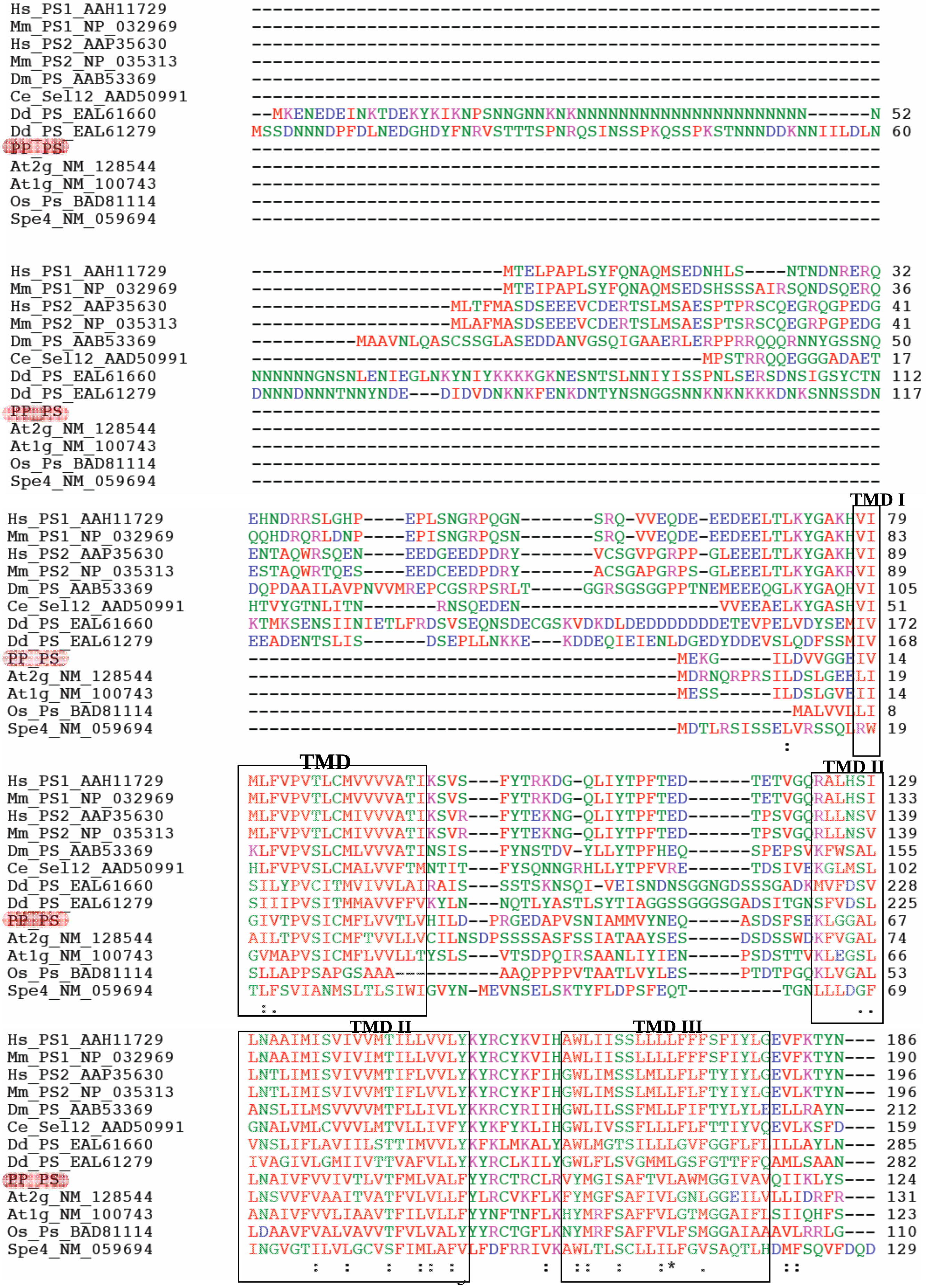
Presenilin



```
Hs_PS1_AAH11729       ------------------------------------------------------------
Mm_PS1_NP_032969      ------------------------------------------------------------
Hs_PS2_AAP35630       ------------------------------------------------------------
Mm_PS2_NP_035313      ------------------------------------------------------------
Dm_PS_AAB53369        ------------------------------------------------------------
Ce_Sel12_AAD50991     ------------------------------------------------------------
Dd_PS_EAL61660        --MKENEDEINKTDEKYKIKNPSNNGNNKNKNNNNNNNNNNNNNNNNNNNNN------N 52
Dd_PS_EAL61279        MSSDNNNDPFDLNEDGHDYFNRVSTTTSPNRQSINSSPKQSSPKSTNNNDDKNNIILDLN 60
PP_PS                 ------------------------------------------------------------
At2g_NM_128544        ------------------------------------------------------------
At1g_NM_100743        ------------------------------------------------------------
Os_Ps_BAD81114        ------------------------------------------------------------
Spe4_NM_059694        ------------------------------------------------------------


Hs_PS1_AAH11729       ------------------------MTELPAPLSYFQNAQMSEDNHLS----NTNDNRERQ 32
Mm_PS1_NP_032969      ------------------------MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQ 36
Hs_PS2_AAP35630       -------------------MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDG 41
Mm_PS2_NP_035313      -------------------MLAFMASDSEEEVCDERTSLMSAESPTSRSCQEGRPGPEDG 41
Dm_PS_AAB53369        ----------MAAVNLQASCSSGLASEDDANVGSQIGAAERLERPPRRQQQRNNYGSSNQ 50
Ce_Sel12_AAD50991     -------------------------------------------MPSTRRQQEGGGADAET 17
Dd_PS_EAL61660        NNNNNNGNSNLENIEGLNKYNIYKKKKGKNESNTSLNNIYISSPNLSERSDNSIGSYCTN 112
Dd_PS_EAL61279        DNNNDNNNTNNYNDE---DIDVDNKNKFENKDNTYNSNGGSNNKNKNKKKDNKSNNSSDN 117
PP_PS                 ------------------------------------------------------------
At2g_NM_128544        ------------------------------------------------------------
At1g_NM_100743        ------------------------------------------------------------
Os_Ps_BAD81114        ------------------------------------------------------------
Spe4_NM_059694        ------------------------------------------------------------

Hs_PS1_AAH11729       EHNDRRSLGHP----EPLSNGRPQGN-------SRQ-VVEQDE-EEDEELTLKYGAKHVI 79
Mm_PS1_NP_032969      QQHDRQRLDNP----EPISNGRPQSN-------SRQ-VVEQDE-EEDEELTLKYGAKHVI 83
Hs_PS2_AAP35630       ENTAQWRSQEN----EEDGEEDPDRY-------VCSGVPGRPP-GLEEELTLKYGAKHVI 89
Mm_PS2_NP_035313      ESTAQWRTQES----EEDCEEDPDRY-------ACSGAPGRPS-GLEEELTLKYGAKRVI 89
Dm_PS_AAB53369        DQPDAAILAVPNVVMREPCGSRPSRLT-----GGRSGSGGPPTNEMEEEQGLKYGAQHVI 105
Ce_Sel12_AAD50991     HTVYGTNLITN-------RNSQEDEN-------------------VVEEAELKYGASHVI 51
Dd_PS_EAL61660        KTMKSENSIINIETLFRDSVSEQNSDECGSKVDKDLDEDDDDDDDETEVPELVDYSEMIV 172
Dd_PS_EAL61279        EEADENTSLIS------DSEPLLNKKE---KDDEQIEIENLDGEDYDDEVSLQDFSSMIV 168
PP_PS                 -----------------------------------------MEKG-----ILDVVGGEIV 14
At2g_NM_128544        -----------------------------------------MDRNQRPRSILDSLGEELI 19
At1g_NM_100743        -----------------------------------------MESS-----ILDSLGVEII 14
Os_Ps_BAD81114        ----------------------------------------------------MALVVLLI 8
Spe4_NM_059694        -----------------------------------------MDTLRSISSELVRSSQLRW 19
                                                                         :

Hs_PS1_AAH11729       MLFVPVTLCMVVVVATIKSVS---FYTRKDG-QLIYTPFTED------TETVGQRALHSI 129
Mm_PS1_NP_032969      MLFVPVTLCMVVVVATIKSVS---FYTRKDG-QLIYTPFTED------TETVGQRALHSI 133
Hs_PS2_AAP35630       MLFVPVTLCMIVVVATIKSVR---FYTEKNG-QLIYTPFTED------TPSVGQRLLNSV 139
Mm_PS2_NP_035313      MLFVPVTLCMIVVVATIKSVR---FYTEKNG-QLIYTPFTED------TPSVGQRLLNSV 139
Dm_PS_AAB53369        KLFVPVSLCMLVVVATINSIS---FYNSTDV-YLLYTPFHEQ------SPEPSVKFWSAL 155
Ce_Sel12_AAD50991     HLFVPVSLCMALVVFTMNTIT---FYSQNNGRHLLYTPFVRE------TDSIVEKGLMSL 102
Dd_PS_EAL61660        SILYPVCITMVIVVLAIRAIS---SSTSKNSQI-VEISNDNSGGNGDSSSGADKMVFDSV 228
Dd_PS_EAL61279        SIIIPVSITMMAVVFFVKYLN---NQTLYASTLSYTIAGGSSGGGSGADSITGNSFVDSL 225
PP_PS                 GIVTPVSICMFLVVTLVHILD--PRGEDAPVSNIAMMVYNEQ-----ASDSFSEKLGGAL 67
At2g_NM_128544        AILTPVSICMFTVVLLVCILNSDPSSSSASFSSIATAAYSES-----DSDSSWDKFVGAL 74
At1g_NM_100743        GVMAPVSICMFLVVLLTYSLS---VTSDPQIRSAANLIYIEN-----PSDSTTVKLEGSL 66
Os_Ps_BAD81114        SLLAPPSAPGSAAA----------AAQPPPPVTAATLVYLES-----PTDTPGQKLVGAL 53
Spe4_NM_059694        TLFSVIANMSLTLSIWIGVYN-MEVNSELSKTYFLDPSFEQT---------TGNLLLDGF 69
                       :.                                                       ..

Hs_PS1_AAH11729       LNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYN--- 186
Mm_PS1_NP_032969      LNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFIYLGEVFKTYN--- 190
Hs_PS2_AAP35630       LNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN--- 196
Mm_PS2_NP_035313      LNTLIMISVIVVMTIFLVVLYKYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYN--- 196
Dm_PS_AAB53369        ANSLILMSVVVVMTFLLIVLYKKRCYRIIHGWLILSSFMLLFIFTYLYLEELLRAYN--- 212
Ce_Sel12_AAD50991     GNALVMLCVVVLMTVLLIVFYKYKFYKLIHGWLIVSSFLLLFLFTTIYVQEVLKSFD--- 159
Dd_PS_EAL61660        VNSLIFLAVIILSTTIMVVLYKFKLMKALYAWLMGTSILLLGVFGGFLFLILLAYLN--- 285
Dd_PS_EAL61279        IVAGIVLGMIIVTTVAFVLLYKYRCLKILYGWLFLSVGMMLGSFGTTFFQAMLSAAN--- 282
PP_PS                 LNAIVFVVIVTLVTFMLVALFYYRCTRCLRVYMGISAFTVLAWMGGIVAVQIIKLYS--- 124
At2g_NM_128544        LNSVVFVAAITVATFVLVLLFYLRCVKFLKFYMGFSAFIVLGNLGGEILVLLIDRFR--- 131
At1g_NM_100743        ANAIVFVVLIAAVTFILVLLFYYNFTNFLKHYMRFSAFFVLGTMGGAIFLSIIQHFS--- 123
Os_Ps_BAD81114        LDAAVFVALVAVVTFVLVALYYYRCTGFLKNYMRFSAFFVLFSMGGAIAAAVLRRLG--- 110
Spe4_NM_059694        INGVGTILVLGCVSFIMLAFVLFDFRRIVKAWLTLSCLLILFGVSAQTLHDMFSQVFDQD 129
                            :  :   :  :: :        :  ::  :   :*  .       ::
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                                   TMD IV                    TMD V           TMD VI
Hs_PS1_AAH11729     ----VAVDYITVALLIWNFGVVGMISIHWKG-PLRLQQAYLIMISALMALVFIKYLPEWT 241
Mm_PS1_NP_032969    ----VAVDYVTVALLIWNFGVVGMIAIHWKG-PLRLQQAYLIMISALMALVFIKYLPEWT 245
Hs_PS2_AAP35630     ----VAMDYPTLLLTVWNFGAVGMVCIHWKG-PLVLQQAYLIMISALMALVFIKYLPEWS 251
Mm_PS2_NP_035313    ----VAMDYPTLFLAVWNFGAVGMVCIHWKG-PLALQQAYLIVISALMALVFIKYLPEWS 251
Dm_PS_AAB53369      ----IPMDYPTALLIMWNFGVVGMMSIHWQG-PLRLQQGYLIFVAALMALVFIKYLPEWT 267
Ce_Sel12_AAD50991   ----VSPSALLVLFGLGNYGVLGMMCIHWKG-PLRLQQFYLITMSALMALVFIKYLPEWT 214
Dd_PS_EAL61660      ----LGLDYVTFVIVVWNFSVGGIVCIFWYS-PKLLNQGYLISISVLMALFFSR-LPDWT 339
Dd_PS_EAL61279      ----LPLDYITFAFLIFNFTVCGIIGVFWYA-HQYVNQLYLVIISVLMAISLTR-LPQWT 336
PP_PS               ----IPIDVITFLICTINFASVGVAAVFFCRMPIMVTQGYLIVIGMLVAFWFTK-LPEWT 179
At2g_NM_128544      ----FPIDSITFLILLFNFSVVGVFAVFMSKFSILITQGYLVWIGVLVAYFFTL-LPEWT 186
At1g_NM_100743      ----IPVDSITCFILLFNFTILGTLSVFAGGIPIVLRQCYMVVMGIVVAAWFTK-LPEWT 178
Os_Ps_BAD81114      ----APLDAATALVLLFNASAVGVLSVFASAVPIVVRQGYMVALAVIVAAWLSR-LPEWT 165
Spe4_NM_059694      DNNQYYMTIVLIVVPTVVYGFGGIYAFFSNS-SLILHQIFVVTNCSLISVFYLRVFPSKT 188
                                 .        *   ..   .   : * :::    :::      :*. :

                      TMD VI
Hs_PS1_AAH11729     AWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVN-------- 293
Mm_PS1_NP_032969    AWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVN-------- 297
Hs_PS2_AAP35630     AWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVG-------- 303
Mm_PS2_NP_035313    AWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMVWTVG-------- 303
Dm_PS_AAB53369      AWAVLAAISIWDLIAVLSPRGPLRILVETAQERNEQIFPALIYSSTVVYALVNTVTPQQS 327
Ce_Sel12_AAD50991   VWFVLFVISVWDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYVLVTAVEN- 273
Dd_PS_EAL61660      TWGILSIVSIYDIFAVLCPGGPLRILIETAQKRNE-NIPAMIYNASIYIGMIYNEDNLEN 398
Dd_PS_EAL61279      IFTLLVIVAIYDLFAVLCPRGPLKVLVELSQERNE-NIPALVY----------------- 378
PP_PS               TWVLLLAMAAYDVVAVLTPRGPLNLLGELAIERDE-DIPALIYEARPTVSGRMQMPPSP- 237
At2g_NM_128544      TWVLLVALALYDIAAVLLPVGPLRLLVEMAISRDE-DIPALVYEARPVIR---------- 235
At1g_NM_100743      TWFILVALALYDLVAVLAPGGPLKLLVELASSRDE-ELPAMVYEARPTVSSGNQ------ 231
Os_Ps_BAD81114      TWVMLIALALYDLVAVLAPRGPLRMLVELASSRDD-ELPALVYESRPTVGPASG------ 218
Spe4_NM_059694      TWFVLWIVLFWDLFAVLAPMGPLKKVQEKASDYSKCVLNLIMFSANEKRLTAGSNQEETN 248
                     : :*  :  :*: *** * ***. : * : . ..  :  :::

Hs_PS1_AAH11729     ---------------------------MAEGDPEAQR-----RVSKNSKYNAESTERESQ 321
Mm_PS1_NP_032969    ---------------------------MAEGDPEAQR-----RVPKNPKYNTQRAERETQ 325
Hs_PS2_AAP35630     ---------------------------MAKLDPSSQG-----ALQLP--YDPEMEE---- 325
Mm_PS2_NP_035313    ---------------------------MAKLDPSSQG-----ALQLP--YDPEMEE---- 325
Dm_PS_AAB53369      -------------------------QATASSSPSSSNSTTTTRATQNSLASPEAAAASGQ 362
Ce_Sel12_AAD50991   --------------------------TTDPREPTSSDSNTSTAFPGEASCSSETPKRPKV 307
Dd_PS_EAL61660      NNNNNNNNNIELNINEVDIENNNNNEDENKNNTEDGNNNNNKNKNNNNNNNNRIENENGA 458
Dd_PS_EAL61279      ------------------------------------------------------------
PP_PS               -----------AQMGSDAERPRVRRWNRRASRSSNPSPDTELGESPMSSGNASQRDSTLT 286
At2g_NM_128544      -----------------NDSRSVQRRVWREQRSSQ---------------NNANRN---- 259
At1g_NM_100743      -----------RRNRGSSLRALVGGGGVSDSGSVELQAVRNHDVNQLGRENSHNMDYN-A 279
Os_Ps_BAD81114      -----------------SSSYASAMGSVEMQPVADPGRSGGNQYDRVEQEDDSSRAVVEM 261
Spe4_NM_059694      ----------EGEESTIRRTVKQTIEYYTKREAQDDEFYQKIRQRRAAINPDSVPTEHSP 298

Hs_PS1_AAH11729     DTVAEN----------------DDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSSSIL 365
Mm_PS1_NP_032969    DSGSGN----------------DDGGFSEEWEAQRDSHLGPHRSTPESRAAVQELSGSIL 369
Hs_PS2_AAP35630     DSYDSF----------------GEPSYPEVFEPPLTGYPG------------EEL----- 352
Mm_PS2_NP_035313    DSYDSF----------------GEPSYPEAFEAPLPGYPG------------EEL----- 352
Dm_PS_AAB53369      RTGNSHPRQNQRDDGSVLATEAEAAGFTQEWSANLSERVARRQIEVQSTQSGNAQRSNEY 422
Ce_Sel12_AAD50991   KRIPQK---------------VQIESNTTASTTQNSGVRVERELAAERPTVQDAN----- 347
Dd_PS_EAL61660      ENSSENGSITPPPTIPNFIKDEKEINRSSGSNGFPNFKKCANDNILIGDAETNDEIVSNA 518
Dd_PS_EAL61279      -----------------------ETGKGSDSN---------------------------- 387
PP_PS               AAVDDSQNLITGPPTEPEVGIIGSRLISSTGEGGALHAV---SIILHENSHMDDDTVPLV 343
At2g_NM_128544      -----------------EVRVVESAEVEEEHVG---------------SSERAEISVPLI 287
At1g_NM_100743      IAVRDIDNVDDGIGNGSRGGLERSPLVGSPSASEHSTSVGTRGNMEDRESVMDEEMSPLV 339
Os_Ps_BAD81114      RDVGGSRSSIRERNLEREAPMAVSVSGHSSNQGGSSQHA-----VIQIEQHEEGETVPLV 316
Spe4_NM_059694      LVEAEPSPIELKEKNSTEELSDDESDTSETSSGSSNLSSSDSSTTVSTSDISTAEECDQK 358

                                                                   TMD VII
Hs_PS1_AAH11729     ---------------------------------------AGEDPEERGVKLGLGDFIFYS 386
Mm_PS1_NP_032969    ---------------------------------------TSEDPEERGVKLGLGDFIFYS 390
Hs_PS2_AAP35630     -----------------------------------------EEEEERGVKLGLGDFIFYS 371
Mm_PS2_NP_035313    -----------------------------------------EEEEERGVKLGLGDFIFYS 371
Dm_PS_AAB53369      R------------------------------TVTAPDQNHPDGQEERGIKLGLGDFIFYS 452
Ce_Sel12_AAD50991   --------------------------------------FHRHEEEERGVKLGLGDFIFYS 369
Dd_PS_EAL61660      E------------------------------SSIDSTISESYVKPKQSIRLGLGDFVFYS 548
Dd_PS_EAL61279      ------------------------------------------------LKLGLGDFIFYS 399
PP_PS               QQQTNSPSSPATLGRSEAEFDHRSRPMNGATQHSEDGDEETGIGLSGAIKLGLGDFVFYS 403
At2g_NM_128544      DRRPEQ------------------------AENSETFLEGIGLGSSGAIKLGLGDFIFYS 323
At1g_NM_100743      ELMGWGDNREE-------------------ARGLEESDNVVDISNRG-IKLGLGDFIFYS 379
Os_Ps_BAD81114      SAASANNAAPNEEHR--------------ENSSSDSGMEFEMFESTRGIKLGLGDFIFYS 362
Spe4_NM_059694      EWDDLVSNSLP-------------------NNDKRPATAADALNDGEVLRLGFGDFVFYS 399
                                       :      :                     ::**:***:***
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                    TMD VII                     TMD VIII                    TMD IX
Hs_PS1_AAH11729     VLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATD 446
Mm_PS1_NP_032969    VLVGKASATASGDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFATD 450
Hs_PS2_AAP35630     VLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTD 431
Mm_PS2_NP_035313    VLVGKAAATGNGDWNTTLACFIAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTD 431
Dm_PS_AAB53369      VLVGKASS--YGDWTTTIACFVAILIGLCLTLLLLAIWRKALPALPISITFGLIFCFATS 510
Ce_Sel12_AAD50991   VLLGKASS--YFDWNTTIACYVAILIGLCFTLVLLAVFKRALPALPISIFSGLIFYFCTR 427
Dd_PS_EAL61660      VLIGKAAS---YQITTVFTVFIAIITGLFLTLILLAVFRRALPALPMSIIFGIIVFFLTF 605
Dd_PS_EAL61279      LLISRAAL---VHMSCVFSTFIAILTGLFLTLLCLAIFKKALPALPISIFLGILFYYLSN 456
PP_PS               VLVGRAAM---YDLMTVYACYLAIVAGLGATLILLAVWQRALPALPISISLGVIFYFLAR 460
At2g_NM_128544      VLVGRAAM---YDLMTVYACYLAIIAGLGITLMLLSVYQKALPALPVSIMLGVVFYFLAR 380
At1g_NM_100743      VLVGRAAM---YDLMTVYACYLAIISGLGCTLILLSVYNRALPALPISIMLGVVFYFLTR 436
Os_Ps_BAD81114      VLVGRAAM---YDLMTVYACYLAIIAGLGCTLILLSICKHALPALPISILLGVTFYFLTR 419
Spe4_NM_059694      LLIGQAAAS--GCPFAVISAALGILFGLVVTLTVFSTEESTTPALPLPVICGTFCYFSSM 457
                    :*:.:*:         . :  :.*: **  **  ::  . : ****:.:  *    : :

                    TMD IX
Hs_PS1_AAH11729     YLVQPFMDQLAFHQFYI 463
Mm_PS1_NP_032969    YLVQPFMDQLAFHQFYI 467
Hs_PS2_AAP35630     NLVRPFMDTLASHQLYI 448
Mm_PS2_NP_035313    NLVRPFMDTLASHQLYI 448
Dm_PS_AAB53369      AVVKPFMEDLSAKQVFI 527
Ce_Sel12_AAD50991   WIITPFVTQVSQKCLLY 444
Dd_PS_EAL61660      KILIQYIYFLGENQIFV 622
Dd_PS_EAL61279      NFLTPFIEALTLSQIFV 473
PP_PS               LVMDPFVLDMSTNLVFF 477
At2g_NM_128544      LLLEVFVVQCSSNLVMF 397
At1g_NM_100743      LLMEPFVVGVTTNLMMF 453
Os_Ps_BAD81114      LLMEPFVVGSSTNLVMF 436
Spe4_NM_059694      FFWEQLYG--------- 465
                     .            .
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PEN-2

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HsPEN2_NP_758844      --------------------------------------------MNLERVSNEEKLNLCR 16
MmPEN2_NP_079774      --------------------------------------------MNLERVSNEEKLNLCR 16
DmPEN_AAM88323        --------------------------------------------MNISKAPNPRKLELCR 16
CePEN2_NP_499459      --------------------------------------------MDISKLTDVKKVDLCK 16
DdPEN2_XP_629118      ------------------------------------------------------------
AtPEN2_Q9FY84         MEATRSDDPS--LNPIRNRNPNPNPNPNPLSTIISS-AQVWPTIDGPLGLTEEASVDYAR 57
OsPEN2_NM_001051998   MEARVAGVPEDEESGLLPRPSAAGRRPSVAAARRAPPPPVWATVDGPLGLPLEEAEGHAR 60
PpPEN2                MAEVEVN----------RRDMEAGESPALTSAALGL--HYWPTIDGPLGVYHEEAVNLAK 48
                      :                                          :

                               TMD I                                    TMD II
HsPEN2_NP_758844      KYYLGGFAFLPFLWLVNIFWFFREAFLVP----AYTEQSQIKGYVWRSAVGFLFWVIVLT 72
MmPEN2_NP_079774      KYYLGGFAFLPFLWLVNIFWFFREAFLAP----AYTEQSQIKGYVWRSAVGFLFWVIILA 72
DmPEN_AAM88323        KYFFAGFAFLPFVWAINVCWFFTEAFHKP----PFSEQSQIKRYVIYSAVGTLFWLIVLT 72
CePEN2_NP_499459      KYFLIGACFLPLVWIVNTFWFFSDAFCKP----INAHRRQIRKYVIASIVGSIFWIIVLS 72
DdPEN2_XP_629118      ---------LTWVWLINILYFIP--YRNS----LN---DKVKWYLKFSLIGFLGYSTIFM 42
AtPEN2_Q9FY84         RFYKFGFALLPWLWFVNCFYFWP-VLR------HSRAFPQIRNYVVRSAIGFSVFTALLS 110
OsPEN2_NM_001051998   RFFLWGFACLPFLWAINCCYFWP-VLRSPATFPSSAAFSRIRPYVVRSAIGFTIFSVVLL 119
PpPEN2                SFYYVGFLCLPWLWFINCLYFLP-VLR------NSRSDPLIRPYVVKSGIGFLVCGSLLL 101
                               *. :* :*  :*                   :: *:  * :*      ::

                      TMD II
HsPEN2_NP_758844      SWITIFQIYRPRWG--ALGDYLSFTIPLGTP----------------------------- 101
MmPEN2_NP_079774      TWITIFQIYRPRWG--ALGDYLSFTIPLGTP----------------------------- 101
DmPEN_AAM88323        AWIIIFQTNRTAWG--ATADYMSFIIPLGSA----------------------------- 101
CePEN2_NP_499459      AWEIFFQHYRAQGL--VWTDFLTFVFPTGRV----------------------------- 101
DdPEN2_XP_629118      GWMGIYLVNRNKWG--AFGDDISITIPFG------------------------------- 69
AtPEN2_Q9FY84         AWALTFSIGGEQLFGPLYDKLVMYNVADR------------------------------- 139
OsPEN2_NM_001051998   TWATTFIIGGERLFGPGWNDLVMYNVADK------------------------------- 148
PpPEN2                SWALTFAYGGEGLLGPSWKHLAVYDIANKYQQYPCNLDSGIILIRNDVTCSFVCHLTWHF 161
                       *   :             .     ..         :   ::::   :   ::  :   :

HsPEN2_NP_758844      ------------------------------------------------------
MmPEN2_NP_079774      ------------------------------------------------------
DmPEN_AAM88323        ------------------------------------------------------
CePEN2_NP_499459      ------------------------------------------------------
DdPEN2_XP_629118      ------------------------------------------------------
AtPEN2_Q9FY84         --------LGLSGLA--------------------------------------- 146
OsPEN2_NM_001051998   --------LGISGFMG-------------------------------------- 156
PpPEN2                PLARRRPNLSIDHYTAYRVSCRDRESECWCPSEILMADLCLHCGDCALKQYPVG 215
                       :      : :       :              :::  : :      :    :
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Nicastrin

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HsNct_BC047621          -------------------MDFNLILES-------LCRGNSVERKIYIPLNKTAPCVRLL 34
MmNct_NM_021607         MATTRGGSGPDPGSRGLLLLSFSVVLAG-------LCGGNSVERKIYIPLNKTAPCVRLL 53
AtNct_Q8GUM5            --MAMGLIRLLSIAFTLVLLSILPLHLSLADEITSIESVPDLQKLMYVAVDG-FPCVRLL 57
OsNct_NM_001054589      --MGGGSTAPLLAAFACVFLAVFPPVAS--GDAATLESVPDLVKAMYINVES-FPCVRLL 55
PpNct_                  -------MAAIARAWGLLLLLLLLPWLA---HGSSIKSVPELESRMYASLAG-FPCVRWL 49
DmNct_NM_143040         -----MEMRLNAASIWLLILSYGATIAQ----------GERTRDKMYEPIGG-ASCFRRL 44
CeNct_NM_060311         -----------MKKWLVIVLIIAGIRCDG--------FSDQVFRTLFIGEGN--ACYRTF 39
                                         :.:               :         ::       .* * :

HsNct_BC047621          NATHQIGCQSSISGDTGVIHVVEKEEDLQ------WVLTDGPNPPYMVLLESKHFTRDLM 88
MmNct_NM_021607         NATHQIGCQSSISGDTGVIHVVEKEEDLK------WVLTDGPNPPYMVLLEGKLFTRDVM 107
AtNct_Q8GUM5            NLSGEIGCSN--PGINKVVAPIIKLKD----------VKD-LVQPHTILVTADEMEDFFT 104
OsNct_NM_001054589      NHSGQVGCSN--PGHDKVIAPIVRFGN----------RNDQLVQPSAVLLPLNQMTDFFL 103
PpNct_                  NLTGELGCAN--PGHGAVSAPILRMGD----------ALD---SPATVLVPAESFEEFVD 94
DmNct_NM_143040         NGTHQTGCSSTYSGSVGVLHLINVEADLE------FLLSSPPSPPYAPMIPPHLFTRNNL 98
CeNct_NM_060311         NKTHEFGCQANRENENGLIVRIDKQEDFKNLDSCWNSFYPKYSGKYWALLPVNLIRRDTI 99
                        * : : **     .   :   :    :                     ::  . :

HsNct_BC047621          EKLKG--RTSRIAGLAVSLTK--PSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQW 144
MmNct_NM_021607         EKLKG--TTSRIAGLAVTLAK--PNSTSSFSPSVQCPNDGFGIYSNSYGPEFAHCKKTLW 163
AtNct_Q8GUM5            RVSTDLSFASKIGGVLVESGSNFQQKLKGFSPDKRFPQAQFSPYEN---------VEYKW 155
OsNct_NM_001054589      RVSNDPELYRKIAGVLVEANG--VDNMLEFSPDRKFPQQAFAPYSN---------LSHHW 152
PpNct_                  RFGDD----KNVVGVLVENGS--QAPGFGASDDARFPQAEFAPYEN---------QSWVW 139
DmNct_NM_143040         MRLKEAGPKNISVVLLINRTN----QMKQFSHELNCPNQYSGLNSTSETCDASN-PAKNW 153
CeNct_NM_060311         SQLKSSKCLSGIVLYNSGESIHPGDESTAASHDAECPNAASDYYLQDKNEEYCERKINSR 159
                                                      * . . *:

HsNct_BC047621          NSLG-NGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLSQNGSAPTFPLCAMQLFSHMHA 203
MmNct_NM_021607         NELG-NGLAYEDFSFPIFLLEDENETKVIKQCYQDHNLGQNGSAPSFPLCAMQLFSHMHA 222
AtNct_Q8GUM5            NSAA-SSIMWRNYNFPVYLLSE-SGISAVHEILSKKKMKHGTYTSDVAEFNMVMETTKAG 213
OsNct_NM_001054589      NPTG-SGIMWNKYDFPVFLLSE-ESTQTLQNLADKNEKSANGYLANVAEFDLVMQTTKAG 210
PpNct_                  NPFG-SGMMHRRLNFPVFFLSSPENIELARRLASQNVEKGSKRPANVVEFNDVMQTTKTG 198
DmNct_NM_143040         NPWG-TGLLHEDFPFPIYYIADLDQVTKLEKCFQDFNNHNYETHALRSLCAVEVKSFMSA 212
CeNct_NM_060311         GAITRDGLMKIDWRIQMVFIDNSTDLEIIEKCYSMFNKPKEDGSSGYPYCGMSFRLANMA 219
                        .     .:      : :  : .       ..  .          .        .     .

HsNct_BC047621          VISTATCMRRS------SIQSTFSINPEIVCDPLSDYNVWSMLKP-----INTTGTLKPD 252
MmNct_NM_021607         VISTATCMRRS------FIQSTFSINPEIVCDPLSDYNVWSMLKP-----INTSVGLEPD 271
AtNct_Q8GUM5            THNSEACLQ------------------EGTCLPLGGYSVWSSLPP-----ISVSSSNNRK 250
OsNct_NM_001054589      THDSESCLR------------------EQSCLPLGGQSVWTSLPP-----ISNSSTKHQK 247
PpNct_                  TPTTESCLG------------------ELSCLPLGGYSVMSTFPP-----VNVSHP-TVK 234
DmNct_NM_143040         AVNTEVCMRRT------NFIN--NLGGSKYCDPLEGRNVYATLYPRKPAIENNLETVHTN 264
CeNct_NM_060311         AGNSEICYRRGKNDAKLFQMNIDSGDAPQLCGAMHSDNIFAFPTPIP---TSPTNETIIT 276
                        .  :  *                       * .: . .: :   *      .

HsNct_BC047621          DRVVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKAP-----DVTTLPRNVMF 307
MmNct_NM_021607         VRVVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALHKAP-----DVTTLSRNVMF 326
AtNct_Q8GUM5            PVVLTVAS-MDTASFFRDKSFGADSPISGLVALLGAVDALSRVD-----GISNLKKQLVF 304
OsNct_NM_001054589      PIIMVTAS-QDSASFFRDRSLGADSPISGLIALLTAVDALSHLH-----DISNLKKQLVF 301
PpNct_                  PVVLAMAS-VDSATFFRDVAPGADSPMSGVIALLAAVDALSHVP-----DFDSFLKRLVF 288
DmNct_NM_143040         EKFILVTCRLDTTTMFDGVGLGAMDSLMGFAVFTHVAYLLKQLLP----PQSKDLHNVLF 320
CeNct_NM_060311         SKYMMVTARMDSFGMIPEISVGEVSVLTSIISVLAAARSMGTQIEKWQKASNTSNRNVFF 336
                           :  :   *:  ::   . *  . : ..     ..  :            .  :.:.*

HsNct_BC047621          VFFQGETFDYIGSSRMVYDMEKGKFPVQLEN------------VDSFVELGQVALRTSLE 355
MmNct_NM_021607         VFFQGETFDYIGSSRMVYDMENGKFPVRLEN------------IDSFVELGQVALRTSLD 374
AtNct_Q8GUM5            LVLTGETWGYLGSRRFLHELDLHSDAVAGLSNT---------SIETVLEIGSVGKGLSGG 355
OsNct_NM_001054589      AVFNGEAWGYLGSRKFLQELDQGADSVNGISSL---------LIDQVLEIGSVGKAISQG 352
PpNct_                  LVFTGEARGYLGSRQFLAQLKKGAFADYGLT-----------SIHQILEVGSVGQASEAT 337
DmNct_NM_143040         VTFNGESYDYIGSQRFVYDMEKLQFPTESTGTPPIAF----DNIDFMLDIGTLDDISNIK 376
CeNct_NM_060311         AFFNGESLDYIGSGAAAYQMENGKFPQMIRSDRTHIHPIRPNELDYILEVQQIGVAKGRK 396
                          : **: .*:**     ::.    .                 :. .:::  :
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HsNct_BC047621          NISGVVLADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFV--------TDTAKA 466
MmNct_NM_021607         NISGVVLADHSGSFHNRYYQSIYDTAENINVTYPEWQSPEEDLNFV--------TDTAKA 485
AtNct_Q8GUM5            QTSAVVLEDFDTNFVNKFYHSHLDDLSNINSSS---VVAAASVVAR--------TLYILA 463
OsNct_NM_001054589      STPGLVLEDFDSQFSNRFYHSTLDGPANVNSSS---IAAAAALIAR--------SLYILA 460
PpNct_                  TVAGVVIEEFDTAFTNKYYNSVDDNSSNVNLPS---LVVAASLVAR--------SLVLLA 441
DmNct_NM_143040         NFNALILNARP---TNKYYHSIYDDADNVDFTYANTSKDFTQLTEVNDFKSLNPDSLQMK 486
CeNct_NM_060311         HVQSVLLAPYGKEYEYQRVNSILDKNEWTEDER---EKAIQEIEAV--------STAILA 503
                           .:::         :  :*  *     :            :

HsNct_BC047621          LADVATVLGRALYELAGGTNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYL 526
MmNct_NM_021607         LANVATVLARALYELAGGTNFSSSIQADPQTVTRLLYGFLVKANNSWFQSILKHDLRSYL 545
AtNct_Q8GUM5            SDN-KDTSNSALGSIHVNASFVEELLTCLLACEPGLSCNLVKDYISPTNTCPGNYAGVIL 522
OsNct_NM_001054589      SAD-LPIDLITLNTIKVNVSLVEELIGCLLKCDPGLSCGIVKSFISPSNSCPSHYVGVFQ 519
PpNct_                  SDNNLRFDSPIFESIQVNMSLVEEMVNCFFGTSPGMRCSLVESLMTASHDVANHYVGVFQ 501
DmNct_NM_143040         VRNVSSIVAMALYQTITGKEYTGTKVANPLMADEFLYCFLQSADCPLFKAAS-YPGSQLT 545
CeNct_NM_060311         AAADYVGVETDEVVAKVDKKLITTIFDCLITSNFWFDCDFMQKLDGGRYHKLFNSYGFNQ 563
                                         . .               :   : .

HsNct_BC047621          GDGPLQHYIAVSSPTNTTYVVQYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQ 586
MmNct_NM_021607         DDRPLQHYIAVSSPTNTTYVVQYALANLTGKATNLTREQCQDPSKVPNESKDLYEYSWVQ 605
AtNct_Q8GUM5            GEPSSKP--YLGYVGDVSRFLWNFLADKTSVQKGNTTSVCSKGVCSKTDEVCIKAESNKE 580
OsNct_NM_001054589      DLPAGTQ--FPSYADDISRFIWNFLADRTSSLAGNSSSCT--GQCHDEGEICVGAEVEGG 575
PpNct_                  ADPSVSPNSMPEVIDDTTRFVWNFLADRTALPREDLHEKCT-LVCKNPDEVCVGATQSQL 560
DmNct_NM_143040         NLPPMRYISVLGGSQESSGYTYRLLGYLLSQLQPDIHRDN-----CTDLPLHYFAGFNNI 600
CeNct_NM_060311         KSTYISMESHTAFPTVLHWLTIFALGSDKETLNVKSEKSCS--HLGQFQAFQMYTYTWQP 621
                                                *.

HsNct_BC047621          GPLHSNETDRLPR-CVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIHARIFLIAS 645
MmNct_NM_021607         GPWNSNRTERLPQ-CVRSTVRLARALSPAFELSQWSSTEYSTWAESRWKDIQARIFLIAS 664
AtNct_Q8GUM5            GTCVVSTTRYVPAYSTRLKYNDGAWTILPQNSSDSMGMVDPVWTESNWDTLRVHVYTVQH 640
OsNct_NM_001054589      GRCVVSTTRYVPAYSTRLKFEDNVWHVLPVNSSDPFSAADPVWTESFWNTIGLRVYAVQA 635
PpNct_                  GQCRVSSTRYVPAYSPRLKFHDYWWQLLPLEAGDKMGAADPVYTESFWNSISIRSYQKED 620
DmNct_NM_143040         GECRLTTQN----------YSHALSPAFLIDGYDWSSGMYSTWTESTWSQFSARIFLRPS 650
CeNct_NM_060311         NPYTGNFSCLKSAIVKKVMVSPAVDSQTP---EEEMNTRYSTWMESVYIIESVNLYLMED 678
                        .    .                           :  .   ..: ** :     . :

                                     TMD
HsNct_BC047621          KELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGAVSY- 689
MmNct_NM_021607         KELEFITLIVGFSILIFSLIVTYCINAKADVLFVAPREPGAVSY- 708
AtNct_Q8GUM5            SAYDNAVLVAGITVTTLAYIGILAAKSIITKALKQD--------- 676
OsNct_NM_001054589      TSYDWLVLLIGIIITVASYFAVIVGRSYISKIIKRD--------- 671
PpNct_                  SWYEELILFIGVFVTFVSILSITCSTSLLRKRLKRA--------- 656
DmNct_NM_143040         NVHQVTTLSVGIVVLIISFCLVYIISSRSEVLFEDLPASNAALFG 695
CeNct_NM_060311         ASFEYTMILIAVISALLSIFAVGRCSETTFIVDEGEPAAEGGEPL 723
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Aph-1

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                                    TMD I                  TMD II
HsAPH1al_NP_001071096     MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLAS 50
MmAph1al_AAH24111         MGAAVFFGCTFVAFGPAFSLFLITVAGDPLRVIILVAGAFFWLVSLLLAS 50
MmAph1as_NP_666216        MGAAVFFGCTFVAFGPAFSLFLITVAGDPLRVIILVAGAFFWLVSLLLAS 50
HsAph1as_NP_057106        MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLAS 50
MmAph1c_NP_080950         MTLPVFFGCAFIAFGPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLLSS 50
MmAph1b_NP_808251         MTAAVFFGCAFIAFGPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSS 50
HsAph1b_Q8WW43            MTAAVFFGCAFIAFGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISS 50
DmAph1_NM_134866          MTLPEFFGCTFIAFGPPFALFVFTIANDPVRIIILIAAAFFWLLSLLISS 50
P.patens_Aph-1            MGVVVGLGYFLIALGPALTIFFSSIAPKPFLTLTVLASALIYLVSLVAAA 50
P.patens_Aph-1a           MGLVAGFGYFLIALGPALTIFGSSVAPKPFLILTVLASALVWLASLNIAA 50
AtAph1_Q8L9G7             MTVAAGIGYALVALGPSLSLFVSVISRKPFLILTVLSSTLLWLVSLIILS 50
OsAph1_NM_001053062       MTVAAGLGYALVALGPAFSLFAGVVARKPFLVLTLLTSTLFWLISLIILS 50
CeAph1_NM_060068          MGYLLTIACYIASFSPSIALFCSFIAHDPVRIILFFLGSFFWLVSLLFSS 50
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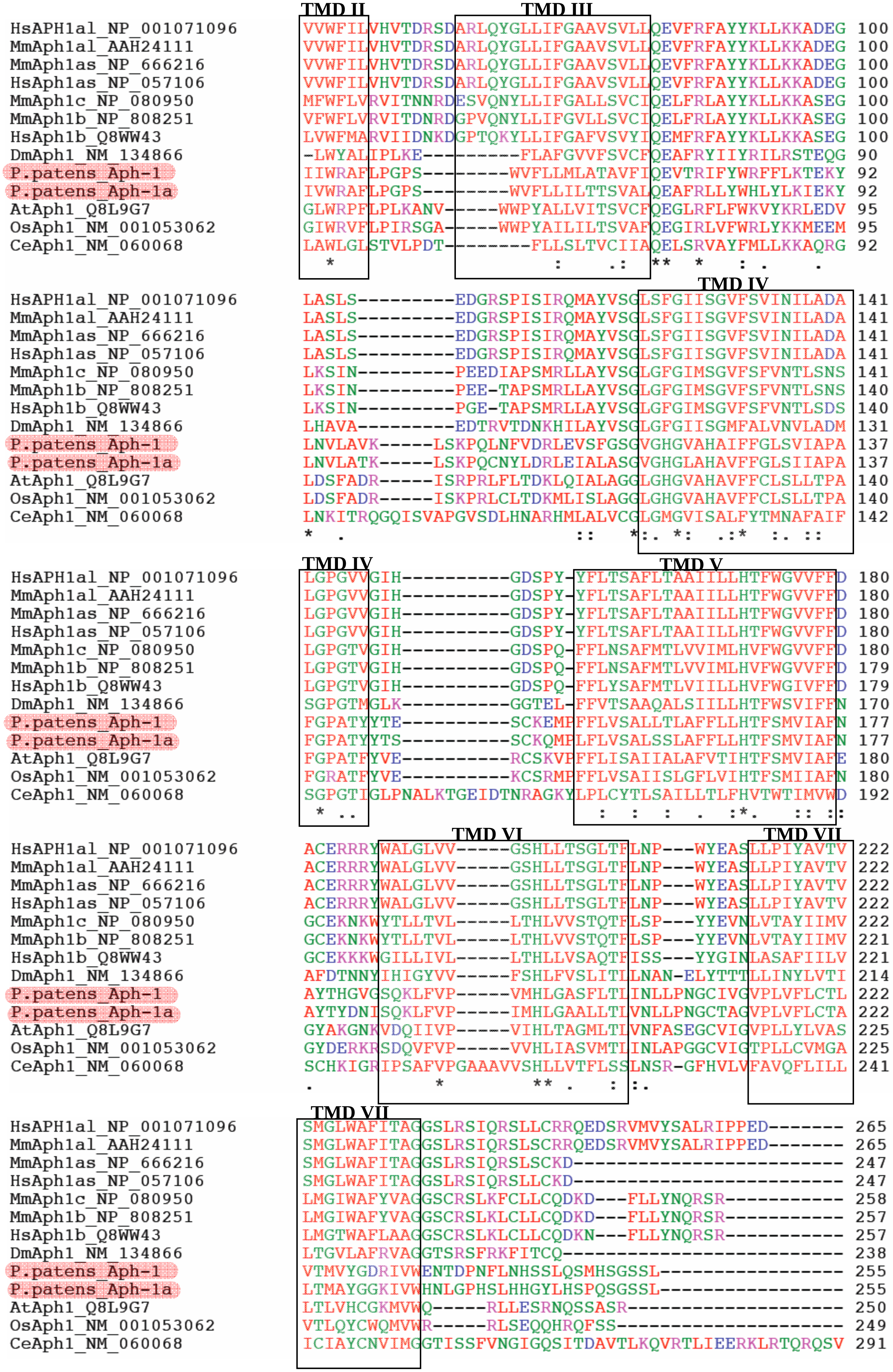

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HsAPH1al_NP_001071096 VVWFILVHVTDRSDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEG 100
MmAph1al_AAH24111     VVWFILVHVTDRSDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEG 100
MmAph1as_NP_666216    VVWFILVHVTDRSDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEG 100
HsAph1as_NP_057106    VVWFILVHVTDRSDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEG 100
MmAph1c_NP_080950     MFWFLVRVITNNRDESVQNYLLIFGALLSVCIQELFRLAYYKLLKKASEG 100
MmAph1b_NP_808251     VFWFLVRVITDNRDGPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEG 100
HsAph1b_Q8WW43        LVWFMARVIIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEG 100
DmAph1_NM_134866      -LWYALIPLKE---------FLAFGVVFSVCFQEAFRYIIYRILRSTEQG 90
P.patens_Aph-1        IIWRAFLPGPS--------WVFLLMLATAVFIQEVTRIFYWRFFLKTEKY 92
P.patens_Aph-1a       IVWRAFLPGPS--------WVFLLILTTSVALQEAFRLLYWHLYLKIEKY 92
AtAph1_Q8L9G7         GLWRPFLPLKANV-----WWPYALLVITSVCFQEGLRFLFWKVYKRLEDV 95
OsAph1_NM_001053062   GIWRVFLPIRSGA-----WWPYAILILTSVAFQEGIRLVFWRLYKKMEEM 95
CeAph1_NM_060068      LAWLGLSTVLPDT--------FLLSLTVCIIAQELSRVAYFMLLKKAQRG 92
                        *                    :    .:  **  *   : .    .

HsAPH1al_NP_001071096 LASLS---------EDGRSPISIRQMAYVSGLSFGIISGVFSVINILADA 141
MmAph1al_AAH24111     LASLS---------EDGRSPISIRQMAYVSGLSFGIISGVFSVINILADA 141
MmAph1as_NP_666216    LASLS---------EDGRSPISIRQMAYVSGLSFGIISGVFSVINILADA 141
HsAph1as_NP_057106    LASLS---------EDGRSPISIRQMAYVSGLSFGIISGVFSVINILADA 141
MmAph1c_NP_080950     LKSIN---------PEEDIAPSMRLLAYVSGLGFGIMSGVFSFVNTLSNS 141
MmAph1b_NP_808251     LKSIN---------PEE-TAPSMRLLAYVSGLGFGIMSGVFSFVNTLSNS 140
HsAph1b_Q8WW43        LKSIN---------PGE-TAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDS 140
DmAph1_NM_134866      LHAVA---------EDTRVTDNKHILAYVSGLGFGIISGMFALVNVLADM 131
P.patens_Aph-1        LNVLAVK-----LSKPQLNFVDRLEVSFGSGVGHGVAHAIFFGLSVIAPA 137
P.patens_Aph-1a       LNVLATK-----LSKPQCNYLDRLEIALASGVGHGLAHAVFFGLSIIAPA 137
AtAph1_Q8L9G7         LDSFADR-----ISRPRLFLTDKLQIALAGGLGHGVAHAVFFCLSLLTPA 140
OsAph1_NM_001053062   LDSFADR-----ISKPRLCLTDKMLISLAGGLGHGVAHAVFFCLSLLTPA 140
CeAph1_NM_060068      LNKITRQGQISVAPGVSDLHNARHMLALVCGLGMGVISALFYTMNAFAIF 142
                      *  .                     ::   *:. *:  .:*  :. ::

HsAPH1al_NP_001071096 LGPGVVGIH----------GDSPY-YFLTSAFLTAAIILLHTFWGVVFFD 180
MmAph1al_AAH24111     LGPGVVGIH----------GDSPY-YFLTSAFLTAAIILLHTFWGVVFFD 180
MmAph1as_NP_666216    LGPGVVGIH----------GDSPY-YFLTSAFLTAAIILLHTFWGVVFFD 180
HsAph1as_NP_057106    LGPGVVGIH----------GDSPY-YFLTSAFLTAAIILLHTFWGVVFFD 180
MmAph1c_NP_080950     LGPGTVGIH----------GDSPQ-FFLNSAFMTLVVIMLHVFWGVVFFD 180
MmAph1b_NP_808251     LGPGTVGIH----------GDSPQ-FFLNSAFMTLVVIMLHVFWGVVFFD 179
HsAph1b_Q8WW43        LGPGTVGIH----------GDSPQ-FFLYSAFMTLVIILLHVFWGIVFFD 179
DmAph1_NM_134866      SGPGTMGLK----------GGTEL-FFVTSAAQALSIILLHTFWSVIFFN 170
P.patens_Aph-1        FGPATYYTE----------SCKEMPFFLVSALLTLAFFLLHTFSMVIAFN 177
P.patens_Aph-1a       FGPATYYTS----------SCKQMPLFLVSALSSLAFFLLHTFSMVIAFN 177
AtAph1_Q8L9G7         FGPATFYVE----------RCSKVPFFLISAIIALAFVTIHTFSMVIAFE 180
OsAph1_NM_001053062   FGRATFYVE----------KCSRMPFFLVSAIISLGFLVIHTFSMIIAFN 180
CeAph1_NM_060068      SGPGTIGLPNALKTGEIDTNRAGKYLPLCYTLSAILLTLFHVTWTIMVWD 192
                       * ..                      :  :  :  .  :*.   :: ::

HsAPH1al_NP_001071096 ACERRRYWALGLVV-----GSHLLTSGLTFLNP---WYEASLLPIYAVTV 222
MmAph1al_AAH24111     ACERRRYWALGLVV-----GSHLLTSGLTFLNP---WYEASLLPIYAVTV 222
MmAph1as_NP_666216    ACERRRYWALGLVV-----GSHLLTSGLTFLNP---WYEASLLPIYAVTV 222
HsAph1as_NP_057106    ACERRRYWALGLVV-----GSHLLTSGLTFLNP---WYEASLLPIYAVTV 222
MmAph1c_NP_080950     GCEKNKWYTLLTVL-----LTHLVVSTQTFLSP---YYEVNLVTAYIIMV 222
MmAph1b_NP_808251     GCEKNKWYTLLTVL-----LTHLVVSTQTFLSP---YYEVNLVTAYIIMV 221
HsAph1b_Q8WW43        GCEKKKWGILLIVL-----LTHLLVSAQTFISS---YYGINLASAFIILV 221
DmAph1_NM_134866      AFDTNNYIHIGYVV-----FSHLFVSLITLLNAN-ELYTTTLLINYLVTI 214
P.patens_Aph-1        AYTHGVGSQKLFVP-----VMHLGASFLTLINLLPNGCIVGVPLVFLCTL 222
P.patens_Aph-1a       AYTYDNISQKLFVP-----IMHLGAALLTLVNLLPNGCTAGVPLVFLCTA 222
AtAph1_Q8L9G7         GYAKGNKVDQIIVP-----VIHLTAGMLTLVNFASEGCVIGVPLLYLVAS 225
OsAph1_NM_001053062   GYDERKRSDQVFVP-----VVHLIASVMTLINLAPGGCVIGTPLLCVMGA 225
CeAph1_NM_060068      SCHKIGRIPSAFVPGAAAVVSHLLVTFLSSLNSR-GFHVLVFAVQFLILL 241
                      .           *        ** .   : :.

HsAPH1al_NP_001071096 SMGLWAFITAGGSLRSIQRSLLCRRQEDSRVMVYSALRIPPED------- 265
MmAph1al_AAH24111     SMGLWAFITAGGSLRSIQRSLSCRRQEDSRVMVYSALRIPPED------- 265
MmAph1as_NP_666216    SMGLWAFITAGGSLRSIQRSLSCKD------------------------- 247
HsAph1as_NP_057106    SMGLWAFITAGGSLRSIQRSLLCKD------------------------- 247
MmAph1c_NP_080950     LMGIWAFYVAGGSCRSLKFCLLCQDKD---FLLYNQRSR----------- 258
MmAph1b_NP_808251     LMGIWAFYVAGGSCRSLKLCLLCQDKD---FLLYNQRSR----------- 257
HsAph1b_Q8WW43        LMGTWAFLAAGGSCRSLKLCLLCQDKN---FLLYNQRSR----------- 257
DmAph1_NM_134866      LTGVLAFRVAGGTSRSFRKFITCQ-------------------------- 238
P.patens_Aph-1        VTMVYGDRIVWENTDPNFLNHSSLQSMHSGSSL----------------- 255
P.patens_Aph-1a       LTMAYGGKIVWHNLGPHSLHHGYLHSPQSGSSL----------------- 255
AtAph1_Q8L9G7         LTLVHCGKMVWQ------RLLESRNQSSASR------------------- 250
OsAph1_NM_001053062   VTLQYCWQMVWR------RLSEQQHRQFSS-------------------- 249
CeAph1_NM_060068      ICIAYCNVIMGGTISSFVNGIGQSITDAVTLKQVRTLIEERKLRTQRQSV 291
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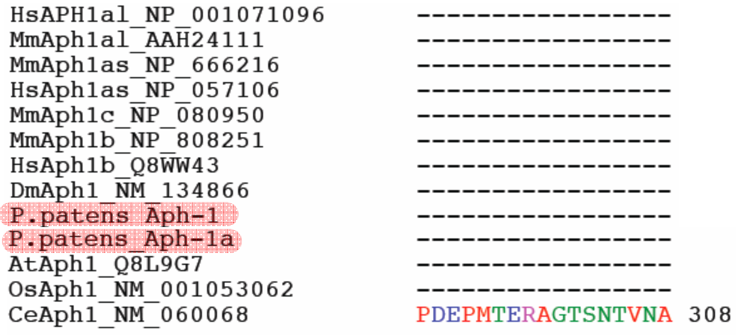

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