```
CLUSTAL O(1.2.4) multiple sequence alignment


NP_003108.2         MGVLKFKHIFFRSFVKSSGVSQIVF-TF----------------LLIPCCLTLNFRAPPV    43
XP_003318802.2      MGVLKFKHIFFRSFVKSSGVSQIVF-TF----------------LLIPCCLTLNFRAPPV    43
XP_003261317.2      MGVLKFKHIFFRSFVKSNGISQIVF-TF----------------LLIPRCLTLNFRAPPV    43
XP_001086882.2      MGVLKFKHIFFRSFVKSSGVSQIVF-TF----------------LLIPCCLTLNFRAPPI    43
NP_001076141.2      MGVLKFKHIFFGSAVEFNRAFQILY-IF----------------LLIPCCLTANFRAPPV    43
XP_002919069.1      MAVLRFQRIFFRSFVGSRGATPVVL-TF----------------LLIPCCLTQEFRAPPF    43
NP_999176.1         MGVQRLQHISFRSFFVPSGAPQVVF-TF----------------LLIPCCLALDFRASPI    43
XP_002686960.3      --MLRHQHISFRNFVGSNGAPQAVF-TF----------------LLVPCCLALNFTAPPL    41
NP_001008413.3      MRMLRRHHISFRSFAGSSGTPQAVF-TF----------------LLLPCCLALDFRAPPL    43
XP_003502178.1      MRVLCLKHSFSGSFLESNGAPQTVL-VF----------------LLLPCCLTGDFRAPPL    43
NP_001166492.1      MGAFTFKHSFFGSFVECSGVLQTVF-IF----------------LLIPCCLA-DKRAPPL    42
NP_001019492.1      MRVLCFKHSFFGSLLESSGLPQTLL-VF----------------LLIRCCLTVDFRAPPL    43
XP_001507937.2      ----RLPHLSSGSWAVCCQASWVAV-VL----------------QLLPWCMALDIQAPPM    39
NP_001073344.1      MGELRFKHLFWGSFVESGGTFQTVL-IF----------------LLIPCSLTVDYRAAPI    43
XP_003502177.1      MGGLPLKHLFWGSFVVSRATFQTVLIIF----------------LLIPCSLTVDYRGGPL    44
XP_002190553.4      -------------------ASGVVF-AT----------------LLVSCCSSLNIRARPL    24
XP_002932242.3      MERVNCEHILYKKLL--------CILCS----------------FLIHTCQSMDMKAPTN    36
NP_001082194.1      -----FQHVLCKKCI--------CILLF----------------CFITSCQSMDIKAPTN    31
XP_002919077.1      MKVLSEGQLRFCVVQPIHLTSC--LVIF----------------IILKSISSLKPARLPI    42
XP_002712114.1      ----------------------------------------------------------PI    2
XP_532444.4         ------------------------LLIF----------------FILKSISSLKPARLPI    20
XP_002818436.2      ----------------------------------------------------------PI    2
NP_084124.1         ----------------------------------------------------------PV    2
XP_003134772.2      ------------------------LLIF----------------FILKSISSLKPARLPV    20
NP_036401.2         ----------------------------------------------------------PI    2
XP_003261316.2      MKVLSEGHLRLCVVQPVHLTSW--LLIF----------------FILKSISCLKPAQLPI    42
XP_003407292.1      -------------------SSW--LLIF----------------FILKSISSLKPARLPI    23
XP_003586042.1      ------------------------LFIL----------------FILKSISSLKPARLPV    20
NP_001094250.1      ----------RCVVQPVHLTSG--LLIF----------------FILKSISSLKPARLPV    32
XP_003221368.2      ----------------------------------------------------------PI    2
XP_003475093.1      -------------IQSIHLTPW--LLVF----------------LSLKSVCSLKPARLPL    29
NP_001090796.1      ----------------------------------------------------------PF    2
XP_003221369.1      ----------------------------------------------------------PL    2
XP_003449274.1      ----------------------------------------------------------PL    2
NP_001074140.1      ----------------------------------------------------------PL    2
XP_003217669.1      ----------------------------------------------------------PI    2
XP_001507903.3      -------------------LSW--LLIS----------------FLLELTSSLKPAQHPI    23
XP_003449275.2      ---------------------------------------------------------PPL    3
XP_001378617.3      --------------------------------------------------------APPI    4
XP_003210019.2      --------------------------------------------------------AAPL    4
XP_414258.3         ---------------------------LVPA-----------VLAVLARQSPEKPSAAPL    22
NP_001080777.1      ----------------------------------------------------------PV    2
NP_001119986.1      -------------------------LSFLPA--FLWLFLGAAANGQLSDSWLNKPTFRPV    33
XP_003221370.3      --------------------------------------------FMLVDGSTAMPTRAPL    16
XP_003448364.1      ---------------------------LLIV--PLWDCL---------FALGLKPTRWPL    22
XP_002189602.4      ----------------------------------------------------------PV    2
NP_001074154.2      ------------------------------------------------------------    0
XP_003448436.2      ----------------------------VL---LHL--------ILISLVSGLHYPNSP-    20
XP_002813763.3      -----------------------------LA--VAW-------------AMELKPTAPPI    16
XP_002935681.1      ---------------------------------YTF--------LLSGLLGWLAAGTDPV    19
XP_001168599.1      -----------------------------LA--VAW-------------AMELKPTAPPI    16
XP_687640.2         ---------HLSGTTRTQRASW--LQVLLLM--LFWTCL---------KAQQLKNTRWPL    38
NP_003764.3         -----------------------------LA--VSW-------------AMELKPTAPPI    16
XP_003476739.1      -----------AGLGPI----V--TLALVLP--VAW-------------AMELKPTGPPI    28
XP_003257153.1      -----------------------------LA--VAW-------------AMELKPTAPPI    16
XP_002758427.1      -----------------------------LV--VAW-------------AMELKPTAPPI    16
XP_001102414.2      ----------------------------------------------------------PL    2
NP_742037.2         --------------------------------------------------------APPI    4
NP_999605.1         -----------------------------LA--VAW-------------ATELKPTAPPI    16
NP_001009754.1      -----------------------------LV--VAW-------------ATELKPTAPPI    16
NP_083196.2         ---------------------------------VLF--------VLLVAPAALKPAMPPV    19
NP_001019491.1      ---------------------------------------------------------PPV    3
NP_776772.1         -----------------------------LV--VAW-------------ATELKPTAPPI    16
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NP_149349.2         ---------------------------LLP---ICA--------LFLTLLDMAQGFRGPL    22
NP_001035086.1      ----------------------------------------------------------P-    1
XP_003502176.1      ---------------------------------------------------------PPV    3
XP_003257149.1      ----------------------------------------------------------PL    2
XP_002813766.6      ----------------------------------------------------------PL    2
NP_001017941.1      ---------------------------LLP---VCT--------LFLNLLSMTQGSRDPV    22
XP_002920567.1      ----------------------------------------------------------PM    2
XP_003476738.1      ----------------------------------------------------------PV    2
NP_999606.1         ---------------------------LLP---ICT--------LFLNLLSVAQGSRDPV    22
XP_002713406.3      -----------------------------------------------------------T    1
XP_003500449.1      -----------------------------------------------------------T    1
XP_001509131.1      ----------------------------------------------------------PV    2
XP_001139800.4      ---------------------------------------------------------PPV    3
NP_032343.3         -----------------------------------------------------------V    1
NP_997499.2         -----------------------------------------------------------M    1
XP_001168796.1      ---------------------------LLP---ICA--------LFLTLLDMAQGFRGPL    22
NP_997482.2         ----------------ITQLGL--TLVV------------------GLTLCLVHVQALLQ    24
NP_001193181.1      ------------------------------------------------------------    0
NP_001186958.1      -------------------------LVL------------------GVALCLGCGQPLPQ    17
NP_999604.1         ------------------------------------------------------------    0
XP_001493753.3      ------------------------------------------------------------    0
NP_001121765.1      -----------------------------------------------------------V    1
NP_821139.2         ------------------------------------------------------------    0
XP_002128103.1      -------------------MSF--SYVFLALGILGSVCHSQSLQS-YLTTSLKDNIWQPP    38
XP_003642042.3      ------------------------------------------------------------    0


NP_003108.2         IPNVPFLWAWNAPSEFCLG-KFDEPLD---MS-LFSFIGSPRINATGQGVTIFYVDRLGY    98
XP_003318802.2      IPNVPFLWAWNAPSEFCLG-KFDEPLD---MS-LFSFIGSPRINVTGQDVTIFYVDRLGY    98
XP_003261317.2      IPNVPFLWAWNAPSEFCLG-KFDEPLD---MS-LFSLTGSPRINVTGQGVTIFYVDRLGY    98
XP_001086882.2      IPNVPFLWAWNAPSEFCLG-KFNEPLD---MS-LFTLMGSPRINITGQGVTIFYVDRLGY    98
NP_001076141.2      IPNVPFLWAWNAPTELCLG-KSGEPLD---TS-LFSLFGSPSKDKTGQGITIFYVDRLGY    98
XP_002919069.1      IPNVSFLWGWNAPTELCAQ-KFNVQLD---LN-LFSLIGSPQKSATGQGITLFYANRLGY    98
NP_999176.1         IPNTTFLWVWNAPTESCAK-KFYMPPD---LS-LFSFVTSPRASVTGQFLTLFYANRLGY    98
XP_002686960.3      IPNIPFLWAWNAPTNHCAE-IFSMPPD---LG-LFSLVGSPQKDVTGQPITLFYADRLGY    96
NP_001008413.3      ISNTSFLWAWNAPVERCVNRRFQLPPD---LR-LFSVKGSPQKSATGQFITLFYADRLGY    99
XP_003502178.1      IPNVPFLWVWNAPTESCLT-KFNEPLD---LS-LFSLVGSPKKSATGQPITIFYTDRLGF    98
NP_001166492.1      IPNVPLLWVWNAPTEFCIG-GTNQPLD---MS-FFSIVGTPRKNITGQSITLYYVDRLGY    97
NP_001019492.1      IPNVPFLCAWNAPTESCAT-RFNQPLD---LS-LFSLVGSPRKTAIGHPVTIFYSDRLGL    98
XP_001507937.2      IPNLPFLSAWNAPTELCAQ-KHDVELD---MS-LFSLVGSTRQEIKGQNITLFYTDRLGY    94
NP_001073344.1      LSNTTFLWIWNVPTERCVG-NVNDPID---LS-FFSLIGSPRKTATGQPVTLFYVDRLGL    98
XP_003502177.1      LPSEILIWVWNVPTEACIG-NFSHSID---LS-LFPIVGSPRKTATGQPVTLFYVDRLGY    99
XP_002190553.4      LSNSPFLSIWNAPTELCTE-RTGVQLD---MN-FFPLIGSTLKTSVGQNITLFYPDRIGY    79
XP_002932242.3      GP-ANFMAIWNAPTELCMR-KFKVNID---IS-LFQITGSPESSTIAQNITIFYTDRLGY    90
NP_001082194.1      GL-SNFMAIWNAPTELCLQ-KFKVKID---VS-LFQIVGTTFNSSIAQNITIFYTDRLGH    85
XP_002919077.1      YQRKPFIAAWNAPTDQCLI-KYNIGLN---LK-MFQVIGSPLAKARGQNVTIFYVNRLGY    97
XP_002712114.1      YQRKPFIAAWNAPTDQCLM-KYNLKLN---LK-MFQVIGSPLAKARGQNVTIFYVNRLGY    57
XP_532444.4         YQRKPFIAAWNAPTDQCLI-KYNIGLN---LK-MFQVIGSPLAKARGQNITIFYVNRLGY    75
XP_002818436.2      YQRKPFIAAWNAPTDQCLI-KYNLRLN---LK-IFPVIGSPLAKARGQNVTIFYVNRLGY    57
NP_084124.1         YQRKPFIAAWNAPTDLCLI-KYNLTLN---LK-VFQMVGSPRLKDRGQNVVIFYANRLGY    57
XP_003134772.2      YQRKPFIAAWNAPTDQCLI-KYNVRLN---LK-MFQVIGSPLARARGQNVTIFYVNRLGY    75
NP_036401.2         YQRKPFIAAWNAPTDQCLI-KYNLRLN---LK-MFPVIGSPLAKARGQNVTIFYVNRLGY    57
XP_003261316.2      YQRKPFIAAWNAPTDQCLI-KYNLRLN---LK-MFPVIGSPLAKARGQNVTIFYVNRLGY    97
XP_003407292.1      YQRKPFIAAWNAPTDQCLI-KYNIRLN---LK-MFQVVGSPLAKARGQNVTIFYVNRLGY    78
XP_003586042.1      YQRKPFIAAWNAPTDQCLI-KYNIRLN---LK-MFQVIGSPLARARGQNVTIFYVNRLGY    75
NP_001094250.1      YQRKPFIAAWNAPTDLCLI-KYNLAVN---LK-VFQMVGSPRLKDRRQNVVIFYANKLGS    87
XP_003221368.2      SRRKPFIAAWNAPTDHCSI-RYNVTIN---LK-MFHVIGSPFAKARGQNVTIFYVNRLGY    57
XP_003475093.1      YQRKPFIAAWNTPTDQCLM-KYKLRLN---LE-MFQVAGSTLTKARGQNVTIFYPRRLGY    84
NP_001090796.1      IQNKPFLAVWNAPTEQCKQ-RYKVDLD---LS-IFDIVANPNETLIGSNVTIFYHTHLGH    57
XP_003221369.1      FPNKAFVVVWNAPTEQCRL-RYDVDLD---LN-VFNVLSNPNETLSGPTVTIFYHTRLGY    57
XP_003449274.1      IGRKPFIAAWNAPLDLCTF-RYNITTN---VNHLFHIQGSPRADWTGQNVTIFYANRLGY    58
NP_001074140.1      LPHRPFVVVWNAPTESCRL-RFKVDLD---LS-VFDIVANHNETLSGPNVTIFYHSHLGY    57
XP_003217669.1      FTRRPFIVAWNVPSQDCQP-RFKVQLD---FS-IFDLQASPNEGFVDQNLTIFYKERLGL    57
XP_001507903.3      FQKKPFVAVWNAPTDQCLF-QYNTGIN---LR-TFHITGSPLAKARGQNVTIFFVNRLGY    78
XP_003449275.2      IPHKPFVVVWNAPTESCRL-RFKVDLD---LS-IFDIVANLNETLSGPNVTIFYHSHLGY    58
XP_001378617.3      FTRRPFLVAWNAPTQDCWP-RFRVSLN---FS-VFDVKASPNEGFVNQNLTIFYRDRLGY    59
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XP_003210019.2      LTRRPFLVAWNAPTQDCKP-RFQVALD---FS-IFDLHASPNEGFVDQNLTIFYKERLGL    59
XP_414258.3         LTRRPFLVAWNAPTQDCKP-RFQVALD---FS-VFDLQASPNEGFVDQNLTIFYKERLGL    77
NP_001080777.1      FTRRPFIIAWNAPTQDCPP-RFNVHLD---LK-LFDLNASPNEGFVDQNLTIFYKERLGM    57
NP_001119986.1      FTRRPFIIAWNAPTQDCPP-RFNVHLD---LK-LFDLNASPNEGFVDQNLTIFYKERLGM    88
XP_003221370.3      FSKKAFVVVWNAPTEQCRL-RYSVDLD---LK-IFNILSNPNESLNGPIVTIFYANRLGF    71
XP_003448364.1      YSRKPLLLAWNAPIEDCAP-RHKIRFQ---LD-QFQIVATPNEGFVNQNLTIFYKERLGL    77
XP_002189602.4      LVNRPFVTIWNIPTERCAE-KYNVSLS---LE-VFDVLANDQQSFTGQDITLFYSDKIGL    57
NP_001074154.2      ----PFVLLWNAPISKCHQ--LKVPLD---LS-LFQAVTTPAR-VHNQSLSLFYKTRLGL    49
XP_003448436.2      FSKVPFLTVWNAPSANCLS-QYGVDLD---LG-MFNIVQNQNQTFMGQNITIFYAEKLGL    75
XP_002813763.3      FTGRPFVVAWDVPTQDCGP-RLKVPLD---LN-AFDVQASPNEGFVNQNITIFYRDRLGL    71
XP_002935681.1      LKGRPFASVWNAPTSPCLD-RFGVTLD---LS-AFDIVLNQNHTFQGSEVVIFYSSQLGF    74
XP_001168599.1      FTGRPFVVAWDVPTQDCGP-RLKVPLD---LN-AFDVQASPNEGFVNQNITIFYRDRLGL    71
XP_687640.2         YSGKPLLLAWNAPTEDCRP-RHDVTFQ---LD-QFQIVASPNEGFTKQNLTIFYQDRLGL    93
NP_003764.3         FTGRPFVVAWDVPTQDCGP-RLKVPLD---LN-AFDVQASPNEGFVNQNITIFYRDRLGL    71
XP_003476739.1      FTGRPFVVAWDVPTQDCGP-RHKVSLD---LK-AFDVQASPNEGFVNQSITIFYYDRLGL    83
XP_003257153.1      FTGRPFVVAWDVPTQDCGP-RLKVPLD---LN-AFDVQASPNEGFVNQNITIFYRDRLGL    71
XP_002758427.1      FTGRPFVVAWDVPTQDCGP-RLKVPLD---LN-AFDVQASPNEGFVNQNITIFYRDRLGL    71
XP_001102414.2      LPNRPFATVWNANTQWCLE-RHSVDVD---VS-IFDVVANPGQTFRGPDMTIFYSSQLGT    57
NP_742037.2         FTGRPFVVAWNVPTQECAP-RHKVPLD---LR-AFDVEATPNEGFFNQNITTFYYDRLGL    59
NP_999605.1         FTGRPFVVAWDVPTQDCGP-RHKVPLDPKDMK-AFDVQASPNEGFVNQNITIFYRDRLGM    74
NP_001009754.1      FTGRPFVVAWDVPTQDCGP-RHKMPLDPKDMK-AFDVQASPNEGFVNQNITIFYRDRLGM    74
NP_083196.2         IKDHPFNVFWAAPTLFCKD-NFNVNMN---LQ-VFNIIPNPFETQSGSTITVFYPKELGY    74
NP_001019491.1      IKNQPFNIFWAAPTLFCKD-NFDVNMN---LQ-AFNIIPNPFETQSGSTIAVFYPKELGY    58
NP_776772.1         FTGRPFVVAWDVPTQDCGP-RHKMPLDPKDMK-AFDVQASPNEGFVNQNITIFYRDRLGM    74
NP_149349.2         LPNRPFTTVWNANTQWCLE-RHGVDVD---VS-VFDVVANPGQTFRGPDMTIFYSSQLGT    77
NP_001035086.1      LIKLPFISIWNAPTERCKS-RFGVELD---LS-VFDIVHNPNQTFMGDNITIFYSDKLGK    56
XP_003502176.1      IKDQPFNIFWAAPTFFCQE-RFGVNMN---LQ-VFGIIPNPLETQSGSTIAIFYPDELGY    58
XP_003257149.1      LPNRPFTTVWNANTQWCLE-RHGVDVD---VS-VFDVVANPGQTFRGPDMTIFYSSQLGT    57
XP_002813766.6      LPNRPFTTVWNANTQWCLE-RHGVDVD---VS-VFDVVVNPGQTFRGPDMTIFYSSQLGT    57
NP_001017941.1      VPNQPFTTIWNANTEWCMK-KHGVDVD---IS-IFDVVTNPGQTFRGPNMTIFYSSQLGT    77
XP_002920567.1      VPNQPFTTIWNANTQWCLE-KYGVDVD---VS-VFDVVANPGQTFRGPDMTIFYSYQLGT    57
XP_003476738.1      VPNQPFITVWNADTQRCLK-NYSVDVD---VS-VFDVVANPGQTFFGPNMTIFYSSKLGT    57
NP_999606.1         VLNRPFTTIWNANTQWCLK-RHGVDVD---VS-VFEVVVNPGQTFRGPNMTIFYSSQLGT    77
XP_002713406.3      VPPKPFTTVWNADTQWCLE-MHGVDVD---VS-VFDVVVNPRQAFRGPNVTIFYSSQLGT    56
XP_003500449.1      VPNKPFITIWNADTYWCLK-NYGVDVD---VS-VFDVIANKEQSFQGPNVTIFYSWQLGT    56
XP_001509131.1      VPNHPFTTIWNADTHTCLE-KFHVDVD---LD-VFDVVANPGEAFMGREMTIFYSNKLGL    57
XP_001139800.4      IKSQPFNIFWAAPTMYCMP-FFNMAIN---LQ-VFNIISNPLETQSGSKIAIFYPNELGY    58
NP_032343.3         VSNRPFITVWNGDTHWCLT-EYGVDVD---VS-VFDVVANKEQSFQGSNMTIFYREELGT    56
NP_997499.2         VSNRPFITVWNADTHWCLK-DHGVDVD---VS-VFDVVANKEQNFQGPNMTIFYREELGT    56
XP_001168796.1      LPNRPFTTVWNANTQWCLE-RHGVDVD---VS-VFDVVANPGQTFRGPDMTIFYSSQLGT    77
NP_997482.2         VPELPFSVLWNVPSARCKT-RFGVHLP---LD-ALGIIANHGQRFHGQNITIFYKNQFGL    79
NP_001193181.1      -PARPFSVLWNVPSARCKN-RFGVPLP---LE-ALGISANRGQHFHGQNVTIFYKNRLGF    54
NP_001186958.1      VPERPFSVLWNVPSAHCEA-RFGVHLP---LN-ALGIIANRGQHFHGQNMTIFYKNQLGL    72
NP_999604.1         -PERPFCVLWNVPSARCKA-RFGVHLP---LE-ALGITANHGQRFHGQNITIFYKSQLGL    54
XP_001493753.3      -PECPFSVLWNVPSAHCKA-RFGVHLP---LE-ALGITANCGQRFHGQKITIFYKNQLGL    54
NP_001121765.1      IGRRGFQVIWNVPTARCQR-RYGVSLP---LQ-QYNIIHNSHQRFQGQNMSIFYQRRLGL    56
NP_821139.2         VPEHPFSVVWNVPSARCKA-HFGVHLP---LD-ALGIVANHGQHFHGQNISIFYKNQFGL    55
XP_002128103.1      LPDRPFIGVWNVDSNRCLT-KYNVPID---LS-SFDIIHNPNEEYVGNQMVIFYAALLGL    93
XP_003642042.3      ----PFAVLWNIPSSRCQR-RFGVGLP---LA-DYGIVENRGGRFAGQNITIFYKNKFGL    51
                         :   *      *                      .         :  ::   :*

NP_003108.2         YPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYMPV-DNLGMAVIDWEEWRPTWARN    157
XP_003318802.2      YPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYMPV-DNLGMAVIDWEEWRPTWARN    157
XP_003261317.2      YPYIDSITGVTVNGGIPQKISLQDHLDKAKQDITFYMPV-DNLGMAVIDWEEWRPTWARN    157
XP_001086882.2      YPYIDLTTGVTVHGGIPQKVSLQDHLDKSKQDILFYMPV-DNLGMAVIDWEEWRPTWARN    157
NP_001076141.2      YPHIDSK-NVSVHGGIPQLGPLQQHLDKAKKDILYYMPT-DNVGLAVIDWEEWRPTWLRN    156
XP_002919069.1      YPHIDEKTGKNVNGGIPQSGNLKKHLEKAKKDIAYYIQT-DSIGLAVIDWENWRPIWVRN    157
NP_999176.1         YPHVDENTGKNVNGGIPQLGSLQRHLDKAEKDILHYMQI-DKVGLSVIDWENWRPTWERN    157
XP_002686960.3      YPKINERTGVHKNGGIPQVASLKKHLDKAEKDIAYYMPI-DNVGLAVIDWENWRPTWVRN    155
NP_001008413.3      YPHIDEKTGKTVFGGIPQLGNLKSHLEKAKNDIAYYIPN-DSVGLAVIDWENWRPTWARN    158
XP_003502178.1      YPHIDDS-NKSIHGGVPQLGSLKSHLEKARDDIQYYMPI-DNVGLAVIDWEDWRPTWSRN    156
NP_001166492.1      YPYIDPHTGAIVHGGLPQLMNLQQHLRKSRQDILFYMPT-DSVGLAVIDWEEWRPTWTRN    156
NP_001019492.1      YPHIDEM-HTAFHGGIPQLGSLKSHLEIAKGDIHHYMPI-DNVGLAVIDWEDWRPTWSRN    156
XP_001507937.2      YPYIDEVTGKSVNTGLPQLCPLDLHLTKAKEDIVNYMPSAEKSGLAVIDWENWRPLWIRN    154
NP_001073344.1      YPHIDAN-QAEHYGGIPQRGDYQAHLRKAKTDIEHYIPD-DKLGLAIIDWEEWRPTWLRN    156
XP_003502177.1      YPHLDTK-LAEHHGGIPQLGNLKNHLDKSKTDIEHYIPV-DKFGLAVIDWEEWRPTWMRN    157
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199	XP_002190553.4	YPYKNEITGEAFNGGLPQLSLLENHLKKAREDIQFYIPSDEQLGLAVIDWENWRPVWIRN	139
200	XP_002932242.3	YPSINETNGKITNGGIPQLTNMDFHLKKVKEDIEYYLPYSKQNGLAVIDWEDWRPIWIRN	150
201	NP_001082194.1	YPSINETNGKISKGGIPQLTNMAFHLKKAKEDIEYYLPSSKQHGLAVIDWEEWRPLYTRN	145
202	XP_002919077.1	YPWYTSQ-GVPINGGLPQNISLQVHLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWARN	156
203	XP_002712114.1	YPWYTSE-GVPINGGLPQNISLQVHLEKADQDINYYIPAKDFSGLAVIDWEYWRPQWARN	116
204	XP_532444.4	YPWYTSQ-GVPINGGLPQNISLQVHLEKADQDINYYIPAEDFNGLAVIDWEYWRPQWARN	134
205	XP_002818436.2	YPWYTSQ-GVPINGGLPQNISLQAHLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWARN	116
206	NP_084124.1	YPWYTSE-GVPINGGLPQNTSLQVHLKKAAQDINYYIPSENFSGLAVIDWEYWRPQWARN	116
207	XP_003134772.2	YPWYTAQ-GVPINGGLPQNISLQVHLEKADQDINYYIPSEDFSGLAVIDWEYWRPQWARN	134
208	NP_036401.2	YPWYTSQ-GVPINGGLPQNISLQVHLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWARN	116
209	XP_003261316.2	YPWYTSQ-GVPINGGLPQNISLQVHLEKADQDINYYIPSEDFSGLAVIDWEYWRPQWARN	156
210	XP_003407292.1	YPWYTSQ-GVPINGGLPQNISLQVHLEKADQDINYYIPAEDFSGLAVIDWEYWRPQWARN	137
211	XP_003586042.1	YPWYTPQ-GVPINGGLPQNISLQVHLEKADQDIRYYIPSEDFSGLAVIDWEYWRPQWARN	134
212	NP_001094250.1	YPWYTSE-GVPINGGLPQNTSLQVHLEKAYQDINYYIPSENFSGLAVIDWEYWRPQWARN	146
213	XP_003221368.2	YPWYTSQ-DVPVNGGLPQNFSLQTHLEKASEDINYYIPDEDFTGLAVIDWEHWRPQWERN	116
214	XP_003475093.1	YPWYTSQ-GVPINGGLPQNTSLKVHLKKVDQDIKYYIPVKDFRGLAVIDWEYWRPQWDRN	143
215	NP_001090796.1	YPYFTDE-GEPVNGGVPQNESLKKHLNKSEHDINRLIPNLDFKGLGVVDWENWRPQWDRN	116
216	XP_003221369.1	YPYFNDN-GDSINGGIPQNQSIIKHLNKAKSDIDHFITMKKFQGLGVIDWENWRPQWDRN	116
217	XP_003449274.1	YPHYTPH-GKAVFGGLPQNCSLDRHLFKAYQDINHFIPAEDFRGLAVIDWEFWRPQWSRN	117
218	NP_001074140.1	YPYYTSS-ETPINGGLPQNQSLSKHLSKARADIDKLIPIKDFHGLGVIDWENWRPQWVRN	116
219	XP_003217669.1	YPYYNAQ-KVAVNGGVPQNSSLEEHLARLAVSISRYIRSEIKEGLAVIDWEEWRPIWIRN	116
220	XP_001507903.3	YPWYNAQ-EDPINGGLPQNASLQTHLIKANQDIRHYISAEDFRGLAMIEWEYWRPQWSCN	137
221	XP_003449275.2	YPYYSNS-GIPINGGLPQNQSISKHLGKARSDIDKLIPHKDFRGLGVIDWENWRPQWVRN	117
222	XP_001378617.3	YPYHDSH-LRPVHGGVPQNSSLMEHLERLPEGVRHYIRSPDREGLAVIDWEDWRPVWIRN	118
223	XP_003210019.2	YPYYNKR-WEPVNGGVPQQSSLAEHLARLQEGIGKYIRSATSEGLAVIDWEEWRPIWMRN	118
224	XP_414258.3	YPYYNKQ-GKPVNGGVPQKSSLAEHLARLQENIGKYIRSATSEGLAVIDWEEWRPIWMRN	136
225	NP_001080777.1	YPYYDEH-GAPVSGGLPQNASLRAHLDKLPDGIQKYIRSRDKDGLAVIDWEEWRPIWVRN	116
226	NP_001119986.1	YPYYDEH-LAPVAGGLPQNASLRAHLDKLPEGIQKYIRSRDKDGLAVIDWEEWRPIWVRN	147
227	XP_003221370.3	YPHFNDS-GDSVNGGIPQKESIIMHLIKASLDIDHSITMKTFQGLGVIDWENWRPQWDRA	130
228	XP_003448364.1	YPYFEQD-ETPVNGGLPQVASRTRHLEKMPEDVKKYIRSEWATGLAVIDWEDWRPLWIRN	136
229	XP_002189602.4	FPYYTSG-GVPVNGGLPQNASLEAHIQQATQDIKVTLHSPDYSGLAVIDWEKWRPLWIRN	116
230	NP_001074154.2	FPYVDLHSMKEYNGGIPQRGNLSASLEKAKEEFLQFIPD-SSSGLAVMDWEEWLPIFDRN	108
231	XP_003448436.2	YPRYSHQ-GEAINGGVPQNSSLDKHLKVARENVNTYIPDRGFPGLGVVDWESWRPEWERN	134
232	XP_002813763.3	YPRFDSA-GRSVHGGVPQNVSLWAHRKMLQKRVEHYIRTQESVGLAVIDWEDWRPVWVRN	130
233	XP_002935681.1	YPYYDES-LSPVNGGLPQNNSLRDHLDKAFMDLLETISHPGFNGVAVVDWESWRPLWARN	133
234	XP_001168599.1	YPRFDSA-GRSVHGGVPQNVSLWAHRKMLQKRVEHYIRTQESAGLAVIDWEDWRPVWVRN	130
235	XP_687640.2	YPYFKPD-STPVYGGLPQAASLTQHLEKMPDGLKKYIKDQAVKGLAVIDWEEWRPLWIRN	152
236	NP_003764.3	YPRFDSA-GRSVHGGVPQNVSLWAHRKMLQKRVEHYIRTQESAGLAVIDWEDWRPVWVRN	130
237	XP_003476739.1	YPHFNEA-GMSVHGGVPQNGSLQEHLGMLRKPVEHYIRTREPAGLAIIDWEHWRPVWVRN	142
238	XP_003257153.1	YPRFDSA-GRSVHGGVPQNVSLWAHRKMLQKRVEHYIRTQESAGLAVIDWEDWRPVWVRN	130
239	XP_002758427.1	YPRFDSA-GRSVHGGVPQNGSLWAHLEMLRDHVEHYIRTPEPAGLAVIDWEDWRPVWVRN	130
240	XP_001102414.2	YPYYTPT-GEPVFGGLPQNASLIAHLARTFQDILAAIPAPDFSGLAVIDWEAWRPRWAFN	116
241	NP_742037.2	YPRFDAA-GMSVHGGVPQNGSLCAHLPMLKEAVERYIQTQEPAGLAVIDWEEWRPVWVRN	118
242	NP_999605.1	YPHFDSV-GRSVHGGVPQNGSLWVHLKMLKGHVEHYIRTQEPAGLAVIDWEDWRPVWVRN	133
243	NP_001009754.1	YPHFNSV-GRSVHGGVPQNGSLWVHLEMLKGHVEHYIRTQEPAGLAVIDWEDWRPVWVRN	133
244	NP_083196.2	YPYFSED-GTSFYGGIPQKVNLSEHLRKSAGDIADAVTLWRSEGLAVIDWEGWRPQWDRN	133
245	NP_001019491.1	YPYFSED-GISFYGGIPQNVNLSEHLRKSANDIANAVSLWRSEGLAVIDWEGWRPQWDRN	117
246	NP_776772.1	YPHFNSV-GRSVHGGVPQNGSLWVHLEMLKGHVEHYIRTQEPAGLAVIDWEDWRPVWVRN	133
247	NP_149349.2	YPYYTPT-GEPVFGGLPQNASLIAHLARTFQDILAAIPAPDFSGLAVIDWEAWRPRWAFN	136
248	NP_001035086.1	YPHYGPN-DEPIYGGVPQNASLNEHLKKADEDLRKNIPDPEFQGLAIIDWEKWRPLWERN	115
249	XP_003502176.1	YPYFSED-RRSIYGGIPQKGNLSEHLKKSASDIADTVTWWRSEGLAVIDWEGWKPQWDRN	117
250	XP_003257149.1	YPYYTPT-GEPVFGGLPQNASLIAHLARTFQDILAAIPAPEFSGLAVIDWEAWRPRWAFN	116
251	XP_002813766.6	YPYYTPS-GEPVFGGLPQNASLIAHLARTFQDILAAIPAPDFSGLAVIDWEAWRPRWAFN	116
252	NP_001017941.1	YPYYTSA-GEPVFGGLPQNASLNAHLARTFQDILAAMPEPRFSGLAVIDWEAWRPRWAFN	136
253	XP_002920567.1	YPYYTSA-GEPVFGGLPQNASLDTHLAHSFQDILAAIPASDFSGLAVIDWEAWRPRWAFN	116
254	XP_003476738.1	YPYYTTT-GEPVFGGLPQNASLGEHLAYAFHDIQATMPAPDFSGLVVIDWEAWRPRWAFN	116
255	NP_999606.1	YPYYTSA-GEPVFGGLPQNASLDVHLNRTFKDILAAMPESNFSGLAVIDWEAWRPRWAFN	136
256	XP_002713406.3	YPYYTPA-GEPVFGGLPQNASLATHLARTFHDILAAMPAPDFSGLVVIDWEAWRPRWAFN	115
257	XP_003500449.1	YPYYTST-GEPIFGGLPQNASLVTHLACTFQDIKAVMPEPDFSGLAVIDWEAWRPRWAFN	115
258	XP_001509131.1	YPSYTSS-GQPLHGGLPQNASLATHLAQAQLDIQAAIPKSNYWGLAVIDWESWRPLWALN	116
259	XP_001139800.4	YPYLSQD-GKSFNGGIPQNVSLSEHLRKTADDIGEGVPWWRSEELVVIDWESWKPQWDRN	117
260	NP_032343.3	YPYYTPT-GEPVFGGLPQNASLVTHLAHTFQDIKAAMPEPDFSGLAVIDWEAWRPRWAFN	115
261	NP_997499.2	YPYYTPT-GEPVFGGLPQNASLVTHLAHAFQDIKAAMPEPDFSGLAVIDWEAWRPRWAFN	115
262	XP_001168796.1	YPYYTPT-GEPVFGGLPQNASLIAHLARTFQDILAAIPAPDFSGLAVIDWEAWRPRWAFN	136
263	NP_997482.2	YPYFGPR-GTAHNGGIPQAVSLDHHLAQAAHQILHNLG-SSFAGLAVLDWEEWYPLWAGN	137
264	NP_001193181.1	YPYLGPR-GTVHNGGIPQAVPLGCHLARAAHQIRHSLW-PGFAGLAVLDWEEWCPLWAGN	112

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NP_001186958.1      YPYFGPR-GTAHNGGIPQALPLDRHLALAAYQIHHSLR-PGFAGPAVLDWEEWCPLWAGN     130
NP_999604.1         YPYFGPR-GTAHNGGIPQAVSLDHHLARAAYQIHRSLR-PGFTGLAVLDWEEWCPLWAGN     112
XP_001493753.3      YPYLGPR-GTAHNGGIPQAVPLDCHLARAAYQIHHSLR-PGFTGLAVLDWEEWSPLWAGN     112
NP_001121765.1      YPYISRE-GVKVNGGLPQEGYLKAHLSLAGVEIREKLR-SSFSGLAVLDWEAWEPVWKWN     114
NP_821139.2         YPYFGPR-GTAHNGGIPQAVSLDHHLARAAHQILHSLG-SSFAGLAVLDWEEWYPLWAGN     113
XP_002128103.1      YPKYGTD-GLAVNGGIPQNGNISAHYEKCVDDIMARIPDSNYNGIAVIDWEAWRPKWERN     152
XP_003642042.3      YPYISPQ-GVPHNGGIPQRAPLRAHLARVAGDVRLRLR-PAFSGLAVVDWEEWRPLWARN     109
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NP_003108.2         -WKP-KDVYKNRSIELVQQQNVQLSLTEATEKAKQEFEKAGKDFLVETIKLGKLLRPNHL     215
XP_003318802.2      -WKP-KDVYKNRSIELVQQQNVQLSLTEATEKAKQEFEKAGKDFLVETIKLGKLLRPNHL     215
XP_003261317.2      -WKP-KDVYKNRSIELVQQQNVQLSLAEATEKAKQEFEKAGKDFMVETIKLGKLLRPNHL     215
XP_001086882.2      -WKP-KDVYKNRSIELVQQQNVQLSLPQATDKAKQEFEKAGKDFMLETIKLGRSLRPNHL     215
NP_001076141.2      -WKP-KDIYRIKSIELVQQQNPQINLTEATKLAKIEFEKAGKCFMEETLKLGRLFRPNHF     214
XP_002919069.1      -WKP-KDIYKHQSIELVQQHHIELNVTEATKIAKADFEKAGKCFMQETLKLGKSLRPNYL     215
NP_999176.1         -WKE-KAIYRRQSIELVQQKNIKLTPAAATKLAKREFEKAGKTFMQETLKLGKLLRPNHL     215
XP_002686960.3      -WKP-KDVYKKASIELVLQQNRHFTLKEATKRAKADFEKAAKSFMQETLKLGKFLRPNHL     213
NP_001008413.3      -WKP-KDVYRDESVELVLQKNPQLSFPEASKIAKVDFETAGKSFMQETLKLGKLLRPNHL     216
XP_003502178.1      -WKP-KDIYKHKSIELVKQQNKQLNITEATRRAKKDFEQAARSFMEGTLKLGKSLRPNHL     214
NP_001166492.1      -WRP-KDIYRNKSIELVKSQHPQYNHSYAVAVAKRDFERTGKAFMLETLKLGKSLRPSSL     214
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XP_001507937.2      -WKP-KDIYRNRSIELVQQKDVTLNFSEAWNIAKVDFEKAARNFMQQSLKLGKTLRPNRL     212
NP_001073344.1      -WKP-KDNYRNKSIELVQSTNPGLSITEATQKAIQQFEEAGRKFMEGTLHLGKFLRPNQL     214
XP_003502177.1      -WKP-KDVYRNKSIALVQANNAGISIEDATQKAKDEFETAGRHFMEETLKLGKSVRPRHL     215
XP_002190553.4      -WGS-KDIYRQESIELVQQRDLSISEAESRTIAKMEFEFAAKSFMLETLKLGIETKPNRL     197
XP_002932242.3      -WAS-KAVYKMNSIEFARQMDITMTHKKAALIAEAQFESAAQNFMLQTLRLGKAMRPNYL     208
NP_001082194.1      -WAS-KAVYKKQSIEFAQQMDITMTHKKAVGIAAAQFESAAKNLMLETLKLGKTMRPNYL     203
XP_002919077.1      -WNT-KDVYRQKSRKLISDMQENISATDIEDLAKETFEESAKAFMKETIELGMKSRPKGL     214
XP_002712114.1      -WNT-KDVYRQKSRKLISDMQANVSATDIEYLAKATFEESAKAFMKETLKLGIKSRPKGL     174
XP_532444.4         -WNT-KDVYRQKSRKLISDMQENVSATDIEYLAKATFEESAKAFMKETIELGIKSRPKGL     192
XP_002818436.2      -WNA-KDVYRQKSRKLISDMGKNVSATDIEYLAKVTFEESAKAFMKETIKLGIKSRPKGL     174
NP_084124.1         -WNT-KDIYRQKSRTLISDMKENISAADIEYSAKATFEKSAKAFMEETIKLGSKSRPKGL     174
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NP_036401.2         -WNS-KDVYRQKSRKLISDMGKNVSATDIEYLAKVTFEESAKAFMKETIKLGIKSRPKGL     174
XP_003261316.2      -WNA-KDVYRQKSRKLISDMGRNVSATDIEYLAKVTFEESAKAFMKETIKLGIKSRPKGL     214
XP_003407292.1      -WNA-KNVYRQKSRKLISETQENVSATDIEYLAKATFEESAKAFMKETIKLGIKSRPKGL     195
XP_003586042.1      -WNT-KDIYRQKSRKLISETQENASAADIEYLAKATFEESAKAFMKETIELGIKSRPKGL     192
NP_001094250.1      -WNT-KDIYRQKSRTLISDMKENISTADIEYLAKATFEKSAKAFMEETIKLGIKSRPKGF     204
XP_003221368.2      -WNT-KNIYRRQSRKLISAMQQNVSTNALEHLAKFSFEQCAKAFMKETIELGIKSRPKGL     174
XP_003475093.1      -WNA-KDVYRRKSKELIFDLQQNVKASDIEYLAKATFEESAKAFMIETIKLGIKRRPKGL     201
NP_001090796.1      -WGS-KLIYRNKSIELVKNHHPTWSDEQLKKKAKEEFDNAAKEFMTKTIALAQEKRSKGL     174
XP_003221369.1      -WGN-KTIYKNKSLELVRKRHPHWPKNAVHKAAKEEFENAGKNFMNSTLSLAENMRPSGL     174
XP_003449274.1      -WHK-KDIYRRKSKELTKKAYINVTAAQVEELARRRFEKSAKIFMLKTIQLGRQLRPSAL     175
NP_001074140.1      -WGS-KDIYRNKSKELIRKLHPGWPQSKVENEAKEVFERAGQVFMNSTLLLAESRRPHGL     174
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XP_003449275.2      -WGS-KDIYRKRSREQIRKLHPNWPESKVEKEAKEGFERAGQAFMNLTLALAQGRRPGGL     175
XP_001378617.3      -WQS-KDVYRKVSRQLVSLRHPTWSQEQVGKQAQYEFEFAARQFMLETLRWAKETRPRQL     176
XP_003210019.2      -WKP-KDVYQEVSRELVKQKQPFWSPEEVNKQAVFEFESAARQFMVRTLRYAKSFRPKQL     176
XP_414258.3         -WKP-KDVYQEVSRELVEQRQPFWSPEKVNKQAVFEFESAARHFMVTTLRYAKSFRPKQL     194
NP_001080777.1      -WQN-KNVYRNNSRNLVASRHPSWPREQVEKEALYDFENAAREFMMETLRHAKNYRPRQL     174
NP_001119986.1      -WQN-KDVYRQNSRNLVSSRHPTWPREKVDKEALYEFENAAREFMTETLRHAKNYRPRQL     205
XP_003221370.3      -WGR-KNIYRDASLELVRKRHPHWPEDAIKKTARKEFENAGRNFMTTTLSLVKKLRPNGL     188
XP_003448364.1      -WEP-KHIYRRHSEELVRQKNPTWTSDRVKRVAQQEFEMSARLFMLDTLKQAKNLRPNQL     194
XP_002189602.4      -WDS-MEIYRQKSEELVQQQHPQWPPKEVEEMAKQQFEKSACDFMNKTLWLGKSLRPSAY     174
NP_001074154.2      -FDL-KKIYMELSINYTLEQNSSLSPQQAATEAKQQFQKEARRFMEETLKKGINLRPRYL     166
XP_003448436.2      -WDT-KKIYQEGSKALVRSKHPDWSPKQVDDAARVEFNKAARNFMEETLKLGQAARPDGL     192
XP_002813763.3      -WQD-KDVYRRSSRQLVASRHPDWPPDRIVKQAQYEFEFAAQQFMLETLRYVKAVRPRHL     188
XP_002935681.1      -WDK-MRVYQQSSQDLVKEFYPHLPPDKVIELAKAEFETAARKLMQSTLELGRALRPKGL     191
XP_001168599.1      -WQD-KDVYRRLSRQLVASRHPDWPPDRIVKQAQYEFEFAAQQFMLETLRYVKAVRPRHL     188
XP_687640.2         -WGP-KLIYRDRSQRLVAEKNPTWPLDQVTKVAQQEFELSARKFMLETLRLAKSLRPQQL     210
NP_003764.3         -WQD-KDVYRRLSRQLVASRHPDWPPDRIVKQAQYEFEFAAQQFMLETLRYVKAVRPRHL     188
XP_003476739.1      -WQD-KDVYRQWSRQLVASRHPDWPKDQIVKEAQYEFEFAARQFMLKTLHYVKSVRPQHL     200
XP_003257153.1      -WQE-KDVYRRSSRQLVASRHPDWPPDRIVKQAQYEFEFAAQQFMLETLRYVKAVRPRHL     188
XP_002758427.1      -WQD-KDVYRRSSRQLVASRHPDWQADRVVKQAQYEFECAARQFMLETLRYVKAVRPRHL     188
XP_001102414.2      -WDT-KDIYRQRSRALVQAQHPDWPVTQVEAVAQDQFQGAARAWMAGTLQLGRALRPRGL     174
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NP_742037.2         -WQE-KDVYRQSSRQLVASRHPDWPSDRIVKQAQYEFEFAARQFMLNTLRYVKAVRPQHL    176
NP_999605.1         -WQD-KDVYRRLSRQLVASRHPDWPPDRVVKQAQYEFEFAARQFMLETLRFVKAFRPQHL    191
NP_001009754.1      -WQD-KDVYRRLSRQLVASHHPDWPPERIVKEAQYEFEFAARQFMLETLRFVKAFRPRHL    191
NP_083196.2         -WGS-RMIYKNHSLAFTRHHHPDWAETKVRTAAQKEFENAGRSFMNVTLTLALEMRPKRL    191
NP_001019491.1      -WGG-RIIYKNHSLAFTRHHHPDWAETKVRTVAQQEFENAGKSLMNVTLTLALEMRPKRL    175
NP_776772.1         -WQD-KDVYRRLSRHLVAIRHPDWPPERVAKEAQYEFEFAARQFMLETLRFVKAFRPRHL    191
NP_149349.2         -WDT-KDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRALRPRGL    194
NP_001035086.1      -WDS-KEVYWKASRAIVKAKHPTWSPDQIETEAVKEFEASSMAFMVETLKLGRRERSGGL    173
XP_003502176.1      -WGS-RIIYKNHSLAFTRHHHPDWSEAKVRTVAQQEFENAGRSFMNITLTLALEMRPKRL    175
XP_003257149.1      -WDT-KDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRALRPRGL    174
XP_002813766.6      -WDT-KDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRALRPRGL    174
NP_001017941.1      -WDT-KDIYRQRSRALVQKQHPDWLAPRVEAAAQDQFEGAAEEWMAGTLKLGQALRPQGL    194
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XP_001509131.1      -WDS-KDVYRERSRALVREEHPDWSSWQVEEEAVIQFQTAARAWMSQTLQLGQTLRPRGL    174
XP_001139800.4      -RGS-RIIYKNHSLAFTRNHHPYWSEMKVETVAQEEFENAGKNFMNITLTLALEMRPKCL    175
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NP_997499.2         -WDS-KDIYQQRSMELVRAEHPDWPETLVEAEAQDQFQEAAQAWMAGTLQLGQVLRPRGL    173
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NP_997482.2         -WGTHRQVYQAASWAWAQQMFPDLNPQEQLHKAQTGFEQAARALMEHTLRLGQMLRPHGL    196
NP_001193181.1      -WGR-RQVYRAASWAWAQWVFPNLDPQEQLHKARVGFEQAARALMEDTLWLGRALQPQGL    170
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XP_001493753.3      -WGR-RRAYQTASWAWAQRVFPYLDPQEQLHKAQTGFEQAARALMEDTLRLGQALQPYGL    170
NP_001121765.1      -FGT-RIVYRKLSKKLVRWEHPDMSEEEVKSKAKLDFELAARQFMEETLRLGLRLCPEGL    172
NP_821139.2         -WGPHRQVYLAASWVWTQQMFPGLDPQEQLHKAHTSFEQAARALMEYTLQLGRTLRPSGL    172
XP_002128103.1      GWGS-GLIYQNKSIEKVKKEHPSWPLNKVKAQAKIEFEEAAKSYMLGTLNLARLMRPKAH    211
XP_003642042.3      -WGR-KRVYQLASQRWAQERGR------GRRLARRAFERAARALMEQTLLLGRSLRPAGL    161
                            *   *                   *   *:  .   :   ::

NP_003108.2         WGYYLFPDCYNHHYKK----PGYNGSCFNVEIKRNDDLSWLWNESTALYPSIYLNTQQSP    271
XP_003318802.2      WGYYLFPDCYNHHYKK----PGYNGSCFNVEIKRNDDLSWLWNESTALYPSIYLNTQQSP    271
XP_003261317.2      WGYYLFPDCYNHHYKK----PGYNGSCFNVEIKRNDDLSWLWNESTALYPSIYLNTQQSP    271
XP_001086882.2      WGYYLFPDCYNHHYRK----PGYNGSCFDVEIKRNDDLSWLWNESTALYPSIYLNTQQSV    271
NP_001076141.2      WGYYLFPDCYNHNYDK----PNYKGICFDIEKKRNDDLDWLWKESTALFPSVYLKSSLQS    270
XP_002919069.1      WGYYLFPDCYNHNYKK----PDYNGSCSDLEKKRNDELNWMWKESTALFPSIYLNTKLKS    271
NP_999176.1         WGYYLFPDCYNHNYHK----PGYNGSCLDIEKRRNDALDWLWKESTALFPSIYLNTRLKP    271
XP_002686960.3      WGYYLFPDCYNHHYNQ----ANYNGSCFDEEKRRNDALNWLWKESTALYPSVYLNTKLKS    269
NP_001008413.3      WGYYLFPDCYNHNHNQ----PTYNGNCPDVEKRRNDDLEWLWKESTALFPSVYLNIRLKS    272
XP_003502178.1      WGFYLFPDCYNNKFHD----LNYNGECPDTEKRRNDGLFWIWKQSTALYPSIYLKTGLKS    270
NP_001166492.1      WGYYLFPDCYNTHFTK----PNYDGHCPPIELQRNNDLQWLWNDSTALYPSVYLTSRVRS    270
NP_001019492.1      WGFYLFPDCYNNNFQD----ANYKGDCPDIEKQRNDALFWIWKESTALYPSIYLKSSLKS    270
XP_001507937.2      WGFYLFPDCYNHNYKS----PNYNGSCFDIEKARNDELQWLWKESTALFPSIYLDTGLRN    268
NP_001073344.1      WGYYLFPDCYNNKFQD----PKYDGQCPAVEKKRNDNLKWLWKASTGLYPSVYLKKDLKS    270
XP_003502177.1      WGYYLFPDCYNNKFQD----PKYDGNCPPVEKQRNDALSWMWKESTGLYPSVYLKKDLGS    271
XP_002190553.4      WGYYLYPDCYNYDYKQN--PHNYTGACLDIEIERNNELNWLWEKSTALYPSIYLETALKS    255
XP_002932242.3      WGFYLFPNCYNYHYKSN--PKQYKGHCPEVEIQRNNKLHWLWKESTALFPNVYLEVALKS    266
NP_001082194.1      WGFYLFPNCYNYHYKSN--PKQYTGHCPKLEIQRNDKLHWLWKESTALFPNIYLEVALKS    261
XP_002919077.1      WGYYLYPDCHNYNVYAP----NYTGSCPEEEVLRNNELSWLWNSSTALYPSIGVRKSLGD    270
XP_002712114.1      WGYYLYPDCHNYNIYAP----NYTGSCPEEEVLRNNELSWLWNSSAALYPSIGVRKALGD    230
XP_532444.4         WGYYLYPDCHNYNVYAP----NYTGSCPEEEVLRNNELSWLWNSSAALYPSIGVRKSLED    248
XP_002818436.2      WGYYLYPDCHNYNVYAP----NYTGSCPEDEVLRNNELSWLWNSSAALYPSIGVWKSLGD    230
NP_084124.1         WGYYLYPDCHNYNVYAT----NYTGSCPEEEVLRNNDLSWLWNSSTALYPAVSIRKSFAD    230
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NP_036401.2         WGYYLYPDCHNYNVYAP----NYSGSCPEDEVLRNNELSWLWNSSAALYPSIGVWKSLGD    230
XP_003261316.2      WGYYLYPDCHNYNVYAP----NYTGSCPEEEVLRNNELSWLWNSSAALYPSIGVWKSLGD    270
XP_003407292.1      WGYYLYPDCHNYNVYAP----NYTGSCPEEEVLRNNELSWLWNSSAALYPSIGVRKSLGD    251
XP_003586042.1      WGYYLYPDCHNYNVYGP----NYTGSCPEEEVLRNNELSWLWNISAALYPSIGVRRSLGD    248
NP_001094250.1      WGYYLYPDCHNYNFYAT----NYTGSCPEEEVLRNNDLSWLWNSSTALYPAVSIRKSFAD    260
XP_003221368.2      WGYYLYPDCHNYNFHDQ----NYTGSCPESEVLRNNELSWLWNSSAALYPSIGIKKFLGN    230
XP_003475093.1      WGYYLYPDCHNYNMDDP----SYTGSCPEEEVLKNNELSWLWDSSTALYPSVVIKKSLRN    257
NP_001090796.1      WGYYLFPDCYNYDYKEN--PQSYTGRCPDIEMTRNDLLKWLWKESNALYPSIYLDYVLKS    232
XP_003221369.1      WGYYLYPDCYNYDYKTD--SNTYTGKCPDIASSRNDLLLWLWKESTALYPSIYLDKRLKS    232
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XP_003449274.1      WGFYLYPDCHNYNLHDQ----NYTGFCPLLERLRNDELVWLWNSSMALYPSVTIRKHHSN    231
NP_001074140.1      WGFYLFPDCYNYGYKQH--PFRYTGECPNIEHVRNDHLMWLWKESTALYPSIYLDCELKS    232
XP_003217669.1      WGYYLFPDCYNHDYSKN--LDSYTGHCPDVEKTRNDHLAWLWKESTALYPSIYLEEVLAN    232
XP_001507903.3      WGYYLYPDCHSYNFHEQ----NYTGSCPEDEVLRNNELFWLWNSSAALYPSISVQKALRN    251
XP_003449275.2      WGFYLFPDCYNYGYKQH--PQHYTGECPNVEHVRNDHLIWLWKESSALYPSIYLDYELKS    233
XP_001378617.3      WGFYLFPDCYNHDYVQN--WSSYTGRCPDVEVSRNDQLAWLWAESSALYPSIYLDPMLKS    234
XP_003210019.2      WGYYLFPDCYNHDYSKN--KESYTGQCPDVEKTRNDQLAWLWNESLALYPSIYLDPLLAS    234
XP_414258.3         WGYYLFPDCYNHDYSKN--KESYTGQCPDVEKTRNDQLAWLWNESMALYPSIYLDPLLAS    252
NP_001080777.1      WGFYLFPDCYNHDYNKN--RDSYTGHCPDVEISRNDQLSWLWEESTALYPSIYLDQILAS    232
NP_001119986.1      WGFYLFPDCYNHDYVKN--RDSYTGQCPDVEISRNDQLSWLWEESTALYPSIYLDQILAS    263
XP_003221370.3      WGYYLYPDCYNYDYKIK--NKIYTGKCPDLEYSRNDLLFWLWKASTALFPSIYLEYMLKS    246
XP_003448364.1      WGFYLFPDCYNHNYMHT--LESYTGRCPDVEESRNDQLKWLWTESTALFPSIYMSSLLRS    252
XP_002189602.4      WGFYGFPDCYNNDFDSL----PYNGTCPDVEQQRNQNLSWLWRGSQALYPSIYLPLCLNG    230
NP_001074154.2      WGYYLFPDCYNYGFDE----SNYTGTCSEYTKQLNNELLWLWEVSTALYPSAYLPVSKSG    222
XP_003448436.2      WGYYGFPNCYNYYSNKS---TGYTGECPPVELKRNDKLLWLWSTSSALYPDIYLSIQMQS    249
XP_002813763.3      WGFYLFPDCYNHDYVQN--WESYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLAS    246
XP_002935681.1      WGFYGFPSCYNYGYKKKNYGQNYTGECPIEEIHRNDNLTWLWEASQALYPDIYLEQALKM    251
XP_001168599.1      WGFYLFPDCYNHDYVQN--WESYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLAS    246
XP_687640.2         WGYYLFPDCYNHNYQTN--LQNYTGQCPDIEVSRNNELKWLWTESTALYPSVYMGKILKD    268
NP_003764.3         WGFYLFPDCYNHDYVQN--WESYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLAS    246
XP_003476739.1      WGFYLFPDCYNHDYVQN--WESYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLAS    258
XP_003257153.1      WGFYLFPDCYNHDYVQN--WESYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLAS    246
XP_002758427.1      WGFYLFPDCYNHDYVQN--WKSYTGRCPDVEVARNDQLAWLWANSTALFPSVYLEETLAS    246
XP_001102414.2      WGFYGFPDCYNYDFLSP----NYTGQCPSGIRAQNDQLGWLWGQSRALYPSIYMPAVLEG    230
NP_742037.2         WGFYLFPDCYNHDYVQN--WDSYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLAS    234
NP_999605.1         WGFYLFPDCYNHDYVQN--WETYTGRCPDVEVSRNDQLAWLWAESTALFPSVYLEETLAS    249
NP_001009754.1      WGFYLFPDCYNHDYVQN--WETYTGRCPDVEVSRNDQLSWLWAESTALFPSVYLEETLAS    249
NP_083196.2         WGFYLYPDCYNYDYRIN--PEFYTGSCPDDEIFRNDQLMWLWEKSAALYPSIYLSKILKS    249
NP_001019491.1      WGFYLYPDCYNYDYRIN--PEFYTGSCPDDEIFRNDQLMWLWEKSAALYPSIYLSKILKS    233
NP_776772.1         WGFYLFPDCYNHDYVQN--WETYTGRCPDVEVSRNDQLAWLWAESTALFPSVYLEETLAS    249
NP_149349.2         WGFYGFPDCYNYDFLSP----NYTGQCPSGIRAQNDQLGWLWGQSRALYPSIYMPAVLEG    250
NP_001035086.1      WGFYGFPCCYNYQYKKN---ETYTGECPALEMKRNDKLAWMWNVSSALYPDIYLDLGLRG    230
XP_003502176.1      WGFYLYPDCYNYDYRIN--PEFYTGRCPDDEIFHNDQLLWLWEKSTALYSSIYLSKILKS    233
XP_003257149.1      WGFYGFPDCYNYDFLSP----NYTGQCPSGIRAQNDQLGWLWGQSRALYPSIYMPAVLEG    230
XP_002813766.6      WGFYGFPDCYNYDFLSP----NYTGQCPSGIRAQNDQLGWLWGQSRALYPSIYMPAVLEG    230
NP_001017941.1      WGFYNFPECYNYDFKSP----NYTGRCPLNICAQNDQLGWLWGQSRALYPSIYLPAALEG    250
XP_002920567.1      WGFYGFPDCYNYDFLSP----NYTGQCPPGISAQNDQLGWLWGQSRALYPSIYMPAELEG    230
XP_003476738.1      WGFYGFPDCYNYNFKSL----NYTGQCPLGIPTENDQLGWLWNQSRALYPSIYIPAALVG    230
NP_999606.1         WGFYGFPDCYNYDFQSS----NYTGQCPPGVSAQNDQLGWLWGQSRALYPSIYLPSALEG    250
XP_002713406.3      WGFYGFPDCYNSDFLSP----NYTGQCAPDTSEQNDQLGWLWNHSCALYPSIYMPAALEG    229
XP_003500449.1      WGYYGFPDCYNHNFLSP----NYTGQCSLNIRDQNDQLDWLWNQSYALYPSVYLPAALMG    229
XP_001509131.1      WGFYGFPACYNYDFKNP----NYTGACPDGIQPLNQELQWLWNQSRALYPSIYLPSELEG    230
XP_001139800.4      WGFYLYPDCYNYDYRIN--PETYTGNCPKDEVLRNDQLLWLWEKSAALYPSIHLDKILKS    233
NP_032343.3         WGYYGFPDCYNNDFLSL----NYTGQCPVFVRDQNDQLGWLWNQSYALYPSIYLPAALMG    229
NP_997499.2         WGYYGFPDCYNYDFLSP----NYTGQCSLSIHDQNDQLGWLWNQSYALYPSIYLPAALMG    229
XP_001168796.1      WGFYGFPDCYNYDFLSP----NYTGQCPSGIRAQNDQLGWLWGQSRALYPSIYMPAVLEG    250
NP_997482.2         WGFYRYPVCGNGWHNMA---SNYTGHCHPAIITRNTQLRWLWAASSALFPSIYLPPRLPP    253
NP_001193181.1      WGFYRFPACGNGWRGTA---SNYTGHCHAAAVARNTQLHWLWAASSALFPSIYLPPRLPP    227
NP_001186958.1      WGFYHYPACGNGWHSMA---SNYTGRCHAATLARNTQLHWLWAASSALFPSIYLPPRLPP    245
NP_999604.1         WGFYHYPACGNGWHGTA---SNYTGHCHAAALARNTQLYWLWAASSALFPSIYLPPGLPP    227
XP_001493753.3      WGFYRFPACGNGWRGMA---SNYTGHCHAATLARNTQLHWLWAASSALFPSIYLPPRLPP    227
NP_001121765.1      WGFYGFPSCYNNNGQGQ---SGYTGKCHNGTEILNDRLGFLWQQSTALYPSIYLWRKLAG    229
NP_821139.2         WGFYRYPACGNGWHKMA---SNYTGHCHAAITTRNTQLRWLWAASSALFPSIYLPPRLPL    229
XP_002128103.1      WGLYLFPDCYNYDKTGK------RMTCTTKTINMNNDIQWLFDASNALYPSTYLGLWFKN    265
XP_003642042.3      WGFYRFPDCFNDDWAKV---ANYTGRCRPAEVQRNDRLRWLWAASAALYPSIYLPPLLPP    218
                    ** * :* * .               *       *  : :::  * .*:    :

NP_003108.2         -V-AATLYVRNRVREAIRVSKIPDA-KSPLPVFAYTRIVFTDQ-------VLKFLSQDEL    321
XP_003318802.2      -V-AATLYVRNRVQEAIRVSKIPDA-KSPLPVFVYTRIVFTDQ-------VLKFLSQDEL    321
XP_003261317.2      -V-AATLYVRNRVREAIRVSKIPDA-KSPLPVFVYARIVFTDQ-------VLKFLSRDEL    321
XP_001086882.2      -V-VATLYVRNRVREAIRVSKIPDA-KNPLPVFVYARLVFTDQ-------VLKFLSREEL    321
NP_001076141.2      -SPKAALFVRNRVQEAIRVSEVPNA-KSPLPIFVYTRLVFTDK-------IFQFLSQDDL    321
XP_002919069.1      -SPYAALYVRNRVWEAIRISQVSSV-KHPLPIFVYARPVFTDV-------SLKYLSEDDL    322
NP_999176.1         -SQ-VALFVRNRVQEAIRVSKVANA-QSPLPVFVYTRPVFSGA-------SSRYLSQDDL    321
XP_002686960.3      -SPQARLFVRNRVQEAIRLSKVANV-KSPLPVFVYTRPVFSDM-------SSKFLSQDDL    320
NP_001008413.3      -TQNAALYVRNRVQEAIRLSKIASV-ESPLPVFVYARPVFTDG-------SSTYLSQGDL    323
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XP_003502178.1       -SQQAVLYVRNRVQEAIRVSKAKDP-QSPVPIFVYSRIVFGDL-------TYRFLSQKDL    321
NP_001166492.1       -SQNGALYVRNRVHESIRVSKLMDD-KNPLPIYVYIRLVFTDQ-------TTTFLELDDL    321
NP_001019492.1       -SPLAALYVRNRVQEAIRMSKVKDP-HNPLPIFVYFRPVFTDL-------TFQYLEQDDL    321
XP_001507937.2       -SGYAPLFVRNRVQEAIRVSKVADP-LNPLPIFVYTRPVFTNA-------PSNYLSQIDL    319
NP_001073344.1       -NRQATLYVRYRVVEAIRVSKVGNA-SDPVPIFVYIRLVFTDR-------TSEYLLEDDL    321
XP_003502177.1       -NRQAALYVRYRVVESVRVSKVRSE-KDPVPIFVYIRLVFTDN-------TSEYLQEVDL    322
XP_002190553.4       -SRNAQLFVRNRVQEAIRTSYVANS-SHPLPVFVYTRPVFTDV-------YEEYLSEDDL    306
XP_002932242.3       -SNNAVMFARHRIQEARRLSSLS---KFTLPIYVYTRPVFTDQ-------PDKFLSEVDL    315
NP_001082194.1       -SSNAALFARHRIQEARRLSTFS---KYAVPIYVYTRPVFTNR-------PDEFLSEVDL    310
XP_002919077.1       -NENILRFSQFRVHESMRISTMTSH-DYALPVFVYTRLGYRNE-------PLFFLSKQDL    321
XP_002712114.1       -SENILRFSQFRVHESLRVSTMTSH-NCSLPVFVYTRLGYRDE-------PLFFLSKQDL    281
XP_532444.4          -NENILRFSRFRVHESLRISTMTSH-DYALPIFVYTRLGYRNE-------PLFFLSKQDL    299
XP_002818436.2       -SENILRFSKFRVHESMRISTMTSH-DYALPVFVYTRLGYRDE-------PLFFLSKQDL    281
NP_084124.1          -SENTLHFSRFRVRESLRISTMTSQ-DYALPVFVYTQLGYKEE-------PLLFLSKQDL    281
XP_003134772.2       -SENTLRFSQFRVHESMRISTVTSH-GYALPVFVYTRLGYRDQ-------PLFFLSKQDL    299
NP_036401.2          -SENILRFSKFRVHESMRISTMTSH-DYALPVFVYTRLGYRDE-------PLFFLSKQDL    281
XP_003261316.2       -SENILRFSKFRVHESMRISTMTSH-DYALPVFVYTRLGYRDE-------PLFFLSKQDL    321
XP_003407292.1       -SENILHFSQFRVHESMRVSAMTSH-DYTLPVFVYTRLGYRDQ-------PLFFLSKQDL    302
XP_003586042.1       -SENVLRFSQFRVHESMRISIMTSR-DHALPVFVYTRLGYRDQ-------PLLFLSKQDL    299
NP_001094250.1       -SENTLHFSQFRVRESLRISTMTSH-DYALPVFVYTRLGYKEE-------PLLFLSKQDL    311
XP_003221368.2       -SENILRFSQFRVNESIRISFMTSH-DYALPVFVYTRLDYRDE-------PLLFLSTQDL    281
XP_003475093.1       -SENVLHFSKFRVQEAMRISTMTSH-KYALPVFVYTRLGYRED-------PLFFLSQQDL    308
NP_001090796.1       -SPNVLKFVHHRVKESMRVASMARK-DYSLPVFVYSRPFYSYT--------LYTLSEADL    282
XP_003221369.1       -SPNSLKFVHYRVKEAIRIASIARK-DYALPVFVYSRPFYAYT--------FQALTEIDL    282
XP_003449274.1       -SISNLHFTQHRIRESLRVASLTSK-EYDLPTYVYLRLGYRDE-------ALNFLTTDDL    282
NP_001074140.1       -STNTVKFVHYRVKEAMRIASIARN-DYTLPVFVYSRPFYAYT--------FVVLSESDL    282
XP_003217669.1       -SINGRKFVRSRVQEALRISRQHHD-DYDLPVFVYTRPTYNRRQ------NLTYLSEMDL    284
XP_001507903.3       -SKNLWLFSWFRVNESLRISTMMSC-DYALPVFVYTRLGYRDA-------PLTFLSKHDL    302
XP_003449275.2       -SSNTVKFVHYRVKEAMRIASIART-DFTLPVFVYSRPFYAYT--------FVVLSESDL    283
XP_001378617.3       -SSNCRKFVRSRVEEALRVAREHHA-GYSLPVFVYTRPTYTQ--------SFTVLSEMDL    284
XP_003210019.2       -TPNSRKFVRARVMEAMRISQQHHE-GYSLPVFVYTRPTYSRK--------MDVLSQPDL    284
XP_414258.3          -TPNSRKFVRARVMEAMRISQQHHE-GYSLPVFVYTRPTYSRK--------MDVLSQPDL    302
NP_001080777.1       -SENGRKFVRSRVREAMRISYRHHK-DYSLPVFVYTRPTYIRK--------LDFLSQMDL    282
NP_001119986.1       -SENGRKFVRSRVREAMRISYRHHK-DYSLPVFVYTRPTYIRK--------LDFLSQMDL    313
XP_003221370.3       -STNALKFVHYRVKEAMRIASIARK-DYALPVFVYSRPFYAYT--------FEPLSEIDL    296
XP_003448364.1       -SASGRQFVRNRVKEGMRLASS-GD-GLARPVFVYTRPTYMNSLE--------QLTETDL    301
XP_002189602.4       T-NKVLAYVRHRVAEAFAVQQGI-L-DSGIPVLPYSQIAFERT--------LDFLSQEDL    279
NP_001074154.2       -SKSAALFVRHQVEEAMRVASLPKH-VHTAPVYVYLRPLLTNQ-------KKLYMNEIDL    273
XP_003448436.2       LSREVLLYCHHRILEAMRAADQV-T-PFAPPVYAYARIVYTYT--------LEFLSQEHL    299
XP_002813763.3       -SRHGRNFVSFRVQEALRVARTHHA-NHALPVYVFTRPTYSR--------RLTGLSEMDL    296
XP_002935681.1       -SEHVGPYVKHRVLEGIRVAK-------DLPVLPYARIVYTYS--------MDFLTQEDL    295
XP_001168599.1       -SRHGRNFVSFRVQEALRVARTHHA-NHALPVYVFTRPTYSR--------RLTGLSEMDL    296
XP_687640.2          -NPKGRQFVRNRVKEGMRLASV-GD-GSARPVFVYTRPTYLTNMTSSNPAELLLLTEMDL    325
NP_003764.3          -SRHGRNFVSFRVQEALRVARTHHA-NHALPVYVFTRPTYSR--------RLTGLSEMDL    296
XP_003476739.1       -SAQGRNFVSFRVQEALRVAQSHHA-NHALPVYVFTRPTYTHTS------KLTGLSEMDL    310
XP_003257153.1       -SRHGRNFVSFRVQEALRVARTHHA-NHALPVYVFTRPTYSR--------RLTGLSEMDL    296
XP_002758427.1       -SAHGRNFVSFRVQEALRVAHTHHA-NHALPVYVFTRPTYSR--------RLRGLSEMDL    296
XP_001102414.2       T-GKSQMYVQHRVAEAFRVAVAA-G-DPNLPVLPYVQIFYDMT--------NHFLPLDEL    279
NP_742037.2          -SKHSRNFVSFRVQEALRVAHTHHA-NHALPVYVFTRPTYTR--------GLTELSQMDL    284
NP_999605.1          -STHGRNFVSFRVQEALRVAHTHHA-NHALPVYVFTRPTYSR--------GLTGLSEMDL    299
NP_001009754.1       -STHGRNFVSFRVQEALRVADVHHA-NHALPVYVFTRPTYSR--------GLTGLSEMDL    299
NP_083196.2          -NLNALKFVHFRVREALRVAEMARK-DYVLPVFIFSRPFYLQS--------IEALSEEDL    299
NP_001019491.1       -DINALKFVHFRVREALRIAEKARK-DYALPVFIFSRPFYLQS--------IEALSEEDL    283
NP_776772.1          -STHGRNFVSFRVQEALRVADVHHA-NHALPVYVFTRPTYSR--------GLTGLSEMDL    299
NP_149349.2          T-GKSQMYVQHRVAEAFRVAVAA-G-DPNLPVLPYVQIFYDTT--------NHFLPLDEL    299
NP_001035086.1       RGQDILLYSRYRILEAMRVREKT-T-HQMTSVFPYARIAFTYS--------MEFLSQDDL    280
XP_003502176.1       -NLNALKFVHFRVREALRVAEMARK-DYVLPVFVFSRPFYLQS--------FEALSEEDL    283
XP_003257149.1       T-GKSQMYVQHRVAEAFRVAVTA-G-DPNLPVLPYVQIFYDMT--------NHFLPLDEL    279
XP_002813766.6       T-GKSQMYVQHRVAEAFRVAVAA-G-DPNLPVLPYVQIFYDMT--------NHFLPLDEL    279
NP_001017941.1       T-KKTQMFVQHRVAEAFRVAAGA-G-DPKLPVLPYMQLFYDMT--------NHFLPAEEL    299
XP_002920567.1       R-GKGQMYVRHRVGEAFRVALGV-G-DPNLPVLPYAQIFYDKT--------NRFLPLDEL    279
XP_003476738.1       T-GKTQRYVRHRVAEAFRVARAA-R-NPSLPVLPYTQIFYEST--------SHLLPMEEL    279
NP_999606.1          T-NKTQLYVQHRVNEAFRVAAAA-G-DPNLPVLPYAQIFHDMT--------NRLLSREEL    299
XP_002713406.3       T-GKEWMYVRHRVTEAFRVATAA-G-NPTLPVLPYAQIFYALT--------NHFLPLEEL    278
XP_003500449.1       TTGKAQLYVRHRVQEAFRVATAS-R-DPKVPILPYVQIFYEMT--------NHLLPLEEL    279
XP_001509131.1       T-GYTWPFVRERVREAFRMAMGT-G-DASLPVLPYAQIYYDKT--------NHFLPLEEL    279
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XP_001139800.4        -SLNALKFVHYQVREAMRVAEMARH-DYVLPVFIFSRPFYLHR--------TEALSQEDL    283
NP_032343.3           T-EKSQMYVRHRVQEALRVAIVS-R-DPHVPVMPYVQIFYEMT--------DYLLPLEEL    278
NP_997499.2           T-GKSQMYVRYRVQEAFRLALVS-R-DPHVPIMPYVQIFYEKT--------DYLLPLEEL    278
XP_001168796.1        T-GKSQMYVQHRVAEAFRVAVAA-G-DPNLPVLPYVQIFYDTT--------NHFLPL---    296
NP_997482.2           -A-YHQTFVRHRLEEAFRVALTGH--AHPLPVLAYVRLTHRSS--------GRFLSLDDL    301
NP_001193181.1        -A-HHQAFVRYRLEEAFRVAIAGH--PHPLPVLAYARLTHRSS--------GRFLSLDEL    275
NP_001186958.1        -A-HHQAFVRHRLEEAFRVALVGH--RHPLPVLAYVRLTHRRS--------GRFLSQDDL    293
NP_999604.1           -A-YHQAFVRYRLEEAFRVALVGH--PHPLPVLAYARLTHRNS--------GRFLSQDEL    275
XP_001493753.3        -A-HHQAFVRYRLEEAFRVALTGH--IHPLPVLAYARLTHRSS--------GRFLSQDDL    275
NP_001121765.1        -HTHAQLMVRHRILEALRVASQHSPGSEPLPVFPYTRVAFIHS--------LTFLNQTDL    280
NP_821139.2           -A-YRQAFVRHRLEEAFRVALLEH--SHPLPVLAYSRLTHRSS--------GRFLSLDDL    277
XP_002128103.1        -TNASMEYVANRVKEALRVDFDRKN-DISAPVYVYNNIFYRKS--------SEFLTQKDI    315
XP_003642042.3        -G-LRRRYVHHRLCEALRLAA------GRLPVVAYSRLSYRRS--------PRFLEPADL    262
                                 :: *.                  : .                 :

NP_003108.2           VYTFGETVALGASGIVIWGTL-SIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVL    380
XP_003318802.2        VYTFGETVALGASGIVIWGTL-SIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVL    380
XP_003261317.2        VYTLGETVALGASGIVIWGSL-SIVRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVL    380
XP_001086882.2        VSTLGETVALGASGIVIWGSL-SITRSMKSCLLLDTYMETILNPYIINVTLAAKMCSQVL    380
NP_001076141.2        VNTIGEIVALGASGIVVWGSH-TLARSMKSCLNLDDYMKNILNPYLINVTLAAKMCNQVL    380
XP_002919069.1        VNTIGETVSLGVSGIIMWGSL-NLSQNVQSCTELDNYMTNTLNPYIINVTLAAKMCNQVL    381
NP_999176.1           VNTIGETVALGASGIVMWGSL-NLSLTMQSCMNLGSYLKTTLNPYLINVTLAAKMCSQVL    380
XP_002686960.3        VSTIGESIALGASGIIMWGSF-NLSLTKQSCMNLSNYLNTILNPYIINVTLAAKMCSQVL    379
NP_001008413.3        VNSVGEIVSLGASGIIMWGSL-NLSLSMQSCMNLGTYLNTTLNPYIINVTLAAKMCSQVL    382
XP_003502178.1        VNTIGETVALGASGMVMWGTL-GLVRSMKSCLNLHDYLENTLNPYLINVTLAAKMCSQTL    380
NP_001166492.1        VHSVGEIVPLGVSGIIIWGSL-SLTRSLVSCIGLENYMKGTLLPYLINVTLAAKMCGQVL    380
NP_001019492.1        VNTIGETVALGASGIVMWGTL-NLSQTMKSCMNLHDYLKTTLNPYIINVTLAAKMCSQTL    380
XP_001507937.2        VNTIGECAALGVSGTVMWGSL-NLTRSVKTCRILDNYMRMTLNPYIINVTLAAKMCSQVL    378
NP_001073344.1        VNTIGEIVALGTSGIIIWDAM-SLAQRAAGCPILHKYMQTTLNPYIVNVTLAAKMCSQTL    380
XP_003502177.1        VNTIGEIVALGPAGIIIWDAM-SLAQRAPGCPILHQYLKTTLNPYIINVTLAAKMCSQTL    381
XP_002190553.4        VNTIGESAALGASGIVIWGDM-NLTQNKNTCRTLDNYLRRTLTPYLINVTMAARICSQVL    365
XP_002932242.3        ANVIGEIAALGADGFVMWGEIKNMTQSKKTCTDLNSYLVKILNPYIINVTLAAKLCSHVL    375
NP_001082194.1        ANVIGEIAALGADGFVMWGDVINMTQSKKACTDLNSYLLKILNPYIINVTLAAKLCSHVL    370
XP_002919077.1        ISTIGESAALGAAGIVIWGDM-NLTSSEGNCTKVKQYVSSDLGSYIVNVTKAAEVCSLHL    380
XP_002712114.1        ISTIGESAALGAAGIVIWGDM-NLTSSKGNCTKVKQFVGSDLGRYIVNVTRAAEVCSLHL    340
XP_532444.4           ISTIGESAALGAAGIVIWGDM-NLTSSEGNCTKVKQYVSSDLGHYIVNVTRAAEVCSIHL    358
XP_002818436.2        VSTIGESAALGAAGIVIWGDM-NLTSSKANCTKVKQFVSSDLGSYIANVTRAAEVCSLHL    340
NP_084124.1           ISTIGESAALGAAGIVVWGDM-NLTSSEENCTKVNRFVNSDFGSYIINVTRAAEVCSRHL    340
XP_003134772.2        ISTIGESAALGAAGFVIWGDM-NLTSSEGNCTKVKQFVSSDLGHYVVNVTRAAEVCSLHL    358
NP_036401.2           VSTIGESAALGAAGIVIWGDM-NLTASKANCTKVKQFVSSDLGSYIANVTRAAEVCSLHL    340
XP_003261316.2        VSTIGESAALGAAGIVIWGDM-NLTSSKANCTKVKQFVNSDLGSYIANVTRAAEVCSLHL    380
XP_003407292.1        ISTIGESAALGAAGIVIWGDL-NLTSSEGNCTKVKQFVSSDLGYYIVNVTGAAEVCSRHL    361
XP_003586042.1        ISTIGESAALGAAGIVIWGDM-NLTSSKGNCTKVKQFVSSDLGSYIVNVTRAAEVCSLHV    358
NP_001094250.1        ISTIGESAALGAAGIVVWGDM-NLTSSAENCTKVNRFVNSDFGSYVINVTTAAEVCSRHL    370
XP_003221368.2        VSTIGESAALGAAGIVIWGDM-NLTSSEVNCTKVKQFIASELGVYIVNVTKAAEVCSWHL    340
XP_003475093.1        INTIGESAALGAAGIVIWGDM-NLTLSEDNCTKVKQFVSSDLGSYIVNVSTAAEICSLHL    367
NP_001090796.1        IYTIGESAALGAAGIVLWGGM-QYASTKESCITVKKYIDGPLGHYLVNVTAAAKMCSKVL    341
XP_003221369.1        VHTIGESAALGAAGVVLWGSI-QYANSYENCLTVKKYIDGPLGHYIMNVTSAAKLCSKVL    341
XP_003449274.1        IHTIGESAALGAAGFVIWGDL-NLTSSRHNCTHVKSFLSHRLGLYITNVTRAAEICSEFL    341
NP_001074140.1        VHTIGESAALGAAGVVLWGSS-EYARSQRNCLTVKKYIDGPLGHYVINVTSAAKLCSKAL    341
XP_003217669.1        ISTIGESAALGAAGAIFWGDA-EDTKSRETCQVLKNYMKENLGRYIVNVTTAADLCSQSQ    343
XP_001507903.3        ISTIGESAALGAAGIVIWGDM-NLTSSEGNCTKVKKFVTSHLGNYLINVTTAAEECSRHH    361
XP_003449275.2        IHTIGESAALGASGVVLWGSS-EYARSQRNCLTVKKYINGPLGHYVINVTSAAKLCSKAL    342
XP_001378617.3        ISTIGESAALGAAGIIFWGDA-YYTKSPETCQKIKEYLESRLAPYLVNVSEAALRCSQDL    343
XP_003210019.2        ISTIGESAALGAAGVIFWGDV-EYTKNRESCQTIKDYMEGDLGRYIVNVTTAAQHCSTTL    343
XP_414258.3           ISTIGESAALGAAGVIFWGDV-EYTKNRESCQTIKDYMEGDLGRYIVNVTTAAQHCSITL    361
NP_001080777.1        ISTIGESAAQGAAGVIFWGDA-EYTKSKETCQMIKRYLEEDLGRYIVNVTTAAELCSQSL    341
NP_001119986.1        ISTIGESAAQGAAGVIFWGDA-EYTKSKETCQMIKKYLDEDLGHYIVNVTTAAELCSQSL    372
XP_003221370.3        VHTIGESAALGAAGVILWGSM-QYASTYKNCLTVKKYIDGPFGHYIVNVTTAANLCSEVL    355
XP_003448364.1        VSTIGESVALGAAGIIMWGDI-AYAHNKTTCSDLDKYLRGTLNQYLLNVSTAAELCSQTL    360
XP_002189602.4        MNTIGESAAQGAAGIILWGSL-DYSTSKEMCLRLKDYVEGPLGHYIVNVTASADLCSQTL    338
NP_001074154.2        VSSIGESAALGASGAVLWGSS-ADYNDKTSCEALSAYLSDKLNPYILNVTTAAHLCSKNL    332
XP_003448436.2        VYTIGESAALGSAGVVLWGDH-ALSKTQATCAAVKSYIDNTLGPYLVNVTSAATLCSQIM    358
XP_002813763.3        ISTIGESAALGAAGVILWGDA-GYTTSTETCQYLKDYLTRLLVPYVVNVSWATQYCSRAQ    355
XP_002935681.1        IQTIGQSAALGAAGIILWGNA-DYSRSEESCLAVKSYIDETLGRYLVNVSSSAMLCSKAV    354
XP_001168599.1        ISTIGESAALGAAGVILWGDA-GYTTSTETCQYLKDYLTRLLVPYVVNVSWATQYCSRAQ    355
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XP_687640.2         VSTIGESVALGVAGVILWGDS-TYASSQATCSSLNEYLRGPLGRYLLNVTSAAEQCSRNL    384
NP_003764.3         ISTIGESAALGAAGVILWGDA-GYTTSTETCQYLKDYLTRLLVPYVVNVSWATQYCSRAQ    355
XP_003476739.1      VSTIGESAALGAAGVILWGDT----SSMETCQYLQKYLTDLLVPYVVNVSWATQYCSWAQ    366
XP_003257153.1      ISTIGESAALGAAGVILWGDA-GYTTSTETCQYLKDYLTRLLVPYVVNVSWATQYCSWAQ    355
XP_002758427.1      ISTIGESAALGAAGVILWGDA-GYTTSTETCQYLKDYLTRLLVPYVVNVSWATQYCSWAQ    355
XP_001102414.2      EHSLGESAAQGAAGVVLWVSW-ENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQAL    338
NP_742037.2         ISTIGESAALGSAGVIFWGDS-VYASSMENCQNLKKYLTQTLVPYIVNVSWATQYCSWTQ    343
NP_999605.1         ISTIGESAALGAAGVILWGDA-GYTTSMETCQYLKDYLTRLLVPYVVNVSWAAQYCSWAQ    358
NP_001009754.1      ISTIGESAALGAAGVILWGDA-GFTTSNETCRRLKDYLTRSLVPYVVNVSWAAQYCSWAQ    358
NP_083196.2         VHTIGESAALGAAGIILWGGY-EYSDTKETCLSVRQTVHGLLGPYVLNVTSAAKLCSQNL    358
NP_001019491.1      VHTIGESAALGAAGIILWGGY-EYSDTKETCLSLQQTVHGLLGPYALNVTSAAKLCSQSL    342
NP_776772.1         ISTIGESAALGAAGVILWGDA-GFTTSNETCRRLKDYLTRSLVPYVVNVSWAAQYCSWAQ    358
NP_149349.2         EHSLGESAAQGAAGVVLWVSW-ENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQAL    358
NP_001035086.1      VHTIGESVALGASGVVLWGDG-NFSRTKRACEAVRDYLDVTLGRYIVNVTEAAFLCSRKV    339
XP_003502176.1      VHTIGESAALGAAGIILWGGH-EYSESKEACLSVQQTIQGLLGPYVFNVTSAAKLCSQSL    342
XP_003257149.1      EHSLGESAAQGAAGVVLWVSW-ENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQAL    338
XP_002813766.6      EHSLGESAAQGAAGVVLWVSW-ENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQAL    338
NP_001017941.1      EHSLGESAAQGAAGVVLWVSW-LSTSTKESCQAIKEYVDTTLGPSILNVTSGARLCSQVL    358
XP_002920567.1      EHSLGESAAQGAAGVVLWVSW-ENTKTKESCQAIKEYVDTTLGPFLLNVTSGALLCSQAL    338
XP_003476738.1      EHTLGESAAQGAAGVVFWVSS-EDTNSKESCQAIKEYMDTTLGPFILNVTSGALLCSQAL    338
NP_999606.1         EHSLGESAAQGAAGVVLWVSW-ENTRTKESCQSIKEYVDTTLGPFILNVTSGALLCSQAV    358
XP_002713406.3      EHSLGESMAQGAAGVVLWVSS-ENTKTKESCLAIKTYVDTTLGPFILNVTSAALLCSQAL    337
XP_003500449.1      EHSIGESAAQGAAGVVVWVSS-ENTTTKESCQTIKEYMDSTLGPFILNVTSAALLCSEAL    338
XP_001509131.1      ENSIGESVAQGVAGVVLWVSW-EDTHTKESCENIKDYVDSTLGPFILNLTSSTQLCSQAL    338
XP_001139800.4      VHTIGESAALGAAGVILWGGY-EYSASKENCLSVQQSIRGPLGHYAVNVTSAAKLCSQSL    342
NP_032343.3         EHSLGESAAQGVAGAVLWLSS-DKTSTKESCQAIKAYMDSTLGPFIVNVTSAALLCSEAL    337
NP_997499.2         EHSLGESAAQGAAGAVLWISS-EKTSTKESCQAIKAYMDSTLGPFILNVTSAALLCSEAL    337
XP_001168796.1      ----------------------------ESCQAIKEYMDTTLGPFILNVTSGALLCSQAL    328
NP_997482.2         MQTIGVSAALGAAGVVLWGDL-SVSSSEEECWRLHDYLVGTLGPYVINVTKAATACSHQR    360
NP_001193181.1      VQTIGVSAALGAAGVVLWGDL-SFSSSEEECWHLHDYLLGTLGPYVINVTRAAVACSHQR    334
NP_001186958.1      VQSIGVSAALGAAGVVLWGDL-SLSSSEEECWHLHDYLVDTLGPYVINVTRAAMACSHQR    352
NP_999604.1         VQTIGVSAALGASGVVLWGDL-SFSSSEEECWHLRGYLVGTLGPYVINVTRAAMACSHQR    334
XP_001493753.3      VQTIGVSAALGAAGVVLWGDL-SFSSSEEECWRLHDYLVGTLGPYVINVTRAATACSQQR    334
NP_001121765.1      EHTLGESAALGAAGVVLWGEL-SFAKSKHQCTLLRDYLSSVLGEYITALRAGVTNCSERL    339
NP_821139.2         MQTIGVSAALGTAGVVLWGDL-SFSSSEEKCWRLHDYLVGTLGPYVINVTKAAMACSHQR    336
XP_002128103.1      IHSSGTAAVLGASGVVFWGDS-ICSKTKEMCENLKYYVENILGPYIKSASDSAAMCSLNT    374
XP_003642042.3      EHTIGESAALGAAGVVLWGDM-SYSRSAESCSSLRHYLVSVLGPYVANVTAAARACSLEQ    321
                                                  *  :   :   :         ..  *.

NP_003108.2         CQEQGVCIRKNWNS-SDYLHLNPDNFAIQLE-----KG-----GKFTVRGKPT--LEDLE    427
XP_003318802.2      CQEQGVCIRKNWNS-SDYLHLNPDNFAIQLE-----KG-----GKFTVRGKPT--LEDLE    427
XP_003261317.2      CQEQGVCIRKDWNS-SDYLHLNPDNFAIQLE-----KG-----GKFTVRGKPT--PEDLE    427
XP_001086882.2      CQEQGVCIRKDWNS-SDYLHLNPDNFDIRLE-----KG-----GKFTVHGKPT--VEDLE    427
NP_001076141.2      CQEQGVCTRKNWDS-NDYLHLNPGNFAIQIG-----NN-----GTYKVDGKPT--LTDLE    427
XP_002919069.1      CQEQGVCIRKHWNS-NDYLHLNPDNFAIQLE-----KS-----GRYTVQGKPT--LEDLQ    428
NP_999176.1         CQEQGVCTRKHWNS-SDYLHLNPANFAIRTG-----KG-----NKYIVHGKPT--LEDLK    427
XP_002686960.3      CHEEGVCTRKHWNS-TDYLHLNPMNFAIQRR-----KY-----GKYTIHGKPT--LEDLL    426
NP_001008413.3      CHNEGVCTRKHWNS-SDYLHLNPMNFAIQTG-----EG-----GKYTVPGTVT--LEDLQ    429
XP_003502178.1      CQDQGICSRKDWNS-DNYLHLSPKNFQIQFV-----RS-----GKYEIRGNPT--LDDLQ    427
NP_001166492.1      CKNQGICTRKDWNT-NTYLHLNATNFDIELQ-----QN-----GKFVVHGKPS--LEDLQ    427
NP_001019492.1      CQNQGICSRKDWNS-NDYLHLSPRNFQIHFI-----KH-----GKYEIIGSPT--LDDLQ    427
XP_001507937.2      CEERGACVRKAWNS-SDYLHLNPANFVIHTT-----ED-----GRYLVNGKPT--YADLK    425
NP_001073344.1      CNEKGMCSRRKESS-DVYLHLNPSHFDIMLT-----ET-----GKYEVLGNPR--VGDLE    427
XP_003502177.1      CEEKGVCSKKNESS-DVYLHLNPSQFYIELT-----KT-----GTYEVHGYPR--VADLQ    428
XP_002190553.4      CQDSGACARKKWNS-SDYLHLNPENIAIQMT-----KD-----GKYTLQGQPS--YQDLQ    412
XP_002932242.3      CQDNGLCTRKNWNT-NTYLHLNSNTLAIE-Q-----KN-----GKYTIKGHAT--HEDLT    421
NP_001082194.1      CQDNGLCTRKHWDT-NTYLHLNSKTLAIE-Q-----KN-----GKYTVEGNPT--YEDLT    416
XP_002919077.1      CRRNGRCRRKVWKA-PDYLHLNPASYHIEAS-----QD-----GEFTVQGKAS--DTDLK    427
XP_002712114.1      CRNNGRCIRKMWRA-PDYLHLNPASFHIAAS-----ED-----GEFIVKGKVS--DTDLA    387
XP_532444.4         CRSNGRCIRKVWKA-PDYLHLNPASYHIEAS-----KD-----GEFIVKGKAS--DMDLE    405
XP_002818436.2      CRNNGRCIRKMWNA-PSYLHLNPTSYHIEAA-----ED-----GEFTVKGKAS--DTDLA    387
NP_084124.1         CKNNGRCVRKTWKA-AHYLHLNPASYHIEAS-----ED-----GEFIVRGRAS--DTDLA    387
XP_003134772.2      CRNNGRCLRKVWKA-PDYLHLNPASYRIEAS-----ED-----GEFTVKGRAS--DRDLA    405
NP_036401.2         CRNNGRCIRKMWNA-PSYLHLNPASYHIEAS-----ED-----GEFTVKGKAS--DTDLA    387
XP_003261316.2      CRNNGRCIRKMWNA-PSYLHLNPASYHIEAS-----ED-----GEFTVKGKAS--DTDLA    427
XP_003407292.1      CGNNGRCVRRRWKA-PDYLHLNPASYHIRAS-----ED-----GDITVTGAAS--DTDLE    408
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XP_003586042.1       CRNNGRCIRKVWKM-PDYLHLNPASYHIEAS-----ED-----GEFTVKGRAS--DTDLA    405
NP_001094250.1       CKNNGRCARKTWKA-AHYLHLNPASYHIEAS-----AD-----REFVVKGRAS--DADLA    417
XP_003221368.2       CQNNGRCIRRNWKA-LNYLHLNPRNFQIEIS-----ED-----QGFTVRGEAS--SADLQ    387
XP_003475093.1       CRSNGRCVRKMWNA-SDYLHLSNKSYRIETS-----GN-----GGFTAKGNVS--DADLI    414
NP_001090796.1       CKKNGRCLRNNIDS-PDYLHLNPNHFKIKK----HFSG-----KGFFATGKPG--WEDIH    389
XP_003221369.1       CKKNGRCIRKNSES-FDYLHLHPQSFKIRFS--KTA-------NKVSVVGKMK--RKDKK    389
XP_003449274.1       CQSNGRCVRRDPHA-RHYLHLSADSYRIHPS-----GD-----GDFAVNGWHS--PHEQQ    388
NP_001074140.1       CKKNGKCVRKSLDS-GAYLHLNPRFFNIRLN--QGIRG-----PCFYVSGHLN--NLDIL    391
XP_003217669.1       CNGHGRCRRRQNDA-NVFLHLNPTSFQILHNDPG-SQA-----PLLEARGKLS--QEDID    394
XP_001507903.3       CGNNGRCTRKAWNA-HDYLHLNPQSYYIEAS-----EN-----EEFMVKGKAS--GTDSE    408
XP_003449275.2       CKKNGRCIRKSLDS-DTYLHLNSRFFHIHHN--SAPSG-----PRFHISGHLN--NHDIL    392
XP_001378617.3       CHGHGRCYRRQPGS-NAFLHLNPQSFRLRPA--ESPEE-----PLFRAEGQFS--PNDLA    393
XP_003210019.2       CQGQGRCLRKNSTA-NVFLHLNPATFQLQHRDKEQPER-----PLIWAKGHLS--HTDIH    395
XP_414258.3          CHGQGRCKRRNSTA-NVFLHLNPATFQLQRRDEEQPQR-----PLIWAKGHLS--HTDVH    413
NP_001080777.1       CNGNGRCLRQDNIT-DAFLHLNSANFQIVSAPKD-SQG-----PSLRAEGKLS--AEDIA    392
NP_001119986.1       CNGNGRCLRQENNT-DAFLHLNPANFQIVSAPKD-FQG-----PSLRAEGKLS--AGDIA    423
XP_003221370.3       CTKNGRCIRKDSES-FDYLHLNPRSFKIRYS--KTM-------KKVYVAGSMK--REDKE    403
XP_003448364.1       CGSHGRCLRRNPNS-DVYLHLNPLTHGIVEK------N-----GKLTVTGELG--KAGGL    406
XP_002189602.4       CSGRGRCVRQDK-Q-QGYLHLDPSRFTIDL----RAGK-----PWLVAQSLEP--GEDIS    385
NP_001074154.2       CQGEGRCVRKNNNS-DDFLHISSESHHIG-R-----NA-----GKYVVTGTPS--ASDLA    378
XP_003448436.2       CSSHGRCQRKDPQS-KAYLHLDPASWKVVSK--RKPNGW----RKYKVLGRLQ--PRHVK    409
XP_002813763.3       CHGHGRCVRRNPSA-STFLHLSTNSFRLVPG--RAPGE-----PQLRPVGELS--WADLD    405
XP_002935681.1       CTGNGRCVRKDPSS-DSHLHLHPDSFRIKR----HPEG-----RGFVVSGQAS--KWDIL    402
XP_001168599.1       CHGHGRCVRRNPSA-STFLHLSTNSFRLVPG--HAPGE-----PQLRPVGELS--WADLD    405
XP_687640.2          CGFRGRCLRKQPNT-DTYLHLSASTHRIERQ------A-----NTLKLTGQMS--EEELG    430
NP_003764.3          CHGHGRCVRRNPSA-STFLHLSTNSFRLVPG--HAPGE-----PQLRPVGELS--WADID    405
XP_003476739.1       CHGHGRCVRRNPTS-NTFLHLNTSSFRLVPG--RVPDG-----LQLQPEGELS--RADLN    416
XP_003257153.1       CHGHGRCVRRNPSA-NTFLHLSTNSFRLVPG--HAPGE-----PQLRPVGELS--WADLD    405
XP_002758427.1       CHGHGRCVRRNPSA-STFLHLSANSFRLVPG--RAPGE-----PQLRPVGNLS--SADRH    405
XP_001102414.2       CSSHGRCVRRPSHP-KALLILNPASFSIQL----TPDG-----GPLSLRGALS--LEDQA    386
NP_742037.2          CHGHGRCVRRNPSA-STFLHLSPSSFRLVPG--RTPSE-----PQLRPEGELS--EDDLS    393
NP_999605.1          CHGHGRCVRRDPSA-NIFLHLSASSFRLVAS--HAPGE-----PQLRPEGELS--WADRN    408
NP_001009754.1       CHGHGRCVRRDPNA-HTFLHLSASSFRLVPS--HAPDE-----PRLRPEGELS--WADRN    408
NP_083196.2          CNSHGRCVRKTPES-SFYLHMPEDSHKNYV----SKKG-----FRFVIPSPSK--LKTIM    406
NP_001019491.1       CNSHGRCIRKTPDS-SFYLHMPEDSQKNSV----TSKG-----VNFVISPKSK--LKAIV    390
NP_776772.1          CHGHGRCVRRDPNA-HTFLHLSASSFRLVPS--HAPDE-----PRLRPEGELS--WADRN    408
NP_149349.2          CSGHGRCVRRTSHP-KALLLLNPASFSIQL----TPGG-----GPLSLRGALS--LEDQA    406
NP_001035086.1       CSSQGRCVRRDPSA-SVYLHLNPEMWSIIPR--AQLPGPITGGPSYVAHRRLWTGQEETS    396
XP_003502176.1       CNSHGRCVRKTVES-SFYLHMPEDSHKSYV----INKG-----FKFVTSARSK--LKTIM    390
XP_003257149.1       CSGHGRCVRRPSHP-KALLLLNPASFSIQL----TPGG-----GPLSLQGALS--LEDQA    386
XP_002813766.6       CSGHGRCVRRPSHP-KALLLLNPASFSIQL----TPGG-----GPLSLRGALS--LEDQA    386
NP_001017941.1       CSGHGRCARRPSYP-KARLILNSTSFSIKP----TPGG-----GPLTLQGALS--LEDRL    406
XP_002920567.1       CSGHGRCARRPSHP-EALLILNPTSFSIQL----TRGG-----GPLTLQGALS--LEDRM    386
XP_003476738.1       CFGHGRCVRRPSHP-DALLILSLASFSIQF----TPGG-----KPLTLKGALS--HEDQA    386
NP_999606.1          CSGHGRCVRRPSHT-EALPILNPSSFSIKP----TPGG-----GPLTLQGALS--LKDRV    406
XP_002713406.3       CSGHGRCARHPSHP-EALLVLSPASFSIQL----TPG------GPLTLQGALS--LKDRV    384
XP_003500449.1       CSGHGRCARRPSYP-EALLTLNPASFSIQI----THDG-----RPPSLKGTLS--LKDQA    386
XP_001509131.1       CSGHGRCARRRDHP-HAFLYLNSSSFSIHR----PPGS-----RHLVLTGKLP--KEDQA    386
XP_001139800.4       CNNHGRCIRKTPES-SFYLHMPESSGKEYV----LNKS-----FRFIISENNK--QKTIK    390
NP_032343.3          CSGHGRCVRHPSYP-EALLTLNPASFSIEL----THDG-----RPPSLKGTLS--LKDRA    385
NP_997499.2          CSGRGRCVRHPSYP-EALLTLSPASFSIEP----THDG-----RPLSLKGTLS--LKDRA    385
XP_001168796.1       CSGHGRCVRRTSHP-KALLLLNPASFSIQL----TPGG-----GPLSLQGALS--LEDQA    376
NP_997482.2          CHGHGRCSWKDPGQMEAFLHLQPD-------------D----------------------    385
NP_001193181.1       CHGHGRCAWQNPGQLEVFLHLQPD-------------G-----------------SPG--    362
NP_001186958.1       CHGHGRCARRDPGQMEAFLHLWPD-------------G-----------------SLG--    380
NP_999604.1          CHGHGRCAWQDPGQLKVFLHLHPG-------------G----------------------    359
XP_001493753.3       CHGHGRCARRDPGQMEAFLHLQPD-------------G----------------------    359
NP_001121765.1       CNAQGRCSRWDPHSHHMIPLLGPH-------------D-----------------ALSLS    369
NP_821139.2          CHGHGRCARKDPGQMEAFLHLQPD-------------D----------------------    361
XP_002128103.1       CNGHGRCV----------------------------------------------------    382
XP_003642042.3       CHGHGRCVRRQPRELSILLHLGAG------------------------------------    345
                     *   * *


NP_003108.2          QFSEKFYCSCYSTL---SCKEKADVKDTDA--------VDVCIA-DGVCIDAFLKPPMET    475
XP_003318802.2       QFSEKFYCSCYSTL---SCKEKADVKDTDA--------VDVCIA-DGVCIDAFLKPPMET    475
XP_003261317.2       QFSEKFYCSCYSTL---SCKERADVKDTDA--------VDVCIA-DGVCIDAFLKPPKET    475
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727   XP_001086882.2      EFSEKFYCSCYTNL---SCKEKADVKDTDA--------VDVCIA-DGVCIDASLKPPVET   475
728   NP_001076141.2      QFSKNFQCSCYTNL---NCKERTDMNNVQT--------VNVCAV-ENVCIDTNVGPQAVT   475
729   XP_002919069.1      QFSKNFYCSCYANV---RCKERVDMTEIHT--------VKVCVA-ADVCIDSFL------   470
730   NP_999176.1         EFSKNFYCSCFANF---HCKERADIENIHA--------INVCIT-EDVCVEAFL------   469
731   XP_002686960.3      QFSENFYCSCYANI---HCKKR-DIKNIHT--------INVCFA-EDVCINASL------   467
732   NP_001008413.3      KFSDTFYCSCYANI---HCKKRVDIKNVHS--------VNVCMA-EDICIDSPVKLQPSD   477
733   XP_003502178.1      YFSKNFRCSCYSNL---NCKERDDLESVST--------VSVCAV-ETACINSFV------   469
734   NP_001166492.1      EFSKNFHCSCYTNV---ACKDRLDVHNVRS--------VNVCTA-NNICIDAVLNFPSLD   475
735   NP_001019492.1      YFSKNFRCSCFSNL---DCKERVDINHVSR--------VNVCTL-EDICINSLV------   469
736   XP_001507937.2      QFSKKFTCRCFAGS---SCKTVVNVTTTSF--------IYVCIA-DDICIEADLNSNLSE   473
737   NP_001073344.1      YFSEHFKCSCFSRM---TCKETSDVKNVQD--------VNVCVG-DNVCIKAKVEP----   471
738   XP_003502177.1      YFSEHFQCSCFTNM---DCQETPDIEDIMD--------VNVCIG-DNICIKAEVEP----   472
739   XP_002190553.4      TFIEKFDCHCYAGH---SCEPRADINDIHY--------LHACIS-EDICI----------   450
740   XP_002932242.3      YFSKHFQCHCNAGR---KCKETFNLKNIGL--------VNVCLPNSNICVKA--------   462
741   NP_001082194.1      YFSKNFKCLCYAGR---TCKELIHLQIIGL--------VNICLPKSNICIKA--------   457
742   XP_002919077.1      AMEEKFSCHCYQGYEGADCRGKKTADGC--------------------------------   455
743   XP_002712114.1      VMAEKFSCHCYQGYEGADCREMKTVDGC--------------------------------   415
744   XP_532444.4         ALEESFSCHCYQGYEGADCRGTKTADGC--------------------------------   433
745   XP_002818436.2      VMADTFSCHCYQGYEGADCRETKTADGC--------------------------------   415
746   NP_084124.1         VMAENFLCHCYEGYEGADCRE---------------------------------------   408
747   XP_003134772.2      VLVERFSCHCYQGYEGTDCREMKRADGC--------------------------------   433
748   NP_036401.2         VMADTFSCHCYQGYEGADCREIKTADGC--------------------------------   415
749   XP_003261316.2      VMADTFSCHCYQGYEGPDCREIKTADGC--------------------------------   455
750   XP_003407292.1      VMAEKFSCHCYQGYKGADCRAMKTPDG---------------------------------   435
751   XP_003586042.1      VLAERFSCHCYQGYQGADCREMKTADGC--------------------------------   433
752   NP_001094250.1      AMAENFLCHCYEGYEGADCRD---------------------------------------   438
753   XP_003221368.2      IMTEKFTCHCYQGFEGENCKKIQTVDG---------------------------------   414
754   XP_003475093.1      VMKQKFFCQCYQGHEGANCQEMKEVDGSTG---LSSC-----------------------   448
755   NP_001090796.1      YMEQRFMCQCY-------------------------------------------------   400
756   XP_003221369.1      AMKEKFMCQCYQGWTGK-------------------------------------------   406
757   XP_003449274.1      LLMERFRCHCYEGHNGENCDSINKVREDKG---PWEEEE---------------------   424
758   NP_001074140.1      DMKQKFTCQCY-------------------------------------------------   402
759   XP_003217669.1      FLQHNFQCHCYQGWRGEGCEEQ--------------------------------------   416
760   XP_001507903.3      VMEEKFSCHCY-------------------------------------------------   419
761   XP_003449275.2      DMKQKFTCQCY-------------------------------------------------   403
762   XP_001378617.3      QLREHFQCQCY-------------------------------------------------   404
763   XP_003210019.2      FLQIHFRCHCYQGWQGNSCQQPA-------------------------------------   418
764   XP_414258.3         FLQTHFRCHCYQGWQGNSCQQSA-------------------------------------   436
765   NP_001080777.1      VLRSQFRCQCY-------------------------------------------------   403
766   NP_001119986.1      TLRSQFRCQCY-------------------------------------------------   434
767   XP_003221370.3      AMEEKFMCQCYQGWS---------------------------------------------   418
768   XP_003448364.1      GFEADFQCQCYS------------------------------------------------   418
769   XP_002189602.4      RLAKEFSCQCY-------------------------------------------------   396
770   NP_001074154.2      DWKSKFTCQCYEDR---NC-----------------------------------------   394
771   XP_003448436.2      LMESEFQCRCYAGWRGQSCSE---------------------------------------   430
772   XP_002813763.3      HLQTHFRCQCYLGWSGEQ------------------------------------------   423
773   XP_002935681.1      YFGEHFYCRCY-------------------------------------------------   413
774   XP_001168599.1      HLQTHFRCQCYLGWSGEQ------------------------------------------   423
775   XP_687640.2         RLRDDFQCQCYNGYSGDDCSIKD-------------------------------------   453
776   NP_003764.3         HLQTHFRCQCYLGWSGEQ------------------------------------------   423
777   XP_003476739.1      YLRTHFRCQCY-------------------------------------------------   427
778   XP_003257153.1      HLQTHFRCQCYLGWSGEQ------------------------------------------   423
779   XP_002758427.1      HLQTHFRCQCY-------------------------------------------------   416
780   XP_001102414.2      QMAVEFKCRCYPGWQGPWCEQKS-------------------------------------   409
781   NP_742037.2         YLQMHFRCHCY-------------------------------------------------   404
782   NP_999605.1         HLQTHFRCQCY-------------------------------------------------   419
783   NP_001009754.1      HLQTHFRCQCY-------------------------------------------------   419
784   NP_083196.2         NMKNGFVCHCY-------------------------------------------------   417
785   NP_001019491.1      NMKNGFVCHCY-------------------------------------------------   401
786   NP_776772.1         HLQMHFRCQCY-------------------------------------------------   419
787   NP_149349.2         QMAVEFKCRCY-------------------------------------------------   417
788   NP_001035086.1      RFADSFRCQCF-------------------------------------------------   407
789   XP_003502176.1      NMKNGFVCHCYYGWYGESCRSHFPNLLSRKNKAPVTAFNSVVFLGMTLCV----------   440
790   XP_003257149.1      QMAVEFKCRCYPGWQGLWCEQKS-------------------------------------   409
791   XP_002813766.6      QMAVEFKCRCYPGWQGPWCEQKS-------------------------------------   409
792   NP_001017941.1      RMAVEFECRCY-------------------------------------------------   417
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XP_002920567.1      RMAVEFQCRCY-------------------------------------------------    397
XP_003476738.1      QMAVEFRCHCY-------------------------------------------------    397
NP_999606.1         QMAEEFQCRCY-------------------------------------------------    417
XP_002713406.3      QMATEFQCHCY-------------------------------------------------    395
XP_003500449.1      QMAMKFKCRCYS------------------------------------------------    398
XP_001509131.1      RMMIEFECHCY-------------------------------------------------    397
XP_001139800.4      DMKNGFVCHCY-------------------------------------------------    401
NP_032343.3         QMAMKFRCRCY-------------------------------------------------    396
NP_997499.2         QMAMKFKCRCYRGWSGEWCKKQ--------------------------------------    407
XP_001168796.1      QMAVEFKCRCYPGWQGPWCEQKS-------------------------------------    399
NP_997482.2         ------------------------------------------------------------    385
NP_001193181.1      -AWESFSCRCYHGWAGPTCQEPRPELRPEEA-----------------------------    392
NP_001186958.1      -DWKSFSCHCYWGWAGPTCQE---------------------------------------    400
NP_999604.1         ------------------------------------------------------------    359
XP_001493753.3      ------------------------------------------------------------    359
NP_001121765.1      DMRSKFKCVCYEGWS---------------------------------------------    384
NP_821139.2         ------------------------------------------------------------    361
XP_002128103.1      ------------------------------------------------------------    382
XP_003642042.3      -SWA--------------------------------------------------------    348


NP_003108.2         EEP-------QIFYNASPSTLSATMFI--------------   495
XP_003318802.2      EES-------QIFYNASPSTLSATMFIVSILFLIISSVASL   509
XP_003261317.2      EES-------QIFYNASPSTLSATMFIVSILFLIISSVVSL   509
XP_001086882.2      EGS-----P-PIFYNTSSSTVSTTMFIVIILFLIISSVVSL   510
NP_001076141.2      YAPKEKKDVAHILSNTTSINSSTTM----------------   500
XP_002919069.1      -----------------------------------------   470
NP_999176.1         -----------------------------------------   469
XP_002686960.3      -----------------------------------------   467
NP_001008413.3      HSSSQEAST-TTFSSISPSTTTATV----------------   501
XP_003502178.1      -----------------------------------------   469
NP_001166492.1      DDDEPPI----------------------------------   482
NP_001019492.1      -----------------------------------------   469
XP_001507937.2      EDFSNSS----------------------------------   480
NP_001073344.1      -----------------------------------------   471
XP_003502177.1      -----------------------------------------   472
XP_002190553.4      -----------------------------------------   450
XP_002932242.3      -----------------------------------------   462
NP_001082194.1      -----------------------------------------   457
XP_002919077.1      -----------------------------------------   455
XP_002712114.1      -----------------------------------------   415
XP_532444.4         -----------------------------------------   433
XP_002818436.2      -----------------------------------------   415
NP_084124.1         -----------------------------------------   408
XP_003134772.2      -----------------------------------------   433
NP_036401.2         -----------------------------------------   415
XP_003261316.2      -----------------------------------------   455
XP_003407292.1      -----------------------------------------   435
XP_003586042.1      -----------------------------------------   433
NP_001094250.1      -----------------------------------------   438
XP_003221368.2      -----------------------------------------   414
XP_003475093.1      -----------------------------------------   448
NP_001090796.1      -----------------------------------------   400
XP_003221369.1      -----------------------------------------   406
XP_003449274.1      -----------------------------------------   424
NP_001074140.1      -----------------------------------------   402
XP_003217669.1      -----------------------------------------   416
XP_001507903.3      -----------------------------------------   419
XP_003449275.2      -----------------------------------------   403
XP_001378617.3      -----------------------------------------   404
XP_003210019.2      -----------------------------------------   418
XP_414258.3         -----------------------------------------   436
NP_001080777.1      -----------------------------------------   403
NP_001119986.1      -----------------------------------------   434
XP_003221370.3      -----------------------------------------   418
XP_003448364.1      -----------------------------------------   418
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XP_002189602.4      -----------------------------------------   396
NP_001074154.2      -----------------------------------------   394
XP_003448436.2      -----------------------------------------   430
XP_002813763.3      -----------------------------------------   423
XP_002935681.1      -----------------------------------------   413
XP_001168599.1      -----------------------------------------   423
XP_687640.2         -----------------------------------------   453
NP_003764.3         -----------------------------------------   423
XP_003476739.1      -----------------------------------------   427
XP_003257153.1      -----------------------------------------   423
XP_002758427.1      -----------------------------------------   416
XP_001102414.2      -----------------------------------------   409
NP_742037.2         -----------------------------------------   404
NP_999605.1         -----------------------------------------   419
NP_001009754.1      -----------------------------------------   419
NP_083196.2         -----------------------------------------   417
NP_001019491.1      -----------------------------------------   401
NP_776772.1         -----------------------------------------   419
NP_149349.2         -----------------------------------------   417
NP_001035086.1      -----------------------------------------   407
XP_003502176.1      -----------------------------------------   440
XP_003257149.1      -----------------------------------------   409
XP_002813766.6      -----------------------------------------   409
NP_001017941.1      -----------------------------------------   417
XP_002920567.1      -----------------------------------------   397
XP_003476738.1      -----------------------------------------   397
NP_999606.1         -----------------------------------------   417
XP_002713406.3      -----------------------------------------   395
XP_003500449.1      -----------------------------------------   398
XP_001509131.1      -----------------------------------------   397
XP_001139800.4      -----------------------------------------   401
NP_032343.3         -----------------------------------------   396
NP_997499.2         -----------------------------------------   407
XP_001168796.1      -----------------------------------------   399
NP_997482.2         -----------------------------------------   385
NP_001193181.1      -----------------------------------------   392
NP_001186958.1      -----------------------------------------   400
NP_999604.1         -----------------------------------------   359
XP_001493753.3      -----------------------------------------   359
NP_001121765.1      -----------------------------------------   384
NP_821139.2         -----------------------------------------   361
XP_002128103.1      -----------------------------------------   382
XP_003642042.3      -----------------------------------------   348
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