

Figure S1. Alignment of AK sequences spanning major taxonomic groups. The alignment of 137 animal, fungal, protist, and plant AK sequences used to construct the phylogenetic tree.

CLUSTAL W(1.81) multiple sequence alignment

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XP_004484680.1/1-405	-----MDKC-KENYISGPV---KTTVLSGDGPKRVLMTPLQPSQN-----
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gi 1617451788 ref XP_007568855.1/1-331	-----MQNKENYEPKG-LQRQF-----
gi 1594674988 ref XP_007185333.1/1-402	-----MDKC-KENSISGP---KTTVPLGDGPKRVPVTQQFPSQN-----
gi 1594654199 ref XP_007175509.1/1-282	-----
gi 1594623572 ref XP_007166415.1/1-344	-----MAQKENAYPWYGRQT-----
gi 1584038001 ref XP_006753367.1/1-368	VAETGQDLQTRSGARAVLEFSNCTSSRLFSSQHVPPPPKAPPLPVSALEPSHWPS-----
gi 1573912300 ref XP_006643864.1/1-292	-----MAIATESCCHE-----
gi 1554569173 ref XP_005878848.1/1-339	-----MTQKENAYPWYGRQT-----
gi 1545541126 ref XP_005635254.1/1-405	-----MDKS-KENCIAGPV---KTAIALGDGPKRVLVTQQVPSQN-----
gi 1545487136 ref XP_005616134.1/1-307	-----MLSGSAQPAESEGE-KTQ-----
gi 1544514002 ref XP_005590555.1/1-471	AGRAGLEAHQPEDPQPLSGRCEREQPSRGLRKASAPSPLLPMSSPKAAVQLGRA-----
gi 1530653727 ref XP_005313062.1/1-365	-----MAYKEN---VTPGTGTSKAYG-----VLSGPGPQVRPRKDPY-----
gi 1528993703 ref XP_005219854.1/1-303	-----MSHRGTARKAGGM-----
gi 1524890835 ref XP_005101959.1/1-332	-----MDPASRVLPKN-----
gi 1514776534 ref XP_004968502.1/1-292	-----MAIATESRGSE-----
gi 1507960369 ref XP_004686961.1/1-405	-----MDKS-KENCISGPV---KTMVPLRDGAKRVPVHQHAPSQS-----
gi 1507953708 ref XP_004684672.1/1-344	-----MAQKENAYPWYGRQT-----
gi 1478517838 ref XP_004433150.1/1-344	-----MAQKENAYPWYGRQT-----
gi 1478512086 ref XP_004430306.1/1-405	-----MDRS-KENCVAGPV---KTTIPLGDGPKRVLVTQQFPSQH-----
gi 1470628341 ref XP_004321082.1/1-402	-----MDKC-KENSISGP---KTTVPLGDGPKRVPVTQQFPSQN-----

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gi|449486478|ref|XP_002195961.2|/1-319 -----MKENHAACP-----
gi|426243291|ref|XP_004015492.1|/1-303 -----MSHRGTARKAGGM-----
gi|426237569|ref|XP_004012730.1|/1-344 -----MAQKENAYPWYGRQT-----
gi|410979749|ref|XP_003996244.1|/1-344 -----MAQKENAYPWYGRQT-----
gi|410953494|ref|XP_003983405.1|/1-405 -----MDKS-KENCVAGPV---KTTIPLGDGPKRVPVTQQFP SQN-----
gi|410914403|ref|XP_003970677.1|/1-332 -----MQNKENYDPKSHTRTFP-----
gi|389641901|ref|XP_003718583.1|/1-397 FEHLNVNDEND---HGDRLVQKS---KISMSTAQISHGSS---RPNLFKVALQSQSANTVT
gi|389635857|ref|XP_003715581.1|/1-400 INPVAVRDLLIR--CSSRPRSDS--RKLPRDAAVGDGNDPRGNTQKEPARRTS--SPR
gi|357126095|ref|XP_003564724.1|/1-291 -----MAISTDSR-SE-----
gi|355703962|gb|EHH30453.1|/1-309 -----MSSPKAAVQLGRA-----
gi|350538969|ref|INP_001233545.1|/1-403 -----MDRS-KENCISGPV---KATAPVG-GPKRVLVTQQFPCQN-----
gi|347966592|ref|XP_321274.5|/1-404 -----MACNKENRKLNGPSSVAA-STGIPSHSGTLLVKKGAGVG---GP
gi|345800233|ref|XP_849906.2|/1-344 -----MTQKENAYPWYGRQT-----
gi|344296517|ref|XP_003419953.1|/1-405 -----MDKS-KENCISGPI---KTTPLGDGPKRVPVTQQFP SQN-----
gi|344290468|ref|XP_003416960.1|/1-345 -----MAQKENAYPWYGRQT-----
gi|344269722|ref|XP_003406697.1|/1-306 -----MFTNVALSFARREWK-----
gi|338709975|ref|XP_001502047.3|/1-304 -----MSLPEAVMKS GSV-----
gi|334312551|ref|XP_001378079.2|/1-402 -----MDIS-KENS VSGPSN--KTAILLGEGPKRVPITQQISSQS-----
gi|332848444|ref|XP_511856.3|/1-344 -----MAQKENAYPWYGRQT-----
gi|330793523|ref|XP_003284833.1|/1-359 -----TTATTKSTITK-----TTSASSTPSTSTPST-----
gi|321461440|gb|EFX72472.1|/1-304 -----METKQPLKENSTN-----
gi|308497987|ref|XP_003111180.1|/1-306 -----MENKPEVIHHD-----
gi|302801442|ref|XP_002982477.1|/1-288 -----M-----
gi|302688103|ref|XP_003033731.1|/1-328 -----MGWRRRTRSAGSRCTATP--
gi|297802712|ref|XP_002869240.1|/1-290 -----MAIPTETQHQ-----
gi|281427796|ref|INP_001164000.1|/1-322 -----MSQRK-----AP
gi|268565413|ref|XP_002639437.1|/1-302 -----MENKQILQT-----
gi|260784959|ref|XP_002587531.1|/1-282 -----
gi|226499040|ref|INP_001148791.1|/1-296 -----MAVATESRGSE-----
gi|224088986|ref|XP_002308590.1|/1-293 -----MAIASDTQPQ-----
gi|215983064|ref|INP_001135979.1|/1-405 -----MGIMDRC-KENCISGP---KTAVPLSDGPKRVPVAAQFP SQN-----
gi|213404608|ref|XP_002173076.1|/1-346 LNRLSVN-----NGS---TVASGRQQLRL LAVSNQM HAN--
gi|198430178|ref|XP_002119314.1|/1-305 -----
gi|196012778|ref|XP_002116251.1|/1-270 -----
gi|168044897|ref|XP_001774916.1|/1-297 -----MGSDADV K YVR-----
gi|159468203|ref|XP_001692272.1|/1-292 -----MLAQRQDAG-----
gi|158297402|ref|XP_317640.3|/1-307 -----CANKSTPTMDDDV FATDGDVN-----
gi|156368106|ref|XP_001627537.1|/1-314 -----
gi|149734120|ref|XP_001489320.1|/1-404 -----MDRS-KENCISGPV---KTTVPLGDGPKRVPVTQQLP-QN-----
gi|149724949|ref|XP_001504864.1|/1-344 -----MTQKENAYPWYGRQT-----
gi|148225464|ref|INP_001085657.1|/1-368 -----MSYKENLIPSSCSSSSSSSS--
gi|146172296|ref|XP_001018388.2|/1-360 -----MKTFDFNYNQSA LQ NQQLKNGTSSQILKNIKDQENKNSSKDQENFK
gi|144226857|ref|INP_001016859.2|/1-360 -----MSYKENLNPSSYTS-----
gi|125524746|gb|EAY72860.1|/1-292 -----MAIATESRCEE-----
gi|115749607|ref|INP_98907.2|/1-344 -----MAQKENAYPWYGRQT-----
gi|115455545|ref|INP_001051373.1|/1-309 -----
gi|115435032|ref|INP_001042274.1|/1-292 -----MAIATESRCEE-----
gi|84000031|ref|INP_001033117.1|/1-402 -----MDRC-KENCISGP---KTAVPLSDGPKRVPVAAQFP SQN-----
gi|83776600|ref|INP_004208.2|/1-344 -----MAQKENSYPWYGRQT-----
gi|76253851|ref|INP_695208.2|/1-397 -----MDRC-KENCVSRPV---KSTVPFG--PKRVLVTEQIP SQH-----
gi|68013217|ref|INP_001018849.1|/1-355 LNCLSVS-----TPS---TTANPGRQQLRL LAVSNQRQVNNV
gi|66815573|ref|XP_641803.1|/1-384 -----TTSTVKSTITKPTTTGATTSTNTSTIPPTTASSSSSSSSSS--
gi|62865639|ref|INP_001015878.1|/1-309 -----MSSPRAVVQLGKA-----
gi|62857967|ref|INP_001016570.1|/1-415 -----MERAVKENLPSNV---KVFHPTMEGPKRIPVTQPPSTQV-----
gi|57525577|ref|INP_001003640.1|/1-405 -----MDSGARSKSSRD LKIHPENEKVSAAGPKRVPVTQS-VQKPVSNP-
gi|50759065|ref|XP_425725.1|/1-409 -----MDRKT KENC PGNPSRATKVANPVVDGPKRVPVPQNSA-QS-----
gi|50303387|ref|XP_451635.1|/1-361 -----MRPSL SRDASDTGRRHSL LQSKLLSIRLSN--
gi|46358064|ref|INP_035627.1|/1-417 GCCKRIGKAVWRRGDMDC-KENCVSRPV---KTTVPFG--PKRVLVTEQIP SQN-----
gi|45198420|ref|INP_985449.1|/1-367 -----MDADAILKKDQ--RRSSLKQRNLLSMLNQTTA
gi|38327570|ref|INP_940838.1|/1-403 -----MDRS-KENCISGPV---KATAPVG-GPKRVLVTQQFPCQN-----
gi|17505246|ref|INP_491714.1|/1-305 -----MENKPPVINLP-----
gi|17137514|ref|INP_477336.1|/1-329 -----MTLSRAKHANRNLPHLLAKVP-----
gi|17136516|ref|INP_476749.1|/1-411 -----MSHPSDHLVPKENAPHRMPEKSAAVHNMQKNLLGKKPNSENMAP
gi|16758580|ref|INP_446201.1|/1-343 -----MAQKENVYPWYGSKT-----
gi|15233958|ref|INP_195009.1|/1-294 -----MAIPTETQHQ-----
gi|15225495|ref|INP_182073.1|/1-288 -----
gi|16708213|gb|IAAF25838.1|/1-282 -----
gi|16325047|ref|INP_015115.1|/1-367 -----MQRNSLVNIKL NANSPSKTTTRPNTSRINK---
gi|2979623|gb|IAC12683.1|/1-345 -----MAQKENAYPWYGSKT-----

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XP_006102660.1/1-339
XP_005673091.1/1-402
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gi|1126479796|ref|XP_006940862.2|/1-308
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gi|1955535802|ref|XP_004439167.2|/1-335
gi|1951053762|ref|XP_014465099.1|/1-416
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gi|1891599507|ref|XP_013025412.1|/1-351
gi|1891565640|ref|XP_013019059.1|/1-351
gi|1884853217|ref|XP_013010870.1|/1-315
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gi|1617451788|ref|XP_007568855.1|/1-331
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---PISASSGQAQRVLCSSNTSHRIPTQA---QKLVS SRKAVQI---QKQKQPQTTPVSH
---TQSGVNTLPQRFVRKEP-----ATPSALVLMRSKAVLEPS-----
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---TPSMVTGPQFVLRKEP-----VTPSALVLMRS-----
---QPA-----AVAGQTMP-----SIPT-----
---DQGT-----AAAGLVEL-----GMPP-----
---NPGALGS---LAKYGAP---GPQFVRKETPAEALL-----
---PQSSLNTLPNIFRKEI-----ATPSATLTMHRSRGLLELS-----
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---IIAE-----KKFPPWSS---PSPG-----
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-YPVTKKDSRGLNKRYS SK-----
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---QAAG-----AAGGPAL-----PVAT-----
-----MNALKDN NF-----
-----MEP-----STST-----
---QPAGEAVTAANQTAQFP-----STPA-----
---ASSLNRG-----
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---QPT-----AAEQTLF-----GVPT-----
---DFLLYVG-----
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-----QHKGSSEGA VVDN-----
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---PQSGLNTLPQFVLRKEA-----ATPSALVLLNRS-----
---RVPGGQVQAQRIPLCPNLAQFVVPVQSAQKALSNOQKPSQNF---LMQFPPTSLVQF
-----TPVSVTGPQFVLRVLPKADAESYVAGPREGCVS-----
---PVSANSQAQRVLCPSNSSQRLPSQV---QKLVS SQKPVQP---LKQKPAQAASAPR
-----MMP-----SIPT-----
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---VLAA-----DEAP-PLP---SAPP-----
-----EKAPPHSQEE-----
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---QHAA-----AAGQTVF-----GAPT-----
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-----DKASAHANEE-----
---ALPASSGQAQRVLCPSNS-QRLPSQA---QKLVS SHKAVPNPN---LKQKQLQANNAPR
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---PVSANSQAQRVLCPSNSSQFVPSQV---QKLVS SQKSVQP---LKQKPTQAASAPR

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gi|449486478|ref|XP_002195961.2|/1-319 -----RPRR-----
gi|426243291|ref|XP_004015492.1|/1-303 ---QPAA-----AAGQSV-----GAPA-----
gi|426237569|ref|XP_004012730.1|/1-344 ---AQPLNTLPQVLRKEA-----VIPSALVMSRS-----
gi|410979749|ref|XP_003996244.1|/1-344 ---TQPLNTLPQVLRKEP-----ATPSALVMSRS-----
gi|410953494|ref|XP_003983405.1|/1-405 ---LLSANSQAQVRLCPSNSSQRIPSQT---QKLVSSHKPVQN---LKQKQLQATSVPR
gi|410914403|ref|XP_003970677.1|/1-332 ----APMTLGGPQVQVKPRAEMDRSAITGPGRECVP-----
gi|389641901|ref|XP_003718583.1|/1-397 SVTLPSQAAQRKMAPPPKSREPPSPSKHKKD-----
gi|389635857|ref|XP_003715581.1|/1-400 QASLESQIREFLHAKKPREQG-AGKEPLEQ-----
gi|357126095|ref|XP_003564724.1|/1-291 -----EKAQHQSQEE-----
gi|355703962|gb|EHH30453.1|/1-309 ---QPAGEAVTAANQTAQQP-----SSPA-----
gi|350538969|ref|INP_001233545.1|/1-403 ---PLPVNSGQAQVRLCPSNSSQVPLQA---QKLVSSHKPVQN---QKQKQLQATSVPH
gi|347966592|ref|XP_321274.5|/1-404 AANTAAGRSNNAAKMVGKVAEGGQHMGG--FKAPQLPAPVVRPAASSSKPVPEKQIT-P
gi|345800233|ref|XP_849906.2|/1-344 ---TQPLNTLPQVLRKDP-----ATPSALVMSRS-----
gi|344296517|ref|XP_003419953.1|/1-405 ---PLSASGQAQVRLCPSNSSQSIPSA---QKLVSSRKPVQS---QKQKPLQITTVPR
gi|344290468|ref|XP_003416960.1|/1-345 ---AQSGLNTLPQVFRKDL-----ATPSALVMSRS-----
gi|344269722|ref|XP_003406697.1|/1-306 ---ELAP-----TERALYD-----VLLE-----
gi|338709975|ref|XP_001502047.3|/1-304 ---RPAV-----PTAGQSQP-----GFPN-----
gi|334312551|ref|XP_001378079.2|/1-402 ---RLPGSSGQAQVRLCSSNP--LLVSSQA---QKNISSHKTSHA---HQSQKLQAPVIH
gi|332848444|ref|XP_511856.3|/1-344 ---APSGLSTLPQVLRKEP-----VTPSALVMSRC-----
gi|330793523|ref|XP_003284833.1|/1-359 -----STPTSTSTSSNSG-----P-----
gi|321461440|gb|EFX72472.1|/1-304 -----QPTVKLEN-----
gi|308497987|ref|XP_003111180.1|/1-306 -----EKSKNNPMK-----
gi|302801442|ref|XP_002982477.1|/1-288 -----VEAPEAVPE-----
gi|302688103|ref|XP_003033731.1|/1-328 ---RSSSPSTRAWQSCACTCCA-----
gi|297802712|ref|XP_002869240.1|/1-290 -----EKEASDA-----A-----
gi|281427796|ref|INP_001164000.1|/1-322 VCQNKENN-----VPRAAAKKGPPAQKG-----
gi|268565413|ref|XP_002639437.1|/1-302 -----KSKNTPNK-----
gi|260784959|ref|XP_002587531.1|/1-282 -----
gi|226499040|ref|INP_001148791.1|/1-296 -----DRASAHANQE-----
gi|224088986|ref|XP_002308590.1|/1-293 -----EKASTEVSGECK-----
gi|215983064|ref|INP_001135979.1|/1-405 ---PVSVNSGQAQVRLCPTNSSQVPSQA---QKLVSIQKPVQT---LKQKPPQAASAPR
gi|213404608|ref|XP_002173076.1|/1-346 ----NNSSTSADALRERQER-----
gi|198430178|ref|XP_002119314.1|/1-305 -----
gi|196012778|ref|XP_002116251.1|/1-270 -----
gi|168044897|ref|XP_001774916.1|/1-297 -----QESQGAGGDSIA-----
gi|159468203|ref|XP_001692272.1|/1-292 -----QAAGTSGGPK-----
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gi|156368106|ref|XP_001627537.1|/1-314 -----
gi|149734120|ref|XP_001489320.1|/1-404 ---LLSANSQAQVRLCPSNSSHRVPSQA---QKLVSSHKPVQN---LKQKQSQATSVPH
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gi|146172296|ref|XP_001018388.2|/1-360 NSQLLSVKSIKKIEQIEQQSDRVQILKVP
gi|144226857|ref|INP_001016859.2|/1-360 ---KFATPSSATAAQVRLRKQPYYSIFTTPSDNLLAQRAQLA-RIT-----
gi|125524746|gb|EAY72860.1|/1-292 -----EKASPHSQEV-----
gi|115749607|ref|INP_898907.2|/1-344 ---AQPLNTLPQVLRKEP-----VTPSALVMSRS-----
gi|115455545|ref|INP_001051373.1|/1-309 -----MEKP-----
gi|115435032|ref|INP_001042274.1|/1-292 -----EKASPHSQEV-----
gi|84000031|ref|INP_001033117.1|/1-402 ---PVSVNSGQAQVRLCPTNSSQVPSQA---QKLVSIQKPVQT---LKQKPPQAASAPR
gi|83776600|ref|INP_004208.2|/1-344 ---APSGLSTLPQVLRKEP-----VTPSALVMSRS-----
gi|76253851|ref|INP_695208.2|/1-397 ---PGSASSGQAQVRLCPSNS-QRVPPQA---QKPVAGQKPVLK-----QLPAASGPR
gi|68013217|ref|INP_001018849.1|/1-355 SLANGKENKRTSNKFNSSLR-----
gi|66815573|ref|XP_641803.1|/1-384 -----SSSSSSSSSSSSSQS-----VP-----
gi|62865639|ref|INP_001015878.1|/1-309 ---QPAGEELATANQTAQQP-----SSPA-----
gi|62857967|ref|INP_001016570.1|/1-415 ---RPPGTAVSAQRILGPSNVQVQVVSQAQ-KPVMSAQKPMSTQKPMQTQGPLRPVTHGH
gi|57525577|ref|INP_001003640.1|/1-405 -HTRVLGAAQGPQVQRPVG-----KTSCLPGDQNTREPEH--KPAAHSKP---
gi|50759065|ref|XP_425725.1|/1-409 ---RPLNSGVQVQVRLCPSNFAQVQVPSQA---QKSSLSNQKLSNNQ--TTQQPRPKLPVQP
gi|50303387|ref|XP_451635.1|/1-361 ---AGKRPSLSRGHAHEKDSI-TSSHHRLSTGPNVNN-----
gi|46358064|ref|INP_035627.1|/1-417 ---LGSASSGQAQVRLCPSNS-QRVPSQA---QKLGAQKQKPAK-----QLPAASVPR
gi|45198420|ref|INP_985449.1|/1-367 TNGAPPQARVQPGKGYRNPQK-VLSPIRNQEMSPGKR-----
gi|38327570|ref|INP_940838.1|/1-403 ---PLPVNSGQAQVRLCPSNSSQRIPLQA---QKLVSSHKPVQN---QKQKQLQATSVPH
gi|17505246|ref|INP_491714.1|/1-305 -----EKETVNTPOK-----
gi|17137514|ref|INP_477336.1|/1-329 -EEHQEPIKNMCLKMMSHDAYGQ-----
gi|17136516|ref|INP_476749.1|/1-411 ASKPLPGSSGALTRKPLGGSNSIASSEGNFQKPMVPS-VKKTTFEAPAPVAPIKKP
gi|16758580|ref|INP_446201.1|/1-343 ---SQSGLNTLPQVLRKEP-----AVTPAQUALMNRS-----
gi|15233958|ref|INP_195009.1|/1-294 -----EKEASDAS-AAAA-----
gi|15225495|ref|INP_182073.1|/1-288 -----MSKKSTESDAGNT-----
gi|16708213|gb|IAAF25838.1|/1-282 -----MEP-----STST-----
gi|16325047|ref|INP_015115.1|/1-367 ----PWIRISHSPQQRNPNKIPSPVREKLNRLPVNNK-----
gi|2979623|gb|IAC12683.1|/1-345 ---SQSGLNTLSQVLRKEP-----ATTSLALVNRS-----

XP_020952967.1/1-297 -----GRRLTIDDFEIGR
XP_012380002.1/1-290 -----IDDFEIGR
XP_006102660.1/1-339 -----NAQPTAAPGQ-----NSNGTPNL-----MRSFTIDDFEIGR
XP_005673091.1/1-402 PVSRLP-SNTQQSEQPQPAAGNNPEKEAASKQK-----NEESKKRQWALEDFEIGR
XP_004484680.1/1-405 PVSKPL-NNTQKSEQSQPPASGSNSGKELESQK-----KEESKKRQWALEDFEIGR
XP_004462482.1/1-349 -----NAQPTA--GQK-TVENSSGTPSFL-----MRSFTIEDFEIGR
Q6NW76.1/1-320 -----SNS-----KVLSIDDFEIGR
NP_999084.2/1-344 -----NTQPTAAPGQK-VVENSSGTPNFS-----TRSFIDDFEIGR
gi|1190438012|ref|XP_020822491.1|/1-365 -----STQPAAVPGRI-GVDSSNMKLNLP-----VHQLKIDDFEIGR
gi|1190373986|ref|XP_020837071.1|/1-405 PASRPP-KSTLNTSEQSQTTPVSASTPGKGETPRQK-----NEETKKRQWALDDFEIGR
gi|1154067554|ref|NP_001153906.2|/1-332 -----TSSVSP-----PKKISIDDFEIGR
gi|1131237831|ref|XP_019799799.1|/1-344 -----NAQPTAAPLQK-VVENNSRTPNFS-----MRSFTIDDFEIGR
gi|1131178530|ref|XP_019784431.1|/1-296 -----VRRLTIDDFEIGR
gi|1126479796|ref|XP_006940862.2|/1-308 -----VRRLTIEDFEIGR
gi|1113784803|ref|XP_019353949.1|/1-376 -----AQRATAVPGRVPEA--GAQVAPQPP-----LKTLSIDDFEIGR
gi|1022987698|ref|XP_016286291.1|/1-365 -----GAQPAALPGRI-GLDNSNVKSNQT-----VRHLKIDDFEIGR
gi|1966994491|ref|XP_014974040.1|/1-344 -----NVQPTAAPGQK-VVENSSGTPNIL-----MRHFTIDDFEIGR
gi|1966965902|ref|XP_015004225.1|/1-398 PVSRLP-SHTPKSKQPLPSAPENNPPEELASKQK-----NEESKKRQWALEDFEIGR
gi|195535802|ref|XP_004439167.2|/1-335 -----VRHFTIDDFEIGR
gi|1951053762|ref|XP_014465099.1|/1-416 SSRPQA-PN-NNEKPHHPVPSANQPEKEGTSKPK-----NQETKKRQWSLDDFEIGR
gi|1946796851|ref|XP_014384184.1|/1-404 PVSRLP-NNTQKSEQQPPAPGKNSKEVASKQK-----NEESKK-QWTLEDFEIGR
gi|1946756071|ref|XP_014392719.1|/1-299 -----SRSLTIDDFEIRC
gi|1922383691|ref|XP_013462066.1|/1-300 -----QRRWILNDFDIGK
gi|1909794683|ref|XP_013153467.1|/1-419 TARSQL-PTKNNEKPPQVVPVPAKNPEAESTSKQKNEETAKKKNEETKKRQWSLDDFEIGR
gi|1891599507|ref|XP_013025412.1|/1-351 -----QKDEPIAGVPSPMGPQ-----WRDFHIGMFEIGK
gi|1891565640|ref|XP_013019059.1|/1-351 -----QQDEPIAGVPSPMGPQ-----WRDFHIGMFEIGK
gi|1884853217|ref|XP_013010870.1|/1-315 -----RRPFTIEDFDIGK
gi|1830244266|ref|XP_012590158.1|/1-296 -----VRRLTIDDFEIGR
gi|1828211890|ref|XP_012558808.1|/1-339 QNSSKGTVKTMLQKSDKPSLEKENQDQKEPKNQK----KENPPPPIDKCWSLSDFDIGK
gi|1820033943|ref|NP_001295465.1|/1-282 -----KKHFTINDFEIGR
gi|1795377289|ref|XP_011750175.1|/1-471 -----MRLKIDDFEIGR
gi|1779989227|ref|XP_011666707.1|/1-321 -----TTAQARTQPVKSAENGHGHDDK-----QMEPKKSWTLKDFDIGR
gi|1761905244|ref|XP_0114402440.1|/1-385 HGTREHLTVPPSAPPPVSSSLGEAPQGGAGTADQ-----SQQPVSCKWGLSDFDIGR
gi|1759175630|ref|XP_011377486.1|/1-303 -----TRQLTIDDFEIGR
gi|1759149200|ref|XP_011368486.1|/1-311 -----NNSEKELASKQK-----NEESKKRQWALEDFEIGR
gi|1759116391|ref|XP_011357226.1|/1-339 -----NAQTAAAPGQ-----NSSGTPNL-----MRSFTIDDFEIGR
gi|1758991346|ref|XP_957232.2|/1-420 -----QPMASASVSSTGTSTSESSSSAGYEQSI-----SPKQFHLGMFEIGR
gi|1743922878|ref|XP_011005517.1|/1-293 -----KRWTLNDFDIGK
gi|1698438703|ref|XP_009757361.1|/1-296 -----KKRWMLNDFDIGK
gi|1697188794|ref|XP_009603442.1|/1-294 -----KRWTVNDFDIGK
gi|1658871623|ref|XP_008418750.1|/1-330 -----SSSNPP-----PKKFTIDDFEIGR
gi|1657559162|ref|XP_008283516.1|/1-424 QNQPKTHVPTVKPELTTPASESAKLEKPNKPAKN----DAANASSSKKPWSLENFDIGR
gi|1657529148|ref|XP_008293493.1|/1-319 -----AASSSV-----SKKISIDDFEIGR
gi|1655887082|ref|XP_008247187.1|/1-292 -----LRLLTIEDFEIGR
gi|1655881324|ref|XP_008272369.1|/1-402 PVSPPP-NNTPKSEQPPPSAPGNNPEKELTSNQK-----NEESKKRQWTLDFDIGR
gi|1655868725|ref|XP_008268971.1|/1-343 -----NAPPTAVLGQK-GMENSSGAPNF-----TRPFTIDDFEIGR
gi|1641774253|ref|XP_008170712.1|/1-431 ISRPPA-PSKNNEEPPQTSLSAKNLEAEGTSVQK-----NEETKKRQWCLDDFEIGR
gi|1620969612|ref|XP_007654691.1|/1-303 -----NIPEKREVPSQKEAPCQK-----NEESKKRQWSLDDFDIGR
gi|1617451788|ref|XP_007568855.1|/1-331 -----SSSNSP-----PKKFTIDDFEIGR
gi|1594674988|ref|XP_007185333.1|/1-402 AVSRPL-SNTQKSEQQLPAPGNNPEKEAASKQK-----NEESKKRQWALEDFEIGR
gi|1594654199|ref|XP_007175509.1|/1-282 -----MRLTIDDFEIGR
gi|1594623572|ref|XP_007166415.1|/1-344 -----NAQPTAAPLQK-VVENNSGTPNFS-----MRSFTIDDFEIGR
gi|1584038001|ref|XP_006753367.1|/1-368 -----VRSLTIDDFEIGR
gi|1573912300|ref|XP_006643864.1|/1-292 -----KRWVLSDFDIGK
gi|1554569173|ref|XP_005878848.1|/1-339 -----NAQPTAAPGQ-----NSNGTPNL-----MRSFTIDDFEIGR
gi|1545541126|ref|XP_005635254.1|/1-405 PASRSL-NNTQKSEQSPSSAPGNNSEKELATKQK-----NEESKKRQWALEDFEIGR
gi|1545487136|ref|XP_005616134.1|/1-307 -----GRRLTIDDFEIGR
gi|1544514002|ref|XP_005590555.1|/1-471 -----MRLKIDDFEIGR
gi|1530653727|ref|XP_005313062.1|/1-365 -----SIQKPAVPGRVPAELSSGAQAQPTP-----QRIFTINDFEIGR
gi|1528993703|ref|XP_005219854.1|/1-303 -----ARRFTVDDFEIGR
gi|1524890835|ref|XP_005101959.1|/1-332 -----ENNSSGGDIASSSD-----SSNGPVKWGLSNFDIGR
gi|1514776534|ref|XP_004968502.1|/1-292 -----KRWVLSDFEVLGK
gi|1507960369|ref|XP_004686961.1|/1-405 AAPRPL-AGTPKSEPP-PSAPGNNSEKEQASKQK-----TEESKKRQWALEDFEIGR
gi|1507953708|ref|XP_004684672.1|/1-344 -----NTQPTAAPGQK-VVENSSGTPNLS-----MRSFTIDDFEIGR
gi|1478517838|ref|XP_004433150.1|/1-344 -----NAQPTAALGQK-VVENSSGTPNLL-----MRSFTIDDFEIGR
gi|1478512086|ref|XP_004430306.1|/1-405 PVSRLP-NSTQKSEQQPSAPGNNSEKERTSKEK-----NEDSKRRQWALEDFEIGR
gi|1470628341|ref|XP_004321082.1|/1-402 SVSRPL-SNTQKSEQQLPAPGNNPEKEAASKQK-----NEESKKRQWALEDFEIGR

gi|470261727|ref|XP_004360485.1|/1-457 -----KKKWTIDDFDIGK
gi|449486478|ref|XP_002195961.2|/1-319 -----QAQNPAAESTSKQKTEET-KKKSEETKKRQWSLDDFEIGR
gi|426243291|ref|XP_004015492.1|/1-303 -----ARRFTIDDFEIGR
gi|426237569|ref|XP_004012730.1|/1-344 -----NAQPTAAPGQK-VVENSSGTLNIP-----KRSFTIDDFEIGR
gi|410979749|ref|XP_003996244.1|/1-344 -----NTQPTAAPGQK-VVENSSGTPNFS-----MRSFTIDDFEIGR
gi|410953494|ref|XP_003983405.1|/1-405 SVSRPL-NNTQKSEQPLPSATGNNSEKELTTKQK-----NEESKKRQWALDDFEIGR
gi|410914403|ref|XP_003970677.1|/1-332 -----SSSTSS-----TRKITIDDFDIGR
gi|389641901|ref|XP_003718583.1|/1-397 -----SVSSSVDELANEVEEASAPR-----VPKEFHLGMFEIGR
gi|389635857|ref|XP_003715581.1|/1-400 -----LQAAQAAAAAALVAQPSAQ-----PVAMHLGMFEIGK
gi|357126095|ref|XP_003564724.1|/1-291 -----KRWVLSDFEVBGK
gi|355703962|gb|EHH30453.1|/1-309 -----MRRLKIDDFEIGR
gi|350538969|ref|NP_001233545.1|/1-403 PVSRL-NNTQKSKQPLPSAPENNPHEELASKQK-----NEESKKRQWALDDFEIGR
gi|347966592|ref|XP_321274.5|/1-404 KTESEPMDDTPADDRPD--AAEQKQSGTDGNQQAQ-----QAKPAKKVWTLNSNDFIGR
gi|345800233|ref|XP_849906.2|/1-344 -----NGQPTAAPGQK-VVENSSGIPNFS-----MRSFTIDDFEIGR
gi|344296517|ref|XP_003419953.1|/1-405 PVSRLP-NNTPKGEQAQPPASGNNSGKELASKQK-----KEESKKRQWALDDFEIGR
gi|344290468|ref|XP_003416960.1|/1-345 -----NAQPTAAPGEKMTENSSTGTPSFL-----MRPFTIDDFEIGR
gi|344269722|ref|XP_003406697.1|/1-306 -----MRRLRIDDFEIGR
gi|338709975|ref|XP_001502047.3|/1-304 -----VRHLTIDDFEIGR
gi|334312551|ref|XP_001378079.2|/1-402 PTSRPP-SSTQNTSEQSQPPVSASIPGKETPRQK-----NEETKKRQWALDDFEIGR
gi|332848444|ref|XP_511856.3|/1-344 -----NVQPTAAPGQK-VMENSSGTPNIL-----TRHFTIDDFEIGR
gi|330793523|ref|XP_003284833.1|/1-359 -----KKKWCIDDFDIGK
gi|321461440|gb|EFX72472.1|/1-304 -----SEWSLDNFEIGR
gi|308497987|ref|XP_003111180.1|/1-306 -----GGKLSIKDFFEIGR
gi|302801442|ref|XP_002982477.1|/1-288 -----ERRWKLADFDIGK
gi|302688103|ref|XP_003033731.1|/1-328 -----PARILTTPVSRRYPT-----REWTLHDFDIGR
gi|297802712|ref|XP_002869240.1|/1-290 -----QKRWTLSDFDIGK
gi|281427796|ref|NP_001164000.1|/1-322 -ALSENK-----AQKGAASDTAQESS-----KGRR---WTLADFDIGK
gi|268565413|ref|XP_002639437.1|/1-302 -----GGKLSINDFEIGR
gi|260784959|ref|XP_002587531.1|/1-282 -----MKS---WKLEDDFEIGR
gi|226499040|ref|NP_001148791.1|/1-296 -----KRWVLSDFEVBGK
gi|224088986|ref|XP_002308590.1|/1-293 -----KRWTLNDFDIGK
gi|215983064|ref|NP_001135979.1|/1-405 PVARPP-SNTQKSKQPQPPAGNNPEKEVASKQK-----NEESKKRQWALDDFEIGR
gi|213404608|ref|XP_002173076.1|/1-346 -----HYSLSSDGNNSKSP-----LRNFHLGMFEIGK
gi|198430178|ref|XP_002119314.1|/1-305 -----MSSANNENKAPEKASTSGRAT-----ASSAKDNASDTWSLKNFDIGK
gi|196012778|ref|XP_002116251.1|/1-270 -----RKRWTLDDFDIGR
gi|168044897|ref|XP_001774916.1|/1-297 -----EKRWSLTDFDIGK
gi|159468203|ref|XP_001692272.1|/1-292 -----RRWTIDDFDIGK
gi|158297402|ref|XP_317640.3|/1-307 -----PYEWSTDDFEVGR
gi|156368106|ref|XP_001627537.1|/1-314 -MAKIPSNHTQTTVSSFNPSITKHKMGSKGGPFK-----LLENMKQKGWNLSDFDIGK
gi|149734120|ref|XP_001489320.1|/1-404 PVPRPL-NNTQRSEQLQPSAGNNSEKELASKEK-----NEESKKRQWALDDFEIGR
gi|149724949|ref|XP_001504864.1|/1-344 -----NAQPTVALGQK-VMENSSGTPNIL-----MRSFTIDDFEIGR
gi|148225464|ref|NP_001085657.1|/1-368 -----PAASSSVPGRVALGTDVASHNTALAEAP-----KRKFTIDDFEIGR
gi|146172296|ref|XP_001018388.2|/1-360 -----KIQWQLSDFELGK
gi|144226857|ref|NP_001016859.2|/1-360 -----PSASSVPGRVAVSMDASSQNTALAEALP-----KRKFTIDDFEIGR
gi|125524746|gb|EAY72860.1|/1-292 -----KRWVLSDFDIGK
gi|115749607|ref|NP_898907.2|/1-344 -----NAQPTAAPGQK-VVENSSGTPNIP-----KRSFTIDDFEIGR
gi|115455545|ref|NP_001051373.1|/1-309 -----EWSMDDFEIGK
gi|115435032|ref|NP_001042274.1|/1-292 -----KRWVLSDFDIGK
gi|84000031|ref|NP_001033117.1|/1-402 PVTRPP-SNTQKSKQPQPPAGNNPEKEVASKQK-----NEESKKRQWALDDFEIGR
gi|83776600|ref|NP_004208.2|/1-344 -----NVQPTAAPGQK-VMENSSGTPDIL-----TRHFTIDDFEIGR
gi|76253851|ref|NP_695208.2|/1-397 PASR-L-SNPQKSEQPPAASGNNSEKEQTSIQK-----TEDSKKRQWTLDDFEIGR
gi|68013217|ref|NP_001018849.1|/1-355 -----KIEEPIAGVPSSAGPQ-----WREFHIGMFEIGK
gi|66815573|ref|XP_641803.1|/1-384 -----KKKWCIDDFDIGK
gi|62865639|ref|NP_001015878.1|/1-309 -----MRRLTVDDFEIGR
gi|62857967|ref|NP_001016570.1|/1-415 QAGKPQGPNNRTPQQTSHSSTPNVEKKGSTDQG--KTLAVPKEEGKKQWCLDDFEIGR
gi|57525577|ref|NP_001003640.1|/1-405 QPKPPLSAETNKTAEPSKQDKPHQTPSSTTSTSSN----TSGSSKSSKAWTLNFDIGR
gi|50759065|ref|XP_425725.1|/1-409 TAGPQV-PSKNSEKPPQAPVPAKSSSEADSVSKQKNEESTKKKKEETKKRQWSLDDFEIGR
gi|50303387|ref|XP_451635.1|/1-361 -----PRRSLMVKK---PNTAHTG-RVPILND-----HNDKFENMTLQDFEIGK
gi|46358064|ref|NP_035627.1|/1-417 PVSR-L-LNPPQKNEQ--PAASGNDSEKEQASLQK-----TEDTKKRQWTLDDFEIGR
gi|45198420|ref|NP_985449.1|/1-367 -----PTLEISELKNVSPINQAHKTGKARAGGV-----PTLSKLQNLKLADFEIGK
gi|38327570|ref|NP_940838.1|/1-403 PVSRLP-NNTQKSKQPLPSAPENNPHEELASKQK-----NEESKKRQWALDDFEIGR
gi|17505246|ref|NP_491714.1|/1-305 -----GGKFTINDFEIGR
gi|17137514|ref|NP_477336.1|/1-329 -----PYDWSPRDFEMGA
gi|17136516|ref|NP_476749.1|/1-411 ESLSKQKPTAASSESSKELGAASSAEKEKTET-----QPQPKKKTWELNNDFEIGR
gi|16758580|ref|NP_446201.1|/1-343 -----NSQSTAVPGQKL TENK--GATALQGSQS-----RQPFTIDNFEIGR
gi|15233958|ref|NP_195009.1|/1-294 -----QKRWTLSDFDIGK
gi|15225495|ref|NP_182073.1|/1-288 -----EKQWSLADFEIGR
gi|16708213|gb|IAAF25838.1|/1-282 -----RKHFINDFEIGR
gi|16325047|ref|NP_015115.1|/1-367 -----KFLDMESSKIPSPIRKATSS-KMIHENK-----KLPKFKSLSDDFELGK
gi|2979623|gb|IAC12683.1|/1-345 -----NSQSTAAPGQKLAENKSQGSTASQGSQN-----KQPFTIDNFEIGR

*::

XP_020952967.1/1-297
XP_012380002.1/1-290
XP_006102660.1/1-339
XP_005673091.1/1-402
XP_004484680.1/1-405
XP_004462482.1/1-349
Q6NW76.1/1-320
NP_999084.2/1-344
gi|1190438012|ref|XP_020822491.1|/1-365
gi|1190373986|ref|XP_020837071.1|/1-405
gi|1154067554|ref|NP_001153906.2|/1-332
gi|1131237831|ref|XP_019799799.1|/1-344
gi|1131178530|ref|XP_019784431.1|/1-296
gi|1126479796|ref|XP_006940862.2|/1-308
gi|1113784803|ref|XP_019353949.1|/1-376
gi|1022987698|ref|XP_016286291.1|/1-365
gi|1966994491|ref|XP_014974040.1|/1-344
gi|1966965902|ref|XP_015004225.1|/1-398
gi|195535802|ref|XP_004439167.2|/1-335
gi|1951053762|ref|XP_014465099.1|/1-416
gi|1946796851|ref|XP_014384184.1|/1-404
gi|1946756071|ref|XP_014392719.1|/1-299
gi|1922383691|ref|XP_013462066.1|/1-300
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gi|1891599507|ref|XP_013025412.1|/1-351
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gi|1884853217|ref|XP_013010870.1|/1-315
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gi|1820033943|ref|NP_001295465.1|/1-282
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gi|1779989227|ref|XP_011666707.1|/1-321
gi|1761905244|ref|XP_0114402440.1|/1-385
gi|1759175630|ref|XP_011377486.1|/1-303
gi|1759149200|ref|XP_011368486.1|/1-311
gi|1759116391|ref|XP_011357226.1|/1-339
gi|1758991346|ref|XP_0957232.2|/1-420
gi|1743922878|ref|XP_011005517.1|/1-293
gi|1698438703|ref|XP_009757361.1|/1-296
gi|1697188794|ref|XP_009603442.1|/1-294
gi|1658871623|ref|XP_008418750.1|/1-330
gi|1657559162|ref|XP_008283516.1|/1-424
gi|1657529148|ref|XP_008293493.1|/1-319
gi|1655887082|ref|XP_008247187.1|/1-292
gi|1655881324|ref|XP_008272369.1|/1-402
gi|1655868725|ref|XP_008268971.1|/1-343
gi|1641774253|ref|XP_008170712.1|/1-431
gi|1620969612|ref|XP_007654691.1|/1-303
gi|1617451788|ref|XP_007568855.1|/1-331
gi|1594674988|ref|XP_007185333.1|/1-402
gi|1594654199|ref|XP_007175509.1|/1-282
gi|1594623572|ref|XP_007166415.1|/1-344
gi|1584038001|ref|XP_006753367.1|/1-368
gi|1573912300|ref|XP_006643864.1|/1-292
gi|1554569173|ref|XP_005878848.1|/1-339
gi|1545541126|ref|XP_005635254.1|/1-405
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IE----GRTHDEKVDLWCIGVLCYELLVGNPPFESSS--HSETYRRITKVDLKFPSS--MP
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPAS--VP
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VT
IE----GRTYNEKVDLWCIGVLCYELLVGNPPFESSS--HNETYRRILKVDVRFPPS--IP
IE----GRTHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYRCISKVEFRYPPF--LS
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VR
VE----QRTYSEMDLWCIGVLCYELLVGNPPFESSS--YSETYRRILKVDVRFPPS--IP
VE----SVEHDSVDLWSLGVLCYEFVVGPPFEAKE--HSDTYRRIQVDLKFPKPIVS
IE----GRTHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYRAISRVEFKFPF--VT
VE----GKEHTEKVDLWSLGVLTYEIVGAPPFEDVSGHSATYKRIKVDLKIPSF--VS
VE----GKEHTEKVDLWSLGVLTYEIVGAPPFEDVSGHSATYRRIKVDLKIPSF--VS
VM----GSTYDEKVDLWCIGVLCYELLVGNPPFESSS--HSETYRRILKVDLRFPPS--MP
IE----GRTYNEKVDLWCIGVLCYELLVGNPPFESSS--HNETYRRILKVDVRFPPS--VP
IE----GKVHDEKVDLWSVGVLCYEFVVGKPPFETES--HDHTYQLISSVKYSFPDY--VS
IE----GKSYNETVDLWCIGVLCYELLVGNPPFESSS--SSETCRRICQVDFRFPSS--MP
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESSS--HSETYRRILKVDVRFPPS--MP
IE----GRMHDDKVDLWSLGVLCYEFVVGKPPFEANT--STETYRRITKVHYQFPYS--VS
VE----EKVHDEKVDLWSLGVLCYEFVVGKPPFETVN--TQDTYKRIVNVDKFPF--SY-VS
IE----GRTYNEKVDLWCIGVLCYELLVGNPPFESSS--HSETCRRILKVDVRFPPS--FP
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VP
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPFS--VP
IRSGSKDNWYNEKVDLWSLGVLTYEIVGAPPFEDTP--IMTQKRIARADMTIPEW--VS
VQ----SVEHDSVDLWSLGVLCYEFVVGIPPEAKE--HSDTYRRIQVDLKFPKPIVS
VE----SVEHDSVDLWSLGVLCYEFVVGPPFEAKE--HSDTYRRIQVDLKFPKPIVS
VE----SVEHDANVDLWSLGVLCYEFVVGPPFEAKE--HSDTYRRIQVDLKFPKPIVS
IE----GHTHSEKVDLWCIGVLCYECLVGNPPFETAS--HSETYKRITKVDLNFPAKV--IS
IE----GKTHDEKVDLWSLGVLCYEFVVGKPPFEANT--HEETYRRISRVEYTPAQTNIS
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFETAS--HSETYKRIMKVDLNFPAKV--IS
IE----GRTYDEKVDLWCIGVLCYELLVGNPPFESSS--HTETYRRILKVDVRFPPS--MS
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYRRISRVEFTFPDF--VT
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPAS--VP
IE----GRTHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYRSISKVEFRFPF--VS
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYRSISKVEYKFPDF--VT
IE----GHTHSEKVDLWCIGVLCYECLVGNPPFETAS--HSETYKRITKVDLNFPAKV--IS
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VP
IE----GRTYNEKVDLWCIGVLCYELLVGNPPFESSS--HNETYRRILKVDVRFPPS--MP
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPFS--MP
IE----QRTYSEMDLWCIGVLCYELLVGNPPFESSS--YSETYRRILKVDVRFPPS--IP
VE----KTEHNDHVDLWSLGVLCYEFVVGAPPFEAKE--HSETYRRIVKVDLKFPKPFVS
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPFS--VP
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VP
IE----RRTYNEKVDLWCIGVLCYELLVGNPPFESSS--HNETYRRILKVDLRFPPS--LP
IE----GRTYDEKVDLWCIGVLCYELLVGNPPFESSS--HSETYRRILKVDVRFPPS--MP
IE----GKTHDEKVDLWCIGVLCYELLVGNPPFESSS--HTETYRRITKVDLQFPF--MS
IE----GRTYDEKVDLWCIGVLCYELLVGNPPFESAS--TSETYRRILKVDLRFPPS--MS
VE----GKTHNEKVDLWSLGVLCYEFVVGKPPFEANT--HSETYRRIVKVDLKFPAS--VS
VE----KTEHDYHVDLWSLGVLCYEFVVGPPFEAKE--HSETYRRIVKVDLKFPKPFVS
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VP
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPFS--VP
IE----GRTHNEKVDLWCIGVLCYELLVGNPPFESAS--HNETYRRIVKVDLKFPAS--VP
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VP
IE----GRMHDEKVDLWSLGVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VP

gi|470261727|ref|XP_004360485.1|/1-457
gi|449486478|ref|XP_002195961.2|/1-319
gi|426243291|ref|XP_004015492.1|/1-303
gi|426237569|ref|XP_004012730.1|/1-344
gi|410979749|ref|XP_003996244.1|/1-344
gi|410953494|ref|XP_003983405.1|/1-405
gi|410914403|ref|XP_003970677.1|/1-332
gi|389641901|ref|XP_003718583.1|/1-397
gi|389635857|ref|XP_003715581.1|/1-400
gi|357126095|ref|XP_003564724.1|/1-291
gi|355703962|gb|EHH30453.1|/1-309
gi|350538969|ref|INP_001233545.1|/1-403
gi|347966592|ref|XP_321274.5|/1-404
gi|345800233|ref|XP_849906.2|/1-344
gi|344296517|ref|XP_003419953.1|/1-405
gi|344290468|ref|XP_003416960.1|/1-345
gi|344269722|ref|XP_003406697.1|/1-306
gi|338709975|ref|XP_001502047.3|/1-304
gi|334312551|ref|XP_001378079.2|/1-402
gi|332848444|ref|XP_511856.3|/1-344
gi|330793523|ref|XP_003284833.1|/1-359
gi|321461440|gb|EFX72472.1|/1-304
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gi|302801442|ref|XP_002982477.1|/1-288
gi|302688103|ref|XP_003033731.1|/1-328
gi|297802712|ref|XP_002869240.1|/1-290
gi|281427796|ref|INP_001164000.1|/1-322
gi|268565413|ref|XP_002639437.1|/1-302
gi|260784959|ref|XP_002587531.1|/1-282
gi|226499040|ref|INP_001148791.1|/1-296
gi|224088986|ref|XP_002308590.1|/1-293
gi|215983064|ref|INP_001135979.1|/1-405
gi|213404608|ref|XP_002173076.1|/1-346
gi|198430178|ref|XP_002119314.1|/1-305
gi|196012778|ref|XP_002116251.1|/1-270
gi|168044897|ref|XP_001774916.1|/1-297
gi|159468203|ref|XP_001692272.1|/1-292
gi|158297402|ref|XP_317640.3|/1-307
gi|156368106|ref|XP_001627537.1|/1-314
gi|149734120|ref|XP_001489320.1|/1-404
gi|149724949|ref|XP_001504864.1|/1-344
gi|148225464|ref|INP_001085657.1|/1-368
gi|146172296|ref|XP_001018388.2|/1-360
gi|144226857|ref|INP_001016859.2|/1-360
gi|125524746|gb|EAY72860.1|/1-292
gi|115749607|ref|INP_898907.2|/1-344
gi|115455545|ref|INP_001051373.1|/1-309
gi|115435032|ref|INP_001042274.1|/1-292
gi|84000031|ref|INP_001033117.1|/1-402
gi|83776600|ref|INP_004208.2|/1-344
gi|76253851|ref|INP_695208.3|/1-397
gi|68013217|ref|INP_001018849.1|/1-355
gi|66815573|ref|XP_641803.1|/1-384
gi|62865639|ref|INP_001015878.1|/1-309
gi|62857967|ref|INP_001016570.1|/1-415
gi|57525577|ref|INP_001003640.1|/1-405
gi|50759065|ref|XP_425725.1|/1-409
gi|50303387|ref|XP_451635.1|/1-361
gi|46358064|ref|INP_035627.1|/1-417
gi|45198420|ref|INP_985449.1|/1-367
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gi|17505246|ref|INP_491714.1|/1-305
gi|17137514|ref|INP_477336.1|/1-329
gi|17136516|ref|INP_476749.1|/1-411
gi|16758580|ref|INP_446201.1|/1-343
gi|15233958|ref|INP_195009.1|/1-294
gi|15225495|ref|INP_182073.1|/1-288
gi|6708213|gb|IAAF25838.1|/1-282
gi|6325047|ref|INP_015115.1|/1-367
gi|2979623|gb|IAC12683.1|/1-345

VN----KQHYDHKVDWVSLGILIEFLCGRSAFCDET--EAVMEKIQKGVVTFP--SYVS
IE----GRTHDEKVDIWSLGVLCYEFVVGKPPFETET--YQETYRAISRVEFKFPPF--VT
IE----GRTYDEKVDLWLCIGVLCYELLVGNPPPFESAS--TSETYRRILKVDLRFPPS--MS
IE----GRTHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPSPS--VP
IE----GRTHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPSPS--VP
IE----GRMHDEKVDLWVLCYEFVVGKPPFEAST--YQETYKRISRVEFTFPDF--VP
IE----GHTHSEKVDLWLCIGVLCYEFVGNPPPFETTS--HSETYKRITKVDLKFPKV--VS
IKSGNKDNTYDEKVDLWVLCYEFVVGGEAPFEDTP--VMTQRRIRADMTIPSPF--VS
IKPRTADKSYDHRVDLWVLCYELLVGEAPFEDTP--AMTHKKITRRDMKVPSPF--VS
VE----KTEHDYHVDIWSLGVLCYEFVYGLPPFEAKE--HSETYRRIVKVDLKFPKPFVS
IE----GRTYDEKVDLWLCIGVLCYELLVGYPPPFESTS--HSETYRRILKVDVRFPLS--MP
IE----GRMHDEKVDLWVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VT
VQ----QOPHTKTVDLWVLCYELLVCGKAPFLATT--YEETYRKIMKVQYTVPPD--VT
IE----GRMHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPSPS--VP
IE----GRMHDEKVDLWVLCYEFVVGKPPFEAST--YQETYNRISRVEFTFPDL--VT
IE----GRMHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPSPS--VP
IE----GRTYDERVDLWLCIGVLCYELLVGNPPPFESPS--HTETYRRILKVDVRFPS--MP
IE----GRTYNEKVDLWLCIGVLCYELLVGNPPPFESNS--HNETYRRILKVDVRFPS--IP
IE----GRMHDEKVDLWVLCYEFVVGKPPFEAET--YQETYRSISKVEYKFPDF--VT
IE----GRMHDEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPAS--VP
VE----NKGYDQTDVWVSLGILIEFLVGHSPFASDE--EQRIFFNNIKENEVHP--SAIS
VE----GRSHDERVDLWVLCYEFVVGSPPFEEK--QDLTYRRICKVDLKFPFAH--LS
IV----GNHSDAVDLWVLCYEFVVGKPPFEHDK--QADTYSIAIKVARFSPDY--VK
VE----NKEHDSVDVWVSLGVLCYEFVFGTPPFEAQK--LSDTYRRIVRVDLKFPKIPVIS
VE----QKEHNERVDLWVLCYEFVIGNPPFEDRDSVNNYRRIASVDLRFPH--MS
VE----SVEHDSVDIWSLGVLCYEFVYGVPPFEAME--HSDTYRRIVQVDLKFPKPIVS
VV----GQTHNEKVDLWVLCYEFVVGKPPFEAPT--FEETYRNISKAYYKFPY--VS
VN----GNSHSDAVDLWVLCYEFVVGKPPFEHEN--QADTYSIAIKAGRFTYPDF--VK
IE----GKMHDEKVDLWVLCYEFVVGKPPFEAE--HSETYRRIVKVDLRFPPH--VT
VE----KAEHDYHVDIWSLGVLCYEFVYGVPPFEAKE--HSETYRRIVKVDLKFPKPFVS
VE----SVEHDSVDIWSLGVLCYEFVYGVPPFEAKE--HSDTYRRIVQVDLKFPKPIVS
IE----GRMHDEKVDLWVLCYEFVVGKPPFEADT--YQETYRRISRVEFTFPDC--VP
VE----GKEHGAKVDLWVLCYEFVVGAPPFEDISGHSATYRRIAKVDLKFPSPF--IS
IE----AKDHADVDLWVLCYEFVVGKPPFETKS--TQETYLRTISLKYSPFPH--VS
II----GDEHDDKVDLWVLCYEFVVGKPPFETKT--HEDTYKRIKVDLKFPENK--LS
VE----GKEHDAVDVWVSLGVLCYEFVYGVPPFEAKK--HSDTYKRIVRVDLRFSPKPIVS
VE----GKEHTTSVDNWSLGVLCYEFVFGGPPFEAPG--HQETYRRIVRVDLKFPDPKPAVS
VD----GKMYDDSDVQWVLCYEFVVGKPPFESQT--TQTTYDKIRRLDVIYPRH--MT
IE----GKEHDEKVDLWVLCYEFVVGKPPFEAE--HNETYRRISRVDLRFPSH--VS
IE----GRMHDEKVDLWVLCYEFVVGKPPFEAST--YQETYKRISRVEFTFPDF--VP
IE----GRTHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPSPS--VP
IE----GKTHNEKVDLWVLCYEFVVGKPPFESQTS--HSETYRRIVKVDLKFPSPF--LS
VE----GNTHNYTVDIWSLGVLCYEFVVGKPPFETKS--YDQTYDRIKKVQFSFP--DYLS
IE----GKTHDEKVDLWVLCYEFVVGKPPFESQTS--HTETYRRIVKVDLKFPSPF--LS
VE----KTEHDYHVDIWSLGVLCYEFVYGVPPFEAKE--HSETYRRIVKVDLKFPKPFVS
IE----GRTHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPSPS--VP
IE----KKAHDHVDNWLWVLCYEFVYGVPPFEAAE--QDDTLRRIVKVDLSFPSTPYVS
VE----KTEHDYHVDIWSLGVLCYEFVYGVPPFEAKE--HSETYRRIVKVDLKFPKPFVS
IE----GRMHDEKVDLWVLCYEFVVGKPPFEADT--YQETYRRISRVEFTFPDC--VP
IE----GRMHNEKVDLWLCIGVLCYELLVGNPPPFESAS--HNETYRRIVKVDLKFPAS--VP
IE----GRMHDEKVDLWVLCYEFVVGKPPFEAHT--YQETYRRISRVEFTFPDF--VT
VE----GKEHTEKVDLWVLCYEFVVGAPPFEDMSGHSATYKRIKVDLKIPSPF--VP
IE----KKGYDQTDVWVSLGILIEFLVGRSPFTSDE--EKNIFHNIQENDVYYP--SSIS
IE----GRTYDEKVDLWLCIGVLCYELLVGYPPPFESAS--HSETYRRILKVDVRFPLS--MP
IE----GRMHDEKVDLWVLCYEFVVGKPPFETDT--HQETYRRISKVEFYQPSY--VS
IE----GKTHDEKVDLWVLCYEFVVGKPPFETKS--HEETYRKISRVEFTYPAH--VS
IE----GRTHDEKVDIWSLGVLCYEFVVGKPPFEAQT--YQETYRAISRVEFKYPLF--VT
IK----SREYNNKVDVWVLCYELLVVGSPPFEEEDT--KEMTYRRILRCDLKFPNL--VS
IE----GRMHDEKVDLWVLCYEFVVGKPPFEAHT--YQETYRRISRVEFTFPDF--VT
IR----SREYNEKVDVWVLCYELLVVGSPPFEEES--KELTYKRILKRNLIFFPDH--VD
IE----GRMHDEKVDLWVLCYEFVVGKPPFEANT--YQETYKRISRVEFTFPDF--VT
VN----GADHSDAVDLWVLCYEFVVGKPPFEHED--QSKTYAAIKARFTYPPDS--VK
VD----GNSYDDSDVQWVLCYEFVVGKPPFESNS--TESTYSKIRMEISYPSH--LS
VQ----GKPHTKNVDLWVLCYEFVVGKPPFEAHT--YQETYRRIVKVDLKFPSPF--IS
IE----GRMHNEKVDLWLCIGVLCYELVMGNPPPFESPS--HSETYRRIVKVDLKFPSPS--MP
VE----SVEHDSVDIWSLGVLCYEFVYGVPPFEAME--HSDTYRRIVQVDLKFPKPIIS
VE----NRDHDYAVDNWLWVLCYEFVYGVPPFEAES--QKDTFKRILKIDLSFPLTPNVS
IA----GKPHTKNVDLWVLCYEFVVGKPPFESST--SSETYRRIVQVDFKLPPEH--VP
VE----SREYDHTIDAWLVLCYEFVVGKPPFEEM--KDTTYKRIAALDIKMPNS--IS
IE----GRMHNEKVDLWLCIGVLCYELVMGNPPPFESPS--HSETYRRIVKVDLKFPSPS--VP

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XP_020952967.1/1-297	LGAQDLIS-----	RLRYQPSDRLPLDQILEHPWV
XP_012380002.1/1-290	PGAQDLIS-----	KLLRYQPSERLPLAQILTHPWV
XP_006102660.1/1-339	VGAQDLIS-----	KLLKHNPSDRLPLAQVSAHPWV
XP_005673091.1/1-402	EGARDLIS-----	RLKHNPSHRPTLKEVLEHPWI
XP_004484680.1/1-405	EGARDLIS-----	RLKHNPSQRPTLKEVLEHPWI
XP_004462482.1/1-349	PGAQDLIS-----	KLLKHNPSERLPLAQVAHPWV
Q6NW76.1/1-320	EGARDLIS-----	KLLRHSPSMRLPLRSVMEHPWV
NP_999084.2/1-344	AGAQDLIS-----	KLLKHNPSDRLPLAQVSAHPWV
gi 1190438012 ref XP_020822491.1/1-365	SGAQDLIS-----	KLLRHNPSERLPLTQVLAHPWV
gi 1190373986 ref XP_020837071.1/1-405	EGARDLIS-----	RLKHNPYQRLTLKELLEHPWI
gi 1154067554 ref NP_001153906.2/1-332	DGARDLIS-----	KLLRHNPNDRLPLQKVMHPWV
gi 1131237831 ref XP_019799799.1/1-344	AGAQDLIS-----	KLLKHNPSERLPLAQVAHPWV
gi 1131178530 ref XP_019784431.1/1-296	LGAQDLIS-----	KLLRYQPSERLPLQVLEHPWV
gi 1126479796 ref XP_006940862.2/1-308	LGARDLIS-----	KLLRYQPLERLPLSQILEHPWV
gi 1113784803 ref XP_019353949.1/1-376	EGARDLIG-----	KLLRHVPAERLPLRAVLEHPWV
gi 1022987698 ref XP_016286291.1/1-365	SGAQDLIS-----	KLLRHNPSERLPLTQVLEHPWV
gi 1966994491 ref XP_014974040.1/1-344	TGAQDLIS-----	KLLRHNPSERLPLAQVSAHPWV
gi 1966965902 ref XP_015004225.1/1-398	EGARDLIS-----	RLKHNPSQRPMLREVLEHPWI
gi 1955535802 ref XP_004439167.2/1-335	LGAKDLIS-----	KLLRYQPLERLPLDQIMEHPWV
gi 1951053762 ref XP_014465099.1/1-416	EGAKDLIS-----	KLLKHNPYHRLPLKDVLEHPWI
gi 1946796851 ref XP_014384184.1/1-404	EGARDLIS-----	RLLMHNPQRLTLKEVLEHPWI
gi 1946756071 ref XP_014392719.1/1-299	LGAQDLIS-----	KLLRYQPSERLPLQVLEHPWV
gi 1922383691 ref XP_013462066.1/1-300	SAAKDLIS-----	QMLVKDSSERLPLHKLEHPWI
gi 1909794683 ref XP_013153467.1/1-419	EGARDLIA-----	KLLKHNPFHRLPLKDVLLHPWI
gi 1891599507 ref XP_013025412.1/1-351	PEAKDLIT-----	RLLRHSPEQRISLEQVVKHPWM
gi 1891565640 ref XP_013019059.1/1-351	PEGKDLIS-----	RLLRHSPEQRISLEQVVKHPWI
gi 1884853217 ref XP_013010870.1/1-315	AGAQDLIS-----	RLLRFPMERLPLSQVAVHPWV
gi 1830244266 ref XP_012590158.1/1-296	LGAQDLIS-----	SLLRYQPSERLPLAQILQHPWV
gi 1828211890 ref XP_012558808.1/1-339	SGARDLIS-----	QLLRKKPSDRLPLADVLKHPWI
gi 1820033943 ref NP_001295465.1/1-282	AGAQDLIS-----	KLLRHHPSERLSLAQVLKHPWV
gi 1795377289 ref XP_011750175.1/1-471	LGARDLIS-----	KLLRYQPLERLPLAQILKHPWV
gi 1779989227 ref XP_011666707.1/1-321	AGARDVIK-----	RLLQHNPANRLPLEQVLAHPWI
gi 1761905244 ref XP_011402440.1/1-385	PGAKDLII-----	KLLKKNPSERLALDEVLEKHSWI
gi 1759175630 ref XP_011377486.1/1-303	LGAQNLIS-----	KLLRYQPLERLPLAQILQHPWV
gi 1759149200 ref XP_011368486.1/1-311	EGARDLIS-----	RLKHNPSQRPTLKEVLEHPWI
gi 1759116391 ref XP_011357226.1/1-339	TGAQDLIS-----	KLLKHNPSERLPLAQVSAHPWV
gi 1758991346 ref XP_957232.2/1-420	KEAKDLIK-----	KLLVLDPEKRLPLEEVENHPWI
gi 1743922878 ref XP_011005517.1/1-293	SAAKDLIS-----	QMLVKDSSERLPLHKLEHPWI
gi 1698438703 ref XP_009757361.1/1-296	SAAKDLIS-----	QMLVKDSSQRLPLKKVLEHPWI
gi 1697188794 ref XP_009603442.1/1-294	SAARDLIS-----	QMLVKDSSQRLALKKLEHPWI
gi 1658871623 ref XP_008418750.1/1-330	DGARDLIS-----	KLLRHNPIDRLPLQNVIGHPWV
gi 1657559162 ref XP_008283516.1/1-424	AGAKDLVA-----	RLKHNPMHRLPIEGVLSPHPW
gi 1657529148 ref XP_008293493.1/1-319	DGARDLIS-----	KLLRHNPIDRLSLQSVIDHPWV
gi 1655887082 ref XP_008247187.1/1-292	LGARDLIS-----	RLRYQPSERLPLAQILRHHPWV
gi 1655881324 ref XP_008272369.1/1-402	EGAKDFIS-----	RLKHNPSHRPTLAEVLEHPWV
gi 1655868725 ref XP_008268971.1/1-343	AGAQDLIS-----	KLLRHNPSDRLTLAQVSAHPWV
gi 1641774253 ref XP_008170712.1/1-431	EGAKDLIV-----	KLLKHNPYQRLPLKDVLAHPWI
gi 1620969612 ref XP_007654691.1/1-303	DGAKDLIS-----	KLLKHNPYQRLTLKEVLEHPWI
gi 1617451788 ref XP_007568855.1/1-331	DGARDLIS-----	KLLRHNPIDRLPLQNVIDHPWV
gi 1594674988 ref XP_007185333.1/1-402	EGARDLIS-----	RLKHNPSQRPTLKEVLEHPWI
gi 1594654199 ref XP_007175509.1/1-282	LGAQDLIS-----	KLLRYQPSERLPLVQILEHPWV
gi 1594623572 ref XP_007166415.1/1-344	AGAQDLIS-----	KLLKHNPSERLPLAQVSAHPWV
gi 1584038001 ref XP_006753367.1/1-368	LGAQDLIS-----	KLLRYQPSERLPLAQVLQHPWV
gi 1573912300 ref XP_006643864.1/1-292	PSAKDLIS-----	QMLVKNSAHLPLHKLEHPWI
gi 1554569173 ref XP_005878848.1/1-339	VGAQDLIS-----	KLLKHNPSDRLPLAQVSAHPWV
gi 1545541126 ref XP_005635254.1/1-405	EGARDLIS-----	RLKHNPSQRPTLKEVLEHPWI
gi 1545487136 ref XP_005616134.1/1-307	LGAQDLVS-----	KLLRYQPLERLPLAQIMEHPWV
gi 1544514002 ref XP_005590555.1/1-471	LGARDLIS-----	KLLRYQPLERLPLAQILKHPWV
gi 1530653727 ref XP_005313062.1/1-365	EGSRDLIT-----	KLLCHNPAERLPLRAVLEHPWV
gi 1528993703 ref XP_005219854.1/1-303	SGARDLIS-----	KLLRFQPLERLPLVRVLEHPWI
gi 1524890835 ref XP_005101959.1/1-332	DGARDLIS-----	KLLRHDPKARLPLEQVLKHPWI
gi 1514776534 ref XP_004968502.1/1-292	PAAKDLIS-----	QMLVKNSAHLPLHKVLEHPWI
gi 1507960369 ref XP_004686961.1/1-405	EGARDFIS-----	RLKHNPSQRPTLKEVLEHPWI
gi 1507953708 ref XP_004684672.1/1-344	SGAQDLIT-----	KLLKHNPSERLPLTQVSAHPWV
gi 1478517838 ref XP_004433150.1/1-344	AGAQDLIS-----	KLLKHNPSERLPLAQVSAHPWV
gi 1478512086 ref XP_004430306.1/1-405	DGARDLIS-----	RLKHNPSQRPTLKEVLEHPWI
gi 1470628341 ref XP_004321082.1/1-402	EGARDLIS-----	RLKHNPSQRPTLKEVLEHPWI

gi 470261727 ref XP_004360485.1 /1-457	MEAQHLIL-----GLLTSDPSERLTMYDVINHPWI
gi 449486478 ref XP_002195961.2 /1-319	EGARDLIS-----RLLKHNPFHRLPLKDVLLHPWI
gi 426243291 ref XP_004015492.1 /1-303	SGARDLIS-----KLLRFQPLERLPLVRVLEHPWI
gi 426237569 ref XP_004012730.1 /1-344	MGAQDLIS-----KLLKHNPSERLPLAQVSAHPWV
gi 410979749 ref XP_003996244.1 /1-344	TGAQDLIS-----KLLKHNPSERLPLAQVSAHPWV
gi 410953494 ref XP_003983405.1 /1-405	EGARDLIS-----RLLKHNPSQRPTLKEVLEHPWV
gi 410914403 ref XP_003970677.1 /1-332	DGARDLIS-----KLLRHNPIDRLTLQNVIDHPWV
gi 389641901 ref XP_003718583.1 /1-397	PECRDLIK-----KLLVLDPVKRLSLDAVQKHPWI
gi 389635857 ref XP_003715581.1 /1-400	REASDLIL-----KLLVVDPNKRLPLDKVLDHPWI
gi 357126095 ref XP_003564724.1 /1-291	PAAKDLIS-----QMLVKNSAHLPLNKVLEHPWI
gi 355703962 gb EHH30453.1 /1-309	LGARDLIS-----KLLRYQPLERLPLAQILKHPWV
gi 350538969 ref INP_001233545.1 /1-403	EGARDLIS-----RLLKHNPSQRPMLREVLEHPWI
gi 347966592 ref XP_321274.5 /1-404	KAASHLIS-----RLLVKDPASRMPLENVAIHPWI
gi 345800233 ref XP_849906.2 /1-344	TGAQDLIS-----KLLKHNPSERLPLSQVSAHPWV
gi 344296517 ref XP_003419953.1 /1-405	VGARDLVS-----RLLKHNPSQRLTLKEVLEHPWI
gi 344290468 ref XP_003416960.1 /1-345	TGAQDLIS-----KLLKHNPSERLPLAQVSAHPWV
gi 344269722 ref XP_003406697.1 /1-306	SGAQDLIS-----KLLRYQPFERLALAQVLEHPWV
gi 338709975 ref XP_001502047.3 /1-304	SGAKDLIS-----KLLRYQPLERLPLDQILEHPWV
gi 334312551 ref XP_001378079.2 /1-402	EGARDLIS-----RLLKHNPYQRLTLKELLEHPWI
gi 332848444 ref XP_511856.3 /1-344	TGAQDLIS-----KLLRHNPSERLPLAQVSAHPWV
gi 330793523 ref XP_003284833.1 /1-359	TDAKDLIS-----KLLISDPHQRLSLDKVINHPWI
gi 321461440 gb EFX72472.1 /1-304	TGAKDLIT-----KLLKSRAEDRIPLRKLLEHSWI
gi 308497987 ref XP_003111180.1 /1-306	KGARDLIG-----KLLVVDPTKRCTLQKVVDHYWV
gi 302801442 ref XP_002982477.1 /1-288	TAAKDLIC-----QLLCKDSSQRLPLKELLAHPWI
gi 302688103 ref XP_003033731.1 /1-328	SDARDLIS-----KLLRHDQDRISLAEVMKHPWI
gi 297802712 ref XP_002869240.1 /1-290	ASAKDLIS-----QMLVKESSQRLPLHKLLEHPWI
gi 281427796 ref INP_001164000.1 /1-322	EGAQDLIR-----KLLVVPNPERLELSQVMKHPWI
gi 268565413 ref XP_002639437.1 /1-302	KGARDLIG-----KLLVVDPRRCSLQEVKDYWV
gi 260784959 ref XP_002587531.1 /1-282	SGARDLIS-----KLLRHNPMLRLPLDSVL SHPW
gi 226499040 ref INP_001148791.1 /1-296	PAAKDLIS-----QMLVKSSAQRLPLHKVLEHPWI
gi 224088986 ref XP_002308590.1 /1-293	SAAKDLIS-----QMLVKDSAERLPLHKLLDHPWI
gi 215983064 ref INP_001135979.1 /1-405	EGARDLIS-----RLLKHNPSQRPTLKEVLEHPWI
gi 213404608 ref XP_002173076.1 /1-346	AEAKDLIS-----RLLQHSPEKRLSLDQVMRHPWI
gi 198430178 ref XP_002119314.1 /1-305	EGARDLIR-----RLLKLEPRHRLPLDSVMAHPWI
gi 196012778 ref XP_002116251.1 /1-270	PEAMDILR-----KLLCRKPSERLSLDGVM SHPW
gi 168044897 ref XP_001774916.1 /1-297	SSARDLIC-----QLLVKDSAQRLPLSKVLTHPW
gi 159468203 ref XP_001692272.1 /1-292	DSAKAFIS-----KLLVKDAHRLPLLEVNQDPWI
gi 158297402 ref XP_317640.3 /1-307	AGAINLIS-----KLLRIPSSSRLTLRDVMMHPWV
gi 156368106 ref XP_001627537.1 /1-314	PGARDLIS-----KLLQHNPNNRLPLKAVLNHPWI
gi 149734120 ref XP_001489320.1 /1-404	EGARDLIS-----RLLKHNPSQRPTLKEVLEHPWI
gi 149724949 ref XP_001504864.1 /1-344	AGAQDLIS-----KLLRHNPSERLPLAQVSAHPWV
gi 148225464 ref INP_001085657.1 /1-368	EGSKDLIS-----KLLRYHPAQLRLPKQVMEHPWV
gi 146172296 ref XP_001018388.2 /1-360	IEVRDLIS-----KILVYEKSQRLDLNNILNHPWI
gi 144226857 ref INP_001016859.2 /1-360	DGSKDLIS-----KLLRYHPPQRLPLKGVMEHPWV
gi 125524746 gb EAY72860.1 /1-292	PAAKDLIS-----QMLVKNSAHLPLHKLLEHPWI
gi 115749607 ref INP_898907.2 /1-344	LGADQLIY-----KLLKHNPSERLPLAQVSAHPWV
gi 115455545 ref INP_001051373.1 /1-309	ADAKDLICKVFFVLLIPIVYVTLKWWELLSFELVRMQLLVKDSNKRLSLDDIMKHPWI
gi 115435032 ref INP_001042274.1 /1-292	PAAKDLIS-----QMLVKNSAHLPLHKLLEHPWI
gi 84000031 ref INP_001033117.1 /1-402	EGARDLIS-----RLLKHNPSQRPTLKEVLEHPWI
gi 83776600 ref INP_004208.2 /1-344	MGAQDLIS-----KLLRHNPSERLPLAQVSAHPWV
gi 76253851 ref INP_695208.2 /1-397	EGARDLIS-----RLLKHNSSQRLTLAEVLEHPWI
gi 68013217 ref INP_001018849.1 /1-355	PDARDLIS-----RLLQHNPEKRMSLEQVMRHPWI
gi 66815573 ref XP_641803.1 /1-384	PEAKDLIS-----RLLVSDPHQRLTLKDVINHPWI
gi 62865639 ref INP_001015878.1 /1-309	LGARDLIS-----KLLRYQPLERLPLAQILKHPWV
gi 62857967 ref INP_001016570.1 /1-415	EGARDLVS-----KLLKHNPNNHRLSLKGVLEHPWI
gi 57525577 ref INP_001003640.1 /1-405	NGSRDLIN-----RLLKHNPMHRLPIQGVMEHPWV
gi 50759065 ref XP_425725.1 /1-409	EGARDLIS-----KLLKHNPFHRLPLKDVLVHPWI
gi 50303387 ref XP_451635.1 /1-361	PQARDLIV-----RLLQFEPSEKRIPLSEVKSHAWI
gi 46358064 ref INP_035627.1 /1-417	EGARDLIS-----RLLKHNASQRLTLAEVLEHPWI
gi 45198420 ref INP_985449.1 /1-367	TEARHLIS-----RLLEYDPGDRIPLKEVKKHPWI
gi 38327570 ref INP_940838.1 /1-403	EGARDLIS-----RLLKHNPSQRPMLREVLEHPWI
gi 17505246 ref INP_491714.1 /1-305	KGARDLIG-----RLLVVDPKARCTLQEQVKEYHWI
gi 17137514 ref INP_477336.1 /1-329	KGCKELIG-----GLLRKESKGRITLVDVMTHYWV
gi 17136516 ref INP_476749.1 /1-411	KAASHLIS-----KLLVLNPQHRLPLDQVMVHPWI
gi 16758580 ref INP_446201.1 /1-343	LGAKDLIS-----KLLKHNPQRLPLEQVSAHPWV
gi 15233958 ref INP_195009.1 /1-294	ASAKDLIS-----QMLVKESSQRLPLHKLLEHPWI
gi 15225495 ref INP_182073.1 /1-288	EEAKNLIS-----QLLVKDPSKRLSIEKIMQHPWI
gi 6708213 gb IAAF25838.1 /1-282	AGAQDLIS-----KLLRYHPSERLSLAQVLEHPWV
gi 6325047 ref INP_015115.1 /1-367	QDAQDLIL-----KLLKYDPKDRMRLGDVKMHPWI
gi 2979623 gb IAC12683.1 /1-345	SGAQDLIS-----KLLKHNPWQRLPLAEVAAHPWV

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XP_020952967.1/1-297 RAHSRRVLPPSTQMVS-----
XP_012380002.1/1-290 QAHSRRVLPPSAQMVS-----
XP_006102660.1/1-339 RAHSRRVLPPSALQSVH-----
XP_005673091.1/1-402 TAN-SKPASSH-KKESTSKQP-----
XP_004484680.1/1-405 TANSKPPSSQKSKESTIQSS-----
XP_004462482.1/1-349 RAHSRRVLPPSALQSV-----
Q6NW76.1/1-320 KANSRRVLPPVCSSEPH-----
NP_999084.2/1-344 RAHSRRVLPPSAPQSV-----
gi|1190438012|ref|XP_020822491.1|/1-365 QTHSRRVLPPCSSRPAH-----
gi|1190373986|ref|XP_020837071.1|/1-405 IANSSKSPSSRKSKESNSTKS-----
gi|1154067554|ref|NP_001153906.2|/1-332 RTNSHRLLPPTCPSKKC-----
gi|1131237831|ref|XP_019799799.1|/1-344 RAHSRRVLPPSALQSV-----
gi|1131178530|ref|XP_019784431.1|/1-296 RAHSRRVLPPSAQMVS-----
gi|1126479796|ref|XP_006940862.2|/1-308 RAHSRRVPPSVQMDS-----
gi|1113784803|ref|XP_019353949.1|/1-376 RANSRRVLPPAYAP-----
gi|1022987698|ref|XP_016286291.1|/1-365 QTHSRRVLPPCSQPAPAH-----
gi|966994491|ref|XP_014974040.1|/1-344 RANSRRVLPPSALQSV-----
gi|966965902|ref|XP_015004225.1|/1-398 TANSKPSNCQ-NRVN-----
gi|955535802|ref|XP_004439167.2|/1-335 RAHSRRVLPPSAQMAS-----
gi|951053762|ref|XP_014465099.1|/1-416 RENSTKSPASRVSEAAGSRKSEANNKT-
gi|946796851|ref|XP_014384184.1|/1-404 TANSKPPSSQKSKESTSKQS-----
gi|946756071|ref|XP_014392719.1|/1-299 QAHSRRVGGPPAPAS-----
gi|922383691|ref|XP_013462066.1|/1-300 VQNAEPSGIYRS-----
gi|909794683|ref|XP_013153467.1|/1-419 TANSTKMPNSRKSDVAALPRTQS-----
gi|891599507|ref|XP_013025412.1|/1-351 LKHKASWSDQ-----
gi|891565640|ref|XP_013019059.1|/1-351 LKFASWNSDQ-----
gi|884853217|ref|XP_013010870.1|/1-315 KAHSRRVLPP-----
gi|830244266|ref|XP_012590158.1|/1-296 RMHSRRVLPPSAQVAS-----
gi|828211890|ref|XP_012558808.1|/1-339 QQHSSMFNKQKQSVNQPTTSSVSLSSS
gi|820033943|ref|NP_001295465.1|/1-282 RKHSQRMLPPCAQMAS-----
gi|795377289|ref|XP_011750175.1|/1-471 QVHSRRVLPPCAQMAS-----
gi|779989227|ref|XP_011666707.1|/1-321 VENSKKKPSSTSSSESQS-----
gi|761905244|ref|XP_011402440.1|/1-385 IENAK-----
gi|759175630|ref|XP_011377486.1|/1-303 QAHSRRVLPPSAHMAS-----
gi|759149200|ref|XP_011368486.1|/1-311 TANSKPPSSSQNKESSSKQS-----
gi|759116391|ref|XP_011357226.1|/1-339 RAHSRRVLPPSALQSV-----
gi|758991346|ref|XP_957232.2|/1-420 LKHCVKGERAANREKMASKMGN-----
gi|743922878|ref|XP_011005517.1|/1-293 VQNVDPGIFRG-----
gi|698438703|ref|XP_009757361.1|/1-296 VQNADPSGVYKG-----
gi|697188794|ref|XP_009603442.1|/1-294 VQNADPSGVYRG-----
gi|658871623|ref|XP_008418750.1|/1-330 KANSRRFLPPTCLTKKP-----
gi|657559162|ref|XP_008283516.1|/1-424 VQNS---TKKPTITLNNEELS-----
gi|657529148|ref|XP_008293493.1|/1-319 RSNHRLLPPTCPAKKS-----
gi|655887082|ref|XP_008247187.1|/1-292 QAHSRRVLPPCAHPAS-----
gi|655881324|ref|XP_008272369.1|/1-402 KAKSSKPPSSCP-DKEPASKQS-----
gi|655868725|ref|XP_008268971.1|/1-343 RAHSRRVLPPSALQSV-----
gi|641774253|ref|XP_008170712.1|/1-431 TTNSTKQPSRRKSEAATSNRTPS-----
gi|620969612|ref|XP_007654691.1|/1-303 TANSKAPNSLKSQESTSTKS-----
gi|617451788|ref|XP_007568855.1|/1-331 KANSRRLLPPTCPTKKP-----
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gi|594654199|ref|XP_007175509.1|/1-282 RAHSRRVLPPSAQMVS-----
gi|594623572|ref|XP_007166415.1|/1-344 RAHSRRVLPPSALQSV-----
gi|584038001|ref|XP_006753367.1|/1-368 QAHSRRVEPPPAPSAS-----
gi|573912300|ref|XP_006643864.1|/1-292 VQNADPSGVYRG-----
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gi|545541126|ref|XP_005635254.1|/1-405 MANSKPPSSSQKNKDSTSKQS-----
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gi|544514002|ref|XP_005590555.1|/1-471 QVHSRRVLPPCAQMAS-----
gi|530653727|ref|XP_005313062.1|/1-365 KANSRRVLPPVFNAPAN-----
gi|528993703|ref|XP_005219854.1|/1-303 RAHSQRVLPPSVPMAP-----
gi|524890835|ref|XP_005101959.1|/1-332 LKYNPDASSSTSSAPSS-----
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gi|470628341|ref|XP_004321082.1|/1-402 TAN-SKPSSSQ-KKESASKQS-----

gi 470261727 ref XP_004360485.1 /1-457	KKNAHPHSLIRT-----
gi 449486478 ref XP_002195961.2 /1-319	TANSTKIPTSRSKSDAAAPSKT-----
gi 426243291 ref XP_004015492.1 /1-303	RAHSQRVLPPSVQRAF-----
gi 426237569 ref XP_004012730.1 /1-344	RAHSRRVLPPSAQSV-----
gi 410979749 ref XP_003996244.1 /1-344	RAHSRRVLPPSALQSV-----
gi 410953494 ref XP_003983405.1 /1-405	TANSSKPSGSKSKESTGKQS-----
gi 410914403 ref XP_003970677.1 /1-332	RSNSRRVLPPICPAKKS-----
gi 389641901 ref XP_003718583.1 /1-397	IKHCVKGERATNREKGRGSD-----
gi 389635857 ref XP_003715581.1 /1-400	VKHCRN-QKASDRLLPSTGNTTPED---
gi 357126095 ref XP_003564724.1 /1-291	VQNADPSGVYRG-----
gi 355703962 gb EHH30453.1 /1-309	QVHSRRVLPPCAQMAS-----
gi 350538969 ref NP_001233545.1 /1-403	TANSSKPSNCQ-NKESASKQS-----
gi 347966592 ref XP_321274.5 /1-404	QLHVDKK-----
gi 345800233 ref XP_849906.2 /1-344	RAHSRRMLPPSAVQAIP-----
gi 344296517 ref XP_003419953.1 /1-405	TANSKKPPSSQ-NKEPTSKQS-----
gi 344290468 ref XP_003416960.1 /1-345	RAHSRRVLPPSALQSV-----
gi 344269722 ref XP_003406697.1 /1-306	QAHSQRVLPPSAQMAS-----
gi 338709975 ref XP_001502047.3 /1-304	RAHSRRVLPPSAQMAS-----
gi 334312551 ref XP_001378079.2 /1-402	IANSKSPSSRKSKESKP-----
gi 332848444 ref XP_511856.3 /1-344	RANSRRVLPPSALQSV-----
gi 330793523 ref XP_003284833.1 /1-359	QKNAHPHSLPTKLGPLPSQMT-----
gi 321461440 gb EFX72472.1 /1-304	LQHLSDVRSRLPTFQIMQPNKA-----
gi 308497987 ref XP_003111180.1 /1-306	TQMVTARKVAEQAQAEKASLRDH---
gi 302801442 ref XP_002982477.1 /1-288	TANADPSGIYAGSGGASA-----
gi 302688103 ref XP_003033731.1 /1-328	VKYRPPKGQIRPSQLGM-----
gi 297802712 ref XP_002869240.1 /1-290	VQNADPSGIYRG-----
gi 281427796 ref NP_001164000.1 /1-322	VSHTEEKSSQ-----
gi 268565413 ref XP_002639437.1 /1-302	TSMLDCSRRAAEKQKAERASLRDH---
gi 260784959 ref XP_002587531.1 /1-282	KDNAATQAESTPAHPHTASHTKS-----
gi 226499040 ref NP_001148791.1 /1-296	VQNADPSGVYREGRSV-----
gi 224088986 ref XP_002308590.1 /1-293	VQNADPSGIFRG-----
gi 215983064 ref NP_001135979.1 /1-405	TAN-SKPSSCQ-KKESTSKQS-----
gi 213404608 ref XP_002173076.1 /1-346	LKHKNWDRPGVDQP-----
gi 198430178 ref XP_002119314.1 /1-305	KANA---KVHKFGPDGRPMD-----
gi 196012778 ref XP_002116251.1 /1-270	VKHVQNDAKN-----
gi 168044897 ref XP_001774916.1 /1-297	VNNADPSGVYNGHN-----
gi 159468203 ref XP_001692272.1 /1-292	KANADPDMLARGN-----
gi 158297402 ref XP_317640.3 /1-307	-----VQMKK-----
gi 156368106 ref XP_001627537.1 /1-314	RMHATPVLEQKPASQR-----
gi 149734120 ref XP_001489320.1 /1-404	TANSSKPSNSQKSKESTSKQP-----
gi 149724949 ref XP_001504864.1 /1-344	RAHSRRVLPPSALQSV-----
gi 148225464 ref NP_001085657.1 /1-368	KANSRRVLPPVYQSSHPK-----
gi 146172296 ref XP_001018388.2 /1-360	QKHNPQNQVTSQVPLQQLNQNIC----
gi 144226857 ref NP_001016859.2 /1-360	KANSRRVLPPVFSQSSK-----
gi 125524746 gb EAY72860.1 /1-292	VQNADPSGVYRG-----
gi 115749607 ref NP_898907.2 /1-344	RTHSRRVLPPSAQSV-----
gi 115455545 ref NP_001051373.1 /1-309	VKNADPSGSCSDQKART-----
gi 115435032 ref NP_001042274.1 /1-292	VQNADPSGVYRG-----
gi 84000031 ref NP_001033117.1 /1-402	IAN-SKPSSCQ-KKESTSKQS-----
gi 83776600 ref NP_004208.2 /1-344	RANSRRVLPPSALQSV-----
gi 76253851 ref NP_695208.2 /1-397	KANSKPPGTGHNSKEATSKSS-----
gi 68013217 ref NP_001018849.1 /1-355	VKYKDSWTRKSESS-----
gi 66815573 ref XP_641803.1 /1-384	KKHAHPKSLEPTKLGPLPSQMTY----
gi 62865639 ref NP_001015878.1 /1-309	QAHSRRVLPPCAQMAS-----
gi 62857967 ref NP_001016570.1 /1-415	IDNSAQKPKRKEGPVTGAQ-----
gi 57525577 ref NP_001003640.1 /1-405	VENS---TKKPTTYTATANN-----
gi 50759065 ref XP_425725.1 /1-409	TANSTKLNNRK-----
gi 50303387 ref XP_451635.1 /1-361	ANNRGSWTDL-----
gi 46358064 ref NP_035627.1 /1-417	KANSKPPGTGHTSKEPTSKSS-----
gi 45198420 ref NP_985449.1 /1-367	EKNKPFW-----
gi 38327570 ref NP_940838.1 /1-403	TANSSKPSNCQ-NKESASKQS-----
gi 17505246 ref NP_491714.1 /1-305	QGMMEAKIRAEKQKQIEKASLRNH---
gi 17137514 ref NP_477336.1 /1-329	KAGMAERELQLQKRRERGKENTARN----
gi 17136516 ref NP_476749.1 /1-411	LAHTQ-----
gi 16758580 ref NP_446201.1 /1-343	RANSRRVLPPSAL-----
gi 15233958 ref NP_195009.1 /1-294	VQNADPSGIYRV-----
gi 15225495 ref NP_182073.1 /1-288	VKNADPKGVCASTDI-----
gi 16708213 gb AAF25838.1 /1-282	REHSRRVLPPCVHGAS-----
gi 6325047 ref NP_015115.1 /1-367	LRNKPFWENKRL-----
gi 2979623 gb AAC12683.1 /1-345	RANSRRVLPPSAL-----