

gi | 31982437 | ref | NP_035071.3 | MEQAVHGESEKRGVITGTHLNDIS-----KAKKCTVIGGSGFLGQHMVEQLLERG--TVNVVFDIH--GGFDNPRVQFFIGDLCNQDLYPALKG--VSTVVFHCASPPFYSNN--KELFYRVNFIGTKT 150
gi | 57164113 | ref | NP_001009399.1 | MEQAVRSSEKRGVITGTHLNDIS-----KAKKCTVIGGSGFLGQHMVEQLLSRG--YAVNVFDVR--GGFDNPRVQFFIGDLCNQDLYPALKG--VSTVVFHCASPPSNN--KELFYRVNFIGTKT 150
gi | 74008671 | ref | XP_538199.2 | MEQAF--GPMRDVTRIRHLLEGLP-----NASKCTVIGGSGFLGQHMVEQLLARG--TVNVVFDIR--GGFDNPRVQFFIGDLCNQDLYPALKG--VSTVVFHCASPPSSNN--KELFYRVNFIGTKN 150
gi | 78369400 | ref | NP_001030559.1 | MEQAA--GEP-----TRICLLEDIP-----KAKRCTVIGGSGFLGQHMVEQLLARG--YAVNVFDIR--GGFDNPRVQFFIGDLCNQDLYPALKG--VSTVVFHCASPPFNN--KELFYRVNFIGTKN 150
gi | 193211614 | ref | NP_001123237.1 | MEPAV--SEPMRDVVARHHLLEDIPKVNADIEKVNQNAKRCVTVIGGSGFLGQHMVEQLLARG--YAVNVFDIQ--GGFDNPRVQFFIGDLCNQDLYPALKG--VSTVVFHCASPPSSNN--KELFYRVNFIGTKN 150
gi | 50745878 | ref | XP_420279.1 | -----MAHFR--S-----TGKCVVIGGSGFLGQHMVEQLLDKG--YSNVVFDIQ--KRFDHNRVQFFIGDLCNKEALLPALQD--VSVAFHCASPPSSDN--KELFYKVNFMGTKA 150
gi | 62955325 | ref | NP_001017674.1 | -----MSPRIR--P-----SSKRCVIGGSGFLGRHLVRLVDRG--TCVNVFDIP--LAYLGVQVTVYQGDLDCKLALVMAKLE--VSVVFHCASPPGSD--GALFORVNDIGTRT 150
gi | 42569340 | ref | NP_180194.2 | -----MSPAA--S-----ETERWCVVVGGRGFAARHLVEMLVRYEM--FHVRIADLAPAILMLDPOENGVLDEGLSRGVVISADLRDKSQVVKAFQ--AEVVFHMAAPDSSIN--HGLQVSNVQGTN 150
gi | 30694041 | ref | NP_849779.1 | -----MVMEV--S-----ETERWCVVVGGRGFAARHLVEMLVRYQM--FHVRIADLAPAVLNPHEETGILGEAIRSRGVQVVSADLRNKTVQVVKFQ--AEVVFHMAAPDSSIN--HGLQVSNVQGTN 150
gi | 115453453 | ref | NP_001050327.1 | -----MAAAAAGG-----GDGRWCVVVGGRGFAARHLVAMLRSGE--WLVRVADLPPAIALDRDEEGILGAALREGRAAYASADLRNKAQVAAAFEG--ADVVFHMAAPDSSIN--PHLYSNVVEGTN 150
gi | 6321437 | ref | NP_011514.1 | -----MSKIDSVLITGGSGFLGLHLIQDFDINPKDIIHFVDRDLPEKLSK--FTFNVDIIFHKGLDLSPPDMENAINESKANVVVHCASPMHGQ--PDIINDIVNVKGTN 150
gi | 50306127 | ref | XP_453025.1 | -----MSSDVKSVLLIGGSGFLGLHLIQDFELKQPQIHFVDRPLDRISK--FTFPDSTITFHQGDLSPADVKALETGATIVVHSAAPMHGNS--QIEVEKVNKGTN 150
gi | 45198519 | ref | NP_985548.1 | -----MPALESVLLVGGSGFLGLHLIEQVWNLTPRPDIYVFDIRPLPKISTC--FTFPDPTKITCYQGDLSAKDVEHAIKS--SGVRVLVHSAAPMHGNS--QIEVEMVNVKGTN 150
gi | 19113533 | ref | NP_596741.1 | -----MP--MNSVLVIG--SGFLGGHIIROLCERE--NLRIAAVDFLEN--EKLLHE--LHG--OFTMYTGDLTQGDIERVFEFPRVVIHTASPVHNL--RDIVFEVNDGTAT 150
gi | 145614678 | ref | XP_001413950.1 | -----MAKPEIKFNLGSVLVGGSGFLGSHIVRMLDDYCKAVSAVLDLRCNRNR--EGVYHDADITNAERLVSVDVPRPDVVIHTASPLAQNSVUVHRDIFYKVNVEGTN 150
gi | 85118539 | ref | XP_965466.1 | -----MAS--EKKPELGSVMVIGGCGFLGHVVRVLLRDYIC--VSVIDLRCNRNR--ESDGVQVFEADITDPARLETIFNQVKPQVVIHTASPAQNS--DVSVALFKKVNVDGTA 150



gi | 31982437 | ref | NP_035071.3 | VIETCREAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--MKPIDYYTEKILQERAVLDANDP--KKNFLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFMINGENLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 57164113 | ref | NP_001009399.1 | VIETCKEAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--MKPIDYYTEKILQERAVLDANDP--KKNFLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFMINGENLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 74008671 | ref | XP_538199.2 | VIETCKEAGVQKLLITSSAVVPEGVN--IKNGTDELPLVA--MKPIDYYTEKILQERAVLDANDP--KRNFLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFMINGENLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 78369400 | ref | NP_001030559.1 | VIETCKEAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--TKPIDYYTEKILQERAVLGAHPD--EKNFLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFMINGENLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 193211614 | ref | NP_001123237.1 | VIETCKEAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--MKPIDYYTEKILQERAVLGAHPD--EKNFLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFMINGENLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 50745878 | ref | XP_420279.1 | VIEACKEAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--KKPIDYYTEKILQEKVLSANDP--DNNFLLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 62955325 | ref | NP_001017674.1 | VIEACKEAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--KKPIDYYTEKILQEKVLSANDP--EKNFLTAIRPHGIFGPRDP--LVLPVILDAARKGKMKFIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 42569340 | ref | NP_180194.2 | VIDACVDEAGVQKLLITSSAVVPEGVD--IKNGTDELPLVA--IKKNDYSATKAEGEELIMKANG--RNLGTCIRPSSIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 30694041 | ref | NP_849779.1 | VIDACIEVGVKRLIYTSAPVDFGVDGHLNLADESLEPP--PKNDYSATKAEGEELIMKANG--RNLGTCIRPSSIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 115453453 | ref | NP_001050327.1 | VIDACIRCKVRLIYTSAPVDFGVDGHLNLADESLEPP--DKFNDSYSATKAEGEELIMKANG--RDGLLTCIRPSSIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 6321437 | ref | NP_011514.1 | VIDMCKKCGVNLVYTSAGVIFNG--QDHNADETWPIP--EVPMDGYNETKAIAEMVLSAND--PNDPFLTALRPAIGIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 50306127 | ref | XP_453025.1 | LLTVAKQCRVKAVVYTSAGVIFNG--QDHNADETWPIP--EVPMDGYNETKAIAEMVLSAND--PNDPFLTALRPAIGIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 45198519 | ref | NP_985548.1 | LLDVAKKCGITAFIYTSAGVIFNG--QDHNADETWPIP--DIPMDGYNETKAIAEMVLSAND--PNDPFLTALRPAIGIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 19113533 | ref | NP_596741.1 | IVEACKKAGVQKLVYTSAGVIFNG--ADLNVDSEQPII--EVHMDAYNESKALAEKQVLEAS--SESLLTAAIRPAGIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 145614678 | ref | XP_001413950.1 | IVEACKKAGVQKLVYTSAGVIFNG--ADLNVDSEQPII--EVHMDAYNESKALAEKQVLEAS--SESLLTAAIRPAGIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300
gi | 85118539 | ref | XP_965466.1 | IVEACKKAGVQKLVYTSAGVIFNG--ADLNVDSEQPII--EVHMDAYNESKALAEKQVLEAS--SESLLTAAIRPAGIFGPGDRLVPSLVAARAGKSKPIIGDGNLVDFTFVENVVHGHILAAEHLSDQ-----AALGG 300



gi | 31982437 | ref | NP_035071.3 | KAFHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 57164113 | ref | NP_001009399.1 | KAFHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 74008671 | ref | XP_538199.2 | KAFHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 78369400 | ref | NP_001030559.1 | KAFHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 193211614 | ref | NP_001123237.1 | KAFHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 50745878 | ref | XP_420279.1 | QAYHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 62955325 | ref | NP_001017674.1 | QAYHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 42569340 | ref | NP_180194.2 | QAYHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 30694041 | ref | NP_849779.1 | QAYHITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 115453453 | ref | NP_001050327.1 | KTYFITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 6321437 | ref | NP_011514.1 | EYFFIITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 50306127 | ref | XP_453025.1 | EYFFIITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 45198519 | ref | NP_985548.1 | EYFFIITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 19113533 | ref | NP_596741.1 | QVFFIITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 145614678 | ref | XP_001413950.1 | EYFFIITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450
gi | 85118539 | ref | XP_965466.1 | EYFFIITNDEPIPFWTFLSRILITGLNVEAPKYHIPVWYAYLAFLLSLLVMVSPVLIQIQTFPIRVALAGTFHHYSCERAKKLFGRPLVMDDAVERTVQSFHLLRDK-----AALGG 450



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gi|31982437|ref|NP_035071.3|----- 600
gi|57164113|ref|NP_001009399.1|----- 600
gi|74008671|ref|XP_538199.2|----- 600
gi|78369400|ref|NP_001030559.1|----- 600
gi|193211614|ref|NP_001123237.1|----- 600
gi|50745878|ref|XP_420279.1|----- 600
gi|62955325|ref|NP_001017674.1|----- 600
gi|42569340|ref|NP_180194.2|----- 600
gi|30694041|ref|NP_849779.1|----- 600
gi|115453453|ref|NP_001050327.1|----- 600
gi|6321437|ref|NP_011514.1|----- 600
gi|50306127|ref|XP_453025.1|----- 600
gi|45198519|ref|NP_985548.1|----- 600
gi|19113533|ref|NP_596741.1|----- 600
gi|145614678|ref|XP_001413950.1|----- 600
gi|85118539|ref|XP_965466.1|----- 600
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.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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SIYYNFVATG---STVVTALSKALLVASVFLFLHGILPEKIFGYTVEKIPASQFHLKDSHDLSELSVSSWNTTVKALRSLCQGNDSFFFKVVFVLLALSAGATSLHIFVIGLPIAFLAFLVYEKKEGEIDSIVVEPKSPACKHK
ILYHNFVAITGSSSVIITAVSKVLLVSSIFMFINIGILPEKM-----
VIYVHLFTCG---YFTITAMAKLFSLLTALFLFIRGILPANVFGHKVKEKLEPSNFHITQVEAHHIAHSVSSIWNLSLVGVLKSLCRGNDWPLFFKVVVFSLLVVSILSSMSSQSAPKIGISMAFLGFKAYEKWEDTIDDLVGNACSVVTHFVQ
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gi|31982437|ref|NP_035071.3|----- 614
gi|57164113|ref|NP_001009399.1|----- 614
gi|74008671|ref|XP_538199.2|----- 614
gi|78369400|ref|NP_001030559.1|----- 614
gi|193211614|ref|NP_001123237.1|----- 614
gi|50745878|ref|XP_420279.1|----- 614
gi|62955325|ref|NP_001017674.1|----- 614
gi|42569340|ref|NP_180194.2|----- 614
gi|30694041|ref|NP_849779.1|----- 614
gi|115453453|ref|NP_001050327.1|----- 614
gi|6321437|ref|NP_011514.1|----- 614
gi|50306127|ref|XP_453025.1|----- 614
gi|45198519|ref|NP_985548.1|----- 614
gi|19113533|ref|NP_596741.1|----- 614
gi|145614678|ref|XP_001413950.1|----- 614
gi|85118539|ref|XP_965466.1|----- 614
-----
.....610....

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DVEKLFGSKKH-
---KVFSGKKID-
G--QSSRQKHAD-
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