

gi | 88900517 | ref | NP_082385.3 | -----MSQVPTIYSDAPDFINFSLLDAEEDTENIDSWFDEKANLENKFLRQSGIGEPFGKNSLRKAKLQCGFVPLKAVDNTYHKEEKENLQKQSIPTNSDCSLLDAKRAVGNTPVPPORRSLRLSAQKDLQEKKN 136
gi | 34858998 | ref | XP_230735.2 | -----MAQVPTIYSDAPDFINFSLLDAEEDTENIDSWFDEKANLENKFLRQSGIGEPFGKNSLRKAKLQCGFVPLKAVDNTYHKEEKENLQKQSIPTNSDCSLLDAKRAVGNTPVPPORRSLRLSAQKDLQEKKN 136
gi | 20127519 | ref | NP_036244.2 | -----MSQVKSYSYDAPDFINFSLLDDEGDTQNIIDSWFEKANLENKLLGKNGTGGGLFOGKTLPRKANLQCAIVPLKAVDNTYHKEEKENLVEQSIPTNSACSSLEVEAAIIRKTPAOPORRSLRLSAQKDLQEKKH 136
gi | 114681424 | ref | XP_001153777.1 | -----MSQVKSYSYDAPDFINFSLLDDEGDTQNIIDSWFEKANLENKLLGKNGTGGGLFOGKTLPRKANLQCAIVPLKAVDNTYHKEEKENLVEQSIPTNSACSSLEVEAAVSRKTPAC--LRRSLRLSAQKDLQEKKH 135
gi | 73991555 | ref | XP_850934.1 | -----MSQVKTISYSDAPDFINFSLLDDEDAQNIIDSWFEKANLENKFSGKNGIAGLFQDKTLPRKPNQCAIVPLRPVNTYHKEEKENLVEQSIPTNSICSSLEVKGTTKNTVPPORRSLRLSAQKDLQEKKH 136
gi | 149642811 | ref | NP_001092368.1 | -----MSQVKTISYSDAPDFINFSLLDDEEDMHIIDSWFEKANLENKFTGKDTGGGLYQKTLPRKANLHR--DVPLRPVNTYHKEEKENLVEQSIPTNSICSSLEVKGTTKNTVPPORRSLRLSAQKDLQEKKH 135
gi | 45383291 | ref | NP_989768.1 | ----------MGRYSFDVFNPCINFALLSD--DVHNDWFWDFQCANLENIPPAEN--LAKLVNSPFAFKLTLSSVLSQMGTKSENCEDEKVELETVVIVTGLSLSWRVTVAEAPFQAGRRPAAKQKQKTPA 130
gi | 145362223 | ref | NP_973754.2 | -----MEAAAEESVSLTVLTVMDVTEFLAP--RWFDFVNGETDESRRAELWFLSALSCAPSE-----SVPRIK--ARRSKFLVAMENAE-----EETLKDKEVLEVVIVTGLSLSQFQKAKAEVAPSKASTVKFSRISSKDAVNNKT 135
gi | 115472277 | ref | NP_001059737.1 | -----MATDANPEAAAPPQLLVDEGEYFCAP--KFFDFVCDTEEEIRAARWFEASASHAPS-----FAPRIKESRAEVKIESLCDFDAEPIPKVEVAVEAAGSAANPQNSDGNVQONKQDSIKLVHEANPEENCVLDGDHKEESD 140
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 88900517 | ref | NP_082385.3 | -----HVASVEMKAKRCVAP--ATDCPPQKRMKVSCHKKLEEEEEE--GSAPATSRKNERETLEKAKGKHTVPGVP-----PAREKVLKSTEEQIEKRLRMOQEVVELRKNNEEFKLLALAGPGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 277
gi | 34858998 | ref | XP_230735.2 | -----HVASVEMKAKRCTAP--HTDVPNPKMKVSHKHKPEEEEEE--GSAPATSRKDD--ETLERAKGKHTVPAVP-----PAREKTVKSTEEQIEKSLRMOQEVVEMRKNNEEFKLLALAGPGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 275
gi | 20127519 | ref | NP_036244.2 | -----HV---KMKAKRCAIPVIIDIEILPSKMKMVSNNKKPEEEE--GSAHQDTAEKNASSPEKAKGRHTVPCMP-----PAKQKFLKSTEEQIEKSMKMOQEVVEMRKNNEEFKLLALAGIGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 275
gi | 114681424 | ref | XP_001153777.1 | -----HV---KMKAKRCAIPVIIDIEILPSKMKMVSNNKKPEEEE--GSAHQDTAEKNASSPEKAKGRHTVPCMP-----PAKQKFLKSTEEQIEKSMKMOQEVVEMRKNNEEFKLLALAGIGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 274
gi | 73991555 | ref | XP_850934.1 | -----G---KMKAKRCAIPALIHIPPSSKMKMVSNNKKPEEEEGS--HQDTSKKHESPEKAKGRHTVSCIQ-----PVRQKTLKSTEEQIEKSMKMOQEVVEMRKNNEEFKLLALAGIGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 276
gi | 149642811 | ref | NP_001092368.1 | -----HV---KMKAKRCAIPVIINFEPPSKMKMV-----KQILKSTEEQIEKSMKMOQEVVEMRKNNEEFKLLALAGIGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 273
gi | 45383291 | ref | NP_989768.1 | -----RVR---VEKNDTILAIKEAPEAKMKMKISSKKEKLTQVS--PKKLLHHPDLS--PARGKNTLTPS--PMLTKNLMAGLTKLQEVEMRKNNEEFKLLALAGIGQPVKKSSTQVTKVDFHFLIDERIKQHPKNC 273
gi | 145362223 | ref | NP_973754.2 | -----VDADDFTEPFDNETRPACTPK-----PMPQSLGAKSVDLK-----KQATARKIASLKNPSTLRKNSQ--AKGSHKSKVGEINLNNTIAITNLIQENIAVKKRQKLDGKRSQILNPK 247
gi | 115472277 | ref | NP_001059737.1 | -----AMLESPPAEDEKESPKSFVPSNAKSDVASSTPKIQRP--PPVKAHTVTPCCKLTVKTEAF--PKVQ-----ATNSSRGLAPLITGSRAPHSALK--SMSVSRSVLKCPRRELLAGKAATAANEIADENAVKKRQKLDGKRSQILNPK 281
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 88900517 | ref | NP_082385.3 | -----EYKQVNFMSSELKHS--PARTRGCTIIPFNLSGKKRTFDEAASYVPLAQQVEAFHKRTPNRYHLRNRK--DES--LLPSK--VNKIARDPQPILOTKYRTRAVTCKSTAEQAELEKLOQVFKARELDPRIFFESGPILPKRA 422
gi | 34858998 | ref | XP_230735.2 | -----EYKQVNFMSSELKHSSTPARTRGCTIIPFNLSGKKRTFDEAASYVPLAQQVEAFHKRTPNRYHLRNRK--DES--LLPSK--VNKIVRDPQPILOTKYRTRAVTCKSTAEQAELEKLOQVFKARELDPRIFFESGPILPKRA 420
gi | 20127519 | ref | NP_036244.2 | -----EYKQVNFMSSELKHS--PARVTKGCTIVKPFNLSGKKRTFDETVSYVPLAQQVEAFHKRTPNRYHLRNRK--DDINLLPSK--SVTKICRDPQTPVLOTKHRARAVTCKSTAELEAELEKLOQVFKARELDPRIFFESGPILPKRA 422
gi | 114681424 | ref | XP_001153777.1 | -----EYKQVNFMSSELKHS--PARVTKGCTIVKPFNLSGKKRTFDETVSYVPLAQQVEAFHKRTPNRYHLRNRK--DDINLLPSK--SVTKICRDPQTPVLOTKHRARAVTCKSTAELEAELEKLOQVFKARELDPRIFFESGPILPKRA 421
gi | 73991555 | ref | XP_850934.1 | -----EYKQVNFMSSELKHS--PARVTKGCTIIPFNLSGKKRTFDETVSYVPLAQQVEAFHKRTPNRYHLRNRK--DDITLLPSK--AGLKICRDPQTPVLOTKQRTFVPLVYKAAADQAELEKLOQVFKARELDPRIFFESGPILPKRA 423
gi | 149642811 | ref | NP_001092368.1 | -----EYKQVNFMSSELKHS--PARVTKGCTIVKPFNLSGKKRTFDETVSYVPLAQQVEAFHKRTPNRYHLRNRK--DDIMPLPSK--VVRICRDPQTPVLOTKHRTRFVPLVYKAAADQAELEKLOQVFKARELDPRIFFESGPILPKRA 379
gi | 45383291 | ref | NP_989768.1 | -----EYKQVNFMSSELKHS--PMMRMPKGTVPKPFNLSGKKRLEDTSSEVSVLAQQVEAFQKRTPSRYHLRNRK--SDEGPAPAKP--VKARLTNPKTPVLOTKHRTRFVPLVYKAAADQAELEKLOQVFKARELDPRIFFESGPILPKRA 420
gi | 145362223 | ref | NP_973754.2 | -----PAILLHKTRNGLVNTGFNLCPSTVTKHTKNGRQVYVREQLAPVLSAELMKKFTQSTRDLVQN-----RPLKTLTRKPEPEFVTSQRARPLRVKSSAELREEMLAKIP--KFRARPNKIIAAPALPAPR 373
gi | 115472277 | ref | NP_001059737.1 | -----TRILPHKGRGGGLAGS--EMSLSAMRKHRRDS--HSLKEVTHYISAAMVVKFESGRELAI--PHNRSLSHEDAAIALQRRKMLMLTRPKPEFQTSRHRVAVRVKSSAELREEMLAKIP--KFRARPNKIIAAPALPAPR 419
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 88900517 | ref | NP_082385.3 | -----PVKPPTPVGFDLIEKRIHERESKSKKTEDEQEFHRSRPCPTKILEDDVVGVEPKKVLPAIVPKSPVFALKNR-----IRVPIK--DEEEKFPV--VIAQOPVPHYGVVYPKPIAABRNVE 533
gi | 34858998 | ref | XP_230735.2 | -----PVKPPTPVGFDLIEKRIHERESKSKKPEDEQEFHRSRPCPTKILEDDVVGVEPKKVLPAIVPKSPVFALKNR-----IRVVKDEEEEPV--VIAQOPVPHYGVVYPKPIAABRNVE 532
gi | 20127519 | ref | NP_036244.2 | -----PVKPPTEPIGFDLIEKRIQERESKSKKTEDEHFHRSRPCPTKILEDDVVGVEPKKVLPAIVPKSPAFALKNR-----IRMPTKDEEEEPV--VIAQOPVPHYGVVYPKPIAABRNVE 534
gi | 114681424 | ref | XP_001153777.1 | -----PVKPPTEPIGFDLIEKRIQERESKSKSDEHFHRSRPCPTKILEDDVVGVEPKKVLPAIVPKSPAFALKNR-----IRMPTKDEEEEPV--VIAQOPVPHYGVVYPKPIAABRNVE 533
gi | 73991555 | ref | XP_850934.1 | -----PVKPPTPVGFDLIEKRIQERESKSKSDEHFHRSRPCPTKILEDDVVGVEPKKVLPAIVPKSPAFALKNR-----IRMPTKDEEEEPV--VIAQOPVPHYGVVYPKPIAABRNVE 535
gi | 149642811 | ref | NP_001092368.1 | -----PVKPPTPVGFDLIEKRIQERESKSKLEEHYEFHRSRPCPTKILEDDVVGVEPKKELPAIVPKSPAFALKNR-----IRMPTKDEEEEPV--MIRAQOPVPHYGVVYPKPIAABRNVE 491
gi | 45383291 | ref | NP_989768.1 | -----PVKELTQPIGFLEKRIQDRNKKQDEEHFHFHRSRPCPTKILEDDVVGVEPKKVLPAIVPKSPVFASKSR-----IRMTSRDEEKKEVEVVIKAHMPHYGVVYPKPIAABRNVE 533
gi | 145362223 | ref | NP_973754.2 | -----SPHILPEQERHLQMARANQHAETSSIASTEVSQKHNDQKHLLTEPKSVPLQITMLRARPITAKTAELEQEELEKAPKFKAKPLNKKIFESKGMGIFCNTKHHITIPQEFHATDERISRPEVLDIFDKLILNLECHEKPLPNTA 523
gi | 115472277 | ref | NP_001059737.1 | -----KAPQLPEFNEFHLMKERA--TRHADTCEASSVGTIRVSS--LHLTWLLISVCKFFLLVS-----LLEI--EENLVEHRAVERADFDHKL 477
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 88900517 | ref | NP_082385.3 | -----VCPFFSFDTRDKERLOLEKIKEMQKGE-----VPKFKALPVPHFDITINLPEKVKVNTQAEPSLETDKRGAYKAEWKHOLEEBEQKQKDAACFKARPNTVIFQEPFVPKKEKKSAAENPSSGLVQEPFOLATEKRAKERQLEKMK 677
gi | 34858998 | ref | XP_230735.2 | -----VCPFFSFDTRDKERLOLEKIKEMQKGE-----VPKFKALPVPHFDITINLPEKVKVNTQAEPSLETDKRGAYKABIWKHOLEEBEQKQKDAACFKARPNTVIFQEPFVPKKEKKSAAENPSSGLVQEPFOLATEKRAKERQLEKMK 676
gi | 20127519 | ref | NP_036244.2 | -----ICPFSSFDSDRDKERLOLEKIKELQKGE-----VPKFKALPLPHFDITINLPEKVKVNTQEPPELCTDRRGALKAQTKWHOLEEBELROOKEAACFKARPNTVISQEPFVPKKEKKSAAEGLSGLVQEPFOLATEKRAKERQLEKMK 678
gi | 114681424 | ref | XP_001153777.1 | -----ICPFSSFDSDRDKERLOLEKIKELQKGE-----VPKFKALPLPHFDITINLPEKVKVNTQEPPELCTDRRGALKAQTKWHOLEEBELROOKEAACFKARPNTVISQEPFVPKKEKKSAAEGLSGLVQEPFOLATEKRAKERQLEKMK 670
gi | 73991555 | ref | XP_850934.1 | -----ICPFSSFDSDRDKERLOLEKIKELQKGE-----VPKFKALPLPHFDITINLPEKVKVNTQEPPELCTDRRGALKAQTKWHOLEEBELROOKEAACFKARPNTVISQEPFVPKKEKKSAAEGLSGLVQEPFOLATEKRAKERQLEKMK 679
gi | 149642811 | ref | NP_001092368.1 | -----ICPFSSFDSDRDKERLOLEKIKELQKGE-----VPKFKALPLPHFDITINLPEKVKVNTQEPPELCTDRRGALKAQTKWHOLEEBELROOKEAACFKARPNTVISQEPFVPKKEKKSAAEGLSGLVQEPFOLATEKRAKERQLEKMK 635
gi | 45383291 | ref | NP_989768.1 | -----VCPFFSFDSDRDKERLOLEKIKELQKGE-----VPKFKALPLPHFDITINLPEKVKVNTQEPPELCTDRRGALKAQTKWHOLEEBELROOKEAACFKARPNTVISQEPFVPKKEKKSAAEGLSGLVQEPFOLATEKRAKERQLEKMK 670
gi | 145362223 | ref | NP_973754.2 | -----VCPFFSFDSDRDKERLOLEKIKELQKGE-----VPKFKALPLPHFDITINLPEKVKVNTQEPPELCTDRRGALKAQTKWHOLEEBELROOKEAACFKARPNTVISQEPFVPKKEKKSAAEGLSGLVQEPFOLATEKRAKERQLEKMK 665
gi | 115472277 | ref | NP_001059737.1 | -----PNPFLNKTEERGAKEKFKYMYKLDVVKARVPAKAPVPTIDYVVPVPPKPEPKQCTQPEPQLESVLRVHEEEMRREREERRRMETBEAQKRLFKAP--VIKEDPIVPEKVRMP-----LLEI--EENLVEHRAVERADFDHKL 477
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi		88900517		ref		NP_082385.3		AEVEAWKLOOLEEVROOEEEOOKEELARLRKELVHKANPIRKYAAVEVKSSLEPLTVPVSPKFSTRFQ-----	745
gi		34858998		ref		XP_230735.2		AEMEAWKLOOLAEVROOEEEOOKEELARLRKELVHKANPIRKYSAVEVKSSLEPLTVPVSPKFSTRFQ-----	744
gi		20127519		ref		NP_036244.2		AEVEACKAOOLEEARLQEEEOOKEELARLRRELVEHKANPIRKYQGLEIKSSDQPLTVPVSPKFSTRFHC-----	747
gi		114681424		ref		XP_001153777.1		AEVEACKAOOLEEARLQEEEOOKEELARLRRELVEHKANPIRKYQGLEIKSSDQPLTVPVSPKFSTRFHC-----	739
gi		73991555		ref		XP_850934.1		AEVEACKVQOLEEARHQEEEOOKEELARLRKELVHKANPIRKYQGVVEVKSSDQPLTVPVSPKFSTRFHC-----	748
gi		149642811		ref		NP_001092368.1		AEVEALKAOOLEEARQOEEEOOKEELARLRKELVHKANPIRKYQGVVEVKSSDQPLTVPVSPKFSTRFHC-----	704
gi		45383291		ref		NP_989768.1		ANLEARREKLEQVROOEEEREKEELAKLRQELVHKANPIRRYRSVEVKPSDQPLTMPKSPNFSDRFRC-----	739
gi		145362223		ref		NP_973754.2		KEKENQYKRYRESSEAAKMVEEERALKQMRKTMVPHARPVPNFNPKPFLPKSNKGTTKAKSPNLRVIKRTERRIMMARPIISAATSASAGQMR	758
gi		115472277		ref		NP_001059737.1		-----	477

.....760.....770.....780.....790.....800.....810.....820.....830.....840....

