

gi | 189458817 | ref | NP_003225.2 | ---MMDQARSAFSNLFGGEP LSYTRFSLARQVDGDNHSHVEMKLADEEENADN-NTK---ANVTKPKRCSGS-----TCVGTIAVIVFVFLIGFMIGYLYGCKGVEPKTECERLAG---EESP--VREEPG---EDFPAAR-RLYWD 125
gi | 50978812 | ref | NP_001003111.1 | ---MMDQARSAFSNLFGGEP LSYTRFSLARQVDGDNHSHVEMKLADEEENVDN-NMRGNHSAVVPKPKRCNGR-----TCVGTIAVIVFVFLIGFMIGYLYGCKRVEPKAGCERPAG---EALGTERTFSELEHYFPELPSRLFWT 134
gi | 11596855 | ref | NP_035768.1 | ---MMDQARSAFSNLFGGEP LSYTRFSLARQVDGDNHSHVEMKLADEEENADN-NMK---ASVRKPKRFNGR-----LCFAAIALVIFVFLIGFMISGYLYGCKRVEQKEECVKLAE---EEDKSEHMET---EDVPTSS-RLYWA 127
gi | 109493400 | ref | XP_341000.3 | ---MMDQARSAFSNLFGGEP LSYTRFSLARQVDGDNHSHVEMKLADEEENADN-NMK---ASVRKPKRFNGR-----LCFAAIALVIVFVFLIGFMIGYLYGCKRVEQKEECVRLAE---AEADKSEHMET---EYVFKSS-RLFWA 126
gi | 119879652 | ref | XP_580860.3 | ---MMDQARSAFSNLFGGEP LSYTRFSLARQVDGDNHSHVEMKLADEEENVDN-NMRGNHSAVVPKPKRCNGR-----TCVGTIAVIVFVFLIGFMIGYLYGCKRVEQKEECVRLAE---EEDKSEHMET---EDVPTSS-RLYWA 132
gi | 45383950 | ref | NP_990587.1 | ---MDHARAALSNLFSVEPMSYTRFSLARQVDGDNHSHVEMKLADEEEDGDIIRGPEHMHVSMAPQDGGSGGCEIPTASYLVDGEGTVEEIQGPP-VIFWF 137
gi | 57770576 | ref | NP_001009917.1 | ---MDQARTLSKLFNGEPRSYTRFSLARQVDGDNHSHVEMKLADEEENADN-NMRGNHSAVVPKPKRCNGR-----TCVGTIAVIVFVFLIGFMIGYLYGCKRVEQKEECVRLAE---EEDKSEHMET---EYVFKSS-RLFWA 128
gi | 82524363 | ref | NP_001009918.2 | MAGTIGQAKMKFSRMVN---SRSYSRFNQSNPQDGSRRVEVFLAVDGEDE-EMDGLTGLNQMQETTRSTGRSEPLNKRILVLCVGAALVFLVFLGLLIGYSVHRKSDNKSEPLETPCS---KEIQAEPPPPVYEPVPSID---WS 138
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 189458817 | ref | NP_003225.2 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 269
gi | 50978812 | ref | NP_001003111.1 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 279
gi | 11596855 | ref | NP_035768.1 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 271
gi | 109493400 | ref | XP_341000.3 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 269
gi | 119879652 | ref | XP_580860.3 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 278
gi | 45383950 | ref | NP_990587.1 | ELKAMLSKLLAKNLVNDLNRVRC-VDSPEAGEADTNMAYIIEEERNF-LDKVWVNDHYIKLVRCG-TKNQVSLN---INGKEE-ILEPDAIVAYSSEGGKPFVYVYVGLKDFEITIQKVAASLNGITIVIVRAGKIIFAEKVA 279
gi | 57770576 | ref | NP_001009917.1 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 265
gi | 82524363 | ref | NP_001009918.2 | DLKRLKLEKLDLTFDTGTLKLLNENSVYPREAGSQKDENLALYVENQREFKLSKVWRDQHFVKIIVKDS-AQNSVIIVD-KNGRLVVLVENPGGYVAYSKAAVITGKLVHANFGTKKDFEDLY---IPVNGSLVIVRAGKIIFAEKVA 276
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 189458817 | ref | NP_003225.2 | NAESLNAGVLIYMDQTKFPVNAELSFHGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPSDWK-TDSTCRMVTSKSK---NVKLVSNVNLKIKILNIFGVKGFVEPDHYVVVGAORDAWGPG 415
gi | 50978812 | ref | NP_001003111.1 | NAQSYNALGVLIYMDQARFPVFNARIFFGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPSAWE-IDPSCRLEFSNKN---NVNLTNNVNLKIRIFNVFVGIKGFVEPDHYVVVGAORDAWGPG 425
gi | 11596855 | ref | NP_035768.1 | NAQSYNALGVLIYMDKKNFVVEADLALFGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPARWN-IDSSCKLESNQ---NVKLVSNVNLKIKILNIFGVKGFVEPDHYVVVGAORDAWGPG 417
gi | 109493400 | ref | XP_341000.3 | NAQSYNALGVLIYMDRNFVVEADLALFGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPPSWN-IDSSCKLESNQ---NVKLVSNVNLKIKILNIFGVKGFVEPDHYVVVGAORDAWGPG 415
gi | 119879652 | ref | XP_580860.3 | NAESLNAGVLIYMDQTKFPVNAELSFHGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPRWIG-TDSSCKLVSDQK---NVKLVSNVNLKIKILNIFGVKGFVEPDHYVVVGAORDAWGPG 424
gi | 45383950 | ref | NP_990587.1 | NARKEAGAVLMDVSLVYDIPFVNAELSFHGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CSEGRKQATHSARGVTIKKTSQIMVVKLDVNNVSMKDKLILNIFGAIGQFVEPDHYVVVGAORDAWGPG 428
gi | 57770576 | ref | NP_001009917.1 | NAASLNAGVLIYMDQTKFPVNAELSFHGHALGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPRWIG-TDSSCKLVSDQK---NVKLVSNVNLKIKILNIFGVKGFVEPDHYVVVGAORDAWGPG 414
gi | 82524363 | ref | NP_001009918.2 | NVAKLGAVALIYDPPANV-DGMD-ELYGHVILGTPDPTGPFPSFNHTQFPSPRSBGLPNIPVQTIISRAAAEKLFNGMEGD-CPRWIG-TDSSCKLVSDQK---NVKLVSNVNLKIKILNIFGVKGFVEPDHYVVVGAORDAWGPG 421
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 189458817 | ref | NP_003225.2 | AA-KSGVGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWA---SKVEKLTLDNAAFPFLAYSIGIPAVSFCFCFE 559
gi | 50978812 | ref | NP_001003111.1 | AA-KSSVGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---NKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 569
gi | 11596855 | ref | NP_035768.1 | VAAKSSVGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---SKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 562
gi | 109493400 | ref | XP_341000.3 | VA-KSSVGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---SKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 559
gi | 119879652 | ref | XP_580860.3 | AA-KSSVGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---SKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 568
gi | 45383950 | ref | NP_990587.1 | VA-KAGTGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---SKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 575
gi | 57770576 | ref | NP_001009917.1 | FA-RSTVGSLLVLELARIITDMIKNDEGFKPKRSIVFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---SKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 563
gi | 82524363 | ref | NP_001009918.2 | VA-KSAVGTALLLKLQAFSDMVLKDFGQPSRRIIFASWSAGDFGSGVATGEWLEGLYSSLHLKAFYIINLDKAVLGTSNFKVSAASPLLYLLEIKTMDQVVKHPVTDG-QFLYQ---DSNWI---SKVEKLSLDNAAFPFLAYSIGIPAVSFCFCFE 560
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 189458817 | ref | NP_003225.2 | ---DIDYPLVGLTMDYKELIERIPELN-KVARAAAEVAGQVVKILTDHVELNLDYERYNSQLLSFVRDLNQYRADIKEM-----GLSLQWLYSARGDFFRATSRLLTDFGNAEKDRFVMMKLDNRVMRVEYHFLSPYVSPRESPPFRH 699
gi | 50978812 | ref | NP_001003111.1 | ---DIDYPLVGLTMDYKELIERIPELN-KMARAAAEVAGQVVKILTDHVELNLDYERYNSQLLSFVRDLNQYRADIKEM-----GLSLQWLYSARGDFFRATSRLLTDFGNAEKDRFVMMKLDNRVMRVEYHFLSPYVSPRESPPFRH 709
gi | 11596855 | ref | NP_035768.1 | ---DADYPLVGLTMDYKELIERIPELN-QMVRTAAEVAGQVVKILTDHVELNLDYERYNSQLLSFVRDLNQYRADIKEM-----GLSLQWLYSARGDFFRATSRLLTDFGNAEKDRFVMMKLDNRVMRVEYHFLSPYVSPRESPPFRH 702
gi | 109493400 | ref | XP_341000.3 | ---DEDYPLVGLTMDYKELIERIPELN-QMVRTAAEVAGQVVKILTDHVELNLDYERYNSQLLSFVRDLNQYRADIKEM-----GLSLQWLYSARGDFFRATSRLLTDFGNAEKDRFVMMKLDNRVMRVEYHFLSPYVSPRESPPFRH 699
gi | 119879652 | ref | XP_580860.3 | ---DIDYPLVGLTMDYKELIERIPELN-KVARAAAEVAGQVVKILTDHVELNLDYERYNSQLLSFVRDLNQYRADIKEM-----GLSLQWLYSARGDFFRATSRLLTDFGNAEKDRFVMMKLDNRVMRVEYHFLSPYVSPRESPPFRH 708
gi | 45383950 | ref | NP_990587.1 | K---DEYRFLDKGDTLENLR-KIDNLD-ALLAAAEEVAGQVVKILTDHVELNLDYERYNSQLLSFVRDLNQYRADIKEM-----GLSLQWLYSARGDFFRATSRLLTDFGNAEKDRFVMMKLDNRVMRVEYHFLSPYVSPRESPPFRH 715
gi | 57770576 | ref | NP_001009917.1 | N---SRFVDFGDFEDINLDLFRSRTLVLAKEAEVAGVTLRLVLDHLLKLNVAKYTIIRSVSVQSRKVESRQMS-GRLEPTLTMQWLLSAGQVDRRAAALTAIRNSDLDMEQCRILNRMIRVEGSLSPYVSPRESPPFRH 709
gi | 82524363 | ref | NP_001009918.2 | SRTTPDYKVFGEKRLRDSVIGQVVELLMAAQVAGMALRLVLDHLLKLNVAKYTIIRSVSVQSRKVESRQMS-GRLEPTLTMQWLLSAGQVDRRAAALTAIRNSDLDMEQCRILNRMIRVEGSLSPYVSPRESPPFRH 710
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



```

:: * * : * * : * . : : : . : : * * * * : * . : . : : .
gi | 189458817 | ref | NP_003225.2 | VFWGS GSH TLP ALLE N L K L R K Q N G A F N E T L F R N Q L A L A T W T I Q G -- A A N A L S G D V W D I D N E F 760
gi | 50978812 | ref | NP_001003111.1 | IFWGS GSH TLP ALV E H L K L R K K K S A F N E T L L R N Q L A L A T W T I Q G -- A A N A L S G D I W D I D N E F 770
gi | 11596855 | ref | NP_035768.1 | IFWGS GSH T L S A L V E N L K L R K N I T A F N E T L F R N Q L A L A T W T I Q G -- V A N A L S G D I W N I D N E F 763
gi | 109493400 | ref | XP_341000.3 | IFWGS GSH T L S A L V E N L R L R K N I T A F N E T L F R N Q L A L A T W T I Q G -- V A N A L S G D I W N I D N E F 760
gi | 119879652 | ref | XP_580860.3 | IFWGS GSH T L S A L L E H L K L R K K N G A F N Q T L L E N Q L A L A T W T I Q G -- A A N A L S G D I W D I D N E F 769
gi | 45383950 | ref | NP_990587.1 | IFFGK G P H T L R S L V E H L Q L L K T N R S V D L N L L R E Q L A L A T W T I K G R P M P W E V I S G K L T M S R E 778
gi | 57770576 | ref | NP_001009917.1 | ILLG S GSH T L A A L L D H L E A I K G G L E S A D I D Q F K N Q F A L A T W T I Q G -- C A N A L A G E V W L D N Q I 770
gi | 82524363 | ref | NP_001009918.2 | IFFGNGWQ T A I D L E N Y L Q D V R D K K A S F I D Q V L N K F A L L T W S I Q G -- C A N D L A G D I W S L D N E I 771
.....760.....770.....780.....790.....800.....810...

```

