

gi 50302207 | ref | XP_451037.1 | -----MADLENIANILSLVVAS--SARTAEQLKELESQEG-FALLLLHVASINPLSLRLGALGFFKFKRRWIDENGN---YLISANDVELVKKVPLM 94
gi 45198791 | ref | NP_985820.1 | -----MVSSSPQLAFARDMSDLTVAHYLGQSVIAS--TARSABQLRGLSESQEG-FALLLLHVVASNNLAASRLGALGFFKFKRRWVDENGE---HLISARDELVKKVPLM 108
gi 6321198 | ref | NP_011276.1 | -----MSDLEIVAKFLAESVIAS--IAKTSERNLRQLETQDG-FGLLLHVIASINPLSLRLGALGFFKFKRRWVDENGN---HLIPANNVELIKKIVPLM 94
gi 145607115 | ref | XP_361520.2 | MPEQTCRGRDGSIAIKLVIGRORREESQKRAODLNVAIGPSHSSPGKMAVVIQEVALLDADLDPO---HHKAEAAALKIEERKPO---FSLLLQLIVNSDALPSKTRLAALCFKFNIRGNVDEBKG---YKLPSEVAALIKQELVGLM 144
gi 32405662 | ref | XP_323444.1 | -----MAANLDHLAQLLQATLDAR---HHRKAETALKEBAKPKF-YSLGILLIVANDAQPSNIRLAALAFKFNIRHNVDENGN---YKLPADBEVAALIKQELVGLM 95
gi 19112322 | ref | NP_595530.1 | -----MDDIPTLLARLNPPT---SKSAEEALKVWELQDSFALKLLNVAEDTVVDINIKLAASLYFKNYIKKHWDSEEGAS---IRISDEVAELIKREIVLGM 93
gi 24584736 | ref | NP_523588.2 | MEVTEANLQLLAGYLQQLTSDPNVRRPAEKLESTELQDN-YPLLILLNLIKAMQMDTTRVAGAAIAFKNYIKRNWAAHLSDGSDRHSERNIKILIVLTM 103
gi 31204951 | ref | XP_311424.1 | MEINENNFERLASVLLQQLTSDPEVRRPAERFIESIHFVSN-YPLLCLLHIDPQVMTTRVAGAAIAFKNYIKRNWAAHLSDGSDRHSERNIKILIVLTM 103
gi 62460562 | ref | NP_001014933.1 | MAMELSDANLOTLEYLKKLLDPPAIRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-DNVIKVCASVTFKNYIKRNWRIVEDE---PNKICEADRVAIKANIVHLM 102
gi 34860723 | ref | XP_342582.1 | MELSDANLOTLEYLKKLLDPPAIRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-DNVIKVCASVTFKNYIKRNWRIVEDE---PNKICEADRVAIKANIVHLM 100
gi 12963737 | ref | NP_076054.1 | MELSDANLOTLEYLKKLLDPPAIRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-DNVIKVCASVTFKNYIKRNWRIVEDE---PNKICEADRVAIKANIVHLM 100
gi 114682541 | ref | XP_001166085.1 | MELSDANLOTLEYLKKLLDPPAIRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-DNVIKVCASVTFKNYIKRNWRIVEDE---PNKICEADRVAIKANIVHLM 100
gi 73992217 | ref | XP_853206.1 | -----M 1
gi 29029559 | ref | NP_001307.2 | MELSDANLOTLEYLKKLLDPPAIRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-DNVIKVCASVTFKNYIKRNWRIVEDE---PNKICEADRVAIKANIVHLM 100
gi 118100584 | ref | XP_417389.2 | MELSDANLOTLEYLKKLLDPPAIRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-DNVIKVCASVTFKNYIKRNWRIVEDE---PNKICEADRVAIKANIVHLM 100
gi 41393069 | ref | NP_958858.1 | MELNDGNLQTLLEYLQKLTSDPAVRRPAEKFLSEVEGNQ-YPLLLLILLEKSG-NEVIRVCASVTFKNYIKRNWRIVEDE---PNKISDPRTAIKANIVHLM 100
gi 15226001 | ref | NP_182175.1 | MEWNRRETLVFLSQCLFNLTSPPEPRRTAERALSDAADQAN-YGLAVLRVAEPAIDQTRHAAAVNFKNHLRSRWHPADGSG-TSPIVDSEKEQIKTLIVSLM 102
gi 115435528 | ref | NP_001042522.1 | -----M 1

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi 50302207 | ref | XP_451037.1 | IQLPGNLQVIGEAISVIAESDFPQRWSTLMDLLISKLS---ADDMVTNAGVLSVAHSICKRWRPLFRSDELFLEIQMVLDFKFAVPLTLMQTVDKQID---EYSSDKARMVILFDVLLLVKLYDLNCDIPAFFEDNMSVGMISMH 237
gi 45198791 | ref | NP_985820.1 | IQLGSHLQVIGESIAVIADSDPFRWPTLLDDLVKLS---AEDMVTNKGVLTVASHIFKRWPLFTSDALVLEIKLVLEKFAVPLHLLQTVDEQIS---ANRADEAKRLRLLFDVLLLVKLYDYDNCODIPAFFEDNMSVGMISMH 251
gi 6321198 | ref | NP_011276.1 | ISLNNLQVIGEAISVIADSDPFRWPTLLDDLVKLS---NDDMVTNKGVLTVASHIFKRWPLFRSDELFLEIKLVLDVFPAPFLLNLLKTVDEQIS---ANEINKASLNLFDVLLLVKLYDYDFNCDIPAFFEDNMSVGMISMH 237
gi 145607115 | ref | XP_361520.2 | ISSPNIQAOLGDAISIIADSDPFRWPTLLDDLVKLS---SDFKIINQVLEVAHSIFKRWPLFRSDELFLEIKLVLDVFPAPFLLNLLKTVDEQIS---AAKGDATQLKGLWQLTMDLLVTRIFDLSDODLPEFFIESNIAELCTLLQ 287
gi 32405662 | ref | XP_323444.1 | ISSPNIQAOLGDAISIIADSDPFRWPTLLDDLVKLS---SDFKIINQVLEVAHSIFKRWPLFRSDELFLEIKLVLDVFPAPFLLNLLKTVDEQIS---AAKGDATQLKGLWQLTMDLLVTRIFDLSDODLPEFFIESNIAELCTLLQ 238
gi 19112322 | ref | NP_595530.1 | LRSTTIQVQLGEVIGVIANFDPDRWDTLLPDLISKLS---AVDMNINAVLSIAHAIFKRWPLFRSDELFLEIKLVLDVFPAPFLLNLLKTVDEQIS---NGPQBAESLNLQVLLVCKVYVDFNCDIPAFFEDNMSVGMISMH 236
gi 24584736 | ref | NP_523588.2 | LHSFVALQKQLSDAIVSIIIGYDFPKKWPQLIDEMVERFA---SGDFNVINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 246
gi 31204951 | ref | XP_311424.1 | LKSPAALQKQLSDAIVSIIIGYDFPKKWPQLIDEMVERFA---SGDFNVINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 246
gi 62460562 | ref | NP_001014933.1 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 245
gi 34860723 | ref | NP_342582.1 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 12963737 | ref | NP_076054.1 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 114682541 | ref | XP_001166085.1 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 73992217 | ref | XP_853206.1 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 144
gi 29029559 | ref | NP_001307.2 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 118100584 | ref | XP_417389.2 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 41393069 | ref | NP_958858.1 | LSSPEIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 15226001 | ref | NP_182175.1 | LSSPRIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 243
gi 115435528 | ref | NP_001042522.1 | LSSPRIQKQLSDAIVSIIIGREDFPKWPDLLTEMVNRFP---SGDFHVIINGVLRVAHSLFKRFRHFKSNELWTEIKLVLDFAFALPLNLFKATIELCS---THANDASALRILFSSLLILSKLFYSLNFODLPEFFEDNMSVGMISMH 252

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi 50302207 | ref | XP_451037.1 | KYLNYQNPILLEDNTEDEEASVLSKVKASIAELIQLYISRYQEEFDPMDVDFNQITWNLLVSLTPPKYDILVSKCMFTVAVARVPKYFELFNTESAMNSIIEKIVLNPVTLRESDEELFEDDPIEYIRRDLEGSDDTRRRACDPLKE 387
gi 45198791 | ref | NP_985820.1 | KYLADNPILLEDETEDEEASVTVKVKSSIAELVQLYISRYEDVDFGPMVEQFIQITWNLLVSLTCKPKYDILVSKCLSMFAVARIPIRYNLFNNEAAINSVTEIKIILPNVTLRSDVLFEDDPIEYIRRDLEGSDDTRRRACDPLKE 401
gi 6321198 | ref | NP_011276.1 | KYLSYSNPILLEDDTEDEEASVILKVKSSIQELVQLYITRYEDVDFGPMINEFIQITWNLLVSLTCKPKYDILVSKCLSMFAVARIPIRYNLFNNEAAINSVTEIKIILPNVTLRSDVLFEDDPIEYIRRDLEGSDDTRRRACDPLKE 387
gi 145607115 | ref | XP_361520.2 | TYLSYSNPILLDG---DDEEETVIMVKSDICSVLTLFYSKFDFFGNIAQEFIPAVVHLLSSIGMEKRVLDGLVSKALQFLAVRIPKYFEIFNNEAAINSVTEIKIILPNVTLRSDVLFEDDPIEYIRRDLEGSDDTRRRACDPLKE 435
gi 32405662 | ref | XP_323444.1 | KYLSYANPFLDD---DEEATPIEILKSDICDALHLFVTKYDFFGGYDFNITSNVNVLLSIVGPKRVDVLSKALHFLAVASVRRHQAIFNNEAAINSVTEIKIILPNVTLRSDVLFEDDPIEYIRRDLEGSDDTRRRACDPLKE 386
gi 19112322 | ref | NP_595530.1 | NQFTVNPBLEG---DEEETNVLKVKASICEVELYITRYEVEFT-MLYDFQVNTWLLTLPDEKVDGLVGMAMFLAVIRIKHAEFQQDVLQQLFILLVLPNLCILRESDEELFEDDPIEYIRRDLEGSDDTRRRACDPLKE 383
gi 24584736 | ref | NP_523588.2 | QLAADVPILRTA---DDHDAVLEHLKASVCENICLYAKKYDEEFKPMQEVAVAVWELLVKKSHIHKYDALVSNALRFLSVAERTHYRHLFEDPNVLASICEKVIIPNDFRVSDEELFEDDPIEYIRRDLEGSDDTRRRACDPLKE 395
gi 31204951 | ref | XP_311424.1 | GLLTVDFVCLKTD---DDHDAVLEHLKASVCENICLYAKKYDEEFKPMQEVAVAVWELLVKKSHIHKYDALVSNALRFLSVAERTHYRHLFEDPNVLASICEKVIIPNDFRVSDEELFEDDPIEYIRRDLEGSDDTRRRACDPLKE 395
gi 62460562 | ref | NP_001014933.1 | TLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 34860723 | ref | NP_342582.1 | TLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 12963737 | ref | NP_076054.1 | TLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 114682541 | ref | XP_001166085.1 | TLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 73992217 | ref | XP_853206.1 | TLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 293
gi 29029559 | ref | NP_001307.2 | TLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 118100584 | ref | XP_417389.2 | SLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 41393069 | ref | NP_958858.1 | NLLTLDNKLQTD---DEEEAGLLELLKSKICDNaALYAQKYDEEFQVLPFRFVAIWNLLVTTGQEVKVDLLVSNAIQFLASVCERPHYKNLFDONTLTSSICEKVIIPNMEFRAADEEAFEDNSEYIRRDLEGSDDTRRRACDPLVG 392
gi 15226001 | ref | NP_182175.1 | KYLSYNPALLES---EEGLTLVDDLRAAICENINHYIEKNEEPEQGLNEFAVVMVTLRDVSKSPSRDLAATAIKFLTSVSTSVHHALPAGDNVKEICQSIIVIPNVSRLVEDEEIFEMNYIFIRRDMEGSDVDRRRACDPLKE 399
gi 115435528 | ref | NP_001042522.1 | -----M 1

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 50302207 | ref | XP_451037.1 | LKEKNESLVTVNVVMVHIKSPFEEYNNQIILNWKHKDLKMLYFLSLAINGKVTNA-GVTSINVMLDVVEFFKSDVVPD*LLN-Q-QAHPILRVDIAIKYVVFNRNOLSKQEQLIEILPVMMAKFLDQKEVVVYTAATIERVFSMRQSAT---- 530
gi | 45198791 | ref | NP_985820.1 | LKEKNESLNLNIVLSHIKKFFKQYHHPQENWKYKDLQCVYLFSLAVKGNVTS-GVSSINAMLDVVDVDFKVEVMSDLNG-H-VPHVILRVDIAIKYIITFRNQTKEHLVQIILPVMANFLDQSEVVVYTAAVIERILSIREFNP---- 544
gi | 6321198 | ref | NP_011276.1 | LKEKNELVNLNIFLAHMKGFVDQYMSDPEKNWKFQDLVLYLFLALANGNINA-GVSSINMLNVDFDFKTEAPLDTNN-IPIHILRVDIAIKYITFRNOLTKAQLIELMPLATFLODEVVVYTAATIERILSIREFNP---- 531
gi | 145607115 | ref | XP_361520.2 | LQENDDKLVTVQVVGQYINHY--LQDAD---WKSXDIAVYLYLSIAAKGAVTAARGVQTVPHVNVDFVQQHITAGDLIKDE-GVEPIKRVNAIKYILNFRNOLSKQEQLIEILPVMMAKFLDQKEVVVYTAAVIERVFLITNEQ---- 573
gi | 32405662 | ref | XP_323444.1 | LLDLDFEALVTVQVSKYINHLKMGKTD---WKAKDTAVYLFALAAKGAVTAAGVQVTVSFVNVDFVQQHITAAADLVAA---GGEPFKVDAIKYILNFRNOLSKQEQLIEILPVMMAKFLDQKEVVVYTAATIERVFLITDDQ---- 525
gi | 19112322 | ref | NP_595530.1 | LLDHFDQKIISVVTTHINANLQOFSNPLLEWKKYVAALQFLSALAIKGQSTRL-GVTSINMLNVDFVAFVENNPKDLPDLPAGVIPHVMVLAEDIKYIITFRNOLSKQEQLIEILPVMMAKFLDQKEVVVYTAATIERVFLITDDQ---- 527
gi | 24584736 | ref | NP_523588.2 | LSINFQKIFGIFQYLERLMLTKYKFNPAWNRSKDQTAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 539
gi | 31204951 | ref | XP_311424.1 | LLQKFEAKVIEIFQYQLVQLLAKYAEANPAANWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 539
gi | 62460562 | ref | NP_001014933.1 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 538
gi | 34860723 | ref | XP_342582.1 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 536
gi | 12963737 | ref | NP_076054.1 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 536
gi | 114682541 | ref | XP_001166085.1 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 536
gi | 73992217 | ref | XP_853206.1 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 537
gi | 29029559 | ref | NP_001307.2 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 536
gi | 118100584 | ref | XP_417389.2 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 536
gi | 41393069 | ref | NP_958858.1 | LCKFFEGPVTGIFSGYVNSMLQYAKNPNVNNWKKHDAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 536
gi | 15226001 | ref | NP_182175.1 | LATNKTQVTEVVLEIQRLSSFSANPANWKKDKCAIYLVTSWASRGG-TQKHGITQANELVNLTEFFVNHILPDLKASVNEFFVPLKADGKIKYIMIFRNOVPEKHLVSIPLLNHLQAESIVVHTYAAHALERLFRMRGN---- 540
gi | 115435528 | ref | NP_001042522.1 |VIILMQK-PGATG---GGTPIVDMSFTSVIVPELQAPDNESPEMLKAGSLRFLKFKRDTIPKATALALPSPVIRFLIHESNVVHSYAATPIENLLIKDMVVPSEA 104



gi | 50302207 | ref | XP_451037.1 | ---SNQLVFKSDIASSEHLLLNFLSLKQKTIPEKLAENEFLMKAVHRVLLITEN-SLGAFALVNLQMLEILKIIISKNPSPIFTHYCFESIADVVIKY---HDSLSTLIDITIPVFLSILGDDIOEFIPYVFOVMAYILLLPA 672
gi | 45198791 | ref | NP_985820.1 | ---SNAMLFVTKNDLINSSEHLLLNFLSLKQKTIPEKLAENEFLMKAVHRVLLITEN-SIKPYAMDILNQLLEIILKIIIAKNPSPNPRFTHYFESVSVVIRYN---HNLNVLIDIMMIPILDLIAEDIOEFIPYVFOVMAYILLLPA 686
gi | 6321198 | ref | NP_011276.1 | ---SPAFIFHKEDISNSTEILLKLNIALILKRGSSPEKLAENEFLMRSIFRVLQTSQED-SIQPLPQLLAIFRIVITIMAKNPNPRFTHYFESIGAILNVTQ---RQNLPLLDVDSMMPTLTVFSEDIQEFIPYVFOVMAYILLLPA 672
gi | 145607115 | ref | XP_361520.2 | ---GQHLFRADIEPLAKDLEHLENLVEKD-RPPTKMQQENEFLMRCIMRVLIVKDGAVL-LLDVLDRLISINVIKPNPNPRFTHYFESIGAILNVTQ---ADASKLEAKLWEPLSIFLNEEDVTEFVYVFOVMAYILLLPA 714
gi | 32405662 | ref | XP_323444.1 | ---GQHLFRADIEPLAKDLEHLENLVEKD-TSAAKQENEFLMRCIMRVLIVKDGAVL-LLDVLDRLISINVIKPNPNPRFTHYFESIGAILNVTQ---NAPQVLLSRLWAPFYLNEEDVTEFVYVFOVMAYILLLPA 667
gi | 19112322 | ref | NP_595530.1 | ---VHIFSLLIAPHILPALNQLL-LIVESASTPKLAENDVLMKAVRRIIMSQE-AILPAASLLQHLKITEVSKNPNPKFPHNYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 670
gi | 24584736 | ref | NP_523588.2 | ---NAIVFGQOILAPVTEELISGLFATLSLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 679
gi | 31204951 | ref | XP_311424.1 | ---KQPIVTKELSPASAEIAGLFAAITVQ---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 679
gi | 62460562 | ref | NP_001014933.1 | ---SATLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 574
gi | 34860723 | ref | XP_342582.1 | ---NATLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 676
gi | 12963737 | ref | NP_076054.1 | ---NTTLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 676
gi | 114682541 | ref | XP_001166085.1 | ---NATLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 676
gi | 73992217 | ref | XP_853206.1 | ---NATLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 577
gi | 29029559 | ref | NP_001307.2 | ---NATLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 676
gi | 118100584 | ref | XP_417389.2 | ---NTTLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 676
gi | 41393069 | ref | NP_958858.1 | ---NTTLFTAABEIAAPVTEILLNFKALITLPL---GSGENEVVMKAIMRSPSVLQS-AAMPFGVALPRLTELLTQVAKNPRPQFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 676
gi | 15226001 | ref | NP_182175.1 | ---ARGNRYAAGDLSFLLQVNLNFKALITLPL---ESENQVLMKAIMRSPSVLQVADI---SAEVAGCTIGGLSILSEVCKNPKNPFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 680
gi | 115435528 | ref | NP_001042522.1 | NVITRAPRYVAADINPAHQIQLVNLNFKALITLPL---ESENQVLMKAIMRSPSVLQVADI---SAEVAGCTIGGLSILSEVCKNPKNPFNHYLFEIAGLIRLSLKSQVQVLSQLENALQVFNQVLLIEDVTEFVYVFOVMAYILLLPA 247



gi | 50302207 | ref | XP_451037.1 | GSMIPSPKQINEALLPAVWELGGVIPAATRLKDFV---KLEQSVYPD--LVPVLGVFORLISKSYDVHGFELLEYIFTFIPAEERLQPFKNIQAVLLORLQNSRTEKYLLKQVFLGVISCK----LGSDFVVOFIDEVQGLFQ 812
gi | 45198791 | ref | NP_985820.1 | GNNIPENVKQLCQPLLSPAVWEMKGNIPAVTRLLKDI---KIDASVYPD--LVPVLGVFORLIASKAYDTQGFELLEYFMNVIPLPSLQVFLKQIIVALLORLQNSRTEKYLLKQVFLGVISCK----LGSDFVVOFIDEVQGLFQ 826
gi | 6321198 | ref | NP_011276.1 | -ATIPESIKPLAQPLLAPNWLKGNIPAVTRLLKDFI---KIDSSVYPD--LVPVLGVFORLIASKAYEVHGFELLEYFMNVIPLPSLQVFLKQIIVALLORLQNSRTEKYLLKQVFLGVISCK----LGSDFVVOFIDEVQGLFQ 811
gi | 145607115 | ref | XP_361520.2 | -TVAPNPNFLNLLKPVLSHTVWETRGVNPVGCARFLSAIIVP---KVAEGIVAEGLHLEAILGIFORLLASKKTEPNADILEAVGSPASALDQVFGTIQSLKFKFETDVPFVFLVLSARGVEAGFGADYFKHAEALQAVFV 861
gi | 32405662 | ref | XP_323444.1 | -GSIPLGDFKALIDAVLQPLSPALWTRGNIPPLAKFLIAAIIIP---KATEEIVKKNFELLSLIFQSLNKGKTDQNAFDILEVICFSVASVLFVFGTIFLLIITKIKNFSVTRVASFYHLVLSARGVEAGLGDYFKHAEALQAVFV 814
gi | 19112322 | ref | NP_595530.1 | -EPLPDFVNLIQPCLSPALWDSKGNIPALVRLLRAMIF---RGPQIFLSKNKFEVPLVGFQKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 816
gi | 24584736 | ref | NP_523588.2 | TGTIPEPYNALFPCLLSPALWDRGNVPLIRLISAFKQSAQIQ---ALGKLSGLLGFQKMIASKANDHEGFYLLQNLISYPAETQNLNRFIFGLLQSLKSKPKYLSGIIFFSFYVVIK---TCGSSQMAOLDIETQNLNFG 822
gi | 31204951 | ref | XP_311424.1 | KSNIPDLYALFPCLLTPALWERPQNVPLIRLRLCAFVQASAQIS---ADDKLVGVGVFORKMIASKANDHEGFYLLQNLISYPAEELGRMRQIFSLFQRLSSKTKFKVRSFIVFLCLYTAR---VGPQALQIMESIQAQMGF 822
gi | 62460562 | ref | NP_001014933.1 | 574
gi | 34860723 | ref | XP_342582.1 | ---DIPSSYMALFPHLLQPVLWERTGNIPALVRLQAFLESGSNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 819
gi | 12963737 | ref | NP_076054.1 | ---DIPSSYMALFPHLLQPVLWERTGNIPALVRLQAFLESGSNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 819
gi | 114682541 | ref | XP_001166085.1 | ---DIPSSYMALFPHLLQPVLWERTGNIPALVRLQAFLESGSNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 819
gi | 73992217 | ref | XP_853206.1 | ---DIPSSYMALFPHLLQPVLWERTGNIPALVRLQAFLESGSNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 720
gi | 29029559 | ref | NP_001307.2 | ---DIPSSYMALFPHLLQPVLWERTGNIPALVRLQAFLESGSNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 819
gi | 118100584 | ref | XP_417389.2 | ---EIPSSYMALFPHLLQPVLWERTGNIPVLRLLQAVLERGASNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 819
gi | 41393069 | ref | NP_958858.1 | ---SIPSSYMALFPHLLQPVLWERTGNIPVLRLLQAVLERGASNTIATAAADKIPGLLGVFORKLIASKANDHOGFYLLNSIIEMPPESVDQYRQIFIFILLFQRLQNSKTKFKIKSFLVFINLYCIK----YCALAQEIFDGIQPKMFG 819
gi | 15226001 | ref | NP_182175.1 | ---TLPSPNYQIFLILLSPESWKRSSQVPAVLRLLQAFILQ---KAPHELVQENRISQVLFQKLVASPTDQGYVILNTIENLNDVSNAPYMKGVSALETRVONKTKVFKSFLVFINLYCIK----HGQAVLVEIMNTVQNIIT 821
gi | 115435528 | ref | NP_001042522.1 | ---PLSQNYMQLFVGLLSNAIWDPPCVPALVLRLLQAFILQ---KIPNELVQENRISQVLFQKLVASPTDQGYVILNTIENLNDVSNAPYMKGVSALETRVONKTKVFKSFLVFINLYCIK----YGPGLVLSVDAIQNIFM 828



gi	50302207	ref	XP_451037.1	QIWNVFDITTSKVGNLDRKIVLAGSLNIVVSGNLF--SKVGNLIVPLDIIVKACS-ESIANVN--EFVDYDAEIEISTFGSSYSRSLSSITEKPYDPLPTVDVHGLRKYTGIVLLEFNQKAGGNFLPQIQQLSEEGKNALTKL	957
gi	45198791	ref	NP_985820.1	QIWSNFIIITALPSIGNLLDRKLLALIGSLNIVVNGSLF--SRVGSLVVPMNVILTAVS-ESIVHK--EYINSEPSDEITTFGSSFSRSLGTAEKSFDPPLSHIDLTRGVKLYIANILTRLDP---SFMNEITMGLSEDAKKALNSL	967
gi	6321198	ref	NP_011276.1	QIWNFIITITLPTIGNLLDRKIALIGVLMVINGOFFQ--SKYPTLISSMNEIIEIASS-QSIANLKN--DYVDLDNLEIISTFGSHFSKLVSISEKPFDPLEIDVNNGVRLYVAEALNKYNAISGNTFLNITLLPQLTQENQVKLNQL	956
gi	145607115	ref	XP_361520.2	PLYLNVVLPVAGFARVPDRKLGVISYTKTLCDSTAF--ETVAKGWGFTCNHLELLELSN-PPKVTGAGDEFIIEADVDDIG-FGVGYTPLNTCKRGRDDDFPEITN--VQTWVSEYMKSANQRTGGKLATPVQRLEDAKAEALAKY	1004
gi	32405662	ref	XP_323444.1	PFYVQVVIPTREFARFSDRKLAVISYSKTLVSKAF--ERYMKGWGFICNALLELLEN-PPKVSAGAGDEILNEADVDDIG-FGIGFTPLSTCKRPPRDFEPEITD--VQWVGFDFLKAADKAHNGLIKAYASERLNDKAKAVLAP	957
gi	19112322	ref	NP_595530.1	QLMSTIILPQAQKLALPLDRKISALGLLRLCDLVLPADAIYENLIIPLLTCLIKLFEMPIEQAQTDADDEELFMDEIDADSMSFQASFSRLATGGKRVDFFPQITD--LKQYCATENMLANRNMGGRLSQIISHLPGDQOSVLSM	963
gi	24584736	ref	NP_523588.2	MLLDRVFIITENKILPKQDRKVMVAVGVTKLLIETPEILQ-QQYATFWPRLHLIDLDFER-PPKLMGLEIGETAGVAEPDAGYQVAFALQTHAQPNDQHLAEIK--DARQFLATLSKFAQARAGEFSLLSL-LEPEVKQVLOKY	966
gi	31204951	ref	XP_311424.1	MVVERVFIIPDINKVSGELEGKIVSVGITKLLCECPMILA-EFVLEWFPQLLQVIVQIFEL-PPD--EASIDGDNFIEIDVPGYQAAYSQLNFAQSKFVDFLPDVG--NVRQHLVONLQGLAQANGGKVRTLIAA-LPADHQEALOKY	963
gi	62460562	ref	NP_001014933.1	-----	574
gi	34860723	ref	XP_342582.1	MVLEKIIIPETQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DSIPDEEHFIDIEDTPGYQAFSOLFAGKKEYPVVGQTVN--NPRVHLAQLHRLSTACPRVPSMVSLSNAEALQYLOGY	962
gi	12963737	ref	NP_076054.1	MVLEKIIIPETQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DSIPDEEHFIDIEDTPGYQAFSOLFAGKKEHDPVGMVN--NPKIHLAOSLHKLSTACPRVPSMVSLSNAEALQYLOGY	962
gi	114682541	ref	XP_001166085.1	MVLEKIIIPETQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DTIPDEEHFIDIEDTPGYQAFSOLFAGKKEHDPVGMVN--NPKIHLAOSLHKLSTACPRVPSMVSLSNAEALQYLOGY	962
gi	73992217	ref	XP_853206.1	MVLEKIIIPETQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DTIPDEEHFIDIEDTPGYQAFSOLFAGKKEHDPVGMVN--NPKIHLAOSLHKLSTACPRVPSMVSLSNAEALQYLOGY	863
gi	29029559	ref	NP_001307.2	MVLEKIIIPETQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DTIPDEEHFIDIEDTPGYQAFSOLFAGKKEHDPVGMVN--NPKIHLAOSLHKLSTACPRVPSMVSLSNAEALQYLOGY	962
gi	118100584	ref	XP_417389.2	MVLEKIIIPETQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DTIPDEEHFIDIEDTPGYQAFSOLFAGKKEHDPVGMVN--NPKIHLAOSLHKLSTACPRVPSMVSLSNAEALQYLOGY	962
gi	41393069	ref	NP_958858.1	MVVERVIVPEVQKVSQVSGNVEKKICAVGITKLLTECPPMMD-NEYTKLWTPLLQSLIGLFL-PEP---DSIPDEEHFIDIEDTPGYQAFSOLFAGKKEHDPVGMVN--NPKIHLAOSLHKLSTACPRVPSMVSLSNAEALQYLOGY	962
gi	15226001	ref	NP_182175.1	AIVVHFVWIPNKLKIMSGMEVKLTAVAATRLICETPALLD-PSAAKLWGKMLD-IVTLVSR-PEQERVLDPE--MPEISENVGYTAAVFKLHAGKKEEDPLKDIKD--PKQFLVAIVSRLSSASPRVFPQIIGENLEQANQTALIQ	963
gi	115435528	ref	NP_001042522.1	IILQRFWIPNLFKIKTIVEVKLTSVASTKILICESALLLD-GAAAQVWGKLLD-IVALLSR-TDQDGAQQDQNDGADADSRISGYSVSVFVRLQYAGKSEDDLLKEVND--PKQFLVTLATLSAQSPGRFPIIEQNVDPAKNGALIQ	533



gi	50302207	ref	XP_451037.1	CTI-----	960
gi	45198791	ref	NP_985820.1	GP-----	969
gi	6321198	ref	NP_011276.1	LVGN-----	960
gi	145607115	ref	XP_361520.2	LS-----	1006
gi	32405662	ref	XP_323444.1	LM-----	959
gi	19112322	ref	NP_595530.1	GYVI-----	967
gi	24584736	ref	NP_523588.2	CDQAGVRIA	975
gi	31204951	ref	XP_311424.1	CAQSGVQIA	972
gi	62460562	ref	NP_001014933.1	-----	574
gi	34860723	ref	XP_342582.1	LQAASVTLL	971
gi	12963737	ref	NP_076054.1	LQAASVTLL	971
gi	114682541	ref	XP_001166085.1	LQAASVTLL	971
gi	73992217	ref	XP_853206.1	LQAASVTLL	872
gi	29029559	ref	NP_001307.2	LQAASVTLL	971
gi	118100584	ref	XP_417389.2	LQAASVTLL	971
gi	41393069	ref	NP_958858.1	LQAASVTQLV	971
gi	15226001	ref	NP_182175.1	CNAVYNGIA	972
gi	115435528	ref	NP_001042522.1	CAAVNTIV	542

