

gi | 28269693 | ref | NP_071449.1 | MVAAPCARLARRSHSALLAALTVLLLOTLVWNFSSLD SGAGE-RRGGAAVGGGEPPE---APAPRRERRDLPAEPAAARGGGGGGGG-GGGGRGPQARARGGGGPEPRGQPASRGALPARALDPHPSPLITLETQDGYFSHRPKEK 145
gi | 82617670 | ref | NP_001032366.1 | MQAAPCARLARRSHSALLAALTVLLLOTLVWNFSSLD SGAGE-RRGGAAVGGGEPPE---PAPRRERRDLPAEPAAARGGGGGGGGCGGGGRGPQARARGGGGPEPRGQPASRGALPARALD-----GYFSHRPKEK 131
gi | 56790277 | ref | NP_001008718.1 | MVAAPCARLARRSHSALLAALTVLLLOTLVWNFSSLD SGAGE-RRGGAAGGTEPPAPP---APAPRRERRDLPPGPAALGACCGGGGGPFPAR-ARARALACPEEPRGQPAGGALPTRALD-----GYFSHRPKEK 134
gi | 120407064 | ref | NP_783576.2 | MVAAPCARLARRSHSALLAALMVLLLOTLVWNFSSLD SGAGEORRAGAAGAEQPE---AAPRRERRDLAAHLPAAARG-----GPGGRAGGGGARGGGGGARAQPASRGALASRARDPQPSPLITLETQDGYFSHRPKEK 138
gi | 34859034 | ref | XP_341913.1 | -----MRSLELFFSVCSFVGRCKAIWLVGVTVF-----MLLME-FDGVFVSHRPKEK 48
gi | 118098014 | ref | XP_414904.2 | ---MPLPIERVGFNAFFFPACFSFCKVGLGPRVSRVPPRFQAFRWSSGAPPVQLAPCCCLGRARRRVEVRCPLGSRALSVPGFLFASREGKLRVAGREGARGPLLEGSAVRSSCARCDCESEPCGRRSILCVADGYFSHRPKEK 147
gi | 292611779 | ref | XP_689440.4 | MFGSLCARLARRSHSALLAALTVLLLOTLVWNFSSLDI---GDRKNDNGRE-----KRDTIGINKAMSEYFK-----SGFQKRHHPPPLGKANRHKQPF-----DGYFSHRPKEK 100
gi | 21358211 | ref | NP_647705.1 | -MQSVYARWLKRYRAFPLILLLVAITOLFLAYKSLDITVGGSGSGFDAAEAP-----ASPPPP 58
gi | 118787075 | ref | XP_556482.2 | --MQKFLRLWRYKVFVLIQFMIVAGVFLAKLLRMLPSGNESSAERDLR-----KLMQDY 57
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 28269693 | ref | NP_071449.1 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 285
gi | 82617670 | ref | NP_001032366.1 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 271
gi | 56790277 | ref | NP_001008718.1 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 274
gi | 120407064 | ref | NP_783576.2 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 279
gi | 34859034 | ref | XP_341913.1 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 189
gi | 118098014 | ref | XP_414904.2 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 191
gi | 292611779 | ref | XP_689440.4 | VRIDSNNSVVKDFENVDNSNFAPRTPQOKKHQPELAKKPPSRQKELLRKLEQEEKGKHIFPGKGPGEVLPDRAAANSSHG-KDVSRR---PPHAR--KTGGG-SPETKYDQPPKCDISGKE-AISALSRASKHCRQIEGTTC 244
gi | 21358211 | ref | NP_647705.1 | -HAQAR---VQPPARTKLTAAQLGFQPCDILAREAISALQRAKTKDREHIAIACAIQAGRFYAPQLRRSCPAGNHTANVILGCFKDEKDRLLAGYYSKSNNSPACKVELCLQSGYVYAGVYGRECFQYDPPPKASKLPDSSC 204
gi | 118787075 | ref | XP_556482.2 | GRSAARDGKLGQNHVLRLLDELDFVPPCELTRKEITVSAIHRAKSSCKAKIVVACEIQAGFYQRLPFCPRGDHSPRALGCFRDEKNRLLSGYYSFKNNPEKICIRLCLQSGYVYAGVYGRECFQYDPPPKASKLPDSSC 207
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 28269693 | ref | NP_071449.1 | RHKLGLLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---NPVRIAFVLVHGRASRQLQRMFKAIYHKDFHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 432
gi | 82617670 | ref | NP_001032366.1 | RHKLGLLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---NPVRIAFVLVHGRASRQLQRMFKAIYHKDFHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 418
gi | 56790277 | ref | NP_001008718.1 | RHKLGLLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---NPVRIAFVLVHGRASRQLQRMFKAIYHKDFHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 421
gi | 120407064 | ref | NP_783576.2 | RHKLGLLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---NPVRIAFVLVHGRASRQLQRMFKAIYHKDFHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 426
gi | 34859034 | ref | XP_341913.1 | RHKLGLLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---NPVRIAFVLVHGRASRQLQRMFKAIYHKDFHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 336
gi | 118098014 | ref | XP_414904.2 | RHKLGLLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---NPVRIAFVLVHGRASRQLQRMFKAIYHKDFHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 438
gi | 292611779 | ref | XP_689440.4 | RHKEHQLMPEKVTRECFLEGKANKNVQWEDSVEYMPA---VPRVRIAFVLMVHGRALRQVRLFKAIYHSHFYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 391
gi | 21358211 | ref | NP_647705.1 | NTKCLGNAKKICGGFYAMNIYETGIKFAQSLTETVTKRADSTVRIAPFLILNRAVROVHRLKALYAPREHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 353
gi | 118787075 | ref | XP_556482.2 | NTKCLGNAKKICGGFYAMNIYETGIKFAQSLTETVTKRADSTVRIAPFLILNRAVROVHRLKALYAPREHYIYHVDKRSNYLHRQVLFQVSRQYVNVVTPWRMATIWGGASLLSTYLQSMRDLEMTDWPWDFFFINLSAADYPIRTN 357
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 28269693 | ref | NP_071449.1 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 578
gi | 82617670 | ref | NP_001032366.1 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 564
gi | 56790277 | ref | NP_001008718.1 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 567
gi | 120407064 | ref | NP_783576.2 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 572
gi | 34859034 | ref | XP_341913.1 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 482
gi | 118098014 | ref | XP_414904.2 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 584
gi | 292611779 | ref | XP_689440.4 | DQLVAFLSRYRDMNFKSHGRDNARFIRKQGLDRLFLECDTHMWRLGDRRIPEGIAVDGSDWFLNRRKFVEYVAFS---TDDLVTKMKQFYSYTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 537
gi | 21358211 | ref | NP_647705.1 | DKLVFLSANPGRNVEVHGGRGTQKFKIQKGLDKTVEVCDTHMWRIGDRKLPAGIQVDDGSDWFLNRRKFVEYVAFS---REDDELLQALLKFRHTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 501
gi | 118787075 | ref | XP_556482.2 | DQLVFLSANPGRNVEVHGGRGTQKFKIQKGLDKTVEVCDTHMWRIGDRKLPAGIQVDDGSDWFLNRRKFVEYVAFS---REDDELLQALLKFRHTLLPAESFFHTVLENSPHCDTMDVNDNLRITNWRKLGCKCQYKHIVDWC GCSFND 507
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 28269693 | ref | NP_071449.1 | FKPDFFHRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 726
gi | 82617670 | ref | NP_001032366.1 | FKPDFFHRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 712
gi | 56790277 | ref | NP_001008718.1 | FKPDFFHRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 715
gi | 120407064 | ref | NP_783576.2 | FKPDFFHRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 720
gi | 34859034 | ref | XP_341913.1 | FKPDFFHRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 630
gi | 118098014 | ref | XP_414904.2 | FKPDFFHRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 732
gi | 292611779 | ref | XP_689440.4 | FKPSDLPFRFOQTAR-PTFFARKFEAVNQEIIGLDYLYLGNYPAGTPGLRSYENYVDEPDGIHSLSDVLTLYHSFARLGLRRAETSLSHTD-GENSCRYPMGHPSVHLYFLADRFGQFLIKHHAITNLA VSKLETLWVMPKVKFK 686
gi | 21358211 | ref | NP_647705.1 | FKPEDWRLQAEQKSLFFARKFEPVNVQAVLLQLEWVWLGFPYTSSEYANLHAYVQSLYHGEDVHSGDGLDARSIGDSVMRLSAR-----QAKLY-PLLEIELTHYLHRDQYKGLVVRHAR-GSTGKPLHLETRVPTQOKG 636
gi | 118787075 | ref | XP_556482.2 | FKPEDWRLQAEQKSLFFARKFEPVNVQAVLLQLEWVWLGFPYTSSEYANLHAYVQSLYHGEDVHSGDGLDARSIGDSVMRLSAR-----QAKLY-PLLEIELTHYLHRDQYKGLVVRHAR-GSTGKPLHLETRVPTQOKG 644
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi | 28269693 | ref | NP_071449.1 | IASPPSDFGRLQFSV--GTDWDAKERLFRNFGGLLGPMDPE-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYKPPLN-----LPLRPGVWTVKILHHWVPAETKFLVAPLTFSNR-----OP 849
gi | 82617670 | ref | NP_001032366.1 | IASPPSDFGRLQFSV--GTDWDAKERLFRNFGGLLGPMDPE-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYKPPLN-----LPLRPGVWTVKILHHWVPAETKFLVAPLTFSNR-----OP 835
gi | 56790277 | ref | NP_001008718.1 | IASPPSDFGRLQFSV--GTDWDAKERLFRNFGGLLGPMDPE-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYKPPLN-----LPLRPGVWTVKILHHWVPAETKFLVAPLTFSNR-----OP 840
gi | 120407064 | ref | NP_783576.2 | VASPPSDFGRLQFSV--GTDWDAKERLFRNFGGLLGPMDPE-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYKPPLN-----LPLRPGVWTVKILHHWVPAETKFLVAPLTFSNR-----OP 843
gi | 34859034 | ref | XP_341913.1 | VASPPSDFGRLQFSV--GTDWDAKERLFRNFGGLLGPMDPE-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYKPPLN-----LPLRPGVWTVKILHHWVPAETKFLVAPLTFSNR-----OP 753
gi | 118098014 | ref | XP_414904.2 | IASPPSDFGRLQFSV--GTDWDAKERLFRNFGGLLGPMDPE-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYKPPLN-----LPLRPGVWTVKILHHWVPAETKFLVAPLTFSNR-----OP 855
gi | 292611779 | ref | XP_689440.4 | FNPPKTFTRLQFAEI--GTDWDAKERIFRNFNMMGPMDEP-----VGMQKWGKGNVVTVIWVDPVNVIAATYDILIEST--AEFTHYRPPLN-----LPLRPGMWTVRVLHHWVPAETRFLIITPLTHHKH-----LP 809
gi | 21358211 | ref | NP_647705.1 | LARNARFKRLRNFEVS--TDFDQKEQIARNFGKLLGQSD--LLLSYTLQANADSGAASHSNLTLWIDPLGRLDQFNELHVEDS--DVINHSKTLK--HPTTPGIWTAKLIQRNSIYALQKFLIAPLAYKQ--YPL 769
gi | 118787075 | ref | XP_556482.2 | VTRSTPLARRLIHLEVS--TEYDEKEQLSRNFRIIGTNAEPALIFRLAPPLET--ERVVKGNATNHSLSAVEWIDPVGITVAASHFTIEDSP--GPLHSFNHFLKAGKLLKPLAEGVWGARLLQKALLGATRPLVTEATFREGRIVENELL 792

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gi | 28269693 | ref | NP_071449.1 | IKPEEALKLHNGPLRNAYMEQSFQSLNPVLSLPIPAQVEQARRN---AASGTALEGWLDSLVGGMWTAMDICATGPTA---CPVMQTCSTAWSSFSPPDKSELGAVKPDGRLR 959
gi | 82617670 | ref | NP_001032366.1 | IKPEEALKLHNGPLRNAYMEQSFQSLNPVLSLPIPAQVEQARRN---AASGTALEGWLDSLVGGMWTAMDICATGPTA---CPVMQTCSTAWSSFSPPDKSELGAVKPDGRLR 945
gi | 56790277 | ref | NP_001008718.1 | IKPEEVLKLNHGPLRNAYMEQSFQSLNPVLSLPIPAQVEQARRN---AGSTGATLEHWLDSLVGGTWTAMDICATGPTA---CPVMQTCSTAWSSFSPPDKSELGAVKPDGRLR 950
gi | 120407064 | ref | NP_783576.2 | IKPEEALKLHNGPRLRNAYMEQSFQSLNPVLSLHINPAQVEQARKN---AAFTGTALEAWLDSLVGGTWTAMDICTTGTPTA---CPVMQTCSTAWSSFSPPDKSELGAVKPDGRLR 953
gi | 34859034 | ref | XP_341913.1 | IKPEEALKLHNGPRLRNAYMEQSFQSLNPVLSLHINPAQVEQARKN---AAFTGTALEAWLDSLVGGTWTAMDICTTGTPTA---CPVMQTCSTAWSSFSPPDKSELGAVKPDGRLR 863
gi | 118098014 | ref | XP_414904.2 | IKQEEAMKYHSGPPKRNAYMEQSFQSLNPVLSLHINPAQVEQARKN---AALVGARLDANVDSLVGSVNSAVDICSTGPTA---CPVMQACTQAWSSLSPPDKSELGAVKPDGRLR 965
gi | 292611779 | ref | XP_689440.4 | IRHEDALKMHNQPAKNSYMEQSFHGLNPIILNIPVHLGQVEAAEHN---AGLTGSELERWVDSLVGDVNSAVDVCSTGPSG---CPVMQTCRETQVWSSLSPPDKSELGAVKPDGRLR 919
gi | 21358211 | ref | NP_647705.1 | AKSSDAEALNA--GLTVALPEDFEMPVQQLQTDDEQFTMREESLAKGKMLQQLHSWIDGLVQFFQLRESQVVEADS---EVSLPLCSQDAPWSSLSAPPDKSELGAVKPDGRLR 876
gi | 118787075 | ref | XP_556482.2 | ERHTRQVLPVRRGSLANTATSKIRAKERKQHPVGHSGDRHADRHWQEAADDQ--QVH--QLNKLVSQFFSIRETCAVAGVERKELVRFVDCSTSWSSLAADPKSELGAVKPDGRLR 905

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