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gi | 21355083 | ref | NP_652013.1 | -----MOKVALLLVAFLLAAVAHFNPSQEKPGLLRVPLHKFQVARRHFADVG-----TELQQLRIR-----VGG--GDVPEPLSNYMDAQQYGPATGSPPONFRVVFDTGSSNLWVPSKKCHLTNTIACLMHNKYDASKSKT 124
gi | 31197673 | ref | XP_307784.1 | -----MARIFGVAVILLAMAVLQ-----YADFVRVALQKAPARDHFRSVC-----TEVRQLRLK-----VGAFTGVPPEPLSNYLDAAQYFGAISIGTTPPOSFKVVFDGSSNLWVPSKQCSFTNTIACLMHNKYDAKSSS 121
gi | 6753556 | ref | NP_034113.1 | -----MKTPTGVLL--LILGLLASS--SFAIRIRPLRKFTIRRTMTEVQ-----GSVEDLILKGPITKYSMQSSPKTTEPVSSELLKNYLDAAQYGGIDIGTTPPOCFVTVVFDGSSNLWVPSIHCCKLLDIAACVWHHKYNDKSSST 130
gi | 42476045 | ref | NP_599161.2 | -----MOTPGVLL--LILGLLAAAS--SSALIRIPLRKFTIRRTMTEVQ-----GSVEDLILKGPITKYSMQSSPKTTEPVSSELLKNYLDAAQYGGIDIGTTPPOCFVTVVFDGSSNLWVPSIHCCKLLDIAACVWHHKYNDKSSST 130
gi | 4503143 | ref | NP_001900.1 | -----MQPSSLLF--LALCLLAAP--ASALVRIPLHKFTIRRTMTEVQ-----GSVEDLILKGPVSKYSQAVPAVTEGPIPEVLKNYMDAQQYGGIDIGTTPPOCFVTVVFDGSSNLWVPSIHCCKLLDIAACVWHHKYNDKSSST 130
gi | 71043798 | ref | NP_001020792.1 | -----MQPSSLLF--LVLGLLAAP--AAALVRIPLHKFTIRRTMTEVQ-----GPVEDLILKGPISKYAOGAPAVTGGPIPEMLRNMYMDAQQYGGIDIGTTPPOCFVTVVFDGSSNLWVPSIHCCKLLDIAACVWHHKYNDKSSST 130
gi | 194679949 | ref | XP_609913.4 | -----MQTPRLLPLLLALGLLAAP--AAAVIRIPLHKFTIRRTMTEVQ-----GPVEHLIAKGPISKYATGEPAVRGGPIPEMLKNYMD--LYGEIGIGTTPPOCFVTVVFDGSSNLWVPSIHCCKLLDIAACVWHHKYNDKSSST 130
gi | 45384002 | ref | NP_990508.1 | -----MAPRGLLV--LILLALVPS--CAALIRIPLRKFTIRRTMTEVQ-----SETPDMNATQFLKFKLG--FADLAEPPELILKNYMDAQQYGGIDIGTTPPOCFVTVVFDGSSNLWVPSVHCHLLDIAACVWHHKYNDKSSST 129
gi | 18858489 | ref | NP_571785.1 | -----MRIRFCCS--LIFPSA--RRRDRIPLKFRLLRRLTSDSG-----RSLLEELVSSSNLKNLGFPAASN--DPTPELILKNYLDAAQYGGIDIGTTPPOCFVTVVFDGSSNLWVPSVHCSLTDIAACVWHHKYNDKSSST 126
gi | 17549909 | ref | NP_510191.1 | -----MNRGILLLLGLLLVQGLVHVKRQKLRVSLKQKPLRLRLLQAGSFEFAKHHRGKYLKNGNHDFDKYQALNVEGEGEDLELRRNYMDAQQYGGITISIGTTPAONFTVIFDTGSSNLWVPSKCKCPYDIACMLHHRYSKSSST 145
gi | 15233518 | ref | NP_192355.1 | MGRFQSFLLVFLSCLLILISTASCERNQDGTIRIGLKKRKLDRSNRLASQ-----LFLKNRGSHWSPKHYFRLNENADMVPLKNYLDAAQYGGIDITIGTTPPOCFVTVVFDGSSNLWVPSIKCYLS--VACVYFSKYKASQSSS 137
gi | 39973863 | ref | XP_368322.1 | -----MKGAMMAAALLG--TAEAGVHTKMKKIPLEEDQLKFDLNAQMRGLG--QKYLGIRESHQQAVFNDVAQAS----GNHPVPIISNFMNAQYFSEITIGTTPPONFKVILDGSSNLWVPS--SCGSIACYLHNKYESSSST 134
gi | 85094599 | ref | XP_959917.1 | -----MKGALLTAALLG--SAQAGVHTMKLKKVPLAQLESVFDVQVHLLG--QKYLGLRTESSHQAQMFKAQDAQVS----GNHPVPIISNFMNAQYFSEITIGTTPPOFHKVILDGSSNLWVPS--SCGSIACYLHNKYESSSST 134
gi | 50306705 | ref | XP_453326.1 | -----MHLNFQSLPLASLLLSAFDVAEAKIHKAKIQKHKLEEDQLKDVFFAEHVAQLG--EKYLNSEQRAYPQESFKDNVDVFAPEGS--SVPLTNYLNAQYFTIITLGSPPQSFVKVILDGSSNLWVPS--AECGSLACFLHTKYDHEASST 145

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gi | 21355083 | ref | NP_652013.1 | :YKNGTEFAIQYGSGLSCYLSQDTPVSIAG-----LDIKDCIFAEALSPEGLVFAAKFDGILGLGYSNISVDKVKPFYAMYEGQLISAPVFSFYLNRDPSAPEGGEIIFGGSDSKHYTGDFTYLVSVDKRAYWFKMDSVTVG 263
gi | 31197673 | ref | XP_307784.1 | FEKNGTAFHIQYGTGSLSCYLSQDTPVIVGG-----VPVEKQIFAEAIQEPGLVFAAKFDGILGLAYKXISVDGVMPPVYFMFNQKIDAPVFSFYLNRDPSAPEGGEIIFGGSDSKHYTGDFTYLVSVDKRAYWFKMDSVTVG 260
gi | 6753556 | ref | NP_034113.1 | YVKNGTSPDIHYGSGSLSCYLSQDTPVVPCKSDQSK--ARGIKVEKQIFGEATKQPGIVFAAKFDGILGMGYPHISVNNVLPVFDNLMQOKLVEKNIFSFYLNDRDPEGQPGGELMLGGDSKYRHHGELSYLNVTRKAYWVHMDQLEVG 278
gi | 42476045 | ref | NP_599161.2 | YVKNGTSPDIHYGSGSLSCYLSQDTPVVPCKSDLG-----GIKVEKQIFGEATKQPGVVFIAAKFDGILGMGYPHISVNNVLPVFDNLMQOKLVEKNIFSFYLNDRDPTGQPGGELMLGGDSRYRHHGELSYLNVTRKAYWVHMDQLEVG 275
gi | 4503143 | ref | NP_001900.1 | YVKNGTSPDIHYGSGSLSCYLSQDTPVVPCKSASSASALGGVQKVERVFGGEATKQPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMQOKLVDQNIQSFYLSRDPDAQPGGELMLGGDSKYRHHGELSYLNVTRKAYWVHMDQVEVA 280
gi | 71043798 | ref | NP_001020792.1 | YVKNGTSPDIHYGSGSLSCYLSQDTPVVPCKSALSG--LAGIKVERQTFGEATKQPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMQOKLVEKNIFSFYLNDRDPAQPGGELMLGGDSKYRHHGELSYLNVTRKAYWVHMDQVDVG 278
gi | 194679949 | ref | XP_609913.4 | YVKNGTTFDIHYGSGSLSCYLSQDTPVVPCKSSSS--PGGVTVQRCITFGEAIKQPGVVFIAAKFDGILGMAYPRISVNNVLPVFDNLMQOKLVEKNIFSFYLNDRDPAQPGGELMLGGDSKYRHHGELSYLNVTRKAYWVHMDQVDVG 278
gi | 45384002 | ref | NP_990508.1 | YVENGTEFAIHYGTGSLSCYLSQDTPVILGN-----LKIKNCFGEAVKQPGITFIAAKFDGILGMAYPRISVVDKVPPEFDPVFNLMQOKLVEKNIFSFYLNDRDPTAQPGGELMLGGDPKYRHHGELSYLNVTRKAYWVHMDSDVDA 268
gi | 18858489 | ref | NP_571785.1 | YVKNGTQFAIQYGSGLSCYLSQDTPCIGD-----IAVEKQIFGEAIKQPGVVFIAAKFDGILGMAYPRISVDGVPVFDMMMSQKVEKNVFSFYLNRDPTQPGGELMLGGDPKYRHHGELSYLNVTRKAYWVHMDGMSIC 265
gi | 17549909 | ref | NP_510191.1 | YKEDGRKMAIQYGTGSMKGFISKDQVCAVG-----VCAEDQFAEATSEPGITFVFAAKFDGILGMAYPEIAVLGQVQVFNLTQKVKVPSNLSFYLNRDPSAPEGGEIIFGGIDSRRYVEPIYVFPVTRKAYWFKMD--KVVG 283
gi | 15233518 | ref | NP_192355.1 | YRKNGRPASTRVGTGAIKSGYFNDDVVKVD-----TVVKEQEFIEATSEPGITFLLAQFDGILGLGFKETISVGNSTPPVWYNNMVEKGLVKEPIFSFYLNRDPEGGEIIVFGVDPKHFRGHEITVFPVHKGWQDFMDQDQIA 276
gi | 39973863 | ref | XP_368322.1 | YKKNGTSPFKIQYGSGLSCYLSQDTPVVPCKSALSG--LAGIKVERQTFGEATKQPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMQOKLVEKNIFSFYLNDRDPAQPGGELMLGGDSKYRHHGELSYLNVTRKAYWVHMDQVDVG 270
gi | 85094599 | ref | XP_959917.1 | YKKNGTSPFKIQYGSGLSCYLSQDTPVVPCKSALSG--LAGIKVERQTFGEATKQPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMQOKLVEKNIFSFYLNDRDPAQPGGELMLGGDSKYRHHGELSYLNVTRKAYWVHMDQVDVG 270
gi | 50306705 | ref | XP_453326.1 | YKANGTEFAIQYGSGLSCYLSQDTPVILGN-----LVIIDQFAEATSEPGITFVFAAKFDGILGLAYDSISVNRVPPVYNNLKNLDDPEVFAFVLDGSDKSEDEGGEASFGGIDEEKYTGELIWLVEVRKAYWVHMDQVDVG 284

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gi | 21355083 | ref | NP_652013.1 | --DLQLCKGGCQVIADTG--TSLIAAPLEAATSINQKIGGT-----PLIQGYV 308
gi | 31197673 | ref | XP_307784.1 | --DAQYCNNGCEAIADTG--TSLIAGPVAEVTAINKAIIGT-----PVLNGEYM 305
gi | 6753556 | ref | NP_034113.1 | N-ELTLCKGGCEAIVDTG--TSLIVGVPVEVKELQKAI GAV-----PLIQGEYM 324
gi | 42476045 | ref | NP_599161.2 | S-ELTLCKGGCEAIVDTG--TSLIVGVPVEVKELQKAI GAV-----PLIQGEYM 321
gi | 4503143 | ref | NP_001900.1 | S-GLTLCKGGCEAIVDTG--TSLMVGVPVEVRELOKAI GAV-----PLIQGEYM 326
gi | 71043798 | ref | NP_001020792.1 | S-SLTLCKGGCEAIVDTG--TSLIVGVPVEVRELOKAI GAV-----PLIQGEYM 324
gi | 194679949 | ref | XP_609913.4 | S-SLTVCKGGCEAIVDTG--TSLIVGVPVEVRELOKAI GAV-----PLIQGEYM 324
gi | 45384002 | ref | NP_990508.1 | N-GLTLCKGGCEAIVDTG--TSLITGPTKEVKELQTAI GAK-----PLIQGEYM 324
gi | 18858489 | ref | NP_571785.1 | S-GLTLCKGGCEAIVDTG--TSLITGPTKEVKELQTAI GAK-----PLIQGEYM 314
gi | 17549909 | ref | NP_510191.1 | S-GVLCSSNGCQAIADTG--TSLIAGPKAIEAIONFIGAE-----PLMGEYM 313
gi | 15233518 | ref | NP_192355.1 | GKPTGYCARCCSAIADSG--TSLITGPTSTVITMINHAIGAQIVSRECKAVVDYQKTMNLNLLAQEDPKKVCSSIGVCAYDGTQSVSMGIQSVVDDGSGLLNQAQCACEMAAVWMEBELIQNQIQERILAYAAELCDHIFPQNOQSA 424
gi | 39973863 | ref | XP_368322.1 | DEVAELDNTG--VILDTG--TSLIALPSQLAELLNSQI GAK-----KQNGQYS 315
gi | 85094599 | ref | XP_959917.1 | KDFAELEHG--VILDTG--TSLIALPSQLAEMLNQAI GAK-----KSWNGQF 315
gi | 50306705 | ref | XP_453326.1 | ERYALEHG--AAIDTG--TSLIALPSGLAEILNAEIGAK-----KQWSGQYS 329

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gi | 21355083 | ref | NP_652013.1 | VS CDLIPQLPVIKFVLGGKTFEGKDYILRVAVMGKTICLSGFMGLDIPPPNGPLWILGDVFIGKYYTEFDMGNDRVGFADAK----- 392
gi | 31197673 | ref | XP_307784.1 | VDCSLIPSLPKITFTLGGKQFTLEGADYILRVAVMGKTICLSGFMGLDIPPNGPLWILGDVFIGKYYTEFDMGNDRVGFATAV----- 389
gi | 6753556 | ref | NP_034113.1 | IPCEKVSSLPTYYLKLGGKNVELHPDKYILKVSCGGKTICLSGFMGMDIPPPSGLWILGDVFIGSYYYTFDRDNNRVGFANAVVL----- 410
gi | 42476045 | ref | NP_599161.2 | IPCEKVSSLPIITFKLGGQNVELHPEKYILKVSCGGKTICLSGFMGMDIPPPSGLWILGDVFIGSYYYTFDREYNRVGFAKAATL----- 407
gi | 4503143 | ref | NP_001900.1 | IPCEKVSSLPAITLKLGGKYKLSPEDYTLKVSCGGKTICLSGFMGMDIPPPSGLWILGDVFIGRYYYTFDRDNNRVGFAEAARL----- 412
gi | 71043798 | ref | NP_001020792.1 | IPCEKVSSLPDVTLKLGGKLYKLSSEDYTLKVSCGGKTICLSGFMGMDIPPPGGLWILGDVFIGCYYYTFDRDQNRVGLAQATL----- 410
gi | 194679949 | ref | XP_609913.4 | IPCEKVSSLPQVTLKLGGKDYALSPEDYALKVSCGAGTTVCLSGFMGMDIPPPGGLWILGDVFIGRYYYTFDRDQNRVGLAEAARL----- 410
gi | 45384002 | ref | NP_990508.1 | ISCDKISSLPVVTLMLGGKPYQLTGEQYVFKVSAGGETICLSGFSGLDVPPPGGLWILGDVFIGPYYYTFDRDNDSVGFAKCV----- 398
gi | 18858489 | ref | NP_571785.1 | VDCKVPTLPTISFSLGGKVSSLTGEQYILKESCGGHDICLSGFMGLDIPPPAGPLWILGDVFIGQYYYTFDRENNRVGFAKAKSV----- 399
gi | 17549909 | ref | NP_510191.1 | ISCDKVPTLPPPVSFVIGGEFSLKGEDYVLVKSCGGKTICLSGFMGLDLPERVGELWILGDVFIGRYYSVFDFDQNRVGFAQAKTADGRPVDPAPRPRSVFDNESESMEQDDE----- 444
gi | 15233518 | ref | NP_192355.1 | VDCGRVSSMPIVTFSIGGSFDLIPODYIFKIGEGVESQCTSGFTAMDIAPPRGLWILGDIFMGPYHTVFDYGKGRVGFAKAA----- 508
gi | 39973863 | ref | XP_368322.1 | IDCKRKDLPDITFRLSGYDFISAYDYILEVSGS---CISTFMAMDIPEPVGLAILGDAFLRRYSIYDLGADTVGIAKAK----- 395
gi | 85094599 | ref | XP_959917.1 | IDCGKSLEDVTFLAGYNFTLGEDYILEVSGS---CLSTFMGMDMPAPVGLAILGDAFLRKYSIYDLGADTVGIATAKR----- 396
gi | 50306705 | ref | XP_453326.1 | VDCSRDSLPDLLNFNGYNFTLAYDYILEVSGS---CISAFTPMDFPEPVGLAILGDAFLRKYSIYDLGADVGLAKAA----- 409

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