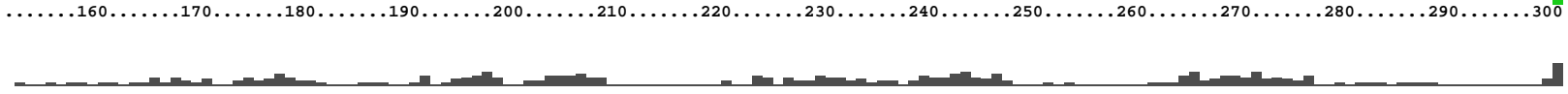


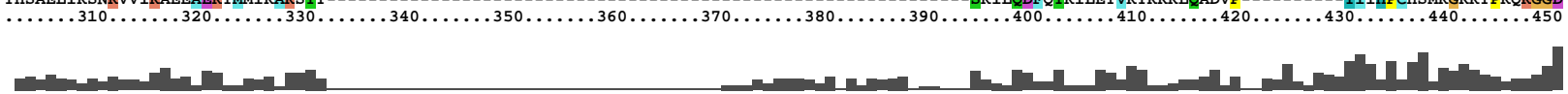
gi | 17137682 | ref | NP_477436.1 | ...MYQPLPPPPVQAPPPPPPPPEEDLSPPG--VGVPSHNYSNESHSSQS...KSLDYVYPTAPAYASSVPSY...DPYQPPAYGTEGAYNEQAQKVGQESHYQYVPAAGS- 108
gi | 158297080 | ref | XP_555381.3 | ...MNHQ--RPPNYSAPPPPPQORNHYLPRGGHTGIPPPGEIASGHSNAGFTMPNFNPPPSLPPAMTRPP...PPAPYAREKPEKSHSPNTSSVHSSSQHAYKRRHP- 103
gi | 73953908 | ref | XP_854135.1 | ...MSFHPGR-GCPRGRGGHGARP-SAPAFRPNLRLLLHPQPPVQYQYPPSAPSTTFSNSPAPNLFPPRPDFVPPPPMPPSAQGLPPPCIRPPFFNHQMRPPFVPPCFPPMPPMPCFNPPVPGAPPGGCTFFPMMP- 138
gi | 194676595 | ref | XP_591998.4 | ...MSFHPGGRCPRGRGGHGARPSAPAFRPNLRLLLHPQPPVQYQYPPSAPSTTFSNSPAPNLFPPRPDFVPPPPMPPSAQGLPPPCIRPPFFNHQMRPPFVPPCFPPMPPPLPCFNPPVPGAPPGGAFPMMP- 140
gi | 155030234 | ref | NP_037367.3 | ...MMCGNTCHRMSFHPGR-GCPRGRGGHGARP-SAPAFRPNLRLLLHPQPPVQYQYPPSAPSTTFSNSPAPNLFPPRPDFVPPPPMPPSAQGLPPPCIRPPFFNHQMRPPFVPPCFPPMPPMPCFNPPVPGAPPGGCTFFPMMP- 147
gi | 114600823 | ref | XP_001157589.1 | ...MMCGNTCHRMSFHPGR-GCPRGRGGHGARP-SAPAFRPNLRLLLHPQPPVQYQYPPSAPSTTFSNSPAPNLFPPRPDFVPPPPMPPSAQGLPPPCIRPPFFNHQMRPPFVPPCFPPMPPMPCFNPPVPGAPPGGCTFFPMMP- 147
gi | 54873615 | ref | NP_081075.2 | ...MPPRPDFVYPPPAAPSAQGLPPPCVFRPPFNHQMRRHFFVPPCFPPMPPMPCFNPPVPGAPPGGCTFFPMMP- 76
gi | 109464509 | ref | XP_226843.4 | ...MCGNTCHRMSYHPGR-GCPRGRGGHGARP-SAPAFRPNLRLLLHPQPPVQYQY...-MPPRPDFVYPPPAAPSAQGLPPPCVFRPPFNHQMRRHFFVPPCFPPMPPMPCFNPPVPGAPPGGCTFFPMMP- 52
gi | 57530438 | ref | NP_001006379.1 | ...MSFHSGR-GCPRGGPGART-FAQYRPNLRLQLHPQPPVQYQYDQQAAPATVSNPATSVMPPRPDFVYPPVPPSTQNPINOCMPRPPFNHQMRRHFFVPPCFPPMPPVPAAPSAPVATATGCTFFPMMP- 138
gi | 160333099 | ref | NP_001103942.1 | ...MSFHAGR-GCPRGR--LPAQGIYHPAPP-RHYDPSAAGPVNPPQGGSSVMPHPDFMSRHFPPPSQAANTLQPCIRPP...VFTEPPPPPP-PPHSDGSTPMP--IQNSYVMYMN- 112
gi | 193202651 | ref | NP_001122460.1 | ...MDEIKMTLNFPRKRRARKKQKQYQRRHHEEMQQLGRRFPQPSISSAPDPVVERIP...LPTSTSAFLPGDSPRLTEKDYETNMMDPP- 92



gi | 17137682 | ref | NP_477436.1 | ...SFLYESYKYVDRYPAYS...NRYPPPERQRYTSSSS...QGYHHYPGYSGRRYEQRHQEHQIQD...SRYAHEPRHGHYA...HR 186
gi | 158297080 | ref | XP_555381.3 | ...PYKGTG--GSQYPPQG...RRYGSPNNVPNTSGG...TGKHPGHYS...SAGKKTASY...TRPSAPRYAPSG...RS 170
gi | 73953908 | ref | XP_854135.1 | ...PPSMHPPPPPVMPQVNYQ--YPPGYSHH--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--DRRERGRSPDRRQDS--RYRSDYDRGRT-RRHRSYERS 275
gi | 194676595 | ref | XP_591998.4 | ...PPSLPHPPPPPVVPQVNYQ--YPPGYSHS--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--ERRERGRSPDRRQDS--RYRSDYDRGRT-RRHRSYERS 277
gi | 155030234 | ref | NP_037367.3 | ...PPSMHPPPPPVMPQVNYQ--YPPGYSHH--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--DRRERGRSPDRRQDS--RYRSDYDRGRT-RRHRSYERS 284
gi | 114600823 | ref | XP_001157589.1 | ...PPSMHPPPPPVMPQVNYQ--YPPGYSHH--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--DRRERGRSPDRRQDS--RYRSDYDRGRT-RRHRSYERS 284
gi | 54873615 | ref | NP_081075.2 | ...PPSMHPPPPPVMPQVNYQ--YPPGYSHS--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--ERRERGRSPERRRPS--RYRSDYDRGRTPPRHSYERS 213
gi | 109464509 | ref | XP_226843.4 | ...PPAVPHPPPPPVVPQVNYQVYVSTGYQQS--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--ERRERGRSPERRRPS--RYRSDYDRGRTPPRHSYERS 52
gi | 57530438 | ref | NP_001006379.1 | ...PPAVPHPPPPPVVPQVNYQVYVSTGYQQS--FPPNFNSFONNPSFPPSANNST--PFRHLPPYPLKAPERRSPERLKHYYDHRHRDHS--GRGERHRSL--ERRERGRSPERRRPS--RYRSDYDRGRTPPRHSYERS 283
gi | 160333099 | ref | NP_001103942.1 | ...IPPPPLPMPSPVPTMPYPTVMSYVPPQQLPPPSFNPAYQPPGSGFKPERSRPP...LHYKIDCSRSPERLRRHDDHRHRGHSYSEYGRNREFGGKRDGCSERRRSDSPRRCKSDYDRGRVS...S 242
gi | 193202651 | ref | NP_001122460.1 | ...VVS 95



gi | 17137682 | ref | NP_477436.1 | ...AKGSHGYGSAARNQVSDYSRCHHERE...RNELEKTRAKPKVETER...DRLLRQWCNFKCEKPEDYVKMNAALS--EADAPVEHWRRSSPABLYVERT---KSE 286
gi | 158297080 | ref | XP_555381.3 | ...HSVPSNTDRLGRPPRDRSASCRRDSDNS...SBERASSRHSRFKVDTER...ABELSKWCNRYCETSEDIARLAEAMA--NDED--RTLWRSSPABLYKR---VSD 268
gi | 73953908 | ref | XP_854135.1 | ...RERERERHRDRSRSPSLERSYKKEYKRSGRSYGLPVVPEPAGCTPELPGELIKNTDQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 423
gi | 194676595 | ref | XP_591998.4 | ...RERERERHRDRSRSPSLERSYKKEYKRSGRSYGLPVVPEPAGCTPELPGELIKNTDQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 388
gi | 155030234 | ref | NP_037367.3 | ...RERERERHRDRSRSPSLERSYKKEYKRSGRSYGLPVVPEPAGCTPELPGELIKNTDQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 432
gi | 114600823 | ref | XP_001157589.1 | ...RERERERHRDRSRSPSLERSYKKEYKRSGRSYGLPVVPEPAGCTPELPGELIKNTDQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 432
gi | 54873615 | ref | NP_081075.2 | ...RERERERHRDRSRSPSLERSYKKEYKRSGRSYGLPVVPEPAGCTPELPGELIKNTDQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 361
gi | 109464509 | ref | XP_226843.4 | ...RERDRDRHRDRSRSPDRSYKKEYKRSGRSYGLPVVPEPAGCTPELPGEMIKTQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 79
gi | 57530438 | ref | NP_001006379.1 | ...RERDRDRHRDRSRSPDRSYKKEYKRSGRSYGLPVVPEPAGCTPELPGEMIKTQWAPPEIVNHRSPREKKRARWEEKDRWSDNQGSKDKNYTSIKEKEPEETMPDKNEE--EELLKPVWIRCTHSENYSSDPMDQVD 394
gi | 160333099 | ref | NP_001103942.1 | ...RHSRDRYRHRDDPGSPSDRHRKHARNRSG...SRERKRRRVEEDKERRDGS...SRERSVNSRREAEETIDRHEEDRGOEELHKPAWIRCTHSENYSSDPMDQVD 351
gi | 193202651 | ref | NP_001122460.1 | ...THSAELIKSNRVIKAEAEKYMIMAKSIT...SKILDQFQKILETVKTKRRLQADV...YIHPCHSMKGRKTQKQGGD 173



gi | 17137682 | ref | NP_477436.1 | ...NEVGRARLQKLCITLDFEELLQRAKRVREKLPVYVPPRKRARRVCKHKKSEAC...SSSSDDDEDFAFKIEQDCMEELSRKQHPQRVHADLWYNDGEMNDGPLCRCSAKSRRIRRHGIVPGETGYKLDQPNNSNAGLKFHYRI 436
gi | 158297080 | ref | XP_555381.3 | ...KVVESARLDALCLTFEELLKRAERIRATTPYVPPRKRARRVCKHKKSEAC...SSSSDDDEDFAFKIEQDCMEELSRKQHPQRVHADLWYNDGEMNDGPLCRCSAKSRRIRRHGIVPGETGYKLDQPNNSNAGLKFHYRI 412
gi | 73953908 | ref | XP_854135.1 | ...STVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 568
gi | 194676595 | ref | XP_591998.4 | ...STVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 577
gi | 155030234 | ref | NP_037367.3 | ...STVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 577
gi | 114600823 | ref | XP_001157589.1 | ...STVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 506
gi | 54873615 | ref | NP_081075.2 | ...STVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 224
gi | 109464509 | ref | XP_226843.4 | ...STVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 539
gi | 57530438 | ref | NP_001006379.1 | ...STVVGTSRLRDLYERFEEELGKROERAKSIRPKWPPPKTKLDEDELE--SSSESCEDEDED--STCS--SSSEVFDVIAEIKRKAHPDRLHDELWYNDPGQMDGDLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNAGRLFHYRI 498
gi | 160333099 | ref | NP_001103942.1 | ...EFTAVSDVSDNSQDEASTSPNTRQAPEADTKTEGVKDEKTCNRRQAKAKLRNFEKER...QTLILKLGIDRKKHPNGIHPDLSFNEKGLNGEGPECKPFIKTCGLKKGHYVAGEDKADCK--KSNENLHYTYLR 314
gi | 193202651 | ref | NP_001122460.1 | ...460...470...480...490...500...510...520...530...540...550...560...570...580...590...600



gi | 17137682 | ref | NP_477436.1 | 158297080 | ref | XP_555381.3 | 73953908 | ref | XP_854135.1 | 194676595 | ref | XP_591998.4 | 155030234 | ref | NP_037367.3 | 114600823 | ref | XP_001157589.1 | 54873615 | ref | NP_081075.2 | 109464509 | ref | XP_226843.4 | 57530438 | ref | NP_001006379.1 | 160333099 | ref | NP_001103942.1 | 193202651 | ref | NP_001122460.1

ISPPNFLLTKPTI... 584
ISPPNFLLTKPTI... 558
VSPPTNFLTDRPT... 715
VSPPTNFLTDRPT... 680
VSPPTNFLTDRPT... 724
VSPPTNFLTDRPT... 724
VSPPTNFLTDRPT... 653
VSPPTNFLTDRPT... 371
VSPPTNFLTDRPT... 686
VSPPTNFLTDRPT... 644
VPLPSENQLYR... 463



gi | 17137682 | ref | NP_477436.1 | 158297080 | ref | XP_555381.3 | 73953908 | ref | XP_854135.1 | 194676595 | ref | XP_591998.4 | 155030234 | ref | NP_037367.3 | 114600823 | ref | XP_001157589.1 | 54873615 | ref | NP_081075.2 | 109464509 | ref | XP_226843.4 | 57530438 | ref | NP_001006379.1 | 160333099 | ref | NP_001103942.1 | 193202651 | ref | NP_001122460.1

ISCSSEWNYVDFIK... 733
MSQNEWDYVDYV... 708
GSKLEGQKAYGES... 857
WEELEWQKYAECK... 822
WEELEWQKYAECK... 866
WEELEWQKYAECK... 866
WEELEWQKYAECK... 795
WEELEWQKYAECK... 513
WEELEWQKYAECK... 828
WEELEWQKYAECK... 786
AIDQFTRN... 597



gi | 17137682 | ref | NP_477436.1 | 158297080 | ref | XP_555381.3 | 73953908 | ref | XP_854135.1 | 194676595 | ref | XP_591998.4 | 155030234 | ref | NP_037367.3 | 114600823 | ref | XP_001157589.1 | 54873615 | ref | NP_081075.2 | 109464509 | ref | XP_226843.4 | 57530438 | ref | NP_001006379.1 | 160333099 | ref | NP_001103942.1 | 193202651 | ref | NP_001122460.1

GHLRFHKSLLD... 875
GHLRFHRSNLV... 850
THHIRYHQLM... 999
THHIRYHQLM... 964
THHIRYHQLM... 1008
THHIRYHQLM... 1016
THHIRYHQLM... 937
THHIRYHQLM... 975
THHIRYHQLM... 650
THHIRYHQLM... 928
CHHIRYFSLDV... 733



gi | 17137682 | ref | NP_477436.1 | 158297080 | ref | XP_555381.3 | 73953908 | ref | XP_854135.1 | 194676595 | ref | XP_591998.4 | 155030234 | ref | NP_037367.3 | 114600823 | ref | XP_001157589.1 | 54873615 | ref | NP_081075.2 | 109464509 | ref | XP_226843.4 | 57530438 | ref | NP_001006379.1 | 160333099 | ref | NP_001103942.1 | 193202651 | ref | NP_001122460.1

LALLAKKLEL... 1025
LAVLAKKLEL... 1000
LAMLAKKLEL... 1148
LAMLAKKLEL... 1113
LAMLAKKLEL... 1157
LAMLAKKLEL... 1165
LAMLAKKLEL... 1086
LAMLAKKLEL... 804
LAMLAKKLEL... 1119
LAMLAKKLEL... 1077
LALLAKKLEL... 883



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gi |17137682|ref|NP_477436.1|
gi |158297080|ref|XP_555381.3|
gi |73953908|ref|XP_854135.1|
gi |194676595|ref|XP_591998.4|
gi |155030234|ref|NP_037367.3|
gi |114600823|ref|XP_001157589.1|
gi |54873615|ref|NP_081075.2|
gi |109464509|ref|XP_226843.4|
gi |57530438|ref|NP_001006379.1|
gi |160333099|ref|NP_001103942.1|
gi |193202651|ref|NP_001122460.1|

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CSEYLYRHFPPEHHEGHLTLRSLVNNRTOAVVCDLGMTYAVYSNPK---ADLTKDRADLLEAFIAGLYVDKGLYCEMFCHVCLFPRLODFIMNODWNPDKSKLOQCCLTLRMDGGEPDIPYKVEASGPNTRVTKVAVYFRG 1147
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1297
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1262
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1306
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1314
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1235
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 953
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1268
ATEYLFHFPPDHHEGHLTLRSLVNNRTOAKVAEELGMEYAITNDKTKRPVALRRTKTLADLLESFIAALYIDKDLEYVHTFMNVCFPPRLKEFILNQDWNPKSLOQCCLTLRTE-GKEPDIPLYKTLQTVGSPHARTYTVAVYFKG 1226
VSDFLYRRFPYHHEGHSLLRSLVSNTOAVVCDLGFTEFVKAQYKTP--PELKLKDKADLVHAFIAGLYVDKGLYVDRGIEHCRAFIRIVFCPRLKHFISEKWNDAKSHLOQWCLAMRDPSSSEPDMPYRVLGIEGPNNRIFKIYAVYK 1031
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350

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gi |17137682|ref|NP_477436.1|
gi |158297080|ref|XP_555381.3|
gi |73953908|ref|XP_854135.1|
gi |194676595|ref|XP_591998.4|
gi |155030234|ref|NP_037367.3|
gi |114600823|ref|XP_001157589.1|
gi |54873615|ref|NP_081075.2|
gi |109464509|ref|XP_226843.4|
gi |57530438|ref|NP_001006379.1|
gi |160333099|ref|NP_001103942.1|
gi |193202651|ref|NP_001122460.1|

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KRLACADGHSIQQAEMNAAKQALENSKDLFP[LDH]ORRVIA[Q]SLKR[KV]RSAGGPGGRGGPGGGGGGGGGGAA[SGSS]GANGE[Q]P[GG]E[DE]LE[DE]G[TE]G[CO]TEGAAAKRTR[Q]KNASE[Q]PRAAAAD[PLP]EVIKME[PLD]IKDE[PL] 1297
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[KEP]D[E]D[IKK]----- 1365
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[KEP]D[E]D[IKK]----- 1330
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[REP]D[E]D[IKK]----- 1374
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[REP]D[E]D[IKK]----- 1382
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[REP]E[AD]E[IKK]----- 1303
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[REP]D[E]A[E]D[IKK]----- 1021
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[REP]D[E]E[ARK]----- 1336
ERIGCGKGPSIQQAEMGAAMDAL[EKYN]--FP[MAH]QKR[FIER]K[YOEL]-----KEMRW[ERE]H[Q]E[REP]D[E]G----- 1289
KRLA[AAESNV]HKAELRVAELALANLES--MSF[SKM]KAKNNSNMRRRL-----E[Q]DTS[D]----- 1083
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500

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gi |17137682|ref|NP_477436.1|
gi |158297080|ref|XP_555381.3|
gi |73953908|ref|XP_854135.1|
gi |194676595|ref|XP_591998.4|
gi |155030234|ref|NP_037367.3|
gi |114600823|ref|XP_001157589.1|
gi |54873615|ref|NP_081075.2|
gi |109464509|ref|XP_226843.4|
gi |57530438|ref|NP_001006379.1|
gi |160333099|ref|NP_001103942.1|
gi |193202651|ref|NP_001122460.1|

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D[ACD]Y[SSV]S[EED]E[FGL]D[DI]S[E]G[E]E[F]A[D]M[ADD]I[S]E[ER]D[ED]V[KP]N[V]E[LE]A[A]V[L]K[E]I[N]E[IR]I[N]D[E]Q[GGG]S[G]T[CGP]V[S]I[L]Q[A]Y[L]K[V]E[G]T[DEL]S[S]D[LE]A[G]E[I]D 1404
----- 1365
----- 1330
----- 1374
----- 1382
----- 1303
----- 1021
----- 1336
----- 1289
----- 1083
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....

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