

gi | 48255935 | ref | NP_000601.3 | MDKFWWHAAG-LCLVPLSLAC---IDLNIICRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAOMEKALSIGFETCRYGFIIEGHVVIPIRIHPNSICAANNNGVYILFS-NTSQYDYICFNASAPPEEDCTSVTDLPLNAFDG-PT 143
gi | 114636964 | ref | XP_001152601.1 | MDKFWWQAAG-LCLVPLSLAC---IDLNIICRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAOMEKALSIGFETCRYGFIIEGHVVIPIRIHPNSICAANNNGVYILFS-NTSQYDYICFNASAPPEEDCTSVTDLPLNAFDG-PT 143
gi | 85540471 | ref | NP_033981.2 | MDKFWWHTAWG-LCLLQLSLAHPHOQIDLNVICRYAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMDOKMLALRKGFTCRYGFIIEGNVVIPIRIHPNAICAAANTGVYILFSNTSHYDYICFNASAPPEEDCTSVTDLPLNSFDG-PV 148
gi | 19923703 | ref | NP_037056.2 | MDKVVWHTAWGLLCLLQLSLAC---QQIDLNVICRYAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAOMELALRKGFTCRYGFIIEGHVVIPIRIHPNAICAAANTGVYILASNTSHYDYICFNASAPPEEDCTSVTDLPLNSFDG-PV 147
gi | 118091486 | ref | XP_001232425.1 | MANFYLLATFG-LCLLKFCLTE---IQFNIIICRYGGVFHVEKNGRYSLTRAEIELCALNSTLALTEQFERAHALGFETCRYGFIIVGHVVIPIRINPYHICAAANTGVYKLANITGRYDAYCYNAIETRSKACEPIERIDTIFLSNQ 145
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 48255935 | ref | NP_000601.3 | LIIIVNRDGTTRYVCKGEYRINPEDIYPSNPTDDDVSSGSSERSSTSGGYIFYIFSTVHPIPEDDS-----PWIIIDSD---LDRIPATILMSTSAATETAATKROETWDFSWLFLPESKNE 257
gi | 114636964 | ref | XP_001152601.1 | LIIIVNRDGTTRYVCKGEYRINPEDIINPSNPTDDDVSSGSSERSSTSGGYIFYIFSTVHPIPEDDG-----PWIIIDSD---LDRIPATILMSTSAATETAATKROENWDFSWLFLPESKNE 257
gi | 85540471 | ref | NP_033981.2 | LIIIVNRDGTTRYSKKGEYRTHQEDIDASNIIIDDVSSGSTIEKSTPESYILHLYLTPTEPTGDDSFIRSLATIASIVVSKSHATAKQNNWIWVWFGNSQSTTQOTQEPITTSATALMTTPETPKRQEAQNWFSWFFQPSSEKSH 297
gi | 19923703 | ref | NP_037056.2 | LIIIVNRDGTTRYSKKGEYRTHQEDIDASNIIIDDVSSGSTIEKSTPPEGYILHLDLPSQPTGDRDDAFFIGSLTATIASIVVSKSHATAKQNNWIWVWFGNSQSTTQOTQDPTTATALMTTPETPKRQEAQNWFSWFFQPSSEKSH 297
gi | 118091486 | ref | XP_001232425.1 | EIVIDNEDGSRYNADG--TRHSGDSSTSGVDNENLGGGSHD-----TTPGDAVIRRSSEFY-----G 203
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 48255935 | ref | NP_000601.3 | LHTTTQAGTSSNIIISAGWEPNEENEDERDRHLSFGSGIDDDDEFISSIISITPRAFHDHTKQNDWQWNPSSHNPEVLLQTTTRMDVDRNGTAYEGNWNPEAHPPLIHHEHHEEETPHSSTIIQATPSSSTTEETATQKEWFGNR 407
gi | 114636964 | ref | XP_001152601.1 | LHTTTQAGTSSNIIISAGWEPNEENEDERDRHLSFGSGIDDDDEFISSIISITPRAFHDHTKQNDWQWNPSSHNPEVLLQTTTRMDVDRNGTAYEGNWNPEAHPPLIHHEHHEEETPHSSTIIQATPSSSTTEETATQKEWFGNR 407
gi | 85540471 | ref | NP_033981.2 | LHTTTKMPGTESNINPTGWEPNEENEDETDKYPNFSFGSGIDDDDEFISSIISITPVSARTEQNDWQWNPSSHNPEVLLQTTTRMDIDRISTAHGENWTPPEPPFNNHEYQDEEETPHATSTT---FNSTABAAATQOETWFONG 444
gi | 19923703 | ref | NP_037056.2 | LHTTTKMPGTESNINPTGWKPNEENEDETDKYPNFSFGSGIDDDDEFISSIISITPVSARTEQNDWQWNPSSHNPEVLLQTTTRMDIDRNSTAHGENWTPPEPPFNNHEYQDEEETPHATSTT---FNSTABAAATQKEKWFENE 447
gi | 118091486 | ref | XP_001232425.1 | VTFYSHMPDHSN---GGGKED---FPVKHYDDEISPTSTDLATAADFFR-----EDDVQHPASTVDSQHEHLLLEVSTQD----- 273
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 48255935 | ref | NP_000601.3 | WHEGYRQTPKEDSHSTIGIAAAAHASHHPMQGRTIPSPEDSSWDFDFNPIISHPMGRGHQAGRRMDMDSSHSITLQPTANPNTGLVEDLDRIGPLSMTTQOSNSQSFSTSHGLEEDKDHPITSTLTSNRRNDVTGRRDPNHSSEGSTLL 557
gi | 114636964 | ref | XP_001152601.1 | WHEGYRQTPREDSHSTIGIAAAAHASHHPMQGRTIPSPEDSSWDFDFNPIISHPMGRGHQAGRRMDMDSSHSITLQPTANPNTGLVEDLDRIGPLSMTTQOSNSQSFSTSHGLEEDKDHPITSTLTSNRRNDVTGRRDPNHSSEGSTLL 557
gi | 85540471 | ref | NP_033981.2 | WQCKNPPTPSEDSHVTEGTTIAS-AHNNHPSQRITIQSQEDVSWDFDFNPIISHPMGRGHQAT-ESKDTGSSHSTTLQPTAAPNTHLVEDLNRIGPLSVTTTQSHSNQFSTLPGEPEDENHPTTSTILPSSIKSGAKDARRGGSLPTDITTSV 592
gi | 19923703 | ref | NP_037056.2 | WQCKNPPTPSEDSHVTEGTTIAS-AHNNHPSQRMTIQSQEDVSWDFDFNPIISHPMGRGHQAT-ESKDTGSSHSTTLQPTAAPNTHLVEDLNRIGPLSVTTTQSHSNQFSTLPGELEGEDHPTTSTVLPSSIKSGR---RRGSLPRDITTSV 592
gi | 118091486 | ref | XP_001232425.1 | -----YWKPYT-----DEERFPSS-----AGRGSTSN 298
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 48255935 | ref | NP_000601.3 | EGYTSHYPHIKESRTIFPVTSATIGSFGVIAVTVG-DNSNVNRSLSGDQDIFHPSGGG--HTTHGSESDGSHSGSDEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINSNGAVEDRKPSELNGEAS 704
gi | 114636964 | ref | XP_001152601.1 | ESYTSHYPHIKESRTIFPVTSATIGSFGVIAVTVG-DNSNVNRSLSGDQDIFHPSGGG--HTTHGSESDGSHSGSDEGGANTTSGPIRTPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINSNGAVEDRKPSELNGEAS 704
gi | 85540471 | ref | NP_033981.2 | EGYTPOYPDIMENGLTFPVTPAKTEVFGETEVTLLANDSNVNVGSLPGDRDSSKDRGSSRVTTHGSELAGHSSANQDSGVTTSGPARRPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINSNGAVEDRKPSELNGEAS 742
gi | 19923703 | ref | NP_037056.2 | EGYTPOYPDIMENGLTFPVTPAKTEVFGETEVTLLANDSNVNVGSLPGDGDSSMDPRGGFDIVTHGSELAGHSSGNQDSGVTTSGPARRPQIPEWLIILASLLALALILAVCIAVNSRRRCGQKKKLVINSNGAVEDRKPSELNGEAS 742
gi | 118091486 | ref | XP_001232425.1 | D--SDQGHK-----GDGEP-----LSSPGLSTTIVLSQPG-NAHVPEWLIIVAAALLALALILAVCIAVNSRRRCGQKKKLVINSNGAVEDRKTRELNGEAS 389
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 48255935 | ref | NP_000601.3 | KSEQMVHLVKNKESSE---FPDQFMIADETRNLQNVDMKIGV 742
gi | 114636964 | ref | XP_001152601.1 | KSEQMVHLVKNKESSE---FPDQFMIADETRNLQNVDMKIGV 742
gi | 85540471 | ref | NP_033981.2 | KSEQMVHLVKNKESSE---FPDQCMIADETRNLQSVDMKIGV 780
gi | 19923703 | ref | NP_037056.2 | KSEQMVHLVKNKESSE---FPDQFMIADETRNLQSVDMKIGV 780
gi | 118091486 | ref | XP_001232425.1 | KSEQMVHLVHKEQNDRTGACDEFLLVDEITQNHQDGMKSGV 431
.....760.....770.....780.....790.....

