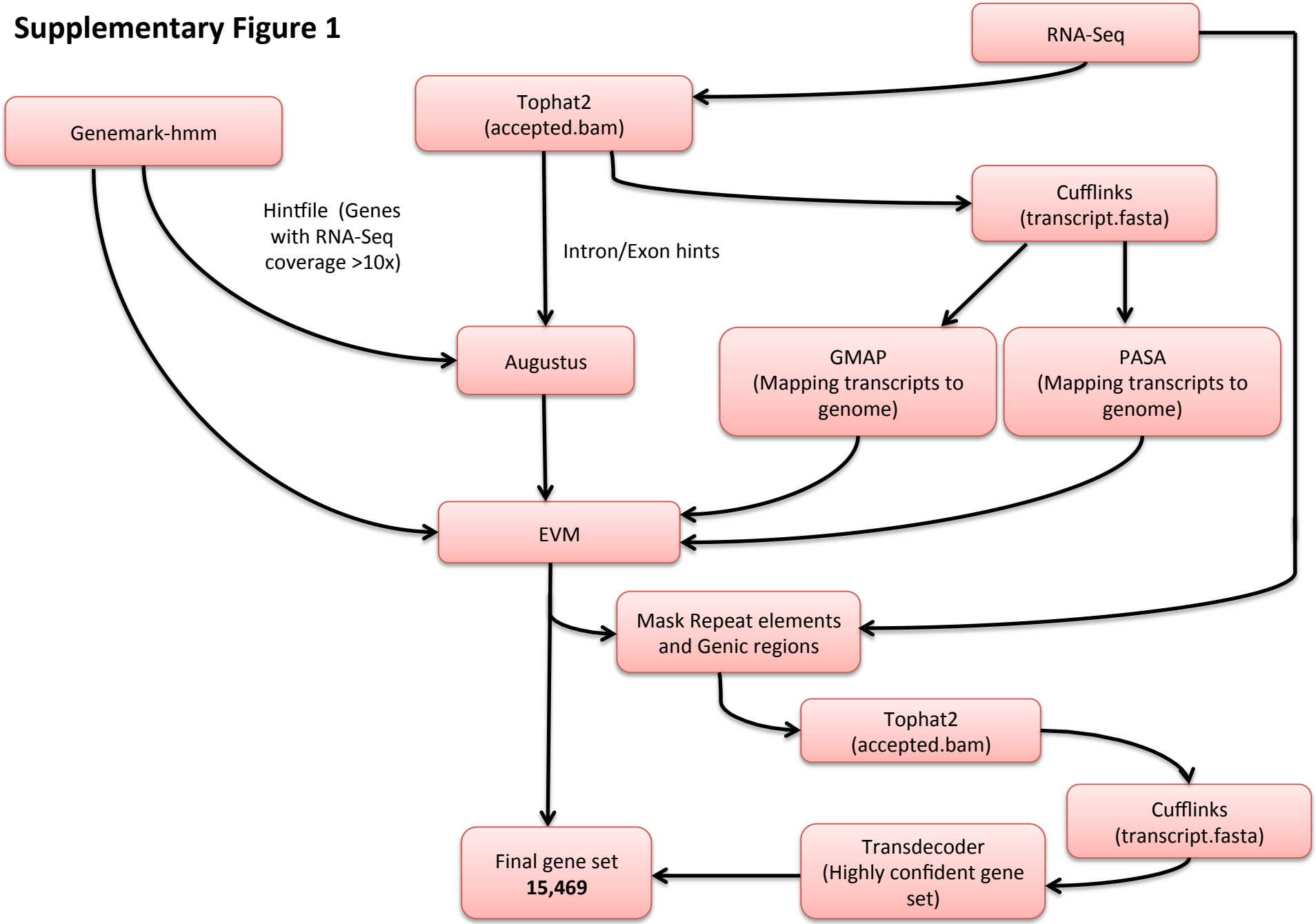
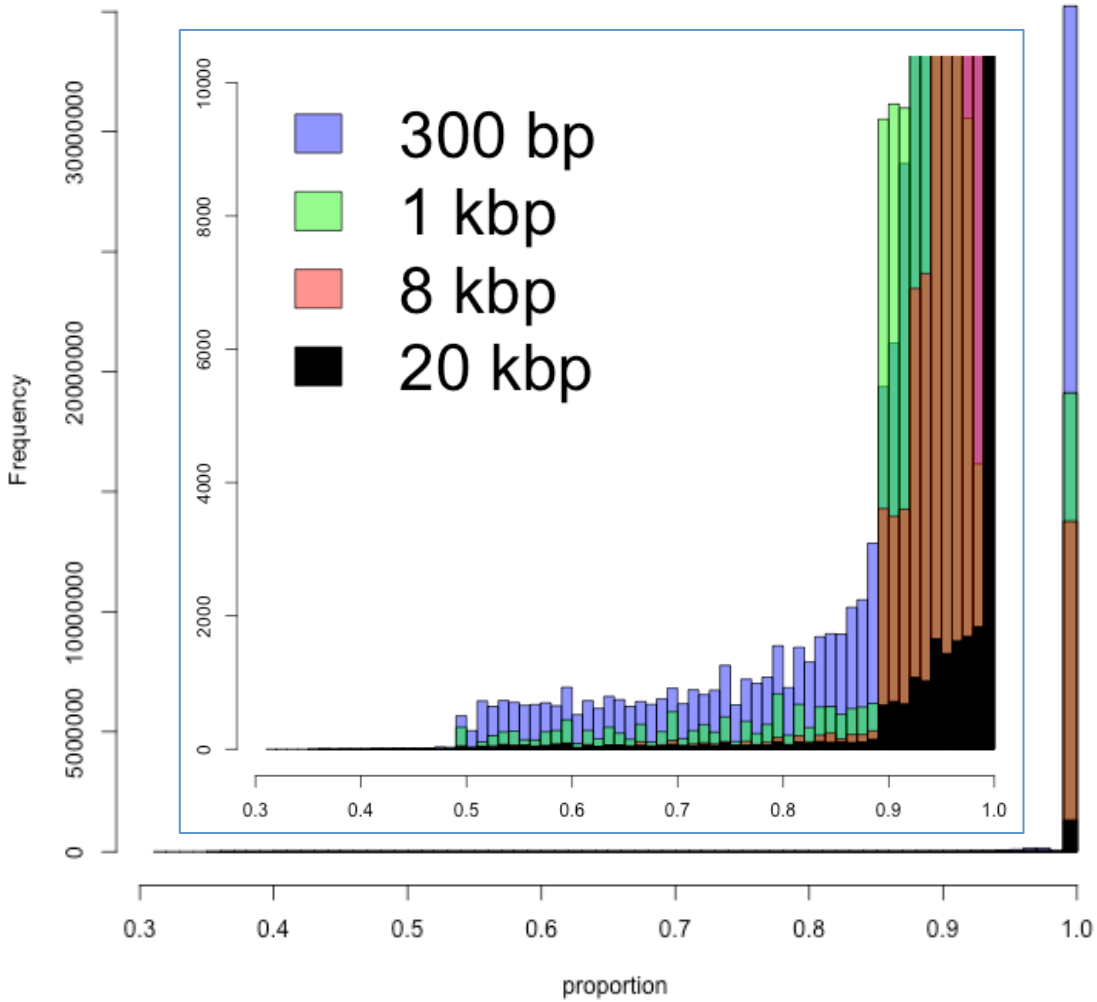
Supplementary Figure 1



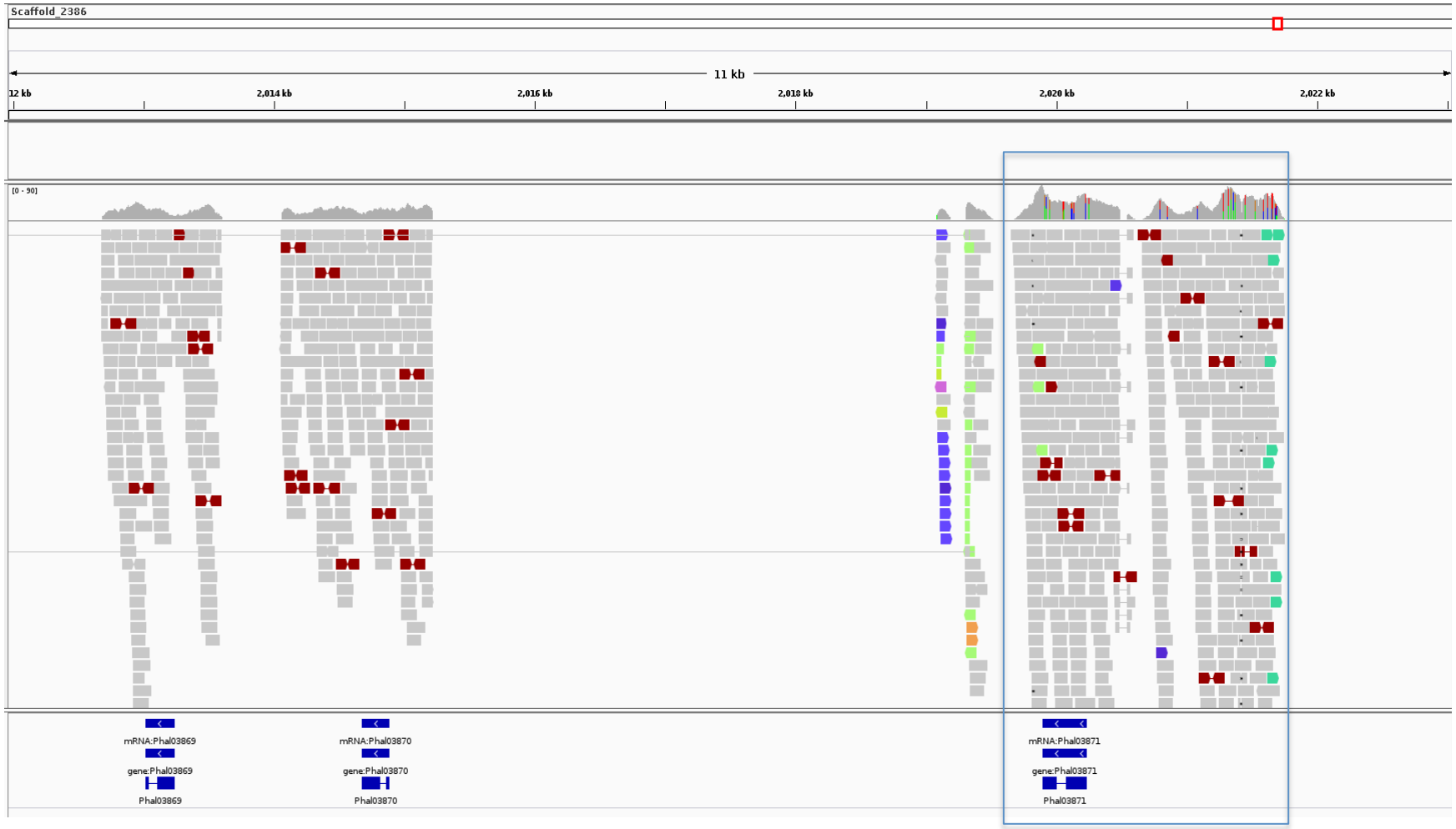
Supplementary Figure 1. Gene prediction pipeline (adapted from *sharma et. al.* 2015): Gene prediction pipeline used to generate highly confident gene models using both *ab-initio* based and transcript mapping based approaches.

Supplementary Figure 2



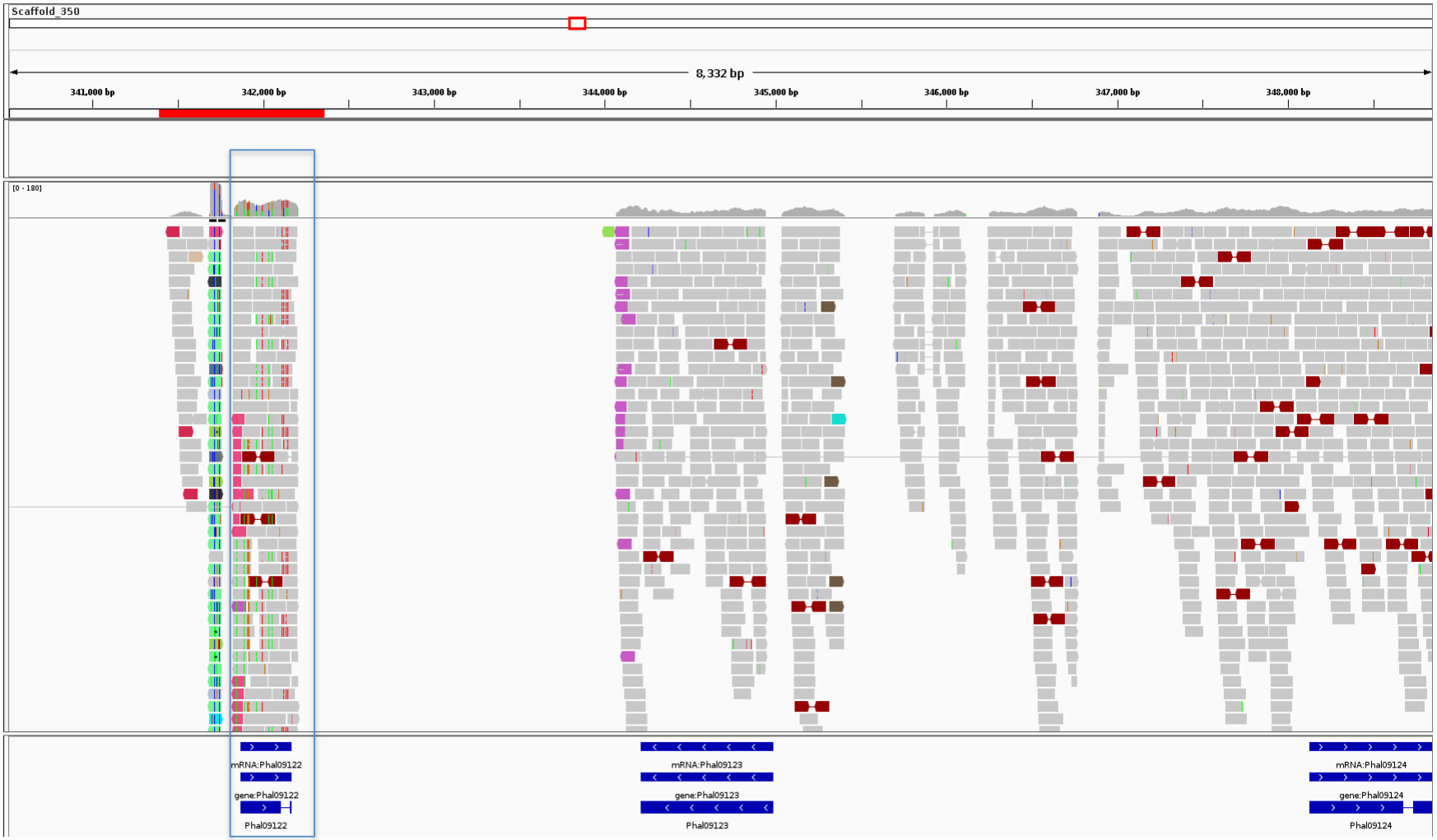
Supplementary Figure 2. Low levels of heterozygosity in *Pl. halstedii*. The histogram shows the frequency distribution for proportions of aligned reads matching the major allele. Proportions are based alignment of sequence reads against the *P. halstedii* reference assembly. Data are color-coded according to which of the four genomic libraries was used to generate the alignments. The inset shows the same data as the main figure but with the vertical axis truncated at 10,000. Heterozygous sites would be expected to generate a major-allele-frequency proportion close to 0.5 whilst homozygous sites would fall close to 1; therefore, in a diploid genome with significant levels of heterozygosity, we would expect a bimodal frequency distribution with peaks close to 0.5 and close to 1. The alignment of sequence reads against the reference genome was performed with BWA (Li & Durbin, 2009) as described in the Methods section.

Supplementary Figure 3



Supplementary Figure 3: A region of apparent heterozygosity on scaffold 2386. We aligned sequence reads from the 300-bp genomic library against the the *P. halstedii* genome assembly using BWA-mem and visualized this 11-kb region of the alignment using IGV. Sequence reads that match multiple sites on the genome are excluded. The region of apparent heterozygosity is indicated in the blue rectangle.

Supplementary Figure 4

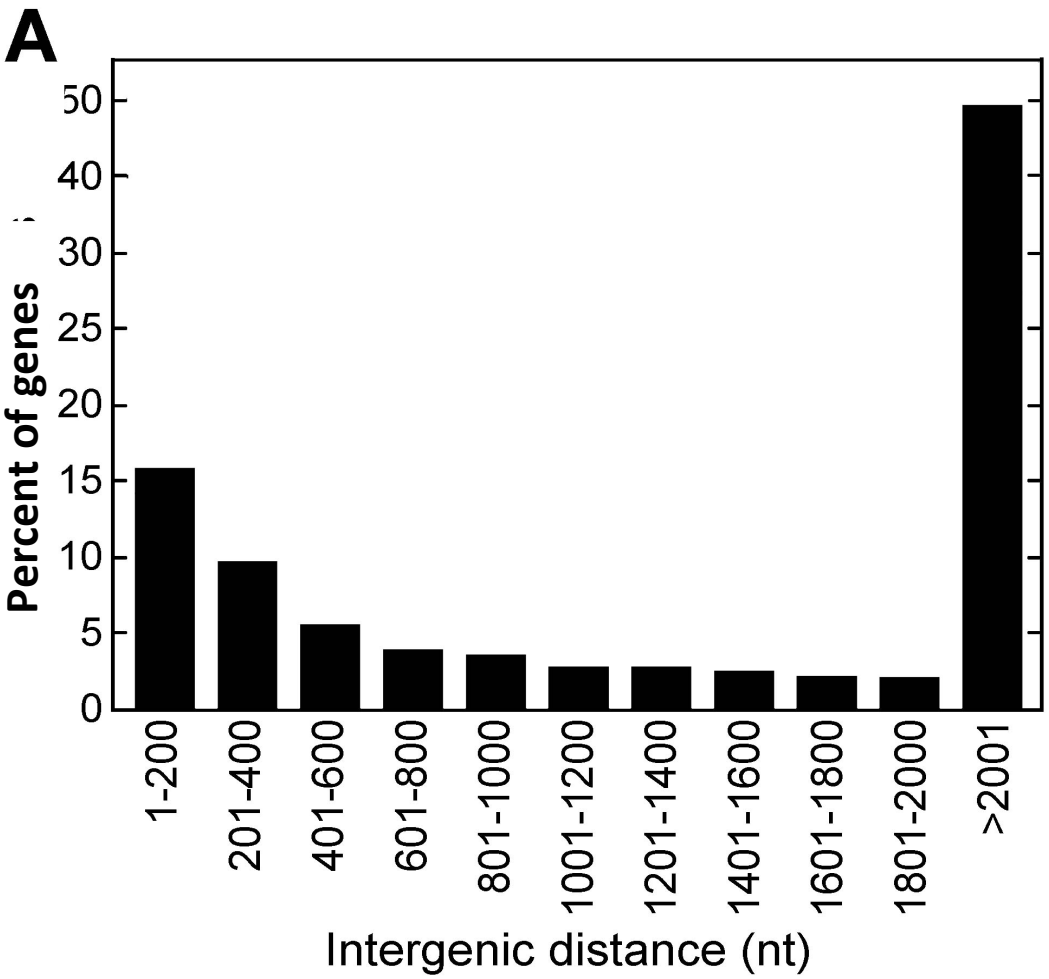


Supplementary Figure 4: A region of apparent heterozygosity on scaffold 350. We aligned sequence reads from the 300-bp genomic library against the the *P. halstedii* genome assembly using BWA-mem and visualized this 8.3-kb region of the alignment using IGV. Sequence reads that match multiple sites on the genome are excluded. The region of apparent heterozygosity is indicated in the blue rectangle.

Supplementary Figure 5

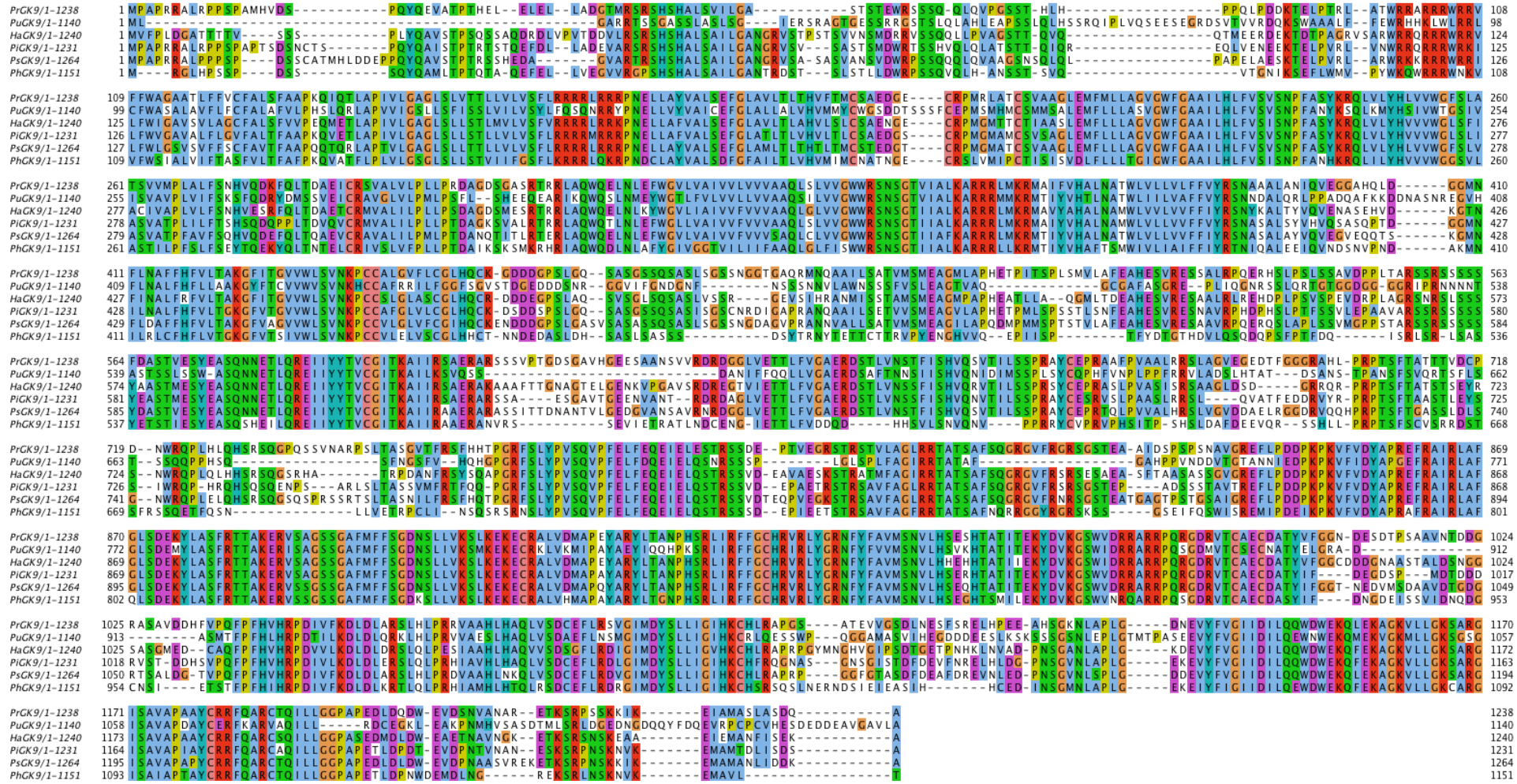
Supplementary Figure 5: A region of apparent heterozygosity on scaffold 350. We aligned sequence reads from the 300-bp, 1-kb and 8-kb genomic libraries against the the *P. halstedii* genome assembly using BWA-mem and visualized this 300-bp region of the alignment using IGV. Sequence reads that match multiple sites on the genome are excluded. The region of apparent heterozygosity is indicated in the blue rectangle.

Supplementary Figure 6



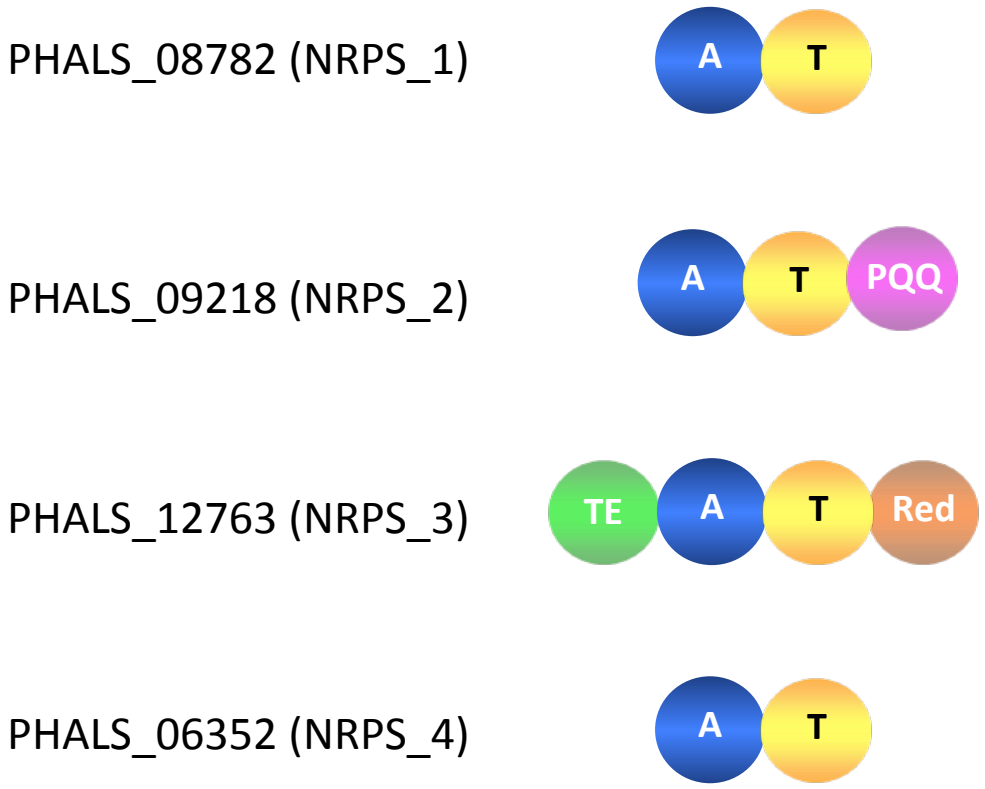
Supplementary Figure 6: Representation of the genome architecture of *Pl. halstedii*.

Supplementary Figure 7



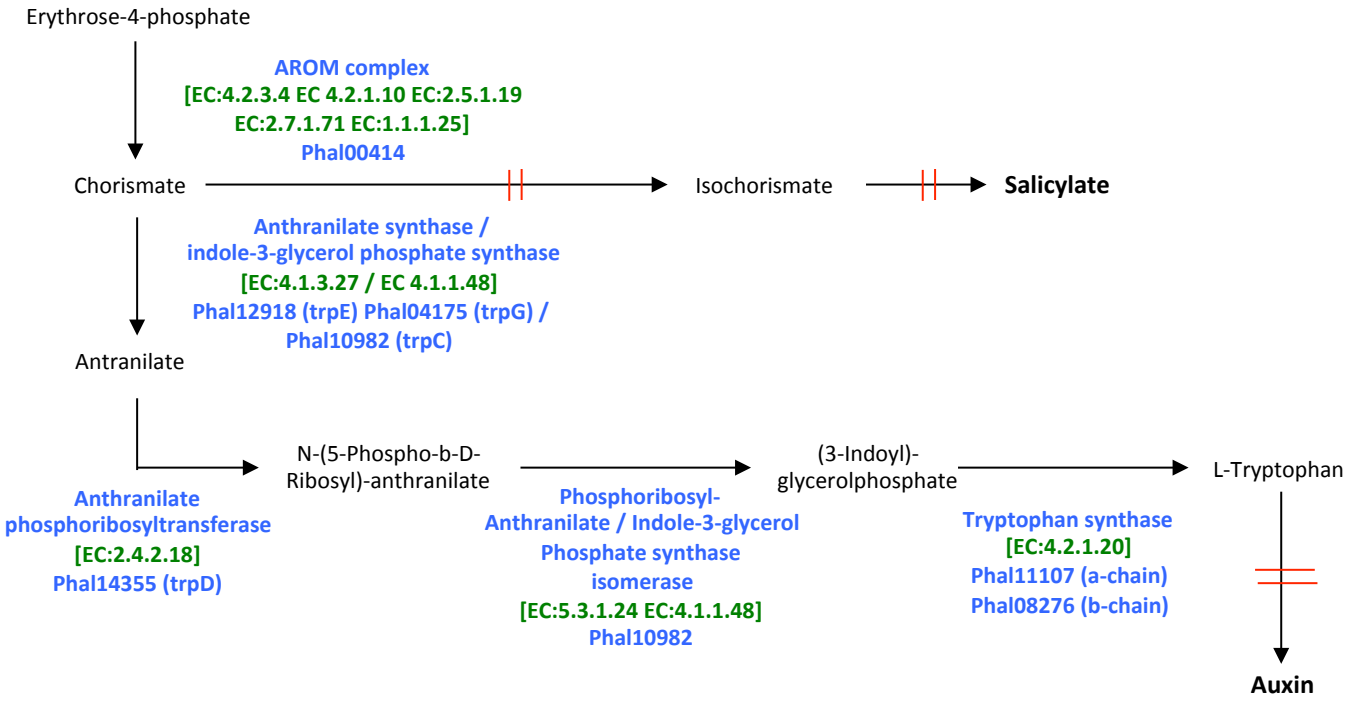
Supplementary Figure 7: Conservation of GK9 in the oomycete genomes.

Supplementary Figure 8



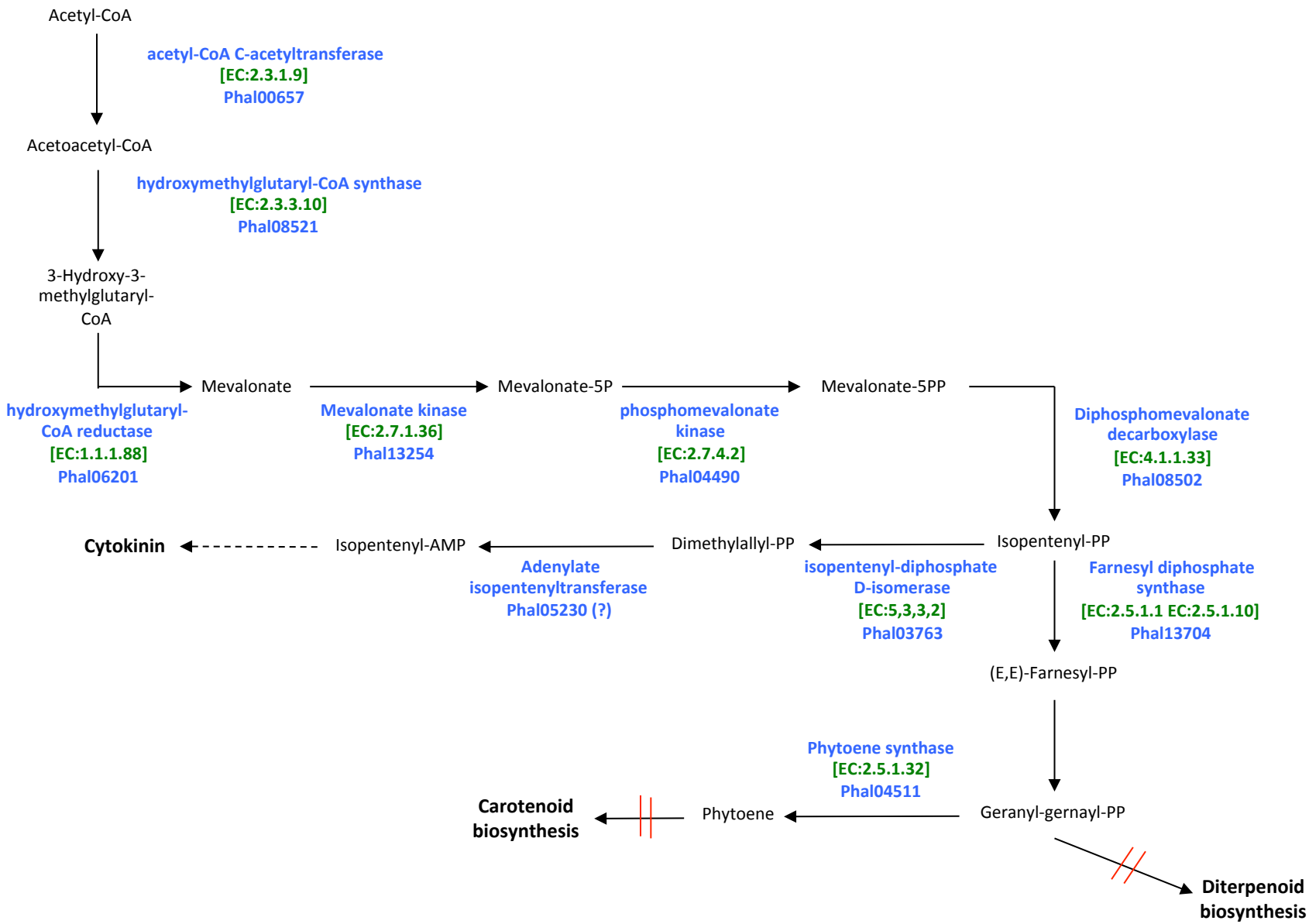
Supplementary Figure 8: Domain organisation of the NRPS encoded in the *P. halstedii* genome. Adelylation (A), thiolation (T), PQQ binding (PQQ), thioesterase (TE), and reductase (Red) domains are shown, which were identified by BLAST-P searches.

Supplementary Figure 9



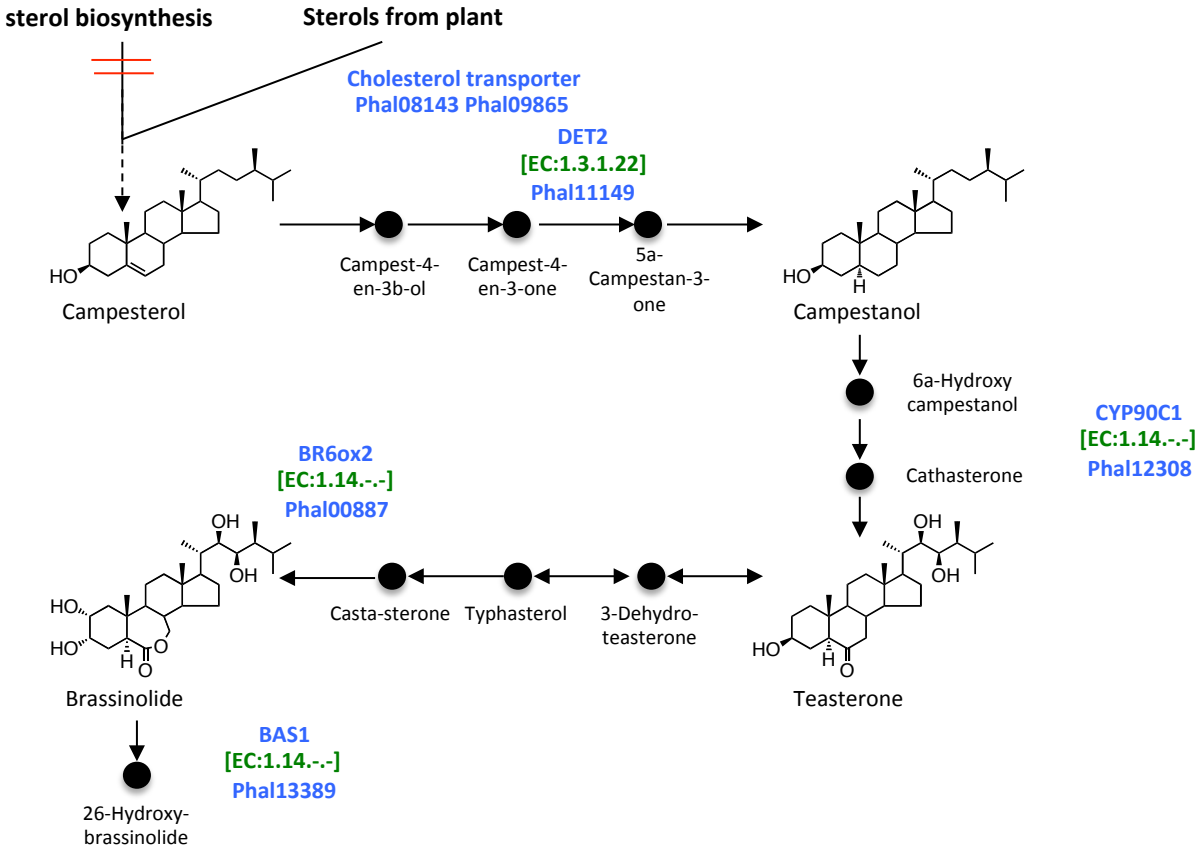
Supplementary Figure 9: Genes involved in the auxin production .

Supplementary Figure 10



Supplementary Figure 10: Non-functional diterpenoid biosynthesis pathway.

Supplementary Figure 11



Supplementary Figure 11: Genes involved in the brassinolide biosynthesis pathway.

Supplementary Figure 12

Phal06084 aligned with HaNLP3 and NLPPya.

Signal peptide
Glutamines in Q-rich region
Conserved cysteines
Heptapeptide motif
Residues making up a cation binding pocket
Residues next to cation binding pocket

```
NLPPya      --MVRFVSALLLAAAGVLASTN-------------------AAVINHDAVPVWPQPEPAD 39
HaNLP3      MKLDGFITTAILAHIPVYARNDYVQEEKQQQLQEPLDGQWKPTTTGHDAIVPFSEPKPVT 60
Phal06084   MSIVSFFSFAVLMVSMIQAQTQNQENLKVTDQQEQLTADWQPKTIPYDQVRGFRQPKPTT 60
              :  *.:  :*    : * .:                     . .  :* :  : :*:*.

NLPPya      ATQALAVRFKPQLDVVNG QPYPAVDPQGNTSGGLKPSGSQAAA R-DMSKAQVYSRSGT 98
HaNLP3      ISEKAGVKFKPLLDVNTG APYAAVNAEGETSGGLQTSGDPESG RGSKYGSQVYGRSTW 120
Phal06084   ISQQVALTFKPQLDIVTG LPYPAVNRLGETSGGLPKDADTETK HGSQFNSQVYGRSTW 120
             ::  .: *** **: .** **.**:  *:*****  ...  : *: .   :***.**

NLPPya      YNGYYAIMYSWYMPKDSPSTGIGHRHDWENVVVWLDN--AASANIVALSASAHSGYKKSF 156
HaNLP3      YNDVWAIMYAWYFPKDSPMLLMGHRHDWENVVVFINDPDEVEPTILG STSWHSGYIKYA 180
Phal06084   FNDVWVMMFSWYFPKDSPFPLLGHRHDWENVVIFIDSPKVPLPKILG SMSYHSEYIKFA 180
            :*. :.:*::**:*****   :**********::::.     ..*:. * * ** * *

NLPPya      PADKSYLDGITAKISYKSTWPLDHELGFTTSAGKQQPLIQWEQMTQAARDALESTDFGNA 216
HaNLP3      P PTDSINGSSVMIKYEHSFPLNHALNITKDAGAYQDLIMWHQMPDLARRALNDTDFGKA 240
Phal06084   P PTFATNGTSVKVKYEDSFPLNHALNVTEKEGTFQDLIMWNQLPPIVRKSLNDTDFGSA 240
            *. .   :* :. :.*: ::**:* *..* . *  * ** *.*:.  .* :*:.****.*

NLPPya      NVPFKS-NFQDKLVKAF-FQ------ 234
HaNLP3      ITPMNDLNFMEKIEAAWPFKTKKDGA 266
Phal06084   NVPMNDWNFLKKVEEAWPFT------ 260
             .*::. ** .*:  *: *
```

Supplementary Figure 12: Multiple alignment of the *Pythium aphanidermatum* NLPPya, the *Hyaloperonospora arabidopsidis* HaNLP3, and the *Plasmopara halstedii* Phal06084. Phal06084 and HaNLP3 both have a Q-rich region and all residues making up the cation-binding pocket. Phal06084 and HaNLP3 also both have an additional disulfide bridge, only found in one branch of a phylogenetic tree of oomycete NLPs.

Supplementary Figure 13

```
NLPPya      --MVRFVSALLLAAAGVLAST------------------------------------ 19
Phal06162   MSIGLLFRVLIACIITIQAQKSSLPNSDDNIIPSKFHAGVTDWSILSPDTHDPRRLENKG 60
Phal06084   MSIVSFFSFAVLMVSMIQAQTQNQEN---------------------------------- 26

Phal14425   MHLTTFLFGAVAVLATVRVDAYSFDLDEDDDKNKLIDSDDDKI----------------- 43
Phal14424   MRYRIILLGAIAFLAAVHADANXXXXXXXXXXXXXX---------------------- 37
Phal13512   MSPRAVFLGVIAILATSHGNAEWADAN------------------------------- 27
Phal14423   MSPRAVLLGAIAILVASHGFAKWADANVS----------------------------- 29
Phal12600   MGLRAIFFGGITILATSLVKAHWINLNVS----------------------------- 29
Phal08480   MTPRAFLFGAITIFTLSYANGYFVFRSVD----------------------------- 29
Phal13513   MNSRALLFVLVALLASVRAN-------------------------------------- 20
Group 1

Phal08947   MFSTVLCAIAFFNLANADNGVQPVINKLQ----------------------------- 29
Phal02474   MLSTVLCAIAFFNLANADDELQPVINKLQ----------------------------- 29
Phal08945   MFLAVFCAIAFFNLANADDGVHPVINKFQ----------------------------- 29
Phal03592   MLSVVLFLVACINVAHADDEQRSTIHKLQ----------------------------- 29
Phal05391   MLSLVLFLVACFNVAHADDEQRSMIHKVQ----------------------------- 29
Phal08445   MRFAIFFLITLCSYAYANDGLEKKANKLP----------------------------- 29
Phal08447   --MRVLSICAAFLSCFVS----VTAQKVA----------------------------- 23
Group 2

Phal05247   MNLWTLAGTLLAILRVCSAQKIDH---------------------------------- 24
Phal13274   MHLWTLAGSLLAALVACSAGKIDH---------------------------------- 24
Phal01213   MKVQAFAVVLFASLFVC-ATCVHP--------------------------------- 23
```

```
NLPPya      ------------------------------------------------------------
Phal06162   GSKSEIIDDDVTPELQVSVYGSKHTAESTVLTKDKVNSTENNIKRTIASNSSRETQFSDQ 120
Phal06084   --------------LKVTDQQEQLTAD------------------------------- 39

Phal14425   ------------------------------------------------------------
Phal14424   ------------------------------------------------------------
Phal13512   ------------------------------------------------------------
Phal14423   ------------------------------------------------------------
Phal12600   ------------------------------------------------------------
Phal08480   ------------------------------------------------------------
Phal13513   ------------------------------------------------------------
Group 1

Phal08947   ------------------------------------------------------------
Phal02474   ------------------------------------------------------------
Phal08945   ------------------------------------------------------------
Phal03592   ------------------------------------------------------------
Phal05391   ------------------------------------------------------------
Phal08445   ------------------------------------------------------------
Phal08447   ------------------------------------------------------------
Group 2

Phal05247   ------------------------------------------------------------
Phal13274   ------------------------------------------------------------
Phal01213   ------------------------------------------------------------
```

```
NLPPya      ------------------------------------------------------------
Phal06162   LFILSGQTVASLTIQSGKHINAVSLLISLPVKKVFNHGGNEGVSKTLTLGIGEHITSTEA 180
Phal06084   ------------------------------------------------------------

Phal14425   ------------------------------------------------------------
Phal14424   ------------------------------------------------------------
Phal13512   ------------------------------------------------------------
Phal14423   ------------------------------------------------------------
Phal12600   ------------------------------------------------------------
Phal08480   ------------------------------------------------------------
Phal13513   ------------------------------------------------------------
Group 1

Phal08947   ------------------------------------------------------------
Phal02474   ------------------------------------------------------------
Phal08945   ------------------------------------------------------------
Phal03592   ------------------------------------------------------------
Phal05391   ------------------------------------------------------------
Phal08445   ------------------------------------------------------------
Phal08447   ------------------------------------------------------------
Group 2

Phal05247   ------------------------------------------------------------
Phal13274   ------------------------------------------------------------
Phal01213   ------------------------------------------------------------
```

```
NLPPya      ------------------------------------------------------------
Phal06162   HWGKLEGRTHLFYVRFNTSMGNSIAGGTKTKTQRIVKAPKGYQLGGFFGHAGNEIIHLGV 240
Phal06084   ------------------------------------------------------------

Phal14425   ------------------------------------------------DYLDSKDDIKS 54
Phal14424   ------------------------------------------------DLFESDDGLST 48
Phal13512   ------------------------------------------------------------
Phal14423   ------------------------------------------------------------
Phal12600   ------------------------------------------------------------
Phal08480   ------------------------------------------------------------
Phal13513   ------------------------------------------------------------
Group 1

Phal08947   ------------------------------------------------------------
Phal02474   ------------------------------------------------------------
Phal08945   ------------------------------------------------------------
Phal03592   ------------------------------------------------------------
Phal05391   ------------------------------------------------------------
Phal08445   ------------------------------------------------------------
Phal08447   ------------------------------------------------------------
Group 2

Phal05247   ------------------------------------------------------------
Phal13274   ------------------------------------------------------------
Phal01213   ------------------------------------------------------------
```

```
NLPPya      ----------------------NAAVINHDAVPVWPQPEPADATQALAVRFKPQLDVVNG 57
Phal06162   IWTSILFIAPNPTTLASSPTPWIQKTMRHDKVVPFKQPKPVTVAEHAAVKFKPQINIVNG 300
Phal06084   ---------------------WQPKTIPYDQVRGFRQPKPTTISQQVALTFKPQLDIVTG 78

Phal14425   GKSTNPYVDDTPDSIDLQSDPSQIVFLGADSVHPFPRTKARTSSQKSALMFQPQLYIEDG 114
Phal14424   DPDASGPGSDFIDPFDPKANIVPVHSIDADNVQPFPESKPCNDSQTTALKYKPRLLITDG 108
Phal13512   ------------------------------PFKQPTPTTDSQKSAIKYQPRLYVVSD 54
Phal14423   -----------KHSAKSRTIPDHYNFVNVNEVQPFKQRKPTTDSQKSAIKYQPRLYVLGA 78
Phal12600   -----------VYPEKPGAVLISPTLMDVDEVQPFYQRKPTTISQESAIKYKPRLYVDEG 78
Phal08480   -----------LDP--------IPDLIDANQVQPFPQPQPETKSQKSAVKYKPSLYIDSG 70
Phal13513   -------------------------IAIDANSVQPFPEQKPQTDSERSALKYKPHLHVSEG 56
Group 1

Phal08947   ----------------------------YDKIKPFPATERDCPINEIALDFQPMLRIESG 61
Phal02474   ----------------------------YDKVKPFPATERDCPINEIALDFQPMLRIESG 61
Phal08945   ----------------------------YDKIKPFPVAKRDCRINEIALDFQPMLRIESG 61
Phal03592   ----------------------------YDEIKPIPGVESNSLINSIALHFQPMLFISSG 61
Phal05391   ----------------------------YDEIEPLPVVARDSLINSIALNFHPMLFVSSG 61
Phal08445   ----------------------------YDSLVPVLPSKPNCRINSIALQFQPELNIKHG 61
Phal08447   ----------------------------YDKARPFDEVKPDCPLNELALMFKPQLHIASG 55
Group 2

Phal05247   ----------------------------DKIKPIEEHEAVNVTEKLAFRYKPSLAVTII 55
Phal13274   ----------------------------DKIKPIEERQPVTLTERLVFKFNPSMKIREE 55
Phal01213   ----------------------------DKIEPFPQPIPTCATQKLALKYKPLLYTSMV 54
                                                                :  .. ::* :
```

```
NLPPya      -CQPYPAVDPQGNTSGGLKPSGSQAAACR-DMSKAQVYSRSGTYNG--YYAIMYSWYMPK 113
Phal06162   -CHPYPAVNATGEISGGLKASGSSDAGCKGSEYGSQVYGRSTWHRG--LWAIMYSWYFPK 357
Phal06084   -CLPYPAVNRLGETSGGLPKDADTETKCHGSQFNSQVYGRSTWFND--VWVMMFSWYFPK 135

Phal14425   -CHPYPAVQSNGSLNAGLEYELFRDPTCEGSPLGSQVYSRSSWYQM--KWATIYTWYFPV 171
Phal14424   -CHPYPAVQSDGAVSAGFEWSRFNRHPCEGSPLGSQVYARSSWYED--KWAVMYVWYFPM 165
Phal13512   -CYPYPAVQANGSLSYGLPWEVFAPTKCNGSPYGSQIYSRSDWYRG--MWAIMYAWYLPR 111
Phal14423   -CYPYPAVQADGSLSEGLPWKIFFQSRCNGSPRGSQIYSRSDWYRG--KWAIMYAWYLPR 135
Phal12600   -CHPYPVVQENGSLSEGMQWKNYFRPSCEGSPRGSQIYSRSDWYQG--KWAMLYTWYLPM 135
Phal08480   -CHPYPAVQANGSLSSGVEWKHNPRASCRGSPLGSQVYSRSDWYKG--KWAIMYTWYFPG 127
Phal13513   -CHPYPAVQQNGSVSAGFEWDEDYSQPCGRSPQGSQIYSRSSWYKG--KWAIMYAWYFPK 113
Group 1

Phal08947   -CHPYPAVDENGYISDGLGVSHWFTD-CLGSPEGSQVYGRAHVYKG--YLAIMYAWYFPR 117
Phal02474   -CHPYPAVDKNGYISDGLGVSHWFTD-CSGSPEGSQVYGRAHVYKG--YLAIMYAWYFPR 117
Phal08945   -CHPYPAVDKNGYVSDGLGVSHWFTD-CSGSPEGSQVYGRAYVFKG--YLAIMYAWYFPR 117
Phal03592   -CHPYPAVDEHGYISNGLGVSHLFTD-CMGSPQGSQVYGRAFAFRG--HLAIMYSWYFPR 117
Phal05391   -CHPYPAVDKHGYISNGLGVSHLFTD-CMDSPKGSQVYGRAFEFKG--HLAIMYTWYFPR 117
Phal08445   -CHPYPAVDDNGYISSGLGVSHFFTD-CMGSPKGSQVYGRAFVYRG--YLAIMYAWYFPR 117
Phal08447   -CHPYPAIDRDGYYSGGLSAFHWATS-CDGSKEGSQVYGRAFYNSDTNVWEVMYAWYFPR 113
Group 2

Phal05247   LCAGYPAVDSDGNFSGGLKPTNGNNG-CTNPPLGSQVYVRIRKYKD--LWAIMYVWYFPK 112
Phal13274   LCVDYPAVDADGNFSGGLKPTNGNSG-CERPPMDSQVYVRVRKYEE--MWAIVYVWYFPK 112
Phal01213   VCVPYAAVDADGEVSDGLKGSNGNDG-CTYARHGSQIYGRIGSYEN--LSAIMYAWYFPK 111
             *  *.::  *  . *.         *      :*:* *            :: **:*
```

Supplementary Figure 13

```
NLPPya      D---SPSTGIGHRHDWENVVVWLDN--AASANIVALSASA-HSGYKKSFPADKSYLDGIT 167
Phal06162   D---TAFPLLGHRHDWEHIIVWIDNPSLYKPRILAVASSA-HSWYTVQSPPHTDRVNGTS 413
Phal06084   D---SPFPLLGHRHDWENVVIFIDSPKVPLPKILGCSMSY-HSEYIKFAPCPTFATNGTS 191
Phal14425   AYDHASPFSTGHRHYWLWAIVWTTDPNPAEGHFLAVSMSG-NFGISSYTLPHIKHLVNGT 230
Phal14424   ALDSVSTFVRGHRHYWLWAIVWTSGPDPDESTFLGVSMSG-DHGITKQLRPKSKYVFNET 224
Phal13512   ALDHSSWLVDGHRHFWTFVVVWTNSPDPNVSTILAASTSGTDNRIKKYLPVKSKYLLDRR 171
Phal14423   ALDQNIWDVDGHSHFWTFVVVWTDSPDPDVSTILAASTSGVGNRIKKYSPLKSKYLLNHK 195
Phal12600   ALDSTAWFVDGHRHFWLWVVIWTDSPDPDDSTILAASMSGFGDEIKKYAPLKSKYLIHDK 195
Phal08480   ALDPTTQFVS----HWLWAIIWTNSPDPDESTLLAVTLPRLADGVKKYSPLHSKYVHNHT 183
Phal13513   AAVHIGRGVSGRRHYWLHAIVWTDEENPNNSSILGVTMSA-GIGLLKRTKIKSHYIIGGT 172
Phal08947   DFMTTPFYV-GHRHGWEHAILWIGG-SSEDAVLLAASVES-TLSYDTYNPVPSKYMKGDH 174
Phal02474   DFMTTPFYV-GHRHGWEHAILWIEG-SSEDAVLLAASVES-TLSYDTYAPVPSKYMKSDH 174
Phal08945   DFMVTPFYV-GHRHGWEHAILWIGG-STEDPVFLAATVES-TFGYKKYSPVPTKYVKSDH 174
Phal03592   DFMTAPFYI-GHRHGWEHAILWFGP-DTENPTLLAVTVES-TFGYKTYAPPPSKYMHGDH 174
Phal05391   DFMSAPFYI-GHRHGWEHAIFWFGA-YRKNPRLLAVTVES-TFGYKTYAPPSSENMHGDH 174
Phal08445   DYVATPFWI-GHRHGWEHAILWFGG-MTEKPELLAVTAKS-LIGYRTYAPPQSKHMDKDR 174
Phal08447   DTMITPVYY-GHNHGWEHAIVYIGV-SSDTPKLLAVAASG-MWSYRTYNPPRSDYVSGNS 170
Phal05247   R---FTSLWPKARHDWEQVVIWIDELT-ETPNVKLVSASYGDDYSKFVPKKSVDSGPTFL 168
Phal13274   R---FQSGWPSARHDWEQAVVWFDDLK-ENPYVVSVATSRGGKYLFFNPSHETTYGPPLH 168
Phal01213   R---FWLGFPIQRHDWKSVVVWLNDLKSMTPTIVAVSMAKSDTRYKTVTKLDLNDFARLQ 168
                         *   : .:           .   :

NLPPya      --AKISYKSTWPLDHELGFTTS---------AGKQQPLIQWEQMTQAARDALE--STDFG 214
Phal06162   --VKVKYAGIWPLNHALTSTTK---------SGEYQDLIMWEQLTEAARQSLQ--QANFG 460
Phal06084   --VKVKYEDSFPLNHALNVTEK---------EGTFQDLIMWNQLPPIVRKSLN--DTDFG 238
Phal14425   TVLLKSHKSLMSARLALDLTEK---------SGEKEDLITWEELTPEARAALSSVKRTEA 281
Phal14424   TVLLKSHEGFFSTRQGLELTKK---------SGGTQNLVTWDQLTPEARTSLSSLFRTEV 275
Phal13512   TLKVKLYQNYWLDKTGLKLTDK---------VGDLQPLITWEQLTDEARAALSSFHYPDW 222
Phal14423   SLKVKLHENHFWDKTGLKLTEK---------VGELQTLITWEQLTDEARAALSSVHYSDW 246
Phal12600   TLKVKSTESRIRKKHGLELTKR---------VGEFQDLITWEQLSDEARAALSNFHRLEK 246
Phal08480   TVKIKSQQSFWLKMHGFELTSR---------SGEFQDLITLDQLTDEAKAALMTNHRPEH 234
Phal13513   TLKLMSYVSFWGRRLALKFTVK---------LGETQDLITWEQLSHEARKALA----LDY 219
Phal08947   --VKLEYTWLGVTHHYLTATKE---------SGEFQDLVMWDNMTENAHISLN--EKVSL 221
Phal02474   --IKLEYTWLGVTHHYLTATKE---------SGEFQDLVMWDNLTENAHKSLN--EKVSL 221
Phal08945   --FKLEYTWLGVTHHYLTATKN---------MGEFQDLVMWNNLTDEARVSLN--EKISL 221
Phal03592   --FKLKYTWLGVTQHYLTATEK---------SGEFQDLIMWDCMDEHVRHSLN--HKVSH 221
Phal05391   --FKLEYTTLIVTHHYLTASER---------TGEFQNLVMWNSMNERARYSLN--HKVSH 221
Phal08445   --FKLKYTWMGVTQHYLSATTS---------PGELQSLVMWDDLPDKARASLK--PRSWS 221
Phal08447   --FKLKYTWIGISHHYLKGTHN---------PGEFQPLIMWENMTSSVRHLFQ--EKTWF 217
Phal05247   LRVETFGP-PSLTITFFPEDYN-----LLDYSSPYY-IILWEQLPEPARAALSD-DNNFG 220
Phal13274   FFPNYFGA-PTLIRESYPVKWK-----FYKEHPRYY-IVMWEQLPEPARAALSD-DKNFG 220
Phal01213   VGSNVVISNTSLRFEYFEFGLRSSNIRLTGHNGQYQKLILWDQLTDPARDALNE-DSNFG 227
                                                  ::  : :   .:  :

NLPPya      NANVPFKS-NFQDKLVKAFFQ----------- 234
Phal06162   MANVPMRDGNFLDKLDTAWSFARLRIQT---- 488
Phal06084   SANVPMNDWNFLKKVEEAWPFT---------- 260
Phal14425   TANSPLQDNKFFSLLEKAYPW----------- 302
Phal14424   TANPPLQDRQYFDILKKAYLW----------- 296
Phal13512   RMETPIQDKWFRYMLSSAYPF----------- 243
Phal14423   RMESPIQDKWFRPMLSSAYPF----------- 267
Phal12600   RANPPIQDKLFYEVLEKSYPF----------- 267
Phal08480   FANPPLQDLRFNEVLQMAFPF----------- 255
Phal13513   KSDTPLQDYRFDGLIKEAYPF----------- 240
Phal08947   NFNSPLSDKRFFKALLKSYPF----------- 242
Phal02474   NFDSPLSDKRFFKALRKSYPF----------- 242
Phal08945   NFNSPLSDKRFFTALRKSYPF----------- 242
Phal03592   NFDPPIRDDRFFHALRKSFPF----------- 242
Phal05391   NFDPPIRDERFFHALRNSFPF----------- 242
Phal08445   HFKPPLADNRFFRALRKAYPF----------- 242
Phal08447   GTKAPFSDDNFFKHLKKARPFYHRT------- 242
Phal05247   DAKFPLRDDQIDQHLEKAYQTEDERNEDR--- 249
Phal13274   DAKCPIRDDKIDHHLEKAYLTDAERKQGKPSK 252
Phal01213   SAVVPFNDNQFKDHLQEAYPLEKV-------- 251
               *: .       :  :
```

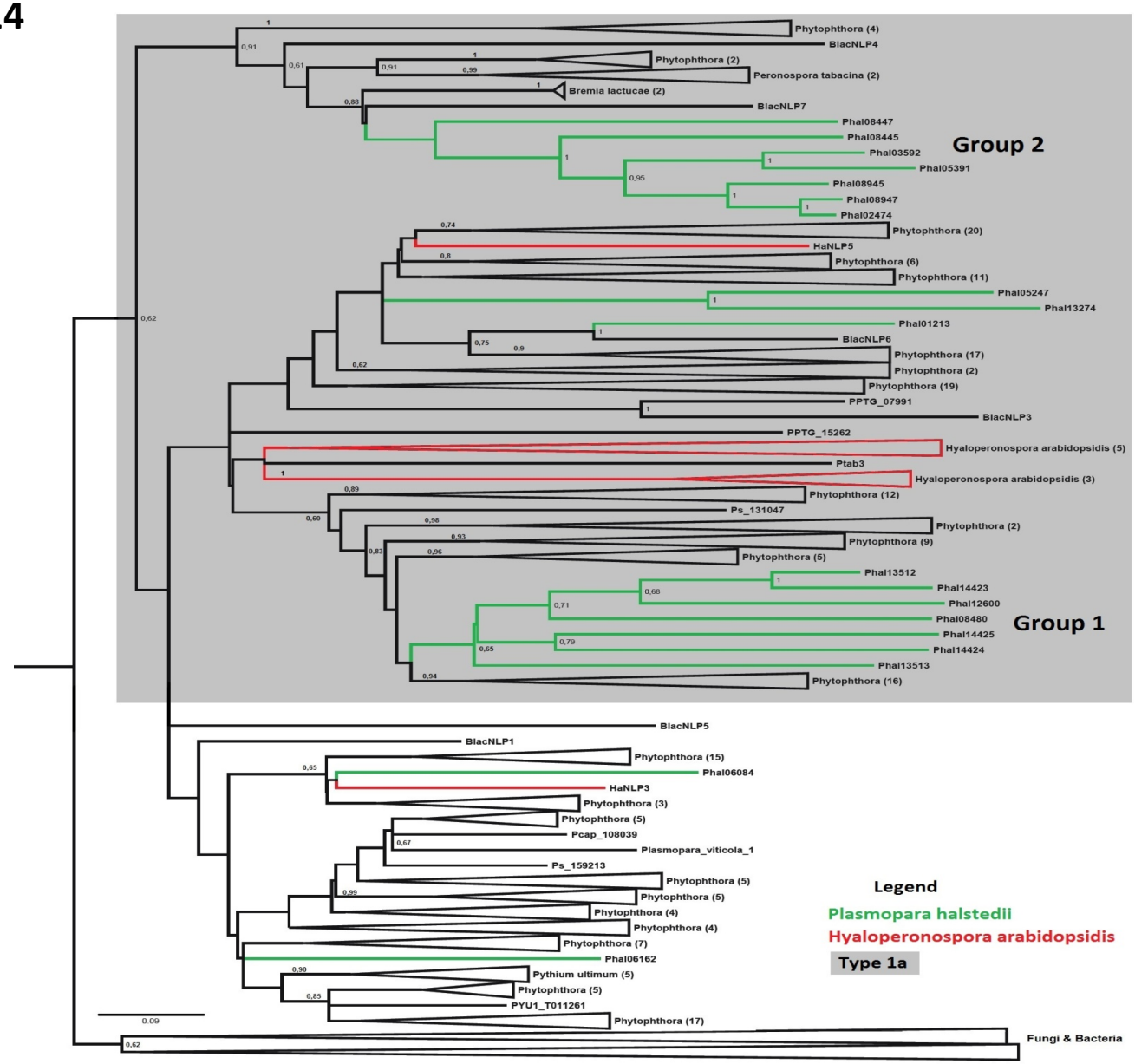
Group 1

Group 2

Legend
Signal peptide
Bad signal peptide
Heptapeptide motif
Conserved cysteine
Kation binding pocket
Next to kation binding pocket

Supplementary Figure 13: Multiple alignment of the *Pythium aphanidermatum* NLPPya and all *Plasmopara halstedii* NLPs. The *Pl. halstedii* genome only encodes two NLPs that contain a complete cation-binding pocket. 17 out of the 19 PhalNLPs contain a functional (D-score>0.45) signal peptide, suggesting they are secreted. Phal06162 contains a 240 aa domain between the signal peptide and the start of the NEP1 domain, a feature not uncommon in this group of NLPs.

Supplementary Figure 14



Supplementary Figure 14: Phylogeny of the 19 PhalNLPs compared with 378 type 1 NLPs of 91 different species (53). Neighbor Joining tree (Mega5, 100 Bootstraps). All signal peptides were removed before alignment. Only bootstrap values >0.6 are shown. 17 of the 19 PhalNLPs are of Type 1a, lacking the acidic cation binding pocket required for induction of necrosis. Two species-specific expansions can be observed, which were named group 1 and group 2. The type 1 NLP Phal06084 clusters together with the well-studied HaNLP3 (54).

Supplementary Figure 15

PhalPseudoNLP1 aligned with its closed relative (Phal14423)

```
Phal14423       ATGAGCCCACGTGCCGTTCTTCTCGGAGCAATTGCTATCCTTGTTGCATCCCATGGCTTT 60
PhalPseudoNLP1  ATGAGCTCTCGCGCCATGCTTCTCGGAATTATTGCCATCTTTGCTGCTTCCTATGGTATA 60
                ****** *:** ***.* *********. :***** *** *** ***:*** **** :*:

Phal14423       GCGAAATGGGCTGACGCTAACGTCTCGAAACACTCAGCAAAGTCACGAACCATTCCCGAC 120
PhalPseudoNLP1  GTGGAAAGGGCTGACGCTGATGTATCTGTACACCCAGAAG---------CTATCTCCTAC 111
                * *.**:************.* **.** .:**** ***.*.         * **  ** **

Phal14423       CATTACAACTTTGTAAATGTCAACGAAGTGCAGCCATTTAAACAGCGTAAACCAACTACG 180
PhalPseudoNLP1  CATTACAACTTTATAAATGTCAACGCAGTGCAGCCCTTTAAACAGCCTAAACCGACGACA 171
                ************.************.*********.********** ******.** **.

Phal14423       GATTCTCAGAAATCTGCGATCAAGTACCAACCACGGCTTTACGTATTGGGTGCATGTTAT 240
PhalPseudoNLP1  GATTCTCAAAGATCTGCCATTAAATACCAACCACGGCTTTCCATTTCGAGCCGATGTCAT 231
                ********.*.****** ** **.****************.*.*:* *.*   **** **

Phal14423       CCATATCCTGCAGTGCAGGCGGATGGATCACTAAGTGAGGGACTTCCCTGGAAAATCTTC 300
PhalPseudoNLP1  CCATATCCTGCAGTGCAGGCGAATGGGTCACTAAATGAGGGACTTCCCTGGAAAGTCTTC 291
                **********************.****.*******.*******************.*****

Phal14423       TTTCAGTCTCGATGTAATGGATCTCCCCGCGGTTCCCAAATTTACTCGCGATCCGATTGG 360
PhalPseudoNLP1  ---CAGTATCGATGTCATGGATCTCCCCACGGTTCTCAAATTTACTCGTGATCCGATTGG 348
                   ****.*******.************.****** ************ ***********

Phal14423       TACCGAGGCAAGTGGGCCATTATGTACGCGTGGTACCTTCCGAGAGCCCTGGACCAAAAC 420
PhalPseudoNLP1  TACCGAGGCAAGTGGGCCATTATGTACGCGTGGTACCTTCCGAAGGCCTTGGACCAAACT 408
                ******************************************.,*** *********.

Phal14423       ATCTGGGATGTTGACGGCCATAGTCATTTTTGGACCTTTGTCGTTGTCTGGACAGACAGC 480
PhalPseudoNLP1  AACTGGTTGGTTGACGGCCATTGTCACTTTTGGACCTGGGTCGTTGTCTGGACAGACAGC 468
                *:**** : ************:**** **********  *********************

Phal14423       CCGGATCCGGATGTCTCGACTATTCTCGCTGCATCAACCTCTGGTGTCGGCAACAGAATT 540
PhalPseudoNLP1  CCTGATCCGAATGTCTCGACCATTCTCGCTGGATCAACAGCTGGCATCGGCGACAAAATC 528
                ** ******.********** ********** ******. **** .*****.***.***

Phal14423       AAAAAATATTCACCACTCAAGTCAAAGTATCTTCTTAACCACAAGTCTTTGAAGGTCAAG 600
PhalPseudoNLP1  AAGAAATACCTACCACTAGAGTCAAAGTATCTTCTTGACAACAAGTCTTTGAAGGTCAAA 588
                **.*****   ******.,******************.**.********************.

Phal14423       CTACACGAAAATCATTTTTGGGATAAGACTGGACTCAAGCTGACAGAAAAAGTTGGTGAG 660
PhalPseudoNLP1  ACACATGAAAGTTATTTATGGAAGAGGACTGGAGTCAAGGTTACCGAAAAAGTCGGT--A 646
                . *** ****.* ****:***.* *.******* ***** * **.******** ***  .

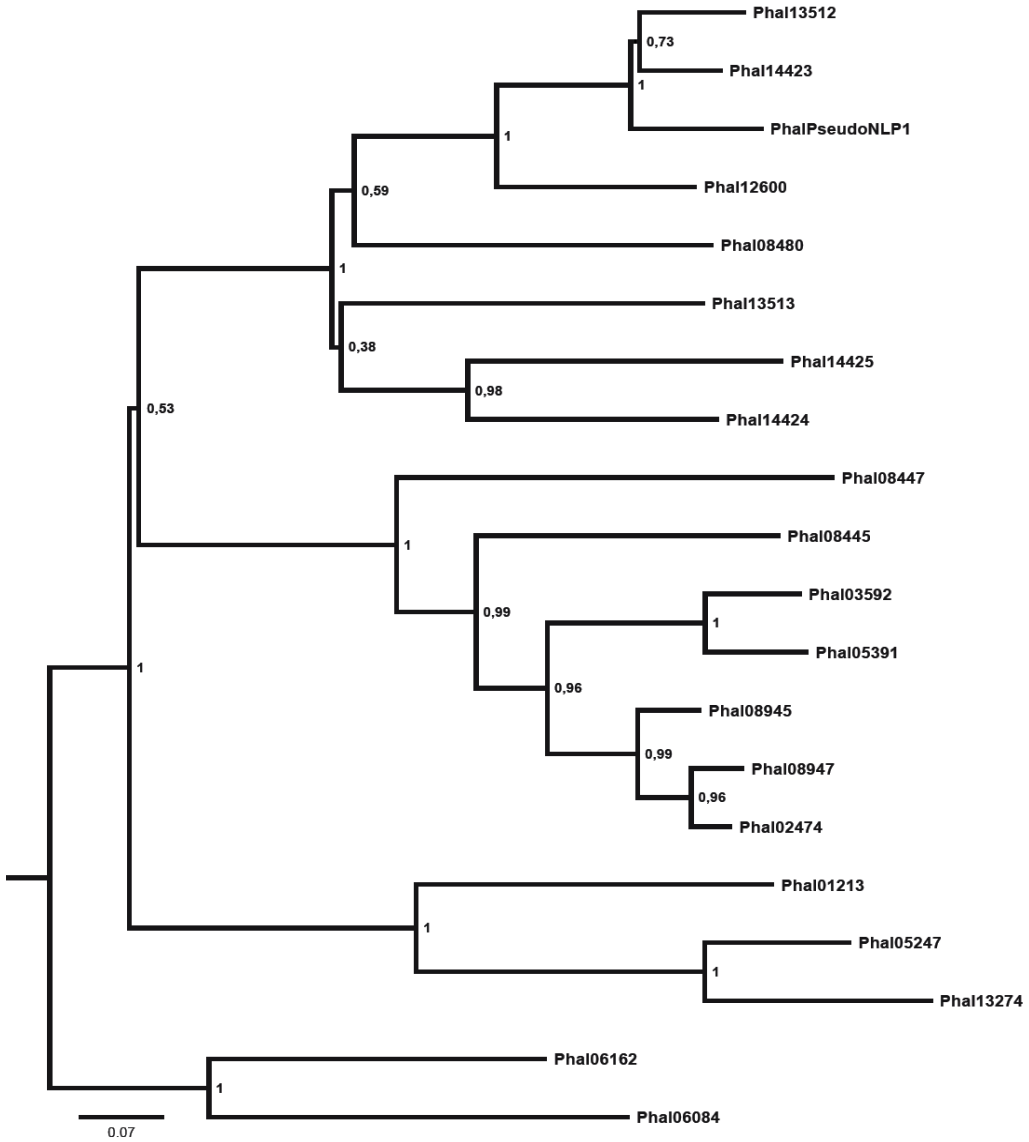
Phal14423       TTGCAGACTCTCATAACTTGGGAGCAGCTTACAGATGAGGCTCGAGCAGCGCTATCTTCT 720
PhalPseudoNLP1  CTGCAGACTCTCATTACTTGGGAGCAGCTTACAGATGAGGCTCGAACAGCGCTATCATCT 706
                 *************:*******************************.***********:***

Phal14423       GTTCATTACTCTGATTGGCGTATGGAGTCGCCAATTCAAGACAAGTGGTTTCGTCCAATG 780
PhalPseudoNLP1  TAGCATTACCCGTATTGGCGTATGGAGTCGCCGATTCAAAACAAGCGTTTTAATCGGACG 766
                 : ****** *  *******************.******.***** * ***.,** .* *

Phal14423       CTAAGTAGTGCTTATCCATTTTAG 804
PhalPseudoNLP1  CTGAAAGCTGCTTATCCATTCTAG 790
                **.*.:. ************ ***
```

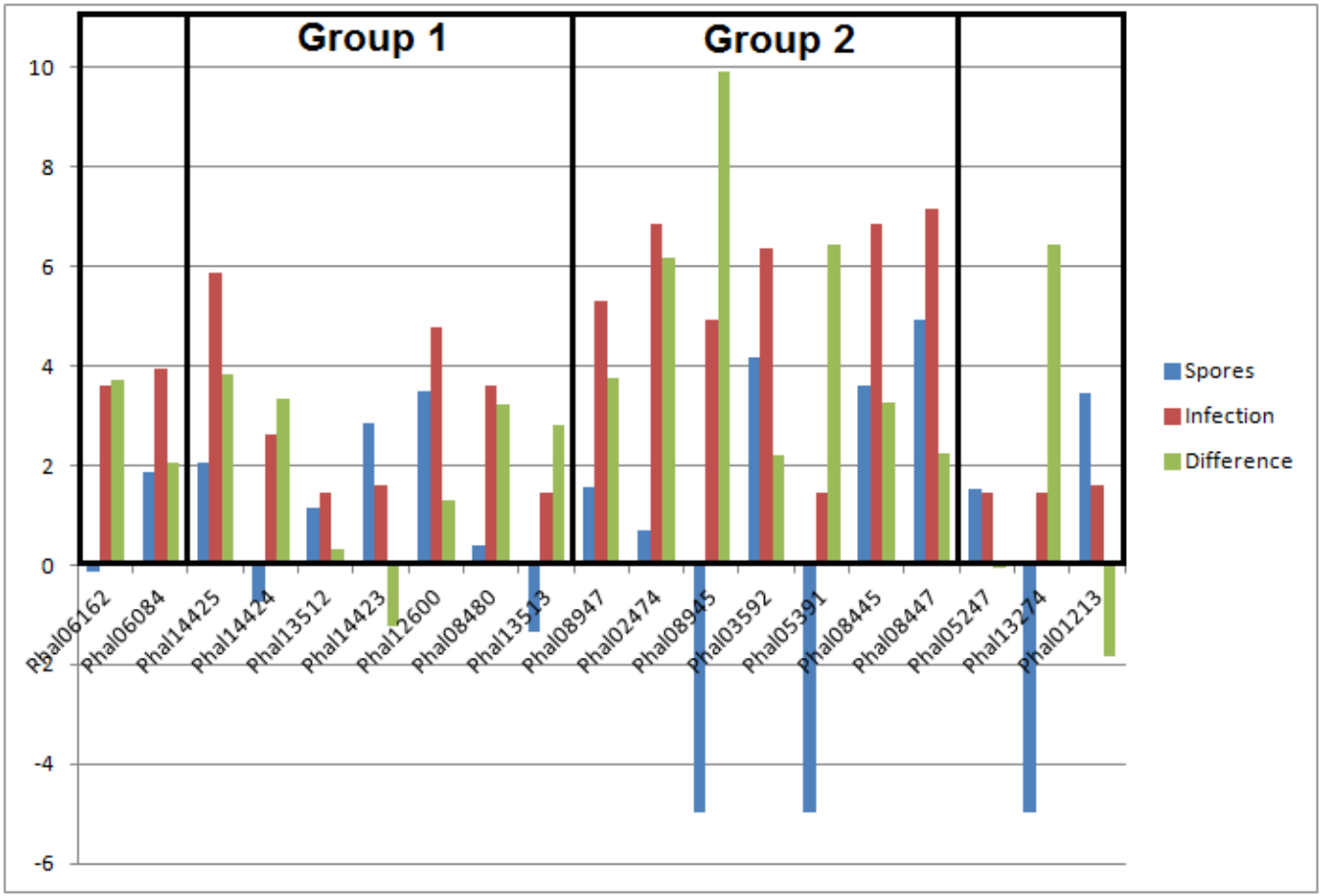
Supplementary Figure 15: Multiple alignment of *PhalPseudoNLP1* and its closest relative *Phal14423*. *PhalPseudoNLP1* encodes a premature stop codon at position 337-339 (indicated in Bold).

Supplementary Figure 16



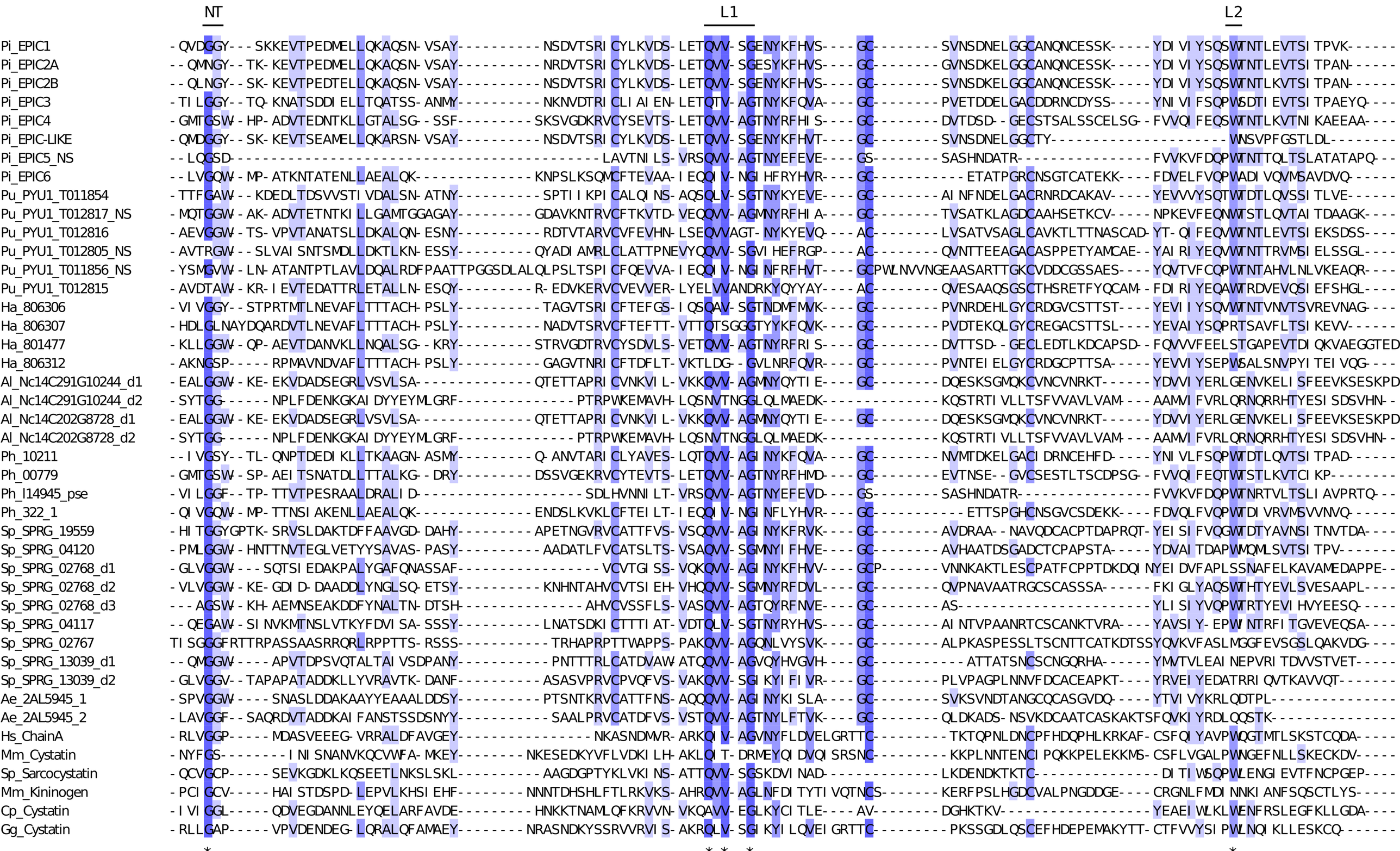
Supplementary Figure 16: DNA-based Maximum Likelyhood tree of all PhalNLP genes, including the pseudogene. The tree is made using Mega5 (100 bootstraps).

Supplementary Figure 17



Supplementary Figure 17: Expression of the PhalNLPs in two different developmental stages. For clarity, the difference, and thus the total up- or down-regulation is included. Values have been derived from the RNA-seq expression profiling (See methods).

Supplementary Figure 18



Supplementary Figure 18: Sequence alignment of Kazal-like domains from seven pathogenic oomycetes. Multiple sequence alignment of 169 Kazal-like domains of seven pathogenic oomycetes. Out of the 169 oomycete Kazal-domains of oomycetes, 60 are from *Phytophthora infestans* (Pi), 37 are from *Pythium ultimum* (Pu), 4 are from *Hyaloperonospora arabidopsidis* (Ha), 8 are from *Albugo laibachii* (Al), 25 are from *Saprolegnia parasitica* (Sp), 30 are from *Plasmopara halstedii* (Ph) and 5 are from *Aphanomyces euteiches* (Ae). The alignment also includes 8 additional known Kazal-like domains present in 2 serine protease inhibitors from crayfish and a protozoan parasite species, respectively. Out of the 8 additional Kazal-like inhibitors, 4 are from the crayfish *Pacifastus leniusculus* (PAPI-1_d1-d2, CAA56043) and 4 from the apicomplexan protozoan parasite *Toxoplasma gondii* (PI-1_d1-d2, AF121778). The amino acid residues that defined the Kazal-like family protease inhibitor domain are marked with asterisks (bottom). The conserved cysteines and their position are numbered in the alignment (top). Cysteine positions three and six shown in grey are missing in some protease inhibitors domains of *P. infestans*. The first suffix indicates the number of the Kazal-like domain from left to right of the C-terminal effector domain in multidomain proteins. The second suffix indicates the P1 amino acid active residue, which is the central to the specificity of Kazal-like inhibitors. The third suffix “NS” when present indicate protease inhibitor domains from proteins that are not predicted to be secreted.

Supplementary Figure 19

```
                   C                   C                   C                   C   C                   C
                   1                   2                   3                   4   5                   6
Pi_EPI1_d1_D       C-PE--Y-C-LDVYD---P--V---GDGE---G------NTYSNECYMKRAKC-H--NE----------TTPPAWKDLVL-----------C
Pi_EPI1_d2_D       C-ST--Y-C-PDVEL---P--V---CGSN--R------VRYGNPEELRIAAC-E--HP--E--LN---IVE-DSG--KA-----------C
Pi_EPI1-LIKE1_d1_D C-PQ--I-C-LDYYT---P--V---ADEE---G------NFYSNECYMKRAKC-E---KN----------SARTNSSSINDD----------
Pi_EPI1-LIKE1_d2_D C-PD--S-C-PDIAL---P--V---CVSD---G------IKYSNPEELKIAAC-K--HP--E--RK---ISTEFSYS--ST----------
Pi_EPI2_d1_D       C-PK--Y-C-LDIDD---P--V---GDEE---G------NMYSNECYMKRAKCAKN---KP----------TDPPFVK---N----------F
Pi_EPI2_d2_D       C-SS--G-C-PDVEL---P--V---CGSD---G------VRYGNPEELKIAAC-E---HP-------ELNIVEAVGMS-----------C
Pi_EPI2-LIKE1_d1_A C-PN-IM-C-PAVYQ---P--V---SDEN---G------VMYPNKKSMEAAKC-K---GP--REN-----PLDEYKR-----------I
Pi_EPI2-LIKE1_d2_D C-AS--A-C-PDVVL---R--V---CGSD---G------VMYSNPEELKIAAC-K---NP-------EQ---NIVEEEG---A-----C
Pi_EPI2-LIKE2_H    C-NF--A-C-FHVMR---P--V---KDEN---G------VMYPNECEMRRARC-RKNEQN----------VDVQGEQ---E----------
Pi_EPI3_E          CADM--L-C-PEVHD---P--V---CGTD--K------VTYPNECDLGLAQC-A---HP-----ERN---ITVFARS---T----------C
Pi_EPI4_d1_T       C-DA--I-C-PTDYE---P--V---CGSD---G------VTYANDCAFGIALC-K---TA-------T---LSLLAVG---E----------C
Pi_EPI4_d2_D       C-PD--A-C-VDVYD---P--V---SDES---G------KTYSNEGYMRMAKC-KDKKKD----------VDILAEY---K----------C
Pi_EPI4_d3_D       C-AA--A-C-PDIYS---P--V---CGSD---G------VTYSSPCHLKLASC-K---KP--K--IK---LVQDSAD---S----------C
Pi_EPI5_R          C-DD--N-C-QRDLM---P--V---CGSD---G------ATYGNDCLLDFAHC-E---NS-------T---ITKLHDG---K----------C
Pi_EPI5-LIKE_R     C-DD--N-G-ERDFT---P--V---CGPD---G------ITYGN---VDFAHC-E---SS-------A---ITKKPDG---D----------C
Pi_EPI6_d1_Q       C-NF--V-C-IQVMS---P--V---TDEN---G------VTYSNECMMHAAKC-KDNGKR----------EDPLEEY---K----------
Pi_EPI6_d2_D       C-PN-IM-C-LDVYE---P--V---TDEN---G------VTYPNKCSMEAAKC-K---GP--REN-----VLDEYKR-----------I
Pi_EPI6_d3_D       C-AS--A-C-PDVEL---P--V---CGSD---G------VRYSNPEELKIAAC-K---NP-------EQ---NIVEEDG---A-----C
Pi_EPI6-LIKE1_d1_Q C-NF--V-C-IQVMR---P--V---TDEN---G------VTYSNKCMMRAAKC-KGNGKR----------EDPLEEY---K----------
Pi_EPI6-LIKE1_d2_D C-PN-IM-C-LDVYG---P--V---TDEN---G------VAYPNKCSMEAAKC-K---GP--REN-----VLDEYKR-----------I
Pi_EPI6-LIKE1_d3_D C-AS--A-C-PDVEL---P--V---CGSD---G------VRYSNPEELKIAAC-K---NP-------EQ---NIVEEDG---A-----C
Pi_EPI6-LIKE2_d1_A C-NF--V-C-IQVMR---P--V---TDEN---G------VTYSNECMMRAAKC-KGKGKR----------EDPLEEY---K----------
Pi_EPI6-LIKE2_d2_A C-PN-IM-C-PAVYQ---P--V---TDEN---G------VTYPNKCSMEAAKC-K---GP--REN-----VLDEYKR-----------I
Pi_EPI6-LIKE2_d3_D C-AS--A-C-PDVEL---P--V---CGSD---G------VRYSNPEELKIAAC-K---NP-------EQ---NIVEKDG---A-----C
Pi_EPI6-LIKE3_d1_K C-NF--A-C-IKMMS---P--V---TDEN---G------VTYSNECMMRAAKC-K---GN--WN-QD---PLEEYKR-----------
Pi_EPI6-LIKE3_d2_D C-PN-IV-C-LDVYE---P--V---TDEN---G------VTYPNQCSMDVEKC-K---GP----------REDVYDEYKRI---------
Pi_EPI6-LIKE3_d3_D C-AT--A-C-PDVKF---Y--V---CGSD---G------VWYSNPCELKIAAC-E---NP-------EQ---NIVEKDG---A-----C
Pi_EPI7_D          C-SQ--V-C-PDVYE---P--V---CGTD--S------VTYSNSCEGLGIASC-K---SP-------EKN---IAKKING---R----------C
Pi_EPI7-LIKE_D     C-PD--A-C-PDVYT---P--V---CGSD---G------NTYSNSCFLGIASC-K---NP-------DKH---IAQASEG---S----------C
Pi_EPI8_d1_D       C-SF--G-C-PDVYE---P--V---CGSN---G------KTYSNSCYLRLESC-Q---NN-------NE---ITEAGNG---E----------C
Pi_EPI8_d2_D       C-PA----C-LDVYE---P--V---TDEN---G------NMYSNECYMKMAKC-KGADDD----------ASMRSDS---P----------
Pi_EPI9_R          C-PT--R-C-TRDYR---P--I---CGSD---I------ITVANKCLFKVGCC-L---DP-------S---LKKFHKG---K----------C
Pi_EPI9-LIKE_R     C-SG--L-C-TRDLM---R--V---CGSN---G------VTYDNECWFEVVCC-E---GP-------G---IKLKNKG---R----------C
Pi_EPI10_d1_D      C-SF--G-C-LDVYK---P--V---CGSN---G------ETYSNSCYLRLASC-K---SN-------NG---ITEAGDG---E----------C
Pi_EPI10_d2_D      C-PD--M-C-LDVYD---P--V---SDEN---G------KEYSNQCYMEMAKC-K---GT--GYDDN---KRSGNP----------
Pi_EPI10_d3_D      C-GD-ML-C-PDNYA---P--V---CGSD---G------ETYPNECDLGITSC-N---HP-------EQN---ITMVGEG----------T
Pi_EPI11_d1_D      C-PS--L-C-TDLFA---P--V---CGSD---G------VTYSNDCYLLLADC-E---SA-------AR---ITKVSDG---K----------C
Pi_EPI11_d2_K      C-SG--V-C-PKILK---P--V---CGSD---G------VTYPNECLLGVADC-E---CS-------D-D---ITKAYDG---E----------C
Pi_EPI11_d3_E      C-ND--V-C-PENFQ---P--V---CGSD---G------VTYSNDCTLEYAQC-T---SG-------GV---ITKVSEG---E----------C
Pi_EPI11_d4_E      C-SE--V-C-PEVFE---P--V---CGSD---G------VTYSDSCFLGIATC-K---DP-------S---IVLAHDG---A----------C
Pi_EPI11_d5_E      C-PD--V-C-IEIFR---P--V---CGSD---G------VTYANSCFLGIASC-H---DP-------S---ITLAHNG---A----------C
Pi_EPI11_d6_E      C-PD--V-C-IEIFR---P--V---CGSD---G------VTYANSCFLGIASC-E---DP-------R---IAQAHEG---P----------C
Pi_EPI11_d7_A      C-PD--I-C-PAIYA---P--V---CGSD---G------VTYSNECLINIASC-N---HP-------ELK---LTKASDG---A----------C
Pi_EPI12_S         C-DK-RN-C-ESHKG---R--V---CSNG---N------QTYATLCDLTSVMC-N---HP-------TRG---VSLAYDG---P----------C
Pi_EPI12-LIKE_D    C-NK-KN-C-KDHVG---P--V---CGND---N------VTYASLCDLTSVMC-E---HP-------ERR---VGMYDG---P----------C
Pi_EPI15_D         C-DQ--V-C-PDVNE---R--V---CGTD---G------VTHTNSCYLGVASC-K---NP-------DKN---IALVSNG---A----------C
Pi_EPI16_D         C-PD--A-C-LDVYS---P--V---IGDD---G------ISYPNECSMQMAKC-K---KS--GKKDD---WASYK-----------
Pi_EPI16-LIKE_Q    C-AG--A-C-MDVDA---P--V---LGDD---G------IWTNACEMRMAKC-E---KS--G-KK---ARTQREA----------L
Pi_EPI17_d1_D      C-DT--E-C-QLISS---P--V---CGSD--H------VTYTNDCAFTVACC-N---AT-------E---LVVANSG---E----------C
Pi_EPI17_d2_M      C-PD--A-C-TMEYS---P--V---TDEN---G------KKYSNECAMRLAKC-KGEAGE-----E---KKIVTFA----------
Pi_EPI18_d1_L      C-KL--N-C-QLISS---P--V---CGSD---N------VSYANSCFLKEARC-S---TG--N-TD---LHVIFRG---L----------C
Pi_EPI18_d2_Q      C-PA--T-C-TQTYS---P--V---CASN---G------QLYGNECRFRQAKC-----SRLGLLAVN---LEPRTLA---E----------C
Pi_EPI19_d1_A      C-SKAFE-CDAVSHA---P--V---CGSD---G------TTYANSCAFASVFC-S---SE--HDADT---LFIQALG---E----------C
Pi_EPI19_d2_R      C-NP--M-C-ERVYD---P--V---CGSD---G------ITYANLCLLEYAEC-R---NP-------N---VKMFGPG---K----------C
Pi_EPI19_d3_Y      CIPE--P-C-PYTFA---P--V---CGSD---G------QTHDNLCLFANAKC-Q---QP-------T---LTVIHEG---E----------C
Pi_KAZAL-LIKE1_P   CADT--P-C-LPEHA---P--V---CGSN---G------VTYENECELGQANC-N---NA-------GLN---VTQVSYG---A----------C
Pi_KAZAL-LIKE2_P   CADT--P-C-LPEHA---P--V---CGSN---S------VTYENECELDQANC-N---NA-------GLN---VTQVSYG---A----------C
Pi_KAZAL-LIKE3_P   CADT--P-C-LPEHA---P--V---CGSN---G------VTYENESELDQANC-N---NA-------GLN---VTQVSYG---A----------C
Pi_KAZAL-LIKE4_P   CADT--P-C-LPEHA---P--V---CGSN---G------VTYENECELDQANC-N---NA-------GLN---VTQVSYG---A----------C
Pi_KAZAL-LIKE5_P   CADT--P-C-LPEHA---P--V---CGSN---G------VTYENECELDQANC-N---NA-------GLN---VTQVSYG---A----------C
Pu_PYU1_T012159_d1_V CHPD--S-C--IVSV---PQLL---CGSD---G------VTYRSICELELACC-T---RP-------D---LKIASMG---A----------C
Pu_PYU1_T012159_d2_E C-SEQEA-C-EESSY---P--I---CGSD---G------VTYQNAGYFDRAYC-K---NN-------D---LVPMGYG---T----------C
Pu_PYU1_T012158_d1_V CHPD--S-C--IVSV---PQLL---CGSD---G------VTYRSICELELACC-T---RP-------D---LKIASMG---A----------C
Pu_PYU1_T012158_d2_E C-SEQEA-C-EESSY---P--I---CGSD---G------VTYQNAGYFDRAYC-K---NN-------D---LVPMGYG---T----------C
Pu_PYU1_T012161_d1_A CAPE--S-CTAAAQK---L--L---CGSD---G------VTYTSACELELAQC-S---HP-------T---LQLASVG---A----------C
Pu_PYU1_T012161_d2_D C-ET-VK-C-GDHAN---P--I---CASN---G------VTYQNACDFDRAYC-K---NK-------E---LAPVSYG---A----------C
Pu_PYU1_T000142_d1_E C-AA--A-C-PENYK---P--L---CGSD---G------KTYSNECMLEYAKC-S---TN-----STT---LTVASDG---E----------C
Pu_PYU1_T000142_d2_S C-LQEIA-C-LSVID---Y--V---CGSD---G------KTYNNACELRKAKC-Q---NP-------S---LTQVSTG---E----------C
Pu_PYU1_T000142_d3_K CTTTT--M-C-TKIYL---P--V---CGSD---D------KTYSNECEFKNAQC-K----A----TSP---LTLKANV---S----------C
Pu_PYU1_T000142_d4_T C-ST--V-C-TTEFN---P--V---CGSN---G------ITYNNACLLKNAQC-T---NS-------T---VTKAADG---A----------C
Pu_PYU1_T010209_d1_A C-SD--A-C-GALYQ---P--V---CGSD---G------VTYPNECTLSVANC-K---SP-------ELK---LTVKSPG---A----------C
Pu_PYU1_T010209_d2_K C-KQ--T-C-SKIRK---P--V---CGSD---G------TMYSNLCILKNAQC-D---NS-------E---IMQMAED---K----------C
Pu_PYU1_T010209_d3_M C-TT--M-C-TMELD---P--V---CGSD---G------KTYSNPCALKNAQC-E---NP-----KSN---IVVKAAG---E----------C
Pu_PYU1_T010209_d4_A C-PS--M-C-TADYT---P--V---CGSD---G------KTYSNKCQLSIAKC-K---NP-----TSN---ISLKSEG---E----------C
Pu_PYU1_T010209_d5_K C-EM--A-C-TKQYA---P--V---CGSN---G------KTYTNSCALKLANC-K---SS--K--KE---ITIRSEG---A----------C
Pu_PYU1_T014337_d1_V C-DR--T-C-EVTDA---A--V---CGND---D------VTYANYCFFSVAAC-K---NK-------T---LALAYTS---P----------C
Pu_PYU1_T014337_d2_L C-DR--F-C-TLEYE---P--V---CGSD---G------VTYGNACAFDEANC-R---AG--G--G---LAVKAVG---T----------C
Pu_PYU1_T013339_d1_A CKAV--K-CDARANT---P--V---CGSD---G------KSYANDCLFEFARC-N---DA-------A---LTLVAKT---S----------C
Pu_PYU1_T013339_d2_R C-NT--D-C-TRELD---Q--M---CGSD---G------KTYNNQCLFDNAKC-L---NP-------A---LVVVKND---A----------C
Pu_PYU1_T009699_d1_D C-DNRSV-C-TDKDP---N--V---CGSD---G------DTYVNKCTFESAYC-D---EP--N--EL---FFIVSDG---A----------C
Pu_PYU1_T009699_d2_L C-QI--K-C-ALDGV---P--V---CGTD---G------KPYINDCHLLAAKC-K---FP-------N---LAKAYNG---A----------C
Pu_PYU1_T009699_d3_R C-NP--I-C-ARVYE---P--V---CGSN---S------VTYANQCLLDYAAC-K---NP-------R---VTKLSNG---K----------C
Pu_PYU1_T009699_d4_S CVPV--A-C-TSEED---P--V---CASN---G------ASYLNTCMFENAQC-Q---FP-------E---LSILHEG---E----------C
Pu_PYU1_T000511_d1_NS_M C-SR--L-C-PMIDS---P--V---CGSD---G------VSYANACYFDEAQC-N---NP-------G---LSIAVHA---L----------C
Pu_PYU1_T000511_d2_NS_D C-DA--I-C-ADIDD---P--V---CTTS---G------TMKNACFLKREQC-K---HP-------Y---VELLRRG---S----------C
Pu_PYU1_T000511_d3_NS_Q C-PA--S-C-GQEYA---P--V---CASS---G------VIYGNECLFRQAKC-----AR--AFASN---FVARDLS---Y----------C
Pu_PYU1_T009700_d1_M CAIGDKRQC-IMYYA---P--V---CASN---G------QTYGNVCQFSSAYC-T---LP-----EAEREGLKIVHDG---E----------C
Pu_PYU1_T009700_d2_D CALF--K-C-SDTGD---G--V---CASD---G------KTYVNACLVRAAGC-A---NP-------G---LFVVSDK---P----------C
Pu_PYU1_T009700_d3_P CMVP--Q-C-APIDK---P--I---CASN---G------KTYMNRCLFSYDEC-K---NP-------S---LRVAHSG---A----------C
Pu_PYU1_T005024_d1_NS_L CTIR--D-C-KLTHD---DVNV---CGSD---G------KTYLNECLFRNAQC-RS--ND--A--LT---RNTNWNG--YR---------
Pu_PYU1_T005024_d2_NS_E C-GHTIT-C-KEIGK---Y--V---CGSD---G------NYYFGYCNLYYAQC-V---DP----------SVEEIE----------
Pu_PYU1_T014335_d1_A C-TLLTE-C-PADPD---P--SESVCGDD---Y------NAYPSACSLLLTHC-Q---HPGAVGPYP---LEGAVPP---T----------C
Pu_PYU1_T014335_d2_M C-AF--V-C-PMFYA---P--V---CTDD---G------HYYENKCYYASARC-R---DT------A---LTEANAD---N----------
Pu_PYU1_T012157_T C-DL--G-C-GTHWS---P--I---CASD---G------VTYRNACTLEEAYC-E---DH------D---VRPLHNG---E----------C
Pu_PYU1_T012160_d1_G CEAI--E-C-SGDWQSDNP---V---CGSN---G------VRYESLCAFELVKC-E---NP-------S---LGDVHVA---P----------C
Pu_PYU1_T012160_d2_D C-EL--S-C-EDLWS---P--I---CGSD---D------VTYRNPCHLEEAFC-R---NH-------Q---VEPTYYG---V----------C
Pu_PYU1_T012156_NS_S C-AR--D-C-GSNRA---P--I---CASD---G------VTYANSCLFDQAHC-V---NN-------E---LLPMHYG---D----------C
Ha_804983_d1_F     C-AI--R-C-AFTGD---R--V---CGSN---N------VTYPNLCLLTLANC-A---NP-------GED---ITVASEG---E----------C
Ha_804983_d2_M     C-AD--A-C-PMIFA---P--V---CGSD---S------ITYGNGCLLGIAHC-E---SK-------G-T---ITQTSEG---Q----------C
Ha_804983_d3_Q     C-PD--L-C-VQTYE---P--V---CGSD---G------VTHNNICMLRAAQC-Y---DP-------S---ITLAYEG---A----------C
Ha_804983_d4_A     C-PD--V-C-LAVFA---P--V---CGSN---D------VTYGNEGELGIFPT-VLAQTN-------S---LIQTAKQRLYI----------
Ai_NC14C621G12264_1_NS_K C-NL--I-KCDKSPFQ---R--V---CGSD---G------KSYPNECQAERMDC-F---EA-------S---LSWDEP----------C
Ai_NC14C621G12264_2_NS_M CTECNMY-C-LDNYD---P--V---CGYSRGIE-------KSYPNECARKNEIC-E---DP-------T---IKP----------
Ai_NC14C188G8390_Q C-NPQPE-C-TQEAD---P--V---CGSN---Y------YTYANRCFLANDRC-T---YP-------H---LSVRADG---I----------
Ai_NC14C84G5389_Q C-NPQPE-C-TQEAD---P--V---CGSN---Y------YTYANRCFLANDRC-T---YP-------H---LSVRADG---I----------
Ai_NC14C177G8157_d1_Y C-ES--I-CAYDYSG---P--A---CGSD---G------HTYPNKCM---TC-L---DS-------G---TKYFHRG---Y----------
Ai_NC14C177G8157_d2_R C-NV--E-C-SRDKE---L--I---CGID---G------QTYINYCHYAVTYC-D----------KRLATLPFLSG---E----------C
Ai_NC14C76G5100_d1_NS_D C-MN--E-C-IDSDS---NSQL---CGTN---G------ITYANLCELKKTGC-T---GT------Q---IALKHFG---V----------C
Ai_NC14C76G5100_d2_NS_N C-AI-AMC-SNNVE---P--V---CDLYPSKL-------TTYQNSCHFRAARC-Q---AL--HGEKG---ELLNGPGEENG---------KLRKREKDAKGKKC
Pn_00020_D         -KHV--L-C-HDDDA---P--V---CGSD---N------KTYPNALLI---RC-------FN----------VTMAYGG---I----------
Pn_00334_R         CID--D-G-TRDGI---P--I---CASN---G------KLYLNMNRFRYNKC-LI---KA--EMNED---ILFADPS---F----------C
Pn_00335_V         C-VD--S-G-SVEDK---P--V---CASN---G------KKYLNEDVFEFHKC-LI---QA--QFGEN---IEIVKME---I----------C
Pn_00336_R         C-YG--H-F-TRDYD---P--V---CGSN---G------KIYSNLSMFTYRQCMMKI QENI-------E---IQVKEMK---Y----------C
Pn_00402_d1_D      C-LL--K-C-SDKNE---P--V---CGSN---G------VTYTNECLLNLANC-E---SS--E---P---ITKVHEG---G----------C
Pn_00402_d2_A      C-PD--M-C-PAIYD---P--V---CASN---G------LTYPSGCALGIASC-Q---SG-----G-A---ITYVSDG---P----------C
Pn_00402_d3_E      C-SD--K-C-IEVYR---P--V---CGTD---N------VTYGNSCFLEFASC-K---NA-------S---ISLAYEG---A----------C
Pn_01542_D         C-TD-VL-C-DDDYA---P--V---CGFD---N------KTYPNACIFQATNC-H---TN----------VTMAYLG---P----------C
Pn_02422_d1_Q      C-DR--V-C-TQDFS---P--V---CGSD---G------NMYSNECIRDLESC-K---SV--E--AG---FGPIANG--VN----------
Pn_02422_d2_E      C-PG--R-C-PEVNE---P--V---CASN---G------ITYANECKFNLAIC-N---SP--Q--LN---VVKTSYEMRQP----------MHSWQC
Pn_02736_d1_A      C-DF--A-C-LAIFD---P--V---CASN---G------ETFSNACEFEQTRC-T---SQ--N--DT---LVIVSQG---A----------C
Pn_02736_d2_D      C-MEKFD-C-LDVYV---P--V---CGSD---G------RTYSNKCSLEKICC-Y---TP-------S---ILILSNE---E----------C
Pn_02736_d3_K      CIES--V-C-TKEFH---P--L---CGSD---G------VMYNNDCLFENAQC-M---NS-------S---LSLAFET---K----------C
Pn_06103_D         C-TD-AL-C-DDGYP---P--V---CGFG---S------KTYPNACIYQATNC-R----------TN--VTMAYSG---PSRDNQRVHLSASATSLNEKSPLI
Pn_06782_D         CTEA--L-C-KDEDA---P--V---CSFD---N------KTYPNAFVGNQWV-H---LS--A--SA---ASSSDKPPLI R----------
Pn_06850_E         C-TD-AL-C-NEDDA---P--V---CGFD---N------KTYVNACIFQAANC-L---TN----------ITMAYSG---P----------C
Pn_07228_d1_I      C-SQLFE-CKIVSYS---P--V---CGSD---G------ITYANYCVFAKKYC-S---LD--QGADT---LYIQSGG---K----------C
Pn_07228_d2_A      C-SL--T-C-QATSN---P--V---CGTD---G------VTYTNDCHLLSTKC-K---HP-------H---LEKRSDG---A----------C
Pn_07228_d3_R      C-NS--M-C-KRLYE---P--I---CGSD---G------VTYANLCLLEYAEC-R---NP-------N---IKVFGPG---K----------C
Pn_07228_d4_D      CIPE--L-C-TDIYA---P--V---CGSD---G------QTHENLCLFSNARC-Q---YP-----NHE---LSIIHDG---E----------C
Pn_09920_d1_T      C-YT--I-C-STDFK---P--V---CGSD---G------VTYTNACAFSIAQC-R---TA-------T---LSLLAVG---E----------C
Pn_09920_d2_D      C-PD--A-C-PDIYD---P--V---SDES---G------KTYTNECYLRMTKC-K---DT--N--HN---LGILAEY----------
Pn_09920_d3_D      C-AP-----C-PDLYS---P--V---CGSD---G------ITYLSLCKLEFASC-K---NP--E--LK---LVQISDD---F----------C
Pn_10391_D         C-TD-AL-C-DDDYS---P--V---CGFD---N------KTYPNACIFQATYC-R---SN----------VTMAYFG---P----------C
Pn_11175_D         C-ND-AL-C-NDDNA---P--V---CGFD---N------KTYPNACIFQATNC-R---TN----------VTIAHLG---P----------C
Pn_11779_d1_D      C-NF--A-C-LDVMK---P--V---CGSD---G------YIYPNKCYRDRASC-E----------SIKAGKGAITE----------
Pn_11779_d2_Y      C-PV-----C-PVYDD---P--V---CGSD---G------ITYTNVCELNWTKC-Q---HP-----ELN---LTHVLDG---T----------C
Pn_13385_d1_D      C-TD-AQ-C-DDDYA---P--V---CGFD---D------KTYPNACIFQATNC-H---TN----------VTMAYLG---P----------C
Pn_13337_D         C-AD-AR-C-DDDNA---P--V---CGFD---N------KTYPNACIFQATNC-R---NP----------VTIAHLG---P----------C
Pn_scaf old_1594_1_E_typical C-TI--Q-C-TREYV---P--V---CDSN---G------QLHANLCLFDVAVC-L---NP----------QLTQEK----------
Sp_SPRG_16334_d1_M C-PI--TVC-PMYYQ---P--V---CGSD---R------VTYSNKCELEVAAC-K---TP-------G---LIMANAT---V----------C
Sp_SPRG_16334_d2_E C-PR--Y-C-LEIYR---P--V---CGSD---G------KTYSNECELNIAAC-K---NP-------S---LTRVRDG---P----------C
Sp_SPRG_16334_d3_K C-PD--A-C-HKMYE---P--V---CGSN---W------VTYANKCLLEAAQC-R---NP-------S---ILLAATG---D----------C
Sp_SPRG_16334_d4_R C-NY--A-C-MRSYD---P--I---CASD---K------RTYSNWCEFSKAVC-K---QP-------E---LTFRSIG---V----------C
Sp_SPRG_05363_d1_D C-PT--V-C-IDLFD---E--V---CGSD---G------KTYTNECKLDIAAC-A---DP-------T---ILKVSKG---A----------C
Sp_SPRG_05363_d2_E C-PI--RGC-IELIS---P--V---CGSD---G------VNYDNECFLRKAKC-T---KP-------E---LTLVSNT---S----------C
Sp_SPRG_11788_d1_K C-EK--A-C-TKDMK---P--V---CGSD---G------VTYNNECLLQNAQC-T----------N---ATMTAVP----------
Sp_SPRG_11788_d2_K C-AM--L-C-DKMYA---P--V---CGSD---N------NTYNSECELSKKAC-N---NP-------T---LKVAKKG---E----------C
Sp_SPRG_11788_d3_D C-PK--V-C-NDVLD---E--V---CGSD---G------KTYNNNCELLKAAC-A---KP----SEK---LTVVSTG---A----------C
Sp_SPRG_10958_d1_K C-DDASP-C-PKGGS---P--V---CATN---G------VTYTNACALAKANC-I---DA-------N---LVLASNG---V----------C
Sp_SPRG_10958_d2_V C-AM--E-C-PVSYD---P--Q---CGSN---G------MTYANVCEFKKAHC-T---NP-------T---VTLDHTG---R----------C
Sp_SPRG_10958_d3_M C-PS--I-C-TMEYA---P--V---CGTD---G------TTYSNGCKLEIARC-RG--GP--K--ST---LRIAHVG---P----------C
Sp_SPRG_10958_d4_D C-PT--A-C-NDKYA---P--V---CGSD---G------HTYVNACNFEKVHC-G---ND-------D---MHIVHGG---A----------C
Sp_SPRG_10958_d5_R CRDR--P-C-NRMFK---P--V---CGSD---N------KTYNNMCLFENAQC-A---NR-------G---LALLHDG---S----------C
Sp_SPRG_13295_d1_K C-EK--A-C-TKDMK---P--V---CGSD---G------VTYNNECLLQNAQC-T----------N---ATMTAVP----------
Sp_SPRG_13295_d2_D C-PK--V-C-NDVLD---E--V---CGSD---G------NTYNSECELLKAAC-A---KP----SEK---LTVVSTG---A----------C
Sp_SPRG_09559_d1_P CAVA----C-PPLKQ---T--Y---CALE---SPSATTFVGTYSSQCNCLVAKC-G---NK----------KV-------Q----------
Sp_SPRG_09559_d2_P CTRKIAK-CKPNEVK---P--SQL---CGSN---G------VTYDNLCFLKAARC-V---KP-------D---IQFIAPG---K----------C
Sp_SPRG_09559_d3_L CGA--K-C-PLTKT---K--V---CASN---GGKTE---LKYCNQCFLDAATC-V---NP-------G---ILKMAA----------
Sp_SPRG_09563_d1_S CAAN----C-TSSKQ---A--VY--CALS---NSTTAYDVSYSQCECLAAKC-K----------NRKVH----------
Sp_SPRG_09563_d2_P CLSKLAR-CKPNQVA---P--V---CGSN---G------VTYDHLCYLKAARC-L---NP-------S---IEFLSPG---K----------C
Sp_SPRG_09563_d3_K CGLG--K-C-SKNKE---K--VKVCATLK---G-AT---IKFKNECLLTAATC-V---NA----------AVTPV-------D----------C
Sp_SPRG_16956_d1_S C-AA--N-C-TSSKQ---V--VY--CALS---NSTTAYDVSFSQCECLAAKC----------------------------------------
Sp_SPRG_16956_d2_P CLSKLAK-CKPNQVA---P--V---CGSN---G------ATYDHLCYLKAARC-L---NP-------S---IEFLSPG---K----------C
Sp_SPRG_16956_d3_K CGLG--K-C-SKTKG---K--EKVCATLK---G-AT---IKFKNECLLTAATC-V---NA----------AVTPV-------D----------C
Ae_11AL6547_d1_E C-IQ--S-C-HEVYQ---P--V---CGSD---G------QTYSNECSLKRESC-L---KG--V--K---VEMKSPG---R----------C
Ae_11AL6547_d2_E C-PR--A-C-IEIFQ---P--V---CGTD---G------VTYANKCTLKQDAC-A---RK--V--S---IQVAHEG---D----------C
Ae_11AL6547_d3_K C-PK--G-C-PKIYH---P--V---CGTD---G------KTYANECTLHLHAC-E---NK-------VD---VAVAHDG---K----------C
Ae_11AL6547_d4_E C-RK--G-C-PEIYH---A--V---CGTD---G------KTYENECTLQRVAC-E---NK-------I D---VAVAHDG---D----------C
Ae_11AL6547_d5_E C-PV--A-C-IEILR---P--V---CGTD---G------KTYDNECFLKRDAC-S---KN--V--H---VQVAHEG---M----------C
Pi_PAPI_d1_L       C-PS--I-C-PLNYK---P--V---CGSD---L------KTYGNSCQLNAAIC-R---NP-------S---LKKLYDG---P----------C
Pi_PAPI_d2_L       C-PS--I-C-PLDYN---P--V---CGTD---G------KTYSNLCALRIEAC-N---NP-----HLN---LRVDYQG---E----------C
Pi_PAPI_d3_L       C-RN--G-C-TLQYD---P--K---CGTD---G------KTYSNLCDLEVAAC-N---NP-----QLN---LKVAYKG---E----------C
Pi_PAPI_d4_Q       C-PT--I-C-TQQYD---P--V---CGTD---G------KTYGNSCELGVAAC-N---NP-----QLN---LKIAYKG---A----------C
Tg_PI-1_d1_R       C-----S-C-PRNLE---L--N---CGGD---H------VTYANHC---IREC-H----------G---VGLLHDG---P----------C
Tg_PI-1_d2_R       C-----A-C-TRELR---L--N---CGVD---G------VTYSNHC---VRKC-E----------R---VKLLHEG---P----------C
Tg_PI-1_d3_L       C-----P-C-PLNLM---L--N---CGVD---G------VTYDNHC---LRRC-R----------R---VELKHEG---P----------C
Tg_PI-1_d4_L       C-----A-C-PLILT---P--N---CGTD---R------KTYPNNC---VREC-A----------G---VKLLHEG---P----------C
                   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
```

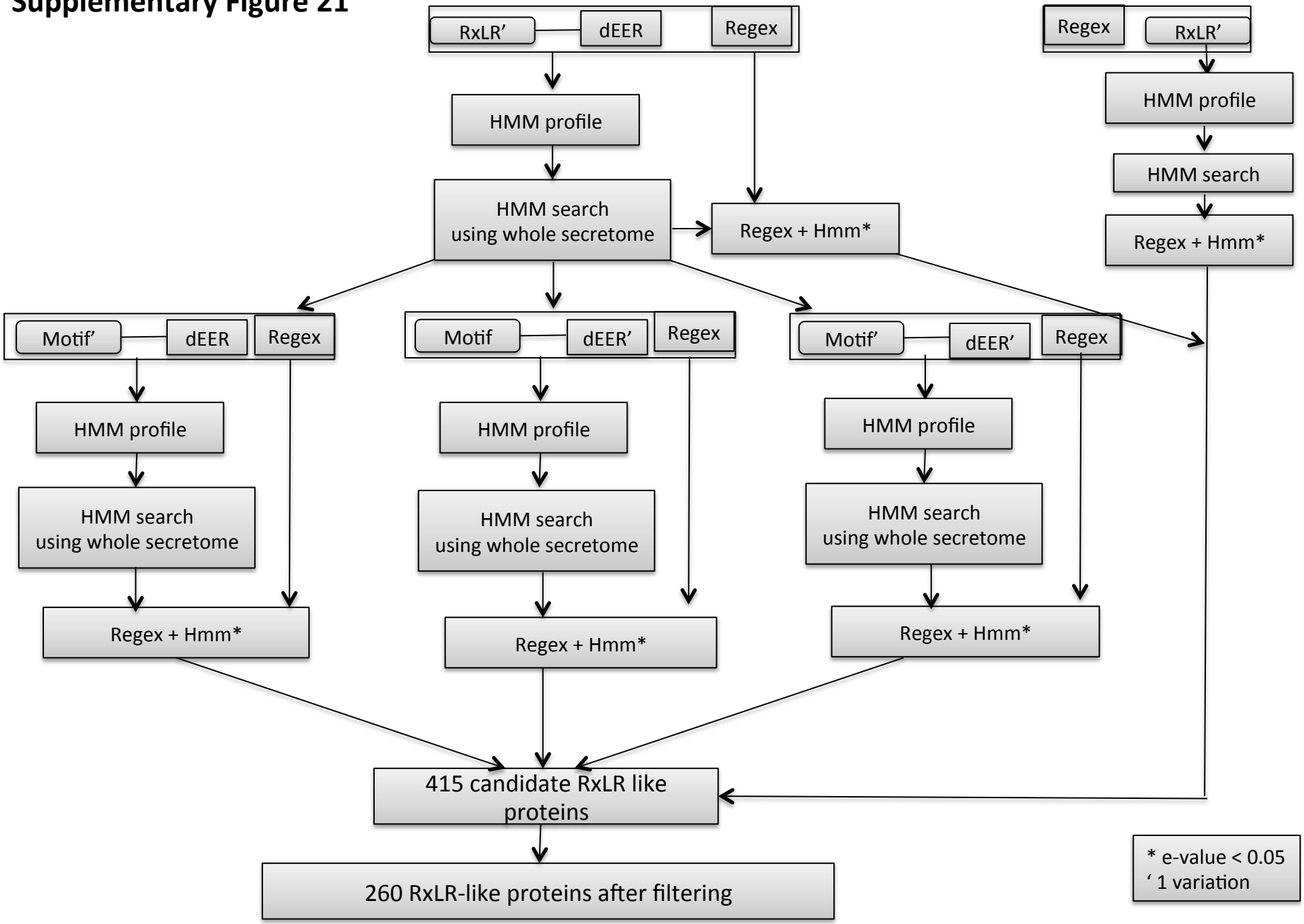
Supplementary Figure 19. Sequence alignment of cystatin-like domains of seven pathogenic oomycetes.
Multiple sequence alignment of 38 cystatin-like domains present in 30 cysteine protease inhibitors (EPICs) of seven pathogenic oomycetes. Out of the 38 oomycete cystatin-like domains, 8 are from *Phytophthora infestans* (Pi), 6 are from *Pythium ultimum* (Pu), 4 are from *Hyaloperonospora arabidopsidis* (Ha), 4 are from *Albugo laibachii* (Al), 9 are from *Saprolegnia parasitica* (Sp), 1 is from *Plasmopara halstedii* (Ph) and 6 are from *Aphanomyces euteiches* (Ae). The alignment also includes 6 cystatin-like domains present in 6 cysteine protease inhibitors from plants (*Carica papaya* Cp Cystatin gi|311505), from animals (insect *Sarcophaga peregrina* Sp_ Sarcocystatin gi|399335, chicken Gg_Cystatin P01038, mouse Mm_Cystatin gi|6226846 Mm_Kininogen gi|12643495, human Hs_ Chain A gi14278690). The proposed active-site residues in cystatins, including the N-terminal trunk (NT), first binding loop (L1) and second binding loop (L2) are indicated in the sequence with a bar (top). The amino acids that define cystatins are marked with asterisks (bottom). The first suffix indicates the number of the cystatin-like domain from left to right of the C-terminal effector domain in multidomain proteins. The second suffix “NS” was added to protease inhibitor domains from proteins that were not predicted to be secreted.

Supplementary Figure 20

CRN predictions on the ORFs of *Pl. halstedii* genome	BlastP	476
	BlastP+HMM (full length/Haas)	200/139
	BlastP + Both HMM	125
	BlastP + Both HMM + SignalP v4 (Probability: 0.6)	33
	BlastP + Both HMM + Manual	55
	BlastP + Both HMM + Manual + SignalP v4 (Probability: 0.6)	16
CRN predictions on the protein sequences of *Pl. halstedii* genome	Constructing *Pl. halstedii* CRNs HMM	49
	Total non-overlapping CRNs in *Pl. halstedii* genome	77

Supplementary Figure 20: Table is representing the number of candidate CRNs predicted in the current study.

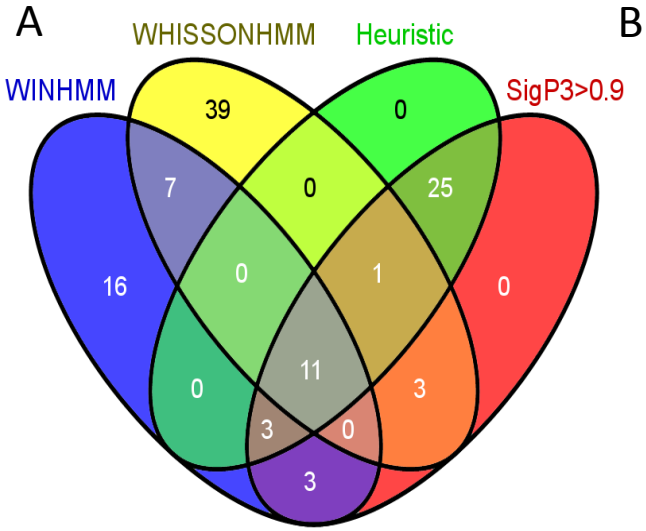
Supplementary Figure 21



Supplementary Figure 21. Pipeline used for predicting RxLR-like proteins form the *P. halstedii* protein sequences.

Supplementary Figure 22

A



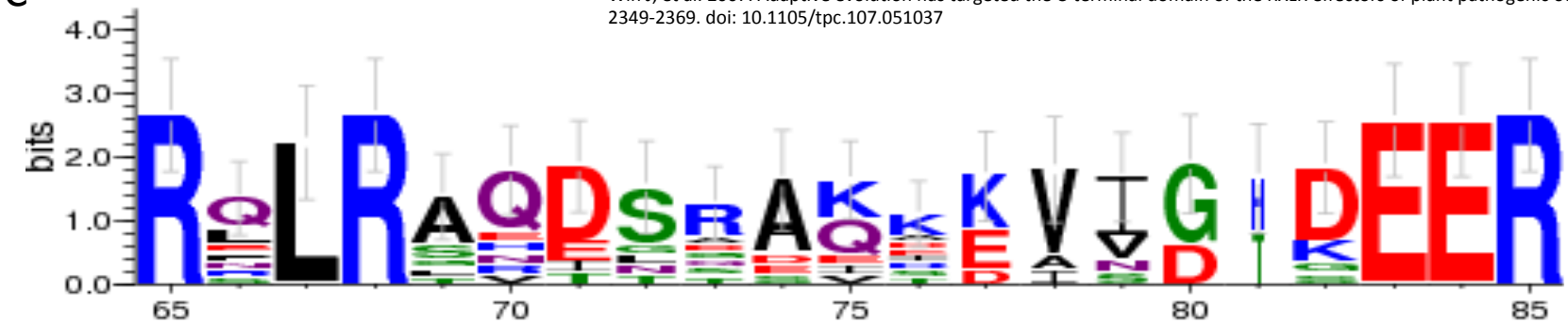
B

	Method	Number (SignalP3 secreted)
RxLR predictions on ORFs of *Pl. halstedii* genome	Heuristic (SigP + RxLR-dEER regex)	40 (40)
	HMM (from Whisson *et al.* 2007)	61 (15)
	HMM (from Win *et al.* 2007)	40 (17)
	Heuristic only	25 (25)
	HMM (Whisson only)	42 (3)
	Hmm (Win only)	19 (3)
	Agreed by heuristic and both HMM	11 (11)
	Agreed by heuristic and >= 1 HMM	15 (15)
	Total by any method	108 (46)
predictions on protein sequences of *Pl. halstedii* genome	Using *Pl. halstedii* HMM using 4 iterations	260
	Total non-overlapping RxLR-like proteins in *Pl. halstedii* genome	274

Whisson SC, et al. 2007. A translocation signal for delivery of oomycete effector proteins into host plant cells. Nature 450: 115-118. doi: 10.1038, nature06203

Win J, et al. 2007. Adaptive evolution has targeted the C-terminal domain of the RXLR effectors of plant pathogenic oomycetes. Plant Cell 19: 2349-2369. doi: 10.1105/tpc.107.051037

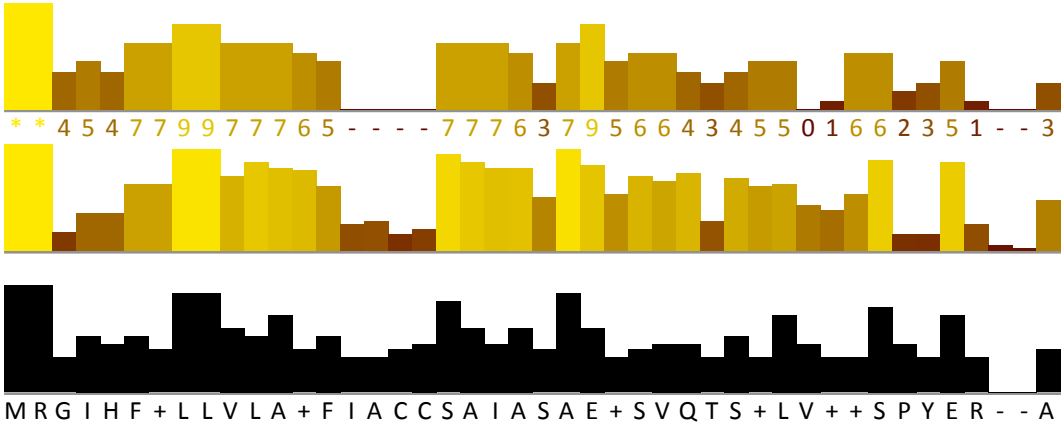
C



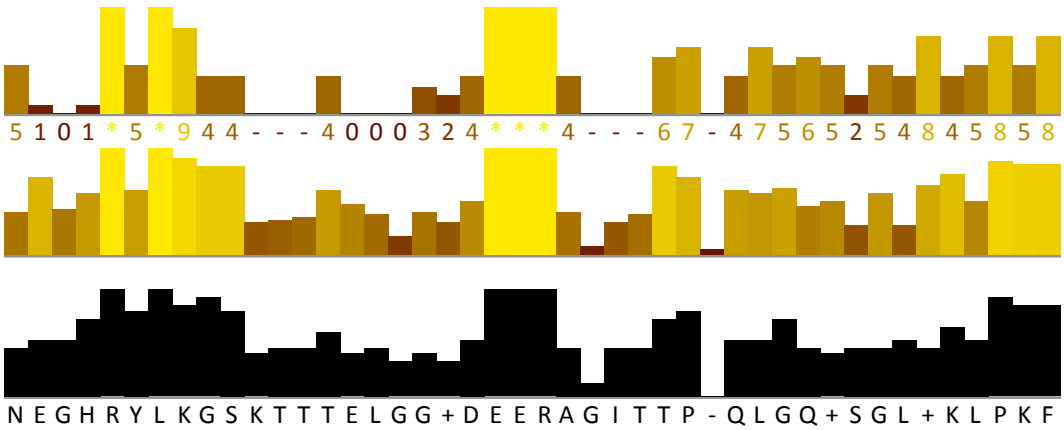
Supplementary Figure 22: (A) Venn-diagram representing the number of RxLR-like effectors predicted from the ORFs of *Pl. halstedii*. **(B)** RxLR-like effector predictions using different methods **(C)** Weblogo visualization of the RxLR-dEER motif of the RxLR-like effectors.

Ortholog 1 Supplementary Figure 23

```
Prm_Prm_76663/1-112      1 M R T T Q L L L L V V A T F I - - - S T A A V A E N S I Q D S A L A T D S I T E T - - A 39
Pso_287018/1-119         1 M R L I Q F F L L V L V T F A V C C S A L A S A E D P N Q M K N T V S T G Q H Q A - - A 42
Prm_Prm_78801/1-125      1 M R V A Q M L L L V V A T F I V C C S A V T D A E N S I Q D N A S T T D S T A E T - - T 42
Pin_PITG_13537T0/1-155   1 M R G I H F F L L A L A S Y - - - - S A I A S A D Q T V E T S S L V N Q S P Y E R - - V 38
Prm_Prm_76660/1-125      1 M R T T Q L L L L V V A T F I A C C S A V T D A E N S I Q V N A L T T D S I T E T - - A 42
Pin_PITG_07736T0/1-120   1 M R I I L Y V V L L L A A H - - - - G T I A T A D N P V E I Q D L E V S T H R K H - - E 38
Pin_PITG_13534T0/1-117   1 M R G I H F F L L A L A S Y - - - - S A I A S A D Q T V E T S S L V N Q S P Y E R - - V 38
Pin_PITG_07766T0/1-115   1 M R A I H L M L L V L V S C - - - - S S I A P A E R A T G M S G V - - N S P F Q P - - E 36
Prm_Prm_78158/1-125      1 M R M A Q L L L L V V A T F I A C C S A V T D A E N S I Q D N A L T T D P T T E I - - A 42
Pin_PITG_19803T0/1-117   1 M R G I H F F L L A L A S Y - - - - S A I A S A D Q T V E T S S L V N Q S P Y E R - - V 38
Prm_Prm_81834/1-132      1 M R M N Q L L L L V I A T F I A R C S T L T D A E R S I Q V D T L A T D S I T E S - - A 42
Pin_PITG_13535T0/1-117   1 M R G I H F F L L A L A S Y - - - - S A I A S A D Q T V E T S S L V N Q S P Y E R - - V 38
Prm_Prm_76672/1-128      1 M R L S L F L L L V V L A F V A C C S T V V A T E E A V Q A S N L V P E S N Q N L - - A 42
Pca_16635/1-455          1 M R Y S H F I L V V A V V F M A C C N T A T T A E S S L G I K A T S A N S P H E V T D T 44
Pin_PITG_13536T0/1-117   1 M R G I H F F L L A L A S Y - - - - S A I A S A D Q T V E T S S L V N Q S P Y E R - - V 38
```




```
Prm_Prm_76663/1-112      40 A K R H R Y L K G G E T T T E L D T A D E E R V - - - A P - S L S M L K D W L K L P K F 79
Pso_287018/1-119         43 T - - - R Y L K G S K T T T D M T S A D E E R F - - - T P - Q F G Q Y W G I F R L P S F 79
Prm_Prm_78801/1-125      43 A K G H R Y L K G S K T T S D V V T V D E E R F - - - T P - K W G M Y L G G L K L P K F 82
Pin_PITG_13537T0/1-155   39 N E G H R Y L K E S - - - T E L G G K G E E R A - I T T S - Q L G Q F S A L F K T P K F 77
Prm_Prm_76660/1-125      43 T K S H R Y L K G S E T T S D V A T V D E E R Y - - - V P - G F G M L L G A L K L P K F 82
Pin_PITG_07736T0/1-120   39 S Q D Y R Y L R G N N E A T K T D G V E E E R T - I S T P - Q F D K L S A L L S P P K F 80
Pin_PITG_13534T0/1-117   39 N E G H R Y L K G S - - - F E L G G K G E E R A - I T T S - Q L G Q F S A L F K T P K F 77
Pin_PITG_07766T0/1-115   37 N E D Q R Y L R G R - - - T K P H E I D E E R A - I R T P - Q L D Q A S S L L K L P K L 75
Prm_Prm_78158/1-125      43 T K D H R Y L K G S K T T S D E A T V D E E R F - - - A P - K F G M F L G G L K L P K F 82
Pin_PITG_19803T0/1-117   39 N E G H R H L K G S - - - T E L G G K G E E R A - I T T P - Q L G Q F S A L F E T P K F 77
Prm_Prm_81834/1-132      43 I E G H R Y L K G S K T T T A L D T V D E E R I G A T T P - N F G M L K G L F K L P K F 85
Pin_PITG_13535T0/1-117   39 N E G H R H L K G S - - - T E L G G K G E E R A - I T T P - Q L G Q F S A L F E T P K F 77
Prm_Prm_76672/1-128      43 G E S H R N L K G S K T T T T A D A E S E E R V G A T T P - N F G M L Q G F L K L P K L 85
Pca_16635/1-455          45 N Q G R R Y L K G S K N E I - - - I A D E E R A - - - A P V G L N K L L G T I R I T N F 82
Pin_PITG_13536T0/1-117   39 N E G H R Y L K G S - - - F E L G G K G E E R A - I T T S - Q L G Q F S A L F K T P K F 77
```

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Prm_Prm_76663/1-112      80 Q R T P K L T S A E K A A E A Q - - - - K K A - - - - D K M F R A W - - - - - - - - - - 105
Pso_287018/1-119         80 - - - A K L P G A Q Q V A F L R Q K F G K G A - - - - G K V I N L W - - - - - - - - - - 106
Prm_Prm_78801/1-125      83 Q S L S K L P L V K Q L A A L K S K L G K K V - - - - A D L Y T K W - - - - - - - - - - 112
```

```
Pin_PITG_13537T0/1-155   78  - - - A N L P L I K Q L N T V R L K L G N K A - - - - G K A F L A F - - - - - - - - - - 104
Prm_Prm_76660/1-125      83  Q G L A K L P L V K Q L A A I K N K F G K K V - - - - G D V Y L K W - - - - - - - - - - 112
Pin_PITG_07736T0/1-120   81  - - - S N L P L I K Q V N K V R I S L A K K L - - - - G S L Y L K K - - - - - - - - - - 107
Pin_PITG_13534T0/1-117   78  - - - A N L P L I K Q L N T V R L K L G N K A - - - - G K A F L A F - - - - - - - - - - 104
Pin_PITG_07766T0/1-115   76  - - - S K L P G I K H L N K F R L Y L A K K A - - - - G N A L T S R - - - - - - - - - - 102
Prm_Prm_78158/1-125      83  Q G L S K L P L L K Q T T L I Q K K L G K K A - - - - A D L Y L K T - - - - - - - - - - 112
Pin_PITG_19803T0/1-117   78  - - - A N L P L I K Q L N T V Q L K L G S K A - - - - G K A Y L A F - - - - - - - - - - 104
Prm_Prm_81834/1-132      86  E S L S K L P L V K Q L V A I Q K K V G K K V G K K I G D I Y L K W - - - - - - - - - - 119
Pin_PITG_13535T0/1-117   78  - - - A N L P L I K Q L N T V Q L K L G S K A - - - - G K A Y L A F - - - - - - - - - - 104
Prm_Prm_76672/1-128      86  Q G L A K L P L I K Q L T Q I S Q K F G K Y S - - - - S N V F Q W L - - - - - - - - - - 115
Pca_16635/1-455          83  Q Q F S K L P F L K Q I A Q I K A K Y G A G V - - - - A K A F A K W R S A Q L N A T A S 122
Pin_PITG_13536T0/1-117   78  - - - A N L P L I K Q L N T V R L K L G N K A - - - - G K A F L A F - - - - - - - - - - 104

Conservation
                         - - - 6 6 * 8 4 7 6 6 5 6 1 6 5 0 1 1 3 4 4 5 - - - - 5 4 7 7 3 2 3 - - - - - - - - - -
Quality
Consensus
                         Q G L A K L P L I K Q L N T + R L K L G K K A - - - - G K A Y L + W - - - - - - - - - -

Prm_Prm_76663/1-112      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_287018/1-119         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_78801/1-125      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_13537T0/1-155   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_76660/1-125      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07736T0/1-120   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_13534T0/1-117   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07766T0/1-115   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_78158/1-125      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_19803T0/1-117   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_81834/1-132      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_13535T0/1-117   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_76672/1-128      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_16635/1-455          123 P E S L F K C S R C Q S V L Y C G R E H Q T E D F A S H K A T C R R I K K M R E K M A Q 166
Pin_PITG_13536T0/1-117   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Conservation
                         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality
Consensus
                         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Prm_Prm_76663/1-112      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_287018/1-119         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_78801/1-125      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_13537T0/1-155   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_76660/1-125      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07736T0/1-120   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

```
Pin_PITG_13534T0/1-117      - - -
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```
Prm_Prm_81834/1-132          - - -
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```
Pin_PITG_13536T0/1-117      - - -
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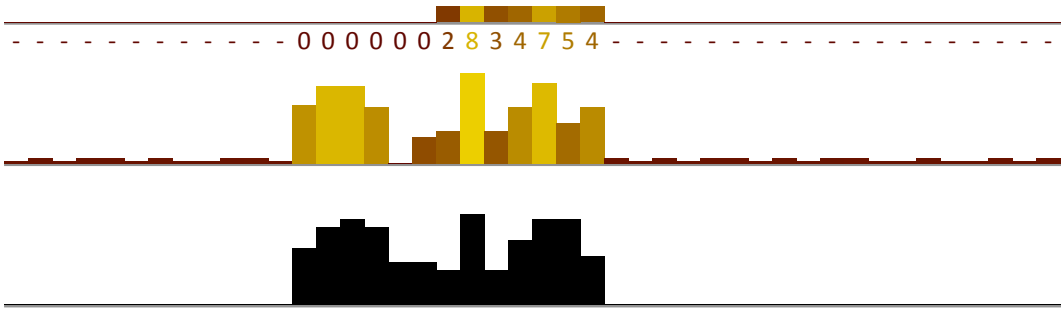


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Prm_Prm_76663/1-112          - - - - - - - - - - - - - - - - - - -
Pso_287018/1-119             - - - - - - - - - - - - - - - - - - -
Prm_Prm_78801/1-125          - - - - - - - - - - - - - - - - - - -
Pin_PITG_13537T0/1-155   137 D F C L S A H A L S C N Q F V I L G S   155
Prm_Prm_76660/1-125          - - - - - - - - - - - - - - - - - - -
Pin_PITG_07736T0/1-120       - - - - - - - - - - - - - - - - - - -
Pin_PITG_13534T0/1-117       - - - - - - - - - - - - - - - - - - -
Pin_PITG_07766T0/1-115       - - - - - - - - - - - - - - - - - - -
Prm_Prm_78158/1-125          - - - - - - - - - - - - - - - - - - -
Pin_PITG_19803T0/1-117       - - - - - - - - - - - - - - - - - - -
Prm_Prm_81834/1-132          - - - - - - - - - - - - - - - - - - -
Pin_PITG_13535T0/1-117       - - - - - - - - - - - - - - - - - - -
Prm_Prm_76672/1-128          - - - - - - - - - - - - - - - - - - -
Pca_16635/1-455              - - - - - - - - - - - - - - - - - - -
Pin_PITG_13536T0/1-117       - - - - - - - - - - - - - - - - - - -
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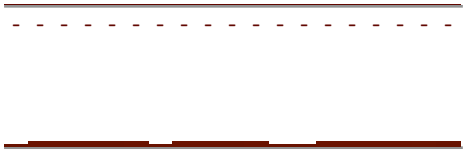
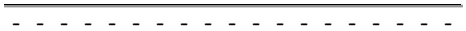
Conservation



Quality

Consensus



Ortholog 2

```
Prm_Prm_74387/1-676      1 M V A K F S P C S L R R C T - - - I L L T I L A L L A C V - G T V S G A T D A N I - - A  38
Prm_Prm_79108/1-468      1 M - A K F S P C S R S R C A - - - I L L A I F A L L T C V - G A V S V A S E S N V - - I  37
Prm_Prm_79110/1-588      1 M I A K L G P R S H R R C A - - - M L L A I F A L L T C V - G A V S V A S E S N V - - I  38
Prm_Prm_79107/1-433      1 M - A K F S P C S R S R C A - - - I L L A I F A L L T C V - G A V S V A S E S N V - - A  37
Pin_PITG_14884T0/1-604   1 M P L K L A L T P R L S Y F - - - I L L A A L A L L V C I H S G S K V A T A S S V I D A  41
Prm_Prm_85872/1-585      1 M V A K F S P C S R S R C A - - - I L P I I L A L L A C V - G A V S G A T D A N I - - A  38
Pca_102742/1-501         1 M S S K A G L I S - - - C A L W L L L L V - - - - - - - - - S T L G V D A H K R L - - -  29
Pin_PITG_14880T0/1-296   1 M P L K I A L T P R F S Y F - - - I L L A A L G L L V C I D S G F K V A T A S N V I D A  41
Prm_Prm_86912/1-294      1 M I A K F S P C S L R R C A - - - Q L L T I F A L L A C V - G A V S G T T D A N I - - A  38
Pso_285707/1-589         1 M V S K S N P L N - - - C S - - - T L L A L L A L A A S V - G R V L A T S H S K I T V A  37
Pin_PITG_13847T0/1-512   1 M V A M I V Q C T R T K Y A H S L I L L V A T A L I I F A - - - - S V V S H S A S - - L  38
Prm_Prm_79119/1-666      1 M - A K F S P C S R S R C A - - - I L L A I F A L L T C V - G A V S V A S E S N V - - A  37
Pso_285703/1-570         1 M A F K A I P A Q R R Y C A - - - I L L V A L A L A V S I - S D A L P T T N S K T F V A  40
Prm_Prm_74367/1-380      1 M V A K A S P C S R S R L A - - - T L L T I V V L L A C V - G G A T V A T D S N T - - G  38
```

Conservation

```
* 0 4 7 4 5 5 3 6 0 0 1 6 5 - - - 6 * 6 5 1 0 2 2 1 0 0 1 - 2 0 0 3 6 4 7 2 4 4 5 - - 1
```

Quality

Consensus

```
M V A K F S P C S R S R C A - - L I L L A I L A L L A C V - G A V S V A T + S N V I + A

Prm_Prm_74387/1-676      39 K - P E T L D R S E G R Q L R G F L R K R S L R T V E E A M K D D D D S E E - R A I - -  78
Prm_Prm_79108/1-468      38 K - P K M L D R A Q G H Q L R G F Q G Y R S L R T F V E I T K D D D D S E E - R V S - -  77
Prm_Prm_79110/1-588      39 K - P K M L D R A Q G H Q L R G F Q G Y R S L R T F V E I T K D D D D S E E - R V S - -  78
Prm_Prm_79107/1-433      38 K - P K T L D R A Q G H Q L R G F Q G Y R S L R T F L E A T K D D D D S E E - R V F - -  77
Pin_PITG_14884T0/1-604   42 R - N D A L D R E V G G Q I - - - - - H R Y L R E S K W T A E Q E D G S P E A R A I G V  79
Prm_Prm_85872/1-585      39 K - P E T L D R S E E R L L R S F H G I R N L R I V E E A M K - D D D S E E - R A I - -  77
Pca_102742/1-501         30 - - - - - - - - - - - - - - - - - - - - - - - L R S - - - - E V S H D N L E D - R V L - -  44
Pin_PITG_14880T0/1-296   42 K - N D A L D C E V G G Q I - - - - - H R Y L R E S K W T A E Q E V G S P E A R A I G V  79
Prm_Prm_86912/1-294      39 K - P E T L G R S E E R L L R S P H G N R N L R T F E E A M K - D D D S E E - R A I - -  77
Pso_285707/1-589         38 S T P V S Y D V V D P N Q V G G - Q T P R H L R A L G - - I E D D D S S V E - R A F - -  75
Pin_PITG_13847T0/1-512   39 K - T I R V D I E T S D R T R S - - - - - - - - - - - - - - - - - - - - - - - - - - - -  53
Prm_Prm_79119/1-666      38 K - P K P L D R A L G R Q L R G F Q G K R S L R T F V E A T K D D D D S E E - R V F - -  77
Pso_285703/1-570         41 S - A P S L D Q A V T - - - - - - Q T H R H L R A - - - - Y E D G V N S E E - K G F - -  70
Prm_Prm_74367/1-380      39 K - P E T - - - S E G R L L R G L Q G - - - - - N F V G T T R N D D E S E E - R A I - -  70
```

Conservation

```
1 - 1 0 0 1 1 0 0 0 0 0 0 0 - - - - - 0 3 1 2 3 0 0 0 - - 0 0 1 0 1 0 0 0 3 - 3 2 0 - -
```

Quality

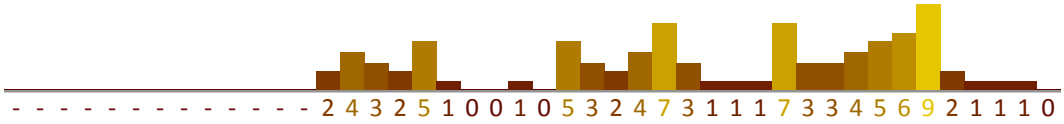
Consensus

```
K - P + T L D R A E G R Q L R G F Q G + R S L R T F V E A T K D D D D S E E A R A I G V

Prm_Prm_74387/1-676      79 - - - - - - - - - - - - - T D A V K K M A Q A A K N K L T S N N Q A T T N K L F K K L Q  109
Prm_Prm_79108/1-468      78 - - - - - - - - - - - - - N E F A K K M I Q A A K N K L T S N N Q A T T N K L F K S L Q  108
Prm_Prm_79110/1-588      79 - - - - - - - - - - - - - N E F A K K M I Q A A K N K L T S N N Q A T T N K L F K S L Q  109
Prm_Prm_79107/1-433      78 - - - - - - - - - - - - - N E F A K K M A Q A A K N K L T S N N Q A T T N K L F K N L Q  108
Pin_PITG_14884T0/1-604   80 K L S A A T V I Q K L I N S Q P T K K L S T R A M E I L T S N N Q R A T D K L F A S L G  123
```

```
Prm_Prm_85872/1-585      78 - - - - - - - - - - - - - T D A V K K M A Q A A K N K L T S N N Q A T T D K L F K K L Q 108
Pca_102742/1-501         45 - - - - - - - - - - - - - D N W K K - - - - - L S L L V K V G S R T K A D K L Y A K H V  70
Pin_PITG_14880T0/1-296   80 K P S T A T V L Q K L I N S Q P T K K R L T R V M G I F T S N N Q R A T D K L F A S L G 123
Prm_Prm_86912/1-294      78 - - - - - - - - - - - - - T D A V K K M A Q A A K N K L T S N N Q A T T D K L F K K L Q 108
Pso_285707/1-589         76 - - - - - - - - - - - - - P E L N S - - - - - M L K I V R P D K Q D K A K N L F V R L K 101
Pin_PITG_13847T0/1-512   54 - - - - - - - - - - - - - A D P P K S L A N R Q L N T I A T D S K E D E D R V - - - - -  79
Prm_Prm_79119/1-666      78 - - - - - - - - - - - - - N E F A K K M A Q A A K N K L T S N N Q A T T D K L F K N L Q 108
Pso_285703/1-570         71 - - - - - - - - - - - - - E G I T K - - - - - L A K M L S P N K Q E A A D K L F I N L K  96
Prm_Prm_74367/1-380      71 - - - - - - - - - - - - - I D A M K Q A A R A A K K K F Y - - - Q T A T D K L F K K V K  98
```

Conservation



```
- - - - - - - - - - - - - 2 4 3 2 5 1 0 0 1 0 5 3 2 4 7 3 1 1 1 7 3 3 4 5 6 9 2 1 1 1 0
```

Quality

Consensus

```
K - S - A T V L Q K L I N N + + A K K M A Q A A K N K L T S N N Q A T T D K L F K K L Q
```

```
Prm_Prm_74387/1-676     110 V G E I D D K L F Q S T Q F K E W V T T V T K N F K T N T E L A Q A S I A S A L V S H F 153
Prm_Prm_79108/1-468     109 V E G T G D K L F Q S A Q F E K W A T T V A K N F K K N P E K A P T S M F S T L A N H Y 152
Prm_Prm_79110/1-588     110 V E G T G D K L F Q S A Q F E K W A T T V A K N F K K N P E K A P T S M F S T L A N H Y 153
Prm_Prm_79107/1-433     109 V E K T G K E L F Q S A Q F E K W A T T V A K N F K K N P E Q A P T S M A S A L V G H Y 152
Pin_PITG_14884T0/1-604  124 V W E V E S K L F A S T P Y Q K W A A S V M K S Y K K N P E K G Q A A I F S T L V R H H 167
Prm_Prm_85872/1-585     109 V G G T D D K L F Q S T Q F K E W V T T V T K N F K T N T E L A Q A S M V S A L V S H F 152
Pca_102742/1-501         71 V G K I T G N F F D T N A F A A W F V A V Q M A Y A K T P A K A K V D M V S S L T A R Y 114
Pin_PITG_14880T0/1-296  124 V W K V E S K L F A S T P Y Q K W A A S V M K S Y K K N P E K G Q A A I F S T L V R H H 167
Prm_Prm_86912/1-294     109 V G G T D D K L F Q S T Q F K E W V T T V T K N F K T N T E L A Q A S M A S A L V S H F 152
Pso_285707/1-589        102 L H E S T S N L F G N P K F Q E W M R S V E K S Y K K T P E A A D A A M V L T M T T Q F 145
Pin_PITG_13847T0/1-512   80 - - - - - - - - - - - - - - - - - - - - - - - N F G I N K - - - - - - - - - - - I K D F  89
Prm_Prm_79119/1-666     109 V E G T G D K L F Q S T Q F E K W A T T V A K N F K K T P E K V P T S M A S A L V S H Y 152
Pso_285703/1-570         97 L Q K E A P D L F G S P K F Q T W M K S I Q K S Y K K T P E A A D A A M V V T L R G Q W 140
Prm_Prm_74367/1-380      99 I K E M D G T L F Q S E Q F K L W E T R V T K N F K Q N T E R A Q A S M V S T L T S R F 142
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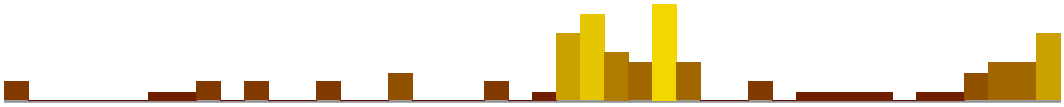
Conservation



```
2 0 0 0 0 0 1 1 2 0 2 0 0 2 0 0 3 0 0 0 2 0 1 7 9 5 4 + 4 0 0 2 0 1 1 1 1 0 1 1 3 4 4 7
```

Quality

Consensus

```
V + G T + D K L F Q S T Q F + K W A T T V + K N F K K N P E K A Q A S M V S T L V S H F
```

```
Prm_Prm_74387/1-676     154 G D E A L A T L L V A A K Q N Y K S A T V A T K L E N A Q L R N W E S A G K T G D D V F 197
Prm_Prm_79108/1-468     153 G D E A L A A L L V T A K Q N Y Q S R T V A T K L E N A Q L Q N W E S A G K T G D D V F 196
Prm_Prm_79110/1-588     154 G D E A L A A L L V T A K Q N Y Q S R T V A T K L E N A Q L Q N W E S A G K T G D D V F 197
Prm_Prm_79107/1-433     153 G D E A L A A L L V T A K Q D L K S R I V A I Q L Q K A Q L Q N W E S A G K T G D D I F 196
Pin_PITG_14884T0/1-604  168 G D D I L A K L V S E A Q P T A A A I R T A K K I E S M Q I A N W V T N R K T E E D I Y 211
Prm_Prm_85872/1-585     153 G D E A - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 156
Pca_102742/1-501        115 G D Q A L A K M L A T T E D D K F I R - - - - E M K A I Q L D N W Q K D K R T V G S V Y 154
Pin_PITG_14880T0/1-296  168 G D D I L A K L V S E A Q P T A A A I R T A K K I E S M Q I A N W V T N R K T E E N I Y 211
Prm_Prm_86912/1-294     153 G D E A L A T L L V A A K Q N Y K S G A V A A K L E N A Q L R N W E S A G K T G D D V F 196
Pso_285707/1-589        146 G D D G L A K L L L L E K T S P D T K E M A T R L E G V Q F K N W I D S K Q T A T G A F 189
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Pin_PITG_13847T0/1-512   90  G A K K L Q K L - - - - - - - - - T E G V Q T K F Q Q Q Q L N R W E A E G K T S D G V F  124
Prm_Prm_79119/1-666     153  G D E A L A A L L V T A K Q N Y Q S R T V A T Q L E N G L L Q N W K S A G K T G D D V F  196
Pso_285703/1-570        141  G D E K L A K V L Q S A M G S S S T K A I A A R L E D V Q F K K W I G E G K T A D D A F  184
Prm_Prm_74367/1-380     143  G D E A L A V S L V T A K Q N S K S R P I A T D L E N A Q L Q N W E S A G K T G D D V F  186
```

Conservation

```
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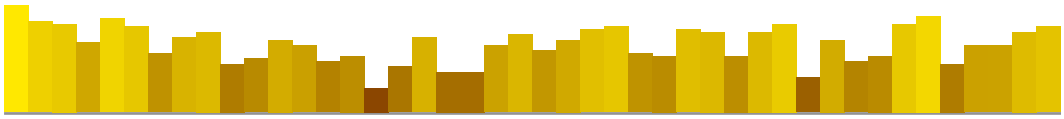
Quality



Consensus

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                         G D E A L A K L L V T A K Q N Y K S R T V A T K L E N A Q L Q N W E S A G K T G D D V F
```

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Prm_Prm_74387/1-676     198  D L L K L N D K G E K L F E S P V A A T W I S Y V T K L N T Q N S D E V I F S S L K K L  241
Prm_Prm_79108/1-468     197  D L L K L N D K G E K L F E S P V A A T W I S Y M T K L N A Q N S D E V I F S S L K K L  240
Prm_Prm_79110/1-588     198  D L L K L N D K G E K L F E S P V A A T W I S Y M T K L N A Q N S D E V I F S S L K K L  241
Prm_Prm_79107/1-433     197  K L L K L N G K G E N L F E T P L A P V W M S Y V T Q L N K E N P G E V I F S S L K K L  240
Pin_PITG_14884T0/1-604  212  K L L K L D A D K E G L L R N P L L N T W V S F V K K L D N E D P Y N L L L L K L T K T  255
Prm_Prm_85872/1-585          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_102742/1-501        155  K L L K L D K E Q D E L L Q S P L I A T W I A Y A T K L D N E D P L G A V F S T L K T Q  198
Pin_PITG_14880T0/1-296  212  K L L K L D A D E K G L L R N P L L N M W I S F V K K L G N E D P Y N L L L L K L R K P  255
Prm_Prm_86912/1-294     197  D L L K L N D K G E K L F E S P V A A T W I S Y V T K L N T Q N S D E V I F S S L K K L  240
Pso_285707/1-589        190  K L L K L D Q D A G D I L K N P L V S T W M S Y V - K L R K E S P I N E M L L Q L K T R  232
Pin_PITG_13847T0/1-512  125  K L L K L D A E G T N I L R S P E L S T W M A F V S K - Q G K D P Y D F L L F K L R R R  167
Prm_Prm_79119/1-666     197  E L L K L S D K G E K L F E T P L A P I W M S Y V T W L N K E N P G E V I F S S L K K L  240
Pso_285703/1-570        185  N L L K L D E K A N D L L K N P V V K T W V S Y V E K L D - V N P Y E L L L A K L E T H  227
Prm_Prm_74367/1-380     187  K L L K L N D K G E K L F E S P M A A T W L A Y L T K L N K K N P E E D M I S S L K R V  230
```

Conservation

```
                         1 2 2 4 2 2 0 2 0 0 0 2 1 1 2 2 2 0 1 0 0 3 1 2 2 1 1 1 2 0 0 0 2 1 0 0 0 1 1 0 1 2 1 1 0
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Quality

Consensus

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                         K L L K L + D K G E K L F E S P L A A T W I S Y V T K L N K E N P + E V I F S S L K K L
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Prm_Prm_74387/1-676     242  F D D E A L A K M I A G A K D S A S T A A T A T K L E Q V Q L N K W M V E G K T V D D I  285
Prm_Prm_79108/1-468     241  Y S D D V L A K M I G G A K N S A N V G A T A K K L E Q V L L S K W M S E G K T I D D I  284
Prm_Prm_79110/1-588     242  Y S D D V L A K M I G G A K N S A N V G A T A K K L E Q V L L S K W M S E G K T I D D I  285
Prm_Prm_79107/1-433     241  Y S N E V L A K M I V G A K N S A S T I V M A D K L E L L L L N R W L R E G K T V D D I  284
Pin_PITG_14884T0/1-604  256  N D E E A L A H M L I A A K G D S L T S S V V R N L E N A L L T A W L R D G K T T G D V  299
Prm_Prm_85872/1-585    157  - - - - - L A K M I A G A K T S A S T A A T A K K L E Q V Q L N K W I S E G K T A D D I  195
Pca_102742/1-501        199  Y N G K D F A T M L L N V K D T D D S F V V A E K L E T L L M K S W Q R E D K S V V D V  242
Pin_PITG_14880T0/1-296  256  N D E E A L A H M L I A A K D N S L T S G V A R N L E S A M L T I W L R D - - - - - - -  292
Prm_Prm_86912/1-294     241  F D D E A L A K M I A G A K N S A S T T A T A T K L E Q V Q L N K W M T E G K T V D D I  284
Pso_285707/1-589        233  Y G D G A L A R M L G L A K Q D S S T S S I A G Q L E E A L V K G W L N K R K T D D Y V  276
Pin_PITG_13847T0/1-512  168  Y D D V D L A K M L V L S K N D A N S K A I A E K L E T L Q L E K W M T D K K S I I D V  211
Prm_Prm_79119/1-666     241  Y S D E V L A K M I V G A K N S A N V G A T A N K L E Y L Q L N K W L S E G K T I D D I  284
Pso_285703/1-570        228  H T A A G L A R T L L V A R Q D Y T T R S I A G K L Q E A Q L E R W S R K K R S A D Y I  271
Prm_Prm_74367/1-380     231  Y D D E A L A K V I T G A Q N S A S T V V L A N T L E R A L M G K W L D E G K T L D E I  274
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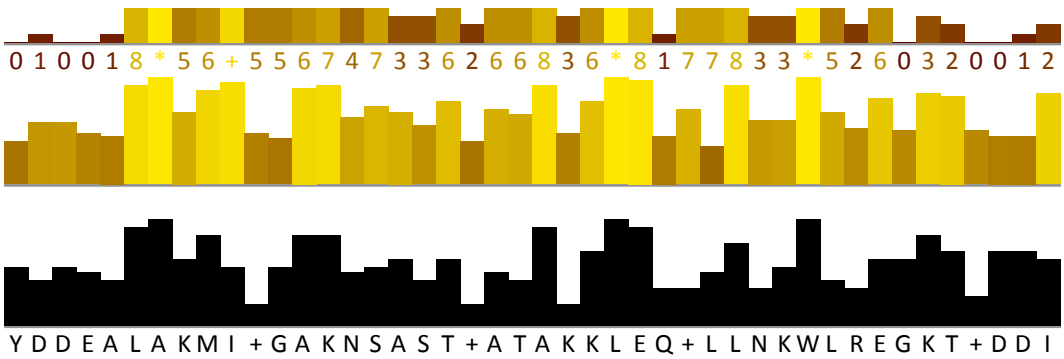
Conservation

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Prm_Prm_74387/1-676      286 F A L L K L N - N E E G K L L Q N T M L T T W M S Y V N L Q - G K N P Y D M I - L V K L 326
Prm_Prm_79108/1-468      285 F K L F K L N - K E G E K L L Q S P M F D T W V S Y - - - - - - - - - - - - - - - - - 309
Prm_Prm_79110/1-588      286 F K L F K L N - K E G E K L L Q S P M L R T W I S Y V D F Q - G K N P Y D L L - L V K L 326
Prm_Prm_79107/1-433      285 F T L L K L N - K D G E K L L Q S P M L R T W I S Y V R W Q - S K D P Y G M I - L V K L 325
Pin_PITG_14884T0/1-604   300 A K L L R L N A D K G E S F L R S A A L P T W L S Y I R Q R - N K D P N K V L - F L E L 341
Prm_Prm_85872/1-585      196 F A L L K L N - N E E G K L L Q N T M L A T W I S Y V N L Q - G K N P Y D M I - L V K L 236
Pca_102742/1-501         243 Y K L L N L D - N E G D L F F Q H P L I D T L I R Y A T V V D K K D S F S G V - F S L L 284
Pin_PITG_14880T0/1-296       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294      285 F A L L K L N - K D G - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 294
Pso_285707/1-589         277 F R L L R L N - R K G A D P F E S P V W N T W V L Y V T K - - H E R P Y E S M - L S V L 316
Pin_PITG_13847T0/1-512   212 F R L L K L N - E E G V T L L K S P M L S I W V S Y A E K L - N K D P Y E L L F L A I K 253
Prm_Prm_79119/1-666      285 F K L F K L N - K E G E K L L Q S P M L R T W I S Y V D L Q - G K N P Y D L L - L V K L 325
Pso_285703/1-570         272 F K L L Q L D - K E G D K L F K N P V L G T W E S Y V T K L D E K N A N E A M - L A V L 313
Prm_Prm_74367/1-380      275 F T L L T L E - T K S - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 284
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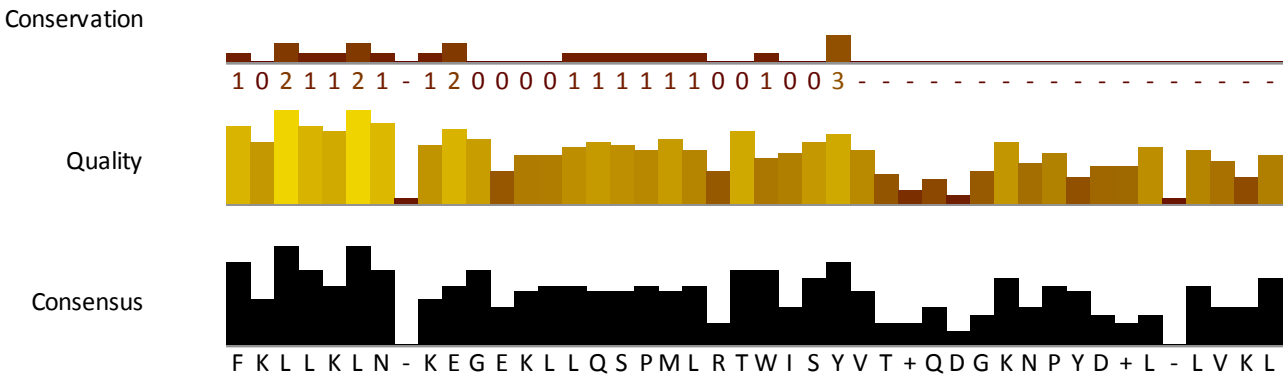


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Prm_Prm_79108/1-468          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_79110/1-588      327 S A H Y D E A G L A K M L V V A K E D G K T P F I A R K L E E V Q L K N W Q - - - - - - 364
Prm_Prm_79107/1-433      326 L T Y Y D E P S L A K I L I A A Q Q D D K T S R L A R K L E E V L L I N W R - - - - - - 363
Pin_PITG_14884T0/1-604   342 Q N R F S D A E L A R V L V A A S R D K N V K I N V T A L Q K L Q L S K W H - - - - - - 379
Prm_Prm_85872/1-585      237 S T H Y D E A G L A K M L V T A K Q D G T A S S I V R K L E E V Q F K N W Q S D G K S A 280
Pca_102742/1-501         285 Q A R Y N E E K M T D M F M T M R D W W P R N I L T D Q L E D L L L K T W Q - - - - - - 322
Pin_PITG_14880T0/1-296       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589         317 K T H Y S E L E I S R M L A A A T G S E S T R G V A T R L A K V R L T S E T - - - - - - 354
Pin_PITG_13847T0/1-512   254 S T S F D E A K L A K M I G S A K G D I Q T G F I A K K M E Q L Q L D K W S - - - - - - 291
Prm_Prm_79119/1-666      326 S A H Y D E T G L A K M L V A A K E D G K T H F I A R K L E E V Q F K N W Q S D G K S A 369
Pso_285703/1-570         314 K I H Y S D E K I G P M F T V A K T S G S A S S V A A R L E H P L L K A W A - - - - - - 351
Prm_Prm_74367/1-380          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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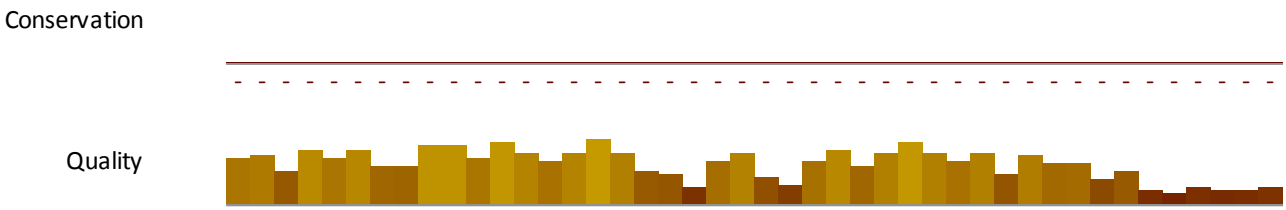

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Consensus
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Prm_Prm_74387/1-676      371 D D V Y N L L K L N L E R G D I L K S P M L T T W I S Y T A K L D E N P Y Q L L L A L L  414
Prm_Prm_79108/1-468          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_79110/1-588          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_79107/1-433          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_14884T0/1-604       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_85872/1-585      281 D D V Y N L L K L N L E R G D I L K S P M L T T W I S Y T A K L D E N P Y Q L L L V K L  324
Pca_102742/1-501             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_14880T0/1-296       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_13847T0/1-512       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_79119/1-666      370 D N V Y N L L K L N L D G D D I L K N P M L T T W I S Y T T K L D E N P Y E L L L A N L  413
Pso_285703/1-570             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_74367/1-380          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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

Quality

Consensus
                             D D V Y N L L K L N L E R G D I L K S P M L T T W I S Y T A K L D E N P Y Q L L L A - L

Prm_Prm_74387/1-676      415 M K Q Y D D A T L T K M F V A A K R G R A T E S I G T K L E E V Q L K S W L S D G K T A  458
Prm_Prm_79108/1-468          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_79110/1-588      365 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - S G G K T P  370
Prm_Prm_79107/1-433      364 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - S D G K T A  369
Pin_PITG_14884T0/1-604   380 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - G R G D T A  385
Prm_Prm_85872/1-585      325 M K R Y D D A T L T K M F V A A K R G R A T K S I S T K L E E V Q L K S W L S D G K T A  368
Pca_102742/1-501         323 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - R Q E K T M  328
Pin_PITG_14880T0/1-296       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589         355 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - V N G G E S A  361
Pin_PITG_13847T0/1-512   292 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - A A G K S G  297
Prm_Prm_79119/1-666      414 L K H Y D D A T L T K M F V A A K R S S A T G F T G T K L G E V Q L K N W L S S G K T A  457
Pso_285703/1-570         352 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - N D G K D A  357
Prm_Prm_74367/1-380          - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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

Quality

Consensus
                             M K - Y D D A T L T K M F V A A K R G R A T - S I G T K L E E V Q L K S W L S D G K T A

Prm_Prm_74387/1-676      459 D D V E K L L Q L N K D G D T L E A S S V W S V W S S Y L T K L D K E N V D E L M E V V  502
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Prm_Prm_79108/1-468        310 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - F M -  311
Prm_Prm_79110/1-588        371 G G I F K L L K L D K E G D D I L A S P V L N T W S S Y L A S L N K G N P D E L M F M K  414
Prm_Prm_79107/1-433        370 D D V F K L L L S N K D G G N V L E N P M L R V W M A Y L T K L D K E N A D K L M F V V  413
Pin_PITG_14884T0/1-604     386 D D I F R H L G L S K E G E E L L E S S V F N T W V S Y V K L V D Y T N T D A L V F S V  429
Prm_Prm_85872/1-585        369 D D V F K L L Q L N K D G D T I F A S S V W S V W S S Y L T K L D K E N A D E L M F V V  412
Pca_102742/1-501           329 D D V F K L L K L E Q Q G D S L F S S K L L S T W V S Y V A K V E - T N P Y N V V F S K  371
Pin_PITG_14880T0/1-296         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589           362 A A A F Q R I K F D E N G E K L F H N - - - - - - A E F V A K A E - R Y G T K D T L Q V  398
Pin_PITG_13847T0/1-512     298 D D V F K S I G L D K E G G K L F E S P A W N T W V A Y L N M Q G - N N A D E I I F S V  340
Prm_Prm_79119/1-666        458 D D V F K L L Q L N K D G D T I L A S S I W S V W S S Y L T K L D K E N A D E L M F V V  501
Pso_285703/1-570           358 A D V F T L F R L D K E G D K L F E N P Q F A T W A Y D I S R Q G R E N P N K V M L S V  401
Prm_Prm_74367/1-380            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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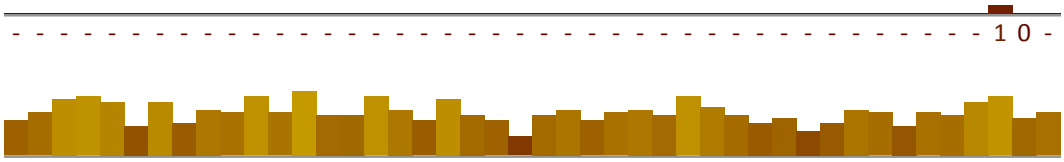
Conservation



Quality

Consensus

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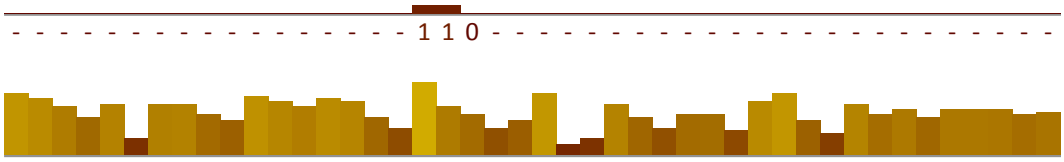
                           D D V F K L L + L + K + G D + L F + S + V W S T W S S Y L T K L D K E N A D E L M F + V

Prm_Prm_74387/1-676        503 L K K H Y G G D E G V A K M V T I A N K E A S - - T K D I G R K L K E E L W R S Q G K D  544
Prm_Prm_79108/1-468        312 - - - - - - - - - - - - - - - - - L K S S A S - - T P S - - - K L Q E E I W R N Q G K T  333
Prm_Prm_79110/1-588        415 L Q E Q Y - G E A G L T S M I A K A K T S A S - - T Q S I A V K L Q E E I W R S Q G K T  455
Prm_Prm_79107/1-433        414 L K K H Y G G D E G V A K M V T A A N K - - - - - - - - - - - - - - - - - - - - - - - -  433
Pin_PITG_14884T0/1-604     430 M K K H Y - S D E I L A K M I A Q A K T - - S V L T R A L A S K L A A E M W R S P G K S  470
Prm_Prm_85872/1-585        413 L K K H Y G G D E G V A K M V G V A N K E T S - - T K D I G R K L E E E L W R S Q G K D  454
Pca_102742/1-501           372 L K S T Y - G E E T L T S M I I Q A R D M P T - A D Y V G T E K V L F K D W V K A K Y T  413
Pin_PITG_14880T0/1-296         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589           399 L R A H Y - T D E R L A A I L N V A S Q A P S K R T K V V A I S L Q L Q L W Q D Q R R S  441
Pin_PITG_13847T0/1-512     341 L R K Q L - G D V G L T N A F A R A N G A N S R L T K D V A T R L E M D I W R M N G H T  383
Prm_Prm_79119/1-666        502 L K K H Y - G D E G V A K I V T V A N K G V S - - T K D V G R K L E E E L W R S Q G K D  542
Pso_285703/1-570           402 M K A H Y - S D E S L E K M M L K A T H L S N - - - S A I V S Q L R S E L W L S Q G K T  441
Prm_Prm_74367/1-380            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

Conservation



Quality

Consensus

```
                           L K K H Y G G D E G L A K M V + V A N K + A S - L T K D I A R K L + E E L W R S Q G K T

Prm_Prm_74387/1-676        545 G D D V F K L L K L D E E G Q K F F E S P A L S T W V S Y V S - - - K L N K Q N P G - -  583
Prm_Prm_79108/1-468        334 A D D I F K L L K L R N S G K K M F S T V D L R T W I S Y V T R L N Q F S K - K P D E F  376
Prm_Prm_79110/1-588        456 A E D V F M L L K L R K S G V N I V D A A G L S T W V S Y V T K L N K L S K - N P D E F  498
Prm_Prm_79107/1-433            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_14884T0/1-604     471 A D D I F K F F Q L D K T G D D L F E A P M F D A W I L Y V E R L N K Y E K - H P D K F  513
Prm_Prm_85872/1-585        455 G D D I F K L L K L D E E G Q T F F E S P A L S T W V S Y V T K L N K L N K Q N P G - -  496
```

```
Pca_102742/1-501          414 V R D A F V H L K L K A E G E E V F E S T A F S T W M A Y A K E L E R T N A - - - - D E 453
Pin_PITG_14880T0/1-296    293 - - - - - - - - - - - - - - - - - - - - - - - - D I W A - - - - - - - - - - - - - - - - 296
Prm_Prm_86912/1-294           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589          442 A D E V F K L L K L E Q A G G S V L R S P F L E T W V L Y A E K L G R V D K - K V G E F 484
Pin_PITG_13847T0/1-512    384 S D D M F K I L K L N E K G D K V F E S P G F T T W V A Y V L K L D G Y K K - T P D E F 426
Prm_Prm_79119/1-666       543 G N D I F K L L K L D E E G Q K F F E S P A L R T W I S Y V T R L N K F N K K S P D - - 584
Pso_285703/1-570          442 V D K A F Q L F K L D E A G K N F L E D P G L G S W V S Y V T T L S K A K K - - S D E F 483
Prm_Prm_74367/1-380       285 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - K V N T N T P D - - 292
```

Conservation

- 0 0 3 1 - - - - - - - 0 0 1 0 - - - - - -

Quality

Consensus

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

```
Prm_Prm_74387/1-676       584 - A I S Q L E K R F G G D I E L A R M I G F A K Q Q A A N A V T E - - - - K V I T Q L Q 622
Prm_Prm_79108/1-468       377 I V I L E L E K Q F - T G A G L A R M L A D A K Y Q A S L I K A E G A E - T L A G K L Q 418
Prm_Prm_79110/1-588       499 V V I S E L E K Q L - T S M T L A R M L A E K I N K I S L T N A E G A A G S V A G K L E 541
Prm_Prm_79107/1-433           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_14884T0/1-604    514 A L F T E L E K R F - D Y V D L A R M L S H A K I Q A E M K G H S V - - - E R L F S L R 553
Prm_Prm_85872/1-585       497 - A I S Q L E K R F G G D I E V A R M I G F A K L K A S N A V T E - - - - K V V T Q L Q 535
Pca_102742/1-501          454 A V L T V L K E R F - G D A E L P R I I A K A K A P I A W D P E D - - - - D I A L V L E 492
Pin_PITG_14880T0/1-296        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589          485 A A I A V L E R R F - G G V E F A K M L S A A K S D G A L K A S - - - - - S V I D Q L Q 522
Pin_PITG_13847T0/1-512    427 A P I R Q L E R H F - G D A T L A R M L A N S K R R A S S A K T K - - - - E Y I K D L Q 465
Prm_Prm_79119/1-666       585 - A I S Q L E K R F - G E M E L A R M I G V A K E K V T T E A T E - - - - K V I A Q L Q 622
Pso_285703/1-570          484 A A I S F L A D R F - R D F E L A K M L S A A K I K N S G G N N - - - - - R V I E E L Q 521
Prm_Prm_74367/1-380       293 - A I S Q L E K R F G S S I K L A K V I A Y A K K R A I T E A T K - - - - A D A T R L Q 331
```

Conservation

- 0 1 0 0 2 0 2 1 1 - 0 0 1 0 1 1 3 1 2 2 0 0 1 0 0 0 0 0 0 0 0 0 - - - - - 0 0 1 0 0 2 1

Quality

Consensus

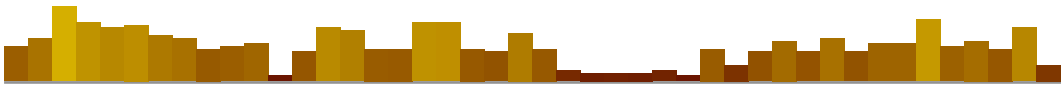
A A I S Q L E K R F G G D + E L A R M L A + A K I K A S L A A T E G A - - K V I T Q L Q

```
Prm_Prm_74387/1-676       623 N L Q F K Q W L G D G - R T L N T I S D K M V S D T M V S A L F D T R N T K V I L D Y S 665
Prm_Prm_79108/1-468       419 A L Q F K K W L K Q G - V T P D S I T K E F T F - - - - - V L I D S T D V K I L L A Y S 456
Prm_Prm_79110/1-588       542 A L Q F K K W L K Q G - A T P N S I A A T F T F - - - - - A - - - R T D L R I S V A Y N 576
Prm_Prm_79107/1-433           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_14884T0/1-604    554 N Q Q F D Q W M N Q K R L D P G R V A A L V A E - - - - - Q P R D I R N N G V V L G F Y 592
Prm_Prm_85872/1-585       536 N L Q F K Q W L A A G - I T P E R V S T K M L L - - - - - T P F D T R N T K V V L D F Y 573
Pca_102742/1-501          493 R L Q - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 495
Pin_PITG_14880T0/1-296        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589          523 K L Q F K K W F K A G - E A P K S V S E K V I N R Q D P - R G L D L R G S D V A Y G Y Q 564
Pin_PITG_13847T0/1-512    466 D W Q F E K W V V E E - T S P N V L S Q L L R K - - - - - K L L G V - - D R V R S D F R 501
Prm_Prm_79119/1-666       623 D L Q F K Q W L A A R - M T P R G L S D K M E L - - - - - T G F D E R N A K V V L D Y V 660
```

```
Pso_285703/1-570      522 T L Q F K K W W E D G - V T P R D I S D M V T - - - - - - K H F D T R G T G V V L G Y H 558
Prm_Prm_74367/1-380   332 D L Q F K Q W L A A G - V T P N N I G T R V M G - - - - - D V F D I R R T Q V S I D Y G 369
```

Conservation

Quality



Consensus

```
+ L Q F K + W L + A G - V T P N S I S D K V T + - - - - - + L F D T R N T K V V L D Y +
```

```
Prm_Prm_74387/1-676   666 D F L K A - - - - - - - - - - - - - - - S A A R T G 676
Prm_Prm_79108/1-468   457 E Y Y T L - - - - - - - - - - - - - - N V G K V N A 468
Prm_Prm_79110/1-588   577 D Y Y K L - - - - - - - - - - - - - - N F G K V T A 588
Prm_Prm_79107/1-433       - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_14884T0/1-604 593 D F Y K A - - - - - - - - - - - - - - N G G S P L Y 604
Prm_Prm_85872/1-585   574 D F Y K T - - - - - - - - - - - - - - I R L S R V I 585
Pca_102742/1-501      496 - - - - - - - - - - - - - - - - - - - K L L S E N 501
Pin_PITG_14880T0/1-296    - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86912/1-294       - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285707/1-589      565 D F Y K A I V A R G G L K D K T R L D S I I E R V 589
Pin_PITG_13847T0/1-512 502 N F L K H - - - - - - - - - - - - - - N P E L S G 512
Prm_Prm_79119/1-666   661 D F V R L - - - - - - - - - - - - - - - - - - - H 666
Pso_285703/1-570      559 D F Y K A - - - - - - - - - - - - - - K P V V D P L 570
Prm_Prm_74367/1-380   370 T F Y R N - - - - - - - - - - - - - - K L A A A T 380
```

Conservation

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

Ortholog 3

```
Prm_Prm_77763/1-152      1 M R L S Y V L L V A - T A T T L L A S G N A L P A - - A T S A D Q A T A I S S T G S S T  41
Prm_Prm_85589/1-159      1 M R L S Y V L L V A - T A T T L L A N G N A L P A - - A T S A D Q A T A I S S T W S S T  41
Pso_354880/1-125         1 M R L S S T T F V V - L A A V L L A S G T A V S K - - A D E T G - V T N V N A V H S P N  40
Prm_Prm_77786/1-157      1 M R L S Y V L L V A - T A T T L L A N G N A L P A - - A T S A D Q A T A I S S T G S S T  41
Pso_286631/1-140         1 M C M S F A L L V A - A A T I L L - - - - - - - - - - - - T T N H A T G V S A L E S T N  31
Pca_13937/1-146          1 M R L S F V V L P A V I A V T F A S S G N A V - - - - A T A D G R N T G L S A I T P P N  40
Pca_13936/1-141          1 M R L S Y V V I P A A I A V T F A S S G N A L - - - - A A A D G S N T G L S A I T S P N  40
Pin_PITG_06290T0/1-160   1 M R K T F L L L I V - - - - T L L G N G S T I S - - - A T T T G N Q A A I S T L E S P V  37
Pca_13953/1-136          1 M R L S Y T L L - - - I I A V F V S S G N A V - - - - A T T N G R T T E L S A M A S P N  37
Prm_Prm_83582/1-154      1 M R L S Y V L L V A - T A T T L L A S G N A L S A - - A T N A D Q T A D I S A M G S P D  41
Pin_PITG_06305T0/1-91    1 M R K A F F P L I V - - - - T L L G N G S A M P A I S A T T T G N Q A T I S T L E S P V  40
Prm_Prm_77765/1-141      1 M R I S Y I L L V A - T A A T L L A S G N A - - - - - A T A S G P T T G D S I M A S P D  38
Prm_Prm_74178/1-144      1 M R F N Y F I L F A - - A A T L F A S C D V V C A - - - - - D V D Q T K L S K M T S P D  37
```

Conservation

```
* 5 5 7 5 4 5 8 0 2 - 0 1 1 6 8 6 2 2 2 2 1 1 - - - - 3 1 0 5 4 0 5 7 3 4 9 3 6 2 7 7 5
```

Quality

Consensus

```
M R L S Y V L L V A - T A T T L L A S G N A L P A - - A T T + G Q A T + I S A M + S P N
```

```
Prm_Prm_77763/1-152      42 E - - - - - - - L I T S H E I D N G A G N D K R F L R S H R V E K E D D D S K E D D D D  78
Prm_Prm_85589/1-159      42 G S S T G S S V L I T S H E I G N G T G N E K R F L R S H R V Q E D D D D S N E D D E D  85
Pso_354880/1-125         41 - - - - - - - - V L A - - - - - - - - G V D K R F L R S H H T E D G E - - - - - - - A K  61
Prm_Prm_77786/1-157      42 G S S T G S S V L I T S H E I G N G A G N E K R F L R S H R V Q E D D D D S N D - - D D  83
Pso_286631/1-140         32 - - - - - - - - L A R S L Q V N E H V G N E T R S L R I H E L E N E D E N D E E - - E E  65
Pca_13937/1-146          41 - - - - - - - - V V A S - - I D T A V G G E K R S L R Y H N N K D L E D D S D D - - - -  70
Pca_13936/1-141          41 - - - - - - - - V V A S - - I D T A V G G E K R S L R Y H T N E D L E D D S D D - - - -  70
Pin_PITG_06290T0/1-160   38 - - - - - - - - L L T H - - - - - - - D T Q K R F L R S H S E A E E G - - - - - - - S E  59
Pca_13953/1-136          38 - - - - - - - - A V A S - - V D T A V G G E K R S L R Y H N N E G L E D E S D D - - - -  67
Prm_Prm_83582/1-154      42 - - - - - - - - L V T S L E I G N G A G D E K R F L R S H R A E E D D D D S N E - - - -  73
Pin_PITG_06305T0/1-91    41 - - - - - - - - L L A S - - - - - - - D T Q K R F L R S H N Q A E E D - - - - - - - S E  62
Prm_Prm_77765/1-141      39 - - - - - - - - L V V S L G T A Q D V G G E T R F L R K H K - - - - D E V S E E - - - E  67
Prm_Prm_74178/1-144      38 - - - - - - - - A A G L S V H A I G A A N E K R R L R S H Y D E D E D E D E D E - - - D  70
```

Conservation

```
- - - - - - - - 7 7 3 0 - - 0 1 0 0 1 5 4 7 6 * 3 * * 2 * 3 0 0 0 0 4 3 0 1 1 3 - - - -
```

Quality

Consensus

```
G S S T G S S V L V + S + E I D N G V G N E K R F L R S H R + E E E D D D S D E D D + +
```

```
Prm_Prm_77763/1-152      79 D D D E E E E E E R K K G P G F F D S Q R L E K M L G N R I Y R S K W F N K W K N S G Y  122
Prm_Prm_85589/1-159      86 D S D E E E E E E R N K G P G F F D S Q R L E K M L N N R I Y R S K W F N K W K N S G Y  129
Pso_354880/1-125         62 L S N Y D N E E R N - - - - G L F G A N T L S N M G K D T I L R F Q M F T K W K A N G Y  101
Prm_Prm_77786/1-157      84 D D E E G E E E E R A G G A N L F K T S K L N E M L S G - I K E F K R Y K K L K A Y G Y  126
Pso_286631/1-140         66 N E G D G E E E E R A G G A N L F A E S K L K Q M M S G - V K L F K R F K N W K A Y G L  108
Pca_13937/1-146          71 E G L E D A E E E E R R G N N M F S A T K L D E M L D G - K Q V M S R F K K W K A F G Y  113
Pca_13936/1-141          71 E G L D D A E E E E R R G N N M F S T T K L D E M L D G - T Q L M S R F K K W Q F L K Y  113
```

```
Pin_PITG_06290T0/1-160   60 E D E F G N A E E R K V G A N L F A D S K L A Q M L N S - R K T F P R F A R W K R E G F 102
Pca_13953/1-136          68 E A L - - L E E E E R K Y T N M F S T T K L D E M L N G - T K M M S R F R K W K A R G Y 108
Prm_Prm_83582/1-154      74 N E N E N E E E E R A G G A N L F T T S K L N E M L S G - V K T F D R F A R W K R D G W 116
Pin_PITG_06305T0/1-91    63 E D E F G N G E E R K V G D R L F A D W K L E Q M L N S - - - - - - - - - - - - - - - - 90
Prm_Prm_77765/1-141      68 D D D D E E E E E R K K G P G F F D S Q R L E K M L G N R I Y R S K W F N R W K D G G Y 111
Prm_Prm_74178/1-144      71 E D E D E D E E E R I K G V D L F K E W K L D Q M L S G - I K E F K R Y K N L K A Y G Y 113
```

Conservation

```
4 4 3 0 0 3 4 * 8 6 0 0 1 1 3 8 * 3 4 6 6 * 3 5 * 7 3 5 - 0 0 0 0 0 0 2 0 1 1 1 0 0 1 1
```

Quality

Consensus

```
E D E E + E E E E R K K G A N L F + T S K L + E M L + G R I K R F K R F K K W K A Y G Y

Prm_Prm_77763/1-152      123 T P G N V E S E M G N K - L Y Q K Y R - I W Y Y Y G P G A R R - - - - - - - - - - - - - 151
Prm_Prm_85589/1-159      130 T P G N V E S E M G N K - L Y Q K Y R - T W Y Y Y G P G A R R - - - - - - - - - - - - - 158
Pso_354880/1-125         102 L P K K I K D D I P R S - - - - - - - - L Y K A Y K I H Y R M - - - - - - - - - - - - - 124
Prm_Prm_77786/1-157      127 T P I K F Q T K L E K M - Y G N K Y K D L W E R Y S A N F Y S - - - - - - - - - - - - - 156
Pso_286631/1-140         109 S P G D V S I R L E N A G K W D D Y K E L Y F T Y Q K Y Y S T - - - - - - - - - - - - - 139
Pca_13937/1-146          114 N T Y N L P D A I Q A - - - - R K Y D E L R K M Y R K F L Y Y - - - - - - - - - - - - - 140
Pca_13936/1-141          114 N M Y N L P D T I L A - - - - S K Y D E L R K M Y R R F L Y Y - - - - - - - - - - - - - 140
Pin_PITG_06290T0/1-160   103 I P S T L R T K L E K L G L W T K Y S G L H T M Y S N N Y Y V H H R E G Q T V K V R V D 146
Pca_13953/1-136          109 N T Y N L P A V T Q K - - - - D K Y T W I R Q K Y R D F L Y H - - - - - - - - - - - - - 135
Prm_Prm_83582/1-154      117 I P T A I F N K F G T K - - - S K Y K E L A S M Y N R N Y D T I R - - - - - - - - - - - 146
Pin_PITG_06305T0/1-91        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_77765/1-141      112 T P I N V Q N N M G N E - L Y Q K Y K - H W Y Y H G P G A L R - - - - - - - - - - - - - 140
Prm_Prm_74178/1-144      114 T P S S L Q T K L T R L - Y G K K Y K D L W E R Y S A N Y Y T - - - - - - - - - - - - - 143
```

Conservation

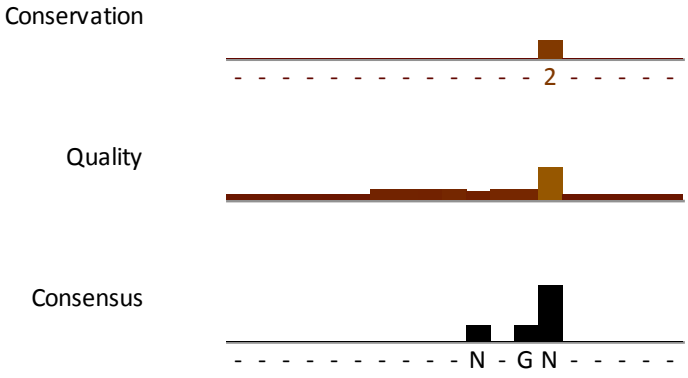
```
0 0 0 0 1 0 0 0 0 0 0 - - - - 1 2 3 1 - 0 0 0 0 3 0 0 0 1 0 0 - - - - - - - - - - - - -
```

Quality

Consensus

```
T P + N L + + K L G N K G L Y Q K Y K E L W + M Y + P N Y Y + - - - - - - - - - - - - -

Prm_Prm_77763/1-152      152 - - - - - - - - - - - - - N - - - - - 152
Prm_Prm_85589/1-159      159 - - - - - - - - - - - - - N - - - - - 159
Pso_354880/1-125         125 - - - - - - - - - - - - - N - - - - - 125
Prm_Prm_77786/1-157      157 - - - - - - - - - - - - - I - - - - - 157
Pso_286631/1-140         140 - - - - - - - - - - - - - I - - - - - 140
Pca_13937/1-146          141 - - - - - - - - - - - - - N Y R K K K 146
Pca_13936/1-141          141 - - - - - - - - - - - - - N - - - - - 141
Pin_PITG_06290T0/1-160   147 L A I I H S R R N T N G G S - - - - - 160
Pca_13953/1-136          136 - - - - - - - - - - - - - N - - - - - 136
Prm_Prm_83582/1-154      147 - - - - - - V K P V N A G R - - - - - 154
Pin_PITG_06305T0/1-91     91 - - - - - - - - - - - - - H - - - - -  91
Prm_Prm_77765/1-141      141 - - - - - - - - - - - - - N - - - - - 141
Prm_Prm_74178/1-144      144 - - - - - - - - - - - - - I - - - - - 144
```


Conservation
2
Quality
Consensus
N
G
N

Ortholog 4

```
Pin_PITG_15679T0/1-271      1 - - - - - - M K V L Q L I A L T A L V S S C V A A S A - - - A D P S G L A K T K S D V D  35
Pin_PITG_05841T0/1-220      1 - - - - - - M R V L Q L I Y V A A L V L R C A A V K T A T K S H T T S T V K I N S E A D  38
Pin_PITG_05846T0/1-263      1 - - - - - - M R V L Q L I C L V A L I S R C A A D T A T T N S H T A S T L K I N S D A D  38
Prm_Prm_73724/1-343         1 - - - - - - M R V L S L V A L I A F V S S C E A T S A V S N S D K V N V A K L D S G I A  38
Pca_14162/1-348             1 - - - - - - M R V L S L V T L L A F V S - - - A Q L I A A N A D Q T G I A A V D S N T A  35
Pin_PITG_06308T0/1-254      1 - - - - - - M Q T I Q L I I F V A F V L S R A A A S I S S F S D P T S I V N I N H D A N  38
Pin_PITG_11952T0/1-270      1 M S R Y S M M L L L R L A V L I T F G L S C A V A L A - - - T D S N N V V K S N P T I -  40
Pso_285308/1-314            1 - - - - - - M R F L F L L V A V A L A S A E A A E S A A M I H E E A G V S S F N T L T -  37
Pca_39353/1-267             1 - - - - - - M R V L S L V T L F T F V S - - - A Q L A A V N A D R T G I A A A D L N T A  35
Pso_286675/1-96             1 - - - - - - M R V L S L L T V I A L V S S C E A A T S A - - - - T T G V V K T D - - I T  32
Prm_Prm_86166/1-353         1 - - - - - - M R V L S L V A L I A L V S S C E A A S A V S N S D K V E V A K L D S G I A  38
Prm_Prm_73707/1-269         1 - - - - - - M R V L S L V A L I A L V S S C E A A S A V S N S D K V E V A K L D S G I A  38
```

Conservation

- - - - - - * 5 5 + 3 * 7 4 6 4 7 8 7 5 0 0 0 8 3 3 5 1 - - 0 2 2 6 4 6 5 4 4 5 0 0 5 1

Quality

Consensus

- - - - - - M R V L S L V A L I A L V S S C A A A S A A S N S D + T G V A K + D S + I A

```
Pin_PITG_15679T0/1-271     36 V L S R V L A - D H E Q T N R S L R R Y D L E G L D S V N - - - - - - - - - - - - - - -  63
Pin_PITG_05841T0/1-220     39 A V S R V L A T - - - Q A T R S L R Q I D Q E K L A E D D - - - - - - - - - - - - - - -  64
Pin_PITG_05846T0/1-263     39 A V S R V L A A D R R Q A T R S L R Q F D H D E L A G G D - - - - - - - - - - - - - - -  67
Prm_Prm_73724/1-343        39 S L P R A L A E H N D Q I K R S L R R H D - - - - - - - - - - - - - - - - - - - - - - -  59
Pca_14162/1-348            36 L L P R V L G V - - - E S K R T L R R Y D P S E F D S E E A V D S D E E A D P V E V A D  76
Pin_PITG_06308T0/1-254     39 R L S R A L A A G Q N Q T Q R S L R Q H E G E D R G A I D - - - - - - - - - - - - - - -  67
Pin_PITG_11952T0/1-270     41 - - - - - - - - K D T Q A L R F L R R Y A F D E E A N R D - - - - - - - - - - - - - - -  61
Pso_285308/1-314           38 - - - - - - - - G G N Q I Q R S L R V Y L - - - - - - - - - - - - - - - - - - - - - - -  50
Pca_39353/1-267            36 L L Q R V L G V - - - E S K R T L R R Y D P S E R D S E G D A D S D - - - - - - - - - -  66
Pso_286675/1-96            33 F L S R A L T A - E Y Q P K R S L R Q Y D E D E L A T L D - - - - - - - - - - - - - - -  60
Prm_Prm_86166/1-353        39 S L S R A L A E H N D Q I K R S L R R H D Y D E L A E V D - - - - - - - - - - - - - - -  67
Prm_Prm_73707/1-269        39 S L P R A L A E H N D Q I K R S L R R H D Y D E L A E V D - - - - - - - - - - - - - - -  67
```

Conservation

0 2 0 3 2 2 1 - - - - 8 4 4 * 5 * * 4 5 3 0 1 0 0 1 0 0 0 - - - - - - - - - - - - - - -

Quality

Consensus

S L S R + L A + H N D Q I K R S L R R Y D + D E L A + V D - - D S D - - - - - - - - - -

```
Pin_PITG_15679T0/1-271     64 - - - - - - S N R E E R N - - S I T M V D D V - - - V T K A S G L V D D V M G K T D D V  96
Pin_PITG_05841T0/1-220     65 - - - - - - D E D E E R G F S I S G P V E T I - - - V T - - - - - - - - - - - - - - -  83
Pin_PITG_05846T0/1-263     68 - - - - - - A E D Q E R G I S I S G P V E K M - - - V T - - - - - - - - - - - - - - -  86
Prm_Prm_73724/1-343        60 - - - - - - - - D E E R Q - Y G T Q L I D D V - - - I T - - - - - - - - - - - K V D D V  80
Pca_14162/1-348            77 S D E E V V S E G E E R V - - G I P G M E K V - - - A S K A T - - - - - - - - K A D D M 107
Pin_PITG_06308T0/1-254     68 - - - - - - - - - - - - - - - - - - - K A D E V - - - V S - - - - - - - - - - - K M K A L  79
Pin_PITG_11952T0/1-270     62 - - - - - - N E D Q E R G I G V S K Q L D D V - - - L L - - - - - - - - - - - K A D E V  85
Pso_285308/1-314           51 - - - - - - G A N E E R G - V G G V K L E N I - - - L T - - - - - - - - - - - - - - -  68
Pca_39353/1-267            67 - - - - - - D E D E E R I - I T I P G I E K I D D A V S K V T - - - - - - - - K T D D M  95
```

```
Pso_286675/1-96          61 - - - - - - S E D E E R A - G T S Q K M E E L - - - V E - - - - - - - - - - - - - - - - 78
Prm_Prm_86166/1-353      68 - - - - - - S G D G E R M - G G A Q L I D D V - - - I T - - - - - - - - - - - K V D D V 90
Prm_Prm_73707/1-269      68 - - - - - - S G N G E R M - G G A Q L I D D V - - - I T - - - - - - - - - - - K A D D V 90
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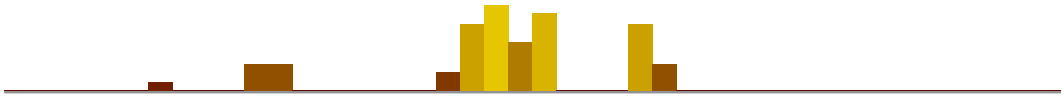
Conservation



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- - - - - - 1 0 0 0 3 3 0 - - 0 0 0 2 7 9 5 8 - - - 7 3 - - - - - - - - - - - - - - - -
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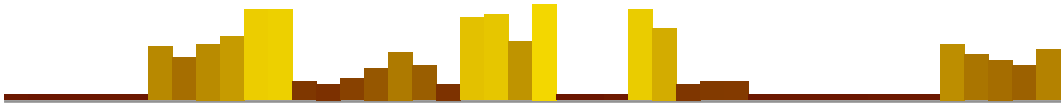
Quality



Consensus

```
- - - - - - S E D E E R G I G G S Q + I + D V - - - V T K A T - - - - - - - K A D D V
```

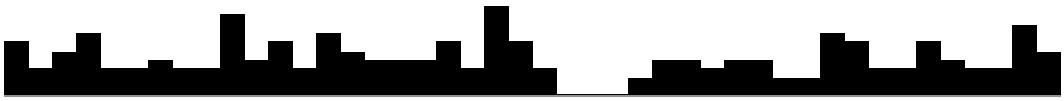
```
Pin_PITG_15679T0/1-271   97 V G K A G - Q F G K V P T K L R D V A T K N M D K I K E M T A R S A L V K T L T G R Y D 139
Pin_PITG_05841T0/1-220   84 - - - - - - - - - K A R T G L K S V L T K I S - - - - - - I E R V L L A S Q L S E R Y P 112
Pin_PITG_05846T0/1-263   87 - - - - - - - - - K F R D G L N A V L S K N P - - - - - V R L R A S L V E Q L S K T Y S 116
Prm_Prm_73724/1-343      81 V T K A T V A E Q K L P S K W T S A L K K F R - - - - - L A N P K T P M Q I V R A K Y P 119
Pca_14162/1-348         108 V P N A - - - - A K G A M K W K I L V Q K N M - - - G Q L V E T A K L V K K L K V G S F 144
Pin_PITG_06308T0/1-254   80 M G T A - - - - K N V P N N L A A L I A K R S K T A G E F V R R P F L V S K L S K R Y N 119
Pin_PITG_11952T0/1-270   86 I G I L - - - - K N V V R K V G G A L I K N S - - - R E T D E Y L R L T R A V S G K Y P 122
Pso_285308/1-314         69 - I F V Q R A K A K L P Q G F T A A A L G N W - - - - - - K G F S R R V D T V M E H Y P 105
Pca_39353/1-267          96 V S K A - - - - A K A S T K W K A L I Q K N I - - - N E L A E T G K L V K T L K A N V L 132
Pso_286675/1-96             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86166/1-353      91 V T K A T V A E Q K L P S K W T S A L K K F R - - - - - L A N P K T P M Q I V R A K Y P 129
Prm_Prm_73707/1-269      91 V M K A T V A E Q K L P S K W T S V L K K Y - - - - - - - - - - - - - - - - - - - - - 112
```

Conservation

```
- - - - - - - - - - 1 1 0 0 0 1 0 0 1 1 0 1 0 0 - - - - - 0 0 0 0 0 0 0 1 0 2 0 0 0 0 0
```

Quality

Consensus



```
V G K A T V A E + K L P + K W T + + L K K N S - - - G E L A E R + + L V K T L S A + Y P
```

```
Pin_PITG_15679T0/1-271  140 Y A - - - - E K L S L S A L K Q L D D I E K V R A V D I K K G I K G S K E T P D G M R R 179
Pin_PITG_05841T0/1-220  113 Y A - - - - Q G L S L S T L K Q L A T I E K L R K I D I E K G I K G S K L T P G S M R R 152
Pin_PITG_05846T0/1-263  117 Y A - - - - D K L S T S T L K Q L E H I E K L R A A D I K K G V K G S K A T P G G M R R 156
Prm_Prm_73724/1-343     120 - - - - - - K G L S S S T M R Q L V Q T E I Q R A D D I A N G V K M V K T G E Y K M Q R 157
Pca_14162/1-348         145 Y S N V E L E K M S L S A L R Q L D D I Q Q L Q K A D I K S N V F G T K A T A N G M R R 188
Pin_PITG_06308T0/1-254  120 I A - - - - D Q L S F S T L K Q L D K I D N M R I V D I K N G I K G N K K T P N G M R R 159
Pin_PITG_11952T0/1-270  123 T A - - - - K E L S L S T L R Q L K K I E A V R K K D I E K G I D V S K A A T D G I H R 162
Pso_285308/1-314        106 - - - - - - K G L S E K A I K E L R T A E T K R F T D Y A M - - - L G P S D K Y N L L R 140
Pca_39353/1-267         133 Y K D V E L E K M S L Q G L R Q L D D I E Q L R K V D I E N K V K G T K K T P D G M R R 176
Pso_286675/1-96             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86166/1-353     130 - - - - - - K G L S S S T M R Q L V Q T E I Q R A D D I A N G V K M V K T G E Y K M Q R 167
Prm_Prm_73707/1-269         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

Conservation

```
- - - - - - 1 0 1 3 0 1 1 1 3 1 2 0 1 0 1 0 0 1 1 0 4 1 0 0 - - - 1 1 0 0 1 0 0 0 1 0 3
```

Quality

```
Pin_PITG_15679T0/1-271     180 V I E P F E G M K V A P K K F L E S H V G R A D Q R Y G K D G S R L L S A N V V M R L N 223
Pin_PITG_05841T0/1-220     153 S M E K F P G M S T V P R Q F L E S H V G R E G Q R F G R D G S R L L S A G V V T R V N 196
Pin_PITG_05846T0/1-263     157 N V E P F P G M S T V P R K F L E S H V G R D G Q R F G K D G S R L L S A G V V T R F N 200
Prm_Prm_73724/1-343        158 Q I D E F P G M K N A P - - L L T S N T G R A E Q L L A D D G S R L L A C I V A S R S A 199
Pca_14162/1-348            189 K M T R T E N M K L P P E Q F L V S H V G R G A Q R L G E N G Q R L L S A A V I S K G D 232
Pin_PITG_06308T0/1-254     160 K I K H F E G M K T A P Q K F L E S H V G R D M Q R Y G K D G S R W L S A G V V T R T T 203
Pin_PITG_11952T0/1-270     163 D I K L F D G N K R V P D K Y M G A H V G R D Q Q R F T E A D T R S L V A G V V T R T N 206
Pso_285308/1-314           141 P M Q G V D E A M I A P N - - L V S L T G R K N Q V L G D A G G R S V V C N V V M R S E 182
Pca_39353/1-267            177 K M E H T A N M K L P P A Q F L E S H I G R D A Q L V G E S G Q R L L S A A V V S K G D 220
Pso_286675/1-96             79 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - K F G H L G F T T R G F 90
Prm_Prm_86166/1-353        168 Q I D E F P G M K N A P - - L L T S N T G R A D Q M L D G D N S R L L A C I V A S R S V 209
Prm_Prm_73707/1-269        113 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - S R L L A C I V A S R S V 125
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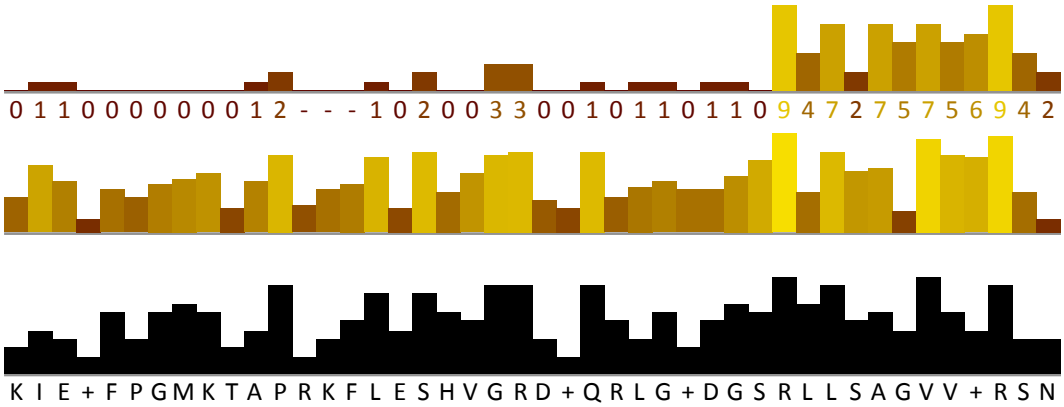


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Pin_PITG_15679T0/1-271     224 D K G E K Q I L L I S S S N P K K G D F L L P K G G W D K G E D V K - K A A L R E V I E 266
Pin_PITG_05841T0/1-220     197 E K G E H Q M L L I S S S N P K K S D F L - P L G - - - - - - - - - - - - - - - - - - 220
Pin_PITG_05846T0/1-263     201 D K G E R E M L M I S S S N P K K R E F L P P K G G W D K G E D I K - T A A L R E V I E 243
Prm_Prm_73724/1-343        200 E K G G G D V L L V S S S N A R K N D W L L P K G G W D K G E T V E - K A A M R E L I E 242
Pca_14162/1-348            233 D I N S K - V L L I S S S D T K K G D F L L P K G G W D H G E T I E - K A V L R E V I E 274
Pin_PITG_06308T0/1-254     204 D Q G E R Q I L L I S S S N P A R G D F L L P K G G W D R G E K I K - K A A L R E V M E 246
Pin_PITG_11952T0/1-270     207 K K G E Q E I L L V S S S K P T K Y E F M I S K G V G K K T R V L K W Q R C V R S L K K 250
Pso_285308/1-314           183 A E G G G - I L L I S S S K L D K Q D F I L P K G G L E K G E I A Y - G A A K R E V L E 224
Pca_39353/1-267            221 D V H G K - V L L I S S S N P K K G D F L L P K G G W D D G E A I E - K A V L R E V I E 262
Pso_286675/1-96             91 D T P V R S - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 96
Prm_Prm_86166/1-353        210 E K G G G D V L L V S S S N A R K N D W L L P K G G W D K G E T V E - H A A M R E L I E 252
Prm_Prm_73707/1-269        126 E K G G G D V L L V S S S N A R K N D W L L P K G G W D K G E T V E - K A A M R E L I E 168
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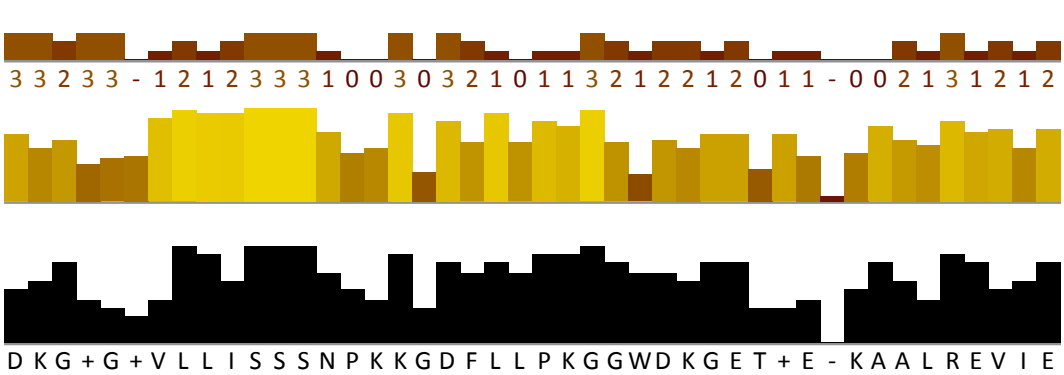


```
Pin_PITG_15679T0/1-271     267 E G G V R - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 271
Pin_PITG_05841T0/1-220         - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_05846T0/1-263     244 E G G V C G Q L W S I L V V D M L T Y L - - - - - - - - - - - - - - - - - - - - - - - 263
```

```
Prm_Prm_73724/1-343      243 E G G V G G T - - - - - - - - - - - - - I M H S L G E T A F K - - - N A L E P S K G Y V 270
Pca_14162/1-348          275 E G G V N G Q - - - - - - - - - - - - - L L H K L G E Y P F K - - - - - - - - - K G A T 296
Pin_PITG_06308T0/1-254   247 E G G V C R A L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 254
Pin_PITG_11952T0/1-270   251 E G Y V D - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 255
Pso_285308/1-314         225 E G G V R Y R S D I F I F Y R W S V L T L V M A L Q V K V K K L K E L G V T L V G D K T 268
Pca_39353/1-267          263 E G G V K - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 267
Pso_286675/1-96              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86166/1-353      253 E G G V G G T - - - - - - - - - - - - - I M H S L G E T A F K - - - N A L E P S K G Y V 280
Prm_Prm_73707/1-269      169 E G G V G G T - - - - - - - - - - - - - I M H S L G E T A F K - - - N A L E P S K G Y V 196

Conservation
                             3 3 1 3 0 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality
Consensus
                             E G G V G G T L - - - - - - - - - - - - - I M H S L G E T A F K - - - N A L E P S K G Y V

Pin_PITG_15679T0/1-271       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_05841T0/1-220       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_05846T0/1-263       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_73724/1-343      271 Y N S F W M K A D D I F D Q W P E S I R Y R I W V S F D D A E K M L K K R P Q M A E I V 314
Pca_14162/1-348          297 A Y A Y M M K A S T V Y D D W A E S I R Y R I W L S Y D D A I T L L G K R D Y M A K V V 340
Pin_PITG_06308T0/1-254       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_11952T0/1-270   256 - R S W I L G A V T I Y T N S R - - - - - - - - - - - - - - - - - - - - - - - - - - - 270
Pso_285308/1-314         269 Y E S F L M R S K K V Y E Q W S E S R R L R V W V R E C Q S I E I P G E T Q L T V R L L 312
Pca_39353/1-267              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_286675/1-96              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86166/1-353      281 Y N S F W M K A D D I F D Q W P E S I R Y R I W V S F D D A E K M L K K R P Q M A E I V 324
Prm_Prm_73707/1-269      197 Y N S F W M K A D D I F D Q W P E S I R Y R I W V S F D D A E K M L K K R P Q M A E I V 240

Conservation
                             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality
Consensus
                             Y N S F W M K A D D I + D Q W P E S I R Y R I W V S F D D A E K M L K K R P Q M A E I V

Pin_PITG_15679T0/1-271       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_05841T0/1-220       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_05846T0/1-263       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_73724/1-343      315 K A T K E K A A L V K T G D L P A M D D T L S K L K F E P                             343
Pca_14162/1-348          341 S T G S N A W W - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 348
Pin_PITG_06308T0/1-254       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_11952T0/1-270       - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285308/1-314         313 F N - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 314
Pca_39353/1-267              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_286675/1-96              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_86166/1-353      325 K A T K E K A A L V K T G D L P A M D D T L S K L K F E P                             353
Prm_Prm_73707/1-269      241 K A T K E K A A L V K T G D L P A M D D T L S K L K F E P                             269
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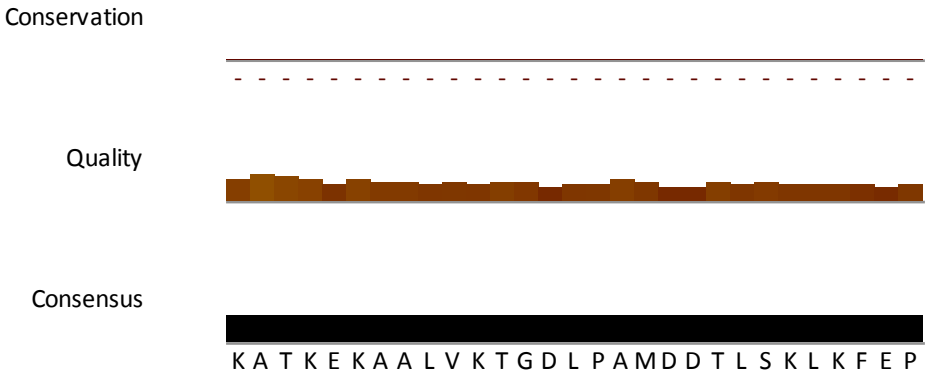
Conservation
Quality
Consensus
K A T K E K A A L V K T G D L P A M D D T L S K L K F E P

Ortholog 5

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Prm_Prm_81825/1-294      1 M R L P S I L V V V S A L T L L A R G T A L - - S A D T D K G V M V - - - - S T M A S P  38
Prm_Prm_81823/1-659      1 M R L P S I L L V V S A L T L F A S G T A L - - S A D T D K G V M V - - - - S T M A S P  38
Prm_Prm_81822/1-293      1 M R L P S I L L V V S A L T L F A S G T A L - - S A D T D K G V M V - - - - S T M A S P  38
Prm_Prm_78748/1-293      1 M R L P S L L A V V S A L T L L A R G T A L - - S A G A D K G M I V - - - - S T M A S P  38
Pin_PITG_07569T0/1-287   1 M R L S T I I L A V S A V T L V A G V N A L C E A A N V D Q A M V M - - - - - P L T Y A  39
Pca_10713/1-289          1 M R L S V I L L A V F A L S S S S V S A T R - - N H P G E T A T A N - - - - T A M Q G V  38
Pin_PITG_07566T0/1-217   1 M R L S N I I L V V N A L T L V A G D N A L C E A A A A D Q A M V M - - - - - P L T Y T  39
Pso_336774/1-303         1 M R L P S I L L A A S A L A L L A S D S A L A A V A G A S E G T K V - - - - S T M A F P  40
Pso_286958/1-293         1 M R L P S I L L A V S A L T V L A S D S A L A A V A G A S E D A K V S T M A S T M A S P  44

Conservation
* * * 7 6 + + 7 8 8 5 * 9 7 5 4 8 3 4 7 7 5 - - 6 4 4 6 6 5 5 5 4 6 - - - - 2 6 9 6 5 5

Quality

Consensus
M R L P S I L L V V S A L T L L A S G T A L + + S A + A D K G + M V - - - - S T M A S P

Prm_Prm_81825/1-294      39 D S G L L D V G H N S G K R F L R V H E T T N E D D G S E E R L S G A N M F N T E K I K  82
Prm_Prm_81823/1-659      39 D S G L L D V G H N S G K R F L R V H E T A N E D D G S E E R L S G A N M F S T K K I K  82
Prm_Prm_81822/1-293      39 D S G L L D V G H N S G K R F L R V H E T A N E D D G S E E R L S G A N M F S T K K I K  82
Prm_Prm_78748/1-293      39 D S G L L D V G R N N G K R F L R V H E T A D G D D H S E E R L S G A N M F N T E K I K  82
Pin_PITG_07569T0/1-287   40 N S V S E D L N N A D G K R Y L R - - - - - S S E N - - E E R L G G A N M F N I K K L E  76
Pca_10713/1-289          39 D G M R T D T - - - N Q M R F L R - - - T E A D D D - - E E R L A G K N M F N A E K I E  74
Pin_PITG_07566T0/1-217   40 K Y V S E D L S N A D G K R Y L R - - - - - S S D D - - E E R L G G A N T F H I K K L E  76
Pso_336774/1-303         41 D L D V L A V S H - S A K R S L H D I E R V D E D D - - E E R W A G A K L F S A A K L E  81
Pso_286958/1-293         45 D L D V L A V S H - S A T R F L R G L E S V G E V D - - E D R L A G D K L F H A A K L K  85

Conservation
5 4 3 3 4 5 6 1 1 - 7 6 5 * 5 * 8 - - - 1 0 5 4 4 8 - - * 9 * 7 8 * 3 6 6 * 4 5 3 * + 7

Quality

Consensus
D S G L L D V G H N S G K R F L R V H E T A N E D D G S E E R L S G A N M F N T K K I K

Prm_Prm_81825/1-294      83 Q A M A D S N Y A K T L F R R W K R N G F E G N D A F D K L K A Y N I G K D N N V Y K L  126
Prm_Prm_81823/1-659      83 Q A M A D S N Y A K T L F R R W K R Y G F G G D D A F N K L K A Y N I D N D N S V Y K L  126
Prm_Prm_81822/1-293      83 Q A M A D P N Y A K T L F R R W K R N G V E A D G A F N K L K A Y N I D N D - N V F R L  125
Prm_Prm_78748/1-293      83 L A I A D S K Y A K T L F R R W K R Y G F E S D D A F K K L T V H N L H K D D N V F Q L  126
Pin_PITG_07569T0/1-287   77 D A L N D T T Y A K T L F R R W K R S G V N E D T I T T K F K N L Q I S L D E N A L E L  120
Pca_10713/1-289          75 K A L Q D T S Y A K T L F R R W K R Y E V E H G A A F D K L I K F N I G K D D K V F G L  118
Pin_PITG_07566T0/1-217   77 D A L N D T T Y A K T L F R R W K R S G V D E D T V T T K F K S M Q I S M D E N A L E L  120
Pso_336774/1-303         82 K A M N D S K Y A E T L M M R W K R H G F D I E D T K L S L E A S K L S K D P R L - - -  122
Pso_286958/1-293         86 R A M D D S K Y A E T L M K R W K R H G Y D I E K A K S I L D V S R Y A K N E K L N A I  129

Conservation
3 * 9 4 * 7 5 * * 7 * * 9 6 * * * * 4 4 6 4 1 4 3 5 4 2 3 8 3 3 2 6 7 2 4 8 0 5 7 0 0 2
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Prm_Prm_81825/1-294      127 Y T N Y V T W L D T H H P L - - G - V V T G D K K M F D E T K L K K A M E D G T Y A N T 167
Prm_Prm_81823/1-659      127 Y T N Y F T W L E T H H P V - - G - V V T G D K K M F D E T K L K K A M G D G T Y A N T 167
Prm_Prm_81822/1-293      126 Y K N Y F T W L K T R H P V - - G - V V T G D K K M F D E T K L K K A M G D G T Y A N T 166
Prm_Prm_78748/1-293      127 Y K N Y L A W L E T H H P L - - G - I V T G D K K M F D R V K L Q K A M G D G T Y A T T 167
Pin_PITG_07569T0/1-287   121 I Q S Y R I W L N A H - - - - - - - A T K T N P K L F D R A K I K K A L E D G T Y A N V 157
Pca_10713/1-289          119 Y K S Y V S W L E K H H P L - - G A E T G G G P N L F S K A K L D K A M K D P K Y E N T 160
Pin_PITG_07566T0/1-217   121 I Q S Y R I W L N A H - - - - - - - A T K T N P K L F D I A K I K K A L E D G T Y A H V 157
Pso_336774/1-303         123 - - - - - - - - - - - - - - - - - - - - - - - - - - - N T A K I Q N A L G D S N Y A K T 139
Pso_286958/1-293         130 Y L K Y A A W L D T H F S R L P G V K P S G G D D L F N K A K L E V A I K D G N Y K R T 173
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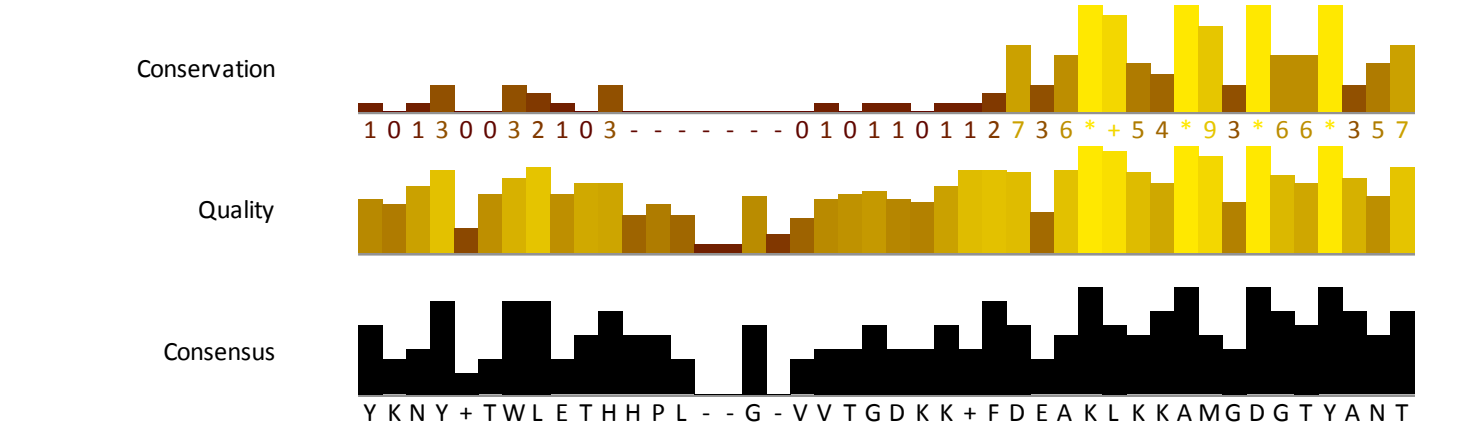


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Prm_Prm_81825/1-294      168 L F G R W K H N R L D S D A V F A R F Q Q M G V K K - D N N L Y K L Y T D Y Y A W L Q I 210
Prm_Prm_81823/1-659      168 L F G R W K R N G L D S D E V F A R F Q K M G V M E - D N N L F K L Y T D Y F A W L Q I 210
Prm_Prm_81822/1-293      167 L F G R W K R N G L D S D E V F T R F Q K M G V K K - D N N L Y K L Y T D Y F A W L Q I 209
Prm_Prm_78748/1-293      168 L F Q R W K R N G I D S D G V F D R F K Q L G V K K - D N I L Y K L Y T D Y F A W L Q I 210
Pin_PITG_07569T0/1-287   158 L Y G R W K R Y G F E S D D V F K R F Q R M G V N K - D D N L Y Q V Y K N Y V T W L N V 200
Pca_10713/1-289          161 M F G R W K R Q G F E S D A A Y N K L L A F N L A S - D A D V Y K I Y T K Y V T W L N I 203
Pin_PITG_07566T0/1-217   158 L Y G R W K R Y G F E S D D V F K R F Q R M G V N K - D D N L Y Q V Y K N Y V T W L N V 200
Pso_336774/1-303         140 L F R E W K T H D H E S T D I L K K L K V L G L R K G D G D G D K L F K N Y A S W L N I 183
Pso_286958/1-293         174 L F K E W K T H N Y E S E A V F K Q L N A L G R K D F D N T L D R L Y V D Y V I W L N V 217
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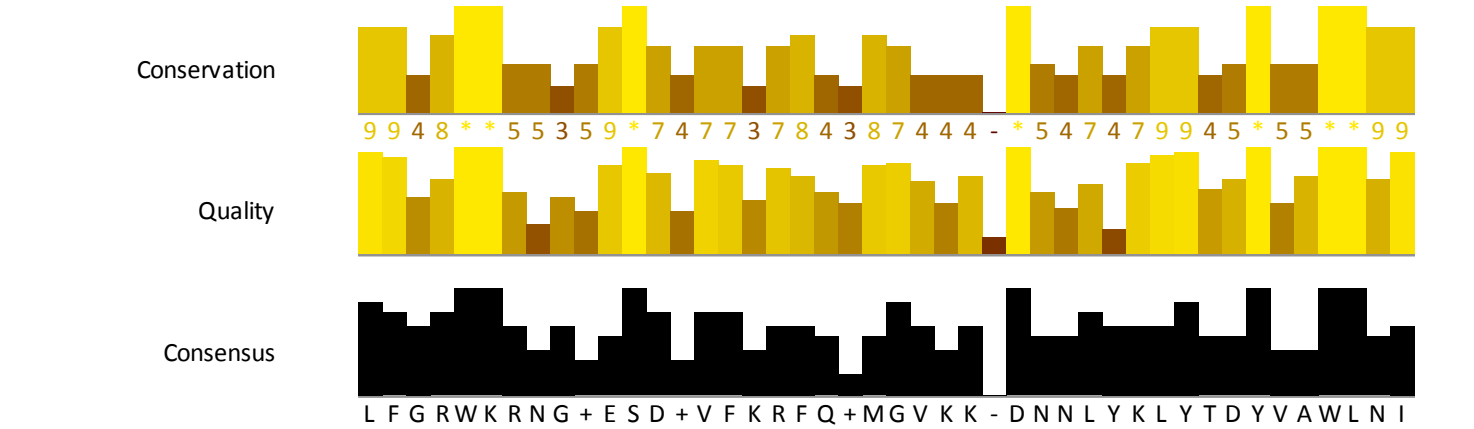


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Prm_Prm_81825/1-294      211 H H P I P G S Q K V S A K Y F L F D S T R L N R A M K D T T F A E K L F A K W K T S G L 254
Prm_Prm_81823/1-659      211 H H P I P G S Q K V S A K D F L F D S T R L N R A M K D T T F A E K L F A K W K T S G L 254
Prm_Prm_81822/1-293      210 H H P I P G S Q K V S A K D F L F D S T R L N R A M K D T T F A E K L F A K W K T S G L 253
Prm_Prm_78748/1-293      211 H H P T A S S K K V L A K D F L F D S T R L N R A M E D K D F A G K L F A K W K T N G M 254
Pin_PITG_07569T0/1-287   201 H H P L K K S T L T T P E A F L F Y P S R I Q R A K S D P A F A E T L F A K W K S S G L 244
Pca_10713/1-289          204 H H P L A K T R K T T A K D F L F N V D R I A R A K K D S E F A E T L F K K W K T S G L 247
Pin_PITG_07566T0/1-217   201 H D P L K K T T L T T P E A F L F - - - - - - - - - - - - - - - - - - - - - - - - - - 217
Pso_336774/1-303         184 H Y P D Q K A K D L A K A K L L F E D T M L L Q A R G D V E L A E R L F R A W K T R G F 227
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Pso_286958/1-293          218 H F P H P D T L K L A N E P L L F K E S M L L K A R T D V D Y A Q S L F W A W K K N - F 260
Conservation                  * 3 * 2 3 3 7 4 3 6 5 3 3 1 8 * * 1 0 2 0 2 0 1 3 0 0 4 0 0 1 3 0 1 2 2 0 1 3 4 1 1 3 1
Quality
Consensus                     H H P + P K S Q K V + A K D F L F D S T R L N R A M K D T T F A E K L F A K W K T S G L

Prm_Prm_81825/1-294       255 D S D L V F T R F R A L G S K K G D N K L D K L Y R N Y Y D W L Q I H Y P T V G - - - - 294
Prm_Prm_81823/1-659       255 D S D P V F V K F R A L G S K K G D N K L D K L Y R D Y F K W L E I H Y P T A G T V V I 298
Prm_Prm_81822/1-293       254 D S D P V F V K F R A L G S K K G D N K L D K L Y R D Y F K W L E I H Y P T A G - - - - 293
Prm_Prm_78748/1-293       255 D S D P V F K R F Q K M G V K T N D - K L Y Q L Y R D Y F A W L Q K N Y P T A G - - - - 293
Pin_PITG_07569T0/1-287    245 D E G P V Y K K L W D M G L K K - D N A I Y K L Y T D Y V L W L D K H F P L P A - - - - 283
Pca_10713/1-289           248 D E K P V Y L K L W D M G L K T - D D E L Y K L Y K N Y V K W L D I H Y P L P A - - - - 286
Pin_PITG_07566T0/1-217        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_336774/1-303          228 T L S E V K Q K L A - - - - K T L A N N D G K L L K Q Y T V W I N N H F P V K P - - - - 263
Pso_286958/1-293          261 S L E K V T E N L K - - - - L T F A N A D N K V L R G Y T N W L I N N F - - - - - - - 292

Conservation                  2 0 0 0 3 0 0 1 1 0 - - - - 1 1 - 1 2 0 0 0 1 2 1 1 0 3 0 0 3 2 0 0 1 2 2 0 0 1 - - - -
Quality
Consensus                     D S D P V F + K + R A + G S K + G D N K L + K L Y R D Y F K W L + I H Y P T A G - - - -

Prm_Prm_81825/1-294           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_81823/1-659       299 N R L V I V P F A V I R R V C L Q N E Y I D V F A V L S R R T K S V S D D T K R R I Q T 342
Prm_Prm_81822/1-293           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_78748/1-293           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07569T0/1-287        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_10713/1-289               - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07566T0/1-217        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_336774/1-303              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_286958/1-293              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Conservation
                              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality

Consensus
                              - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Prm_Prm_81825/1-294           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_81823/1-659       343 L L R R W K Q I D I G I T E A A N E A K D N V K Y L F T L E K F I I P L Y N G T P S S I 386
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Prm_Prm_81822/1-293        - - -
```

Consensus

- -

Prm_Prm_81825/1-294 -
Prm_Prm_81823/1-659 475 E F N E M K I F G K F N L F C R R V M K L I D M F T T I P P V L V A A H G R H G S A V G 518
Prm_Prm_81822/1-293 -
Prm_Prm_78748/1-293 -
Pin_PITG_07569T0/1-287 -
Pca_10713/1-289 -
Pin_PITG_07566T0/1-217 -
Pso_336774/1-303 -
Pso_286958/1-293 -

Conservation

- -

Quality

Consensus

- -

Prm_Prm_81825/1-294 -
Prm_Prm_81823/1-659 519 G T V S I N S Y G R H L S D S Y R D L N P A Y F H I A A V I L L G S L N S I F I V D V T 562
Prm_Prm_81822/1-293 -
Prm_Prm_78748/1-293 -
Pin_PITG_07569T0/1-287 -
Pca_10713/1-289 -
Pin_PITG_07566T0/1-217 -
Pso_336774/1-303 -
Pso_286958/1-293 -

Conservation

- -

Quality

Consensus

- -

Prm_Prm_81825/1-294 -
Prm_Prm_81823/1-659 563 A G S E S S A A K S T M Y A K T R R L S W I F E T Y T D G P L V P S G S Y T T G A Y Y Y 606
Prm_Prm_81822/1-293 -
Prm_Prm_78748/1-293 -
Pin_PITG_07569T0/1-287 -
Pca_10713/1-289 -
Pin_PITG_07566T0/1-217 -
Pso_336774/1-303 -
Pso_286958/1-293 -

Conservation

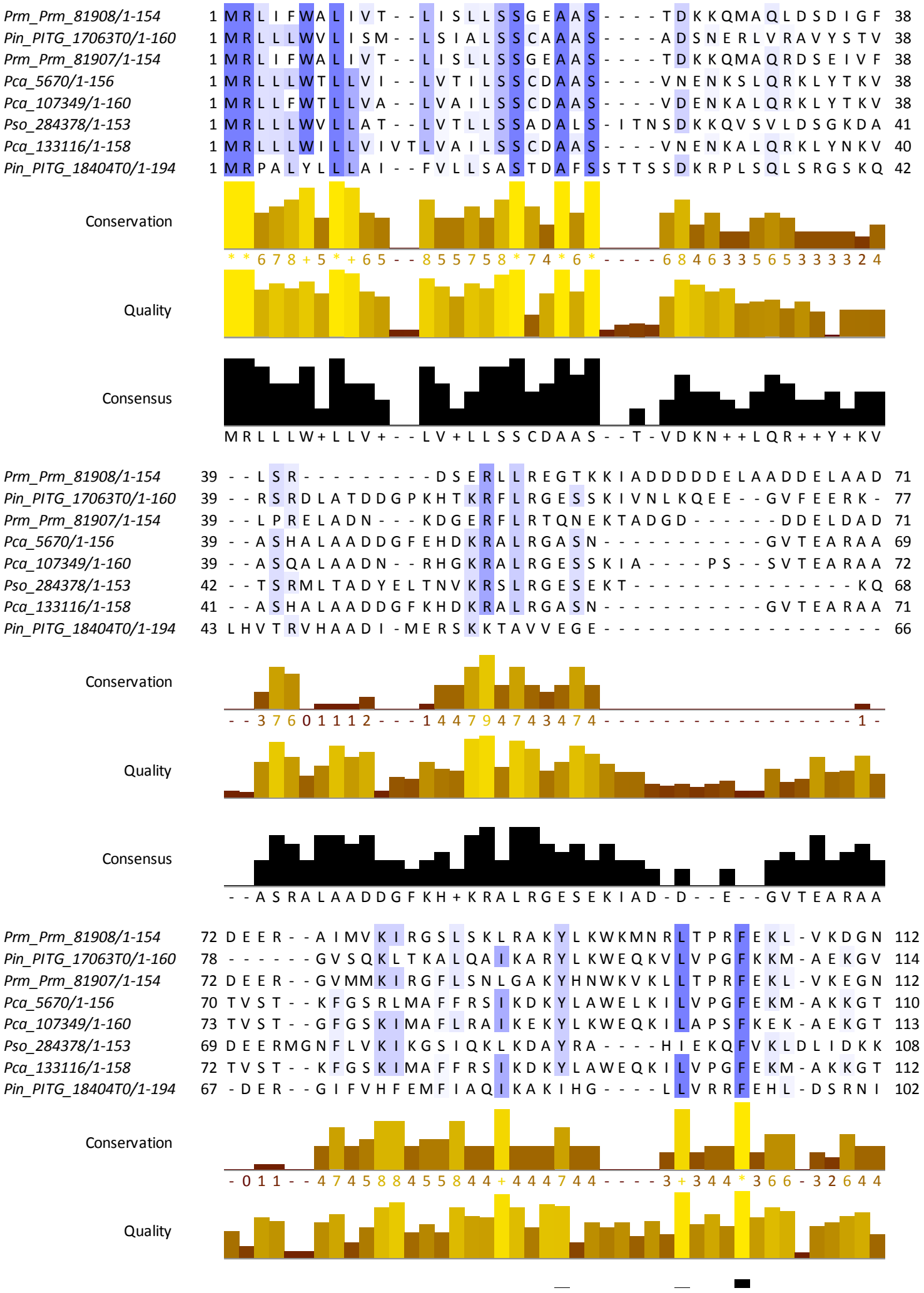
Conservation

Quality

Consensus

Prm_Prm_81825/1-294		- - -

Ortholog 6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Pin_PITG_17063T0/1-160 1 MRLLLWVLISM--LSIALSSCAAAS----ADSNERLVRAVYSTV 38
Prm_Prm_81907/1-154 1 MRLIFWALIVT--LISLLSSGEAAS----TDKKQMAQRDSEIVF 38
Pca_5670/1-156 1 MRLLLWTLLVI--LVTILSSCDAAS----VNENKSLQRKLYTKV 38
Pca_107349/1-160 1 MRLLFWTLLVA--LVAILSSCDAAS----VDENKALQRKLYTKV 38
Pso_284378/1-153 1 MRLLLWVLLAT--LVTLLSSADALS-ITNSDKKQVSVLDSGKDA 41
Pca_133116/1-158 1 MRLLLWILLVIVTLVAILSSCDAAS----VNENKALQRKLYNKV 40
Pin_PITG_18404T0/1-194 1 MRPALYLLLAI--FVLLSASTDAFSSTTSSDKRPLSQLSRGSKQ 42
Conservation
**678+5*+65--85578*74*6*----6846335653333 24
Quality
Consensus
MRLLW+LLV+--LV+LLSSCDAAS--T-VDKN++LQR++Y+KV
Prm_Prm_81908/1-154 39 --LSR----------DSERLLREGTKKIADDDDDDELAADDELAAD 71
Pin_PITG_17063T0/1-160 39 --RSRDLATDDGPKHTKRFLRGESSKIVNLKQEE--GVFEERK- 77
Prm_Prm_81907/1-154 39 --LPRELADN---KDGERFLRTQNEKTADGD-----DDELDAD 71
Pca_5670/1-156 39 --ASHALAADDGFEHDKRALRGASN----------GVTEARAA 69
Pca_107349/1-160 39 --ASQALAADN--RHGKRALRGESSKIA----PS--SVTEARAA 72
Pso_284378/1-153 42 --TSRMLTADYELTNVKRSLRGESEKT----------KQ 68
Pca_133116/1-158 41 --ASHALAADDGFKHDKRALRGASN----------GVTEARAA 71
Pin_PITG_18404T0/1-194 43 LHVTRVHAADI-MERSKKTAVVEGE---------- 66
Conservation
--3760111 2---1447947434 74----------1-
Quality
Consensus
--ASRALAADDGFKH+KRALRGESEKIAD-D--E--GVTEARAA
Prm_Prm_81908/1-154 72 DEER--AIMVKIRGSLSKLRAKYLKWKMNRLTPRFEKL-VKDGN 112
Pin_PITG_17063T0/1-160 78 ------GVSQKLTKALQAIKARYLKWEQKVLVPGFKKM-AEKGV 114
Prm_Prm_81907/1-154 72 DEER--GVMMKIRGFLSNLGAKYHNWKVKLLTPRFEKL-VKEGN 112
Pca_5670/1-156 70 TVST--KFGSRLMAFFRSIKDKYLAWELKILVPGFEKM-AKKGT 110
Pca_107349/1-160 73 TVST--GFGSKIMAFLRAIKEKYLKWEQKILAPSFKEK-AEKGT 113
Pso_284378/1-153 69 DEERMGNFLVKIKGSIQKLKDAYRA----HIEKQFVKLDLIDKK 108
Pca_133116/1-158 72 TVST--KFGSKIMAFFRSIKDKYLAWEQKILVPGFEKM-AKKGT 112
Pin_PITG_18404T0/1-194 67 -DER--GIFVHFEMFIAQIKAKIHG----LLVRRFEHL-DSRNI 102
Conservation
-011--4745884558444+4447444----3+344*366-3264 4
Quality

```
Consensus                                   + + E R - - G F G + K I M + F L R + I K A K Y L + W E Q K I L V P + F E K L - A K K G T

Prm_Prm_81908/1-154          113  S L D D V K K M Y R I - - - - - G Q W G T P S R N K R F Y K L F E E W V K T N - Y P N G  150
Pin_PITG_17063T0/1-160       115  T Y S E L R D T F R V R M M N S G R W G T P S G F K R Y A R L Y S E W L H R T - G R S H  157
Prm_Prm_81907/1-154          113  S L D D V K K M Y G I - - - - - G E G G T P S R N K R F Y K L F E E W A K T N - Y P N G  150
Pca_5670/1-156               111  T Y T Q V R E D F R T R L N W S G L W G T P S G F K R Y A K L Y R T W L E K N - H Y S Q  153
Pca_107349/1-160             114  T Y S E V L A N Y R T R L N W S G L W G T P S G F K R Y A R L Y E T W L K N N P K Y S H  157
Pso_284378/1-153             109  T P D D L Y K E Y R R - - - - - A P W G V S K L K K K A Y K G Y A A Y Y K R E - H P N W  146
Pca_133116/1-158             113  T Y T Q V R E D F R T R L N W S G L W G T P S G F K R Y A K L Y K T W L E K N - H Y S H  155
Pin_PITG_18404T0/1-194       103  T P D K L A K D Y Q I - - - - - G T M A A L A R S K R F I K L Y A D W Y R K R - H P S W  140

Conservation                                9 4 7 5 9 2 3 5 9 4 4 - - - - - + 2 6 + 6 4 4 3 3 * 9 6 5 9 7 9 3 4 + 5 6 6 6 - 4 3 9 3

Quality

Consensus                                   T Y D D V R K D Y R + R L N W S G L W G T P S G F K R Y A K L Y E + W L K K N - H P S H

Prm_Prm_81908/1-154          151  L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_17063T0/1-160       158  L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_81907/1-154          151  L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_5670/1-156               154  L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_107349/1-160             158  L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_284378/1-153             147  V - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_133116/1-158             156  L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_18404T0/1-194       141  V H P K I P P D S C D G P T C L N A Q T Q T Y Q R S P C R S P R T K F A V Q V R H C L L  184

Conservation                                9 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Quality

Consensus                                   L - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Prm_Prm_81908/1-154          152  - - - - - - - P K Q                                                                      154
Pin_PITG_17063T0/1-160       159  - - - - - - - - A K                                                                      160
Prm_Prm_81907/1-154          152  - - - - - - - P K Q                                                                      154
Pca_5670/1-156               155  - - - - - - - - A V                                                                      156
Pca_107349/1-160             159  - - - - - - - - A V                                                                      160
Pso_284378/1-153             148  - - - - S S I P K K                                                                      153
Pca_133116/1-158             157  - - - - - - - - A V                                                                      158
Pin_PITG_18404T0/1-194       185  P R L A S A C T G S                                                                      194

Conservation                                - - - - - - - - 5 3
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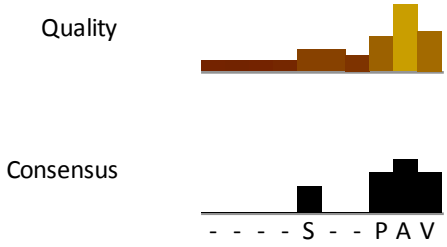
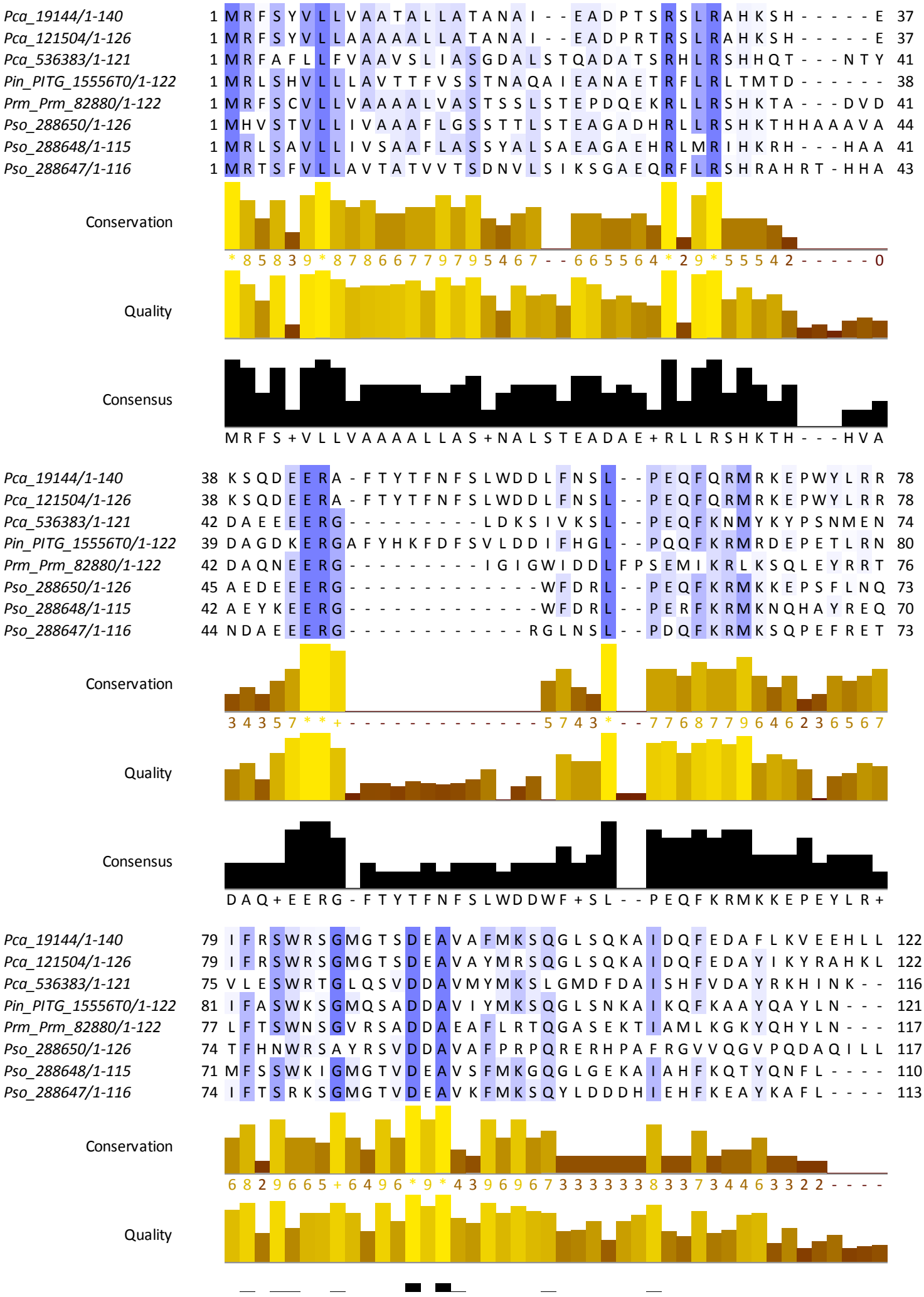

Quality
Consensus
- - - - S - - P A V

Ortholog 7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Pca_121504/1-126 1 M R F S Y V L L A A A A A L L A T A N A I - - E A D P R T R S L R A H K S H - - - - - E 37
Pca_536383/1-121 1 M R F A F L L F V A A V S L I A S G D A L S T Q A D A T S R H L R S H H Q T - - - N T Y 41
Pin_PITG_15556T0/1-122 1 M R L S H V L L L A V T T F V S S T N A Q A I E A N A E T R F L R L T M T D - - - - - - 38
Prm_Prm_82880/1-122 1 M R F S C V L L V A A A A L V A S T S S L S T E P D Q E K R L L R S H K T A - - - D V D 41
Pso_288650/1-126 1 M H V S T V L L I V A A A F L G S S T T L S T E A G A D H R L L R S H K T H H A A A V A 44
Pso_288648/1-115 1 M R L S A V L L I V S A A F L A S S Y A L S A E A G A E H R L M R I H K R H - - - H A A 41
Pso_288647/1-116 1 M R T S F V L L A V T A T V V T S D N V L S I K S G A E Q R F L R S H R A H R T - H H A 43
Conservation
* 8 5 8 3 9 * 8 7 8 6 6 7 7 9 7 9 5 4 6 7 - - 6 6 5 5 6 4 * 2 9 * 5 5 5 4 2 - - - - - 0
Quality
Consensus
M R F S + V L L V A A A A L L A S + N A L S T E A D A E + R L L R S H K T H - - - H V A
Pca_19144/1-140 38 K S Q D E E R A - F T Y T F N F S L W D D L F N S L - - P E Q F Q R M R K E P W Y L R R 78
Pca_121504/1-126 38 K S Q D E E R A - F T Y T F N F S L W D D L F N S L - - P E Q F Q R M R K E P W Y L R R 78
Pca_536383/1-121 42 D A E E E E R G - - - - - - - - - L D K S I V K S L - - P E Q F K N M Y K Y P S N M E N 74
Pin_PITG_15556T0/1-122 39 D A G D K E R G A F Y H K F D F S V L D D I F H G L - - P Q Q F K R M R D E P E T L R N 80
Prm_Prm_82880/1-122 42 D A Q N E E R G - - - - - - - - - I G I G W I D D L F P S E M I K R L K S Q L E Y R R T 76
Pso_288650/1-126 45 A E D E E E R G - - - - - - - - - - - - - W F D R L - - P E Q F K R M K K E P S F L N Q 73
Pso_288648/1-115 42 A E Y K E E R G - - - - - - - - - - - - - W F D R L - - P E R F K R M K N Q H A Y R E Q 70
Pso_288647/1-116 44 N D A E E E R G - - - - - - - - - - - - R G L N S L - - P D Q F K R M K S Q P E F R E T 73
Conservation
3 4 3 5 7 * * + - - - - - - - - - - - - - 5 7 4 3 * - - 7 7 6 8 7 7 9 6 4 6 2 3 6 5 6 7
Quality
Consensus
D A Q + E E R G - F T Y T F N F S L W D D W F + S L - - P E Q F K R M K K E P E Y L R +
Pca_19144/1-140 79 I F R S W R S G M G T S D E A V A F M K S Q G L S Q K A I D Q F E D A F L K V E E H L L 122
Pca_121504/1-126 79 I F R S W R S G M G T S D E A V A Y M R S Q G L S Q K A I D Q F E D A Y I K Y R A H K L 122
Pca_536383/1-121 75 V L E S W R T G L Q S V D D A V M Y M K S L G M D F D A I S H F V D A Y R K H I N K - - 116
Pin_PITG_15556T0/1-122 81 I F A S W K S G M Q S A D D A V I Y M K S Q G L S N K A I K Q F K A A Y Q A Y L N - - - 121
Prm_Prm_82880/1-122 77 L F T S W N S G V R S A D D A E A F L R T Q G A S E K T I A M L K G K Y Q H Y L N - - - 117
Pso_288650/1-126 74 T F H N W R S A Y R S V D D A V A F P R P Q R E R H P A F R G V V Q G V P Q D A Q I L L 117
Pso_288648/1-115 71 M F S S W K I G M G T V D E A V S F M K G Q G L G E K A I A H F K Q T Y Q N F L - - - - 110
Pso_288647/1-116 74 I F T S R K S G M G T V D E A V K F M K S Q Y L D D D H I E H F K E A Y K A F L - - - - 113
Conservation
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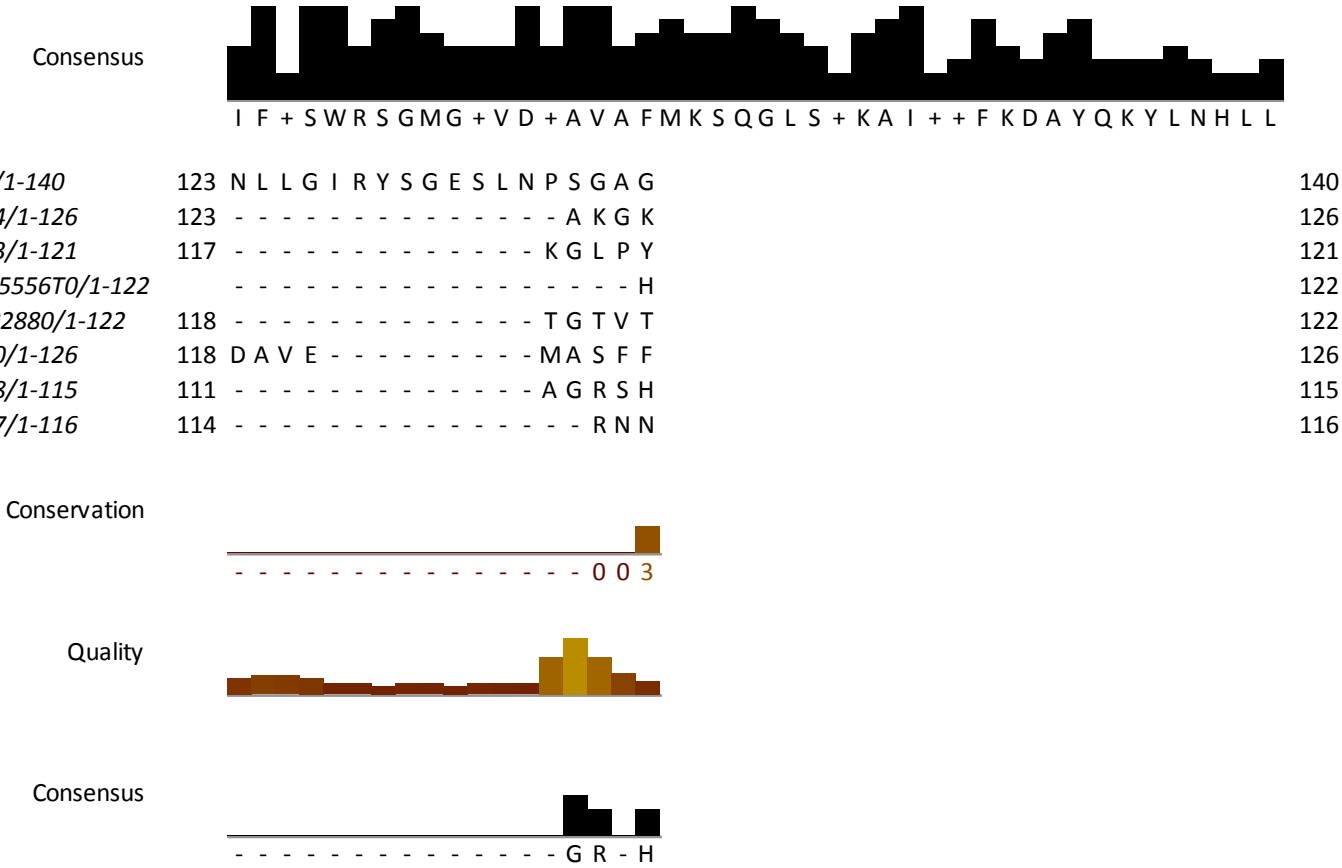
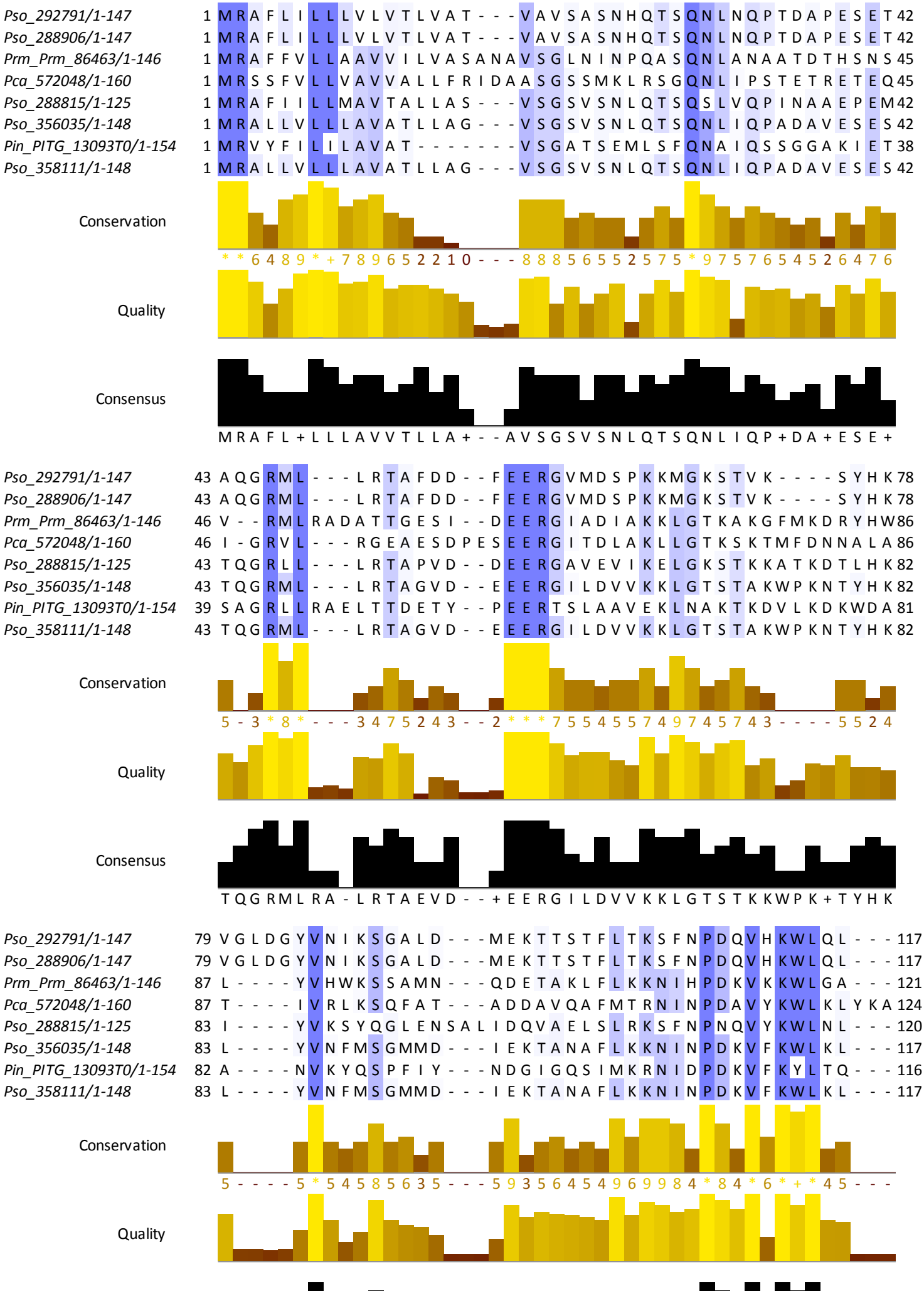
Quality


Consensus
I F + S W R S G M G + V D + A V A F M K S Q G L S + K A I + + F K D A Y Q K Y L N H L L
Pca_19144/1-140 123 N L L G I R Y S G E S L N P S G A G 140
Pca_121504/1-126 123 - - - - - - - - - - - - - - A K G K 126
Pca_536383/1-121 117 - - - - - - - - - - - - - - K G L P Y 121
Pin_PITG_15556T0/1-122 - - - - - - - - - - - - - - - - - - H 122
Prm_Prm_82880/1-122 118 - - - - - - - - - - - - - - T G T V T 122
Pso_288650/1-126 118 D A V E - - - - - - - - - - M A S F F 126
Pso_288648/1-115 111 - - - - - - - - - - - - - - A G R S H 115
Pso_288647/1-116 114 - - - - - - - - - - - - - - - R N N 116
Conservation
- - - - - - - - - - - - - - - - 0 0 3
Quality
Consensus
- - - - - - - - - - - - - - - G R - H

Ortholog 8


Pso_292791/1-147 1 MRAFLILLLVLVTLVAT---VAVSASNHQTSQNLNQPTDAPESET 42
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Prm_Prm_86463/1-146 1 MRAFFVLLAAVVILVASANAVSGLNINPQASQNLANAATDTHSNS 45
Pca_572048/1-160 1 MRSSFVLLVAVVALLFRIDAASGSSMKLRSGQNLIPSTETRETEQ 45
Pso_288815/1-125 1 MRAFIILLMAVTALLAS---VSGSVSNLQTSQSLVQPINAAEPEM 42
Pso_356035/1-148 1 MRALLVLLLAVATLLAG---VSGSVSNLQTSQNLIQPADAVESES 42
Pin_PITG_13093T0/1-154 1 MRVYFILILAVAT-------VSGATSEMLSFQNAIQSSGGAKIET 38
Pso_358111/1-148 1 MRALLVLLLAVATLLAG---VSGSVSNLQTSQNLIQPADAVESES 42
Conservation
**6489*+7896522 10---8885655257 5*9757654526476
Quality
Consensus
MRAFL+LLLAVVTLLA+--AVSGSVSNLQTSQNLIQP+DA+ESE+
Pso_292791/1-147 43 AQGRML---LRTAFDD--FEERGVMDSPKKMGKSTVK----SYHK 78
Pso_288906/1-147 43 AQGRML---LRTAFDD--FEERGVMDSPKKMGKSTVK----SYHK 78
Prm_Prm_86463/1-146 46 V--RMLRADATTGESI--DEERGIADIAKKLGTKAKGFMKDRYHW 86
Pca_572048/1-160 46 I-GRVL---RGEAESDPESEERGITDLAKLLGTKSKTMFDNNALA 86
Pso_288815/1-125 43 TQGRLL---LRTAPVD--DEERGAVEVIKELGKSTKKATKDTLHK 82
Pso_356035/1-148 43 TQGRML---LRTAGVD--EEERGILDVVKKLGTSTAKWPKNTYHK 82
Pin_PITG_13093T0/1-154 39 SAGRLLRAELTTDETY--PEERTSLAAVEKLNAKTKDVLKDKWDA 81
Pso_358111/1-148 43 TQGRML---LRTAGVD--EEERGILDVVKKLGTSTAKWPKNTYHK 82
Conservation
5-3*8*---34752 43--2***755455574 9745743----5524
Quality
Consensus
TQGRMLRA-LRTAEVD--+EERGILDVVKKLGTSTKKWPK+TYHK
Pso_292791/1-147 79 VGLDGYVNIKSGALD---MEKTTSTFLTKSFNPDQVHKWLQL--- 117
Pso_288906/1-147 79 VGLDGYVNIKSGALD---MEKTTSTFLTKSFNPDQVHKWLQL--- 117
Prm_Prm_86463/1-146 87 L----YVHWKSSAMN---QDETAKLFLKKNIHPDKVKKWLGA--- 121
Pca_572048/1-160 87 T----IVRLKSQFAT---ADDAVQAFMTRNINPDAVYKWLKLYKA 124
Pso_288815/1-125 83 I----YVKSYQGLENSALIDQVAELSLRKSFNPNQVYKWLNL--- 120
Pso_356035/1-148 83 L----YVNFMSGMMD---IEKTANAFLKKNINPDKVFKWLKL--- 117
Pin_PITG_13093T0/1-154 82 A----NVKYQSPFIY---NDGIGQSIMKRNIDPDKVFKYLTQ--- 116
Pso_358111/1-148 83 L----YVNFMSGMMD---IEKTANAFLKKNINPDKVFKWLKL--- 117
Conservation
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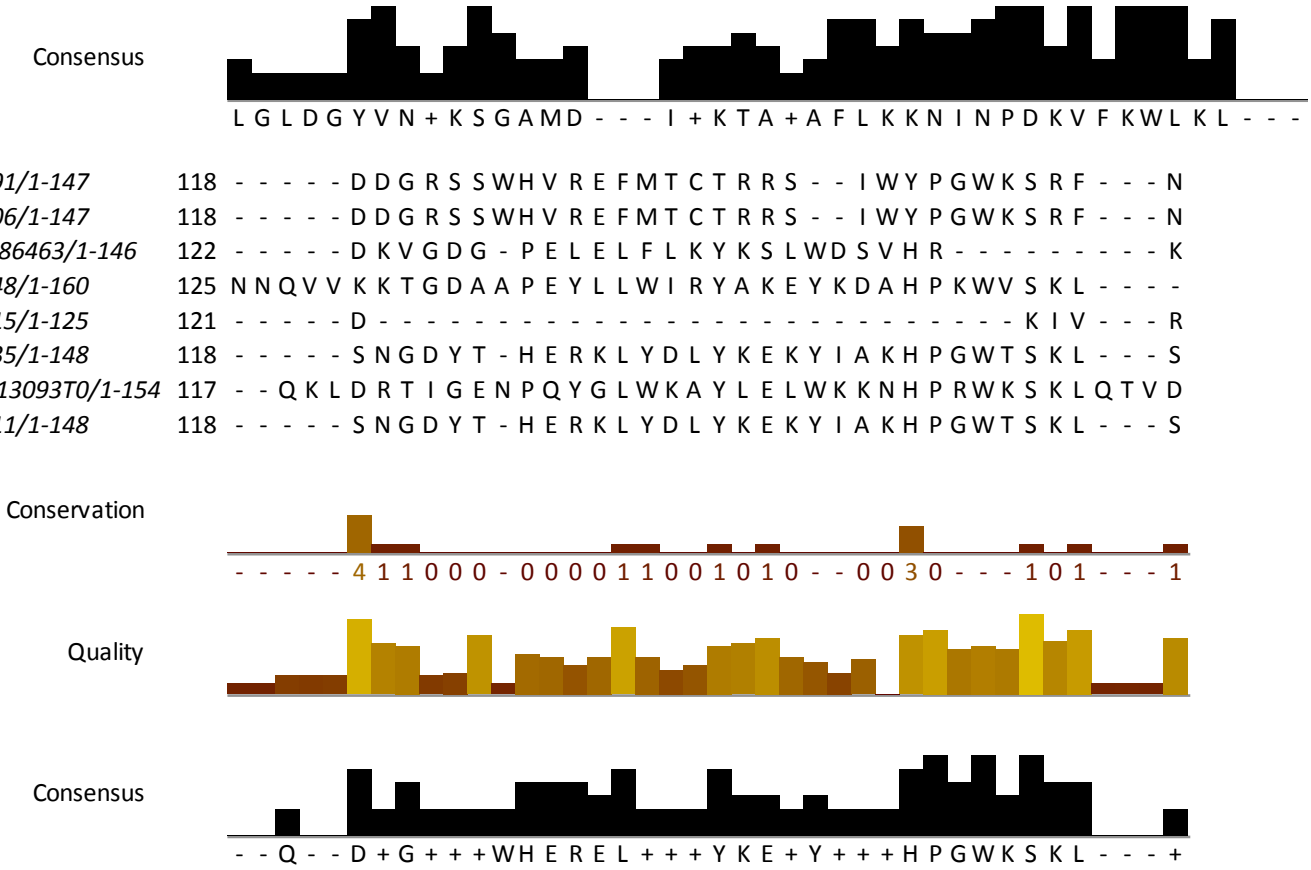
Quality


Consensus
L G L D G Y V N + K S G A M D - - - I + K T A + A F L K K N I N P D K V F K W L K L - - -
Pso_292791/1-147 118 - - - - - D D G R S S W H V R E F M T C T R R S - - I W Y P G W K S R F - - - N 147
Pso_288906/1-147 118 - - - - - D D G R S S W H V R E F M T C T R R S - - I W Y P G W K S R F - - - N 147
Prm_Prm_86463/1-146 122 - - - - - D K V G D G - P E L E L F L K Y K S L W D S V H R - - - - - - - - - K 146
Pca_572048/1-160 125 N N Q V V K K T G D A A P E Y L L W I R Y A K E Y K D A H P K W V S K L - - - - 160
Pso_288815/1-125 121 - - - - - D - K I V - - - R 125
Pso_356035/1-148 118 - - - - - S N G D Y T - H E R K L Y D L Y K E K Y I A K H P G W T S K L - - - S 148
Pin_PITG_13093T0/1-154 117 - - Q K L D R T I G E N P Q Y G L W K A Y L E L W K K N H P R W K S K L Q T V D 154
Pso_358111/1-148 118 - - - - - S N G D Y T - H E R K L Y D L Y K E K Y I A K H P G W T S K L - - - S 148
Conservation
- - - - - 4 1 1 0 0 0 - 0 0 0 0 1 1 0 0 1 0 1 0 - - 0 0 3 0 - - - 1 0 1 - - - 1
Quality
Consensus
- - Q - - D + G + + + W H E R E L + + + Y K E + Y + + + H P G W K S K L - - - +

Ortholog 9

```
Prm_Prm_76339/1-146      1 M R V - - T H F L L V A T A T L Y S - C N A V S A A S G D A D Q A K L S M V T S T D A A  41
Pso_288968/1-82          1 M R L - - T Y F L L V A A S T F L S T V D A S A - - - G G I - K A E L P A L T S T D A A  38
Pca_14853/1-131          1 M R F - - S H V L L L A T A A L I S S C N A T A I V P G E G - - - - - Q V T T S A D V A  37
Pca_15117/1-144          1 M R S - - Y H F L L L A T A A L L S S C N A T A A V L C E G - - - - - Q V M T S A D A A  37
Pin_PITG_12276T0/1-140   1 M R T A S S F F V L V S T V L L F A S A K A V R - - - - - - - P T K H S E M A T T D I D  37
Pca_19651/1-140          1 M R F - - S Y F L L L T S A A I L S N S N A T A T V S G E G - - - - - H V M T S A D A -  36
Pin_PITG_11839T0/1-155   1 M G I - - I Y F L L V T A S - L L S S Y N A N A A I L G D D - Q T R M Y T V A S T D A A  40
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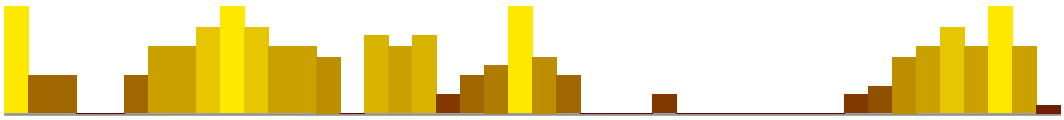
Conservation



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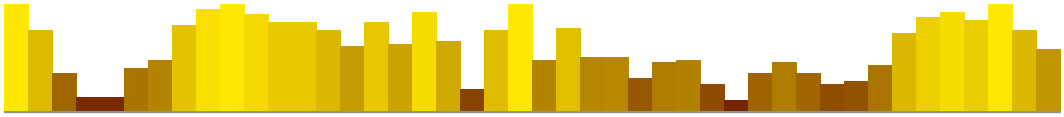
Quality



Consensus

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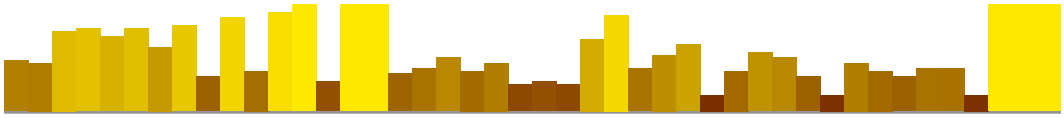
M R F - - S + F L L V A T A A L L S S C N A T A A V + G E G - Q + K L + V M T S T D A A
```

```
Prm_Prm_76339/1-146      42 V P V R A L D T V N G K R L L R S Y Y E A D K D D E A D E A D E A - D E Y D A A - E E E  83
Pso_288968/1-82          39 V P A R A V D T S N G K R F L R A Y Y T - - - - D D E D E K D E - - D D E D E K Y E E E  76
Pca_14853/1-131          38 V P V R A L E T R N G K R S L R - Y Y D A E E E D E T D K Y D Q K N G K Y D D D - E E E  79
Pca_15117/1-144          38 V P V R A L G T S N S K R S L R - Y Y D T E E E D E T D K H H Q K N D K Y D E D - E E E  79
Pin_PITG_12276T0/1-140   38 K Q I E P A N I G S D Q R F L R V H T - - - - - S E A V E E G A K D F A Y I N E - E E E  75
Pca_19651/1-140          37 - P A R A L E T N N G K R S L R - Y Y A A - - - D E D D K Y D Q K N G K Y D D D E E E E  75
Pin_PITG_11839T0/1-155   41 A L V R V V D T R N V K R L L R I N H E - - - - G E D D - - - - - - - - - - - - - E E E  67
```

Conservation

```
1 5 7 8 6 7 4 6 3 9 4 7 * 4 * * - 5 5 0 - - - - 5 9 4 5 2 0 0 0 - - 0 0 1 0 0 0 - * * *
```

Quality



Consensus

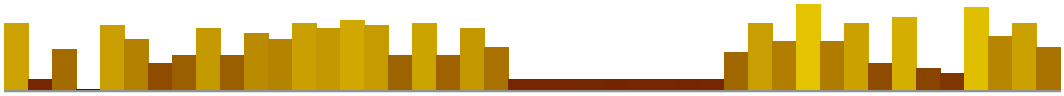
```
V P V R A L D T + N G K R S L R - Y Y + A E E E D E + D + Y D Q K N D K Y D + D - E E E
```

```
Prm_Prm_76339/1-146      84 R G V M T P A Q I R K W T A R A E E W V E - - - - - - - - - R G K T Q G Q M R D K F T G  118
Pso_288968/1-82          77 R - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_14853/1-131          80 R - V M T A A Q I A K W T A K A G E W V E - - - - - - - - - Q G K T P A Y I K D K L T A  113
Pca_15117/1-144          80 R - T W S A A Q I D K W T A K A D E W V D - - - - - - - - - L G K T P A Y I K A K L T A  113
Pin_PITG_12276T0/1-140   76 R - T R S Q E W V N K W S A R A A E W V G - - - - - - - - - K G L T R G Q I A E K Y G I  109
Pca_19651/1-140          76 R - N F T A A Q L A K W T E K A E S W V S - - - - - - - - - K N R T P A Y I K D K L T G  109
Pin_PITG_11839T0/1-155   68 I - V N N P W E T N L Y N S K N G E L S G L R K I N L L F K E G K T P A Q V W Y K L S G  110
```

Conservation

```
5 - 1 0 2 0 0 1 0 0 1 3 2 0 3 1 0 1 1 1 0 - - - - - - - - - 0 1 0 2 0 3 1 1 0 0 4 1 1 1
```

Quality



Consensus

```
                                   R - V M T A A Q I + K W T A K A + E W V + - - - - - - - - - K G K T P A + I K D K L T G

Prm_Prm_76339/1-146       119  L R G V M N - - - A K D K E K Y N L F L A A Y L R - - - - - - - - - - - - - - - A H P - -  143
Pso_288968/1-82            78  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - A N P - -   80
Pca_14853/1-131           114  F N G V M S - - - D K N K E K I L S V - - - - - - - - - - - - - - - - - - - - - - - - -  129
Pca_15117/1-144           114  F N G V M S - - - D K N R K K Y E L F L A K W G R - - - - - - - - - - - - - - - A N P D E  140
Pin_PITG_12276T0/1-140    110  K K G R R T D P R S K N K Q K Y N L F L A A S L K - - - - - - - - - - - - - - - K H P - -  137
Pca_19651/1-140           110  M N G L M T - - - A E N R K K Y E L F T A A Y G R - - - - - - - - - - - - - - - A N P H A  136
Pin_PITG_11839T0/1-155    111  L G A G M I - - - Q K N G M K F N L F F L Q S I T L C I P A T L A S Q D E V L A I S H S  151

Conservation
                                   1 0 3 0 0 0 - - - 0 2 2 0 0 4 1 0 0 1 - - - - - - - - - - - - - - - - - - - - - - - 1 0 1 - -

Quality

Consensus
                                   + N G V M + - - - + K N K + K Y N L F L A A + + R - - - - - - - - - - - - - - - A N P H -

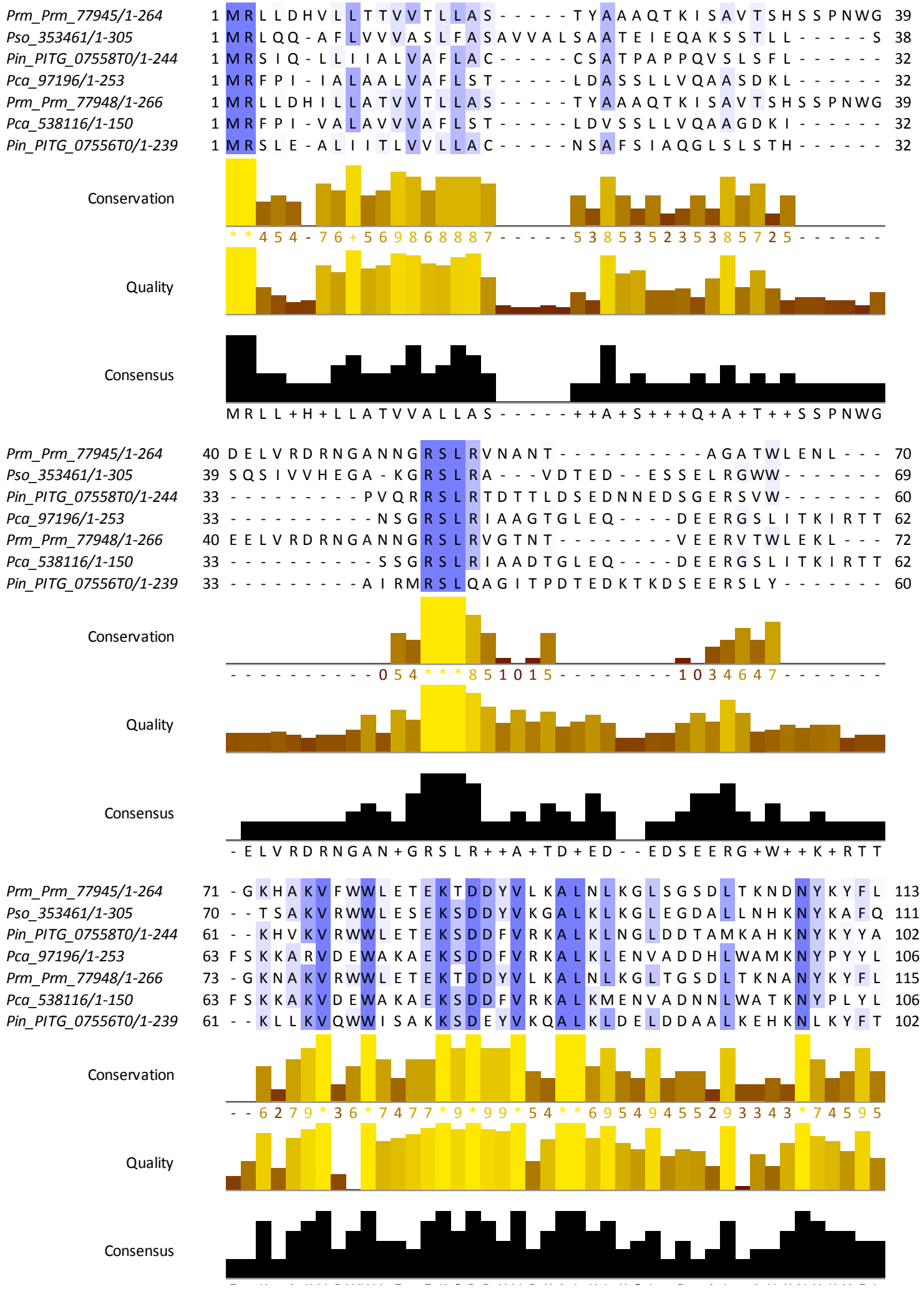
Prm_Prm_76339/1-146       144  - G G I                                                                                  146
Pso_288968/1-82            81  - - D L                                                                                   82
Pca_14853/1-131           130  - - R G                                                                                  131
Pca_15117/1-144           141  F G R R                                                                                  144
Pin_PITG_12276T0/1-140    138  - G G I                                                                                  140
Pca_19651/1-140           137  L D R L                                                                                  140
Pin_PITG_11839T0/1-155    152  L N I T                                                                                  155

Conservation
                                   - - 2 3

Quality

Consensus
                                   L G R +
```

Ortholog 10


Prm_Prm_77945/1-264 1 MRLLDHVLLTTVVTLLAS-----TYAAAQTKISAVTSHSSPNWG 39
Pso_353461/1-305 1 MRLQQ-AFLVVVASLFASAVVALSAATEIEQAKSSTLL-----S 38
Pin_PITG_07558T0/1-244 1 MRSIQ-LLIIALVAFLAC-----CSATPAPPQVSLSFL------ 32
Pca_97196/1-253 1 MRFPI-IALAALVAFLST-----LDASSLLVQAASDKL------ 32
Prm_Prm_77948/1-266 1 MRLLDHILLATVVTLLAS-----TYAAAQTKISAVTSHSSPNWG 39
Pca_538116/1-150 1 MRFPI-VALAVVVAFLST-----LDVSSLLVQAAGDKI------ 32
Pin_PITG_07556T0/1-239 1 MRSLE-ALIITLVVLLAC-----NSAFSIAQGLSLSTH------ 32
Conservation
**454-76+5698688887-----53853523538572 5------
Quality
Consensus
MRLL+H+LLATVVALLAS-----++A+S+++Q+A+T++SSPNWG
Prm_Prm_77945/1-264 40 DELVRDRNGANNGRSLRVNANT----------AGATWLENL--- 70
Pso_353461/1-305 39 SQSIVVHEGA-KGRSLRA---VDTED--ESSELRGWW------- 69
Pin_PITG_07558T0/1-244 33 ---------PVQRRSLRTDTTLDSEDNNEDSGERSVW------- 60
Pca_97196/1-253 33 ----------NSGRSLRIAAGTGLEQ----DEERGSLITKIRTT 62
Prm_Prm_77948/1-266 40 EELVRDRNGANNGRSLRVGTNT--------VEERVTWLEKL--- 72
Pca_538116/1-150 33 ----------SSGRSLRIAADTGLEQ----DEERGSLITKIRTT 62
Pin_PITG_07556T0/1-239 33 ---------AIRMRSLQAGITPDTEDKTKDSEERSLY------- 60
Conservation
---------054***851015--------1034647------
Quality
Consensus
-ELVRDRNGAN+GRSLR++A+TD+ED--EDSEERG+W++K+RTT
Prm_Prm_77945/1-264 71 -GKHAKVFWWLETEKTDDYVLKALNLKGLSGSDLTKNDNYKYFL 113
Pso_353461/1-305 70 --TSAKVRWWLESEKSDDYVKGALKLKGLEGDALLNHKNYKAFQ 111
Pin_PITG_07558T0/1-244 61 --KHVKVRWWLETEKSDDFVRKALKLNGLDDTAMKAHKNYKYYA 102
Pca_97196/1-253 63 FSKKARVDEWAKAEKSDDFVRKALKLENVADDHLWAMKNYPYYL 106
Prm_Prm_77948/1-266 73 -GKNAKVRWWLETEKTDDYVLKALNLKGLTGSDLTKNANYKYFL 115
Pca_538116/1-150 63 FSKKAKVDEWAKAEKSDDFVRKALKMENVADNNLWATKNYPLYL 106
Pin_PITG_07556T0/1-239 61 --KLLKVQWWISAKKSDEYVKQALKLDELDDAALKEHKNLKYFT 102
Conservation
--6279*36*7477*9*99*54**69549455293343*74595
Quality
Consensus

```
                                   F + K + A K V R W W L E + E K S D D Y V R K A L K L K G L + D + A L + A H K N Y K Y F L

Prm_Prm_77945/1-264        114 K F A K K A E S Y R L N K W L R N D F P T Y E A W K E L G L Q K - V R T I E Q L N Q I R 156
Pso_353461/1-305           112 Y F L K K S E D Y K I N K W Y R N E Y T T Y Q G W Q E L G L N K K I T L G K D L D K I R 155
Pin_PITG_07558T0/1-244     103 Y F A K K A E D Y L F N K W L R N H V P T F E A W K S L N L G K - I T K A D Q L K E I A 145
Pca_97196/1-253            107 R F L E K T E A K K I N D W L I G D V P T Y G A W V K L G L G S - I - - - D D I E K V K 146
Prm_Prm_77948/1-266        116 K F A K K A E S N R R A M W V R K D F P T Y Q V W K E L G L Q G - V R T V E Q L N Q I R 158
Pca_538116/1-150           107 R F L E K A E A A K I K N W L I G D V S T Y G A W A K L G L N S - L - - - D D M D K A K 146
Pin_PITG_07556T0/1-239     103 Y F Q Y E K R H N L L S K A F R R N L P T F E V W K K L N L D K - I T S R D Q L K D I Y 145

Conservation
                               6 * 5 5 7 4 8 2 3 5 4 4 4 6 6 5 4 4 6 7 * 9 4 8 * 3 4 * 7 * 4 4 - 9 - - - 6 7 9 5 5 7 3
Quality
Consensus
                               Y F + K K A E + Y K I N K W L R N D V P T Y E A W K + L G L + K - I T T - D Q L + K I R

Prm_Prm_77945/1-264        157 N T K E F G I Y K R Y V N E F D D Y V Y R S M V A G Y N P - P K V M V V S G A T K A E M 199
Pso_353461/1-305           156 N T D E F K V Y K H Y V N Y F D K F V L I S L K A G D K P - P K W M V A R G P S D A E M 198
Pin_PITG_07558T0/1-244     146 N T K N F I S Y S R F V K Q Y D D N V V S T L N A G Y N P - P V V A V A R G A S E A E I 188
Pca_97196/1-253            147 T T A A F K T Y E K F V K E Y D D Q A I A L W K D Y K I P - - - I P V A K A T S P T E M 187
Prm_Prm_77948/1-266        159 N T K V F A V Y K R Y V N E F D N Y V Y R S M V A G Y N P - P K V M V A R G A P K A E M 201
Pca_538116/1-150           147 R A A A - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 150
Pin_PITG_07556T0/1-239     146 Q A A D F R A Y S R Y V K M F D N S V V G L V N G G V G T V P R V M I A R G A T D P E I 189

Conservation
                               7 7 3 3 2 0 0 3 1 3 2 3 1 0 2 4 1 0 2 1 0 0 1 0 1 1 0 0 1 - - - 1 0 2 2 1 3 1 1 0 1 3 1
Quality
Consensus
                               N T + + F K V Y K R Y V + E F D D Y V + R S + + A G Y N P - P K V M V A R G A S + A E M

Prm_Prm_77945/1-264        200 T A R V E I M A E A K R S E A Y A K V A L G L T V - - P G R P R L T L T G K P L E K H D 241
Pso_353461/1-305           199 T A R T E I M A E A R R P A K Y A K L A L G L T E T T D N S K L K L L T D K A L E E S S 242
Pin_PITG_07558T0/1-244     189 T A R T M I M A S A R R D D D V A K V L L G L T K - - P G Y P R R V L D G N A L T Q H D 230
Pca_97196/1-253            188 N A R M D I L A A A K R G D D Y A K K V L G L D N - - - - - - - - - V T G S A L I S H V 222
Prm_Prm_77948/1-266        202 T A R V E I M A E A K R S E L Y A K V A L G L T V - - P G R R G I T L K G E A L K K H D 243
Pca_538116/1-150           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07556T0/1-239     190 T A R T I L M A R E G R S D N V A K V L L G L T E - - A D D P F R V L S G A K L I Q H Q 231

Conservation
                               2 3 3 0 0 2 1 3 0 0 0 3 1 0 0 1 3 4 1 1 2 3 2 2 0 - - - - - - - - - 2 1 1 0 0 2 0 1 1 0
Quality
Consensus
```

```
                                   T A R T E I M A E A K R S D D Y A K V A L G L T + - - P G R P R R + L T G K A L + + H D

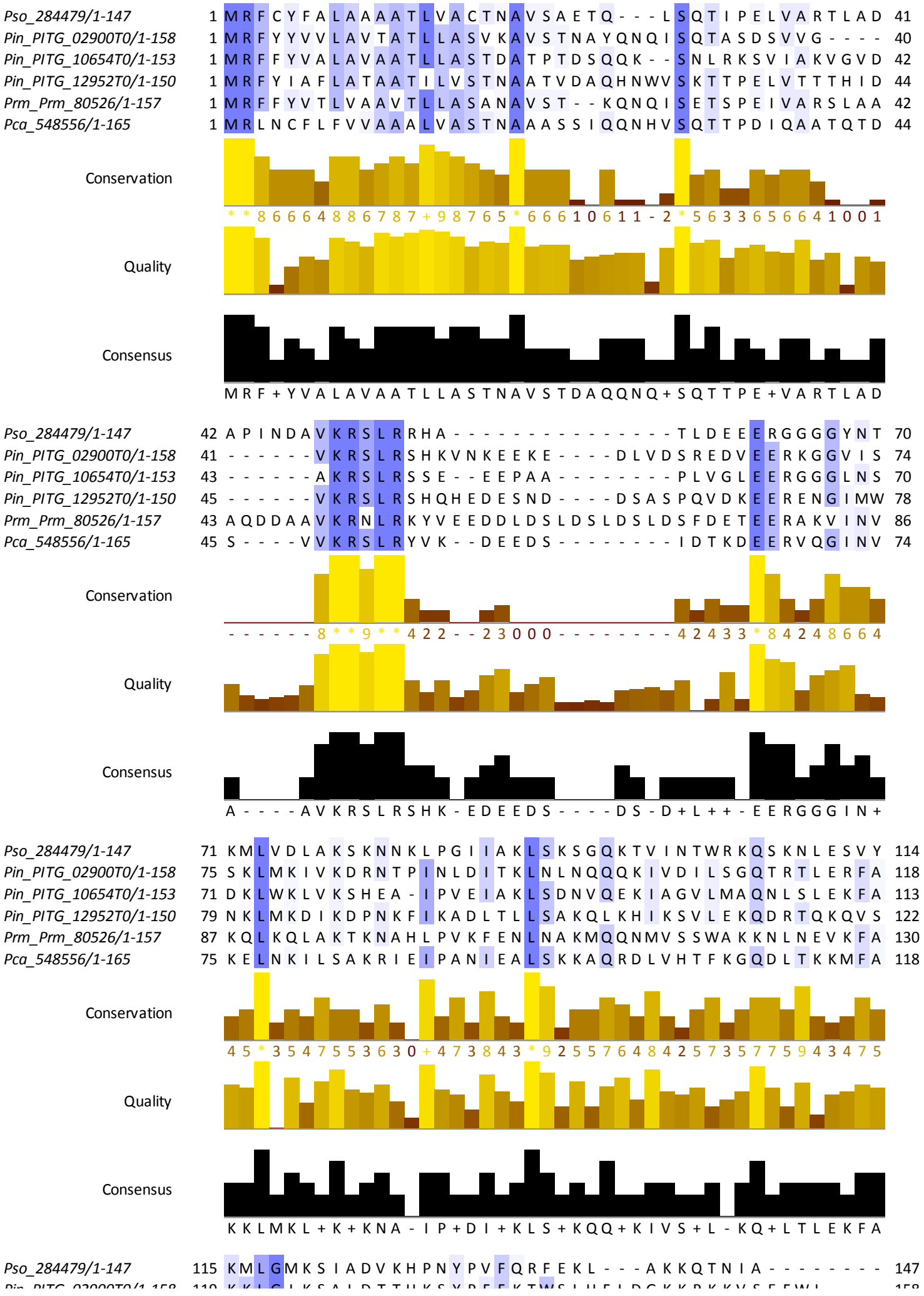
Prm_Prm_77945/1-264        242 N Y G Y F K L F L A E A A K V A K S T N K V - - - - - - - - - - - - - - - - - - - - - - - 263
Pso_353461/1-305           243 D F K Y F V L F L K K K E P V L T E E L K K L E A R V L P N Q L R S N K R Y Q E L L E E 286
Pin_PITG_07558T0/1-244     231 E Y K Y Y Q L F K E A K T - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 243
Pca_97196/1-253            223 N Y Q Y F E H Y R R T V K R L Q D P K K K L N R L P T I - - - - - - - - - - - - - - - - 250
Prm_Prm_77948/1-266        244 D Y G Y F E L F L A E A A K V A K T P I K V - - - - - - - - - - - - - - - - - - - - - - - 265
Pca_538116/1-150                - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_07556T0/1-239     232 D Y K Y F E L F - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 239

Conservation
                                   1 2 0 3 2 0 1 2 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality
Consensus
                                   D Y K Y F E L F L A E + A K V A K - - - K V - - - - - - - - - - - - - - - - - - - - - -

Prm_Prm_77945/1-264                - - - - - - - - - - - - - - - - - - - A                                             264
Pso_353461/1-305           287 M G W V K K Y V T A A N A G G A P R G                                                   305
Pin_PITG_07558T0/1-244             - - - - - - - - - - - - - - - - - - - S                                             244
Pca_97196/1-253            251 - - - - - - - - - - - - - - - - - T E R                                                 253
Prm_Prm_77948/1-266                - - - - - - - - - - - - - - - - - - - A                                             266
Pca_538116/1-150                   - - - - - - - - - - - - - - - - - - -
Pin_PITG_07556T0/1-239             - - - - - - - - - - - - - - - - - - -

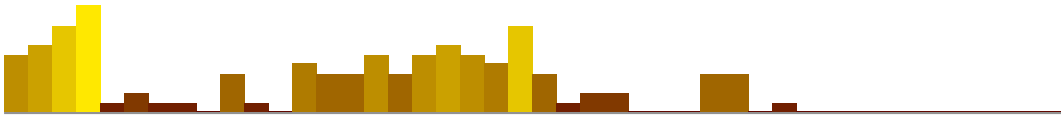
Conservation
                                   - - - - - - - - - - - - - - - - - - -
Quality
Consensus
                                   - - - - - - - - - - - - - - - - - - A
```

Ortholog 11


Pso_284479/1-147 1 MRFCYFALAAAATLVACTNAVSAETQ---LSQTIPELVARTLAD 41
Pin_PITG_02900T0/1-158 1 MRFYYVVLAVTATLLASVKAVSTNAYQNQISQTASDSVVG---- 40
Pin_PITG_10654T0/1-153 1 MRFFYVALAVAATLLASTDATPTDSQQK--SNLRKSVIAKVGVD 42
Pin_PITG_12952T0/1-150 1 MRFYIAFLATAATILVSTNAATVDAQHNWVSKTTPELVTTTHID 44
Prm_Prm_80526/1-157 1 MRFFYVTLVAAVTLLASANAVST--KQNQISETSPEIVARSLAA 42
Pca_548556/1-165 1 MRLNCFLFVVAAALVASTNAAASSIQQNHVSQTTPDIQAATQTD 44
Conservation
**86664886787+98765*66610611-2*5633656641001
Quality
Consensus
MRF+YVALAVAATLLASTNAVSTDAQQNQ+SQTTPE+VARTLAD
Pso_284479/1-147 42 APINDAVKRSLRRHA----------TLDEEERGGGGYNT 70
Pin_PITG_02900T0/1-158 41 ------VKRSLRSHKVNKEEKE----DLVDSREDVEERKGGVIS 74
Pin_PITG_10654T0/1-153 43 ------AKRSLRSSE--EEPAA--------PLVGLEERGGGLNS 70
Pin_PITG_12952T0/1-150 45 ------VKRSLRSHQHEDESND----DSASPQVDKEERENGIMW 78
Prm_Prm_80526/1-157 43 AQDDAAVKRNLRKYVEEDDLDSLDSLDSLDSFDETEERAKVINV 86
Pca_548556/1-165 45 S----VVKRSLRYVK--DEEDS--------IDTKDEERVQGINV 74
Conservation
------8**9**422--23000--------42433*84248664
Quality
Consensus
A----AVKRSLRSHK-EDEEDS----DS-D+L++-EERGGGIN+
Pso_284479/1-147 71 KMLVDLAKSKNNKLPGIIAKLSKSGQKTVINTWRKQSKNLESVY 114
Pin_PITG_02900T0/1-158 75 SKLMKIVKDRNTPINLDITKLNLNQQQKIVDILSGQTRTLERFA 118
Pin_PITG_10654T0/1-153 71 DKLWKLVKSHEA-IPVEIAKLSDNVQEKIAGVLMAQNLSLEKFA 113
Pin_PITG_12952T0/1-150 79 NKLMKDIKDPNKFIKADLTLLSAKQLKHIKSVLEKQDRTQKQVS 122
Prm_Prm_80526/1-157 87 KQLKQLAKTKNAHLPVKFENLNAKMQQNMVSSWAKKNLNEVKFA 130
Pca_548556/1-165 75 KELNKILSAKRIEIPANIEALSKKAQRDLVHTFKGQDLTKKMFA 118
Conservation
45*3547553630+473843*9255764842573577594347 5
Quality
Consensus
KKLMKL+K+KNA-IP+DI+KLS+KQQ+KIVS+L-KQ+LTLEKFA
Pso_284479/1-147 115 KMLGMKSIADVKHPNYPVFQRFEKL---AKKQTNIA-------- 147

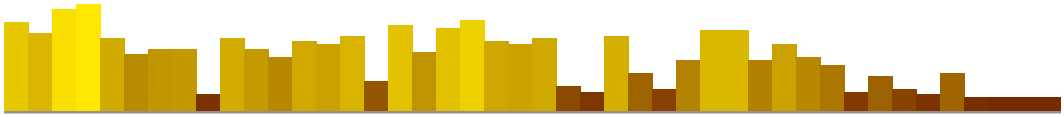
```
Pin_PITG_02900T0/1-158    119 K K L G T K S A L D T T H K S Y P F F K T W S L H F L D G K K P K K V S E F W T - - - - 158
Pin_PITG_10654T0/1-153    114 K K V G M D G A H D T A H R N N P F F Q K W K A N F L D G K K P K K I P E E W I - - - - 153
Pin_PITG_12952T0/1-150    123 K K L G - - - - - - - - N Q N S K F V E E W K E S F R V R K K P K P Q W - - - - - - - - 150
Prm_Prm_80526/1-157       131 K K L G L K S V N D V G N K N Y P A F Q K F R E M F T - - - - - - - - - - - - - - - - - 157
Pca_548556/1-165          119 T K L G M R D V D D V A N R H Y P F F E K W E H L F R P G K K E K K V P E M L I G N H E 162
```

Conservation



```
6 7 9 * 1 2 1 1 0 4 1 0 5 4 4 6 4 6 7 6 5 9 4 1 2 2 0 - 0 4 4 0 1 0 0 0 - - - - - - - -
```

Quality



Consensus

```
K K L G M K S + - D V A + + N Y P F F Q K W + E L F + D G K K P K K + P E - W I - - - -
```

```
Pso_284479/1-147          - - -
Pin_PITG_02900T0/1-158    - - -
Pin_PITG_10654T0/1-153    - - -
Pin_PITG_12952T0/1-150    - - -
Prm_Prm_80526/1-157       - - -
Pca_548556/1-165          163 Y Y Y                                                                                 165
```

Conservation

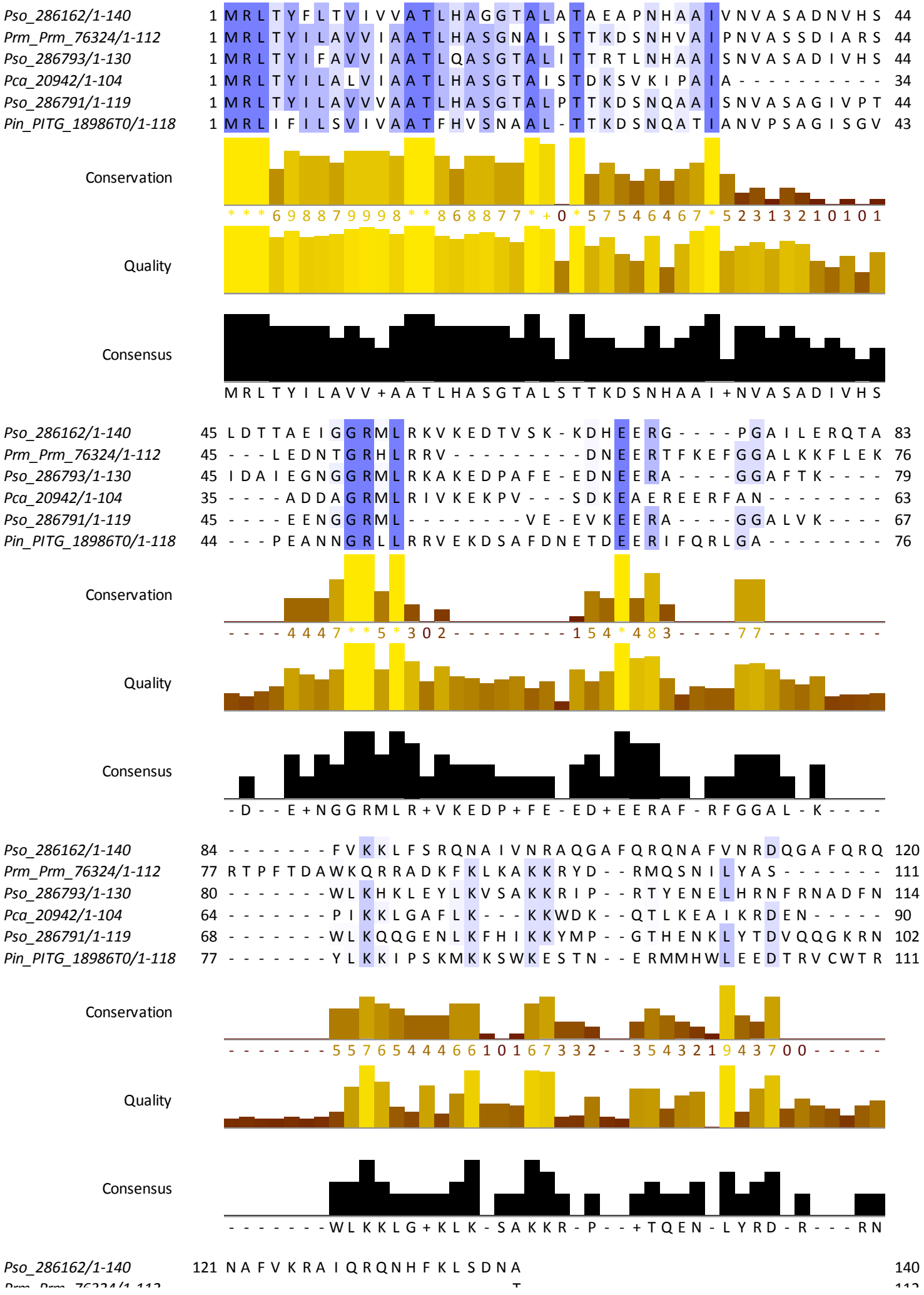
```
- - -
```

Quality

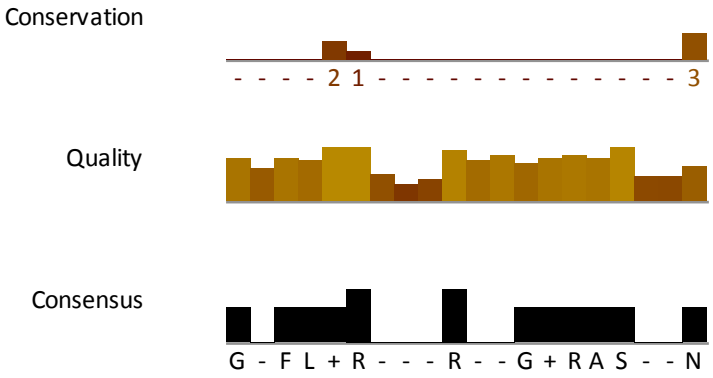
Consensus

```
- - -
```

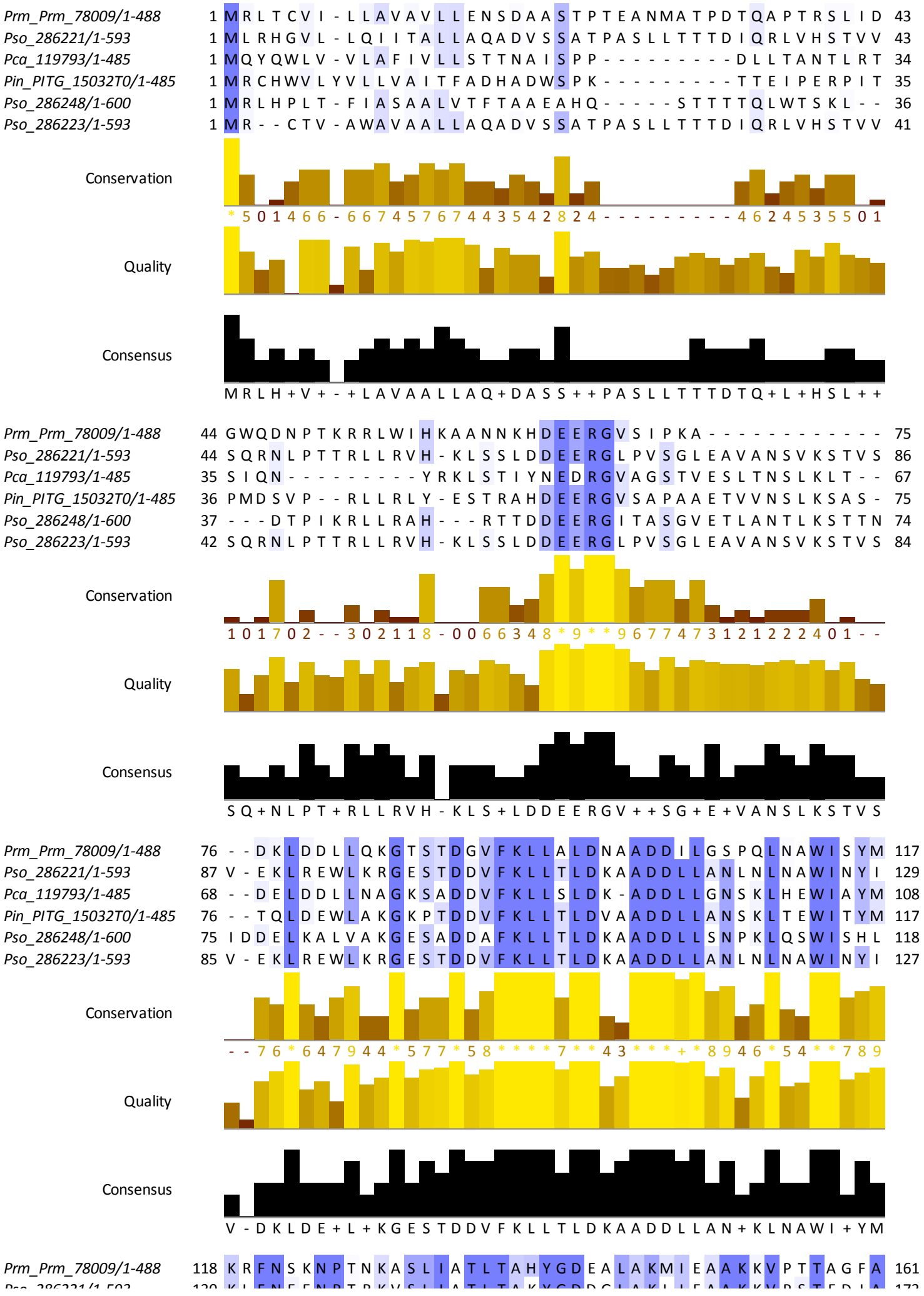
Ortholog 12


Pso_286162/1-140 1 MRLTYFLTVIVVATLHAGGTALATAEAPNHAAIVNVASADNVHS 44
Prm_Prm_76324/1-112 1 MRLTYILAVVIAATLHASGNAISTTKDSNHVAIPNVASSDIARS 44
Pso_286793/1-130 1 MRLTYIFAVVIAATLQASGTALITTRTLNHAAISNVASADIVHS 44
Pca_20942/1-104 1 MRLTYILALVIAATLHASGTAISTDKSVKIPAIA---------- 34
Pso_286791/1-119 1 MRLTYILAVVVAATLHASGTALPTTKDSNQAAISNVASAGIVPT 44
Pin_PITG_18986T0/1-118 1 MRLIFILSVIVAATFHVSNAAL-TTKDSNQATIANVPSAGISGV 43
Conservation
***6988799 98**8688 77*+0*5754646 7*5231321010 1
Quality
Consensus
MRLTYILAVV+AATLHASGTALSTTKDSNHAAI+NVASADIVHS
Pso_286162/1-140 45 LDTTAEIGGRMLRKVKEDTVSK-KDHEERG----PGAILERQTA 83
Prm_Prm_76324/1-112 45 ---LEDNTGRHLRRV---------DNEERTFKEFGGALKKFLEK 76
Pso_286793/1-130 45 IDAIEGNGGRMLRKAKEDPAFE-EDNEERA----GGAFTK---- 79
Pca_20942/1-104 35 ----ADDAGRMLRIVKEKPV---SDKEAEREERFAN-------- 63
Pso_286791/1-119 45 ----EENGGRML--------VE-EVKEERA----GGALVK---- 67
Pin_PITG_18986T0/1-118 44 ---PEANNGRLLRRVEKDSAFDNETDEERIFQRLGA------- 76
Conservation
----4447**5*302--------154*483----77--------
Quality
Consensus
-D--E+NGGRMLR+VKEDP+FE-ED+EERAF-RFGGAL-K----
Pso_286162/1-140 84 -------FVKKLFSRQNAIVNRAQGAFQRQNAFVNRDQGAFQRQ 120
Prm_Prm_76324/1-112 77 RTPFTDAWKQRRADKFKLKAKKRYD--RMQSNILYAS------- 111
Pso_286793/1-130 80 -------WLKHKLEYLKVSAKKRIP--RTYENELHRNFRNADFN 114
Pca_20942/1-104 64 -------PIKKLGAFLK---KKWDK--QTLKEAIKRDEN----- 90
Pso_286791/1-119 68 -------WLKQQGENLKFHIKKYMP--GTHENKLYTDVQQGKRN 102
Pin_PITG_18986T0/1-118 77 -------YLKKIPSKMKKSWKESTN--ERMMHWLEEDTRVCWTR 111
Conservation
-------5576544466101673 32--3543219437 00-----
Quality
Consensus
-------WLKKLG+KLK-SAKKR-P--+TQEN-LYRD-R---RN
Pso_286162/1-140 121 NAFVKRAIQRQNHFKLSDNA 140

Pfm_Pfm_76324/1-112		- I	112
Pso_286793/1-130	115	G R F K R N - - - Q A A N I R A S I - N	130
Pca_20942/1-104	91	- - - - R R K W I R E Q G F E P R - - D	104
Pso_286791/1-119	103	A E M L K R - - - R D S G I R A A M G N	119
Pin_PITG_18986T0/1-118	112	G L I L D T - - - - - - - - - - - - - - L	118



Ortholog 13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Pso_286221/1-593 1 M L R H G V L - L Q I I T A L L A Q A D V S S A T P A S L L T T T D I Q R L V H S T V V 43
Pca_119793/1-485 1 M Q Y Q W L V - V L A F I V L L S T T N A I S P P - - - - - - - - - D L L T A N T L R T 34
Pin_PITG_15032T0/1-485 1 M R C H W V L Y V L L V A I T F A D H A D W S P K - - - - - - - - - T T E I P E R P I T 35
Pso_286248/1-600 1 M R L H P L T - F I A S A A L V T F T A A E A H Q - - - - - S T T T T Q L W T S K L - - 36
Pso_286223/1-593 1 M R - - C T V - A W A V A A L L A Q A D V S S A T P A S L L T T T D I Q R L V H S T V V 41
Conservation
* 5 0 1 4 6 6 - 6 6 7 4 5 7 6 7 4 4 3 5 4 2 8 2 4 - - - - - - - - - 4 6 2 4 5 3 5 5 0 1
Quality
Consensus
M R L H + V + - + L A V A A L L A Q + D A S S + + P A S L L T T T D T Q + L + H S L + +
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Pso_286221/1-593 44 S Q R N L P T T R L L R V H - K L S S L D D E E R G L P V S G L E A V A N S V K S T V S 86
Pca_119793/1-485 35 S I Q N - - - - - - - - - Y R K L S T I Y N E D R G V A G S T V E S L T N S L K L T - - 67
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Pso_286248/1-600 37 - - - D T P I K R L L R A H - - - R T T D D E E R G I T A S G V E T L A N T L K S T T N 74
Pso_286223/1-593 42 S Q R N L P T T R L L R V H - K L S S L D D E E R G L P V S G L E A V A N S V K S T V S 84
Conservation
1 0 1 7 0 2 - - 3 0 2 1 1 8 - 0 0 6 6 3 4 8 * 9 * * 9 6 7 7 4 7 3 1 2 1 2 2 2 4 0 1 - -
Quality
Consensus
S Q + N L P T + R L L R V H - K L S + L D D E E R G V + + S G + E + V A N S L K S T V S
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Pso_286221/1-593 87 V - E K L R E W L K R G E S T D D V F K L L T L D K A A D D L L A N L N L N A W I N Y I 129
Pca_119793/1-485 68 - - D E L D D L L N A G K S A D D V F K L L S L D K - A D D L L G N S K L H E W I A Y M 108
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Pso_286248/1-600 75 I D D E L K A L V A K G E S A D D A F K L L T L D K A A D D L L S N P K L Q S W I S H L 118
Pso_286223/1-593 85 V - E K L R E W L K R G E S T D D V F K L L T L D K A A D D L L A N L N L N A W I N Y I 127
Conservation
- - 7 6 * 6 4 7 9 4 4 * 5 7 7 * 5 8 * * * * 7 * * 4 3 * * * + * 8 9 4 6 * 5 4 * * 7 8 9
Quality
Consensus
V - D K L D E + L + K G E S T D D V F K L L T L D K A A D D L L A N + K L N A W I + Y M
Prm_Prm_78009/1-488 118 K R F N S K N P T N K A S L I A T L T A H Y G D E A L A K M I E A A K K V P T T A G F A 161

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Pca_119793/1-485        109 K A F N Q K T P S E R T S V I A T L T A H Y G D D G V A K M V E A A K H V R T T S A L A 152
Pin_PITG_15032T0/1-485  118 K L F N Q A N P K K Q T S L I R T L T T H Y G D E A L A K M V V A A K Q V P D T A T F A 161
Pso_286248/1-600        119 E L F N E Q N P S K K T T L I A T L T A H Y G D E A L T R I I E Q G K R V A S T E A T A 162
Pso_286223/1-593        128 K L F N E E N P T Q K V S L I A T L T A K Y G D D G L A K L I E A A K K V P S T E D I A 171

Conservation            7 3 * * 6 3 + * 5 5 7 6 9 9 * 4 * * * 7 9 * * * 9 + 9 7 9 9 9 4 6 + * 6 * 3 7 * 4 5 5 *
Quality
Consensus               K L F N E + N P T K K T S L I A T L T A H Y G D + + L A K M I E A A K K V P S T E + + A

Prm_Prm_78009/1-488     162 K R V Q T E L V Q R W L V A G E T - - - - - - - - - - - - - - - - - - - - - - - - - - 178
Pso_286221/1-593        174 K R V Q A E Q L Q S W L A D M K T T K E V F A L L A L D K A A D D L L A S P L L N T W L 217
Pca_119793/1-485        153 K R V Q A E Q T Q R W L V D G K T - - - - - - - - - - - - - - - - - - - - - - - - - - 169
Pin_PITG_15032T0/1-485  162 K R L Q T E Q L Q L W L N Q G K S - - - - - - - - - - - - - - - - - - - - - - - - - - 178
Pso_286248/1-600        163 N R I Q A K Q F E A W L A G G Q S A D D V F K L L A L D K A K E E L I G S P L L D S W L 206
Pso_286223/1-593        172 K R V Q A E Q L Q S W L A D M K T T K E V F A L L A L D K A A D D L L A S P L L N T W L 215

Conservation            6 * 9 * 7 7 7 5 8 3 * * 6 4 8 6 9 - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality
Consensus               K R V Q A E Q L Q + W L A D G K T T K E V F A L L A L D K A A D D L L A S P L L N T W L

Prm_Prm_78009/1-488     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_286221/1-593        218 S Y M K L V N E D S T K K - T S L L A T L T A H Y G A D G V S K M I E S A K R V P S T A 260
Pca_119793/1-485        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
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Pso_286248/1-600        207 G Y M K F F N K E K P K K Q T S L I S T L A A H Y N E F E L A E M I G S A R K V P S T A 250
Pso_286223/1-593        216 S Y M K L V N E D S T K K - T S L L A T L T A H Y G A D G V S K M I E S A K R V P S T A 258

Conservation            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality
Consensus               S Y M K L V N E D S T K K - T S L L A T L T A H Y G A D G V S K M I E S A K R V P S T A

Prm_Prm_78009/1-488     179 - - - - - - - - - - - - - - - - - - - - - - - - P D K V F A L L K L D E A G A G L F A Q P Q 200
Pso_286221/1-593        261 T M A K R L E N E Q I R R W I A D E M - - Y P I D V F T L L K L D K S G A Q L F T Q P Q 302
Pca_119793/1-485        170 - - - - - - - - - - - - - - - - - - - - - - - - P T Q V F Q L L K L D E A G T D L F T Q P Q 191
Pin_PITG_15032T0/1-485  179 - - - - - - - - - - - - - - - - - - - - - - - - P D D V F T L L K L D K A G Q K V F T H P E 200
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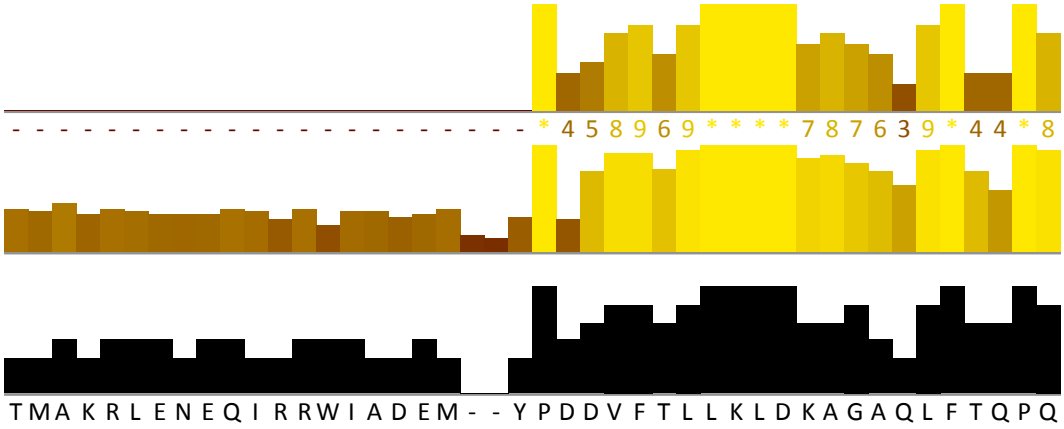


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Pso_286221/1-593        303 V N T W L K F V D D F G K A N P N T E K T L F - - - - - - - - - - - - - - - - - - A V L 328
Pca_119793/1-485        192 I V T W A K Y F E D F H K V K P N K E A T L F - - - - - - - - - - - - - - - - - - T F L 217
Pin_PITG_15032T0/1-485  201 M V S W A K Y V G D F N K V N P D K P V T L F - - - - - - - - - - - - - - - - - - S T L 226
Pso_286248/1-600        295 V T A W M K Y M A A Y N N K N P K E K V S F L K S W E Y V V E D E K E V W K L V D S P L 338
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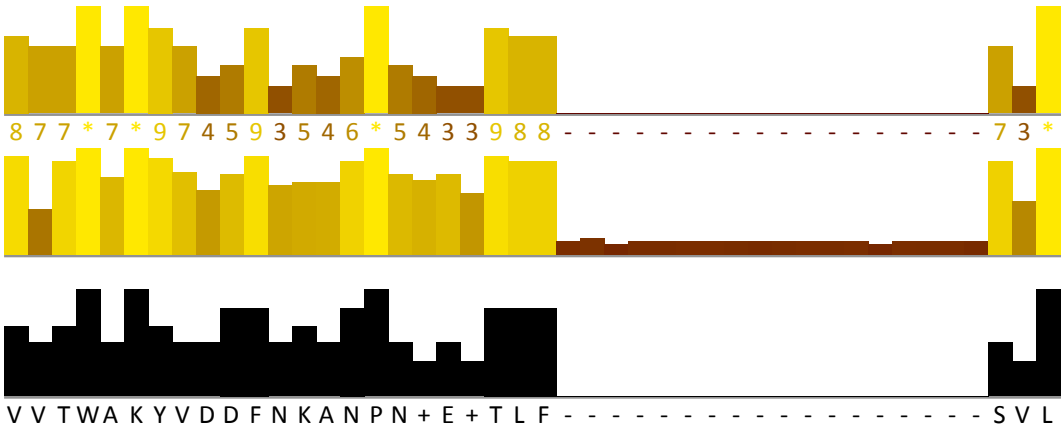


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Pca_119793/1-485        218 Q P R Y - - T E A T L A H M L I A A E K V P A T K S I A T R V Q A E L T S L W L - - - - 255
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Pso_286248/1-600        339 R K A Y - - N D E E L V T M L I A A K K V P S T E K M A R R V Q A E L T Q S W M - - - - 376
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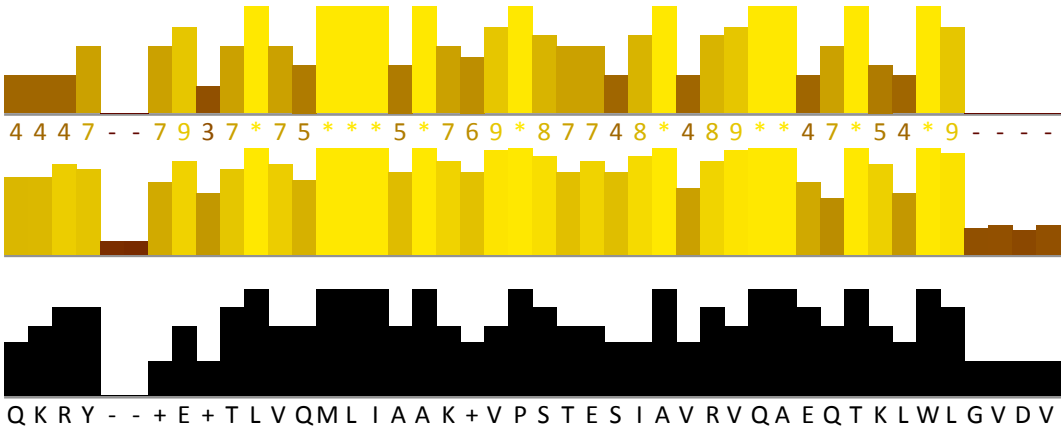


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Pca_119793/1-485        256 T N K V E - - P A D V F K L L Q L D - - E I G M P L L K D P V F N A W V K Y T D D F H K 295
Pin_PITG_15032T0/1-485  265 N T Q K E - - P G D V F K L L R L D - - K E G H D I I Q N P L F R A W V Q Y T D D F R K 304
Pso_286248/1-600        377 K D P K N H L P D D I F D L L K L T - - - D K E T L L G D P L F S A W L K Y L D E F N Y 417
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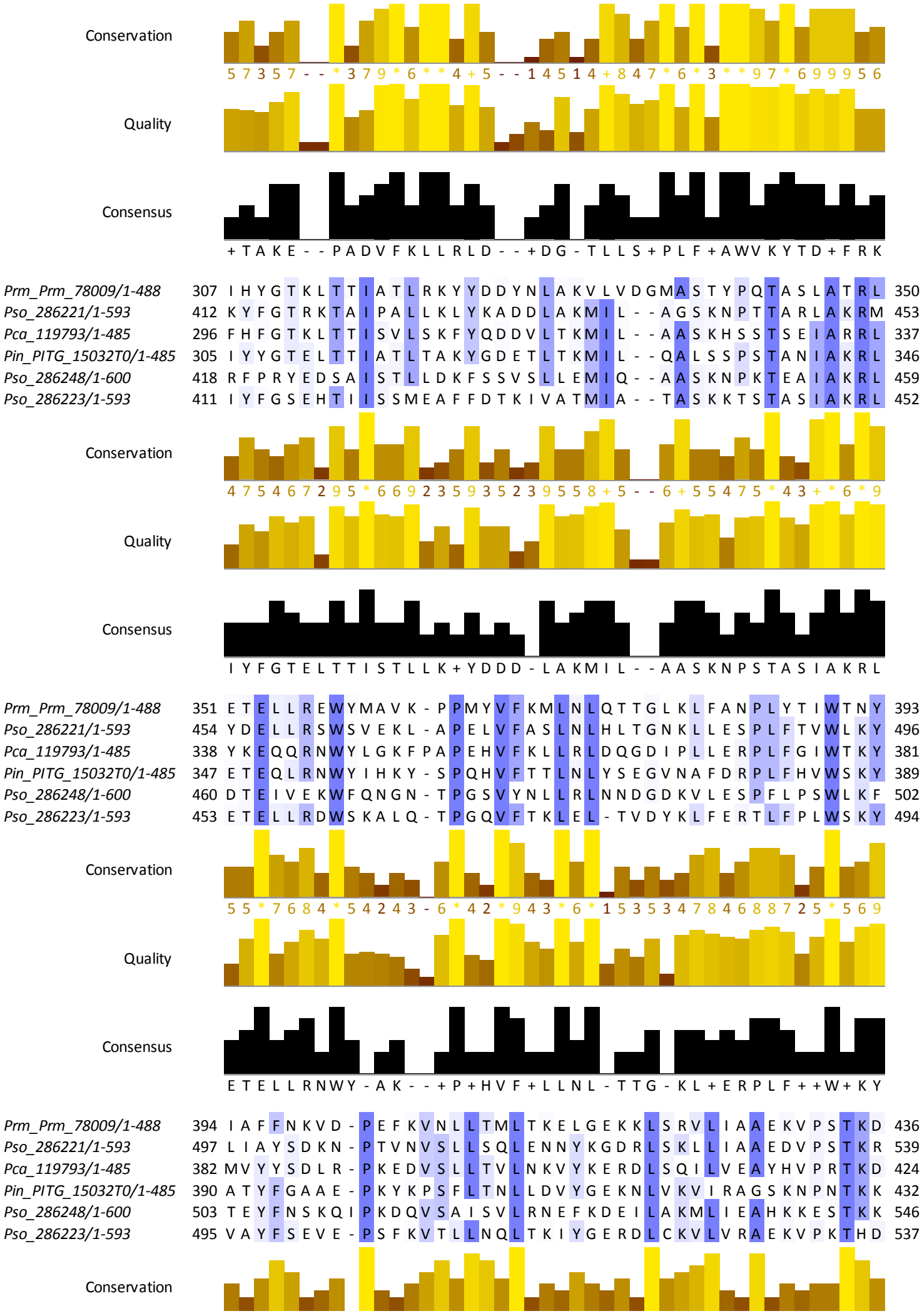
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Quality
Consensus
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Prm_Prm_78009/1-488 307 I H Y G T K L T T I A T L R K Y Y D D Y N L A K V L V D G M A S T Y P Q T A S L A T R L 350
Pso_286221/1-593 412 K Y F G T R K T A I P A L L K L Y K A D D L A K M I L - - A G S K N P T T A R L A K R M 453
Pca_119793/1-485 296 F H F G T K L T T I S V L S K F Y Q D D V L T K M I L - - A A S K H S S T S E I A R R L 337
Pin_PITG_15032T0/1-485 305 I Y Y G T E L T T I A T L T A K Y G D E T L T K M I L - - Q A L S S P S T A N I A K R L 346
Pso_286248/1-600 418 R F P R Y E D S A I S T L L D K F S S V S L L E M I Q - - A A S K N P K T E A I A K R L 459
Pso_286223/1-593 411 I Y F G S E H T I I S S M E A F F D T K I V A T M I A - - T A S K K T S T A S I A K R L 452
Conservation
4 7 5 4 6 7 2 9 5 * 6 6 9 2 3 5 9 3 5 2 3 9 5 5 8 + 5 - - 6 + 5 5 4 7 5 * 4 3 + * 6 * 9
Quality
Consensus
I Y F G T E L T T I S T L L K + Y D D D - L A K M I L - - A A S K N P S T A S I A K R L
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Pso_286221/1-593 454 Y D E L L R S W S V E K L - A P E L V F A S L N L H L T G N K L L E S P L F T V W L K Y 496
Pca_119793/1-485 338 Y K E Q Q R N W Y L G K F P A P E H V F K L L R L D Q G D I P L L E R P L F G I W T K Y 381
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Pso_286248/1-600 460 D T E I V E K W F Q N G N - T P G S V Y N L L R L N N D G D K V L E S P F L P S W L K F 502
Pso_286223/1-593 453 E T E L L R D W S K A L Q - T P G Q V F T K L E L - T V D Y K L F E R T L F P L W S K Y 494
Conservation
5 5 * 7 6 8 4 * 5 4 2 4 3 - 6 * 4 2 * 9 4 3 * 6 * 1 5 3 5 3 4 7 8 4 6 8 8 7 2 5 * 5 6 9
Quality
Consensus
E T E L L R N W Y - A K - - + P + H V F + L L N L - T T G - K L + E R P L F + + W + K Y
Prm_Prm_78009/1-488 394 I A F F N K V D - P E F K V N L L T M L T K E L G E K K L S R V L I A A E K V P S T K D 436
Pso_286221/1-593 497 L I A Y S D K N - P T V N V S L L S Q L E N N Y K G D R L S K L L I A A E D V P S T K R 539
Pca_119793/1-485 382 M V Y Y S D L R - P K E D V S L L T V L N K V Y K E R D L S Q I L V E A Y H V P R T K D 424
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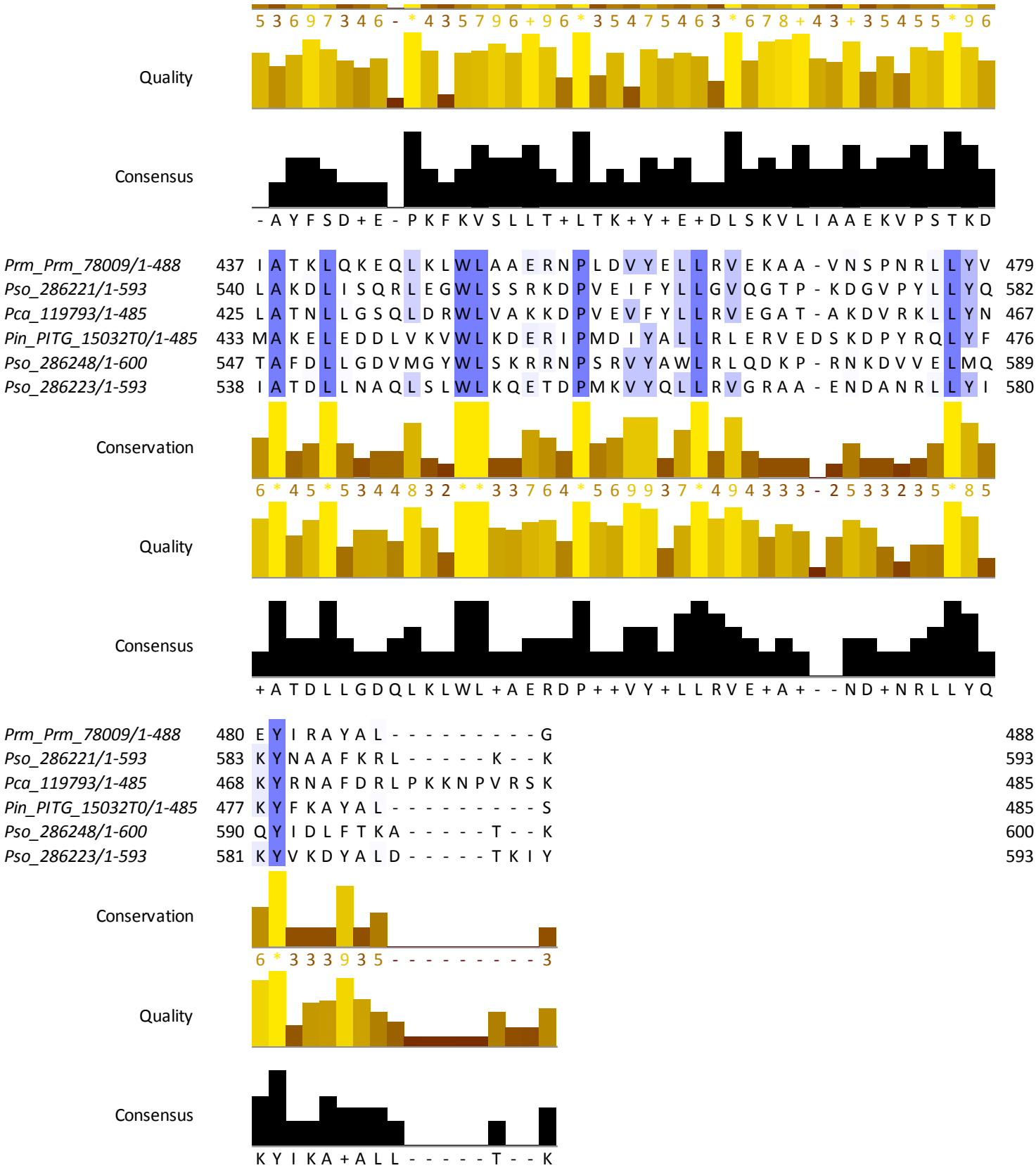
Conservation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Consensus
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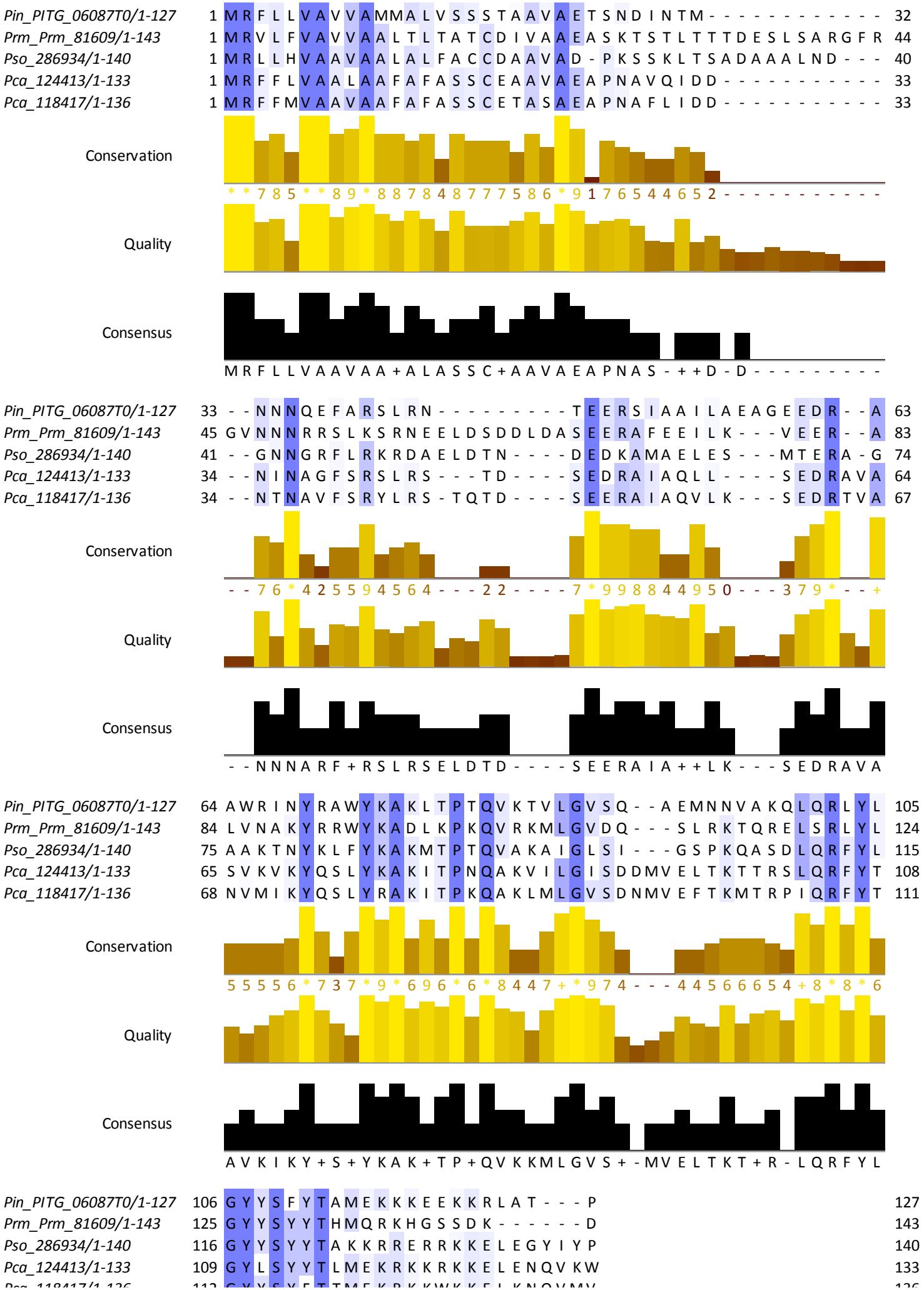
Ortholog 14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Pso_286934/1-140 1 MRLLHVAAVAALALFACCDAAVAD-PKSSKLTSADAAALND- - - 40
Pca_124413/1-133 1 MRFFLVAALAAFAFASSCEAAVAEAPNAVQIDD- - - - - - - - - - - 33
Pca_118417/1-136 1 MRFFMVAAVAAFAFASSCETASAEAPNAFLIDD- - - - - - - - - - - 33
Conservation
* * 7 8 5 * * 8 9 * 8 8 7 8 4 8 7 7 7 5 8 6 * 9 1 7 6 5 4 4 6 5 2 - - - - - - - - - - -
Quality
Consensus
MRFLLVAAVAA+ALASSC+AAVAEAPNAS-++D-D- - - - - - - - -
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Prm_Prm_81609/1-143 45 GVNNNRRSLKSRNEELDSDDLDASEERAFEEILK- - - VEER- - A 83
Pso_286934/1-140 41 - - GNNGRFLRKRDAELDTN- - - - DEDKAMAELES- - - MTERA-G 74
Pca_124413/1-133 34 - - NINAGFSRSLRS- - - TD- - - - SEDRAIAQLL- - - - SEDRAVA 64
Pca_118417/1-136 34 - - NTNAVFSRYLRS-TQTD- - - - SEERAIAQVLK- - - SEDRTVA 67
Conservation
- - 7 6 * 4 2 5 5 9 4 5 6 4 - - - 2 2 - - - - 7 * 9 9 8 8 4 4 9 5 0 - - - 3 7 9 * - - +
Quality
Consensus
- - NNNARF+RSLRSELDTD- - - - SEERAIA++LK- - - SEDRAVA
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Pso_286934/1-140 75 AAKTNYKLFYKAKMTPTQVAKAIGLSI- - - GSPKQASDLQRFYL 115
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Conservation
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Quality
Consensus
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Pin_PITG_06087T0/1-127 106 GYYSFYTAMEKKKEEKKRLAT- - - P 127
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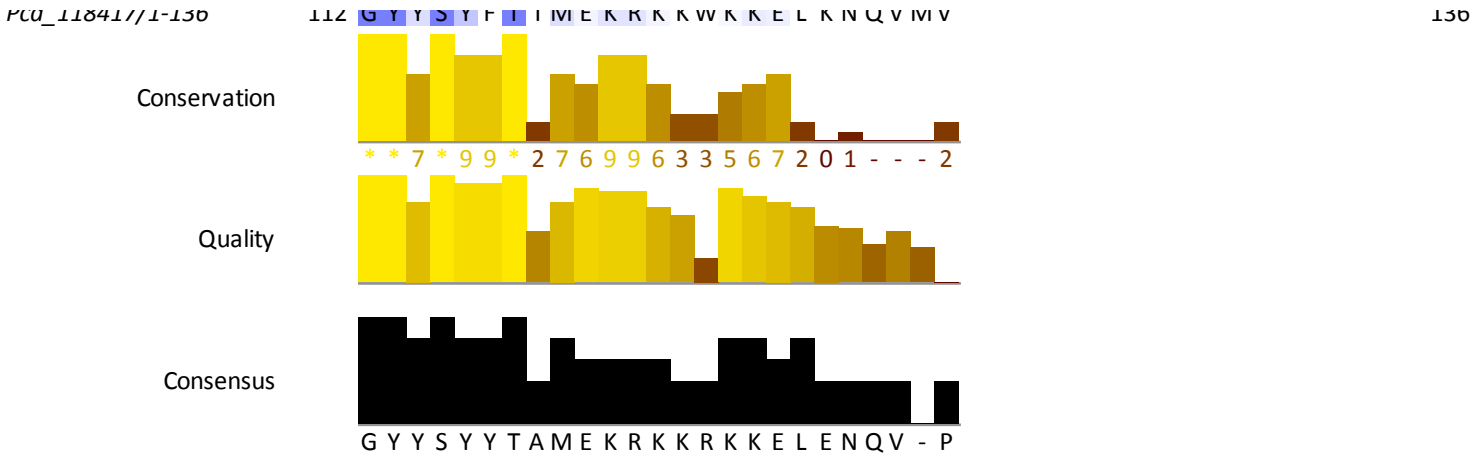
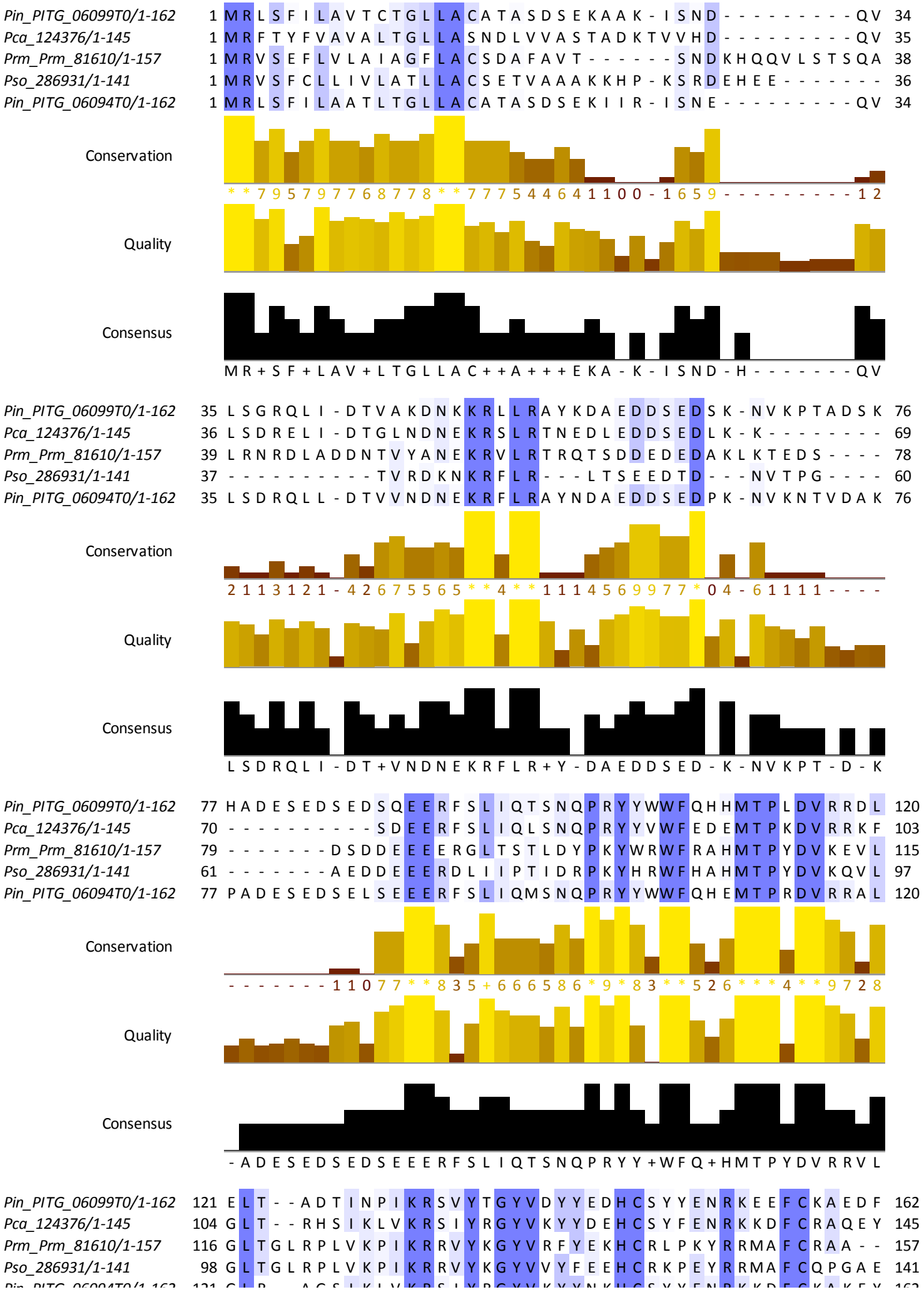

Pca_118417/1-136
112
136
Conservation
Quality
Consensus
* * 7 * 9 9 * 2 7 6 9 9 6 3 3 5 6 7 2 0 1 - - - 2
G Y Y S Y Y T A M E K R K K R K K E L E N Q V - P

Ortholog 15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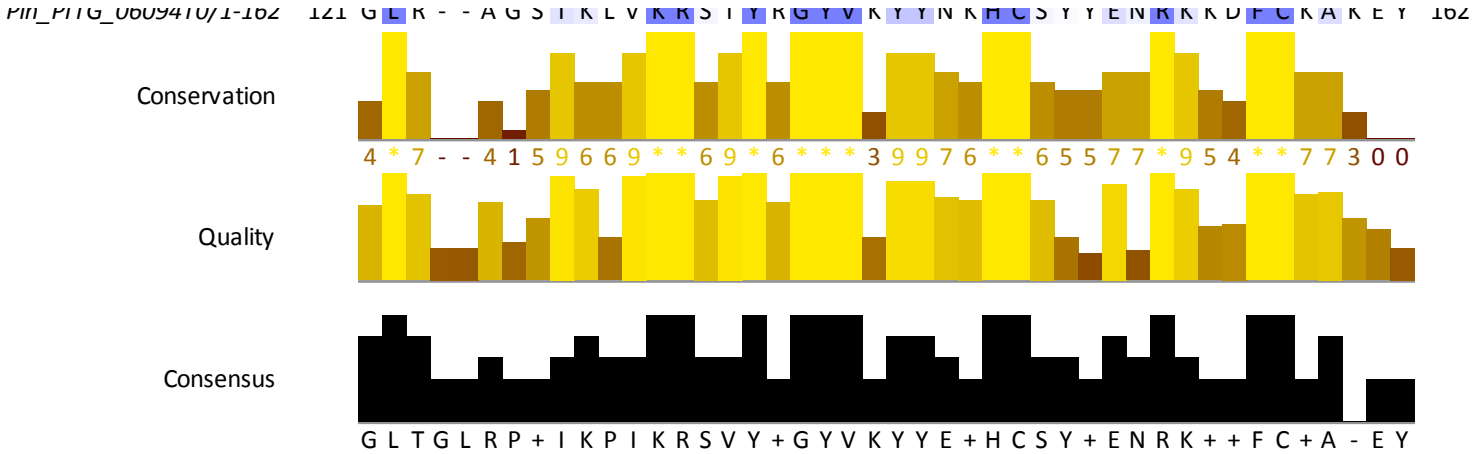
Pca_124376/1-145 1 MRFTYFVAVALTGLLASNDLVVASTADKTVVHD---------QV 35
Prm_Prm_81610/1-157 1 MRVSEFLVLAIAGFLACSDAFAVT------SNDKHQQVLSTSQA 38
Pso_286931/1-141 1 MRVSFCLLIVLATLLACSETVAAAKKHP-KSRDEHEE------- 36
Pin_PITG_06094T0/1-162 1 MRLSFILAATLTGLLACATASDSEKIIR-ISNE---------QV 34
Conservation
79579776877 877754464110 0-1659---------12
Quality
Consensus
MR+SF+LAV+LTGLLAC++A+++EKA-K-ISND-H-------QV
Pin_PITG_06099T0/1-162 35 LSGRQLI-DTVAKDNKKRLLRAYKDAEDDSEDSK-NVKPTADSK 76
Pca_124376/1-145 36 LSDRELI-DTGLNDNEKRSLRTNEDLEDDSEDLK-K-------- 69
Prm_Prm_81610/1-157 39 LRNRDLADDNTVYANEKRVLRTRQTSDDEDEDAKLKTEDS---- 78
Pso_286931/1-141 37 ----------TVRDKNKRFLR---LTSEEDTD---NVTPG---- 60
Pin_PITG_06094T0/1-162 35 LSDRQLL-DTVVNDNEKRFLRAYNDAEDDSEDPK-NVKNTVDAK 76
Conservation
2113121-4267555 65**4**1114569977*04-6111 1----
Quality
Consensus
LSDRQLI-DT+VNDNEKRFLR+Y-DAEDDSED-K-NVKPT-D-K
Pin_PITG_06099T0/1-162 77 HADESEDSEDSQEERFSLIQTSNQPRYYWWFQHHMTPLDVRRDL 120
Pca_124376/1-145 70 ----------SDEERFSLIQLSNQPRYYVWFEDEMTPKDVRRKF 103
Prm_Prm_81610/1-157 79 -------DSDDEEEERGLTSTLDYPKYWRWFRAHMTPYDVKEVL 115
Pso_286931/1-141 61 -------AEDDEEERDLIIPTIDRPKYHRWFHAHMTPYDVKQVL 97
Pin_PITG_06094T0/1-162 77 PADESEDSELSEEERFSLIQMSNQPRYYWWFQHEMTPRDVRRAL 120
Conservation
-------1107 7**835+666586*9*83**526***4**9728
Quality
Consensus
-ADESEDSEDSEEERFSLIQTSNQPRYY+WFQ+HMTPYDVRRVL
Pin_PITG_06099T0/1-162 121 ELT--ADTINPIKRSVYTGYVDYYEDHCSYYENRKEEFCKAEDF 162
Pca_124376/1-145 104 GLT--RHSIKLVKRSIYRGYVKYYDEHCSYFENRKKDFCRAQEY 145
Prm_Prm_81610/1-157 116 GLTGLRPLVKPIKRRVYKGYVRFYEKHCRLPKYRRMAFCRAA-- 157
Pso_286931/1-141 98 GLTGLRPLVKPIKRRVYKGYVVYFEEHCRKPEYRRMAFCQPGAE 141



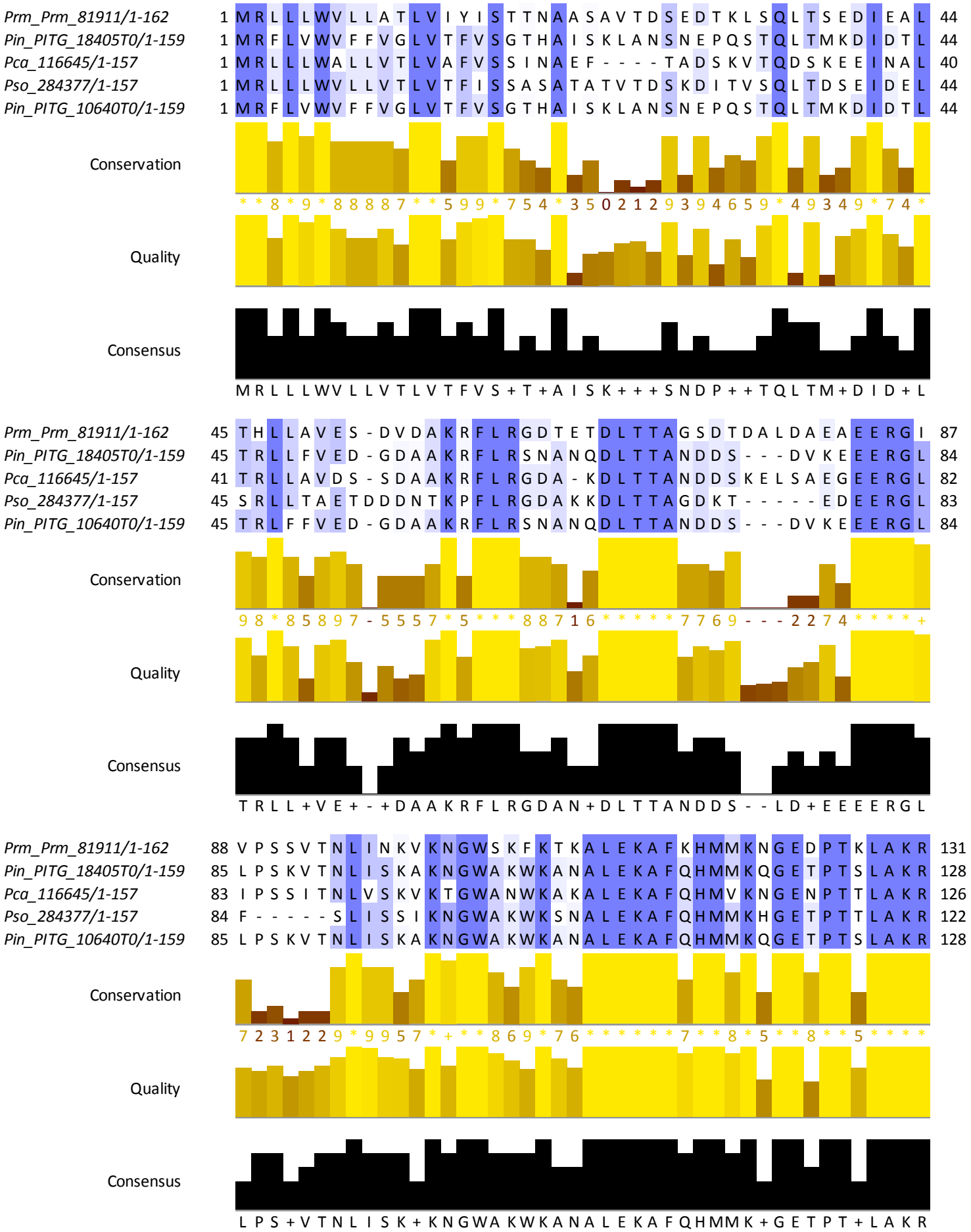
Pin_PITG_06099T0/1-162
Pca_124376/1-145
Prm_Prm_81610/1-157
Pso_286931/1-141
Pin_PITG_06094T0/1-162

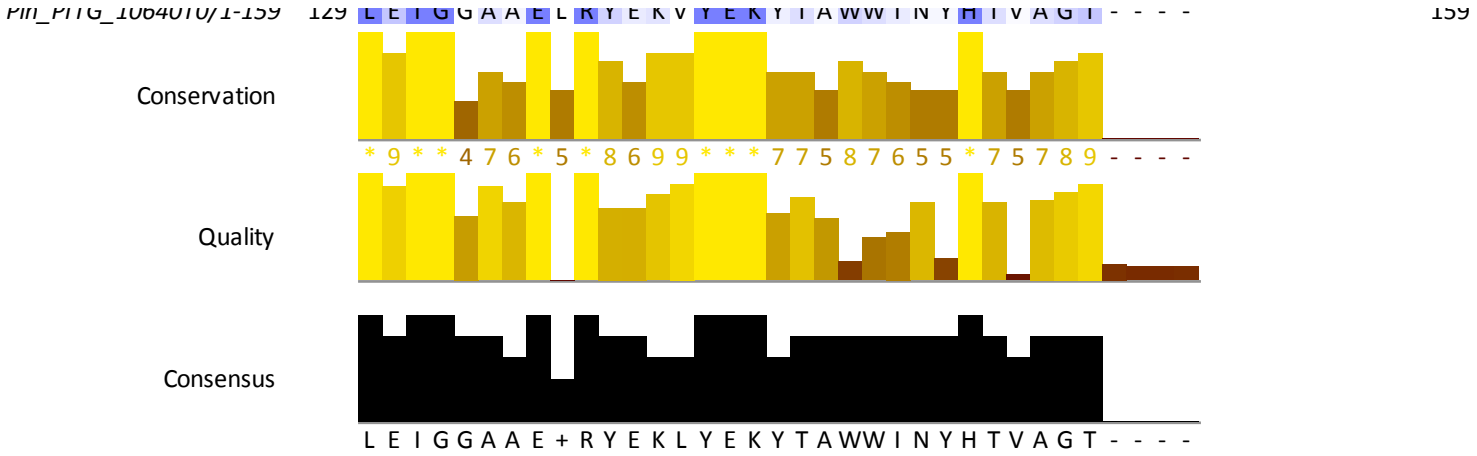
Conservation

Quality

Consensus

Ortholog 16


Prm_Prm_81911/1-162 1 MRLLLWVLLATLVIYISTTNAASAVTDSEDTKLSQLTSEDIEAL 44
Pin_PITG_18405T0/1-159 1 MRFLVWVFFVGLVTFVSGTHAISKLANSNEPQSTQLTMKDIDTL 44
Pca_116645/1-157 1 MRLLLWALLVTLVAFVSSINAEF----TADSKVTQDSKEEINAL 40
Pso_284377/1-157 1 MRLLLWVLLVTLVTFISSASATATVTDSKDITVSQLTDSEIDEL 44
Pin_PITG_10640T0/1-159 1 MRFLVWVFFVGLVTFVSGTHAISKLANSNEPQSTQLTMKDIDTL 44
Conservation
Quality
Consensus
MRLLLWVLLVTLVTFVS+T+AISK+++SNDP++TQLTM+DID+L
Prm_Prm_81911/1-162 45 THLLAVES-DVDAKRFLRGDTETDLTTAGSDTDALDAEAEERGI 87
Pin_PITG_18405T0/1-159 45 TRLLFVED-GDAAKRFLRSNANQDLTTANDDS---DVKEEERGL 84
Pca_116645/1-157 41 TRLLAVDS-SDAAKRFLRGDA-KDLTTANDDSKELSAEGEERGL 82
Pso_284377/1-157 45 SRLLTAETDDDNTKPFLRGDAKKDLTTAGDKT-----EDEERGL 83
Pin_PITG_10640T0/1-159 45 TRLFFVED-GDAAKRFLRSNANQDLTTANDDS---DVKEEERGL 84
Conservation
Quality
Consensus
TRLL+VE+-+DAAKRFLRGDAN+DLTTANDDS--LD+EEEERGL
Prm_Prm_81911/1-162 88 VPSSVTNLINKVKNGWSKFKTKALEKAFKHMMKNGEDPTKLAKR 131
Pin_PITG_18405T0/1-159 85 LPSKVTNLISKAKNGWAKWKANALEKAFQHMMKQGETPTSLAKR 128
Pca_116645/1-157 83 IPSSITNLVSKVKTGWANWKAKALEKAFQHMVKNGENPTTLAKR 126
Pso_284377/1-157 84 F-----SLISSIKNGWAKWKSNALEKAFQHMMKHGETPTTLAKR 122
Pin_PITG_10640T0/1-159 85 LPSKVTNLISKAKNGWAKWKANALEKAFQHMMKQGETPTSLAKR 128
Conservation
Quality
Consensus
LPS+VTNLISK+KNGWAKWKANALEKAFQHMMK+GETPT+LAKR
Prm_Prm_81911/1-162 132 LEIGGAAEPRYEKLYEKYTAWWINYHTNAGT---- 162
Pin_PITG_18405T0/1-159 129 LEIGGAAELRYEKVYEKYTAWWINYHTVAGT---- 159
Pca_116645/1-157 127 LDIGRTVEGRHHRLYEKFTAWWINYHTVAGT---- 157
Pso_284377/1-157 123 LEIGGATEPRYERLYEKLVDQLPHDHRYLSSGCDY 157


Pin_PITG_10640T0/1-159
129
L E I G G A A E L R Y E K V Y E K Y T A W W I N Y H T V A G T - - - -
159
Conservation
* 9 * * 4 7 6 * 5 * 8 6 9 9 * * * 7 7 5 8 7 6 5 5 * 7 5 7 8 9 - - - -
Quality
Consensus
L E I G G A A E + R Y E K L Y E K Y T A W W I N Y H T V A G T - - - -

Ortholog 17

```
Pin_PITG_15225T0/1-221     1 M R V Y F A L L A - V F A S A L V I - - - E S D G K A I T S I Q L - - - - - - - - - - - 29
Pca_101904/1-270           1 M R F C F V V L A T V F - - - - A L L S S E T P A I A T A E K H S E A L S F I N G N N Y 40
Pin_PITG_15226T0/1-224     1 M S V C Y I V P S L V F I V A L S F M T S S C E A K T T V H I Y A - - - - - - - - - - - 33
Pso_285899/1-213           1 M R V G Y V L L A V L A - - - - V L V R N C A A T S A T A L S N E A G V S T T H T L N P 40
Prm_Prm_83274/1-323        1 M R A C L V L L A A A F A N S N V T L A G P V S G P S T A S - - - - - - T L V N D F Q P 38

Conservation
                           * 6 6 6 7 7 9 6 8 0 7 7 - - - - 6 5 1 0 1 3 6 3 7 2 7 6 6 1 0 1 0 - - - - - - - - - - - -

Quality

Consensus
                           M R V C + V L L A - V F A - A L V L L - S E - - + K A T A S I - - - - - S - - N - - N P

Pin_PITG_15225T0/1-221    30 - K R T E K R L L R R Y G M G D T D I T E N T K D E E R A - - - - - - - - - - - - - - - 57
Pca_101904/1-270          41 - G G T A N R S L R S H D - - - - - - K V N A V E E E R A - - - - - - - - - - - - - - - 62
Pin_PITG_15226T0/1-224    34 - G Q I K K R H L R S Y G V G D V D M K D K T S G E E R A - - - - - - - - - - - - - - - 61
Pso_285899/1-213          41 W A E H D K R F P R S H - - - - - - - - - - A D H D E K S - - - - - - - - - - - - - - - 59
Prm_Prm_83274/1-323       39 - E G S S K R F L R S Y D M S D L N V N E G A G E E E R G I D L T K L D D V I N V V K G 81

Conservation
                           - 3 3 2 3 6 * 2 6 * 6 8 1 - - - - - - 1 0 0 7 2 2 9 * 9 8 - - - - - - - - - - - - - - - -

Quality

Consensus
                           - G G T - K R F L R S Y + M G D - D - K E N A - E E E R A - - - - - - - - - - - - - - - -

Pin_PITG_15225T0/1-221     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pca_101904/1-270           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_15226T0/1-224     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pso_285899/1-213           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Prm_Prm_83274/1-323       82 D K V M D A A K L D D V I N A A K T K K V I D A A K V D D V I N T A N A D K V I D A A K 125

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

Quality

Consensus
                           - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Pin_PITG_15225T0/1-221    58 - - - - - - - - - - - - - - - - - - - - - G N V S P S F F Q R L N N A D E I V G A L K N Q 81
Pca_101904/1-270          63 - - - - - - - - - - - - - - - - - - - - - - I D A D K L V K L L N P D D I A A A L K N Y 84
Pin_PITG_15226T0/1-224    62 - - - - - - - - - - - - - - - - - - - - - G S I D P K T I A D L L Q A D D I V S A L K S H 85
Pso_285899/1-213          60 - - - - - - - - - - - - - - - - - - - - - - T L A K I D D L V D P V K L D A A L S G L 80
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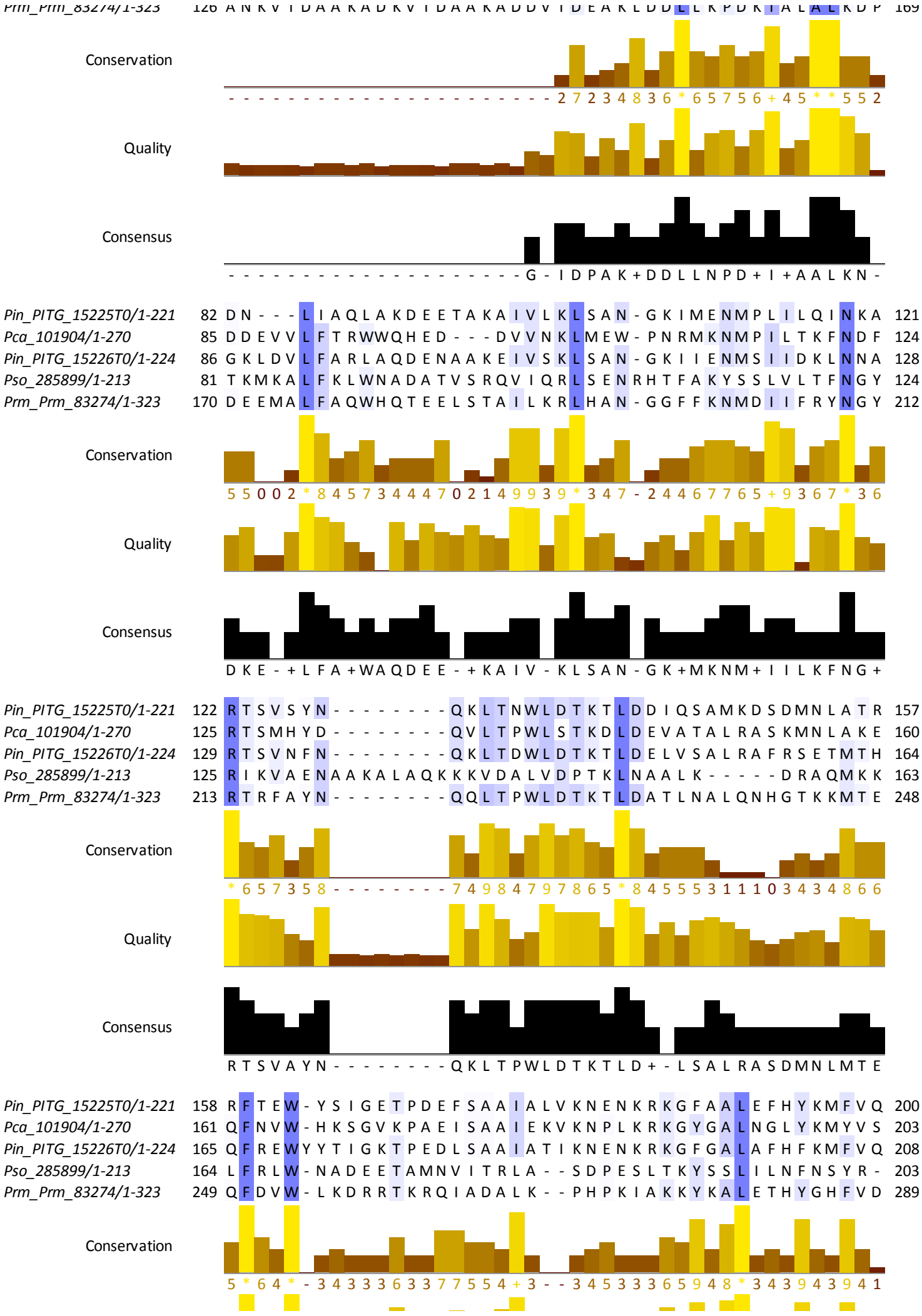
Prm_Prm_83274/1-323 126 A N K V I D A A K A D K V I D A A K A D D V I D E A K L D D L L K P D K I A L A L K D P 169
Conservation
- 2 7 2 3 4 8 3 6 * 6 5 7 5 6 + 4 5 * * 5 5 2
Quality
Consensus
- G - I D P A K + D D L L N P D + I + A A L K N -
Pin_PITG_15225T0/1-221 82 D N - - - L I A Q L A K D E E T A K A I V L K L S A N - G K I M E N M P L I L Q I N K A 121
Pca_101904/1-270 85 D D E V V L F T R W W Q H E D - - - D V V N K L M E W - P N R M K N M P I L T K F N D F 124
Pin_PITG_15226T0/1-224 86 G K L D V L F A R L A Q D E N A A K E I V S K L S A N - G K I I E N M S I I D K L N N A 128
Pso_285899/1-213 81 T K M K A L F K L W N A D A T V S R Q V I Q R L S E N R H T F A K Y S S L V L T F N G Y 124
Prm_Prm_83274/1-323 170 D E E M A L F A Q W H Q T E E L S T A I L K R L H A N - G G F F K N M D I I F R Y N G Y 212
Conservation
5 5 0 0 2 * 8 4 5 7 3 4 4 4 7 0 2 1 4 9 9 3 9 * 3 4 7 - 2 4 4 6 7 7 6 5 + 9 3 6 7 * 3 6
Quality
Consensus
D K E - + L F A + W A Q D E E - + K A I V - K L S A N - G K + M K N M + I I L K F N G +
Pin_PITG_15225T0/1-221 122 R T S V S Y N - - - - - - - - Q K L T N W L D T K T L D D I Q S A M K D S D M N L A T R 157
Pca_101904/1-270 125 R T S M H Y D - - - - - - - - Q V L T P W L S T K D L D E V A T A L R A S K M N L A K E 160
Pin_PITG_15226T0/1-224 129 R T S V N F N - - - - - - - - Q K L T D W L D T K T L D E L V S A L R A F R S E T M T H 164
Pso_285899/1-213 125 R I K V A E N A A K A L A Q K K K V D A L V D P T K L N A A L K - - - - - D R A Q M K K 163
Prm_Prm_83274/1-323 213 R T R F A Y N - - - - - - - - Q Q L T P W L D T K T L D A T L N A L Q N H G T K K M T E 248
Conservation
* 6 5 7 3 5 8 - - - - - - - - 7 4 9 8 4 7 9 7 8 6 5 * 8 4 5 5 5 3 1 1 1 0 3 4 3 4 8 6 6
Quality
Consensus
R T S V A Y N - - - - - - - - Q K L T P W L D T K T L D + - L S A L R A S D M N L M T E
Pin_PITG_15225T0/1-221 158 R F T E W - Y S I G E T P D E F S A A I A L V K N E N K R K G F A A L E F H Y K M F V Q 200
Pca_101904/1-270 161 Q F N V W - H K S G V K P A E I S A A I E K V K N P L K R K G Y G A L N G L Y K M Y V S 203
Pin_PITG_15226T0/1-224 165 Q F R E W Y Y T I G K T P E D L S A A I A T I K N E N K R K G F G A L A F H F K M F V Q 208
Pso_285899/1-213 164 L F R L W - N A D E E T A M N V I T R L A - - S D P E S L T K Y S S L I L N F N S Y R - 203
Prm_Prm_83274/1-323 249 Q F D V W - L K D R R T K R Q I A D A L K - - P H P K I A K K Y K A L E T H Y G H F V D 289
Conservation
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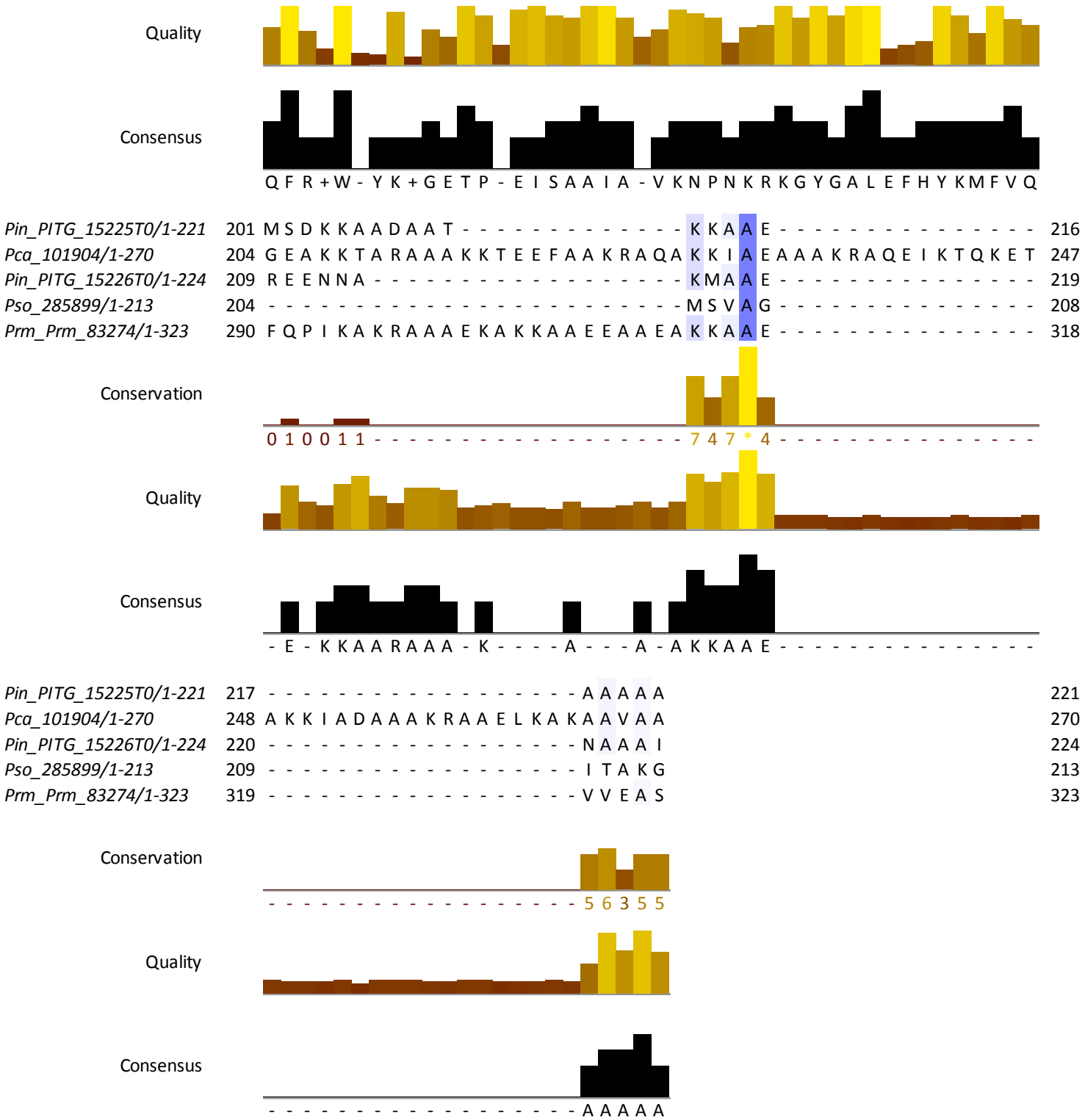
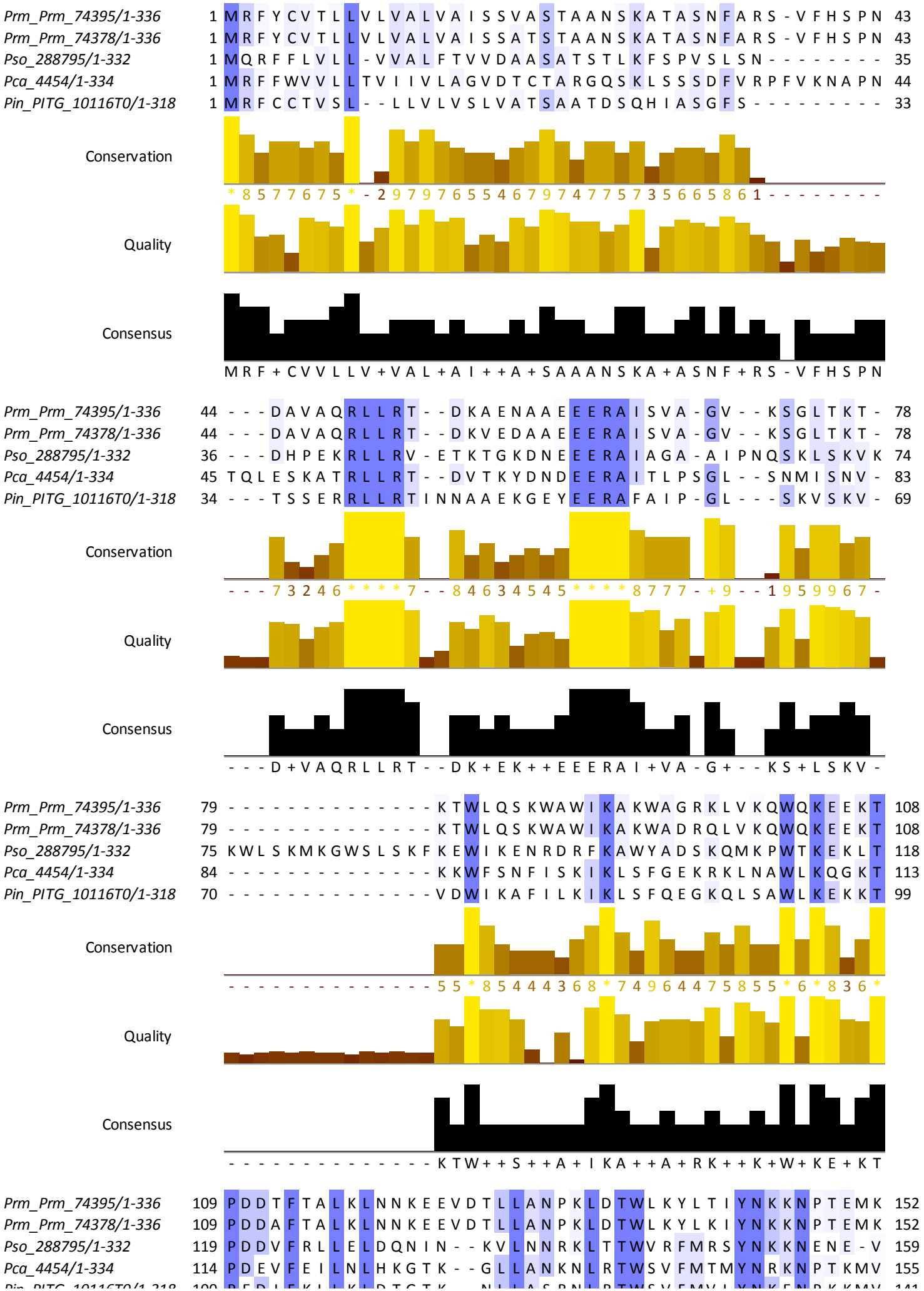

Quality
Consensus
Q F R + W - Y K + G E T P - E I S A A I A - V K N P N K R K G Y G A L E F H Y K M F V Q
Pin_PITG_15225T0/1-221 201 M S D K K A A D A A T - - - - - - - - - - - - - K K A A E - - - - - - - - - - - - - - - 216
Pca_101904/1-270 204 G E A K K T A R A A A K K T E E F A A K R A Q A K K I A E A A A K R A Q E I K T Q K E T 247
Pin_PITG_15226T0/1-224 209 R E E N N A - - - - - - - - - - - - - - - - - - K M A A E - - - - - - - - - - - - - - - 219
Pso_285899/1-213 204 - M S V A G - - - - - - - - - - - - - - - 208
Prm_Prm_83274/1-323 290 F Q P I K A K R A A A E K A K K A A E E A A E A K K A A E - - - - - - - - - - - - - - - 318
Conservation
0 1 0 0 1 1 - - - - - - - - - - - - - - - - - - - 7 4 7 * 4 - - - - - - - - - - - - - - -
Quality
Consensus
- E - K K A A R A A A - K - - - - A - - - A - A K K A A E - - - - - - - - - - - - - - -
Pin_PITG_15225T0/1-221 217 - - - - - - - - - - - - - - - - - - - A A A A A 221
Pca_101904/1-270 248 A K K I A D A A A K R A A E L K A K A A V A A 270
Pin_PITG_15226T0/1-224 220 - - - - - - - - - - - - - - - - - - - N A A A I 224
Pso_285899/1-213 209 - - - - - - - - - - - - - - - - - - - I T A K G 213
Prm_Prm_83274/1-323 319 - - - - - - - - - - - - - - - - - - - V V E A S 323
Conservation
- - - - - - - - - - - - - - - - - - - 5 6 3 5 5
Quality
Consensus
- - - - - - - - - - - - - - - - - - - A A A A A

Ortholog 18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Prm_Prm_74378/1-336 1 MRFYCVTLLVLVALVAISSATSTAANSKATASNFARS-VFHSPN 43
Pso_288795/1-332 1 MQRFFLVLL-VVALFTVVDAASATSTLKFSPVSLSN-------- 35
Pca_4454/1-334 1 MRFFWVVLLTVIIVLAGVDTCTARGQSKLSSSDFVRPFVKNAPN 44
Pin_PITG_10116T0/1-318 1 MRFCCTVSL--LLVLVSLVATSAATDSQHIASGFS--------- 33
Conservation
8577675-2979765546797477573566586 1--------
Quality
Consensus
MRF+CVVLLV+VAL+AI++A+SAAANSKA+ASNF+RS-VFHSPN
Prm_Prm_74395/1-336 44 ---DAVAQRLLRT--DKAENAAEEERAISVA-GV--KSGLTKT- 78
Prm_Prm_74378/1-336 44 ---DAVAQRLLRT--DKVEDAAEEERAISVA-GV--KSGLTKT- 78
Pso_288795/1-332 36 ---DHPEKRLLRV-ETKTGKDNEEERAIAGA-AIPNQSKLSKVK 74
Pca_4454/1-334 45 TQLESKATRLLRT--DVTKYDNDEERAITLPSGL--SNMISNV- 83
Pin_PITG_10116T0/1-318 34 ---TSSERRLLRTINNAAEKGEYEERAFAIP-GL---SKVSKV- 69
Conservation
---73246****7--84634545****8777-+9--1959967-
Quality
Consensus
---D+VAQRLLRT--DK+EK++EEERAI+VA-G+--KS+LSKV-
Prm_Prm_74395/1-336 79 ----------KTWLQSKWAWIKAKWAGRKLVKQWQKEEKT 108
Prm_Prm_74378/1-336 79 ----------KTWLQSKWAWIKAKWADRQLVKQWQKEEKT 108
Pso_288795/1-332 75 KWLSKMKGWSLSKFKEWIKENRDRFKAWYADSKQMKPWTKEKLT 118
Pca_4454/1-334 84 ----------KKWFSNFISKIKLSFGEKRKLNAWLKQGKT 113
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Conservation
----------55*854443 68*74964475855*6*836*
Quality
Consensus
----------KTW++S++A+IKA++A+RK++K+W+KE+KT
Prm_Prm_74395/1-336 109 PDDTFTALKLNNKEEVDTLLANPKLDTWLKYLTIYNKKNPTEMK 152
Prm_Prm_74378/1-336 109 PDDAFTALKLNNKEEVDTLLANPKLDTWLKYLKIYNKKNPTEMK 152
Pso_288795/1-332 119 PDDVFRLLELDQNIN--KVLNNRKLTTWVRFMRSYNKKNENE-V 159
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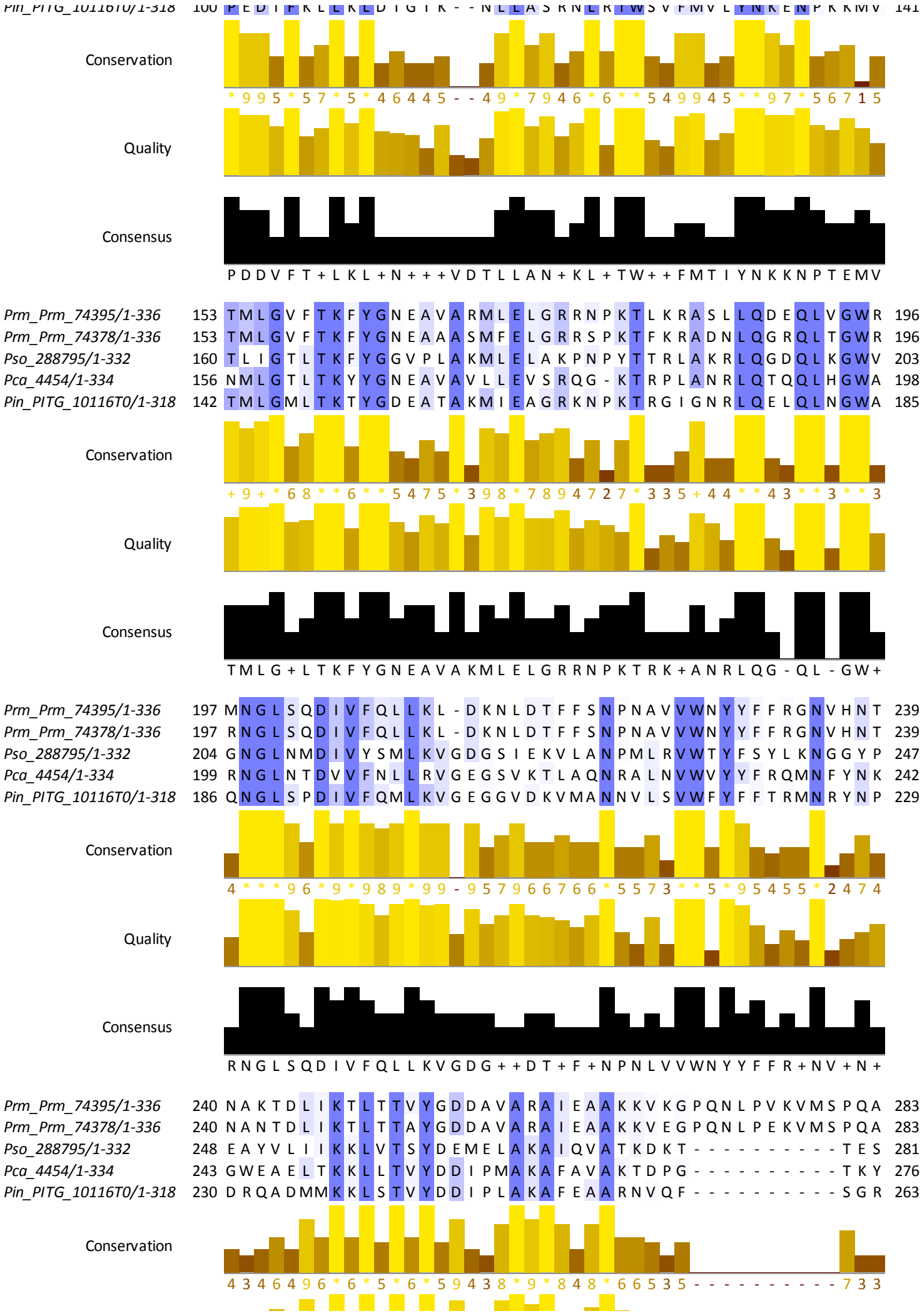
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Quality
Consensus
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Pca_4454/1-334
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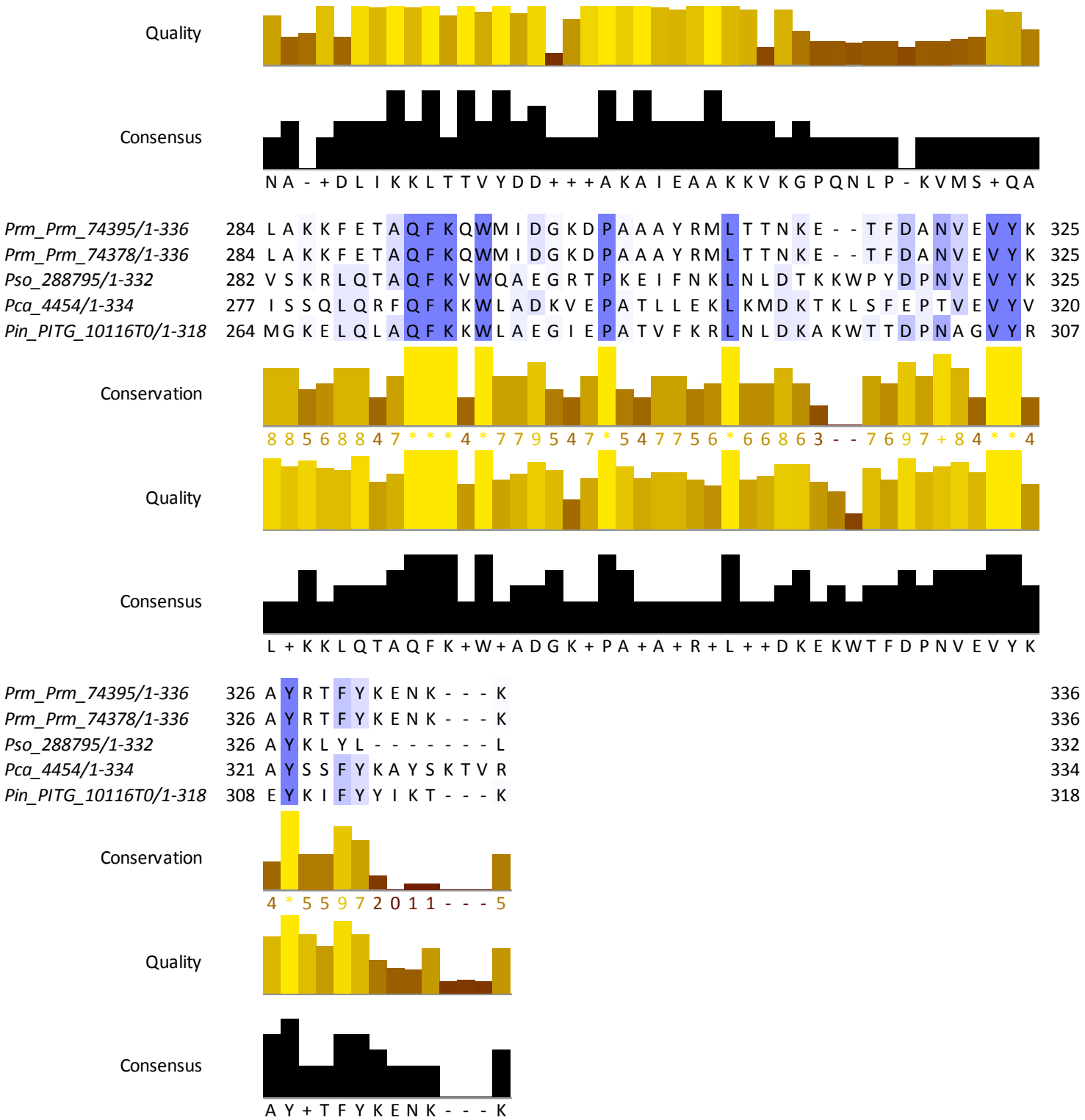
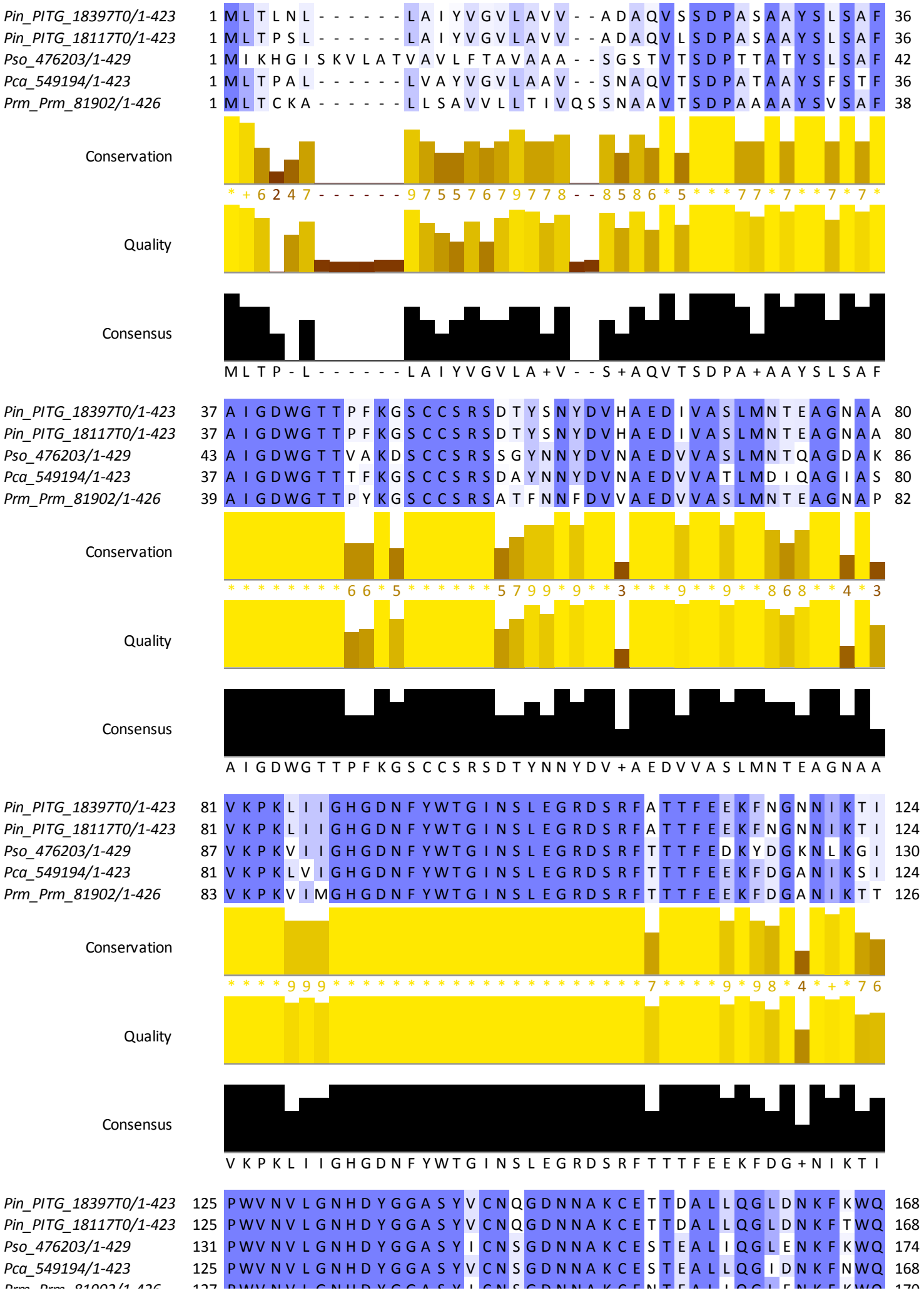

Quality
Consensus
N A - + D L I K K L T T V Y D D + + + A K A I E A A K K V K G P Q N L P - K V M S + Q A
Prm_Prm_74395/1-336 284 L A K K F E T A Q F K Q W M I D G K D P A A A Y R M L T T N K E - - T F D A N V E V Y K 325
Prm_Prm_74378/1-336 284 L A K K F E T A Q F K Q W M I D G K D P A A A Y R M L T T N K E - - T F D A N V E V Y K 325
Pso_288795/1-332 282 V S K R L Q T A Q F K V W Q A E G R T P K E I F N K L N L D T K K W P Y D P N V E V Y K 325
Pca_4454/1-334 277 I S S Q L Q R F Q F K K W L A D K V E P A T L L E K L K M D K T K L S F E P T V E V Y V 320
Pin_PITG_10116T0/1-318 264 M G K E L Q L A Q F K K W L A E G I E P A T V F K R L N L D K A K W T T D P N A G V Y R 307
Conservation
8 8 5 6 8 8 4 7 * * * 4 * 7 7 9 5 4 7 * 5 4 7 7 5 6 * 6 6 8 6 3 - - 7 6 9 7 + 8 4 * * 4
Quality
Consensus
L + K K L Q T A Q F K + W + A D G K + P A + A + R + L + + D K E K W T F D P N V E V Y K
Prm_Prm_74395/1-336 326 A Y R T F Y K E N K - - - K 336
Prm_Prm_74378/1-336 326 A Y R T F Y K E N K - - - K 336
Pso_288795/1-332 326 A Y K L Y L - - - - - - - L 332
Pca_4454/1-334 321 A Y S S F Y K A Y S K T V R 334
Pin_PITG_10116T0/1-318 308 E Y K I F Y Y I K T - - - K 318
Conservation
4 * 5 5 9 7 2 0 1 1 - - - 5
Quality
Consensus
A Y + T F Y K E N K - - - K

Ortholog 19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Pso_476203/1-429 1 MIKHGISKVLATVAVLFTAVAAA--SGSTVTSDPTTATYSLSAF 42
Pca_549194/1-423 1 MLTPAL------LVAYVGVLAAV--SNAQVTSDPATAAYSFSTF 36
Prm_Prm_81902/1-426 1 MLTCKA------LLSAVVLLTIVQSSNAAVTSDPAAAAYSVSAF 38
Conservation
*+6247------9755767977 8--8586*5***77*7**7*7*
Quality
Consensus
MLTP-L------LAIYVGVLA+V--S+AQVTSDPA+AAYSLSAF
Pin_PITG_18397T0/1-423 37 AIGDWGTTPFKGSCCSRSDTYSNYDVHAEDIVASLMNTEAGNAA 80
Pin_PITG_18117T0/1-423 37 AIGDWGTTPFKGSCCSRSDTYSNYDVHAEDIVASLMNTEAGNAA 80
Pso_476203/1-429 43 AIGDWGTTVAKDSCCSRSSGYNNYDVNAEDVVASLMNTQAGDAK 86
Pca_549194/1-423 37 AIGDWGTTTFKGSCCSRSDAYNNYDVNAEDVVATLMDIQAGIAS 80
Prm_Prm_81902/1-426 39 AIGDWGTTPYKGSCCSRSATFNNFDVVAEDVVASLMNTEAGNAP 82
Conservation
*******66*5*****5799*9**3***9**9**868**4*3
Quality
Consensus
AIGDWGTTPFKGSCCSRSDTYNNYDV+AEDVVASLMNTEAGNAA
Pin_PITG_18397T0/1-423 81 VKPKLIIGHGDNFYWTGINSLEGRDSRFATTFEEKFNGNNIKTI 124
Pin_PITG_18117T0/1-423 81 VKPKLIIGHGDNFYWTGINSLEGRDSRFATTFEEKFNGNNIKTI 124
Pso_476203/1-429 87 VKPKVIIGHGDNFYWTGINSLEGRDSRFTTTFEDKYDGKNLKGI 130
Pca_549194/1-423 81 VKPKLVIGHGDNFYWTGINSLEGRDSRFTTTFEEKFDGANIKSI 124
Prm_Prm_81902/1-426 83 VKPKVIMGHGDNFYWTGINSLEGRDSRFTTTFEEKFDGANIKTT 126
Conservation
****999*********************7*****9*98*4*+*76
Quality
Consensus
VKPKLIIGHGDNFYWTGINSLEGRDSRFTTTFEEKFDG+NIKTI
Pin_PITG_18397T0/1-423 125 PWVNVLGNHDYGGASYVCNQGDNNAKCETTDALLQGLDNKFKWQ 168
Pin_PITG_18117T0/1-423 125 PWVNVLGNHDYGGASYVCNQGDNNAKCETTDALLQGLDNKFTWQ 168
Pso_476203/1-429 131 PWVNVLGNHDYGGASYICNSGDNNAKCESTEALIQGLENKFKWQ 174
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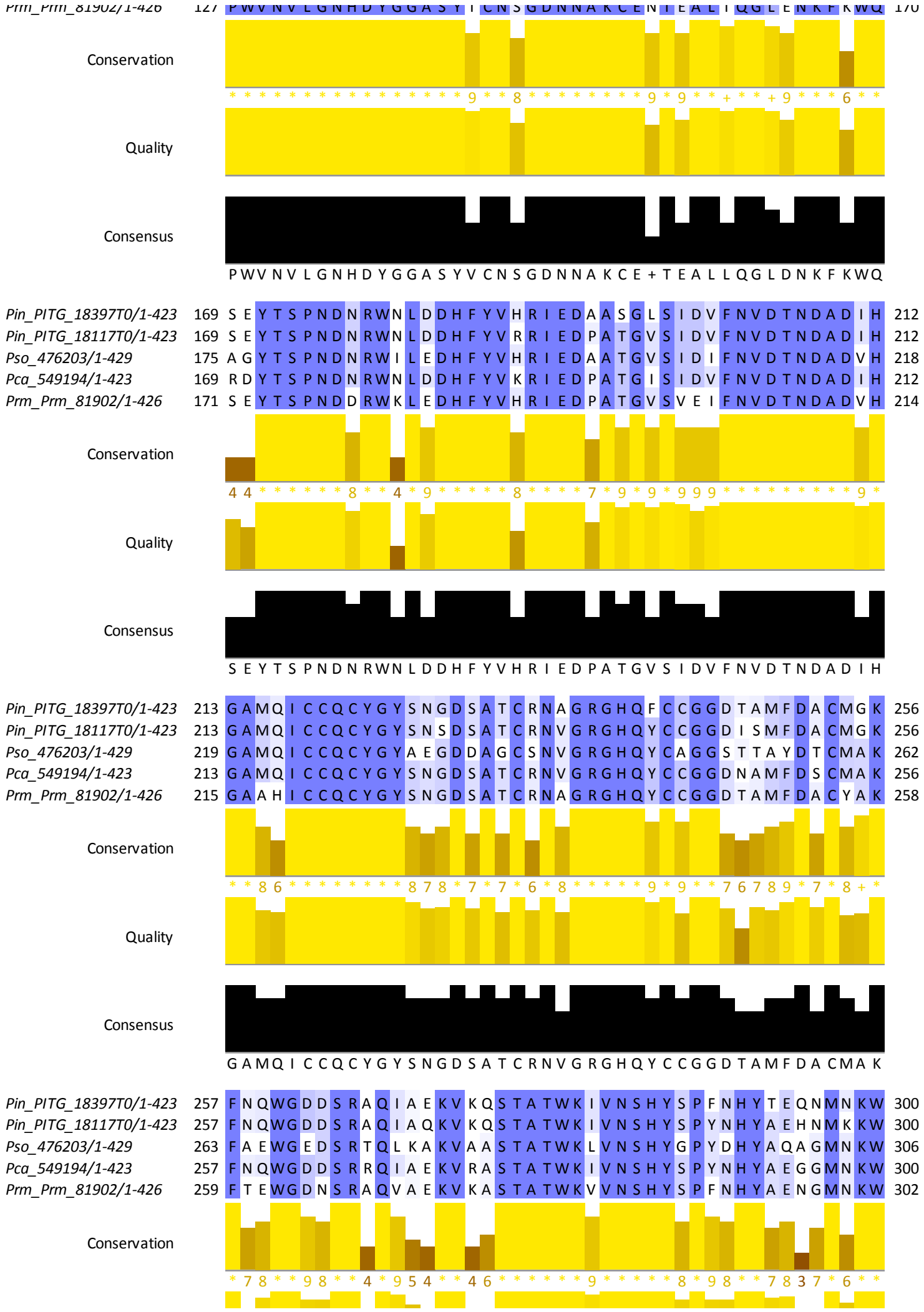
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Conservation
Quality
Consensus
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Pin_PITG_18117T0/1-423 169 SEYTSPNDNRWNLDDHFYVRRIEDPATGVSIDVFNVDTNDADIH 212
Pso_476203/1-429 175 AGYTSPNDNRWILEDHFYVHRIEDAATGVSIDIFNVDTNDADVH 218
Pca_549194/1-423 169 RDYTSPNDNRWNLDDHFYVKRIEDPATGISIDVFNVDTNDADIH 212
Prm_Prm_81902/1-426 171 SEYTSPNDDRWKLEDHFYVHRIEDPATGVSVEIFNVDTNDADVH 214
Conservation
Quality
Consensus
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Pin_PITG_18397T0/1-423 213 GAMQICCQCYGYSNGDSATCRNAGRGHQFCCGGDTAMFDACMGK 256
Pin_PITG_18117T0/1-423 213 GAMQICCQCYGYSNSDSATCRNVGRGHQYCCGGDISMFDACMGK 256
Pso_476203/1-429 219 GAMQICCQCYGYAEGDDAGCSNVGRGHQYCAGGSTTAYDTCMAK 262
Pca_549194/1-423 213 GAMQICCQCYGYSNGDSATCRNVGRGHQYCCGGDNAMFDSCMAK 256
Prm_Prm_81902/1-426 215 GAAHICCQCYGYSNGDSATCRNAGRGHQYCCGGDTAMFDACYAK 258
Conservation
Quality
Consensus
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Pin_PITG_18397T0/1-423 257 FNQWGDDSRAQIAEKVKQSTATWKIVNSHYSPFNHYTEQNMNKW 300
Pin_PITG_18117T0/1-423 257 FNQWGDDSRAQIAQKVKQSTATWKIVNSHYSPYNHYAEHNMKKW 300
Pso_476203/1-429 263 FAEWGEDSRTQLKAKVAASTATWKLVNSHYGPYDHYAQAGMNKW 306
Pca_549194/1-423 257 FNQWGDDSRRQIAEKVRASTATWKIVNSHYSPYNHYAEGGMNKW 300
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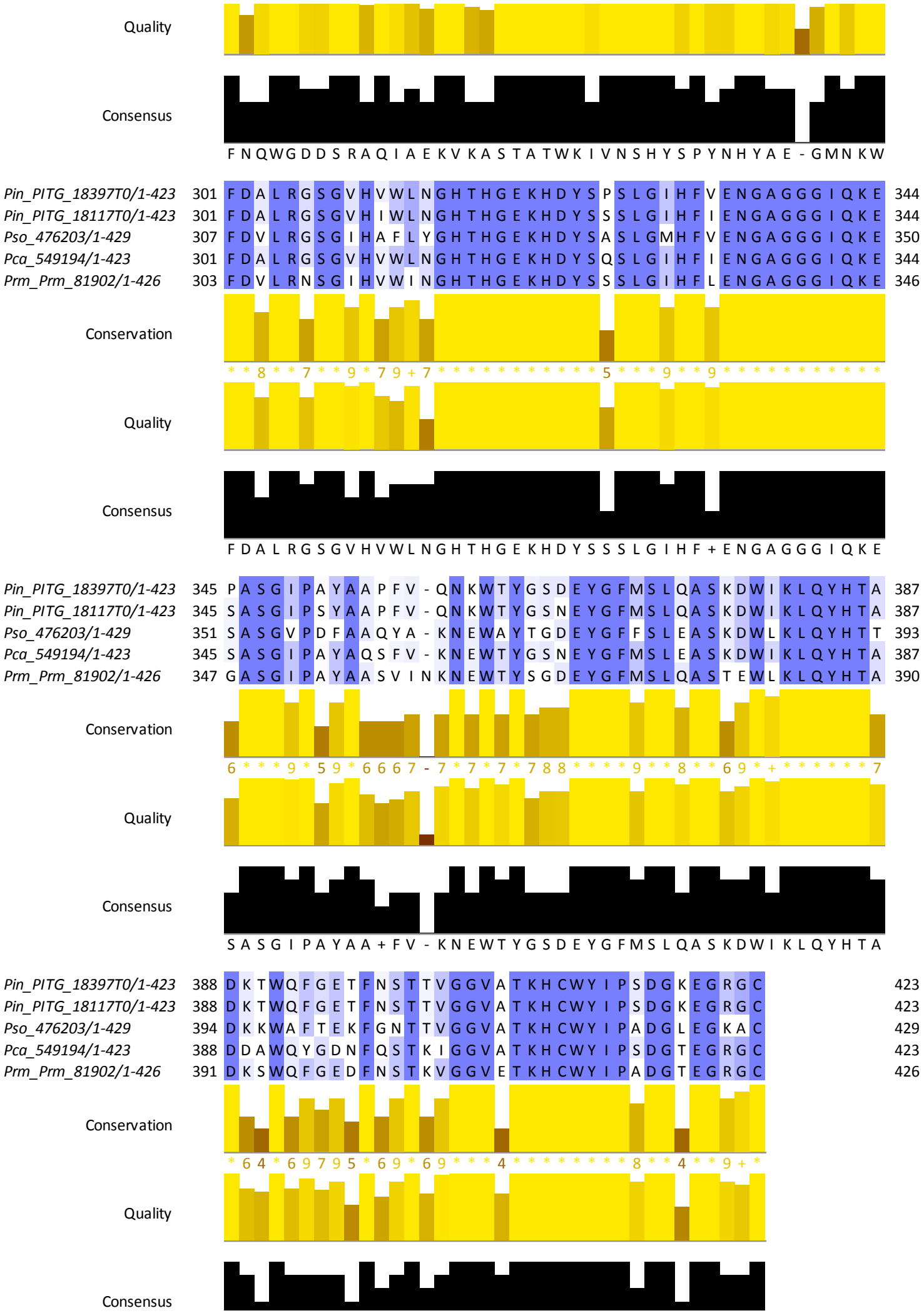
Conservation


Quality
Consensus
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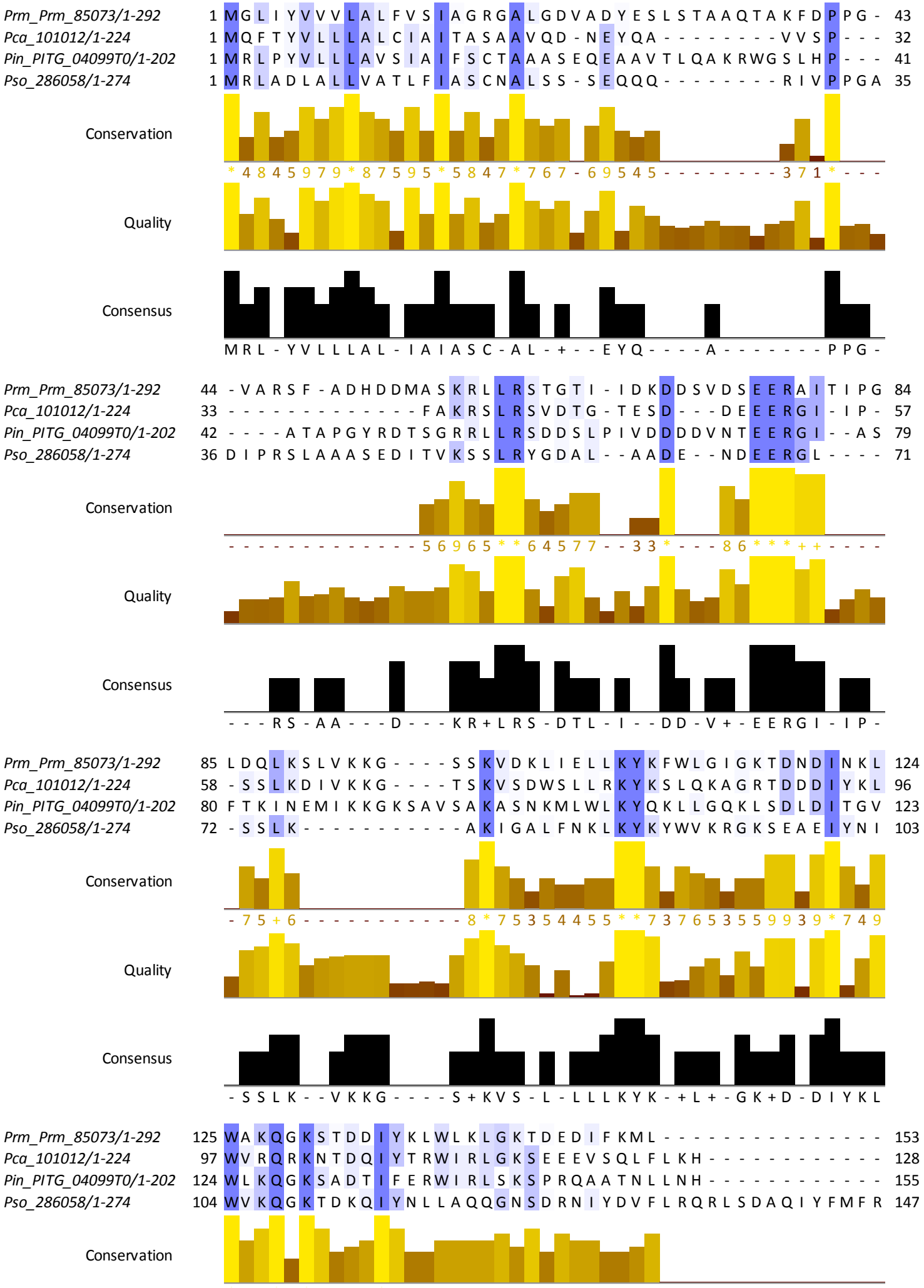
Pin_PITG_18397T0/1-423 301 F D A L R G S G V H V W L N G H T H G E K H D Y S P S L G I H F V E N G A G G G I Q K E 344
Pin_PITG_18117T0/1-423 301 F D A L R G S G V H I W L N G H T H G E K H D Y S S S L G I H F I E N G A G G G I Q K E 344
Pso_476203/1-429 307 F D V L R G S G I H A F L Y G H T H G E K H D Y S A S L G M H F V E N G A G G G I Q K E 350
Pca_549194/1-423 301 F D A L R G S G V H V W L N G H T H G E K H D Y S Q S L G I H F I E N G A G G G I Q K E 344
Prm_Prm_81902/1-426 303 F D V L R N S G I H V W I N G H T H G E K H D Y S S S L G I H F L E N G A G G G I Q K E 346
Conservation
* * 8 * * 7 * * 9 * 7 9 + 7 * * * * * * * * * * * 5 * * * 9 * * 9 * * * * * * * * * *
Quality
Consensus
F D A L R G S G V H V W L N G H T H G E K H D Y S S S L G I H F + E N G A G G G I Q K E
Pin_PITG_18397T0/1-423 345 P A S G I P A Y A A P F V - Q N K W T Y G S D E Y G F M S L Q A S K D W I K L Q Y H T A 387
Pin_PITG_18117T0/1-423 345 S A S G I P S Y A A P F V - Q N K W T Y G S N E Y G F M S L Q A S K D W I K L Q Y H T A 387
Pso_476203/1-429 351 S A S G V P D F A A Q Y A - K N E W A Y T G D E Y G F F S L E A S K D W L K L Q Y H T T 393
Pca_549194/1-423 345 S A S G I P A Y A Q S F V - K N E W T Y G S N E Y G F M S L E A S K D W I K L Q Y H T A 387
Prm_Prm_81902/1-426 347 G A S G I P A Y A A S V I N K N E W T Y S G D E Y G F M S L Q A S T E W L K L Q Y H T A 390
Conservation
6 * * * 9 * 5 9 * 6 6 6 7 - 7 * 7 * 7 * 7 8 8 * * * * 9 * * 8 * * 6 9 * + * * * * * * 7
Quality
Consensus
S A S G I P A Y A A + F V - K N E W T Y G S D E Y G F M S L Q A S K D W I K L Q Y H T A
Pin_PITG_18397T0/1-423 388 D K T W Q F G E T F N S T T V G G V A T K H C W Y I P S D G K E G R G C 423
Pin_PITG_18117T0/1-423 388 D K T W Q F G E T F N S T T V G G V A T K H C W Y I P S D G K E G R G C 423
Pso_476203/1-429 394 D K K W A F T E K F G N T T V G G V A T K H C W Y I P A D G L E G K A C 429
Pca_549194/1-423 388 D D A W Q Y G D N F Q S T K I G G V A T K H C W Y I P S D G T E G R G C 423
Prm_Prm_81902/1-426 391 D K S W Q F G E D F N S T K V G G V E T K H C W Y I P A D G T E G R G C 426
Conservation
* 6 4 * 6 9 7 9 5 * 6 9 * 6 9 * * * 4 * * * * * * * * 8 * * 4 * * 9 + *
Quality
Consensus

[redacted]

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

Ortholog 20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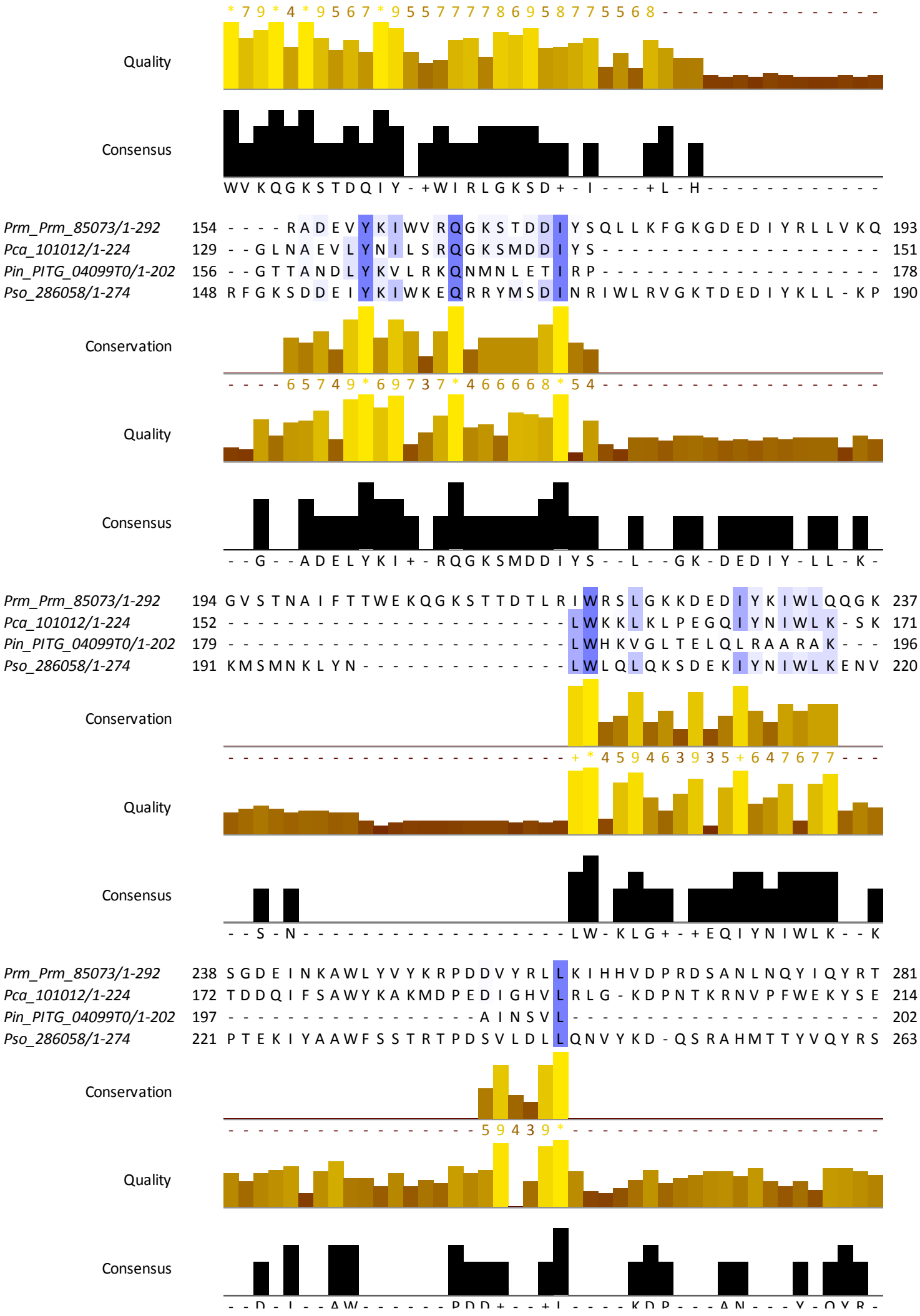
Pin_PITG_04099T0/1-202 1 MRLPYVLLLAVSIAIFSCTAAASEQEAAVTLQAKRWGSLHP--- 41
Pso_286058/1-274 1 MRLADLALLVATLFIASCNALSS-SEQQQ--------RIVPPGA 35
Conservation
*4845979*87595*5847*767-69545--------371*---
Quality
Consensus
MRL-YVLLLAL-IAIASC-AL-+--EYQ----A-------PPG-
Prm_Prm_85073/1-292 44 -VARSF-ADHDDMASKRLLRSTGTI-IDKDDSVDSEERAITIPG 84
Pca_101012/1-224 33 ----------FAKRSLRSVDTG-TESD---DEEERGI-IP- 57
Pin_PITG_04099T0/1-202 42 ----ATAPGYRDTSGRRLLRSDDSLPIVDDDDVNTEERGI--AS 79
Pso_286058/1-274 36 DIPRSLAAASEDITVKSSLRYGDAL--AADE--NDEERGL---- 71
Conservation
----------56965**64577--33*---86***++----
Quality
Consensus
---RS-AA---D---KR+LRS-DTL-I--DD-V+-EERGI-IP-
Prm_Prm_85073/1-292 85 LDQLKSLVKKG----SSKVDKLIELLKYKFWLGIGKTDNDINKL 124
Pca_101012/1-224 58 -SSLKDIVKKG----TSKVSDWSLLRKYKSLQKAGRTDDDIYKL 96
Pin_PITG_04099T0/1-202 80 FTKINEMIKKGKSAVSAKASNKMLWLKYQKLLGQKLSDLDITGV 123
Pso_286058/1-274 72 -SSLK----------AKIGALFNKLKYKYWVKRGKSEAEIYNI 103
Conservation
-75+6----------8*75354455**73765355993 9*749
Quality
Consensus
-SSLK--VKKG----S+KVS-L-LLLKYK-+L+-GK+D-DIYKL
Prm_Prm_85073/1-292 125 WAKQGKSTDDIYKLWLKLGKTDEDIFKML---------- 153
Pca_101012/1-224 97 WVRQRKNTDQIYTRWIRLGKSEEEVSQLFLKH---------- 128
Pin_PITG_04099T0/1-202 124 WLKQGKSADTIFERWIRLSKSPRQAATNLLNH---------- 155
Pso_286058/1-274 104 WVKQGKTDKQIYNLLAQQGNSDRNIYDVFLRQRLSDAQIYFMFR 147
Conservation


Quality
Consensus
Conservation
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Pca_101012/1-224
Pin_PITG_04099T0/1-202
Pso_286058/1-274

Prm_Prm_85073/1-292	282	A Y N D M L G I S N L	292
Pca_101012/1-224	215	F Y R - A K K Y R T S	224
Pin_PITG_04099T0/1-202		- - - - - - - - - - -	
Pso_286058/1-274	264	Y F N E N Y G I R E W	274

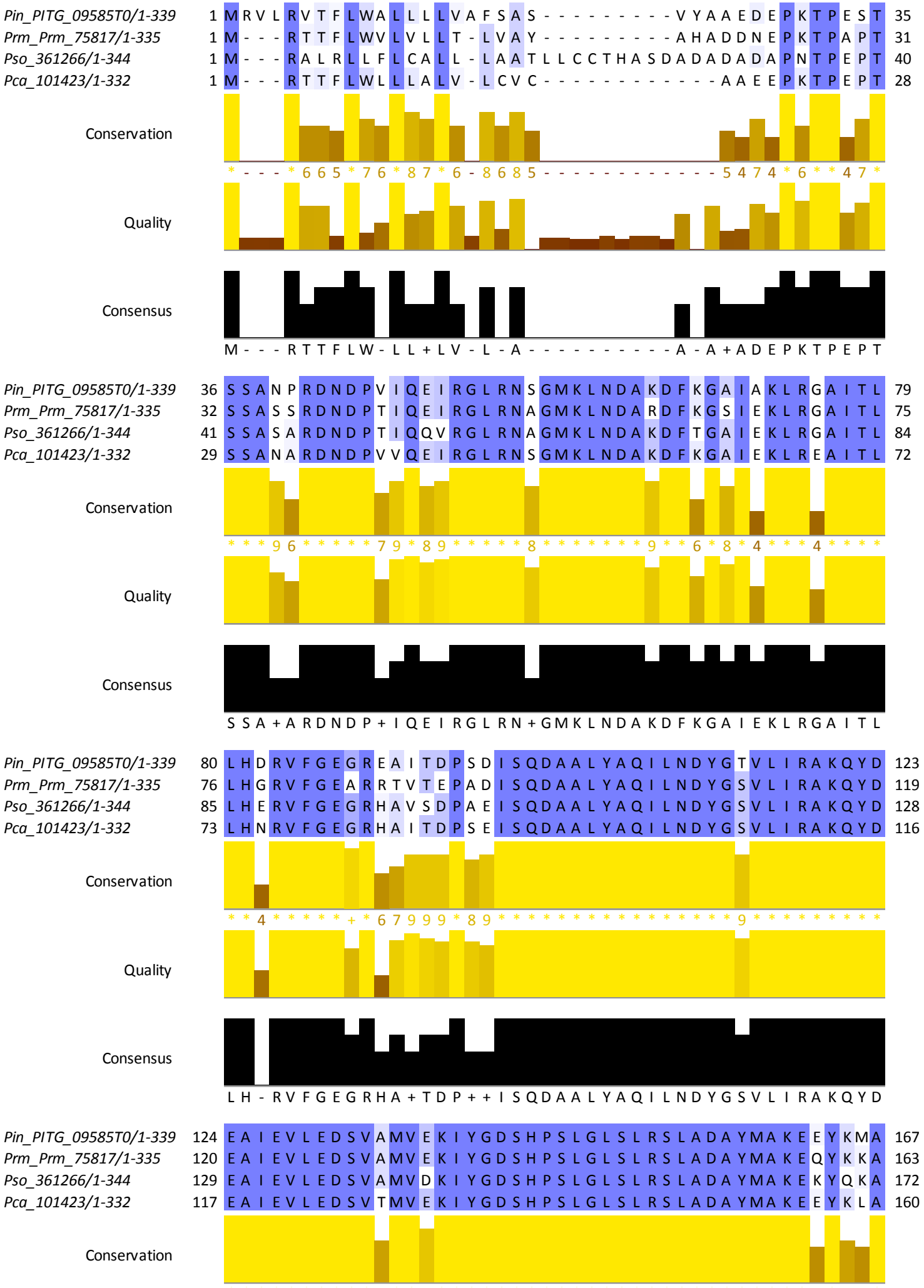
Conservation

Quality

Consensus

- Y N - - - G I R - -

Ortholog 21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Prm_Prm_75817/1-335 1 M---RTTFLWVLVLLT-LVAY---------AHADDNEPKTPAPT 31
Pso_361266/1-344 1 M---RALRLLFLCALL-LAATLLCCTHASDADADADAPNTPEPT 40
Pca_101423/1-332 1 M---RTTFLWLLLALV-LCVC----------AAEEPKTPEPT 28
Conservation
*---*665*76*87*6-8685----------5474*6**47*
Quality
Consensus
M---RTTFLW-LL+LV-L-A----------A-A+ADEPKTPEPT
Pin_PITG_09585T0/1-339 36 SSANPRDNDPVIQEIRGLRNSGMKLNDAKDFKGAIAKLRGAITL 79
Prm_Prm_75817/1-335 32 SSASSRDNDPTIQEIRGLRNAGMKLNDARDFKGSIEKLRGAITL 75
Pso_361266/1-344 41 SSASARDNDPTIQQVRGLRNAGMKLNDAKDFTGAIEKLRGAITL 84
Pca_101423/1-332 29 SSANARDNDPVVQEIRGLRNSGMKLNDAKDFKGAIEKLREAITL 72
Conservation
96**79*89*****8*******9**6*8*4***4****
Quality
Consensus
SSA+ARDNDP+IQEIRGLRN+GMKLNDAKDFKGAIEKLRGAITL
Pin_PITG_09585T0/1-339 80 LHDRVFGEGREAITDPSDISQDAALYAQILNDYGTVLIRAKQYD 123
Prm_Prm_75817/1-335 76 LHGRVFGEARRTVTEPADISQDAALYAQILNDYGSVLIRAKQYD 119
Pso_361266/1-344 85 LHERVFGEGRHAVSDPAEISQDAALYAQILNDYGSVLIRAKQYD 128
Pca_101423/1-332 73 LHNRVFGEGRHAITDPSEISQDAALYAQILNDYGSVLIRAKQYD 116
Conservation
4***+*67999*89*********************9*******
Quality
Consensus
LH-RVFGEGRHA+TDP++ISQDAALYAQILNDYGSVLIRAKQYD
Pin_PITG_09585T0/1-339 124 EAIEVLEDSVAMVEKIYGDSHPSLGLSLRSLADAYMAKEEYKMA 167
Prm_Prm_75817/1-335 120 EAIEVLEDSVAMVEKIYGDSHPSLGLSLRSLADAYMAKEQYKKA 163
Pso_361266/1-344 129 EAIEVLEDSVAMVDKIYGDSHPSLGLSLRSLADAYMAKEKYQKA 172
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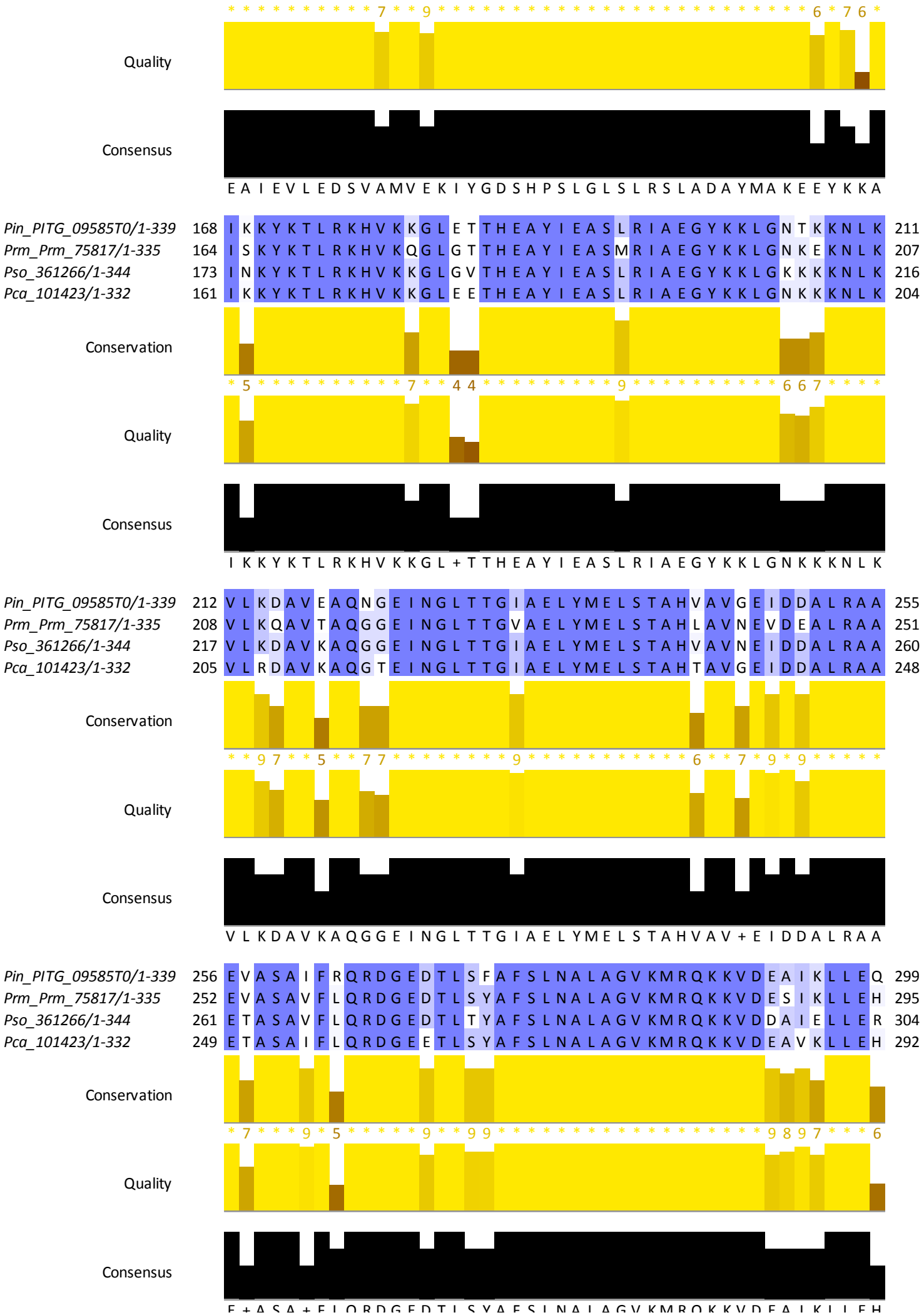
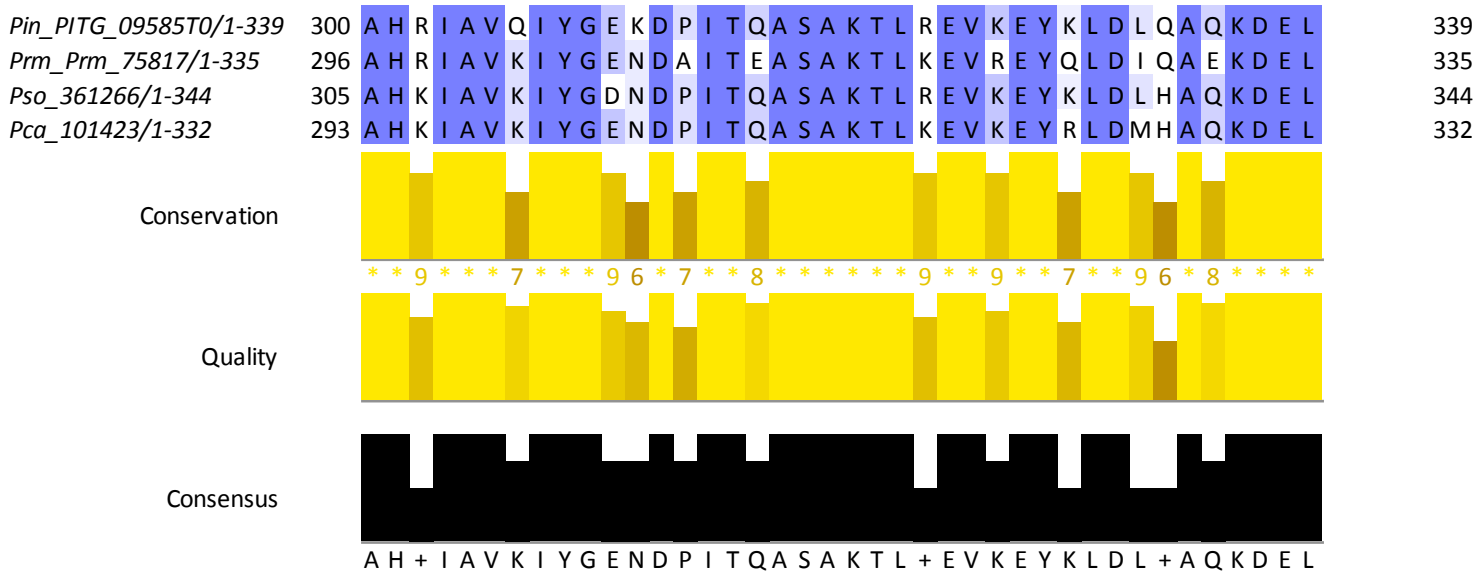
Conservation


Quality
Consensus
E A I E V L E D S V A M V E K I Y G D S H P S L G L S L R S L A D A Y M A K E E Y K K A
Pin_PITG_09585T0/1-339 168 I K K Y K T L R K H V K K G L E T T H E A Y I E A S L R I A E G Y K K L G N T K K N L K 211
Prm_Prm_75817/1-335 164 I S K Y K T L R K H V K Q G L G T T H E A Y I E A S M R I A E G Y K K L G N K E K N L K 207
Pso_361266/1-344 173 I N K Y K T L R K H V K K G L G V T H E A Y I E A S L R I A E G Y K K L G K K K N L K 216
Pca_101423/1-332 161 I K K Y K T L R K H V K K G L E E T H E A Y I E A S L R I A E G Y K K L G N K K K N L K 204
Conservation
Quality
Consensus
I K K Y K T L R K H V K K G L + T T H E A Y I E A S L R I A E G Y K K L G N K K K N L K
Pin_PITG_09585T0/1-339 212 V L K D A V E A Q N G E I N G L T T G I A E L Y M E L S T A H V A V G E I D D A L R A A 255
Prm_Prm_75817/1-335 208 V L K Q A V T A Q G G E I N G L T T G V A E L Y M E L S T A H L A V N E V D E A L R A A 251
Pso_361266/1-344 217 V L K D A V K A Q G G E I N G L T T G I A E L Y M E L S T A H V A V N E I D D A L R A A 260
Pca_101423/1-332 205 V L R D A V K A Q G T E I N G L T T G I A E L Y M E L S T A H T A V G E I D D A L R A A 248
Conservation
Quality
Consensus
V L K D A V K A Q G G E I N G L T T G I A E L Y M E L S T A H V A V + E I D D A L R A A
Pin_PITG_09585T0/1-339 256 E V A S A I F R Q R D G E D T L S F A F S L N A L A G V K M R Q K K V D E A I K L L E Q 299
Prm_Prm_75817/1-335 252 E V A S A V F L Q R D G E D T L S Y A F S L N A L A G V K M R Q K K V D E S I K L L E H 295
Pso_361266/1-344 261 E T A S A V F L Q R D G E D T L T Y A F S L N A L A G V K M R Q K K V D D A I E L L E R 304
Pca_101423/1-332 249 E T A S A I F L Q R D G E E T L S Y A F S L N A L A G V K M R Q K K V D E A V K L L E H 292
Conservation
Quality
Consensus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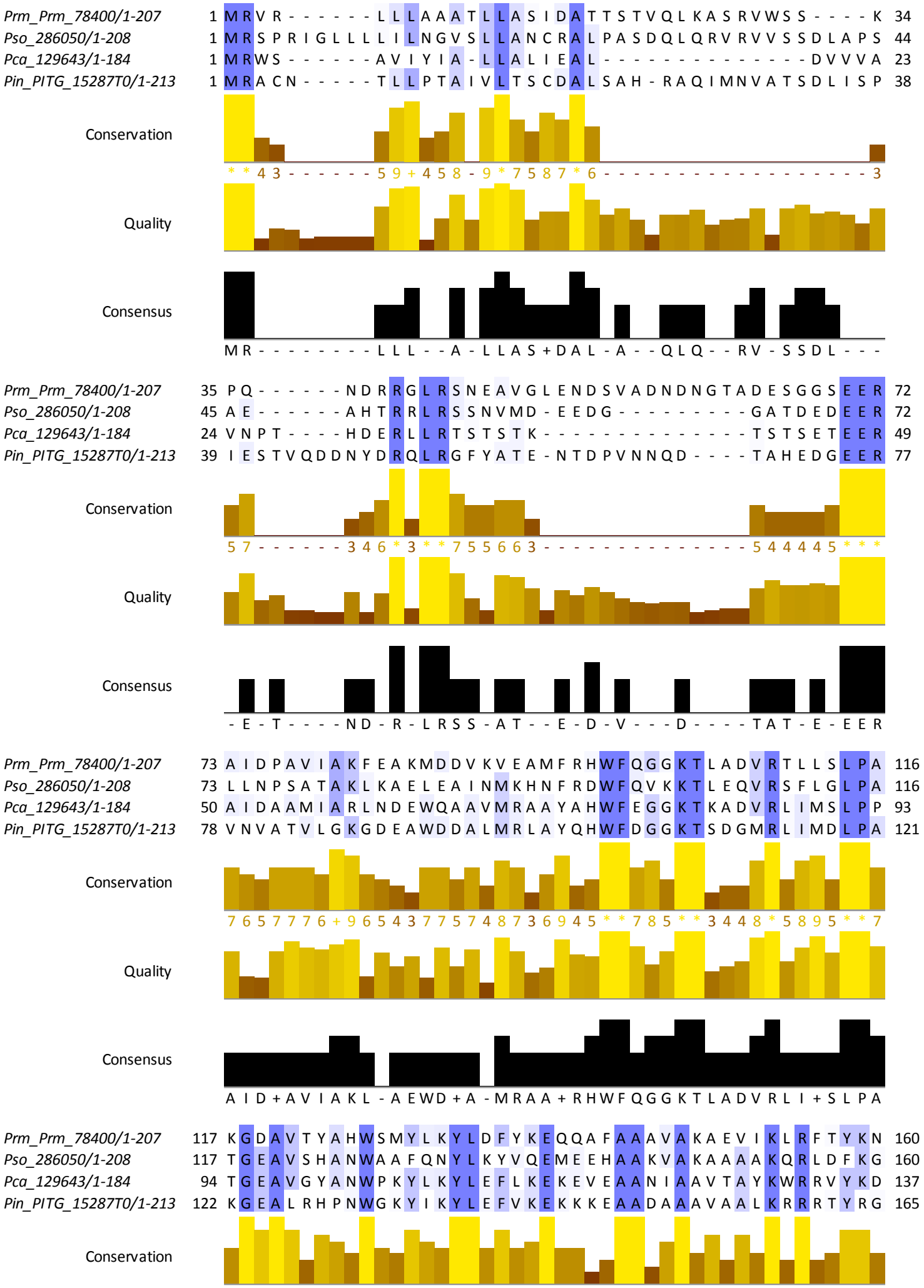
Prm_Prm_75817/1-335 296 A H R I A V K I Y G E N D A I T E A S A K T L K E V R E Y Q L D I Q A E K D E L 335
Pso_361266/1-344 305 A H K I A V K I Y G D N D P I T Q A S A K T L R E V K E Y K L D L H A Q K D E L 344
Pca_101423/1-332 293 A H K I A V K I Y G E N D P I T Q A S A K T L K E V K E Y R L D M H A Q K D E L 332
Conservation
* * 9 * * * 7 * * * 9 6 * 7 * * 8 * * * * * * 9 * * 9 * * 7 * * 9 6 * 8 * * * *
Quality
Consensus
A H + I A V K I Y G E N D P I T Q A S A K T L + E V K E Y K L D L + A Q K D E L

Ortholog 22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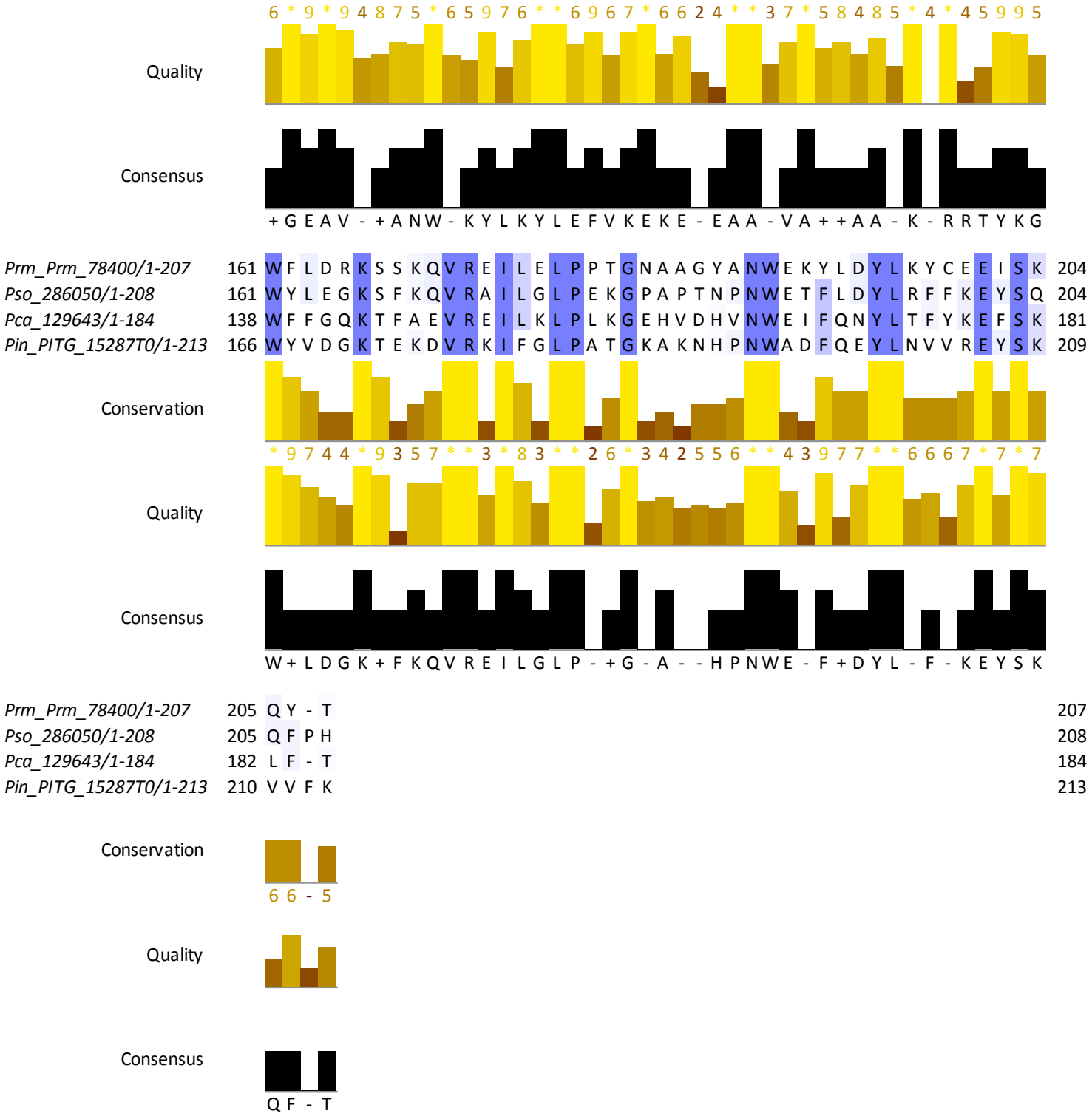
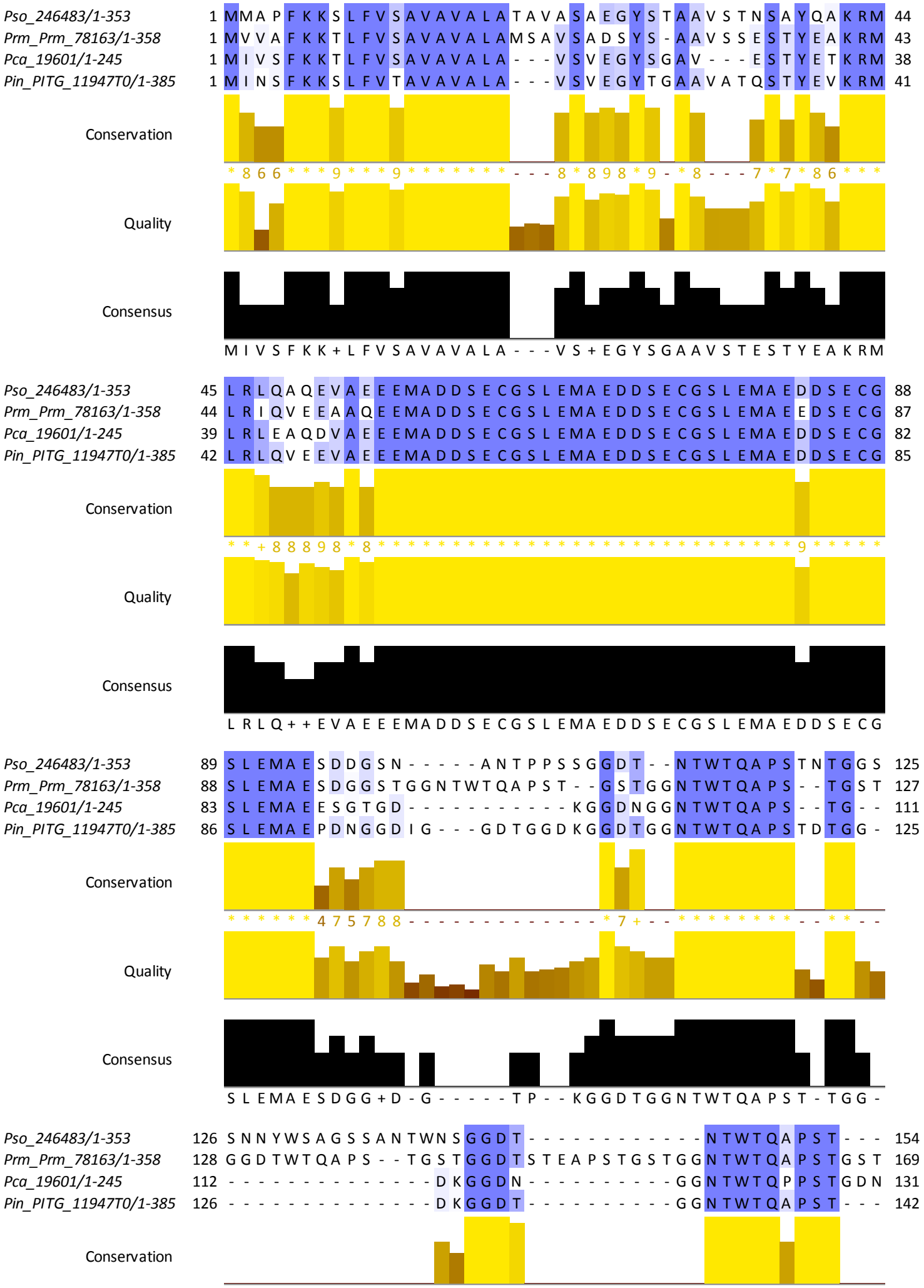
Pso_286050/1-208 1 MRSPRIGLLLLILNGVSLLANCRALPASDQLQRVRVVSSDLAPS 44
Pca_129643/1-184 1 MRWS------AVIYIA-LLALIEAL----------DVVVA 23
Pin_PITG_15287T0/1-213 1 MRACN-----TLLPTAIVLTSCDALSAH-RAQIMNVATSDLISP 38
Conservation
**43-------59+458-9*7587*6----------3
Quality
Consensus
MR---------LLL--A-LLAS+DAL-A--QLQ--RV-SSDL---
Prm_Prm_78400/1-207 35 PQ------NDRRGLRSNEAVGLENDSVADNDNGTADESGGSEER 72
Pso_286050/1-208 45 AE------AHTRRLRSSNVMD-EEDG---------GATDEDEER 72
Pca_129643/1-184 24 VNPT----HDERLLRTSTSTK----------TSTSETEER 49
Pin_PITG_15287T0/1-213 39 IESTVQDDNYDRQLRGFYATE-NTDPVNNQD----TAHEDGEER 77
Conservation
57------346*3**75663----------544445***
Quality
Consensus
-E-T----ND-R-LRSS-AT--E-D-V---D----TAT-E-EER
Prm_Prm_78400/1-207 73 AIDPAVIAKFEAKMDDVKVEAMFRHWFQGGKTLADVRTLLSLPA 116
Pso_286050/1-208 73 LLNPSATAKLKAELEAINMKHNFRDWFQVKKTLEQVRSFLGLPA 116
Pca_129643/1-184 50 AIDAAMIARLNDEWQAAVMRAAYAHWFEGGKTKADVRLIMSLPP 93
Pin_PITG_15287T0/1-213 78 VNVATVLGKGDEAWDDALMRLAYQHWFDGGKTSDGMRLIMDLPA 121
Conservation
7657776+9654377574873694 5**785**3448*5895**7
Quality
Consensus
AID+AVIAKL-AEWD+A-MRAA+RHWFQGGKTLADVRLI+SLPA
Prm_Prm_78400/1-207 117 KGDAVTYAHWSMYLKYLDFYKEQQAFAAAVAKAEVIKLRFTYKN 160
Pso_286050/1-208 117 TGEAVSHANWAAFQNYLKYVQEMEEHAAKVAKAAAAKQRLDFKG 160
Pca_129643/1-184 94 TGEAVGYANWPKYLKYLEFLKEKEVEAANIAAVTAYKWRRVYKD 137
Pin_PITG_15287T0/1-213 122 KGEALRHPNWGKYIKYLEFVKEKKKEAADAAAVAALKRRRTYRG 165
Conservation


6 * 9 * 9 4 8 7 5 * 6 5 9 7 6 * * 6 9 6 7 * 6 6 2 4 * * 3 7 * 5 8 4 8 5 * 4 * 4 5 9 9 5
Quality
Consensus
+ G E A V - + A N W - K Y L K Y L E F V K E K E - E A A - V A + + A A - K - R R T Y K G
Prm_Prm_78400/1-207 161 W F L D R K S S K Q V R E I L E L P P T G N A A G Y A N W E K Y L D Y L K Y C E E I S K 204
Pso_286050/1-208 161 W Y L E G K S F K Q V R A I L G L P E K G P A P T N P N W E T F L D Y L R F F K E Y S Q 204
Pca_129643/1-184 138 W F F G Q K T F A E V R E I L K L P L K G E H V D H V N W E I F Q N Y L T F Y K E F S K 181
Pin_PITG_15287T0/1-213 166 W Y V D G K T E K D V R K I F G L P A T G K A K N H P N W A D F Q E Y L N V V R E Y S K 209
Conservation
* 9 7 4 4 * 9 3 5 7 * * 3 * 8 3 * * 2 6 * 3 4 2 5 5 6 * * 4 3 9 7 7 * * 6 6 6 7 * 7 * 7
Quality
Consensus
W + L D G K + F K Q V R E I L G L P - + G - A - - H P N W E - F + D Y L - F - K E Y S K
Prm_Prm_78400/1-207 205 Q Y - T 207
Pso_286050/1-208 205 Q F P H 208
Pca_129643/1-184 182 L F - T 184
Pin_PITG_15287T0/1-213 210 V V F K 213
Conservation
6 6 - 5
Quality
Consensus
Q F - T

Ortholog 23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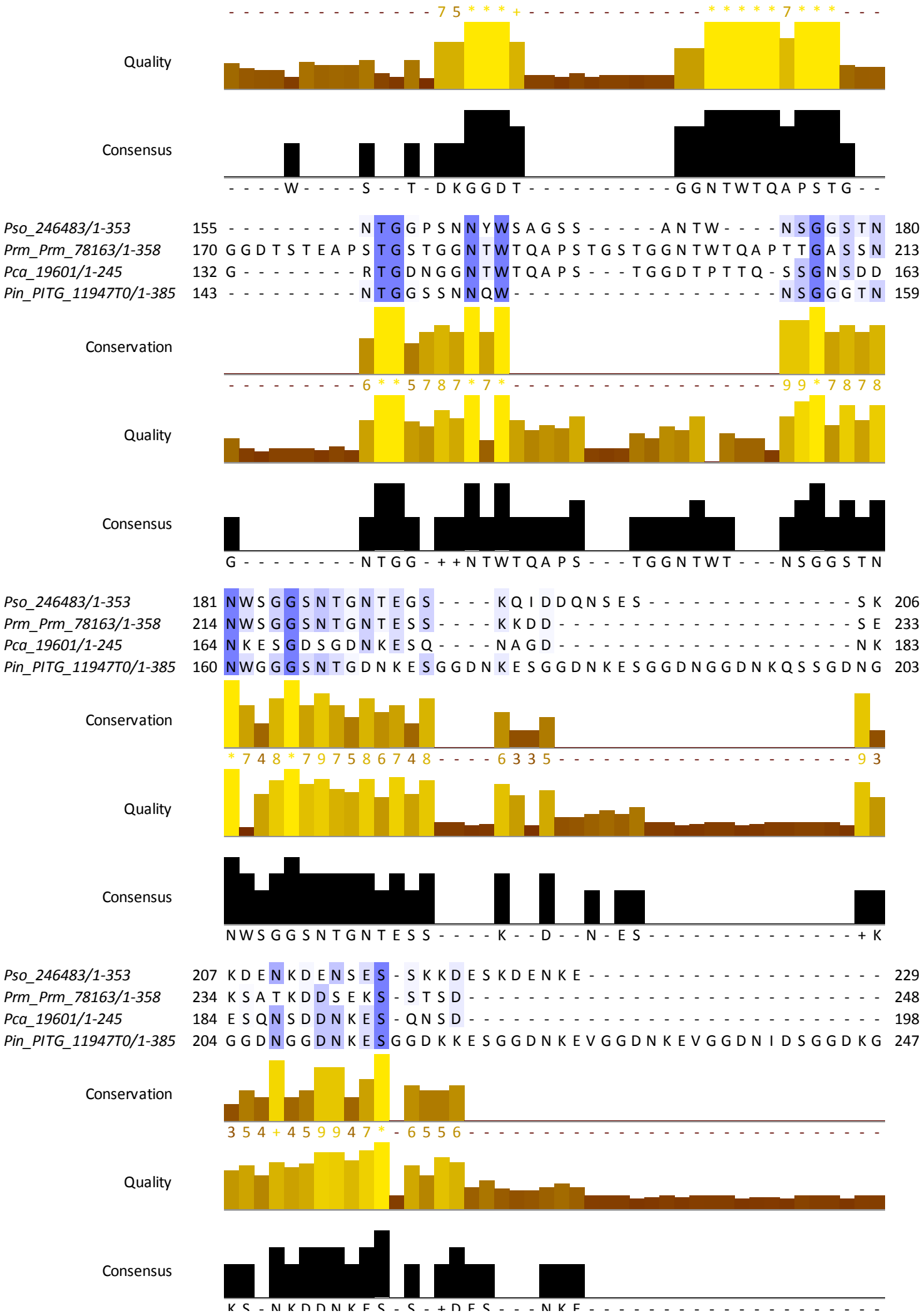
Prm_Prm_78163/1-358 1 MVVAFKKTLFVSAVAVALAMSAVSADSYS-AAVSSESTYEAKRM 43
Pca_19601/1-245 1 MIVSFKKTLFVSAVAVALA---VSVEGYSGAV---ESTYETKRM 38
Pin_PITG_11947T0/1-385 1 MINSFKKSLFVTAVAVALA---VSVEGYTGAAVATQSTYEVKRM 41
Conservation
*866****9*****9*******---8*898*9-*8---7*7*86***
Quality
Consensus
MIVSFKK+LFVSAVAVALA---VS+EGYSGAAVSTESTYEAKRM
Pso_246483/1-353 45 LRLQAQEVAEEEMADDSECGSLEMAEDDSECGSLEMAEDDSECG 88
Prm_Prm_78163/1-358 44 LRIQVEEAAQEEMADDSECGSLEMAEDDSECGSLEMAEEDSECG 87
Pca_19601/1-245 39 LRLEAQDVAEEEMADDSECGSLEMAEDDSECGSLEMAEDDSECG 82
Pin_PITG_11947T0/1-385 42 LRLQVEEVAEEEMADDSECGSLEMAEDDSECGSLEMAEDDSECG 85
Conservation
+88898*8*******************************9*****
Quality
Consensus
LRLQ++EVAEEEMADDSECGSLEMAEDDSECGSLEMAEDDSECG
Pso_246483/1-353 89 SLEMAESDDGSN-----ANTPPSSGGDT--NTWTQAPSTNTGGS 125
Prm_Prm_78163/1-358 88 SLEMAESDGGSTGGNTWTQAPST--GSTGGNTWTQAPS--TGST 127
Pca_19601/1-245 83 SLEMAEESGTGD----------KGGDNGGNTWTQAPS--TG-- 111
Pin_PITG_11947T0/1-385 86 SLEMAEPDNGGDIG---GDTGGDKGGDTGGNTWTQAPSTDTGG- 125
Conservation
******47578 8----------*7+--*******--**--
Quality
Consensus
SLEMAESDGG+D-G-----TP--KGGDTGGNTWTQAPST-TGG-
Pso_246483/1-353 126 SNNYWSAGSSANTWNSGGDT----------NTWTQAPST--- 154
Prm_Prm_78163/1-358 128 GGDTWTQAPS--TGSTGGDTSTEAPSTGSTGGNTWTQAPSTGST 169
Pca_19601/1-245 112 ----------DKGGDN----------GGNTWTQPPSTGDN 131
Pin_PITG_11947T0/1-385 126 ----------DKGGDT----------GGNTWTQAPST--- 142
Conservation


Quality
Consensus
Pso_246483/1-353 155 - - - - - - - - - - N T G G P S N N Y W S A G S S - - - - - A N T W - - - - N S G G S T N 180
Prm_Prm_78163/1-358 170 G G D T S T E A P S T G S T G G N T W T Q A P S T G S T G G N T W T Q A P T T G A S S N 213
Pca_19601/1-245 132 G - - - - - - - - R T G D N G G N T W T Q A P S - - - T G G D T P T T Q - S S G N S D D 163
Pin_PITG_11947T0/1-385 143 - - - - - - - - - - N T G G S S N N Q W - N S G G G T N 159
Conservation
Quality
Consensus
Pso_246483/1-353 181 N W S G G S N T G N T E G S - - - - K Q I D D Q N S E S - - - - - - - - - - - - - - - S K 206
Prm_Prm_78163/1-358 214 N W S G G S N T G N T E S S - - - - K K D D - S E 233
Pca_19601/1-245 164 N K E S G D S G D N K E S Q - - - - N A G D - N K 183
Pin_PITG_11947T0/1-385 160 N W G G G S N T G D N K E S G G D N K E S G G D N K E S G G D N G G D N K Q S S G D N G 203
Conservation
Quality
Consensus
Pso_246483/1-353 207 K D E N K D E N S E S - S K K D E S K D E N K E - 229
Prm_Prm_78163/1-358 234 K S A T K D D S E K S - S T S D - 248
Pca_19601/1-245 184 E S Q N S D D N K E S - Q N S D - 198
Pin_PITG_11947T0/1-385 204 G G D N G G D N K E S G G D K K E S G G D N K E V G G D N K E V G G D N I D S G G D K G 247
Conservation
Quality
Consensus

```
Pso_246483/1-353        230 - E N K D D G G N T - - E N A A D T S V Q Q Q T Q G D I G G E - - - - - - - - - - - - - 257
Prm_Prm_78163/1-358     249 - - - - - - - - N T - - E S S A D S S V Q Q T A Q G S V G G E - - - - - - - - - - - - - 269
Pca_19601/1-245         199 - - - - - - - - D N - - K E S Q N S G D K K G S Q - - - - - - - - - - - - - - - - - - - 213
Pin_PITG_11947T0/1-385  248 G D N K Q Q G G D N G G D N K K S G G D N K E S G G D N G G D K K E S G G E N T G D S V 291

Conservation
                            - - - - - - - - 8 + - - 6 6 4 4 7 7 8 5 6 7 4 7 6 - - - - - - - - - - - - - - - - - - -
Quality

Consensus
                            - - N K - - G G + + - - E N S A D S + + Q + - S Q G D - G G E - - - - - - - - - - - - -

Pso_246483/1-353        258 S D P E V A G E A N P E I G G E A D S E C G S L A M A E D D S E C G S L Q M A E D D S E 301
Prm_Prm_78163/1-358     270 A D P - - - - - - S S E I A G E A D S E C G S L A M A E - D S E C G S L E M A E D G S E 306
Pca_19601/1-245             - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Pin_PITG_11947T0/1-385  292 Q Q G E I G G E A - - E I G G E G D S E C G S L E M A E D D S E C G S L D M A E D D S E 333

Conservation
                            - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Quality

Consensus
                            - D P E - - G E A - - E I G G E A D S E C G S L A M A E D D S E C G S L - M A E D D S E

Pso_246483/1-353        302 C G S L E M A E D S E C G S L E M A E D N G D K Q D Y S G F K S N I D F S T F Q G T D A 345
Prm_Prm_78163/1-358     307 C G S L E M A E D S E C G S L E M A E G S S D N Q E Y S G S K S D I T F S T F Q G T D T 350
Pca_19601/1-245         214 - - - - - - - - - - - - - - - - - - - - N S D D N K E Y T G S K S D I D F S T F Q G - D A 237
Pin_PITG_11947T0/1-385  334 C G S L E M A E P D N G G D - N G G N T G G D K G G D T G G D I G G D E G G N T G G D N 376

Conservation
                            - - - - - - - - - - - - - - - - - - - - 5 7 5 * 6 4 4 5 9 * 5 6 5 5 7 8 5 8 7 6 9 * - * 7
Quality

Consensus
                            C G S L E M A E D S E C G S L E M A E - S G D + Q E Y + G S K S D I D F S T F Q G T D A

Pso_246483/1-353        346 N A G T V - S P Q 353
Prm_Prm_78163/1-358     351 N A G T V - A P Q 358
Pca_19601/1-245         238 N V G T V - A P Q 245
Pin_PITG_11947T0/1-385  377 G G N T E G S T G 385

Conservation
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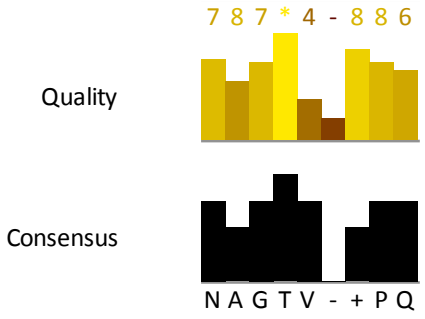
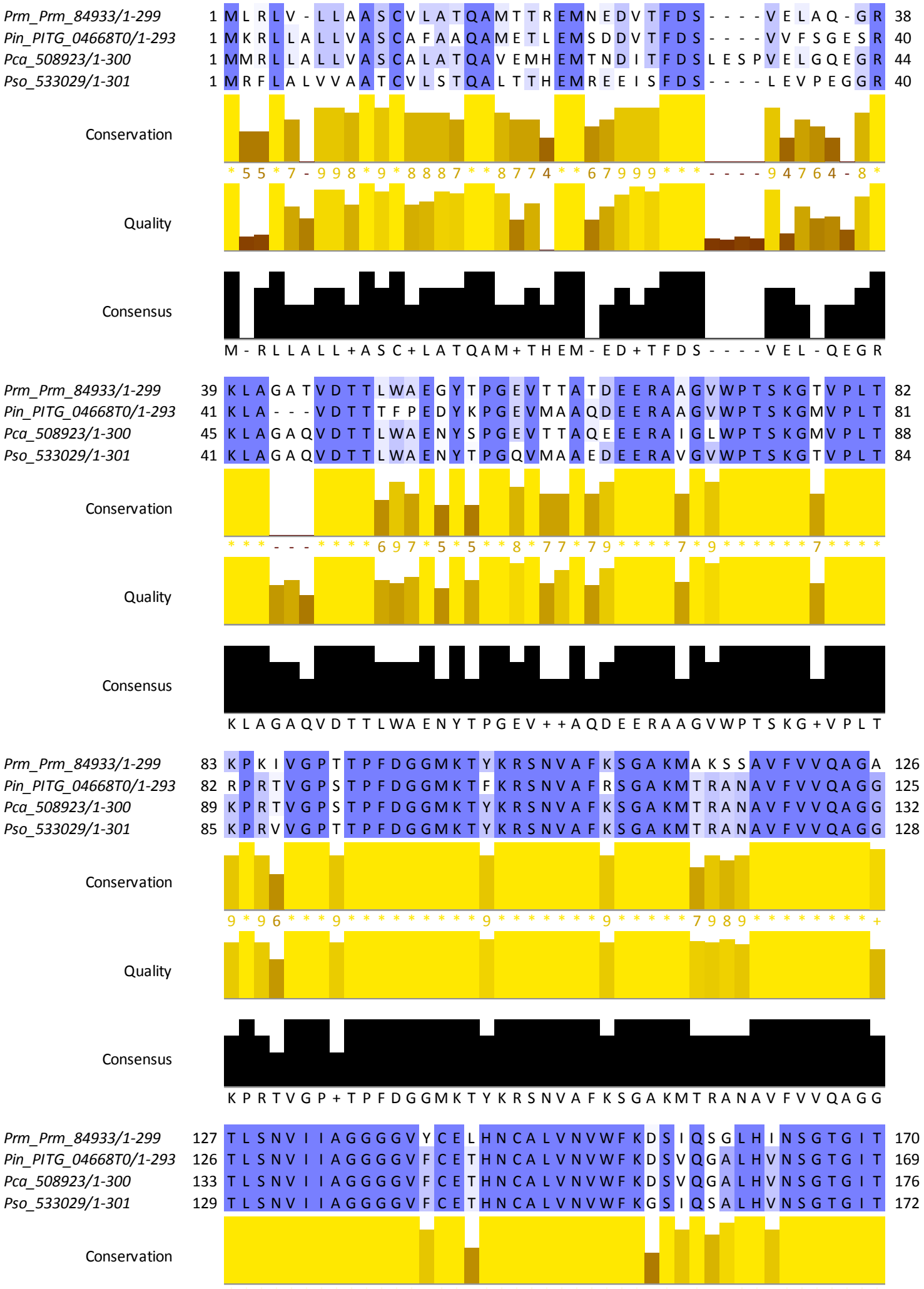

7 8 7 * 4 - 8 8 6
Quality
Consensus
N A G T V - + P Q

Ortholog 24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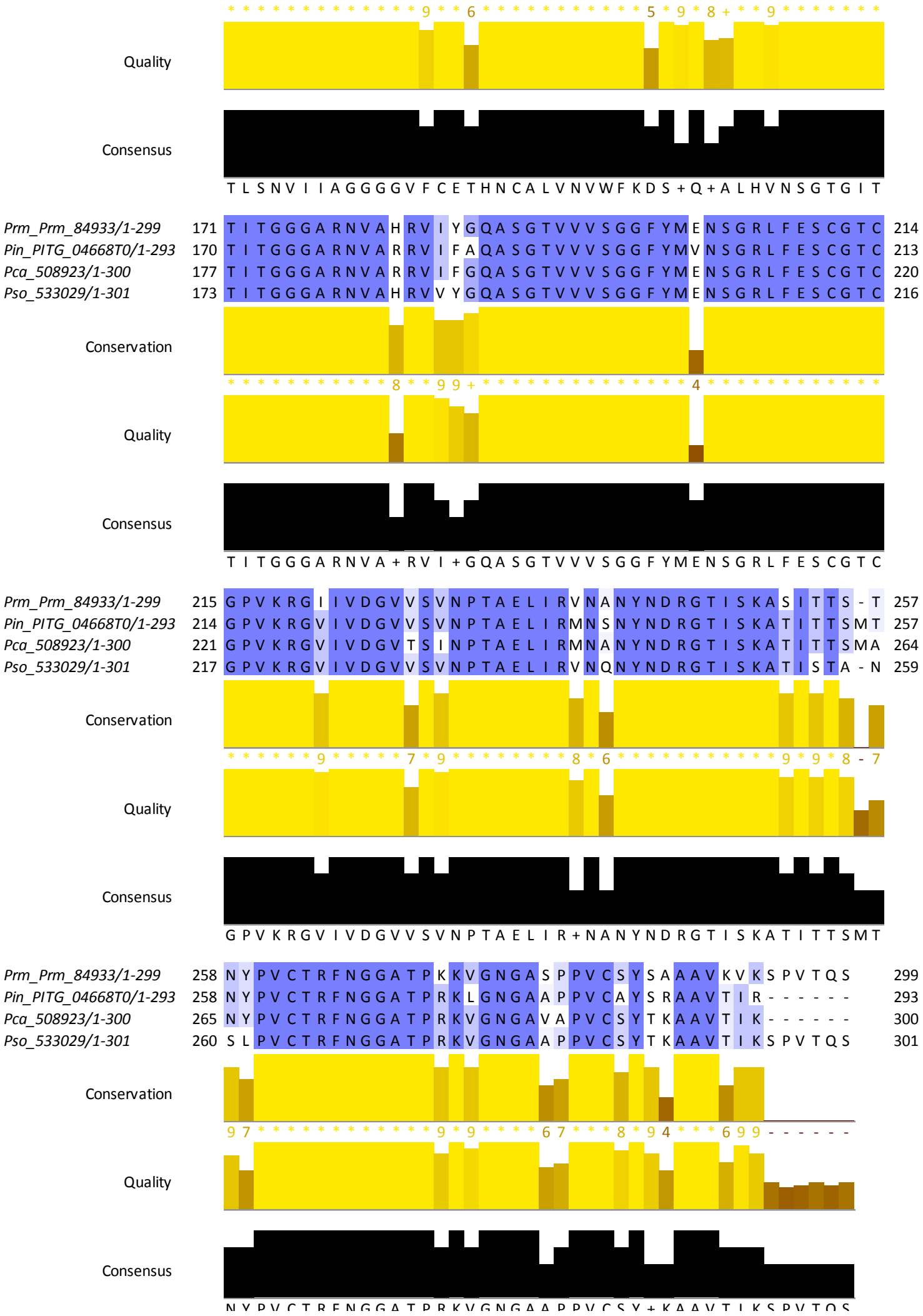
Pin_PITG_04668T0/1-293 1 M K R L L A L L V A S C A F A A Q A M E T L E M S D D V T F D S - - - - V V F S G E S R 40
Pca_508923/1-300 1 M M R L L A L L V A S C A L A T Q A V E M H E M T N D I T F D S L E S P V E L G Q E G R 44
Pso_533029/1-301 1 M R F L A L V V A A T C V L S T Q A L T T H E M R E E I S F D S - - - - L E V P E G G R 40
Conservation
* 5 5 * 7 - 9 9 8 * 9 * 8 8 8 7 * * 8 7 7 4 * * 6 7 9 9 9 * * * - - - - 9 4 7 6 4 - 8 *
Quality
Consensus
M - R L L A L L + A S C + L A T Q A M + T H E M - E D + T F D S - - - - V E L - Q E G R
Prm_Prm_84933/1-299 39 K L A G A T V D T T L W A E G Y T P G E V T T A T D E E R A A G V W P T S K G T V P L T 82
Pin_PITG_04668T0/1-293 41 K L A - - - V D T T T F P E D Y K P G E V M A A Q D E E R A A G V W P T S K G M V P L T 81
Pca_508923/1-300 45 K L A G A Q V D T T L W A E N Y S P G E V T T A Q E E E R A I G L W P T S K G M V P L T 88
Pso_533029/1-301 41 K L A G A Q V D T T L W A E N Y T P G Q V M A A E D E E R A V G V W P T S K G T V P L T 84
Conservation
* * * - - - * * * * 6 9 7 * 5 * 5 * * 8 * 7 7 * 7 9 * * * * 7 * 9 * * * * * * 7 * * * *
Quality
Consensus
K L A G A Q V D T T L W A E N Y T P G E V + + A Q D E E R A A G V W P T S K G + V P L T
Prm_Prm_84933/1-299 83 K P K I V G P T T P F D G G M K T Y K R S N V A F K S G A K M A K S S A V F V V Q A G A 126
Pin_PITG_04668T0/1-293 82 R P R T V G P S T P F D G G M K T F K R S N V A F R S G A K M T R A N A V F V V Q A G G 125
Pca_508923/1-300 89 K P R T V G P S T P F D G G M K T Y K R S N V A F K S G A K M T R A N A V F V V Q A G G 132
Pso_533029/1-301 85 K P R V V G P T T P F D G G M K T Y K R S N V A F K S G A K M T R A N A V F V V Q A G G 128
Conservation
9 * 9 6 * * * 9 * * * * * * * * 9 * * * * * * 9 * * * * * 7 9 8 9 * * * * * * * +
Quality
Consensus
K P R T V G P + T P F D G G M K T Y K R S N V A F K S G A K M T R A N A V F V V Q A G G
Prm_Prm_84933/1-299 127 T L S N V I I A G G G G V Y C E L H N C A L V N V W F K D S I Q S G L H I N S G T G I T 170
Pin_PITG_04668T0/1-293 126 T L S N V I I A G G G G V F C E T H N C A L V N V W F K D S V Q G A L H V N S G T G I T 169
Pca_508923/1-300 133 T L S N V I I A G G G G V F C E T H N C A L V N V W F K D S V Q G A L H V N S G T G I T 176
Pso_533029/1-301 129 T L S N V I I A G G G G V F C E T H N C A L V N V W F K G S I Q S A L H V N S G T G I T 172
Conservation


Quality
Consensus
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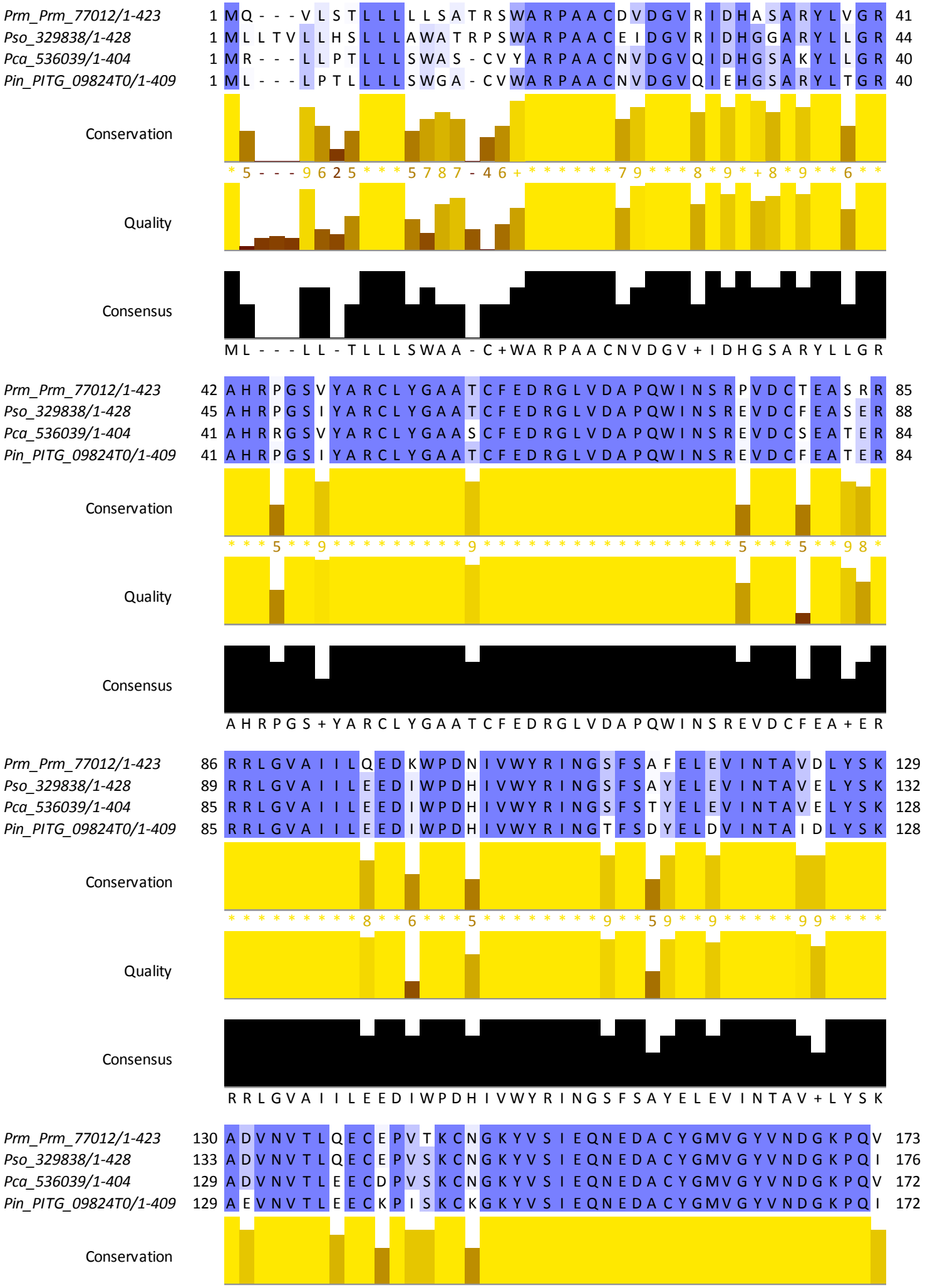
N T T V C T R T N C G A T T R R V G N G A A T T V C S T T R A A V T T R S T V T Q S

Ortholog 25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Pca_536039/1-404 1 MR---LLPTLLLSWAS-CVYARPAACNVDGVQIDHGSAKYLLGR 40
Pin_PITG_09824T0/1-409 1 ML---LPTLLLLSWGA-CVWARPAACNVDGVQIEHGSARYLTGR 40
Conservation
*5---9625***5787-46+******79***8*9*+8*9**6**
Quality
Consensus
ML---LL-TLLLSWAA-C+WARPAACNVDGV+IDHGSARYLLGR
Prm_Prm_77012/1-423 42 AHRPGSVYARCLYGAATCFEDRGLVDAPQWINSRPVDCTEASRR 85
Pso_329838/1-428 45 AHRPGSIYARCLYGAATCFEDRGLVDAPQWINSREVDCFEASER 88
Pca_536039/1-404 41 AHRRGSVYARCLYGAASCFEDRGLVDAPQWINSREVDCSEATER 84
Pin_PITG_09824T0/1-409 41 AHRPGSIYARCLYGAATCFEDRGLVDAPQWINSREVDCFEATER 84
Conservation
5**9******9**********5***5**98*
Quality
Consensus
AHRPGS+YARCLYGAATCFEDRGLVDAPQWINSREVDCFEA+ER
Prm_Prm_77012/1-423 86 RRLGVAIILQEDKWPDNIVWYRINGSFSAFELEVINTAVDLYSK 129
Pso_329838/1-428 89 RRLGVAIILEEDIWPDHIVWYRINGSFSAYELEVINTAVELYSK 132
Pca_536039/1-404 85 RRLGVAIILEEDIWPDHIVWYRINGSFSTYELEVINTAVELYSK 128
Pin_PITG_09824T0/1-409 85 RRLGVAIILEEDIWPDHIVWYRINGTFSDYELDVINTAIDLYSK 128
Conservation
*******8**6***5*********9**59**9*****99****
Quality
Consensus
RRLGVAIILEEDIWPDHIVWYRINGSFSAYELEVINTAV+LYSK
Prm_Prm_77012/1-423 130 ADVNVTLQECEPVTKCNGKYVSIEQNEDACYGMVGYVNDGKPQV 173
Pso_329838/1-428 133 ADVNVTLQECEPVSKCNGKYVSIEQNEDACYGMVGYVNDGKPQI 176
Pca_536039/1-404 129 ADVNVTLEECDPVSKCNGKYVSIEQNEDACYGMVGYVNDGKPQV 172
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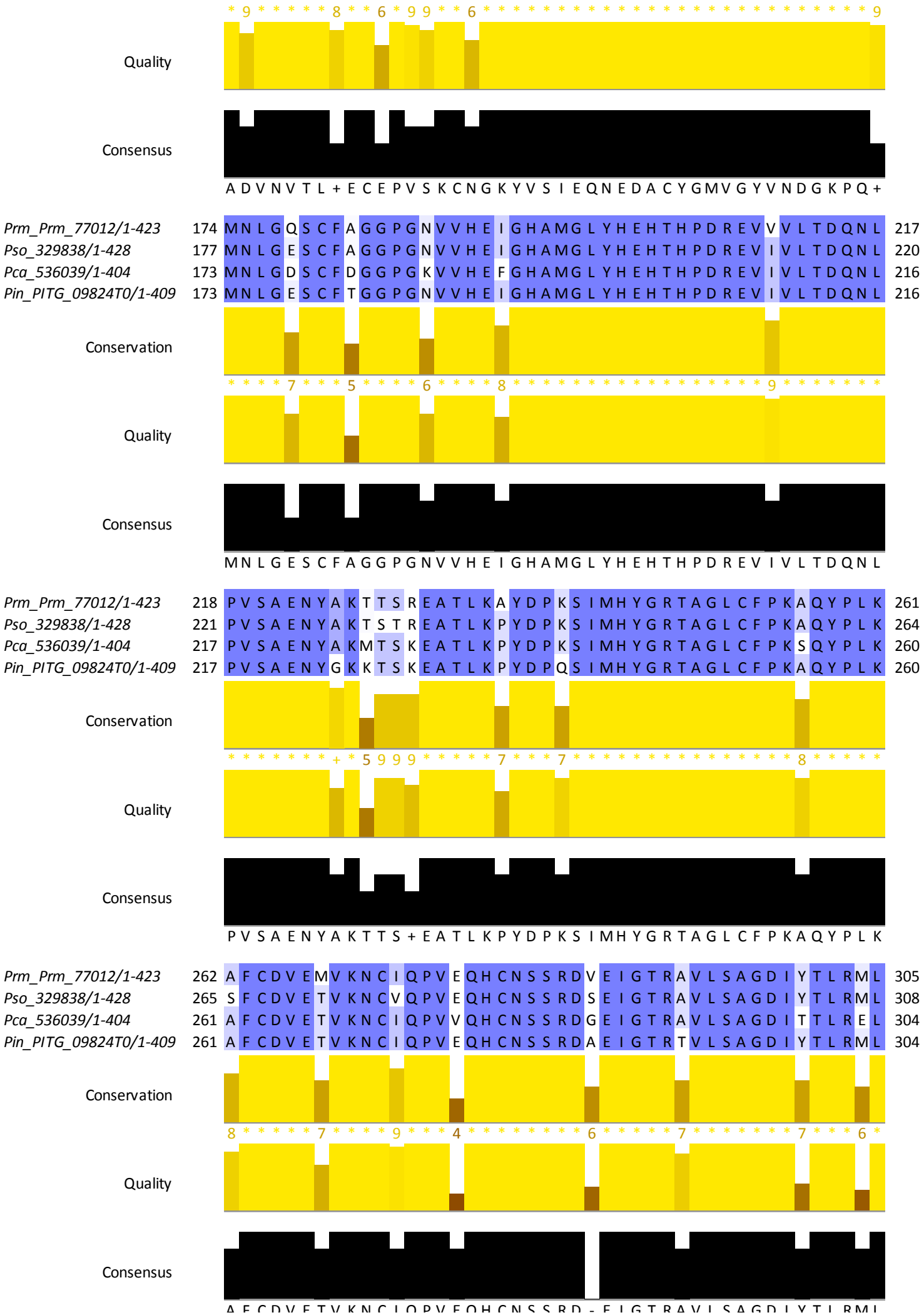
Conservation


Quality
Consensus
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Conservation
Quality
Consensus
M N L G E S C F A G G P G N V V H E I G H A M G L Y H E H T H P D R E V I V L T D Q N L
Prm_Prm_77012/1-423 218 PVSAENYAKTTSREATLKAYDPKSIMHYGRTAGLCFPKAQYPLK 261
Pso_329838/1-428 221 PVSAENYAKTSTREATLKPYDPKSIMHYGRTAGLCFPKAQYPLK 264
Pca_536039/1-404 217 PVSAENYAKMTSKEATLKPYDPKSIMHYGRTAGLCFPKSQYPLK 260
Pin_PITG_09824T0/1-409 217 PVSAENYGKKTSKEATLKPYDPQSIMHYGRTAGLCFPKAQYPLK 260
Conservation
Quality
Consensus
P V S A E N Y A K T T S + E A T L K P Y D P K S I M H Y G R T A G L C F P K A Q Y P L K
Prm_Prm_77012/1-423 262 AFCDVEMVKNCIQPVEQHCNSSRDVEIGTRAVLSAGDIYTLRML 305
Pso_329838/1-428 265 SFCDVETVKNCVQPVEQHCNSSRDSEIGTRAVLSAGDIYTLRML 308
Pca_536039/1-404 261 AFCDVETVKNCIQPVVQHCNSSRDGEIGTRAVLSAGDITTLREL 304
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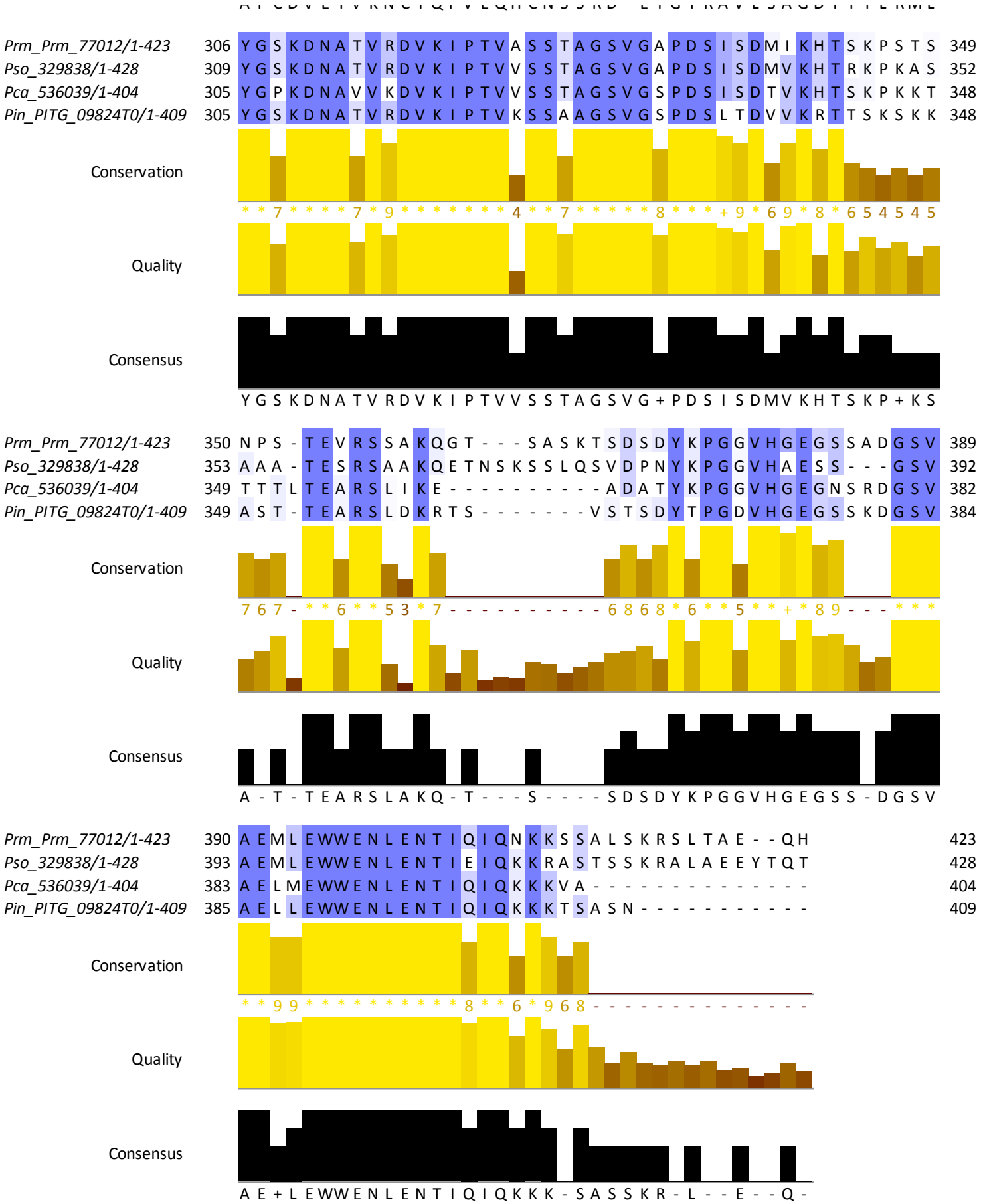
Conservation
Quality
Consensus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Pca_536039/1-404 305 YGPKDNAVVKDVKIPTVVSSTAGSVGSPDSISDTVKHTSKPKKT 348
Pin_PITG_09824T0/1-409 305 YGSKDNATVRDVKIPTVKSSAAGSVGSPDSLTDVVKRTTSKSKK 348
Conservation
Quality
Consensus
YGSKDNATVRDVKIPTVVSSTAGSVG+PDSISDMVKHTSKP+KS
Prm_Prm_77012/1-423 350 NPS-TEVRSSAKQGT---SASKTSDSDYKPGGVHGEGSSADGSV 389
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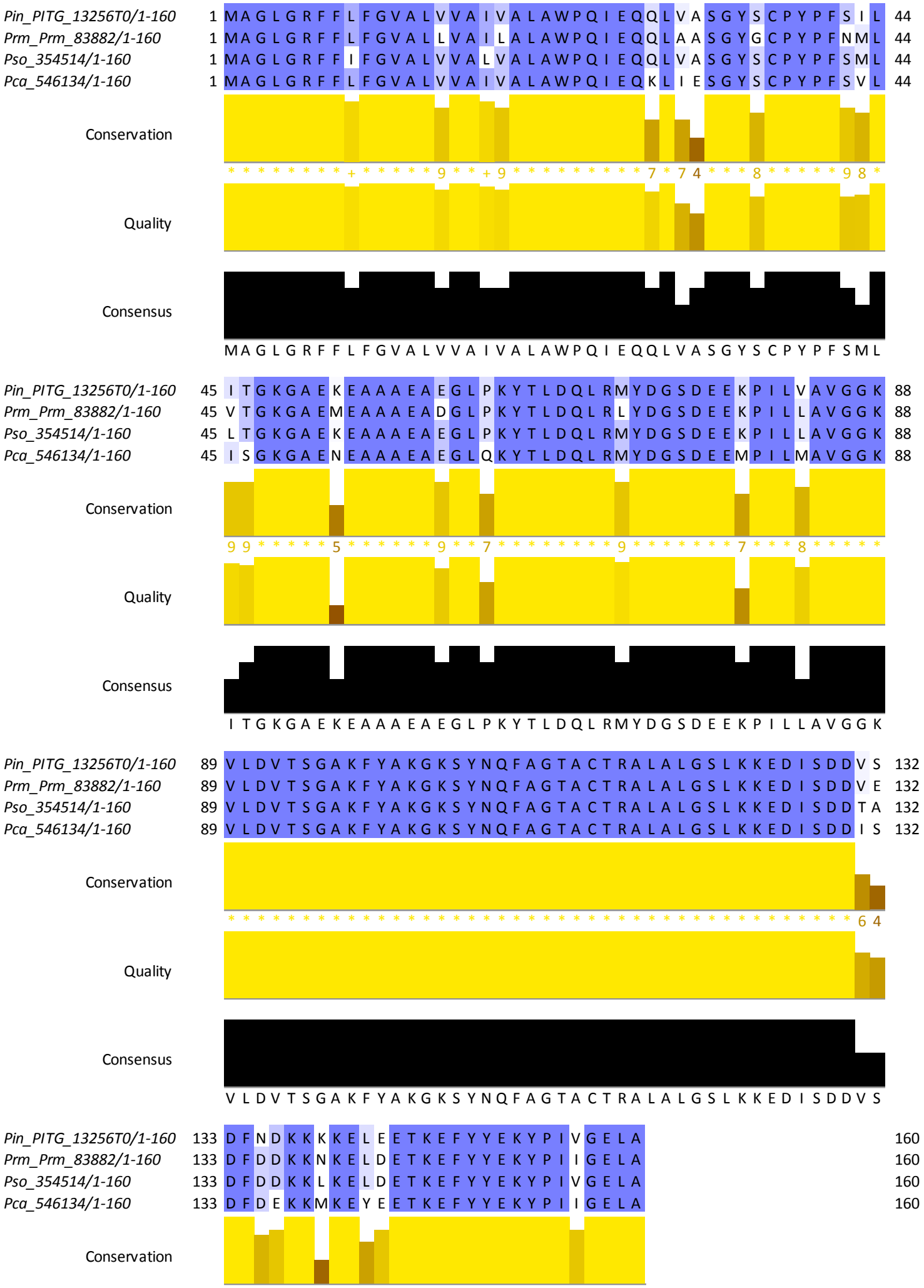
Ortholog 26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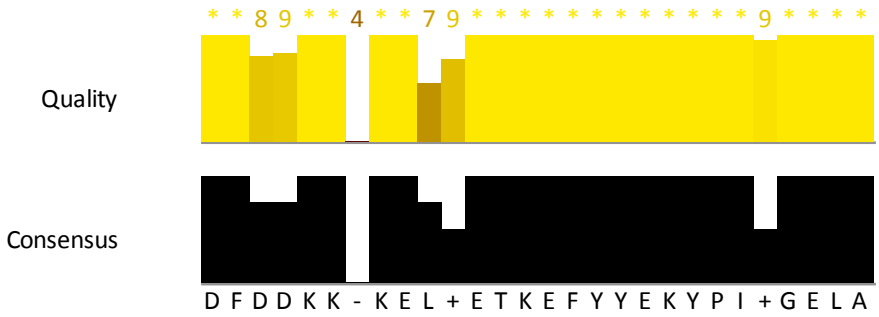
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Ortholog 27

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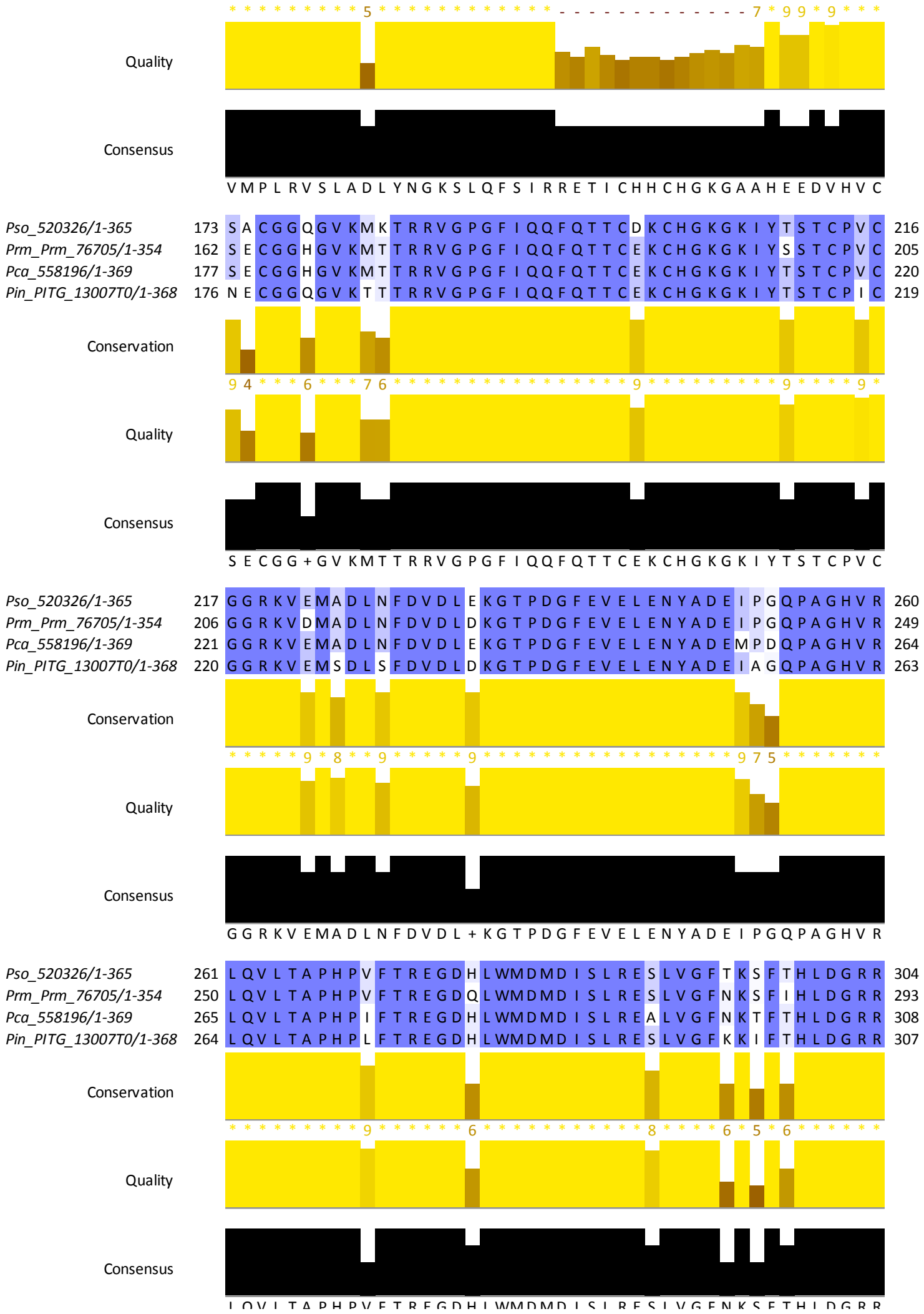
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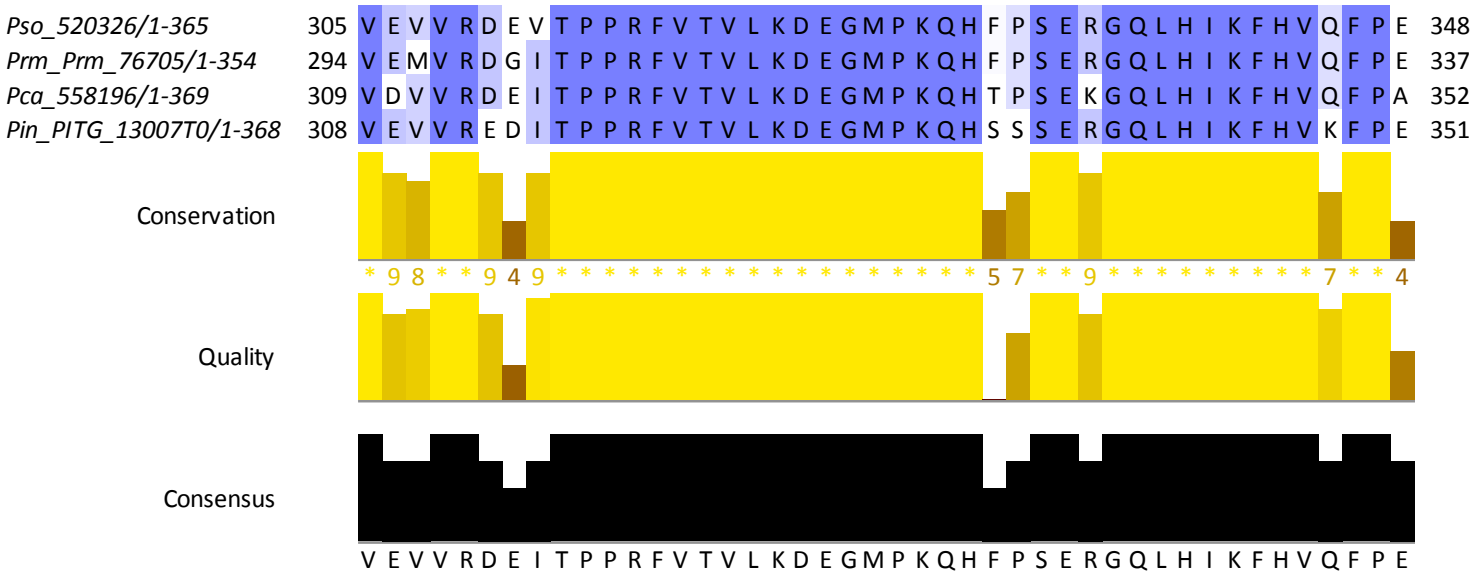
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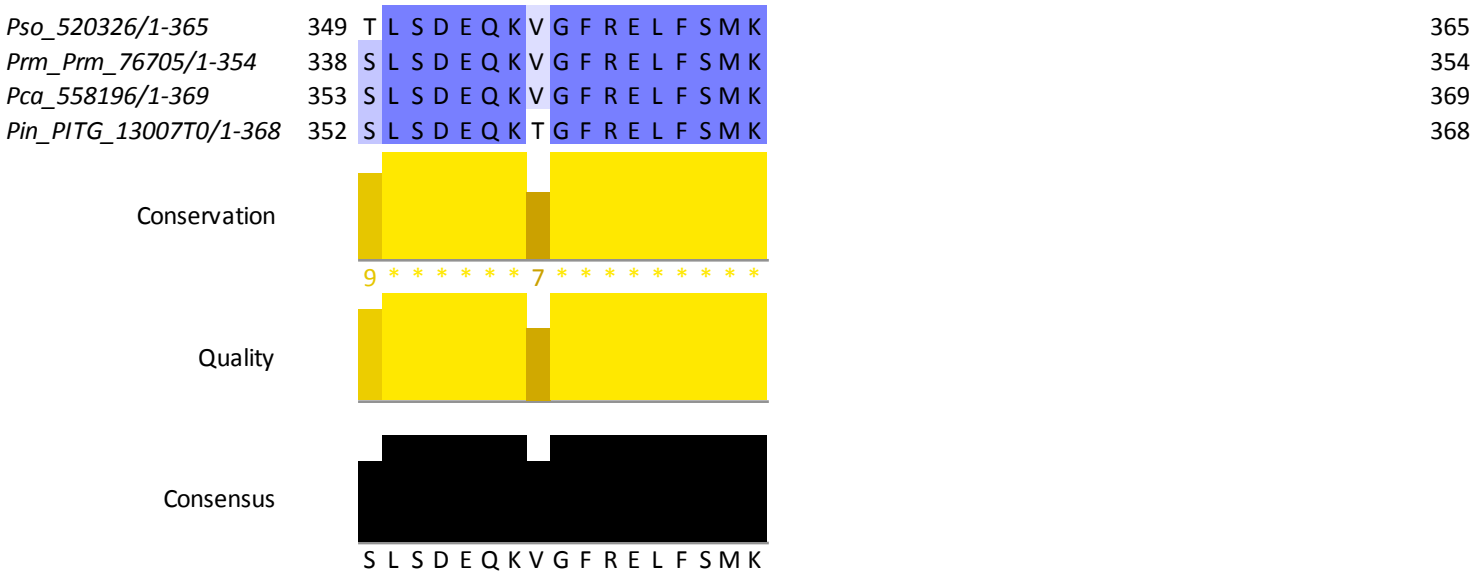
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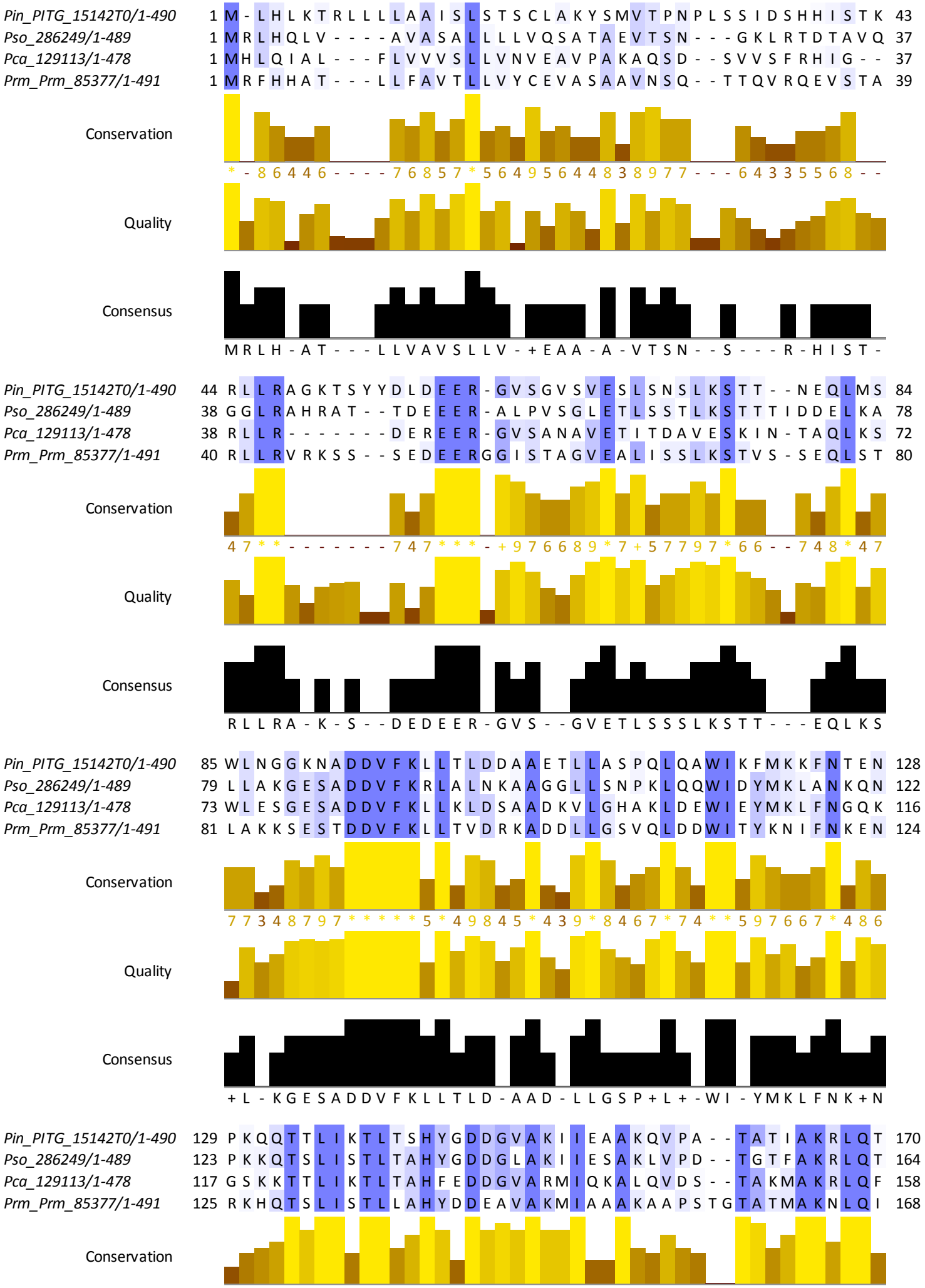
Ortholog 28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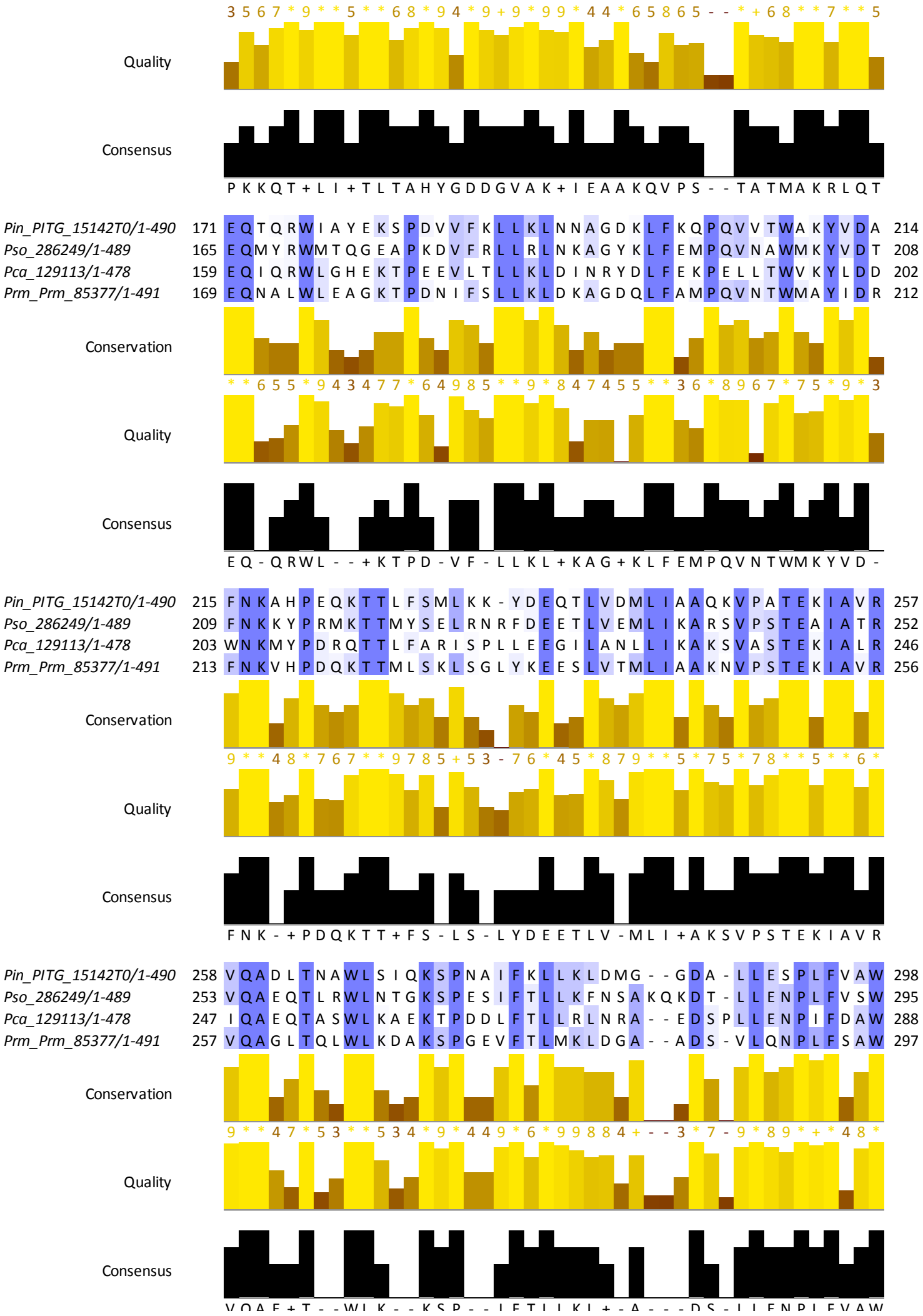
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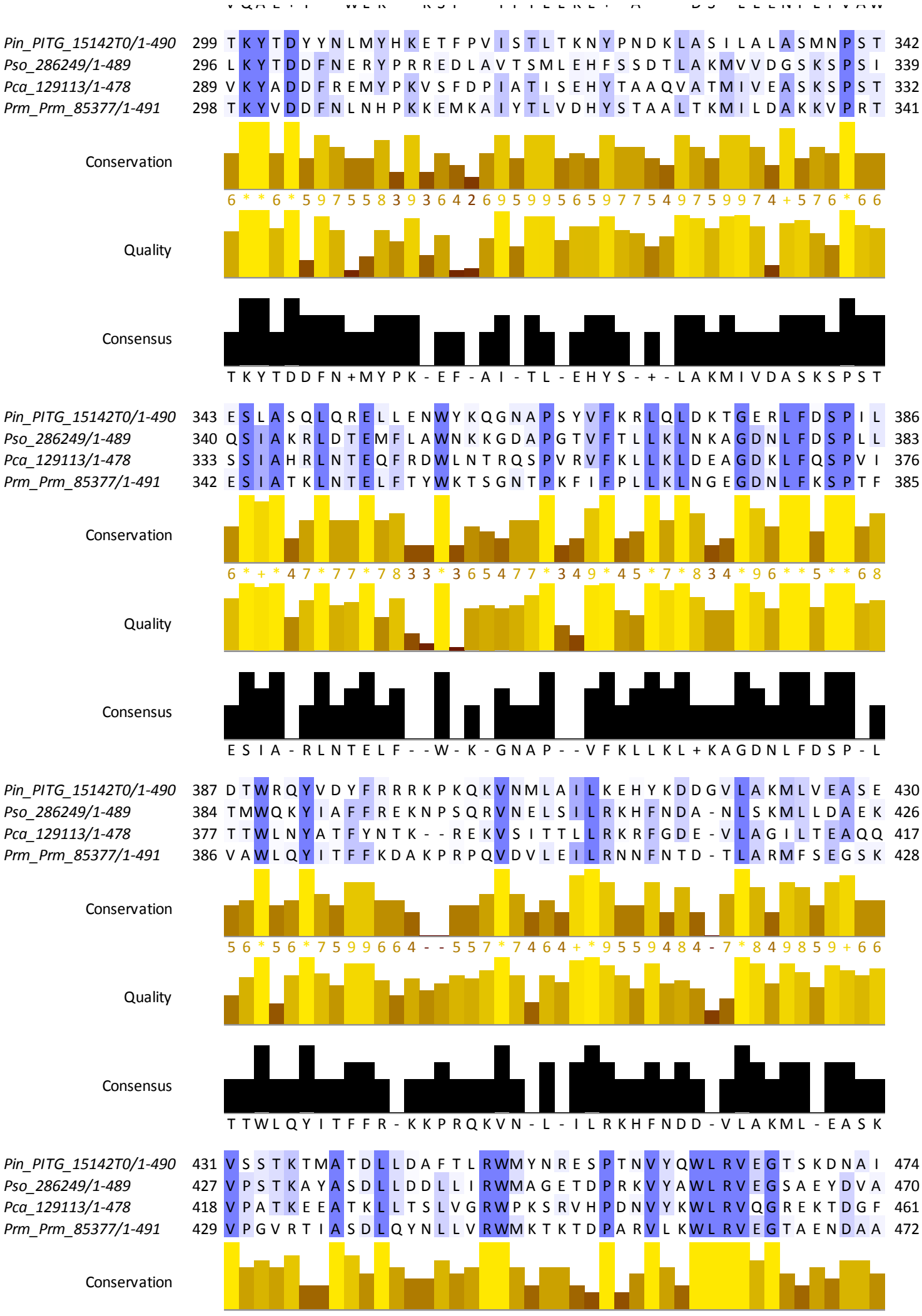
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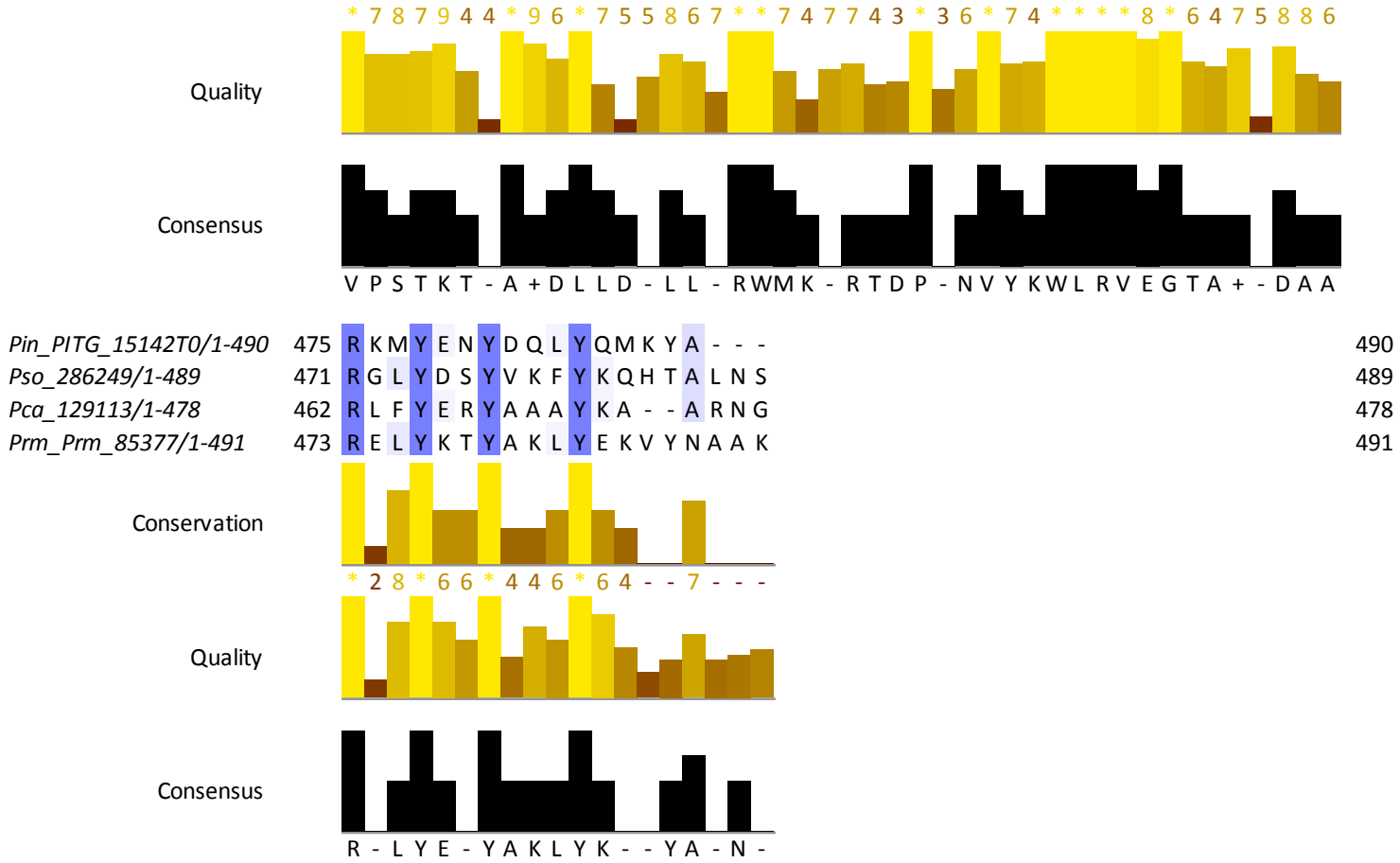
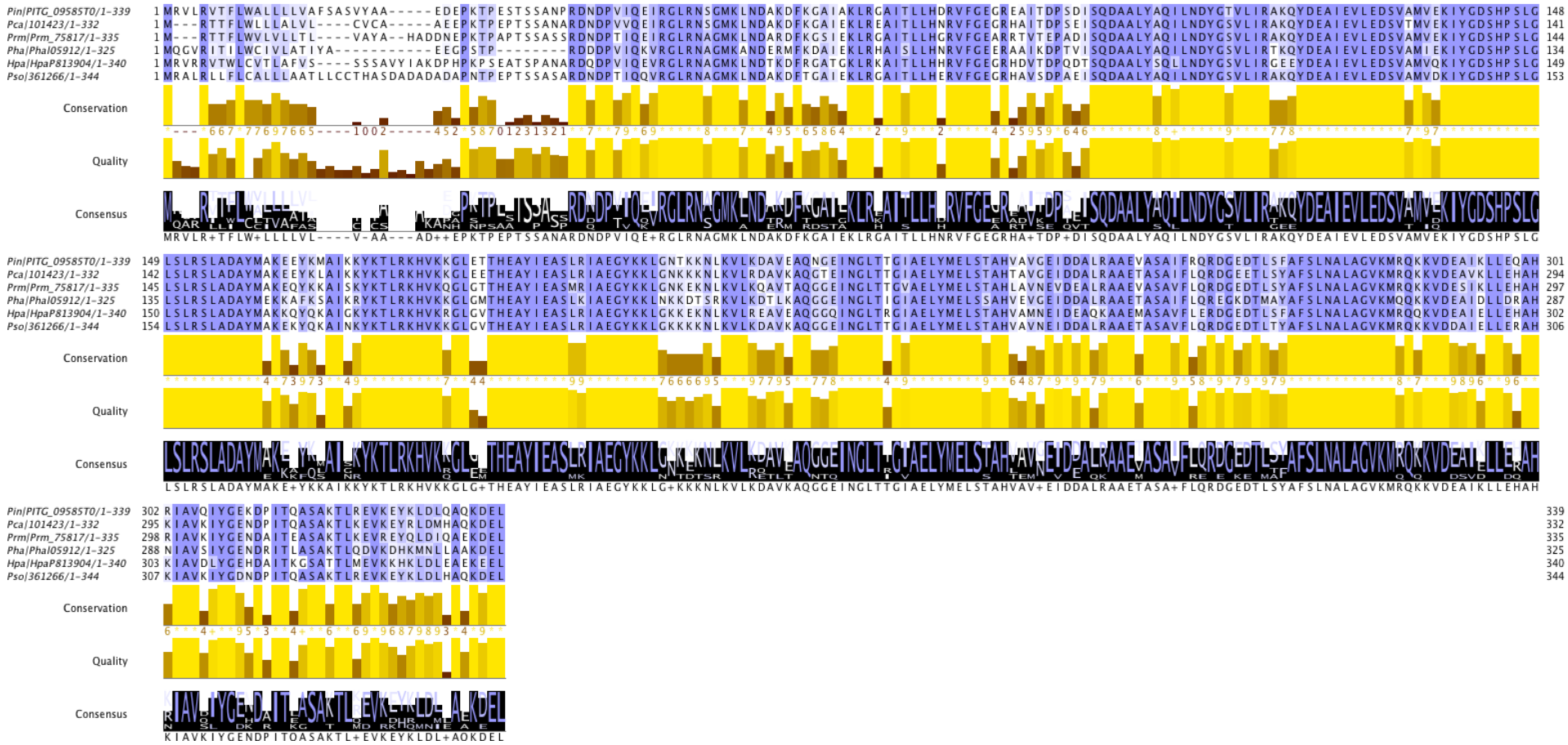


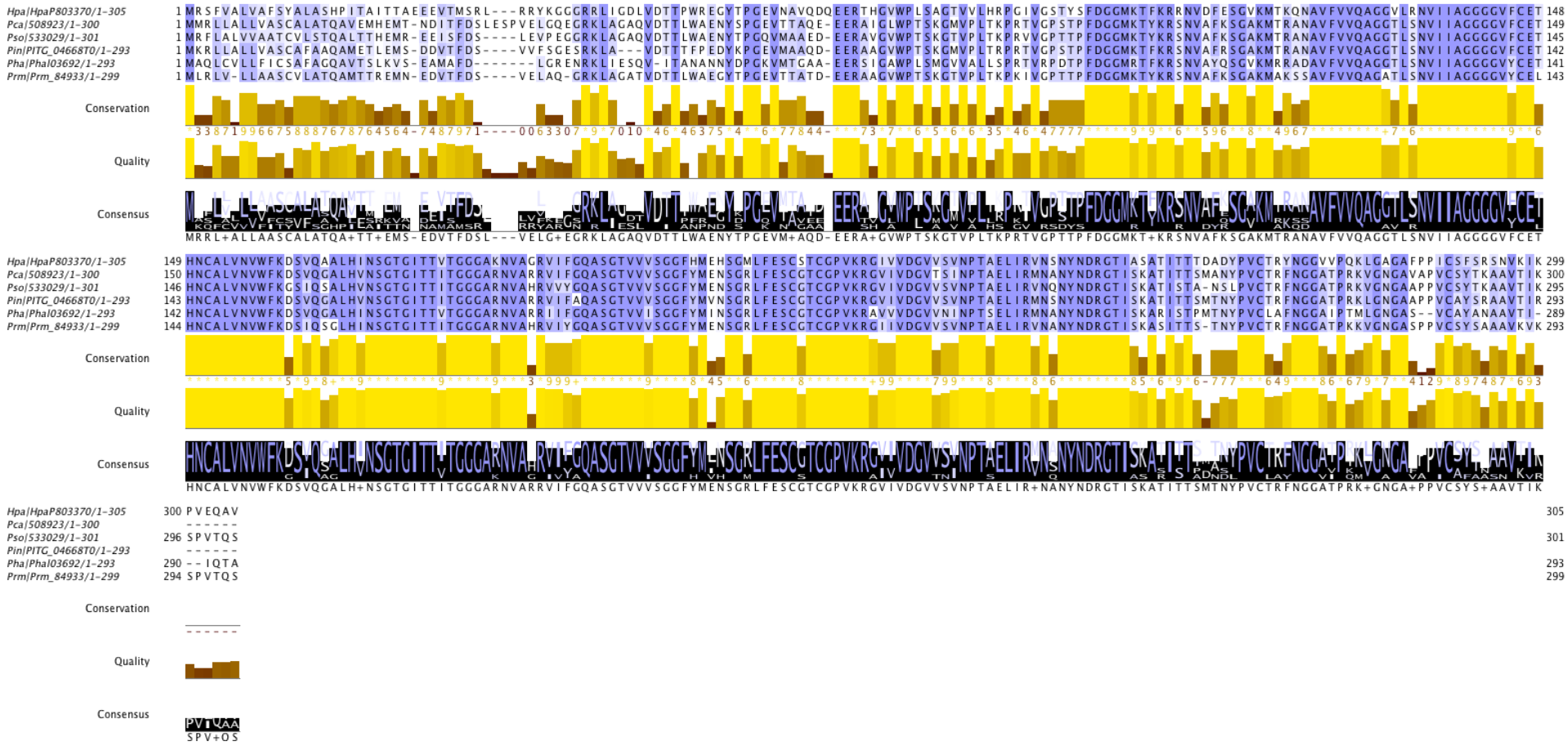
Supplementary Figure 23: Multiple sequence alignments of the 28 orthologs of RxLR-like effectors.

Supplementary Figure 24



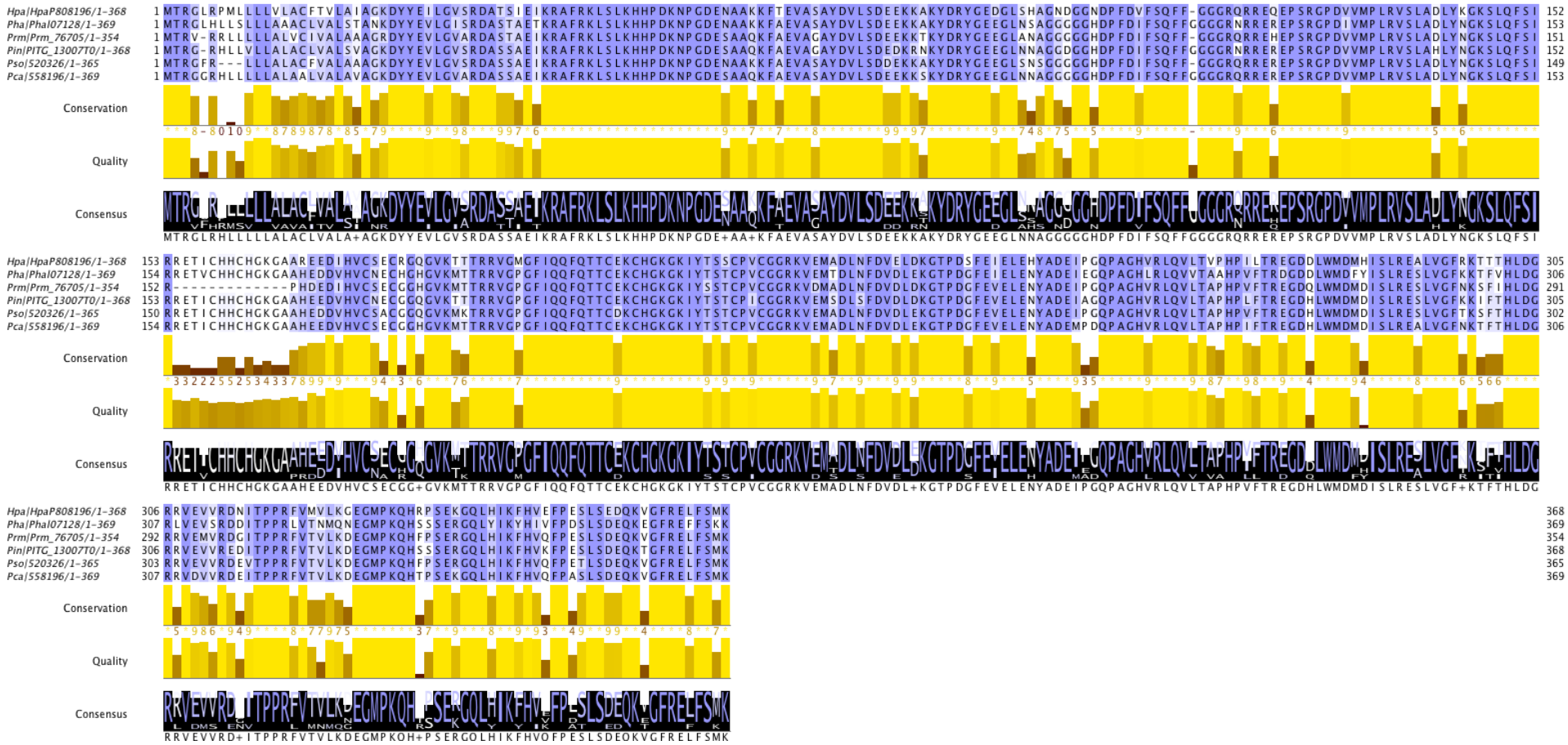
Supplementary Figure 24: Multiple sequence alignment of the RxLR-like proteins of Ortholog 1.

Supplementary Figure 25



Supplementary Figure 25: Multiple sequence alignment of the RxLR-like proteins of Ortholog 2.

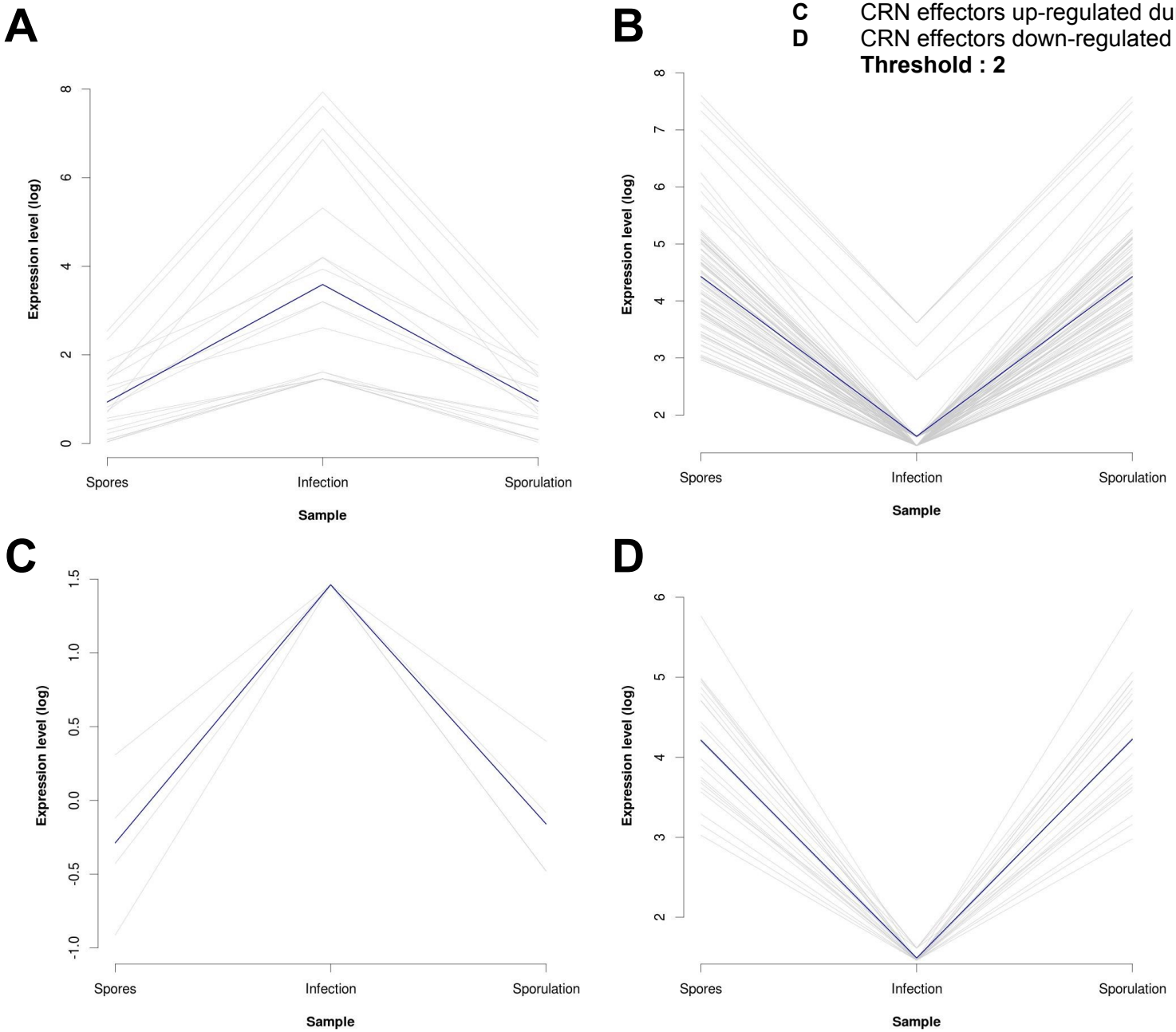
Supplementary Figure 26



Supplementary Figure 26: Multiple sequence alignment of the RxLR-like proteins of Ortholog 3.

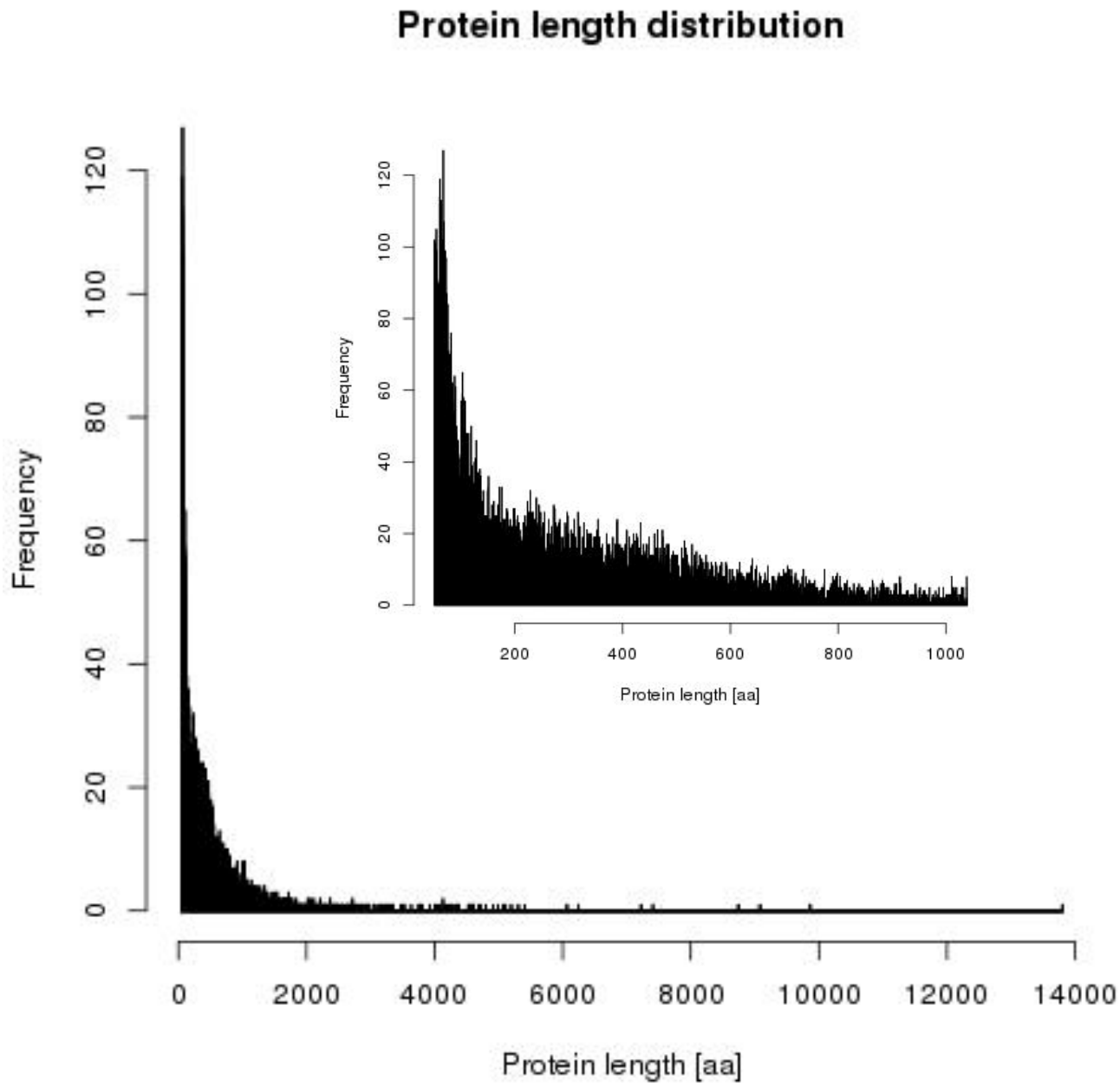
Supplementary Figure 27

A RxLR effectors up-regulated during infection
B RxLR effectors down-regulated during infection
C CRN effectors up-regulated during infection
D CRN effectors down-regulated during infection
Threshold : 2



Supplementary figure 27: Expression profiling of the candidate RxLR and CRNs encoding genes. Expression values have been estimated in terms of log2.

Supplementary Figure 28



Supplementary Figure 28: Protein length distribution.