

gi | 6678463 | ref | NP\_033471.1 | -MEAEELIGSSVT -IDS IMNKMRDIKKNIN--EDCTDELSLSKICADHT--ETVNOIMRVGNTPENWLNFLLLKLEKNSP-LNDLLNKLIGRYSQAIEALPPDKYGNESFARIOVRLAELKAIQEPDDARDYFOMARENCKKFAFVH 150  
gi | 109483730 | ref | XP\_236477.4 | -MEAEELIGRNLV -IDS IMNKMRDIKKNIN--EDLTDELNLKIKVCVDPDENSETVNOIMMVENTPENWLNFLLLKLEKNSPP-LNDALLNKLIGRYSQAIEALPPDKYGNESFARIOVRLAELKAIQEPDDAHDYFOMARENCKKFAFVH 150  
gi | 73973853 | ref | XP\_539016.2 | -MEAEEDVGGREL -IDS IMNKVRDIKKNFKN--EDLTDELNLKLNKVSADSDNSGTVNOIMMANNPEDWLNLLLLKLEKNSVP-LNDALLNKLIGRYSQAIEALPPDKYGNESFARIOVRFELKAIQEPDDARDYFOMARENCKKFAFVH 150  
gi | 119901123 | ref | XP\_603264.3 | -MEAEELSGKELT -IDS IMNKMRDIKKNFKN--EDLTDELNLKLTASTDTTNSGTVNOIMMANNPEDWLNLLLLKLEKNSVP-LNDALLNKLIGRYSQAIEALPPDKYGNESFARIOVRFELKAIQEPDDARDYFOMARENCKKFAFVH 150  
gi | 262399361 | ref | NP\_001160163.1 | -MESEDLSGREL -IDS IMNKVRDIKKNFKN--EDLTDELNLKLNKISADTTNSGTVNOIMMANNPEDWLSLLLLKLEKNSVP-LSDALLNKLIGRYSQAIEALPPDKYGNESFARIOVRFELKAIQEPDDARDYFOMARENCKKFAFVH 150  
gi | 114608216 | ref | XP\_001146752.1 | -MESEDLSGREL -IDS IMNKVRDIKKNFKN--EDLTDELNLKLNKISADTTNSGTVNOIMMANNPEDWLNLLLLKLEKNSVP-LSDALLNKLIGRYSQAIEALPPDKYGNESFARIOVRFELKAIQEPDDARDYFOMARENCKKFAFVH 150  
gi | 118088789 | ref | XP\_419867.2 | MESEEDLSERGLPRIASIMSRVRLDKNKNYRDNLTDELNLKTKISADTTNSGTVNRIMTINPEDWLLRLLLEKKGIPMDLISLNRLLIGRYSQAIVTALPAKKSSEDENYARILVRFELKAIQEPEDARDYFOMARENCKKFAFVH 150  
gi | 28077097 | ref | NP\_778207.1 | -MDEESLERQMO -IAMLCQKLAAMMKQLFN--EDDDYIN-----QAISSNSPDT CRTFLSNLEKKGIPQADPSSLKSLMDSYTRVRESMPLKGYKSNESYAKMLVRFELKAIQEPDARDYFOMARENCKKFAFVH 150  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 6678463 | ref | NP\_033471.1 | VSFQFELSGNKKSEQLLHKAVETGAVPLQMLETAMRNHLHKKQLLPEEDKKSVSASTVLSAQ-----EPFSSSLGN-----VQNRSI-----CESRGQAQAARVLYGENLPP-----GDAEVRHONP-----FKG 300  
gi | 109483730 | ref | XP\_236477.4 | VSFQFELSGNKKSEQLLHKAVETGAVPLQMLETAMRNHLHKKQLLPEEDKKSLSASTVLTAA-----EPFSSSLGN-----LQNRKSSCDPKVQAAAARILYGENMPP-----KDAEVRSHRNP-----LKG 300  
gi | 73973853 | ref | XP\_539016.2 | ISFAQFELSGNFKKSKOLLHKAVECGAVPLEMLEIATONLNLOKQQLLEEEKKLSVSMVLTITQ-----EPFSSSLGN-----LQNRNISCDRSGOTTKARFLYGENLPP-----QDAEIGHRNS-----LKG 300  
gi | 119901123 | ref | XP\_603264.3 | ISFAQFELSGNFKKSKOLLHKAVECGAAPLEMLEIATONLNLOKQQLLEEEKKLSASTVSSAA-----EPFSSSLGN-----LQNRNISCDRSGOTTKARFLYGENLPP-----QDTIEIGYRNP-----LKG 300  
gi | 262399361 | ref | NP\_001160163.1 | ISFAQFELSGNFKKSKOLLKAVERGAVPLEMLEIATONLNLOKQQLLEEEKKLSASTVLTAA-----EPFSSSLGN-----LQNRNISCDRSGOTTKARFLYGENMPP-----QDAEIGHRNS-----LKG 300  
gi | 114608216 | ref | XP\_001146752.1 | ISFAQFELSGNFKKSKOLLKAVERGAVPLEMLEIATONLNLOKQQLLEEEKKLSASTVLTAA-----EPFSSSLGN-----LQNRNISCDRSGOTTKARFLYGENLPP-----QDAEIGHRNS-----LKG 300  
gi | 118088789 | ref | XP\_419867.2 | VAFQFELSGNFKKSKOLLKAVECSAVPLEMLEIATONLNLOKQQLLEEEKKLSASTVLTAA-----EPFSSSLGN-----LQNRNISCDRSGOTTKARFLYGENLPP-----QDAEIGHRNS-----LKG 300  
gi | 28077097 | ref | NP\_778207.1 | VAAQFELLCGNMKCKTMIILQKAFENNAKPRHVLAAAVRNLIKTKRQLLHEDKENLSYALDHTQGGRRRGGACELKPKSSTPLHSSDQKFPQENGFVWRTGSOHRRRTAMAERVPMVPLSIPENETSSDSCAKAKAFAFPTHSSGFSRQ 300  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 6678463 | ref | NP\_033471.1 | TH-----AAKRSQPFQ-----RVPVNLN-----SPDFYVKTDS-----AVTQLTTRLALS-----VPLPYVCLLHLLLA-----LAGLAKSGPDRDAILPG-----SRPRGSDSYE-----LRGLKPIOT----- 450  
gi | 109483730 | ref | XP\_236477.4 | TN-----KTKRSQPFQ-----RVPVNLN-----SPDYVKTDS-----AVPQPTKRRKISGSE-----VRSIMPG-----SKSFGNDSYE-----LRGLKPIQA----- 450  
gi | 73973853 | ref | XP\_539016.2 | TN-----KAKRSQPFQ-----RVPVNLN-----SPD-YGKIDGS-----VLPSPFKRQISGSE-----VRDIIVSG-----SKSSGNDSE-----LRHLKSIQI----- 450  
gi | 119901123 | ref | XP\_603264.3 | TS-----KAKRSQPFQ-----RVPVNLN-----SPDSHEKMDVS-----VAPHFTRKHISGSE-----CRDITIPG-----CKSSGNDSE-----LRHLKSVON----- 450  
gi | 262399361 | ref | NP\_001160163.1 | TN-----KTKQSQPFQ-----RVPVNLN-----SPDCDKVTDD-----VVPFCMKRQTSRSE-----CRDLVPPG-----SKPSGNDSCB-----LRNLKSVON----- 450  
gi | 114608216 | ref | XP\_001146752.1 | TN-----KTKQSQPFQ-----RVPVNLN-----SPDCDKVTDD-----VVPFCMKRQTSRSE-----CRDLVPPG-----SKPSGNDSCB-----LRNLKSVON----- 450  
gi | 118088789 | ref | XP\_419867.2 | LN-----KSNQACPFQ-----RVPVNLN-----SPDKVLTDFDDVQVQTDV-----LNASVMKROVSRSE-----CTALIPFPPLSEPKPSNDSCD-----PADSKLLOE----- 450  
gi | 28077097 | ref | NP\_778207.1 | SGSSVRSFAFLCSKKGTPDGGVSLNLIKPPVI-----SPDYLRREDIEEGHTI-----ALLNRAEKREARTSEI-----DINDIISINSGCCAFILKLNLEKRAPHSDAAFSLKLLDCYSKVFAR-----FPLAEHCKTESYARMLVRYAELKGIQEDPEDAADI 450  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 6678463 | ref | NP\_033471.1 | -----IYLDKSLVNEKSSSE-----LMSDLIALKSKTDS-----LTKLEE-----KPEIAERRPQWQSTRK-----ECVFNQPAAFAPLRHVED-----VTPKADKE-----SPPI 600  
gi | 109483730 | ref | XP\_236477.4 | -----IHLKDSLVEKSSSE-----LMSDLVTLKSKTDS-----LTKLEEPK-----VRQPEIPEIRRHQWQSAKRP-----GCGIINSAAFAPQWHPED-----VTPKADKEKCTIVEQLAFSVSKQSPPI 600  
gi | 73973853 | ref | XP\_539016.2 | -----INSKESLMSDEKSSSE-----LDLDSVTLKKNKSESSLLTKLEEK-----EHOEQNVTVNQKQWQSVKRS-----ECVFNQPAVASENLWQIPE-----VSRKVDTEQKQIFEQPAFVSVKQSPPI 600  
gi | 119901123 | ref | XP\_603264.3 | -----VRSKEPVIDEKSSSE-----LITDSVTLKKNKSESSFLTKLEEK-----EHOELKVPSELKQWQSKRKS-----ECANQNAAFPSQWQIPE-----VTPKIDTEQKQIFEQPAFVSVKQSPPI 600  
gi | 262399361 | ref | NP\_001160163.1 | -----SHEKPEPLVDEKSSSELIITDSITLKNKTESLLAKLEEK-----EYOPEVPEPESNQKQWQSKRKS-----ECINONPAASNNHWQIPE-----LARKVNTER-----HTIFEQPVFVSVKQSPPI 600  
gi | 114608216 | ref | XP\_001146752.1 | -----SHEKPEPLVDEKSSSELIITDSITLKNKTESLLAKLEEK-----EYOPEVPEPESNQKQWQSKRKS-----ECINONPAASNNHWQIPE-----LARKVNTER-----HTIFEQPVFVSVKQSPPI 600  
gi | 118088789 | ref | XP\_419867.2 | -----NSVOLQMLD-----ENSLTAIINSVTLKKNKIDTSLVMKREENKLOYELKIPESRSMESQOQSSSAEYRQCFDQIKLNCVNRKRWKPE-----VMOQNCYRERSLEQSAHPLSRRLSPDP 600  
gi | 28077097 | ref | NP\_778207.1 | FSIARSHCKAFAFVHIAHAHAFELSRGNSRKS-----VSILQKALS-----NARPIELLC-----AIRNLKSGKTLTLLPADLQES-----EAENVEAQNYIKREENAKAP-----EDHQKPFSEKTESSEWKPALITKH-----SPEDRKALEPVSSES-----SHHAVR 600  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 6678463 | ref | NP\_033471.1 | SVPKWLDPKSACEIPSSSSLDYMKCFKIPVVKNDFFPACPSSTIPYSQLARLQOQQOGLSPLQLS-----LQISGSSSINECISVNGRIYSILKIQISGGSSKVFQVLEKQIINAIKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 109483730 | ref | XP\_236477.4 | SVPKWLDPKSACEIPSSSSLDYMKCFKIPVVKNDFFPACPSSTIPYSQLARLQOQQOGLSPLQLS-----LQISGSSSINECISVNGRIYSILKIQISGGSSKVFQVLEKQIINAIKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 73973853 | ref | XP\_539016.2 | SAPTWDPKSLCKIPSSSALDDYMKCFRIPVVKNDFFPACQLSTIPYSQLAHFOQQOGLSIPVPLQAT-----LQISASS-----INECISVNGRIYSILKIQISGGSSKVFQVLEKQIHAIKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 119901123 | ref | XP\_603264.3 | SVPKWLDPKSICKIPSNALDDYMKCFRIPVVKNDFFPACQLSTIPYSQLAYFOQQOGLSIPVPLQAT-----LQISASS-----INECISVNGRIYSILKIQISGGSSKVFQVLEKQIHAIKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 262399361 | ref | NP\_001160163.1 | SISKWFDPKSICKIPSSNLDYMKCFRIPVVKNDFFPACQLSTIPYQACFOQQOGLSILAPLQAT-----LQVLAASSANECSVNGRIYSILKIQISGGSSKVFQVLEKQIYAIKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 114608216 | ref | XP\_001146752.1 | SISKWFDPKSICKIPSSNLDYMKCFRIPVVKNDFFPACQLSTIPYQACFOQQOGLSILAPLQAT-----LQVLAASSANECSVNGRIYSILKIQISGGSSKVFQVLEKQIYAIKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 118088789 | ref | XP\_419867.2 | AVSKKNELLYVCGIPSS-----TCTDYMECFRIPVVKNDFFPACQLSTIPYSQLPYLPHTPATIPFNQMG-----LQVSGSIPSN-----EAVNGRIYSILKIQISGGSSKVFQVLEKQIYAVKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
gi | 28077097 | ref | NP\_778207.1 | PAPLRLNPSLSCQIPNYRQNP-----NSFVIPVVKQRPVIVSVPATAQKMCPTALPCTPSGVSIIQPPPTQPSAFSNESITIKGKOFFIFKMIIRGSSKVFQVLEKQIYAVKVVNLEADSDQIESYRNEIAYLNKLOQHSDKIIRL 750  
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|6678463|ref|NP\_033471.1| YDYEITTEQYIYVMVECGNIDLNSWLKSKKSLNPWERKSYWKNMLEAVHIIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENSKIRTKVSPRSDVWSLGCILYYMTYGRTPFOHI 900  
gi|109483730|ref|XP\_236477.4| YDYEITDRYIYVMVECGNIDLNSWLKSKKSLNPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRIKTKISPRSDVWSLGCILYYMTYGRTPFOHI 900  
gi|73973853|ref|XP\_539016.2| YDYEITDQYIYVMVECGNIDLNSWLKSKKSLNPWERKSYWKNMLEAVYTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRKSRSKISPKSDVWSLGCILYYMTYGRTPFOHI 900  
gi|119901123|ref|XP\_603264.3| YDYEITDQYIYVMVECGNIDLNTWLNKSKKSLNPWERKSYWKNMLEAVYTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRKSRSKISPKSDVWSLGCILYYMTYGRTPFOHI 900  
gi|262399361|ref|NP\_001160163.1| YDYEITDQYIYVMVECGNIDLNSWLKSKKSLNPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRKSRSKISPKSDVWSLGCILYYMTYGRTPFOHI 900  
gi|114608216|ref|XP\_001146752.1| YDYEITDQYIYVMVECGNIDLNSWLKSKKSLNPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRKSRSKISPKSDVWSLGCILYYMTYGRTPFOHI 900  
gi|118088789|ref|XP\_419867.2| YSVEITDQYIYVMVECGNIDLNSWLKSKKSLNPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRKSRSKISPKSDVWSLGCILYYMTYGRTPFOHI 900  
gi|28077097|ref|NP\_778207.1| YDYEITSSYIYMLMECGHLDLNTWLNKSKKSLNPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMLKLIIDFGIANQMOPDITSIVKDSQVGTVNYMPEAIRDMSSS-RENGRKSRSKISPKSDVWSLGCILYYMTYGRTPFOHI 900  
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi|6678463|ref|NP\_033471.1| INQVSKLHAIINPAHEIEFPEISEKDLRDLVLCCLVRNPKERISIPPELLHPVVOIQP--HPGSMARGANDEMKYVGLQVLGLNSPNSILKTAKTLYERNCGEGQDSSSS-KTFDKK-RERK 1024  
gi|109483730|ref|XP\_236477.4| INQVSKLHAIIDPSHEIEFPEISEKDLRDLVLCCLVRNPKERISIPPELLAHPVVOIQP--HPGSMARAGTDEMKYVGLQVLGLNSPNSILKAAKTLYERNCGESQAPSSS-KTSDKK-RERE 1024  
gi|73973853|ref|XP\_539016.2| INQISKLHAIIDPNHEIEFDPDIPEKDLQDVLKCLLRDPKORISIPPELLAHPVVOIQP--HPGNQMARKTTEEMKYVGLQVLGLNSPNSILKAAKTLYDRYSSGESHDSSSSKTFENK-WEKK 1024  
gi|119901123|ref|XP\_603264.3| INQISKLHAIIDPNHEIEFDPDIPEKDLQDVLKCLLRDPKORISIPPELLAHPVVOIQP--HPGNQMARKTTEEMKYVGLQVLGLNSPNSILKAAKTLYEQYSSGESHSSSSKTLAKK-WDRK 1024  
gi|262399361|ref|NP\_001160163.1| INQISKLHAIIDPNHEIEFDPDIPEKDLQDVLKCLLRDPKORISIPPELLAHPVVOIQP--HPVNMARGTTEEMKYVGLQVLGLNSPNSILKAAKTLYEHYSSGESHSSSS-KTFEKK-RGKK 1024  
gi|114608216|ref|XP\_001146752.1| INQISKLHAIIDPNHEIEFDPDIPEKDLQDVLKCLLRDPKORISIPPELLAHPVVOIQP--HPGNQMARKTTEEMKYVGLQVLGLNSPNSILKAAKTLYEHYSSGESHSSSS-KTFEKK-RGKK 1024  
gi|118088789|ref|XP\_419867.2| INTRKLLVAIVDPHYEIEFPDIAEKDLQDVLKCLLRNPKORISVSELLVHPVVOIQPQCQTGVANAKGAEVVKRILGQVLGLNSPNSISRAARTLYEQCNKSLDVAFAKSSGSKSWTAK 1024  
gi|28077097|ref|NP\_778207.1| INQISKLHAIIDPSHEIDFDPDIPEKDLQDVLKCLLRNPKORISVSELLVHPVVOIQP--QPAPPEAETSSDFKRIINLNLVLAQHPNSIARAASNLMAMCNSGRKLDVRCVKSSSCTLWK-- 1024  
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....

