```
AQP0 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000026455      MWELRSASFWRAIFAEFFATLFYVFFGLGASLRWAPGPLHVLQVALAFGLALATLVQTVG 60
ENSRNOT00000004223      MWELRSASFWRAIFAEFFATLFYVFFGLGSSLRWAPGPLHVLQVALAFGLALATLVQTVG 60
ENST00000257979         MWELRSASFWRAIFAEFFATLFYVFFGLGSSLRWAPGPLHVLQVAMAFGLALATLVQSVG 60
                        *****************************:***************:***********:**

ENSMUST00000026455      HISGAHVNPAVTFAFLVGSQMSLLRAFCYIAAQLLGAVAGAAVLYSVTPPAVRGNLALNT 120
ENSRNOT00000004223      HISGAHVNPAVTFAFLVGSQMSLLRAFCYIAAQLLGAVAGAAVLYSVTPPAVRGNLALNT 120
ENST00000257979         HISGAHVNPAVTFAFLVGSQMSLLRAFCYMAAQLLGAVAGAAVLYSVTPPAVRGNLALNT 120
                        *****************************:******************************

ENSMUST00000026455      LHAGVSVGQATTVEIFLTLQFVLCIFATYDERRNGRMGSVALAVGFSLTLGHLFGMYYTG 180
ENSRNOT00000004223      LHAGVSVGQATTVEIFLTLQFVLCIFATYDERRNGRMGSVALAVGFSLTLGHLFGMYYTG 180
ENST00000257979         LHPAVSVGQATTVEIFLTLQFVLCIFATYDERRNGQLGSVALAVGFSLALGHLFGMYYTG 180
                        **..*******************************::***********:***********

ENSMUST00000026455      AGMNPARSFAPAILTRNFSNHWVYWVGPIIGGGLGSLLYDFLLFPRLKSVSERLSILKGA 240
ENSRNOT00000004223      AGMNPARSFAPAILTRNFSNHWVYWVGPIIGGGLGSLLYDFLLFPRLKSVSERLSILKGA 240
ENST00000257979         AGMNPARSFAPAILTGNFTNHWVYWVGPIIGGGLGSLLYDFLLFPRLKSISERLSVLKGA 240
                        *************** **:******************************:*****:****

ENSMUST00000026455      RPSDSNGQPEGTGEPVELKTQAL 263
ENSRNOT00000004223      RPSDSNGQPEGTGEPVELKTQAL 263
ENST00000257979         KPDVSNGQPEVTGEPVELNTQAL 263
                        :*. ****** *******:****
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AQP1 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000004774      MASEIKKKLFWRAVVAEFLAMTLFVFISIGSALGFNYPLERN-QTLVQDNVKVSLAFGLS 59
ENSRNOT00000015692      MASEIKKKLFWRAVVAEFLAMTLFVFISIGSALGFNYPLERN-QTLVQDNVKVSLAFGLS 59
ENSGALT00000008364      MASEFKKKMFWRAVVAEFLAMILFIFISIGSALGFNFPVSVNGTSATQDNVKVSLAFGLS 60
ENST00000311813         MASEFKKKLFWRAVVAEFLATTLFVFISIGSALGFKYPVGNN-QTAVQDNVKVSLAFGLS 59
ENST00000265298         ------------------------------------------------------------


ENSMUST00000004774      IATLAQSVGHISGAHLNPAVTLGLLLSCQISILRAVMYIIAQCVGAIVATAILSGITSSL 119
ENSRNOT00000015692      IATLAQSVGHISGAHLNPAVTLGLLLSCQISILRAVMYIIAQCVGAIVASAILSGITSSL 119
ENSGALT00000008364      IATMAQSVGHISGAHLNPAVTLGLLLSCQISIFKALMYILAQCLGAVVATAILSGVTSSL 120
ENST00000311813         IATLAQSVGHISGAHLNPAVTLGLLLSCQISIFRALMYIIAQCVGAIVATAILSGITSSL 119
ENST00000265298         ------------------------------------MYIIAQCVGAIVATAILSGITSSL 24
                                                            ***:***:**:**:*****:****

ENSMUST00000004774      VDNSLGRNDLAHGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALG 179
ENSRNOT00000015692      LENSLGRNDLARGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALG 179
ENSGALT00000008364      PYNSLGLNALAKGINAGQGLGIEIIATLQLVLCVLATTDRRRNDVSGSAPLAIGLSVALG 180
ENST00000311813         TGNSLGRNDLADGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALG 179
ENST00000265298         TGNSLGRNDLADGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALG 84
                          **** * ** *:*:*********.****************.*:.**************

ENSMUST00000004774      HLLAIDYTGCGINPARSFGSAVLTRNFSNHWIFWVGPFIGGALAVLIYDFILAPRSSDFT 239
ENSRNOT00000015692      HLLAIDYTGCGINPARSFGSAVLTRNFSNHWIFWVGPFIGSALAVLIYDFILAPRSSDFT 239
ENSGALT00000008364      HLLAIDYTGCGINPARSFGSALIANNFENHWIFWVGPIIGGAGAALIYDFILAPRSSDLT 240
ENST00000311813         HLLAIDYTGCGINPARSFGSAVITHNFSNHWIFWVGPFIGGALAVLIYDFILAPRSSDLT 239
ENST00000265298         HLLAIDYTGCGINPARSFGSAVITHNFSNHWIFWVGPFIGGALAVLIYDFILAPRSSDLT 144
                        *********************:::.**.*********:**.* *.*************:*

ENSMUST00000004774      DRMKVWTSGQVEEYDLDADDINSR-----------------VEMKPK------------- 269
ENSRNOT00000015692      DRMKVWTSGQVEEYDLDADDINSR-----------------VEMKPK------------- 269
ENSGALT00000008364      DRVKVWTSGQVEEYDLEGDDMNSR-----------------VEMKPK------------- 270
ENST00000311813         DRVKVWTSGQVEEYDLDADDINSR-----------------VEMKPK------------- 269
ENST00000265298         DRVKVWTSGQVEEYDLDADDINSRSFLGTKIYQFTHSLEVVEEVKERDPPASRPSEHDGR 204
                        **:*************:.**:***                  *:* :

ENSMUST00000004774      ------------------------
ENSRNOT00000015692      ------------------------
ENSGALT00000008364      ------------------------
ENST00000311813         ------------------------
ENST00000265298         CARKSPLAPKLLTDSPAQVPGILP 228
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AQP2 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000023752      MWELRSIAFSRAVLAEFLATLLFVFFGLGSALQWASSPPSVLQIAVAFGLGIGTLVQALG 60
ENSRNOT00000000324      MWELRSIAFSRAVLAEFLATLLFVFFGLGSALQWASSPPSVLQIAVAFGLGIGTLVQALG 60
ENST00000199280         MWELRSIAFSRAVFAEFLATLLFVFFGLGSALNWPQALPSVLQIAMAFGLGIGTLVQALG 60
                        *************:******************:*..: *******:**************

ENSMUST00000023752      HVSGAHINPAVTVACLVGCHVSFLRAAFYVAAQLLGAVAGAAILHEITPVEIRGDLAVNA 120
ENSRNOT00000000324      HVSGAHINPAVTVACLVGCHVSFLRAAFYVAAQLLGAVAGAAILHEITPVEIRGDLAVNA 120
ENST00000199280         HISGAHINPAVTVACLVGCHVSVLRAAFYVAAQLLGAVAGAALLHEITPADIRGDLAVNA 120
                        *:********************.*******************:******.:*********

ENSMUST00000023752      LHNNATAGQAVTVELFLTMQLVLCIFASTDERRSDNLGSPALSIGFSVTLGHLLGIYFTG 180
ENSRNOT00000000324      LHNNATAGQAVTVELFLTMQLVLCIFASTDERRGDNLGSPALSIGFSVTLGHLLGIYFTG 180
ENST00000199280         LSNSTTAGQAVTVELFLTLQLVLCIFASTDERRGENPGTPALSIGFSVALGHLLGIHYTG 180
                        * *.:*************:**************.:* *:*********:*******::**

ENSMUST00000023752      CSMNPARSLAPAVVTGKFDDHWVFWIGPLVGAVIGSLLYNYLLFPSTKSLQERLAVLKGL 240
ENSRNOT00000000324      CSMNPARSLAPAVVTGKFDDHWVFWIGPLVGAIIGSLLYNYLLFPSAKSLQERLAVLKGL 240
ENST00000199280         CSMNPARSLAPAVVTGKFDDHWVFWIGPLVGAILGSLLYNYVLFPPAKSLSERLAVLKGL 240
                        ********************************::*******:***.:***.*********

ENSMUST00000023752      EPDTDWEEREVRRRQSVELHSPQSLPRGSKA 271
ENSRNOT00000000324      EPDTDWEEREVRRRQSVELHSPQSLPRGSKA 271
ENST00000199280         EPDTDWEEREVRRRQSVELHSPQSLPRGTKA 271
                        ****************************:**
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AQP3 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000055327      MGRQKELMNRCGEMLHIRYRLLRQALAECLGTLILVMFGCGSVAQVVLSRGTHGGFLTIN 60
ENSRNOT00000013803      MGRQKELMNRCGEMLHIRYRLLRQALAECLGTLILVMFGCGSVAQVVLSRGTHGGFLTIN 60
ENST00000297991         MGRQKELVSRCGEMLHIRYRLLRQALAECLGTLILVMFGCGSVAQVVLSRGTHGGFLTIN 60
ENSGALT00000003868      MGRQKDVLATIEEHLRIRNKLVRQALAECLGTLILVLFGCGSVAQIVLSRGTHGGFLTVN 60
ENST00000343952         MGRQKELVSRCGEMLHIRYRLLRQALAECLGTLILVMFGCGSVAQVVLSRGTHGGFLTIN 60
ENST00000379492         ------------------------------------MFGCGSVAQVVLSRGTHGGFLTIN 24
                                                            :********:************:*

ENSMUST00000055327      LAFGFAVTLGILVAGQVSGAHLNPAVTFAMCFLAREPWIKLPIYALAQTLGAFLGAGIVF 120
ENSRNOT00000013803      LAFGFAVTLAILVAGQVSGAHLNPAVTFAMCFLAREPWIKLPIYTLAQTLGAFLGAGIVF 120
ENST00000297991         LAFGFAVTLGILIAGQVSGAHLNPAVTFAMCFLAREPWIKLPIYTLAQTLGAFLGAGIVF 120
ENSGALT00000003868      LAFGFAVMLGILIAGQVSGGHLNPAVTFAMCFLAREPWIKLPVYALAQTLGAFLGAGIVF 120
ENST00000343952         LAFGFAVTLGILIAGQVSGAHLNPAVTFAMCFLAREPWIKLPIYTLAQTLGAFLGAGIVF 120
ENST00000379492         LAFGFAVTLGILIAGQVSGAHLNPAVTFAMCFLAREPWIKLPIYTLAQTLGAFLGAGIVF 84
                        ******* *.**:******.**********************:*:***************

ENSMUST00000055327      GLYY--DAIWAFANNELFVSGPNGTAGIFATYPSGHLDMVNGFFDQFIGTAALIVCVLAI 178
ENSRNOT00000013803      GLYY--DAIWAFAGNELVVSGPNGTAGIFATYPSGHLDMVNGFFDQFIGTAALIVCVLAI 178
ENST00000297991         GLYY--DAIWHFADNQLFVSGPNGTAGIFATYPSGHLDMINGFFDQFIGTASLIVCVLAI 178
ENSGALT00000003868      GLYHAPDAIWAFGSNHLYVTGENATAGIFATYPSQHLNVVNGFFDQFIGTASLIVCVLAI 180
ENST00000343952         GLYY--DAIWHFADNQLFVSGPNGTAGIFATYPSGHLDMINGFFDQDRPALVVGAHRVPT 178
ENST00000379492         GLYY--DAIWHFADNQLFVSGPNGTAGIFATYPSGCTYISR----------SSGTCFCHN 132
                        ***:  **** *..*.* *:* *.**********    : .             .

ENSMUST00000055327      VDPYNN--PVPRGLEAFTVGLVVLVIGTSMGFNSGYAVNPARDFGPRLFTALAGWGSEVF 236
ENSRNOT00000013803      VDPYNN--PVPRGLEAFTVGLVVLVIGTSMGFNSGYAVNPARDFGPRLFTALAGWGSEVF 236
ENST00000297991         VDPYNN--PVPRGLEAFTVGLVVLVIGTSMGFNSGYAVNPARDFGPRLFTALAGWGSAVF 236
ENSGALT00000003868      VDPFNN--PVPPGLEAFTVGFVVLVIGTSMGFYSGYAVNPARDFGPRLFTAIAGWGTEVF 238
ENST00000343952         PGLHCGCLRVPADDRLPPGAAPTLQRGREC------EAGPCEAQGADLSGQGSPLRCPGL 232
ENST00000379492         AGMKGG---VKSGHKFHVCFCFVL----------------FLMYVADVTVLGIRDGRPHF 173
                         .   .   *  . .       .*                     . :           :

ENSMUST00000055327      TTGRHWWWVPIVSPLLGSIAGVFVYQLMIGCHLEQPPPSTEEENVKLAHMKHKEQI 292
ENSRNOT00000013803      TTGQNWWWVPIVSPLLGSIGGVFVYQLMIGCHLEQPLPSTEAENVKLAHMKHKEQI 292
ENST00000297991         TTGQHWWWVPIVSPLLGSIAGVFVYQLMIGCHLEQPPPSNEEENVKLAHVKHKEQI 292
ENSGALT00000003868      WTGKQWWWVPIVAPFLGAIAGVIVYQLMIGCHDEPSPPASEQETVKLANVKHKERV 294
ENST00000343952         EHPL-----TVQGPLP---RSPLHDPPFQAKELPIYPHPTTAPSGFPLDLAQIAP- 279
ENST00000379492         RKGR-----HSFNPLL---NNVLFYFYIKKNKINMCL------------------- 202
                                     *:     . :    :   .
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AQP4 - CLUSTAL W (1.83) multiple sequence alignment


ENST00000339532         ------------------------------------------------------------
ENST00000383168         ------------------------------------------------------------
ENSGALT00000024413      ------------------------------------------SKCARLCKCESIMVAFKG 18
ENSGALT00000036809      ------------------------------------------------------------
ENSMUST00000115856      MVHGFGCFVFFFLISLSSLWASEDSTCNSTLPLCHLATTLDCCKCGHSCSRESIMVAFKG 60
ENSMUST00000079081      --------------------------------MSDRAAARRWGKCGHSCSRESIMVAFKG 28
ENST00000383170         ------------------------------------------------------------
ENSRNOT00000048109      ------------------------------------------------------------
ENSRNOT00000021961      ------------------------------------------------------------


ENST00000339532         ------------------------------------------------------------
ENST00000383168         ------------------------------------------------------------
ENSGALT00000024413      VWTQPFWKAVSAEFLAMLIFVLLSLGSTINWGGSEKPLPVDMVLISLCFGLSIATMVQCF 78
ENSGALT00000036809      ------------------------------------------------------------
ENSMUST00000115856      VWTQAFWKAVSAEFLATLIFVLLGVGSTINWGGSENPLPVDMVLISLCFGLSIATMVQCF 120
ENSMUST00000079081      VWTQAFWKAVSAEFLATLIFVLLGVGSTINWGGSENPLPVDMVLISLCFGLSIATMVQCF 88
ENST00000383170         ------------------------------------------------------------
ENSRNOT00000048109      ------------------------------------------------------------
ENSRNOT00000021961      ------------------------------------------------------------


ENST00000339532         ----------------MSDRPTARRWGKCGPLCTREN----------------------- 21
ENST00000383168         ----------------MSDRPTARRWGKCGPLCTRENIMVAFKGVWTQAFWKAVTAEFLA 44
ENSGALT00000024413      GHISGGHINPAVTVAMVCTRKISLAKSVFYILAQCLG----------------------- 115
ENSGALT00000036809      ------HINPAVTVAMVCTRKISLAKSVFYILAQCLG----------------------- 31
ENSMUST00000115856      GHISGGHINPAVTVAMVCTRKISIAKSVFYIIAQCLG----------------------- 157
ENSMUST00000079081      GHISGGHINPAVTVAMVCTRKISIAKSVFYIIAQCLG----------------------- 125
ENST00000383170         ---------CTLAGEGMSDRPTARRWGKCGPLCTREN----------------------- 28
ENSRNOT00000048109      ----------------MSDGAAARRWGKCGPPCSRES----------------------- 21
ENSRNOT00000021961      ----------------MSDGAAARRWGKCGPPCSRES----------------------- 21
                                        :.    :   .     .   .

ENST00000339532         ------------------------------------------------------------
ENST00000383168         MLIFVLLSLGSTINWGGTEKPLPVDMVLISLCFGLSIATMVQCFGHISGGHINPAVTVAM 104
ENSGALT00000024413      ------------------------------------------------------------
ENSGALT00000036809      ------------------------------------------------------------
ENSMUST00000115856      ------------------------------------------------------------
ENSMUST00000079081      ------------------------------------------------------------
ENST00000383170         ------------------------------------------------------------
ENSRNOT00000048109      ------------------------------------------------------------
ENSRNOT00000021961      ------------------------------------------------------------


ENST00000339532         ----------------------IMGAGILYLVTPPSVVGGLGVTMVHGNLTAG------- 52
ENST00000383168         VCTRKISIAKSVFYIAAQCLGAIIGAGILYLVTPPSVVGGLGVTMVHGNLTAG------- 157
ENSGALT00000024413      ---------------------AIVGAGILYLITPPSVVGGLGVTAVHGDLSAG------- 147
ENSGALT00000036809      ---------------------AIVGAGILYLITPPSVVGGLGVTAVHGDLSAG------- 63
ENSMUST00000115856      ---------------------AIIGAGILYLVTPPSVVGGLGVTTVHGNLTAG------- 189
ENSMUST00000079081      ---------------------AIIGAGILYLVTPPSVVGGLGVTTVHGNLTAG------- 157
ENST00000383170         --------------------IMVAFKGVWTQAFWKAVTAEFLAMLIFVLLSLGSTINWGG 68
ENSRNOT00000048109      --------------------IMVAFKGVWTQAFWKAVTAEFLAMLIFVLLSVGSTINWGG 61
ENSRNOT00000021961      --------------------IMVAFKGVWTQAFWKAVTAEFLAMLIFVLLSVGSTINWGG 61
                                              :   *:       :*.. : .  :.  *: *

ENST00000339532         --HGLLVELIIT---FQLVFTIFASCDSKRT--DVTGSIALAIGFSVAIGHLFAINYTGA 105
ENST00000383168         --HGLLVELIIT---FQLVFTIFASCDSKRT--DVTGSIALAIGFSVAIGHLFAINYTGA 210
ENSGALT00000024413      --HGLLVELIIT---FQLVFTIFASCDSKRS--DVTGSVALAIGFSVAIGHLFAINYTGA 200
ENSGALT00000036809      --HGLLVELIIT---FQLVFTIFASCDSKRS--DVTGSVALAIGFSVAIGHLFAINYTGA 116
ENSMUST00000115856      --HGLLVELIIT---FQLVFTIFASCDSKRT--DVTGSIALAIGFSVAIGHLFAINYTGA 242
ENSMUST00000079081      --HGLLVELIIT---FQLVFTIFASCDSKRT--DVTGSIALAIGFSVAIGHLFAINYTGA 210
ENST00000383170         TEKPLPVDMVLISLCFGLSIATMVQCFGHISGGHINPAVTVAMVCTRKISIAKSVFYIAA 128
ENSRNOT00000048109      SENPLPVDMVLISLCFGLSIATMVQCFGHISGGHINPAVTVAMVCTRKISIAKSVFYITA 121
ENSRNOT00000021961      SENPLPVDMVLISLCFGLSIATMVQCFGHISGGHINPAVTVAMVCTRKISIAKSVFYITA 121
                          : * *::::    * * :: :..* .: :  .:. ::::*:  :  *.   :: *  *

ENST00000339532         SMNPAR------------------------------------------------------ 111
ENST00000383168         SMNPAR------------------------------------------------------ 216
ENSGALT00000024413      SMNPAR------------------------------------------------------ 206
ENSGALT00000036809      SMNPA------------------------------------------------------- 121
ENSMUST00000115856      SMNPAR------------------------------------------------------ 248
ENSMUST00000079081      SMNPAR------------------------------------------------------ 216
ENST00000383170         QCVG-------------------------------------------------------- 132
ENSRNOT00000048109      QCLGAIIGAGILYLVTPPSVVGGLGVTTIN------------------------------ 151
ENSRNOT00000021961      QCLGAIIGAGILYLVTPPSVVGGLGVTTVHGNLTAGHGLLVELIITFQLVFTIFASCDSK 181
                        .

ENST00000339532         -----------------------------------SFGPAVIMGNWENHWIYWVGPIIGA 136
ENST00000383168         -----------------------------------SFGPAVIMGNWENHWIYWVGPIIGA 241
ENSGALT00000024413      -----------------------------------SFGPAVIMGKWENQWVYWVGPIIGA 231
ENSGALT00000036809      ------------------------------------------------------------
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ENSMUST00000115856      -----------------------------------SFGPAVIMGNWANHWIYWVGPIMGA 273
ENSMUST00000079081      -----------------------------------SFGPAVIMGNWANHWIYWVGPIMGA 241
ENST00000383170         -------------------------------------------------------PIIGA 137
ENSRNOT00000048109      -------------------------YTGASMNPARSFGPAVIMGNWENHWIYWVGPIIGA 186
ENSRNOT00000021961      RTDVTGSVALAIGFSVAIGHLFAINYTGASMNPARSFGPAVIMGNWENHWIYWVGPIIGA 241


ENST00000339532         VLAGGLYEYVFCPDVEFKRRFKEAFSKAAQQTKGSYMEVEDNRSQVETDDLILKPGVVHV 196
ENST00000383168         VLAGGLYEYVFCPDVEFKRRFKEAFSKAAQQTKGSYMEVEDNRSQVETDDLILKPGVVHV 301
ENSGALT00000024413      VLAGALYEYVYCPDMELKRRFKDVFSKATQPSKGKYIEVDDTRSHVETDDLILKPGIVHV 291
ENSGALT00000036809      ------------------------------------------------------------
ENSMUST00000115856      VLAGALYEYVFCPDVELKRRLKEAFSKAAQQTKGSYMEVEDNRSQVETEDLILKPGVVHV 333
ENSMUST00000079081      VLAGALYEYVFCPDVELKRRLKEAFSKAAQQTKGSYMEVEDNRSQVETEDLILKPGVVHV 301
ENST00000383170         VLAGGLYEYVFCPDVEFKRRFKEAFSKAAQQTKGSYMEVEDNRSQVETDDLILKPGVVHV 197
ENSRNOT00000048109      VLAGALYEYVFCPDVELKRRLKEAFSKAAQQTKGSYMEVEDNRSQVETEDLILKPGVVHV 246
ENSRNOT00000021961      VLAGALYEYVFCPDVELKRRLKEAFSKAAQQTKGSYMEVEDNRSQVETEDLILKPGVVHV 301


ENST00000339532         IDVDRGEEKKGKDQSGEVLSSV 218
ENST00000383168         IDVDRGEEKKGKDQSGEVLSSV 323
ENSGALT00000024413      IDIDRSEDKKGRDPSSEVLSSV 313
ENSGALT00000036809      ----------------------
ENSMUST00000115856      IDIDRGEEKKGKDSSGEVLSSV 355
ENSMUST00000079081      IDIDRGEEKKGKDSSGEVLSSV 323
ENST00000383170         IDVDRGEEKKGKDQSGEVLSSV 219
ENSRNOT00000048109      IDIDRGDEKKGKDSSGEVLSSV 268
ENSRNOT00000021961      IDIDRGDEKKGKDSSGEVLSSV 323
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AQP5 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000042340      ----------------------------------MKKEVCSVAFFKAVFAEFLATLIFVF 26
ENSRNOT00000024102      ----------------------------------MKKEVCSLAFFKAVFAEFLATLIFVF 26
ENSMUST00000088200      ----------------------------------MKKEVCSVAFFKAVFAEFLATLIFVF 26
ENSRNOT00000040874      ----------------------------------MKKEVCSLAFFKAVFAEFLATLIFVF 26
ENST00000293599         ----------------------------------MKKEVCSVAFLKAVFAEFLATLIFVF 26
ENSGALT00000041244      -----------------------------------------------------STLIFVF 7
ENSGALT00000041246      -------------------------------------EILTLAFARAVFVEFISTLIFVF 23
ENSGALT00000004288      APPDQQRQWELSSKAVVFFAPRVHRGSHPPPTPTMKREILTLAFARAVFVEFISTLIFVF 60
                                                                             :******

ENSMUST00000042340      FGLGSALKWPSALPTILQISIAFGLAIGTLAQALGPVSGGHINPAITLALLIGNQISLLR 86
ENSRNOT00000024102      FGLGSALKWPSALPTILQISIAFGLAIGTLAQALGPVSGGHINPAITLALLIGNQISLLR 86
ENSMUST00000088200      FGLGSALKWPSALPTILQISIAFGLAIGTLAQALGPVSGGHINPAITLALLIGNQISLLR 86
ENSRNOT00000040874      FGLGSALKWPSALPTILQISIAFGLAIGTLAQALGPVSGGHINPAITLALLIGNQISLLR 86
ENST00000293599         FGLGSALKWPSALPTILQIALAFGLAIGTLAQALGPVSGGHINPAITLALLVGNQISLLR 86
ENSGALT00000041244      IGLGSALKWPSALPSILQISLAFGLAIGTLVQAFGHISGAHINPAVTIAFFVGNQISFLR 67
ENSGALT00000041246      IGLGSALKWPSALPSILQISLAFGLAIGTLVQAFGHISGAHINPAVTIAFFVGNQISFLR 83
ENSGALT00000004288      IGLGSALKWPSALPSILQISLAFGLAIGTLVQAFGHISGAHINPAVTIAFFVGNQISFLR 120
                        :*************:****::*********.**:* :**.*****:*:*:::*****:**

ENSMUST00000042340      AIFYVAAQLVGAIAGAGILYWLAPGNARGNLAVN---ALSNNTTPGKAVVVELILTFQLA 143
ENSRNOT00000024102      AVFYVAAQLVGAIAGAGILYWLAPLNARGNLAVN---ALNNNTTPGKAMVVELILTFQLA 143
ENSMUST00000088200      AIFYVAAQLVGAIAGAGILYWLAPGNARGNLAVN---AQQHNTRQGRGGGVNLDFPAGPL 143
ENSRNOT00000040874      AVFYVAAQLVGAIAGAGILYWLAPLNARGNLAVNAVTEQQHNAWQGHGGGVNLDFPASPL 146
ENST00000293599         AFFYVAAQLVGAIAGAGILYGVAPLNARGNLAVN---ALNNNTTQGQAMVVELILTFQLA 143
ENSGALT00000041244      TLFYVIAQLVGAIAGAGILYGVTPANTRGNLAIN---SLNNNTTPGQAVVVEMILTFQLA 124
ENSGALT00000041246      TLFYVIAQLVGAIAGAGILYGVTPANTRGNLAIN---SLNNNTTPGQAVVVEMILTFQLA 140
ENSGALT00000004288      TLFYVIAQLVGAIAGAGILYGVTPANTRGNLAIN---SLNNNTTPGQAVVVEMILTFQLA 177
                        :.*** ************** ::* *:*****:*     .:*:  *:.  *:: :.

ENSMUST00000042340      LCIFSSTDSRRTSPVGSPALSIGLSVTLGHLVGIYFTGCSMNPARSFGPAVVMNRFSPSH 203
ENSRNOT00000024102      LCIFSSTDSRRTSPVGSPALSIGLSVTLGHLVGIYFTGCSMNPARSFGPAVVMNRFSPSH 203
ENSMUST00000088200      HLLLHGLPP--HQPGGLPSLIHWLVGHTGPSCGDLLHRLFHEPSPIFRPCGGHESVQPLS 201
ENSRNOT00000040874      HLLLHRLSP--NQPCGLPSLIHWLVCHTGPSCGDLLHRLFHEPSPIFRPCGGHEPVQPLS 204
ENST00000293599         LCIFASTDSRRTSPVGSPALSIGLSVTLGHLVGIYFTGCSMNPARSFGPAVVMNRFSPAH 203
ENSGALT00000041244      ACIFASTDNRRNGNVGSPALSIGLSVAVGHLVGVSVRGGTIGWKKSMEPSVTKKERSIAV 184
ENSGALT00000041246      ACIFASTDNRRNGNVGSPALSIGLSVAVGHLVGVSVRG---GWGRNFS-RMPILILSPIA 196
ENSGALT00000004288      ACIFASTDNRRNGNVGSPALSIGLSVAVGHLVGL--------YCCQLNPAKEVAQSSPPW 229
                          ::           * *:*   *    *   *             :         .

ENSMUST00000042340      WVFWVGPIVGAVLAAILYFYLLFPSSLSLHDRVAVVKGTYEPEEDWEDHREERKKTIELT 263
ENSRNOT00000024102      WVFWVGPIVGAMLAAILYFYLLFPSSLSLHDRVAVVKGTYEPEEDWEDHREERKKTIELT 263
ENSMUST00000088200      LGLLGRTIVGAVLAAILYFYLLFPSSLSLHDRVAVVKGTYEPEEDWEDHREERKKTIELT 261
ENSRNOT00000040874      LGLLGR-IVGAMLAAILYFYLLFPSSLSLHDRVAVVKGTYEPEEDWEDHREERKKTIELT 263
ENST00000293599         WVFWVGPIVGAVLAAILYFYLLFPNSLSLSERVAIIKGTYEPDEDWEEQREERKKTMELT 263
ENSGALT00000041244      CVFWVGPILGACLAALLYFYILVPYCMNMSDRVAIVKGTYESEEEWEEQREERKKSMELT 244
ENSGALT00000041246      FVFWVGPILGACLAALLYFYILVPYCMNMSDRVAIVKGTYESEEEWEEQREERKKSMELT 256
ENSGALT00000004288      WVFWVGPILGACLAALLYFYILVPYCMNMSDRVAIVKGTYESEEEWEEQREERKKSMELT 289
                          :    *:** ***:****:*.* .:.: :***::*****.:*:**::******::***

ENSMUST00000042340      AH 265
ENSRNOT00000024102      AH 265
ENSMUST00000088200      AH 263
ENSRNOT00000040874      AH 265
ENST00000293599         TR 265
ENSGALT00000041244      PP 246
ENSGALT00000041246      PP 258
ENSGALT00000004288      PP 291
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AQP6 - CLUSTAL W (1.83) multiple sequence alignment


ENSRNOT00000000323      MEPGLCNRAYLLVGGLWTAISKALFAEFLATGLYVFFGVGSVLPWPVALPSVLQVAITFN 60
ENSRNOT00000049837      MEPGLCNRAYLLVGGLWTAISKALFAEFLATGLYVFFGVGSVLPWPVALPSVLQVAITFN 60
ENSMUST00000023754      MEPGLCSRAYLLVGGLWTAISKALFAEFLATGLYVFFGVGSVLPWPVALPSVLQIAITFN 60
ENSGALT00000016693      ------------------------------------------------------------
ENST00000315520         ------------------------------------------------------------
ENST00000394984         ------------------------------------------------------------
ENST00000394985         ------------------------------------------------------------


ENSRNOT00000000323      LATATAVQISWKTSGAHANPAVTLAYLVGSHISLPRAVAYIAAQLAGATVGAALLYGVTP 120
ENSRNOT00000049837      LATATAVQISWKTSGAHANPAVTLAYLVGSHISLPRAVAYIAAQLAGATVGAALLYGVTP 120
ENSMUST00000023754      LATATAVQISWKTSGAHANPAVTLAYLVGSHISLPRAMAYIAAQLAGATAGAALLYGVTP 120
ENSGALT00000016693      ------------------------------------------------------------
ENST00000315520         -----------------------------------------------------------M 1
ENST00000394984         -----------------------------------------------------------M 1
ENST00000394985         -----------------------------------------------------------M 1


ENSRNOT00000000323      GGVRETLGVNVVHNSTSTGQAVAVELVLTLQLV-LCVFASMDSRQ--TLGSP-----AAM 172
ENSRNOT00000049837      GGVRETLGVNVVHNSTSTGQAVAVELVLTLQLV-LCVFASMDSRQ--TLGSP-----AAM 172
ENSMUST00000023754      GGIRETLGVNVVHNSTSTGQAVAVELVLTLQLV-LCVFASMDGRQ--TLASP-----AAM 172
ENSGALT00000016693      -----------LHNETTTGQAVTVELFLTFQLV-LCIFASTDERREDNMGSP-----ALS 43
ENST00000315520         DAVEPGGRGWASMLACRLWKAISRALFAEFLATGLYVFFGVGSVMRWPTALPSVLQIAIT 61
ENST00000394984         DAVEPGGRGWASMLACRLWKAISRALFAEFLATGLYVFFGVGSVMRWPTALPSVLQIAIT 61
ENST00000394985         DAVEPGGRGWASMLACRLWKAISRALFAEFLATGLYVFFGVGSVMRWPTALPSVLQIAIT 61
                                           :*::  *.  :  . * :* . .       . *     *

ENSRNOT00000000323      IGTSVALGHLIGIYFTGCSMNPARSFGPAVIVG---KFAVHWIFWVGPLTGAVL-ASLIY 228
ENSRNOT00000049837      IGTSVALGHLIGIYFTGCSMNPARSFGPAVIVG---KFAVHWIFWVGPLTGAVL-ASLIY 228
ENSMUST00000023754      IGTSVALGHLIGIYFTGCSMNPARSFGPAVIVG---KFAVHWIFWVGPLTGAVL-ASLIY 228
ENSGALT00000016693      IGLSVAVGHLLGIRYTGCSMNPARSFAPAVIVG---DFSDHWVFWVGPLVGAAA-ASIIY 99
ENST00000315520         FNLVTAMAVQVTWKASGAHANPAVTL--AFLVGSHISLPRAVAYVAAQLVGATVGAALLY 119
ENST00000394984         FNLVTAMAVQVTWKASGAHANPAVTL--AFLVGSHISLPRAVAYVAAQLVGATVGAALLY 119
ENST00000394985         FNLVTAMAVQVTWKASGAHANPAVTL--AFLVGSHISLPRAVAYVAAQLVGATVGAALLY 119
                        :.  .*:.  :    :*.  *** ::  *.:**   .:.    : .. *.**.  *:::*

ENSRNOT00000000323      NFILFPDTKTVAQRLAILVGTT----------KVEKVVDLEPQKKE-------------- 264
ENSRNOT00000049837      NFILFPDTKTVAQRLAILVGTT----------KVEKVVDLEPQKKE-------------- 264
ENSMUST00000023754      NFILFPDTKTVAQRLAILVGTT----------KVEKVVDLEPQKKE-------------- 264
ENSGALT00000016693      NYVLFPQSKTFSERLAIFKG-------------------MEPEEDW-------------- 126
ENST00000315520         GVMPGDIRETLGINVVRNSVSTGQAVAVELLLTLQLVLCVFASTDSRQTSGSPATMIGIS 179
ENST00000394984         GVMPGDIRETLGINVAPPTSS---------------ALRLFPSSS--------------- 149
ENST00000394985         GVMPGDIRETLGINVVRNSVSTGQAVAVELLLTLQLVLCVFASTDSRQTSGSPATMIGIS 179
                        . :     :*.. .:.                       : .. .

ENSRNOT00000000323      --------SQTNSEDTEVSV---------------------------------------- 276
ENSRNOT00000049837      --------SQTNSEDTEVSV---------------------------------------- 276
ENSMUST00000023754      --------SQTNSEDTECLTSPCEEAVRSFSFTLGLC----------------------- 293
ENSGALT00000016693      --------AEREA----------------------------------------------- 131
ENST00000315520         VALGHLIGIHFTGCSMNPARSFGPAIIIGKFTVHWVFWVGPLMGALLASLIYNFVLFPDT 239
ENST00000394984         --------LHLEACLTRP------------FSIS-------------------------- 163
ENST00000394985         VALGHLIGIHFTGCSMNPARSFGPAIIIGKFTVHWVFWVGPLMGALLASLIYNFVLFPDT 239
                                 .  .

ENSRNOT00000000323      -------------------------------------------
ENSRNOT00000049837      -------------------------------------------
ENSMUST00000023754      -------------------------------------------
ENSGALT00000016693      -------------------------------------------
ENST00000315520         KTLAQRLAILTGTVEVGTGAGAGAEPLKKESQPGSGAVEMESV 282
ENST00000394984         -------------------------------------------
ENST00000394985         KTLAQRLAILTGTVEVGTGAGAGAEPLKKESQPGSGAVEMESV 282
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AQP7 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000030136      ----------------MAPRSVLETIQSVL--QKNMVREFLAEFLSTYVMMVFGLGSVAH 42
ENSMUST00000054945      ----------------MAPRSVLETIQSVL--QKNMVREFLAEFLSTYVMMVFGLGSVAH 42
ENSMUST00000116345      ----------------MAPRSVLETIQSVL--QKNMVREFLAEFLSTYVMMVFGLGSVAH 42
ENSRNOT00000012975      ----------------MAG-SVLENIQSVL--QKTWVREFLAEFLSTYVLMVFGLGSVAH 41
ENST00000297988         MVQASGHR-RSTRGSKMVSWSVIAKIQEIL--QRKMVREFLAEFMSTYVMMVFGLGSVAH 57
ENST00000379507         --MGSGHCLRSTRGSKMVSWSVIAKIQEIL--QRKMVREFLAEFMSTYVMMVFGLGSVAH 56
ENST00000379506         --MGSGHCLRSTRGSKMVSWSVIAKIQEIL--QRKMVREFLAEFMSTYVMMVFGLGSVAH 56
ENST00000379503         -----------------MGWATFTD-------QGEEGLEPSGPWKTSHTR---------- 26
ENSGALT00000003866      ---------------------MLEKIQKMLTIRSNSVRELLAEALGMYILMVLGLSSVAQ 39
                                              :         :     *  .     :

ENSMUST00000030136      MVLGE-NSGSYLGVNLGFGFGVTMGVHVAGGISGAHMNAAVTFTNCALGRMTWKKFPVYV 101
ENSMUST00000054945      MVLGE-NSGSYLGVNLGFGFGVTMGVHVAGGISGAHMNAAVTFTNCALGRMTWKKFPVYV 101
ENSMUST00000116345      MVLGE-NSGSYLGVNLGFGFGVTMGVHVAGGISGAHMNAAVTFTNCALGRMTWKKFPVYV 101
ENSRNOT00000012975      MVLGE-RLGSYLGVNLGFGFGVTMGIHVAGGISGAHMNAAVTFTNCALGRMAWKKFPIYV 100
ENST00000297988         MVLNK-KYGSYLGVNLGFGFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYV 116
ENST00000379507         MVLNK-KYGSYLGVNLGFGFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYV 115
ENST00000379506         MVLNK-KYGSYLGVNLGFGFGVTMGVHVAGRISGAHMNAAVTFANCALGRVPWRKFPVYV 115
ENST00000379503         ----------------------------------AHMNAAVTFANCALGRVPWRKFPVYV 52
ENSGALT00000003866      TVLGKGEFGQYLSINLGFGIGVTMGIHAAGGISGAHLNAAITLTHCMFGNLPWRKLPVYL 99
                                                          **:***:*:::* :*.:.*:*:*:*:

ENSMUST00000030136      LGQFLGSFSAAATTYLIFYGAINHFAGGDLLVTGSKATANIFATYLPEYMTLWRGFLDEA 161
ENSMUST00000054945      LGQFLGSFSAAATTYLIFYGAINHFAGGDLLVTGSKATANIFATYLPEYMTLWRGFLDEA 161
ENSMUST00000116345      LGQFLGSFSAAATTYLIFYGAINHFAGGDLLVTGSKATANIFATYLPEYMTLWRGFLDEA 161
ENSRNOT00000012975      LGQFLGSFLAAATTYLIFYGAINHYAGGELLVTGPKSTANIFATYLPEHMTLWRGFVDEV 160
ENST00000297988         LGQFLGSFLAAATIYSLFYTAILHFSGGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEA 176
ENST00000379507         LGQFLGSFLAAATIYSLFYTAILHFSGGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEA 175
ENST00000379506         LGQFLGSFLAAATIYSLFYTAILHFSGGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEA 175
ENST00000379503         LGQFLGSFLAAATIYSLFYTAILHFSGGQLMVTGPVATAGIFATYLPDHMTLWRGFLNEA 112
ENSGALT00000003866      LGQFLGSFLAAATIFGLYYDALHDYTNGNFTVTGPTATASIFSTYPSPYMSLTGGFFTEF 159
                        ******** **** : ::* *: .::.*:: ***. :**.**:** . :*:*  **. *

ENSMUST00000030136      FVTGMLQLCLFAITDKKNSPALQGTEPLVIGILVTVLGVSLGMNSGYAINPSRDLPPRLF 221
ENSMUST00000054945      FVTGMLQLCLFAITDKKNSPALQGTEPLVIGILVTVLGVSLGMNSGYAINPSRDLPPRLF 221
ENSMUST00000116345      FVTGMLQLCLFAITDKKNSPALQGTEPLVIGILVTVLGVSLGMNSGYAINPSRDLPPRLF 221
ENSRNOT00000012975      FVTGMLQLCIFAITDKLNSPALQGTEPLMIGILVCVLGVSLGMNTGYAINPSRDLPPRFF 220
ENST00000297988         WLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIF 236
ENST00000379507         WLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIF 235
ENST00000379506         WLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIF 235
ENST00000379503         WLTGMLQLCLFAITDQENNPALPGTEALVIGILVVIIGVSLGMNTGYAINPSRDLPPRIF 172
ENSGALT00000003866      IATVMLLLGILVIHDEKNNGALKGTHALLTGILVLGIGMGMGMNTGYAINPSRDLPPRIF 219
                          * ** * ::.* *: *. ** **..*: ****  :*:.:***:*************:*

ENSMUST00000030136      TFIAGWGKQVFRAGNNWWWVPVVAPLLGAYLGGIVYLGLIHPSIPQDPQRLENFTARDQK 281
ENSMUST00000054945      TFIAGWGKQVFRAGNNWWWVPVVAPLLGAYLGGIVYLGLIHPSIPQDPQRLENFTARDQK 281
ENSMUST00000116345      TFIAGWGKQVFRAGNNWWWVPVVAPLLGAYLGGIVYLGLIHPSIPQDPQRLENFTARDQK 281
ENSRNOT00000012975      TFIAGWGKKVFSAGNNWWWVPVVAPLLGAYLGGIVYLGLIHAGIP--PQ----------- 267
ENST00000297988         TFIAGWGKQVFSNGENWWWVPVVAPLLGAYLGGIIYLVFIGSTIPREPLKLEDSVAYEDH 296
ENST00000379507         TFIAGWGKQVFSNGENWWWVPVVAPLLGAYLGGIIYLVFIGSTIPREPLKLEDSVAYEDH 295
ENST00000379506         TFIAGWGKQVFR------YCPCPGPFL--------------------------------- 256
ENST00000379503         TFIAGWGKQVFR------YCPCPGPFL--------------------------------- 193
ENSGALT00000003866      TAIAGWGVDVFRAGNYWWWVPVVAPTLGSLAGGLIHKLLID--IHNQPVLERGNEKGQTV 277
                        * ***** .**       : *  .* *

ENSMUST00000030136      VTASYKNAASANISGSVPLEHF------------------------ 303
ENSMUST00000054945      VTASYKNAASANISGSVPLEHF------------------------ 303
ENSMUST00000116345      VTASYKNAASANISGSVPLEHF------------------------ 303
ENSRNOT00000012975      --------------GS------------------------------ 269
ENST00000297988         GITVLPKMGSHEPTISPLTPVSVSPANRSSVHPAPPLHESMALEHF 342
ENST00000379507         GITVLPKMGSHEPTISPLTPVSVSPANRSSVHPAPPLHESMALEHF 341
ENST00000379506         ----------------------------------------------
ENST00000379503         ----------------------------------------------
ENSGALT00000003866      VESS------------------------------------------ 281
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AQP8 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000033023      MSGEQTPMCSMDLPEVKVKTS--MAGRCRVFWYEQYVQPCIVELVGSALFIFIGCLSVIE 58
ENSMUST00000098056      MPAEHAPTS--------------------CFCSQLYR----------------------- 17
ENSRNOT00000019939      FSLRQTPMCSMDLREIKGKETNMADSYHGMSWYEQYIQPCVVELLGSALFIFIGCLSVIE 60
ENST00000219660         MSG-EIAMCEPEFGNDKAREPS-VGGRWRVSWYERFVQPCLVELLGSALFIFIGCLSVIE 58
ENSGALT00000009629      LGGQPSTKEAMEMVDAERPPAK-------QNWYECYVLPCLAELLGSAAFVFIGCLSVVE 53
                        :     .                          : :                          

ENSMUST00000033023      NSPNTGLLQPALAHGLALGLIIATLGNISGGHFNPAVSLAVTVIGGLKTMLLIPYWISQL 118
ENSMUST00000098056      ------------------------LG----GHFNPAVSLAVTVIGGLKTMLLIPYWISQL 49
ENSRNOT00000019939      NSPNTGLLQPALAHGLALGLIIATLGNISGGHFNPAVSLAVTLVGGLKTMLLIPYWVSQL 120
ENST00000219660         NGTDTGLLQPALAHGLALGLVIATLGNISGGHFNPAVSLAAMLIGGLNLVMLLPYWVSQL 118
ENSGALT00000009629      DSIGTGLLQPALVHGLSIVPIVVSLGNISGAHINPVVSLGIWLVGGMKLIMLIPYCIAQL 113
                                                **    .*:**.***.  ::**:: ::*:** ::**

ENSMUST00000033023      FGGLIGAALAKVVSPEERFWNASGAAFAIVQEQEQVAEALGIEIILTMLLVLAVCMGAVN 178
ENSMUST00000098056      FGGLIGAALAKVVSPEERFWNASGAAFAIVQEQEQVAEALGIEIILTMLLVLAVCMGAVN 109
ENSRNOT00000019939      FGGMIGAALAKVVSPEERFWNASGAAFAIVQEQEQVAEALGVEIVMTMLLVLAVCMGAVN 180
ENST00000219660         LGGMLGAALAKAVSPEERFWNASGAAFVTVQEQGQVAGALVAEIILTTLLALAVCMGAIN 178
ENSGALT00000009629      CGGILGAALTKAVASSLNFDSRVGGAFGIIRTNAQIGPALGNEIILTTFLLLVVCMTAVN 173
                         **::****:*.*:.. .* .  *.**  :: : *:. **  **::* :* *.*** *:*

ENSMUST00000033023      EKTMGPLAPFSIGFSVIVDILAGGSISGACMNPARAFGPAVMAGYWDFHWIYWLGPLLAG 238
ENSMUST00000098056      EKTMGPLAPFSIGFSVIVDILAGGSISGACMNPARAFGPAVMAGYWDFHWIYWLGPLLAG 169
ENSRNOT00000019939      EKTMGPLAPFSIGFSVIVDILAGGGISGACMNPARAFGPAVMAGYWDFHWIYWLGPLLAG 240
ENST00000219660         EKTKGPLAPFSIGFAVTVDILAGGPVSGGCMNPARAFGPAVVANHWNFHWIYWLGPLLAG 238
ENSGALT00000009629      GETKSPLAPVCIALTVVINIIVGGSISGPCMNPARAFGPAVIANYWLYHWVYWVGPLIGC 233
                         :* .****..*.::* ::*:.** :** ************:*.:* :**:**:***:. 

ENSMUST00000033023      LFVGLLIRLLIGDEKTRLILKSR 261
ENSMUST00000098056      LFVGLLIRLLIGDEKTRLILKSR 192
ENSRNOT00000019939      LFVGLLIRLFIGDEKTRLILKSR 263
ENST00000219660         LLVGLLIRCFIGDGKTRLILKAR 261
ENSGALT00000009629      LISSLLIRFVIGDRKIRLFLK-- 254
                        *: .**** .*** * **:**  
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AQP9 - CLUSTAL W (1.83) multiple sequence alignment


ENSMUST00000113569      --------------------MPSEKDRAKKNLVQRLALKSCLAKETLSEFLGTF------ 34
ENSMUST00000113570      --------------------MPSEKDRAKKNLVQRLALKSCLAKETLSEFLGTF------ 34
ENSMUST00000074465      --------------------MPSEKDRAKKNLVQRLALKSCLAKETLSEFLGTF------ 34
ENSMUST00000060917      MAWQFYLFVCLFVYLFIYVCAPMHTSASENGLLESALLPPSFHHVDSRDGAQVIRPGNRD 60
ENSRNOT00000021442      --------------------MPSEKDGAKKSLMQRLALKSRIAKETLSEFLGTF------ 34
ENST00000219919         --------------------MQPEGAEKGKSFKQRLVLKSSLAKETLSEFLGTF------ 34
ENSGALT00000006776      ------------------------------------------------------------
ENSGALT00000039255      -------------------EEAKMSRKNKRSLKEKFALKNSLVKEALSEFLGTF------ 35


ENSMUST00000113569      IMIVLGCGSIAQAVLSREKAGGIITINIGFATAVVMA-LYATFGVSGGHINPAVSFAMCT 93
ENSMUST00000113570      IMIVLGCGSIAQAVLSREKAGGIITINIGFATAVVMA-LYATFGVSGGHINPAVSFAMCT 93
ENSMUST00000074465      IMIVLGCGSIAQAVLSREKAGGIITINIGFATAVVMA-LYATFGVSGGHINPAVSFAMCT 93
ENSMUST00000060917      FYLVLGCGSIAQAVLSREKAGGIITINIGFATAVVMA-LYATFGVSGGHINPAVSFAMCT 119
ENSRNOT00000021442      IMIVLGCSSIAQAVLSRERFGGIITINIGFASAVVMA-LYVTFGISGGHINPAVSFAMCA 93
ENST00000219919         ILIVLGCGCVAQAILSRGRFGGVITINVGFSMAVAMA-IYVAGGVSGGHINPAVSLAMCL 93
ENSGALT00000006776      ----------------------------GSSIAVYTCGVYVGGNFSGGHINPAVSLAMCV 32
ENSGALT00000039255      IMITLGCGCVGQAVLSRGAHGGPMTISVGFAMAVTTA-VYVSGGVSGGHINPAVSLAMCV 94
                                                    * : **  . :*.  ..**********:***

ENSMUST00000113569      FGRMEWFKFPFYVGAQLLGAFVGAATVFGIYYDGLMAFADGKLLITGENGTAFIFATYPK 153
ENSMUST00000113570      FGRMEWFKFPFYVGAQLLGAFVGAATVFGIYYDGLMAFADGKLLITGENGTAFIFATYPK 153
ENSMUST00000074465      FGRMEWFKFPFYVGAQLLGAFVGAATVFGIYYDGLMAFADGKLLITGENGTAFIFATYPK 153
ENSMUST00000060917      FGRMEWFKFPFYVGAQLLGAFVGAATVFGIYYDGLMAFADGKLLITGENGTAFIFATYPK 179
ENSRNOT00000021442      FGRMEWFKFPFYVGAQFLGAFVGAATVFGIYYDGLMAFAGGKLLVVGENATAFIFATYPA 153
ENST00000219919         FGRMKWFKLPFYVGAQFLGAFVGAATVFGIYYDGLMSFAGGKLLIVGENATAHIFATYPA 153
ENSGALT00000006776      AGRLKWTKLPIYILAQFLGAFVGAAAVFGIYHDAFMEYSNGTLEVTGPYATAHIFATYPA 92
ENSGALT00000039255      AGRLKWTKLPIYILAQFLGAFVGAAAVFGIYHDAFMEYSNGTLEVTGPYATAHIFATYPA 154
                         **::* *:*:*: **:********:*****:*.:* ::.*.* :.*  .**.******

ENSMUST00000113569      PFVSVPGAFVDQSP---------------------------------------------- 167
ENSMUST00000113570      PFVSVPGAFVDQVVSTMFLLLIVFAIFDSRNLGVPRGLEPIVIGLLIIVISCSLGLNSGC 213
ENSMUST00000074465      PFVSVPGAFVDQVVSTMFLLLIVFAIFDSRNLGVPRGLEPIVIGLLIIVISCSLGLNSGC 213
ENSMUST00000060917      PFVSVPGAFVDQVVSTMFLLLIVFAIFDSRNLGVPRGLEPIVIGLLIIVISCSLGLNSGC 239
ENSRNOT00000021442      PFISTPGAFVDQVVSTMFLLLIVFAMFDSRNLGVPRGLEPVVIGLLIIVLSCSLGLNSGC 213
ENST00000219919         PYLSLANAFADQVVATMILLIIVFAIFDSRNLGAPRGLEPIAIGLLIIVIASSLGLNSGC 213
ENSGALT00000006776      PYLSLINGFADQVMSTAVLLLVIFAIFDTRNNRVPKGLEPVVVGLLIIVLTCSLGMNSGC 152
ENSGALT00000039255      PYLSLINGFADQVMSTAVLLLVIFAIFDTRNNRVPKGLEPVVVGLLIIVLTCSLGMNSGC 214
                        *::*  ..*.**

ENSMUST00000113569      --------WPRRITHIKGS-----------------SRILSAIRG--------------- 187
ENSMUST00000113570      AMNPARDLSPRLFTALAGWGFEVFTFGNNFWWIPVVGPMIGAVLGGLIYVLFIQMHHSNP 273
ENSMUST00000074465      AMNPARDLSPRLFTALAGWGFEVFTFGNNFWWIPVVGPMIGAVLGGLIYVLFIQMHHSNP 273
ENSMUST00000060917      AMNPARDLSPRLFTALAGWGFEVFTFGNNFWWIPVVGPMIGAVLGGLIYVLFIQMHHSNP 299
ENSRNOT00000021442      AMNPARDLSPRLFTALAGWGFEVFTVGNNFWWIPVVGPMIGAFLGGLIYILFIQMHHSKL 273
ENST00000219919         AMNPARDLSPRLFTALAGWGFEVFRAGNNFWWIPVVGPLVGAVIGGLIYVLVIEIHHPEP 273
ENSGALT00000006776      AMNPARDLGPRLFTAIAGWGMEVFTAGNNWWWVPIVAPMLGGVLGALTYIIFIEVHHSD- 211
ENSGALT00000039255      AMNPARDLGPRLFTAIAGWGMEVFTAGNNWWWVPIVAPMLGGVLGALTYIIFIEVHHSD- 273
                                 ** :* : *                  . ::... *

ENSMUST00000113569      ---VEHRP-------------- 192
ENSMUST00000113570      DPEVKAEPAENNLEKHELSVIM 295
ENSMUST00000074465      DPEVKAEPAENNLEKHELSVIM 295
ENSMUST00000060917      DPEVKAEPAENNLEKHELSVIM 321
ENSRNOT00000021442      DPDMKAEPSENNLEKHELSVIM 295
ENST00000219919         DSVFKTEQSEDKPEKYELSVIM 295
ENSGALT00000006776      ---NQQGEENDVYDKYELTNM- 229
ENSGALT00000039255      ---NQQGEENDVYDKYELTNM- 291
                            :
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AQP10 - CLUSTAL W (1.83) multiple sequence alignment


ENST00000324978      MVFTQAPAEIMGHLRIRSLLARQCLAEFLGVFVLMLLTQGAVAQAVTSGETKGNFFTMFL 60
ENST00000355197      MVFTQAPAEIMGHLRIRSLLARQCLAEFLGVFVLMLLTQGAVAQAVTSGETKGNFFTMFL 60
                     ************************************************************

ENST00000324978      AGSLAVTIAIYVGGNVSGAHLNPAFSLAMCIVGRLPWVKLPIYILVQLLSAFCASGATYV 120
ENST00000355197      AGSLAVTIAIYVGGNVSGAHLNPAFSLAMCIVGRLPWVKLPIYILVQLLSAFCASGATYV 120
                     ************************************************************

ENST00000324978      LYHDALQNYTGGNLTVTGPKETASIFATYPAPYLSLNNGFLDQVLGTGMLIVGLLAILDR 180
ENST00000355197      LYHDALQNYTGGNLTVTGPKETASIFATYPAPYLSLNNGFLDQVLGTGMLIVGLLAILDR 180
                     ************************************************************

ENST00000324978      RNKGVPAGLEPVVVGMLILALGLSMGANCGIPLNPARDLGPRLFTYVAGWGPEVFSAGNG 240
ENST00000355197      RNKGVPAGLEPVVVGMLILALGLSMGANCGIPLNPARDLGPRLFTYVAGWGPEVFRWET- 239
                     *******************************************************   .

ENST00000324978      WWWVPVVAPLVGATVGTATYQLLVALHHPEGPEPAQDLVSAQHKASELETPASAQMLECK 300
ENST00000355197      ------------DSPGAG-------LHSPS---------SAKG-----SVPGSTALCL-- 264
                                  : *:.       ** *.         **:      ..*.*: :

ENST00000324978      L 301
ENST00000355197      -
```

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AQP11 - CLUSTAL W (1.83) multiple sequence alignment


ENSRNOT00000018091      MSALLGLPPEVQDTCISLGLMLLVVLFMGLARVIARQQLH-RPMVHAFVLEFLATFQLCY 59
ENSRNOT00000038705      MSALLGLPPEVQDTCISLGLMLLVVLFMGLARVIARQQLH-RPMVHAFVLEFLATFQLCY 59
ENSMUST00000055379      MSALLGLRPEVQDTCISLGLMLLFVLFVGLARVIARQQLH-RPVVHAFVLEFLATFQLCC 59
ENSMUST00000084986      MSALLGLRPEVQDTCISLGLMLLFVLFVGLARVIARQQLH-RPVVHAFVLEFLATFQLCC 59
ENST00000313578         MSPLLGLRSELQDTCTSLGLMLSVVLLMGLARVVARQQLH-RPVAHAFVLEFLATFQLCC 59
ENSGALT00000002458      ASGTVAMAAG--GIWMSLGLMAAVVAAVGLCRSLALRRLHARPHLCSFLLELLSTFQVCA 58
                         *  :.: .   .   *****  .*  :**.* :* ::** **   :*:**:*:***:*

ENSRNOT00000018091      CTHELQLLSEQDSGHPTWTLTLIYFFSLVHGLTLVGTASNPCGVMMQMILGGMSPEMGAV 119
ENSRNOT00000038705      CTHELQLLSEQDSGHPTWTLTLIYFFSLVHGLTLVGTASNPCGVMMQMILGGMSPEMGAV 119
ENSMUST00000055379      CTHELQVLSEQDSAHPTWTLTLIYFFSLVHGLTLVGTASNPCGVMMQMILGGMSPEMGAV 119
ENSMUST00000084986      CTHELQVLSEQDSAHPTWTLTLIYFFSLVHGLTLVGTASNPCGVMMQMILGGMSPEMGAV 119
ENST00000313578         CTHELQLLSEQHPAHPTWTLTLVYFFSLVHGLTLVGTSSNPCGVMMQMMLGGMSPETGAV 119
ENSGALT00000002458      CTNELSLLGNTEP-RPHTALTLTYGFTVLHGLTLPGSTCNPCGTLQPLWGGRTSARAGGL 117
                        **:**.:*.: .. :*  :*** * *:::***** *::.****.:  :  *  *.. *.:

ENSRNOT00000018091      RLMAQLVSALCSRYCISALWSLSLTKYHFDERILACRNPINTDISKAIIIEAICSFIFHS 179
ENSRNOT00000038705      RLMAQLVSALCSRYCISALWSLSLTKYHFDERILACRNPINTDISKAIIIEAICSFIFHS 179
ENSMUST00000055379      RLLAQLVSALCSRYCISALWSLSLTKYHYDERILACRNPIHTDMSKAIIIEAICSFIFHS 179
ENSMUST00000084986      RLLAQLVSALCSRYCISALWSLSLTKYHYDERILACRNPIHTDMSKAIIIEAICSFIFHS 179
ENST00000313578         RLLAQLVSALCSRYCTSALWSLGLTQYHVSERSFACKNPIRVDLLKAVITEAVCSFLFHS 179
ENSGALT00000002458      KIWAQFAAAVLARVFMHFIWRLEMAESHLGALTQGCGNPMQTTEVQAFCIELLFSVVFQL 177
                        :: **:.:*: :*     :* * ::: * .    .* **:..   :*.  * : *.:*:

ENSRNOT00000018091      ALLHFQEVRTKLRIHVLAALITFLAYAGGSLTGALFNPALALSLHFPCFDESFYKFFVVY 239
ENSRNOT00000038705      ALLHFQEVRTKLRIHVLAALITFLAYAG-------------------------------- 207
ENSMUST00000055379      ALLHFQEVRTKLRIHLLAALITFLAYAG-------------------------------- 207
ENSMUST00000084986      ALLHFQEVRTKLRIHLLAALITFLAYAGGSLTGALFNPALALSLHFPCFDELFYKFFVVY 239
ENST00000313578         ALLHFQEVRTKLRIHLLAALITFLVYAGGSLTGAVFNPALALSLHFMCFDEAFPQFFIVY 239
ENSGALT00000002458      TILQVENIKPSYRVHAVALLITMLVFAG-------------------------------- 205
                        ::*:.::::.. *:* :* ***:*.:**

ENSRNOT00000018091      WVAPSLGVLLMILMFSFFLPWLHNNQLSNKKE 271
ENSRNOT00000038705      -------VLLMILMFSFFLPWLHNN------- 225
ENSMUST00000055379      -------VLMMILMFSFFLPWLHNNQMTNKKE 232
ENSMUST00000084986      WLAPSVGVLMMILMFSFFLPWLHNNQMTNKKE 271
ENST00000313578         WLAPSLGILLMILMFSFFLPWLHNNHTINKKE 271
ENSGALT00000002458      --------------------------------
```

AQP12 - CLUSTAL W (1.83) multiple sequence alignment

```
ENSMUST00000059676      MASLNVSLCFFFATCAICEVARRASKALLPAGTYASFARGAVGAAQLAACCLEMRVLVEL 60
ENSRNOT00000005935      MASLNVSLSFFFATCAICEVARRASKALLPAGTYASFAREAVGAAQLAACCLEMRVLVEL 60
ENSGALT00000010387      MAGLNVSIAFFFLVLGTCEAFRRLSKRLLAPGLLVCLTAELAGSLQLCSGCLELRMLLEI 60
ENST00000337801         MAGLNVSLSFFFATFALCEAARRASKALLPVGAYEVFAREA------------MRTLVEL 48
ENST00000373309         ---------------------NQPAPALSPQ----------------------------- 10
                                             .: :  * .

ENSMUST00000059676      GPWAGGFGPDLLLTLVFLLFLVHGVTFDGASANPTVALQEFLMVEASLPNTLLKLSAQVL 120
ENSRNOT00000005935      GPWAGGFGPDLLLTLVFLLFLVHGVTFDGASANPTVALQEFLMVEASLPSTLLKLLAQVL 120
ENSGALT00000010387      GPWGG-LSPDVVLTLLFLLFVVHAACANGAASNPTVSLQEFLLFECSLVATVAKLLAQCV 119
ENST00000337801         GPWAGDFGPDLLLTLLFLLFLAHGVTLDGASANPTVSLQEFLMAEQSLPGTLLKLAAQGL 108
ENST00000373309         ------------------------VSCRHSSSGGPGRWQEFLMAEQSLPGTLLKLAAQGL 46
                                                .    :::. .   ****: * **  *: ** ** :

ENSMUST00000059676      GAQAACALTQRCWAWELSELHLLQSLMAAHCSSTLRTSVLQGMLVEGACTFFFHLSLLHL 180
ENSRNOT00000005935      GAQAACALTQRCWTWELSELHLLQSLMAVHCSSTLRTSVLQGTLVEGACTFLFHLSLLHL 180
ENSGALT00000010387      GTGMGWALTKLYWSWELTQLHLIQNLMASECSSSIRTSPHLGALVEAACSFFFHLILLRV 179
ENST00000337801         GMQAACTLMRLCWAWELSDLHLLQSLMAQSCSSALRTSVPHGALVEAACAFCFHLTLLHL 168
ENST00000373309         GMQAACTLMRLCWAWELSDLHLLQSLMAQSCSSALRTSVPHGALVEAACAFCFHLTLLHL 106
                        *   . :* :  *:***::***:*.***  ***::***   * ***.**:* *** **::

ENSMUST00000059676      QHSLLVYRVPALALLVTLMAYTAGPYTSAFFNPALAASVTFHCPGNTLLEYAHVYCLGPV 240
ENSRNOT00000005935      QRSLLVYRAPALALLVTAMAYTAGPYTSAFFNPALAASVTFHCSGNTLLEYAHVYCLGPV 240
ENSGALT00000010387      RRSPAVCRVPVLAATVTFLTYVAAPATGAFFNPALATASTFLCAGSSLQDYIQVYWLGPL 239
ENST00000337801         RHSPPAYSGPAVALLVTVTAYTAGPFTSAFFNPALAASVTFACSGHTLLEYVQVYWLGPL 228
ENST00000373309         RHSPPAYSGPAVALLVTVTAYTAGPFTSAFFNPALAASVTFACSGHTLLEYVQVYWLGPL 166
                        ::*  .   *.:*  **  :*.*.* *.********:: ** *.* :* :* :** ***:

ENSMUST00000059676      AGMILAVLLHQGHLPR------LFQR-----NLFYRQKSKYRTPRGKLSPG--------- 280
ENSRNOT00000005935      AGMILAVLLHQGHLPR------FFER-----NLFYRQKSKYRTPRVKLSPG--------- 280
ENSGALT00000010387      AGMLAALLLYQGNIPR------FFQK-----NLLYGQKSKYKIPKARVMHA--------- 279
ENST00000337801         TGMVLAVLLHQGRLPH------LFQR-----NLFYGQKNKYRAPRGKPAPA--------- 268
ENST00000373309         TEEQHGEVMEPPLGPRSGDSGPWLQRPRWSPHLLLHLLSDTRLHLTEVPEGQLGSYGILE 226
                        :    . ::     *:       :::     :*:    .. :    .   .

ENSMUST00000059676      -------------SVDAKM-HKGE---------------- 290
ENSRNOT00000005935      -------------SVDTKM-LKGE---------------- 290
ENSGALT00000010387      -------------EDGEQQ-QKGK-----GEKSNPAPRA- 299
ENST00000337801         -------------SGDTQTPAKGSSVREPGRSGVEGPHSS 295
ENST00000373309         AFFSFCWLYTGEVSGAMPQPPLGGKDRSWGSLRHLALRW- 265
                                     .        *
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