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gi | 73945697 | ref | XP_851025.1 | MISSQALGSKCEQIFNLHLFLVFLACLTFEDIECTHCWDTRGRGFTIAGWSVLKQVIALFSLILCYIVGRFRFEDDGTIAGHRQWTRSRREPKMAVNVYSTSVTSDNLSRHDMLAWINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 115496618 | ref | NP_001068802.1 | -----MAVNVYSTSVTSDNLSRHDMLAWINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 6912494 | ref | NP_036457.1 | -----MAVNVYSTSVTSDNLSRHDMLAWINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 114681760 | ref | XP_001154462.1 | -----MAVNVYSTSVTSDNLSRHDMMSHTASGPHAF TSA-----RKEGVVRRSSRGRAGGVVWRFRFEDDGTIAGCGQWTRCRPKMAVNVYSTSVTSDNLSRHDMWGINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 7106301 | ref | NP_031922.1 | -----MAVNVYSTSVTSDNLSRHDMLAWINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 78097100 | ref | NP_612518.2 | -----MAVNVYSTSVTSDNLSRHDMLAWINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 71894959 | ref | NP_001026031.1 | -----MAVNVYSTSVTSDNLSRHDMLAWINESLQLNLTKIEQLCSGAAYCOFMDMLFPFSGIALK 150
gi | 47271390 | ref | NP_998805.1 | -----MAVNVYSTSVTSDNLSRHDMLAWINESLQMNFTKIELLCSGAAYCOFMDMLFPFSGIALK 150
gi | 15240262 | ref | NP_201528.1 | -----MATNIGMMDSAYFVGRSEILAWINSTLQNLSKVEEACSGAVHCQLMDSVHPGIVPMH 150
gi | 115482758 | ref | NP_001064972.1 | -----MAASNIGMDGAYFVGRNELAWINSTLQNLSKVEEACSGAVACQLMDSVHPGIVPMH 150
gi | 145615185 | ref | XP_360052.2 | -----MGESRELVQWLNSLQLNLTKIEQCCGAALCOVDSSIFL-DVPMS 150
gi | 164428973 | ref | XP_957714.2 | -----MLVAPATPRARSGNTNFRVDVGLTINVHSQELLQWINSLQLNLTKIEQCCGAALCOVDSSIFG-DIPMS 150
gi | 19114590 | ref | NP_593678.1 | -----MSESRELLAWINQVTSSLGLTRIEDCGKGYAMIQIFDSIQ-DPLK 150
gi | 6320853 | ref | NP_010932.1 | -----MSAGIGSRTELLWLNGLLNLNYKLEECGGAAYCOIMDSIYG-DLPMN 150
gi | 50304189 | ref | XP_452044.1 | -----MAGIGSRSELLWLNGLLNLNYKLEECGGAAYCOIMDSIYG-DLPMN 150
gi | 45184847 | ref | NP_982565.1 | -----MSGMGESELLWLNGLLNLNYKLEECGGAAYCOIMDSIYG-DLPMH 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 73945697 | ref | XP_851025.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 115496618 | ref | NP_001068802.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAMAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 6912494 | ref | NP_036457.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 114681760 | ref | XP_001154462.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 7106301 | ref | NP_031922.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 78097100 | ref | NP_612518.2 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 71894959 | ref | NP_001026031.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 47271390 | ref | NP_998805.1 | KVKFQAKLEHEYIQNFELIQAGFKRMGVDKIIPVDKLVKKGFQDNFEFVQWFKFFDANYDGKDYDPVAARQ-----GOETAVAPSLVAPALNKPKKPLSSSAAPORPIATHRTATPKA-----GPGVVR 300
gi | 15240262 | ref | NP_201528.1 | KVNFDAKSEYEMIQNYKVLQDVFNLKIKTKHIEVSKLKGRPLDNLFQMWMMKYCDSVNGQHNVHALER-----REASKGGKEATRAATQSSGKSSSAAPPRPSSNGTRKHEPENTGT-----HHSSTGNHHH 300
gi | 115482758 | ref | NP_001064972.1 | KVNFDAKTEYEMIQNYKVLQDVFNLKIKTKHIEVSKLKGRPLDNLFQMWMMKYCDSVNGQHNVHALER-----RESSKGGKEATRAATQSSGKSSSAAPPRPSSNGTRKHEPENTGT-----HHSSTGNHHH 300
gi | 145615185 | ref | XP_360052.2 | RVKFNVNSEYAIIQNFKLQNTFTKHQVDDKIPVAGLVKCMDNLEFLQWVKRFWDQYPGGEYDAVAR-----KGAP-----LGAAGGGGGAAVRPAVAGGAAARRAGGTPTTTG-----AARAG-----LG 300
gi | 164428973 | ref | XP_957714.2 | RVKFNVNSEYAIIQNFKLQNTFTKHQVDDKIPVAGLVKCMDNLEFLQWVKRFWDQYPGGEYDAVAR-----KGAP-----LGAAGGGGGAAVRPAVAGGAAARRAGGTPTTTG-----AARAG-----LG 300
gi | 19114590 | ref | NP_593678.1 | KVNFECNNEYQYINNKVLQQVFLKGIDKVDPERLSRCKMDNLEFLQWVKRFWDQYPGGEYDAVAR-----KGAP-----LGAAGGGGGAAVRPAVAGGAAARRAGGTPTTTG-----AARAG-----LG 300
gi | 6320853 | ref | NP_010932.1 | RVKFNATAEYFQTNYKILQSCFSRHGIEKTVYVDKLIRCKFQDNLEFLQWLKKHWIRHKDESYDPDARRKYRPILNNSAAK-----PRTVSNPTAKRSSTGTGSAMSGGLATRHSLGINGSRKLSVTQ-----QLVA 300
gi | 50304189 | ref | XP_452044.1 | RVNFCAGSEYEYFNYKILQSCFTKHKIEKSVLVERLKCRFQDNLEFLQWIKFWTQHKDESYDAEVRRKGR-----AGPSN-----NKREVSSTASKPP--IRHRSNIQNNIRKSSNEQ-----LLS 300
gi | 45184847 | ref | NP_982565.1 | RVKFDARAEYESLTNFKILQSCFTKHKIEKTVFVDRLLKCRFQDNLEFLQWMMRRFWIQDKDESPYPESRRKSVRPYMRAPAQPPSHAPKRRSLATFAATCTAAPRLQKARAAAGAGGAVATRVPSGAPARGLATAGAGEQVAA 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 73945697 | ref | XP_851025.1 | KNPGVGNGDDEAAELMQCVNVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----NPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 115496618 | ref | NP_001068802.1 | KNPGVGNGDDEAAELMQCVNVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----NPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 6912494 | ref | NP_036457.1 | KNPGVGNGDDEAAELMQCVNVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----DPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 114681760 | ref | XP_001154462.1 | KNPGVGNGDDEAAELMQCVNVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----DPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 7106301 | ref | NP_031922.1 | KNPGVGNGDDEAAELMQCVNVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----DPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 78097100 | ref | NP_612518.2 | KNPGMGNGDDEAAELMQCVNVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----DPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 71894959 | ref | NP_001026031.1 | K-----AAGDESAGLIEQINVLKLVEDLEKERDFYFGKLRNIELICQE-----NEGEN-----DPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 47271390 | ref | NP_998805.1 | RPG--AGGDEREABLIQELNILKSTIQDMEKERDFYFGKLRNIELICQE-----NEGEN-----DPVLQRIVDILYATDEG-----FVIPDEGGPQEEQEEV----- 450
gi | 15240262 | ref | NP_201528.1 | SSKPSAKQSKPVAPDBEKITELKLYIDSLEKERDFYFSKLRDVEILQS-----PDTEH-----LPVNAIHKVLYAAEDEVGAETQ-----LSPIAEGSERRNSVTESQRKLIVN 450
gi | 115482758 | ref | NP_001064972.1 | SAKPSPANS-ACPANDEQITELKLYDSLEKERDFYFSKLRDVEILQS-----PDVEH-----LPVNAIHKVLYAAEDEVGAETQ-----LSPIAEGSERRNSVTESQRKLIVN 450
gi | 145615185 | ref | XP_360052.2 | NSKANPALQENATLK-----EVVGLERERDFYFSKLRDIELLVQS-----AVEEDPETEKEDG-----LVKQIQAILSTEEG-----FETPAEG 450
gi | 164428973 | ref | XP_957714.2 | NSAANQALQQEVATLK-----EVVGLERERDFYFSKLRDIELLVQS-----AVEEDPETEKEDG-----LVKQIQAILSTEEG-----FETPAEG 450
gi | 19114590 | ref | NP_593678.1 | AVLRAKQAQQITSLETOLYEVNETFGLERERDFYFNKLREIEILVOT-----HLTTSP-----MLERIQAILSTEDG-----FELPPDQPADLTTALDHDTNNV-----ABEAG 450
gi | 6320853 | ref | NP_010932.1 | IQAELTKSQETIGSLNEIEIQYKGVSTLEIEREFYFNKLRDIEILVHT-----TQDLINEGVKFNDETIGHCGNGGGALLRFVKKVESILYAEG-----FEMNDGEDELNDKNLGEHGIVPNOGGYANSG 450
gi | 50304189 | ref | XP_452044.1 | LQELSETRNLSLEKECSQYKLNTALKERDFYFGKLRDIEILIAGS-----TQDLCEGVYNDKE-----LRPFLNRIQQILYAEG-----FEP-----FVENVEQASTNP----- 450
gi | 45184847 | ref | NP_982565.1 | LQELSAAEHKINKLTEMVQYQDAMSLMERERDFYFGKLRDIEILVQS-----TQDLFKEGVYNDDP-----ELNRLLGKVSQILSTEG-----FEVANGADGNEYEVEAGTRME 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|73945697|ref|XP_851025.1|-----487
gi|115496618|ref|NP_001068802.1|-----487
gi|6912494|ref|NP_036457.1|-----487
gi|114681760|ref|XP_001154462.1|-----487
gi|7106301|ref|NP_031922.1|-----487
gi|78097100|ref|NP_612518.2|-----487
gi|71894959|ref|NP_001026031.1|-----487
gi|47271390|ref|NP_998805.1|-----487
gi|15240262|ref|NP_201528.1|-----487
gi|115482758|ref|NP_001064972.1|--LVDVAATITLSPRRLSDASDVKCSGSSPLLTC-487
gi|145615185|ref|XP_360052.2|--LLEFGMASSRRLSDISDVQLCG-SPLTSFT487
gi|164428973|ref|XP_957714.2|-----EVDDE--TF487
gi|19114590|ref|NP_593678.1|-----AADDE--TF487
gi|6320853|ref|NP_010932.1|MDLKDSETRVPSAPDFVHARLQSLEVDDENIITF487
gi|50304189|ref|XP_452044.1|VNGNEGSNDVLMONDEGEVGSNNLIIDEE--TF487
gi|45184847|ref|NP_982565.1|-----CVEGOVLENLITDDE--TF487
.....460.....470.....480.....

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