

```

gi | 19922206 | ref | NP_610917.1 | -----MFGRQSGGLGSSNLS-NLVEFRAGRMMNVG-----KMHVDPDRKGLVYVYQEDGLIHFCWKDRIT-EGKVEDDLIVFPDDFEYKRVDCKGRVYVILKFKSSRRMFFWMOEPKTDKDEQCRRINELLNPPSAHQRGGGG 136
gi | 158297918 | ref | XP_001689089.1 | --MSGLPFGSSALGSSSGNRHLVEFRAGRMMNVN-----KMHVDPDRKGLVYVYQEDGLIHFCWKDRIT-EGTVEDDLILFPDDCEFKKIDYVKNGRVYVILKFKSSRRLLFFWMOEPKTRDDEWCRRLINEVINPPSGNSIGSGGR 141
gi | 31981027 | ref | NP_062796.2 | MTTSGALFP-SLVPGRSGSSKYLVEFRAGKMSLKG-----TIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGTVEDDLIIFPDDCEFKRVVPCPSGRVYVILKFKAGSKRLLFFWMOEPKTDQDEEHCRKVNECLNPPMPGSLGASGS 142
gi | 13928990 | ref | NP_113896.1 | MTTSGALFP-SLVPGRSGSSIKYLVEFRAGKMSLKG-----TIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGTVEDDLIIFPDDCEFKRVVPCPSGRVYVILKFKAGSKRLLFFWMOEPKTDQDEEHCRKVNECLNPPMPGTLGASGS 142
gi | 28373194 | ref | NP_783163.1 | MTTSGALFP-SLVPGRSGANLKYLVEFRAGKMSLKG-----TIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGNVEDDLIIFPDDCEFKRVVPCPSGRVYVILKFKAGSKRLLFFWMOEPKTDQDEEHCRKVNEYLNPPMPGALGASGS 142
gi | 73992416 | ref | XP_534476.2 | MTTSGALFP-SLVPGRSGSSNKYLVEFRAGKMSLKG-----TIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGNVEDDLIIFPDDCEFKRVVPCPSGRVYVILKFKAGSKRLLFFWMOEPKTDQDEEHCRKVNEYLNPPMPGALGTSGS 142
gi | 122692585 | ref | NP_001073751.1 | MTTSGALFP-SLVPGRSGSSNKYLVEFRAGKMSLKG-----TIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGNVEDDLIIFPDDCEFKRVVPCPSGRVYVILKFKAGSKRLLFFWMOEPKTDQDEEHCRKVNEYLNPPMPGALGASGS 142
gi | 45382833 | ref | NP_989982.1 | MTTSGALFP-SLVPGRSGSSSKYLVEFRAGKMSLKG-----TIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGNVEDDLIIFPDDCEFKRVVPCCTGRVYVILKFKAGSKRLLFFWMOEPKTDKDEEHCRKVNEYLNPPMPGALGNA 142
gi | 76253863 | ref | NP_957307.2 | -MSSGALFP-SLVSGSSSSSKYLVEFRAGKMSLKG-----STIVTPDKRRKGLVYIQOTDDSLIHFCWKDRIT-EGNVEDDLIIFPDDCEFKRVNCTGRVYVILKFKAGSKRLLFFWMOEPKTDKDEEYCRKVNEYLNPPMPGALGSGG 141
gi | 18401185 | ref | NP_565626.1 | -MSSSEAPFVMQEMLEFRAGKMSLQG-----TRVVPDARKGLVRIARGDEGLIHFWQLDRN-QNTVEDDQIVFPDEALFEKVNOS-DRVYILKFNSSDRKLLFFWMOEPRAEGDAELGSSVNOYLNQPLEFFPGEGLAA 132
gi | 115465819 | ref | NP_001056509.1 | -----MESTEP-LQDIMCEFRAGKMSLDG-----IRVVPDTRKGLVRIARGDEGLIHFWQLDRG-QNLVEVDQIVFPDEEAVFEKVTOS-GRVYILKFNSSDRKLLFFWMOEPRAEGDAELGSSVNOYLNQPLEFFPGEGLAA 126
gi | 25152916 | ref | NP_498387.2 | -MAAMFVNTRVAVSSGHIVVEFRAGKMSLQD-----MRKVVAPKPKGLVFIKQSDNMLIHFCWKDRIT-EGAVDDLIIFPDDAEFKAVPCCTGKVMYMLKFKSGD-MKLFWIDQSTPDVDDKLVKVKVTDALNKPPTSRFAASRA 142
gi | 19113539 | ref | NP_596747.1 | -----MLLITFAKPKKGLVYVIMNRDAYGLIHFWQAKNLDLENLEP-----TGAVVDDLIIFVSSCECTGRVYVILKFKAGSSAHSRLFYVMOESADNNTSVAERINYSYIKQDLDLPARSDVA 125
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

gi | 19922206 | ref | NP_610917.1 | N-----DGDLYMLNMSQQQLMFLG-GVGMGGLSSLLGQMN-----SRTPSSRNT-----SGGGGASALQTPENVSVPRPSPAPK-SGSSRSSN-----VNSQVGEAGS----- 232
gi | 158297918 | ref | XP_001689089.1 | NCGND-----NCDLYMLNMSQQQLMFLG-GVGMGGLSSLLGSMIRNSGNSSRTSAATPSNRS-SLAINNGGCGSTTPSAAVNAPSTIPRPAKTSGTNKTNSAGSAGTIGPISTIPVGRNAGSAGTADGGTRILLSDLQNVL 284
gi | 31981027 | ref | NP_062796.2 | SGHELSALGGEGGLQSLLLGNMHSQMLMOLIGPAGLGGGLGALGTPGLASLLGSSGPPASSSSSSSSRSQAAVTPSS-----STSSARATPAPAPAAAATSPSPAPSSGNG-----TST-----AASPTOP-----IQLSDLQSL 271
gi | 13928990 | ref | NP_113896.1 | SGHELSALGGEGGLQSLLLGNMHSQMLMOLIGPAGLGGGLGALGTPGLASLLGSSGPPASSSSSSSSRSQAAVTPSS-----TSSARATPAPAPAAAATSPSPAPSSGNG-----TST-----AASPTOP-----IQLSDLQSL 271
gi | 28373194 | ref | NP_783163.1 | SGHELSALGGEGGLQSLLLGNMHSQMLMOLIGPAGLGGGLGALGTPGLASLLGSSGPPASSSSSSSSRSQAAVTPSS-----TSSARATPAPAPAAAATSPSPAPSSGNG-----AST-----AASPTOP-----IQLSDLQSL 271
gi | 73992416 | ref | XP_534476.2 | GGHELSALGGEGGLQSLLLGNMHSQMLMOLIGPAGLGGGLGALGTPGLASLLGSSGPPASSSSSSSSRSQAAVTPSS-----TSSARATPAPAPAAAATSPSPAPSSGNG-----TST-----AASPTOP-----IQLSDLQSL 271
gi | 122692585 | ref | NP_001073751.1 | GGHELSALGGEGGLQSLLLGNMHSQMLMOLIGPAGLGGGLGALGTPGLASLLGSSGPPASSSSSSSSRSQAAVTPSS-----TSSARATPAPAPAAAATSPSPAPSSGNG-----TST-----AASPTOP-----IQLSDLQSL 271
gi | 45382833 | ref | NP_989982.1 | GGHELSALGGEGGLQSLLLGNMHSQMLMOLIGPAGLGGGLGALGTPGLASLLGSSGPPASSSSSSSSRSQAAVTPSS-----TSSARATPAPAPAAAATSPSPAPSSGNG-----TSS-----ATSPTOP-----IQLSDLQSL 271
gi | 76253863 | ref | NP_957307.2 | GGHELSALG-EGGLQSLLLGNMHSQMLMOLIGPTGLG-----GLGALAGPGLASLLGSSGPPATSSSTSSSSRSQAAATPSSG-SAARLSSQAPTFVVPVPAATSSGSPVTPPTTAA-----QIFSLPAGPASTOP-----IQLSDLQSL 275
gi | 18401185 | ref | NP_565626.1 | ATTELEDMEDNISRAGNLVVP-----NLSSEVE-DVTSS-----GPVKLADLQRLNLSGGPVGLAGDQDEG-----QIFSLPAGPASTOP-----IQLSDLQSL 198
gi | 115465819 | ref | NP_001056509.1 | EAEMSHEDTADDISSRAGNLVVP-----HMTADLAGETISAA-----GPVRLLEDLQRLLSAIQ-PSDAVADEFDAG-----QIFSLPAGPASTOP-----IQLSDLQSL 191
gi | 25152916 | ref | NP_498387.2 | GSNANIDRQSAGGLISLSDMNAFLGGIDQ-----QLMSLIQSLQGGNDLTPISVPRGEDASEADCEP-----ETNAAEESNPLSLNPAIQQLFNLR-----QIFSLPAGPASTOP-----IQLSDLQSL 238
gi | 19113539 | ref | NP_596747.1 | TVSDMMEVDIVQES-----PIAIPTESSKES-----IGAPNSDEINSEAVRNLLATISQAQFGG-----QIFSLPAGPASTOP-----IQLSDLQSL 184
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

```



```

gi | 19922206 | ref | NP_610917.1 | -----VDADAPGRSLIDLSIALPGADAINQIADPEHVKTILIVLHPESEVDVDDRKOQIKDNITSPFOQALAQF-SALQSAQLGPVVIKQFELSNEAFAAFAFSGNLEDVFRALERLPPGATMGG-----KPSASKKASDPETPVSVA 373
gi | 158297918 | ref | XP_001689089.1 | SGISATGVDSGGRRNIDLASAVN-SOILASIIISDOEKVDALVAHLPOLE-GDENKKEQLKETISSPFOQALSMFSAALQSGOLGPVVSQFQLNADAVAAANAGDLEQFVKALENSEKTPASEASGANRKSAGSSTSDPKPKSEVAK 432
gi | 31981027 | ref | NP_062796.2 | AAMNVPAGPGGSGQ--VDLASVLT-PEIMAPILANADVOERLLPYLPSGESLPOT-ADEIIONTLTSPFOQALGMFSAALASGOLGFLMCOFGLPAEAVEAANKGDVEAFAKAMONNARSDDPKEGDTR-DKKDEEEDMSLD 407
gi | 13928990 | ref | NP_113896.1 | AAMNVPAGPGGSGQ--VDLASVLT-PEIMAPILANADVOERLLPYLPSGESLPOT-ADEIIONTLTSPFOQALGMFSAALASGOLGFLMCOFGLPAEAVEAANKGDVEAFAKAMONNARSDDPKEGDTR-DKKDEEEDMSLD 407
gi | 28373194 | ref | NP_783163.1 | AAMNVPAGPGGSGQ--VDLASVLT-PEIMAPILANADVOERLLPYLPSGESLPOT-ADEIIONTLTSPFOQALGMFSAALASGOLGFLMCOFGLPAEAVEAANKGDVEAFAKAMONNARSDDPKEGDTR-DKKDEEEDMSLD 407
gi | 73992416 | ref | XP_534476.2 | AAMNVPAGPGGSGQ--VDLASVLT-PEIMAPILANADVOERLLPYLPSGESLPOT-ADEIIONTLTSPFOQALGMFSAALASGOLGFLMCOFGLPAEAVEAANKGDVEAFAKAMONNARSDDPKEGDTR-DKKDEEEDMSLD 406
gi | 122692585 | ref | NP_001073751.1 | AAMNVPAGPGGSGQ--VDLASVLT-PEIMAPILANADVOERLLPYLPSGESLPOT-ADEIIONTLTSPFOQALGMFSAALASGOLGFLMCOFGLPAEAVEAANKGDVEAFAKAMONNARSDDPKEGDTR-DKKDEEEDMSLD 407
gi | 45382833 | ref | NP_989982.1 | AAMNVPAGPGGSGQ--VDLASVLT-PEIMAPILANADVOERLLPYLPSGESLPOT-ADEIIONTLTSPFOQALGMFSAALASGOLGFLMCOFGLPAEAVEAANKGDVEAFAKAMONNARSDDPKEGDTR-DKKDEEEDMSLD 406
gi | 76253863 | ref | NP_957307.2 | AAMNVPAMPTGSG--VDLASVLT-PDVMAPILANPEVQRLPYLPSGESLPQ--ADEIIONTLTSPFOQALSMFSAALASGOLGFLMCOFGLPSEAVDAANKGDVEAFAKAMEGSD-SKTDDGDSK-DKKDDDEDMSLD 410
gi | 18401185 | ref | NP_565626.1 | -----LALGDILK-PELIMPLEALPVOERLSHLPEGHSRAED-----ILELQSPFRQVDAFTYVLRITGID-ITQFGIDPSPRYKFT-----VDSFLEALEDVSDQS-----RDAMES----- 300
gi | 115465819 | ref | NP_001056509.1 | -----LGLGDILK-PDLVPLMETLPIEC-LASVLPPEGWTAED-----ILELQSPPLRQVEAFTYVLRITGID-ITQFGIDPSPRYKFT-----VDSFLEALEDVSDQS-----RDAMES----- 306
gi | 25152916 | ref | NP_498387.2 | -----SQKKEAVVSLATALS-NETVAEVARN--HAELAPHLPTSDPPARE-----LSEIVRTPFRQVDAFTYVLRITGID-ITQFGIDPSPRYKFT-----VDSFLEALEDVSDQS-----RDAMES----- 372
gi | 19113539 | ref | NP_596747.1 | -----STVDLCEILK-PSNLTDLQCEGVIDRLMPYMPDTPNNLEG-----VLAIVSSPQYALRSFQALNSPGGVNIIISALGLSDEANPEGGALQFLKALARFVSRNNGSE-----RDAMES----- 291
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

```



```

gi | 19922206 | ref | NP_610917.1 | DENIDPAHEKQEEKK--- 389
gi | 158297918 | ref | XP_001689089.1 | EENGHGKTONKDDDEMAG 451
gi | 31981027 | ref | NP_062796.2 | ----- 407
gi | 13928990 | ref | NP_113896.1 | ----- 407
gi | 28373194 | ref | NP_783163.1 | ----- 407
gi | 73992416 | ref | XP_534476.2 | ----- 406
gi | 122692585 | ref | NP_001073751.1 | ----- 407
gi | 45382833 | ref | NP_989982.1 | ----- 406
gi | 76253863 | ref | NP_957307.2 | ----- 410
gi | 18401185 | ref | NP_565626.1 | ----- 300
gi | 115465819 | ref | NP_001056509.1 | ----- 306
gi | 25152916 | ref | NP_498387.2 | VD----- 374
gi | 19113539 | ref | NP_596747.1 | ----- 291
.....460.....

```