

Supplementary Information

TableS1. Protein sequences of all members of the HMA1-4 gene family

Sequences with their names highlighted in green were taken into account in the phylogenetic analysis while sequences with their names highlighted in yellow were not. Indeed, the latter sequences either were too short, or corresponded to pseudogenes.

>AhHMA1

AWRVANAVGITEVYCNLKPEDKLNHVKNISREAGGGLIMVGEIN DAPALAAATIGIVLAQRASATAIAVADILL
LRDTITGVPFCVAKSRQTTSLVKQNALALTSIFVAALPSVLGFVPLWLTVLLHEGGTLLVCLNSVRGLNDPSWS
WKQDIVHLINKLSSQEPSISSNSLSSVEPAH

>AhHMA3

MAEGEEAKKKNLQTSYFDVVGICCTSEVSVIVGDVLRPLDGVKEFSVIVPSRTVIVVHDTFLISPLQIVKALNQAR
LEASVRPYGETSLKSQWSPFFAILSGVFLALSFFKYFYSLLEWLAVVAVVAGIFPILAKAVASVTRFRDLINALT
FIAVIATLCMQNFTEAATIVFLFSVADWLESSAAHKASTVMSSLSLAPRKAVIAETGHEVDVDEVRIINTIVSVK
AGESIPIDGVVVDGSCDVDEKTLTGESFPVSKQRDSTVLAATINLNGYIKVKTALARDCVVAKMTKLVEEAQKS
QTKTQRFIDKCSRYTTPAVVLAACFAVIPVLLKQLDLSHWFHLALVVLVSGCPCGLILSTPIATFCALTKAAMS
GFLIKTGDCLLETAKIKIVAFDKTGTITKAEFMVSDFRSLSHNINLHNLVWVSSIESKSSHPMAAALIDYARSV
SVEPKPDLVENFQNFPGEGVYGRIDGQDIYIGNKRIAQRAGCLTVPDMEANMKRGTIGYIYIGAKLSGSFNLID
SCRYGVAQALKELKSLGIKTAMLTGDNDAALSTQEQLENALDIVHSELLPQDKARIIDEFKIQGPTMMVGDGLN
DAPALAKADIGLSMIGISGSALATETGDIILMSNDIRKIPKGMRLAKRSHKKVIENVVLSVSIKGAIMVLAFLVGY
LVWAAVLADAGTCLLVILNSMMLLRDEREAVSTCYRASSSPVKLEEDEAEDLEVGLLQKSEETNKKSCCSGSCSG
PKDNQOK

>AhHMA4-1

MASQNKKEEKKVKKLQKSYFDVLGICCTSEVPIIENILKSLDGVKEYSVIVPSRTVIVVHDSLLISPFQIAKAL
NQARLEANVRVNGETNFKNKWSPFFAVVSGLLLLLSFLKFVYSPLRWLAVAAVAAGIYPILAKAFASIRRLRDI
NILVITVIATLAMQDFMEAAAVVFLFTIADWLETRASYRATAVMQSLMSLAPQKAI I AETGEEVEVDEVKYSTV
VAVKAGETIPIDGIVVDGNCEVDEKTLTGAEFPVPKQKDSVWAGTINLNGYISVKTTSLAGDCVAVKMAKLVEE
AQSSKTKSQRLLDKCSQYYTPAIIVVSACVAIVPVMKVHNLKHWFLALVVLVSGCPCGLILSTPVATFCALTK
AATSGLLIKSADYLDTLISKIKIAAFDKTGTITRGEFIVIDFKLSRDISLRSLLYWVSSVESKSSHPMAATIVDY
AKSVSVEPRPEEVEDYQNFPGEGIYKIDGNDIYIGNKRIASRAGCSTVPEIEVDTKGGKTVGYVYVGERLAGVF
NLSDACRSQVQAMKELKSLGIKTAMLTGDSQAAAMHAQEQLGNALDVVHGELLPEDKSKI IQEFKKEGPTAMVG
DGVNDAPALATADIGISMGISGSALATQTGHIILMSNDIRRIPOAVKLARRARRKVIENVCLSIILKAGILALAF
AGHPLIWAAVLVDVGTCLLVILNSMMLLRREKKKIGNKKCYRASTMLNKRKLEGDDDDAVDLEAGLLTKSGNGQC
KSSCCGDKKQEKVMMKPSKTSDDHSHPGCCGDKKQGNVPLVRDGGCSEETRAKAVGDMVSLSSCKKSSHVKH
DLKMKGGSGCCANKSEKVEEVVAKSCCEKPKQOMESAGDCKSSHCEEKHAEEIVLPVQMIGQALTGLEIELQTK
ETCKTRCCDNKEKAKKKGLLLSSEDTSYLEKGVLIKDEGNCKSACQKTGTVKESCHEKAPLDIETKLVSCGNTEG
EVGEQTDLEIKIEGDCKSGCCSDEKQTEITLASEEETDSTDCSSGCCMDKEEVTQICGLETEGGGDCKSHCCGT
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CKEKEKRHSKSCCRSYAKEFCSHRHHHHHHHHVSA

>AhHMA4-2

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NILVITVIATLAMQDFMEAAAVVFLFTIADWLETRASYRATAVMQSLMSLAPQKAI I AETGEEVEVDEVKYSTV
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AQSSKTKSQRLLDKCSQYYTPAIIVVSACVAIVPVMKVHNLKHWFLALVVLVSGCPCGLILSTPVATFCALTK
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DLKMKGGSGCCANKSEKVEEVVAKSCCEKPKQOMESAGDCKSSHCEEKHAEEIVLPVQMIGQALTGLEIELQTK
ETCKTRCCDNKEKAKKKGLLLSSEDTSYLEKGVLIKDEGNCKSACQKTGTVKQSCHEKAPLDIETKLVSCGNTEG
EVGEQTDLEIKIEGDCKSGCCSDEKQTEITLASEEETDSTDCSSGCCMDKEEVTQICGLETEGGGDCKSHCCGT
GLTQEGSSKLGNVESAQFGGCGTVKVVSSQSCSTSDLVLSDLQVKKDEHCESSHGAVKVEETCCKVKIPEACAPE
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>AhHMA4-3

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NILVITVIATLAMQDFMEAAAVVFLFTIADWLETRASYRATAVMQSLMSLAPQKAI I AETGEEVEVDEVKYSTV

61 VAVKAGETIPIDGIVVDGNCEVDEKTLTGEAFVVPKQKDSSVWAGTINLNGYISVKTTSLAGDCVVAKMAKLVVEE
62 AQSSKTKSQRLLDKCSQYYTPAIIVVSACVAIVPVMKVHNLKHWFLALVVLVSGPCGLILSTPVAATFCALTK
63 AATSGLLIKSADYLDLTLKIKIAAFDKTGTITRGEFIVIDFKLSRDITLRLSLLYWVSSVESKSSHPMAATIVDY
64 AKSVSVEPRPEEVEDYQNFPGEGIYGKIDGNDIYIGNKRIASRAGCSTVPETEIDTKGGKTVGYVYVGERLAGVF
65 NLSDACRSGVSVQAMKELKSLGIKTAMLTGDSQAAAMHAQEQLGNALDVVHGELLPEKSKIIQEFKKEGPTAMVG
66 DGVNDAPALATADIGISMGISGSALATQTGHIILMSNDIRRIPOAVKLARRARRKVIENVCLSIILKAGILALAF
67 AGHPLIWAAVLVDVGTCLLVILNSMLLLREKKKIGNKKCYRASTSMNNGRKLKLEGDDDDAVDLEAGLLTKSGNGQC
68 KSSCCGDKKNQEKVMMKPSKTSDDHSHPGCCGDKKQGNVPLVRDGGCSEETRKAVGDMVSLSSCKKSSHVKH
69 DLKMKGGSGCCANKSEKVEEVVAKSCCEKPKQOMESAGDCKSSHCEEKHAEEIVLPVQMIGQALTGLEIELQTK
70 ETCKTRCCDNKEKAKKGLLLSSEDTSYLEKGVLIKDEGNCKSACQKTGTQVKSCHAKAPLDIETKLVSCGNTGEG
71 EVGEQTDLEIKIEGDKSGCCSDEKQTEITLASEEEADSTDCSSGCCMDKEEVTQICGLETEGGGDCCKSHCCGT
72 GLTQEGSSKLGNETAQSOGCGTVKVSQSCCTSSTDLVLSLQVTKDEHCESSHGAVKQVETCKVKIPEACAPE
73 CEKEKRHSKSCCRSYAKEFCSHRHHHHHHHHHHVSA
74 >AHMA1-1
75 MEPAALTRSSSLTRFPYRRGLATLRLARVNSFSVLTTPKTLRRKPLPLSISSSLSLPPRSIRIRAVEDHHHDDHHH
76 DDEQDHDHHHHHHHHHQHGCCSVELKAESKPQKVLFGFAKTIGWVRLANLREHLHLCCSAAAMFLAAAACPYLA
77 PKPYIKSLQNAFMIVGFPLVGVASLDMADIAGGKVNIVHLMALAAAFASVFMGNALEGGLLAMFNLAHIAEEF
78 FTSRSMVDVKELKESNPDSALLIEVLNGVNPNISDLSYKSVPVHSVEVGSYILVGTGEIVPVDCEVYQGSATITI
79 EHLTGEVPLEAKAGDRVPGGARNLDGRMIVKATKAWNDSTLNKIVQLTEEAHSNPKLQRLWDEFGENYSKVVV
80 VLSLAIAFLGPFLFKWPFLLSTAACRGSVYRALGLMVAASPCALAVAPLAYATAISSCARKGILLKGAQVLDALAS
81 CHTVAFDKTGTTLTGGTLTCKAIEPIYGHQGGNNSVTTCCIPNCEKEALAVAAAMEKGTTHPIGRAVVDHSGVD
82 LPSIFVESFEYFPGRGLTATVNGAKSVAEESRLRKASLGSIEFITSFLKSEDESKQIKDAVNASLYGNDVFVHAAL
83 SVDQKVTLIHLEDQPRPGVSGVIAELKSWARLRVMMLTGDHDSAWRVANAVGITEVYCNLKPEDKLNHVKNIAR
84 EAGGGLIMVGEINDAPALAAATVGIVLAQRASATAIADVADILLRDNITGVFPFCVAKSRQTTSLVKQNIALALT
85 SIFLAALPSVLGFVPLWLTVLLHEGGTLLVCLNSVRGLNDPSWSWKQDIVHLINKLSSQEPSTISSNSLSSVEPA
86 H
87 >AHMA1-2
88 MESAALLHSSLTRFSCRQNSTLRLSRLNSTTLPRDVLIRTTNSNTLPRRSRLRFAKAAACENHHHHYHHEHDDHHHQ
89 NHHQHCCSVELTVSNHLQKLLKFAKAIWIRLANFLRENHLCCSSVVLFLAAAACPHLMIPKPYITPIQNSFM
90 IVAFPLVGISASLDMADIAGGKVNIVHLMALAAAFASVFMGNALEGGLLTMFNLAHIAEEFFTSRSMVDVKELN
91 ESNPDSALDIVDNDENVNFFDLTYKSVHVMKAAVEVGSYILVGTGEIVPVDCEVYQGNATITIEHLTGEVPLEAK
92 AGDRVPGGARTLNGRIIVKATKAWNESTLNKILQVTEEAHSNPKLERWLYEFGEIYKVVVVLVSAI AFLGPFL
93 FKLPLVLTACRGSVYRALGFLVAASPCALAVAPLAYATAISSCARKGILLKGGQVLDALASCHTIGFDKGTTLT
94 TGGLTCKAIEPIYGHQEGNNSVNPCCMPNCENEALAVAAAMEKGTTHPIGRAMVDHSGVDLPSVSVESFEYF
95 PGRGLTATVNCIESVTEGRKLRKASLGSVEFITSLFESQDESRIKNAVNSSLYGNDVFHAVLSLDQKVTLIHLE
96 DQPREVSKVLTELKSWGKMRIMMLTGDHESAWRVANAVGIDEVYCNLKPEDKLDHVKNISEGSGGGGLIMVGE
97 GINDGPALAAATVGIVLAQRASASAIADVADVLLQDNITGVFPFCIAKSRQTTSLVKQNVAIALTSIFLAALPSVL
98 GFLPLWLTVLLHEGGTLLVCLNSIRSLNDPSWSWKQDIVHELHLSKTHQHKTYRDGN
99 >AHMA2
100 MASKKMTKSYFDVLGICCTSEVPLIENILKSMGDGVEKSVIIVPSRTVIIVVHDTLILSQFQIVKALNQARLEANVR
101 VTGETNFRNKWSPFAMVSGLLLLLFFKYLYSPFRWLAVAAVAGIYPIAKAVASLARFRIDINILVIITVGA
102 TIGMRDYTEAGVVVFLFTIAEWLQSRASYKASAVMQSLMSLAPQKAMIAETGEEVQVDELKINTVIAVKAGETIP
103 IDGVVVDGNEVDEKTLTGEAFVVPKLRDSTVWAGTINLNGYITVKTALAEDEVVAKMAKLVVEEAQNSKTETQR
104 FIDKCSQYYTPAIIILISVCFAAIPFALKVHNLKHWIHLALVVLVSGPCGLILSTPVAATFCALTKAATSGLLIK
105 ADYLETLAKIKVAFDKTGTITRGEFIVMDFQSLSEDISLHSLLYWVSSAESKSSHPMAAALVDYAKSVSVEPKP
106 EAVEDYQNFPGEGIYGKIDGKEVYIGNKRIASRSGCSSVPDQVVDTKGGKTIYVYVVGKTLGSGVFNLSDACRSGV
107 AQAMKELKALGIKTAMLTGDNQAAAMHAQEQLGNAMDIVRAELLPEGKSEIIEKFMREEGSTAMVGDGLNDAPAL
108 ATADIGISMGVSGSAIATETGNIILMSNDIRRIPOAIKLARRAKRVVENVVTSITMKGAILALAFAGHPLIWA
109 VLADVGTCLLVILNSMLLLSDNHKTGNKCYRESSSSIVEKLEGDAAGDMEAGLLPKISDKHCKSGCCGKTQVK
110 VMQPAKSSSDHSHSGCCEKQKQDNVTVVKKSSCAEPVDLVQGHDSGCCGNKSQPNQHEVQQSCHNKPSGLDIGT
111 GSQHEGSSTVVNLEGDEQEEVKVSVKCCSSPADLAVTSLKVKSDGHSKSSCCCESSKRDKEGASSQVTKKACKS
112 NCSREKSHHGSSCCSSYAKECCSHHHHHHTRANGIGSLKEIVIE
113 >AHMA3
114 MAEGEEAKKNLQTSYFDVVGICCSSEVSIVGDVLRPLDGVEKFSVIVPSRTVIIVVHDTFLISPLQIVKALNQAR
115 LEASVTRPYGDTSLKSQWSPFAIVSGVFLAVSFFKYFYNLLEWLAIAAVVAGIFPIAKAVASVTRFRDINGLT
116 LIAVIATLCMQDFTEAATIVFLFSVADWLESSAAHKASTVMSSLSLAPRKAVIDATGLEVDVDEVRIINTIVSVK
117 AGESIPIDGVVVDGSDVDEKTLTGESFPVSKQRESTVLAATINLNGYIKVKTALARDCVVAKMTKLVEEAQKS
118 QTKTQRFIDKCSRYYPVAVVLAACFAVIPALLKQVNLSHWFLALVVLVSGPCGLILSTPVAATFCALTKAATS
119 GFLIKTGDCLTLAKIKIVAFDKTGTITKAEFMVSDFRSLSHNINLHNLWVSSIESKSSHPMAAALIDYARLI
120 FVEPKPDIVENFQNFPGEGVYGRIDGQDIYIGNKRIQRAGCLTVPMEANMKRGTIGYIYIGAKLSGSFTLLD
121 GCRYGVAQALKELKSLGIKTAMLTGDNDAAMSTQEQIENALDIVHSELLPQDKARIDEFKIQGPTMMVGDGLN
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123 LVWAAVLADAGTCLLVILNSMMLLRDEREAVSTCYRASSSSPVKLEEDEAEEDLEVGLLQKSEETSCKKSCSSGCCS
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125 >AlhMA4-1
126 MASQNKQEEKKVKKLQKSYFDVLGICCTSEVPI IENILKALDGVKEYSVIVPSRTVIVVHDSLLISPFQIGKAL
127 NQARLEANVRVNGETNFKNKWSPFAVVGILLLLSFLKFVYSPLRWLAVAAVAAGIYPI LAKAFASIRRLRID I
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135 AGHPLIWA AVLVDVGTCLLVILNSMMLLLREKKKIGNKKCYRASTSM LNGRKLEGDDDDVV DLEAGLLKKSNGQC
136 NSSCCGDKKNQEKVMMKPSKTS SDHSHPGCYGDKKQDKVKPLVRD GCCGEETRAKAVGDI I SLSSCKKSSHVKH
137 DLKMKGGSGCCANKSEKVEEVVAKSCCEKSKQOMESAGDCKSSHCEEKHAEEI VVPVQI IGQALTGLEIELQRK
138 EPCKTSCCDNKEEKVKEIGLLLASEDKSYPEKGVLIKDEGNCKSGCENKGTVTQRCHKEAGLDMETGVSCDLKLV
139 CCGKTEGEVGEQTDLEIKIEGHCESRCCSDEKQTEITLASEEETDDQDCSSGCCVNEGIVKQSSHEKKHVLVE
140 KEGLDMETGVCCDDLKLVCCGNTEGEVEEQDLEIKNEGHCKSGCCNDEKQTAETLASEEETDSTDCSSGCCMD
141 KEEVTKICGEKPVSLVVSGLETE GGGDCKSHCCGTGLTQEGSSKLVNVE SAQSGGCGTVKVSSQSCCTSSTDLVL
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143 >AlhMA4-2
144 ATAVMQSLMSLAPQKAI I AETGEEVEVDEVKISTVAVKAGETIPIDGIVVDGNCEVDEKTLTGEAFVVPKQRDS
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147 FKSLSRDITLRSLLYWSSVESKSSHPMAATIVDYAKSVSVEPRPEEVEDYQNFPGEGIYGKIEGNDIYIGNKRI
148 ASRAGCSTEIEVDTKGGNTVGYVYVGERLAGVFNLSDACRSGV SQAMTELKSLGIKTAMLTGDSQAAAMHAQEQL
149 GNVLDVVH GELLPEDKSKI IQEFKKEGPTAMVGDGVNDAPALAIADIGISMGISGSALATQTGHI IILMSNDIRRI
150 POAVKLARRARRKVVENVFLS IILKAGILALAFAGHPLIWA AVLVDVGTCLLVILNSMMLLLREKKKIGNKKCYRA
151 STSM LNGRKLEGDDDDVV DLEAGLLTKSGNGQCNSSCCGDKKNQEKVMMKPSKTS SDHSHPGCCGDKKQDKVK
152 PLVRD GCCGEETRAKAVGDMVSLSSCKKSSHVKHDLKMKGGSGCCANKSEKVEEVVAKSCCEKPKQOMESAGDCKS
153 GHCEEKHAEEI VVPVQI IGQALTGLEIELQRKECKTSCCDNKEEKVKEIGLLLASEDKSYPEKVLIKDEGNCK
154 KSGCENKGTVTQRCHKEAGLDMETGVSCDLKLVCCGKTEGEVAGKTDLEIKIEGHCESRCCSDEKQTEITLASE
155 EETDDQDCFSGCCHGLFLGCCMDKEVTKICGEKPVSLVVSGLETE GGGDCKSHCCGTCLTQEGSSKLVNVE SAQS
156 GCGTVKVSSQSCCTSSTDLVLS DLQVKKDEQCESSNRAVKSETCCKVKIPEACASKCKEKEKRHNKSGCCRSYA
157 KEFCSHRHHHHHHHHHHHHH VIA
158 >AtHMA1
159 MEPATLTRSSSLTRFPYRRGLSTLRLARVNSFSLIPPKTLRQKPLRISASLNLPPRSIRLRAVEDHHHDHHHDD
160 EQDHHHHHHHHHQGCCSVELKAESKPQKMLFGFAKAI GWVRLANYLREHLHLCCSAAAMFLAAAVCPYLAPEPY
161 IKSLQNAFMIVGFPLVGV SASLDALMDIAGGKVN I HVLMALAAAFASVFMGNALEGGLLAMFNLAHIAEFPF TSR
162 SMVDVKELKESNPDSALLIEVHNGNPNISDLSYKSVPVHSVEVGSYVVLVGTGEIVPV DCEVYQGSATITIEHLT
163 GEVPLEAKAGDRVPGGARNLDGRMIVKATKAWNDSTLNKIVQLTEEAHSNPKLQRWLDEFGENYSKVVVVLSL
164 AIAFLGPF LFKWPF LSTAACRGSVYRALGLMVAASPCALAVAPLAYATAISSCARKGILLKGAQVLDALASCHTI
165 AFDKGTGLTGLTCKAIEPIYGHOGGTNSSVITCCIPNCEKEALAVAAMEKGTTHPIGRAVVDH SVGKDLPSI
166 FVSTEFYFPGRGLTATVNGVKTVAEESRLRKASLGSIEFITS LFKSEDESKQIKDAVNASSYKDFVHAALSVDQ
167 KVTLIHLEDQPRPGVSGVIAELKSWARLRVMMLTGDHDSAWRVANAVGITEVYCNLKPEDKLNHVKNIAREAGG
168 GLIMVGE GINDAPALAAATV GIVLAQRASATAIAVADILLRDNITGV PFCVAKSRQTTSLVKQONVALALTSIFL
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170 >AtHMA2
171 MASKKMTKSYFDVLGICCTSEVPLIENILNSMDGVKEFSVIVPSRTVIVVHDTLILSQFQIVKALNQAQLEANVR
172 VTGETNFKNKWSPFAVVGILLLLSFFKYLYSPFRWLAVA AVVAGIYPI LAKAVASLARFRIDINILVVVTVGA
173 TIGMQDYTEAAVVVFLFTIAEWLQSRASYKASAVMQSLMSLAPQKAVIAETGEEVEVDELKTN TVIAVKAGETIP
174 IDGVVVDGNCEVDEKTLTGEAFVVPKLDSTVWAGTINLNGYITVNTTALAEDCVVAKMAKLVEEAQNSKTETQR
175 FIDKCSKYYP AII LISICFVAIPFALKVHNLKHWHLALVVLV SACPCGLILSTPVATFCALTKAATSGLLIKG
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177 EAVEDYQNLPGEGIYGKIDGKEVYIGNKRIASRAGCLSVPDIDVDTKGGKTI GYVYVGETLAGVFNLSDACRSGV
178 AQAMKELKSLGIKIAMLTGDNHAAAMHAQEQLGNAMDIVRAELLPEDKSEIKQLKREEGPTAMVGDGLNDAPAL
179 ATADIGISMGVSGSALATETGNI IILMSNDIRRIPOAIKLA KRAKRVVENVVISITMKGAILALAFAGHPLIWA A
180 VLADVGTCLLVILNSMMLLLSDKHKTGNKCYRESSSSSVLIAEKLEGDAAGDMEAGLLPKISDKHCKPGCCGTKTQ
181 EKAMKPAKTS SDHSHSGCCETKQKDKVTVVKKNCAEPVDLGHGHD SGCCGDKSQOPHQHEVQVQQSCHNKPSGL
182 DSGCCGK SQOPHQHELOQSCHDKPSGLDIGTGPKHEGSSTLVNLEGDAKEELKVLVNGCCSSPADLAITSLKVK
183 SDSHCKSNCS SRERCHHSNCCRSYAKESCSHDHHTRAHGVGTLKEIVIE
184 >AtHMA3

185 MAEGEESKKMNLQTSYFDVVGICCSSEVSVIGNVLRQVDGVKEFSVIVPSRTVIVVHDTFLISPLQIVKALNQAR
186 LEASVRPYGETSLKSQWSPFAIVSGVLLVLSFFKYFYSPLEWLAI VAVVAGVFPILAKAVASVTRFRDLINALT
187 LIAVIATLCMQDFTEAATIVFLFSVADWLESSAAHKASIVMSSLMSLAPRKAVIADTGLEVDVDEVGINTVVSVK
188 AGESIPIDGVVVDGSCDVDEKTLTGESFPVSKQRESTVMAATINLNGYIKVKTALARDCVVAKMTKLVEEAQKS
189 QTKTQRFIDKCSRYTTPAVVVSAACFVAVPVLKQVLDLHWFHLALVVLVSGCPCGLILSTPVATFCALTKAATS
190 GFLIKTGDCLETLAKIKIVAFDKTGTITKAEFMVSDFRSLSPSINLHKLNNWVSSIECKSSHPMAAALIDYAVISV
191 SVEPKPDIVENFQNFPGEGVYGRIDGQDIYIGNKRIAQRAGCLTDNVPDIEATMKRGTIGYIYMGAKL TGSFNL
192 LDGCRYGVAQALKELKSLGIQTAMLTGDNQDAAMSTQEQLLENALDIVHSELLPQDKARIIDDFKIQGPTMMVGDG
193 LNDAPALAKADIGISMGISGSALATETGDIILMSNDIRKIPKGMRLAKRSHKKVIENVVLSVSIKGAIMVLGFVG
194 YPLVWAAVLADAGTCLLVILNSMILLRDEREAVSTCYRSSTSSPVKLEEDEVEDLEVGLLQKSEETSCKSCCSGC
195 CSGPKDNQOK
196 >AtHMA4
197 MALQNKEEEKKVKKLQKSYFDVLGICCTSEVPIIENILKSLDGVKEYSVIVPSRTVIVVHDSLLISPFQIAKAL
198 NEARLEANVRVNGETSFKNKWSPFAVVSGLLLLLSFLKFVYSPLRWLAVAAVAAGIYPIILAKAFASIKRPRIDI
199 NILVIITVIATLAMQDFMEAAAVVFLFTISDWLETRASYKATSVMQSLMSLAPQKAI I AETGEEVEVDEVKVDTV
200 VAVKAGETIPIDGIVVDGNCEVDEKTLTGAEFPVPKQRDSTVWAGTINLNGYICVKTTSLAGDCVVAKMAKLVVEE
201 AQSSTKSQRLIDKCSQYYPAILVLSACVAIVPVMKVHNLKHWFLALVVLVSGCPCGLILSTPVATFCALTK
202 AATSGLLIKSADYDLTSLKIKIVAFDKTGTITRGEFVIDFKLSRDINLRSLLYVWVSSVESKSSHPMAATIVDY
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408 EGVHLHCKASNE DNGAINNTVNIKLEADHSNSKRGN TSNKPMENRETNNCKSCRRGSSQFKIGKSCAGLNKREV G
409 GCCKSYMKECCRKHGDIRMAVRGGLNE I I I E
410 **>EphMA1-1**
411 MEPAILSRSSSLTRFPFRGGLATLRLARVNSFSIFPNTLLRRKPFHLRISASLSLPRQSIRLRAVEDHHHDDHHH
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422 **>EphMA1-2**
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434 **>EphMA2**
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436 NVRVTGETNFKNKWSPFAVVSGLVLLLSFFKYVYSPFRWLAVAAVAGIYPILAKSVASIASRRIDINILVVI T

437 VGATLGMRDYTEAAAVVFLFTIAEWLQSRASYKASAVMQSLMSLAPQKAVIAETGEEVEVDDLKISTVIAVKAGE
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 508 **>FvHMA-B**
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608 CQSIADFDTGTLTTGKLMCKAIEPIHGHLVDASNGVDPSCCTPNCESEALAVAAAAMEKGTTHPIGRAVLKHSVGRD
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610 SVDKKTTLFHFDEDEPTGVCEVIYTLREKAKLRIMMLTGDHESQAORVAKAVCIEEVHFSLKPEDKLNKVKAVSR
611 EGGGGLIMVGDGINAPALAAATVGVILAQRASATAVAVADVLLQDNLCVVPFCIAKARQTTSLVKQSVALLT
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613 VPL
614 >HvHMA1-2
615 MPTFPFAGCSATPRGMQFRAASAASSAAPRLQPSARLLRLWRPRPFAHHLPSKPLPVASVPPVLLPRARRSLAFT
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617 PLNSVGRLOVALIAVAFPLVGVSAALDALVDIADGKINIHVLMALAAAFASVFMGNLSLEGGLLAMFSLAHTAEY
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621 CQSIADFDTGTLTTGKLMCKAIEPIHGHLVDNRNLNDSSCCTPSCSEALAVAAAAMEKGTTHPIGRAVLDHYVVK
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623 CIDEVHCCCLKPEDKLNKVKAVSSRGGSLIMVGDGINAPALAAATVGVVLAQRASATAVAAADVLLQDNICGVP
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654 >JcHMA-A
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667 >LsHMA-A
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671 >LsHMA-B
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675 >MtHMA-A
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687 CNDI

688 >MtHMA-B

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703 >NchMA4

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720 >NtHMA-A

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740 >NtHMA-B

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1005 VKAGEVVPIDGVVVDGRSEVDESTLTGESFPVAKQPDSQVWAGTLNIDGYIAVRRTAMADNSAVAKMARLVEEAQ
1006 NSRSKTQRLIDTCAKYYPVAVVMAAGVAVIPVAIRAHHLKHWFQLALVLLVSACPCALVLSTPVATFCALLTAA
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1010 NDAPALAKADVGVSMGVSGSAVAMETSHITLMSNDIRRIKAIQLARRTHRTIIVNIIFSVITKLAIVGLALS GH
1011 PLIWA AVLADVGT CMLVIMYSMLLLRSKGRKAKCCASSQHGS HAKKHCVSRHCS DGPCKSTGCSKESSAGKHG
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1016 SSCCGHSHTMLKLPEIVVE
1017 >SbHMA3-1
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1024 DKVEMSQLLYWVSSIESKSSHPMAAALVEYSQSKSIQPKPENVTFRIFPGEGISGVINGRQIFIGNRRIMARSS
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1193 GMNDAPALAKADVGSMGVSGSAVAMETSHITLMSNDIRRIPMAVQLARRTHRTIVVNIVFSVITKLAIVGLALA
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1195 KESPSAGKHACSDHGHATHCKEPSNHRPERHACHDHGSHNHCKEPPSSHVVTEKHVCHDHGNTSHSCEEAGNQL
1196 LLVESHG CNDHGHGSHDRCKELSSPRFTSKHECHDHEHSHCKEKP KTPCADSEAAACHGHGHEHRHCEGDSHSH
1197 ATGEHG CHEHDAHSHCEEHGHSDTAVEHACEHECHGEHQTVHAVETHHCHDHDHEHGQHELGEIEEPEKDC HDHS
1198 HHCCEHPHGKDKVA AEPVEEVTISIAALPKDEGHHHSEEQHNGEHCRKAKDCGGGGGAAPT DCAASKNCCGVKGG
1199 DACSSVQAARARETGPCCRSYVKCPR TAAASRSSCCGHSM LKLPEIVVE

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1201 MGSVEERLLPPPPARSADAGAGGAKSGKWEKTYLDVLGVCCSAEVALVERLLKPIDGVRVAVTVVPSRTVIVEHD
1202 LAAVSQSHIVKALNKAGLEASVRAYGSSGVVARWPSPYTVASGALLLASLFAPLLPSLRWLALAAACAGAPPMVL
1203 RALAAGLALDINALMLVAVAGAAALGDYAEAGAI VFLFTTAEWLET LACTKASAGMSSLMS MVPPTV VLAQTGEV
1204 VGV RDVGVGAVVAVRAGEVVPVDGVVV DGOSEVDESSLTGESFPVPKQQAQEVWAGTMNLDGYIAVRTTALADNS
1205 TVARMQRLVEAAQNSRSKTQRLVDS CAKYYTPAVVAVAAGVALV PLLLGP RGAQDPKRWFQLALVLLVSACPCAL
1206 VLSTPVATFCALLRAARMGVLIKGGDVLES LGEIRVAAFDKTGTITKGEFSVHGFHVVDKVGMSQLLYWVSSIE
1207 SKSSHPMATALVEYAQSKSIQPEPTSVTDFRIY PPEGISGAINGRQIFIGNTRIMARSSCYAAGAGPEMEGQQGA
1208 SIGHVIVDGDHVA AFSLSDDCRTGAAEAIRELRSMGIRSVMLTGDSKAAA SRAQRQLGGALEEVHSELLPADKVA
1209 LVGDLKARAGPTLMVGDGMNDAPALATADVGVAMGLSGSAAAMETSHATLMSSDLLRVPAAVRLGRRARATVAAN
1210 VIASVGAKA AVLALAAAWRPALVWAVLADVGTCLLVVLHSM LLLWDPAGAGWRRRGGGGDPEACRATARSLAMRS
1211 QLAEASNGAAGTAQGRRPGGGT KAGCHCCRETSE PSEQDHTAVVV DIPA PSAERPGVVAPTAATGCCSSSAREAC
1212 ATPTT VTTVNSAPRGCCGGIGEGDTRENARTSCCTDARDSPKKAGQQC NARCCSWGKQNTLKCQAQDTISNLK

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1213
1214 MPGPAVEAAAARGGGCCGKTAGKWEKTYLDVLGICCTAEVALVERLLAPINGVRVAVTVVPSRTVIVDHD TAAVVSQ
1215 FHIVKVLNKAGLEASVRAYGSSAGAPGRWPS PFIVACGVLLAASLFAPLLPPLRWLAVAAACVGSQPMLLRFAFAA
1216 AGKLTLDINILMLIAVAGAVALGSYTEAGAI VFLFTVAEWLET LACTKASAGMSSLMSV PKTVVLAETGQVVMG
1217 GDVAVGTVVAVRAGDVVPVDGVVVGGQSEVDESSLTGESFPVPKQAQSEVWAGTINLDGYISVRTTALAENSTVA
1218 KMERLVEEAQNSRSRTQRLIDSCAKHYTPAVV VLAAGVVLV PVLGAPDLEHWFRLSLVLLVSACPCALV LSTPV
1219 ATFCALLRAARMGLLVKGGNVLES LGEVRVAAFDKTGTITRGEFSIKDFLVVRDKVQMSQLLYWVSSIESKSSHP
1220 MAAALVEYAQSKSIQPKPEDVTETCIYHGEG IYGAINGKHIYIGNERIMARSSCRQQEAGHRET DGLKGVSVGLV
1221 ICDGDLVGKFSLSDT CRTGAAEA IQLRSMGIKSVMLTG DSEAAAKHAQEQLGGVLEELHSGLLPEDKVR LIRGL
1222 QARHGATLMVGDGMNDAPALAAADVGVSMGLSGSAAAIETSHATLMSGDVL RVPKAVRLGRRTRRTIAVNVASSV
1223 GAKA AVLALAVAWRPV LWWAVLADVGTCLLVVLHSM LLLRDAARARRRRCGGASKACCATA CKAPKTACCATASKA
1224 CGATTVKPVATRPQAGAGKADRPGGDKHGNGKDDCHRCCHKQSKLPEDAVVIAIPVRAVEHRKDAAAHEKAEG
1225 NAAGCCGGAPASAACCAEAHGG EDEVCIVISARSPCCSTARSRSASP K DAMCCGSGGKDGGAI SALVC

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1226
1227 MPGPAVEAAARS GGDHGGCCGKAAGKWEKTYLDVLGICCTAEVALVERLLTPIQGVRAVTVVPSRTVIVDHD T
1228 AAVSQFHIVKVLNKAGLEASVRAYGSSAGAGGRWPS PFTVACGALLALSLLAPLLPPLRWLAVAAACVGSQPMLL
1229 RAFAAAGKLTLDINILMLIAVAGSVALGSFTEAGAI VFLFTVAEWLET LACSKASAGMSSLMS TVPKTVVLAETG
1230 QVVMGMDVAVGTVVAVRAGDVVPVDGVVVGGHSEVDESSLTGESFPVPKQQAQSEVWAGTINLDGYISVRTTALAE
1231 NSTVAKMERLVEEAQNSRSRTQRLIDSCAKHYTPAVV VLAAGVVLV PALLGARDLELEHWFRLSLVLLVSACPCA
1232 LVLSTPVATFCALLRAARMGLLVKGGNVLES LGEVRVAAFDKTGTITRGEFSIKDFHVVDK VEMNQLLYWVSSI
1233 ESKSSHPMAAALVEYAQSKSVQPKPENVTETCIYHGEG IYGVMDGKQIYIGNERI IARSSCRHHQHAGHQETDGL
1234 KGV SIGHVICD GDLVGKFSLSDT CRTGAAEA IQLRSMGIKSVMLTG DSAAA AKHAQEQLGGVLEELHAGLLPED
1235 KVRLVRGLQARHGATLMVGDGMNDAPALAAADVGVSMGLSGSAAAIETSHAALMSGDILRVPKAVRLGRRARRTI
1236 AVNVASSVGA KAAVLA LAVAWRPV LWWAVLADVGTCLLVVLHSM LLLR DGAARRPRCCASATA CKSKQASKPCCA
1237 TVKPVATTRHRHGHGHHGAGAGK PTLGGDKQKDC HGCCQKESKPPEDAVVIAIPGRAVEHRKEAFPHENAG
1238 AGGCCAAAHA EDEVCIVISARSPCCSTARSRS GSPKDALCCHGSGGKDGGAI SALVC

1239