

gi|38373673|ref|NP_055073.2|MPIRPDLOOLEKCIDALRKNDFKPLKLLQIDICEDVKIKCSKOFFHKVDNLICRELNKEIDHNVSAILLVSVGRGCKNIVLGOAGLLMIKQGLIQKMWAVFEKSKDITIQSGNSKDEAVLNMIEDLVDLLLVHIDVSDGKKQVVESS 150
gi|114682866|ref|XP_514753.2|MPIRPDLOOLEKCIDALRKNDFKPLKLLQIDICEDVKIKCSKOFFHKVDNLICRELNKEIDHNVSAILLVSVGRGCKNIVLGOAGLLMIKQGLIQKMWAVFEKSKDITIQSGNSKDEAVLNMIEDLVDLLLVHIDVSDGKKQVVESS 150
gi|73992653|ref|XP_534470.2|MPIRPDLOOLEKCIDALRKNDFKPLKLLQIDICEDVKIKCSKOFFHKVDNLICRELNKEIDHNVSAILLVSVGRGCKNIVLGOAGLLMIKQGLIQKMWAVFEKSKDITILRRGNSKDEAVLNMIEDLVDLLLVHIDVSDGRRQVVESS 150
gi|109689713|ref|NP_796165.2|MPVVRPDLOOLEKCIDALRKNDFKPLKLLQIDICEDVKIKCSKOFFRKLDDLICRELNKKDICTVSSILLISIGRCSKNIFILGOTGLQMIKQGLVQKMWVWFENSKBIILNQOSKDEAVMMNIEDLVDLLLVHIDVSDGKGNQVLES 150
gi|18543333|ref|NP_570091.1|MPVVRPDLOOLEKCIDALRKNDFKPLVLLQIDICEDVKIKCSKOFFRKLDDLICRELHKKDICTISNILLISIGRCSKNIFILGOTGLQMIKQGLVQKMWVWFENSKBIILNQOSKDEAVMMNIEDLVDLLLVHIDVSDGKGNQVLES 150
gi|118100648|ref|XP_417396.2|-----MAPLQDHVVEKLVDEAFKDNFQALEKFLKKEEETILRCRQFMAKLDKLFIR-----WFEKARKLWVEAGPSKNEGLIKLADLDFDVLMMVVECKEGAYEVTES 103
gi|189535810|ref|XP_685048.3|1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|38373673|ref|NP_055073.2|FVPRICSLVIDSRVNICIQEIIKKMNAMLKMPDAR---KILSNQEMILMSSMGERILDAGDYDLOVGIVEALCRMTTEKQROELAHQWFSMDFIAKAFKRIKDSSEFETDCRIFLNLVNGMLGDKRR-VFTFPCLSAFLDKYELQIP 296
gi|114682866|ref|XP_514753.2|FVPRICSLVIDSRVNICIQEIIKKMNAMLKMPDAR---KILSNQEMILMSSMGERILDAGDYDLOVGIVEALCRMTTEKQROELAHQWFSMDFIAKAFKRIKDSSEFETDCRIFLNLVNGMLGDKRR-VFTFPCLSAFLDKYELQIP 296
gi|73992653|ref|XP_534470.2|FVPRICSLVIDSRVNICIQEIIKKMNAMLKMPDAR---KILSNQEMILMSSMGERILDAGDYDLOVGIVEALCRMTTEKQROELAHQWFSMDFIAKAFKRIKDSSEFETDCRIFLNLVNGMLGDKRR-VFTFPCLSAFLDKYELQIP 296
gi|109689713|ref|NP_796165.2|FIPQICALVIDSRVNFCCIQAALKMNLMLDRIPDAN---KILSNQEMILMSSMGERILDVGDYELQVGIVEALCRMTTEKRRQELAEWFSMDFIANAFKIKDCSEFETDCRIFLNLVNGMLGDKRR-VFTFPCLSAFLGKYELQIP 296
gi|18543333|ref|NP_570091.1|FIPQICALVIDSRVNFCCIQAALKMNLMLDRIPDAN---KILSNQEMILMSSMGERILDVGDYELQVGIVEALCRMTTEKRRQELAEWFSMDFIANAFKIKDCSEFETDCRIFLNLVNGMLGDKRR-VFTFPCLSAFLGKYELQIP 296
gi|118100648|ref|XP_417396.2|-----LLSHIGKLASDAKINIIIQEAARKLNAVLAEPTELKKKKILSSQEAASSMMIGVACRILKGGDYDLOVSLMEALCRMVSPARNEELADSWFTMTFVSAFKKIKDSSEFETDCRIFLNLVNGMLGDKRRVSYSPCLEAFLEKHELLMP 253
gi|189535810|ref|XP_685048.3|.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|38373673|ref|NP_055073.2|SDEKLEEFWIDFNLGSHLSFYIAG--DNDHHEAVTVPEEKVQIYSIEVRESKLLIILKNIIVKISKREGEKELLYFDASLEITNVQKIFGANKHRESIRKQGISVAKTSLHILFD---ASGSQILVPSQISPVGEEIVLSLKEKS 441
gi|114682866|ref|XP_514753.2|SDEKLEEFWIDFNLGSHLSFYIAG--DNDHHEAVTVPEEKVQIYSIEVRESKLLIILKNIIVKISKREGEKELLYFDASLEITNVQKIFGANKHRESIRKQGISVAKTSLHILFD---ASGSQILVPSQISPVGEEIVLSLKEKS 441
gi|73992653|ref|XP_534470.2|SDEKLEEFWIDFNLGSHLSFYIAG--DNDHHEAVTVPEEKVQIYSIEVRESKLLIILKNIIVKISKREGEKELLYFDASLEITNVQKIFGANKHRESIRKQGISVAKTSLHILFD---ASGSQILVPSQISPVGEEIVLSLKEKS 441
gi|109689713|ref|NP_796165.2|SDEKLEEFWIDFNLGSHLSFYIAG--DEEDHHEAVTVPEEKVQIYSIEVRESKLLIILKNIIVKISKREGEKELLYFDASLEITNVQKIFGANKHRESIRKQGISVAKTSLHILFD---ASGSQILVPSQISPVGEEIVLSLKEKS 441
gi|18543333|ref|NP_570091.1|SDEKLEEFWIDFNLGSHLSFYIAG--DNDHHEAVTVPEEKVQIYSIEVRESKLLIILKNIIVKISKREGEKELLYFDASLEITNVQKIFGANKHRESIRKQGISVAKTSLHILFD---ASGSQILVPSQISPVGEEIVLSLKEKS 441
gi|118100648|ref|XP_417396.2|-----MNVGNQDGEKFFLYFDSILKIEDVARKIYGLNCKEFSKQSMSEVAKTIVHIVFD---ESGSQILVPSQISPVGEEIVLSLKEKS 82
gi|189535810|ref|XP_685048.3|KDEKLEAFWIDFNLGSHLSFYIAG--DNDHHEAVTVPEEKVQIYSIEVRESKLLIILKNIIVKISKREGEKELLYFDASLEITNVQKIFGANKHRESIRKQGISVAKTSLHILFD---ASGSQILVPSQISPVGEEIVLSLKEKS 403
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|38373673|ref|NP_055073.2|KSPKPEFAK-PSKYIKNSDKGNRNSOLEKTIIPSKRKMSEASMIVSGADRYTMRSPVLFNNTSIPPRRRRIKPPLOMTSSAEKPSVQTSENRVDNAASLKSRSSEGRHRRDIDKHIKTAKVENTENKNVFEFNONFSELODVPIDSQ- 589
gi|114682866|ref|XP_514753.2|KSPKPEFAK-PSKYIKNSDKGNRNSOLEKTIIPSKRKMSEASMIVSGADRYTMRSPVLFNNTSIPPRRRRIKPPLOMTSSAEKPSVQTSENRVDNAASLKSRSSEGRHRRDIDKHIKTAKVENTENKNVFEFNONFSELODVPIDSQ- 589
gi|73992653|ref|XP_534470.2|NSQKEDAK-PPKNIKSSQVDGKNSOLEKTIIPSKRKMSEASMIVSGADRYTMRSPVLFNNTSIPPRRRRIKPPLOMTSSAEKPSVQTSENRVDNAASLKSRSSEGRHRRDIDKHIKTAKVENTENKNVFEFNONFSELODVPIDSQ- 588
gi|109689713|ref|NP_796165.2|DIQKKLVN-PLELGNSSS-----DEIITIPSKRKMSEASMIVSGADRYTMRSPVLFNNTSIPPRRRRIKPPLOMTSSAEKPSVQTSENRVDNAASLKSRSSEGRHRRDIDKHIKTAKVENTENKNVFEFNONFSELODVPIDSQ- 579
gi|18543333|ref|NP_570091.1|NLQKKLIN-PLELGNSSS-----DRDRKMSSEASMIVSGADRYTMRSPVLFNNTSIPPRRRRIKPPLOMTSSAEKPSVQTSENRVDNAASLKSRSSEGRHRRDIDKHIKTAKVENTENKNVFEFNONFSELODVPIDSQ- 584
gi|118100648|ref|XP_417396.2|KCKIKQLPGSQRSLNKNNDCKCKDGSFKITISCRKRMSEASVLPAPARFPTRSPLFISTSTP-SKGRFLPLPKMSSVERSSNAENGTIRKLNLYQQLTENGQCTSDN----- 192
gi|189535810|ref|XP_685048.3|ERKKEELRDLMMSKISCNVTSLSFHCENNQTAHVISAQSTPAAHTEQKTKSLKAEKLFH-KHIPVDKVVEMVQDDKNEEETFDKGVVDPQPVKRLSLISLGLWLSLSSIKRVSVSGSLLAGKDAKKCAMNGSSLPPQRL 552
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|38373673|ref|NP_055073.2|AAEKRDHTILPGVLDNICGNKIHSKWACWTPVTINIELCNNORASTSSGDILNODIVINKKLTQKSSSSISDHNSEGTGKVKYKKEQTDHIKIDKAEVEVCKKHNOQ-NHPKYSQKNTENAKQSDWPVESETTFKSVLLNKTIEESLI 738
gi|114682866|ref|XP_514753.2|PVEKRDAHALPGVLDNICGNKIHSKWACWTPVTINIELCNNORASTSSGDILNODIVINKKLTQKSSSSISDHNSEGTGKVKYKKEQTDHIKIDKAEVEVCKKHNOQ-NHPKYSQKNTENAKQSDWPVESETTFKSVLLNKTIEESLI 738
gi|73992653|ref|XP_534470.2|AVGKKKPVLPGLVYINICGNKMPKWSWCTPVTINIELCNNORASTSSGDILNODIVINKKLTQKSSSSISDHNSEGTGKVKYKKEQTDHIKIDKAEVEVCKKHNOQ-NHPKYSQKNTENAKQSDWPVESETTFKSVLLNKTIEESLI 736
gi|109689713|ref|NP_796165.2|AVGKVKPVLPGLVD-ISKNTIHSRWACWTPVTITIKLNNORSRALPGDICTODTGVNKKCKKQKSVS---DDDSEETQKGVYKSKDVIKCNKSE--EAEFCERNIDEG-NHPKYSQKNTANAKKNDWHIESETTFKSVLLNKTIEESLI 722
gi|18543333|ref|NP_570091.1|AVEKVKPVLPGLVD-ISKNTIHSRWACWTPVTITIKLNNORSRALPGDICTODTGVNKKCKKQKSVS---DDDSEETQKGVYKSKDVIKCNKSE--EAEFCERNIDEG-NHPKYSQKNTANAKKNDWHIESETTFKSVLLNKTIEESLI 727
gi|118100648|ref|XP_417396.2|-----EPCETECNLR----- 202
gi|189535810|ref|XP_685048.3|SPAQCASRILP-----QKDLHTQLQRLEEVLKQVQVTDGHAVERGSLASKTAGQEKEDTEKSVKSLPAKSTOORRKSQVGNISDHDNITDAADSMVKMISRH-----YKKGAKAASPFTNIA 668
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|38373673|ref|NP_055073.2| YRKKYILSKDVNTAICDKNPSASKNVQSHRKAELKELTSELNSWDSKQKMRKESKSGKEFTNVAESLISQINRKYKTKDDIKSTRKLKESLINSDFSNKPVVQLSKEKVKQKSYRKLKTTFVNVVTECPVNDVYVFNFLNGADDPPIIKLGIQ 888
gi|114682866|ref|XP_514753.2| YKKKYILSKDVNTAICDKNPSASKNVQSHRKAELKELTSELNSWDLRQKMRKESKSGKEFTDVAESLISQINRKYKTKDDIKSTRKLKESLINSDFSNKPVVQLSKEKVKQKSYRKLKTTFVNVVTECPVNDVYVFNFLNGADDPPIIKLGIQ 888
gi|73992653|ref|XP_534470.2| YRKKYILSKDVNTAICDKNPSASKNVQSHRKAELKELTSELNSWDLRQKMRKESKSGKEFTDVAESLISQINRKYKTKDDIKSTRKLKESLINSDFSNKPVVQLSKEKVKQKSYRKLKTTFVNVVTECPVNDVYVFNFLNGADDPPIIKLGIQ 886
gi|109689713|ref|NP_796165.2| YKKTCLVLSKDVNTAICDKSPSRRKSRNHTKSRKELMSLTSCELEDEIPVRENSKGRKFTGAESESLINQISRRYVNSPSMMSTRKLKPEPQDGGFSGKPPDLQFN--KVQRKSYRKLKATVVNVVTECPVNDVYVFNFLNGADDPPIIKLGIQ 869
gi|18543333|ref|NP_570091.1| YKKTCLVLSKDVNTAICDKSPSRRKSRNHTKSRKELMSLTSCELEDEIPVRENSKGRKFTGAESESLINQISRRYVNSPSMMSTRKLKPEPQDGGFSGKPPDLQFN--KVQRKSYRKLKATVVNVVTECPVNDVYVFNFLNGADDPPIIKLGIQ 873
gi|118100648|ref|XP_417396.2| -----KSKIRBEAELPERKGVCEGVLRKLLPEANGATEKQTSDRVQ-----INPVSVSRVYDVYVFNFLNGADDPPIIKLGIQ 273
gi|189535810|ref|XP_685048.3| STNRNLFNKSCGSSSTEKNAAKRSRLPKLDNKSQKPLQNTIEDIYAFTEDEPKISVKSDFVFNESSELSISLNRRNSAKRPALPKGTANAKKYLFDGTDTDNMDISWLSKANRPPK--PKVADYSRQPKATFPADSTFKSPYSVPA 817
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi|38373673|ref|NP_055073.2| EFQATAKEACADRSIRLVGPRNHDELKSSVKTDKDKIITNHOKNLFSDTETEYRCDDSKTDISWLREP--KSKPOLIDYSRNKNVNRHKSQKSS-----RSSLEKQSPSSKMTPSKNITKMKDKTIP 1010
gi|114682866|ref|XP_514753.2| EFQATAKEACADRSIRLVGPRNHDELKSSVKTDKDKIITNHOKNLFSDTETEYRCDDSKTDISWLREP--KSKPOLIDYSRNKNVNRHKSQKSS-----RSSLEKQSPSSKMTPSKNITKMKDKTIP 1010
gi|73992653|ref|XP_534470.2| EFQATAKEARVNSIKLIGLNRHDELTSKTKDKDKIITDPKNNLNFSDTETEYRCDDSKTDISWLREP--KSKPOLIDYSRNKNVNRHKSQKSSKSLFRFILLQLLFLKLEMLCWLIRPSSLEKQSPSSKMTPSKNITKMKDKTIP 1034
gi|109689713|ref|NP_796165.2| EFQATREASMDNSLKLIV--KNHDEHDFLTKDKDKRMLSSYEKKTLLSDTETEYRCDDSKTDISWLREP--KTK--RLMDYSRNKNVNRHKSQKSS-----RSSLEKQSPSSKMTPSKNITKMKDKTIP 987
gi|18543333|ref|NP_570091.1| YNQATREASMDNSIKLVVDRNRDRRSLKTKDERLSS--HERKTLFSDTETEYRCDDSKTDISWLREP--KSK--RLMDYSRNKNVNRHKSQKSS-----RSSLEKQSPSSKMTPSKNITKMKDKTIP 993
gi|118100648|ref|XP_417396.2| -----PKHFLSDTETEYRCDDSKTDISWLKSKAPKPIIDYSRNKNVNRHKSQKSS-----DPPCOMDAPKRAKPKKPECKKQSSVIDEIME 369
gi|189535810|ref|XP_685048.3| KPVKEQTKPKRKRQKQK---IAEHEHDKWQSSINNKITGRPRRAAALIKYREPSDSSQSQTESENAPPPKKAIVRVVPTQEI VSAHTTAQ-----EKRRKQSPVDTKQHEKNGRKTETAFABI 937
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi|38373673|ref|NP_055073.2| RIRLPRKATKTKKNYKDLNS--ESECEQEPFSHSFKENIPVKEENIHSRMKIVKLPKQKQKVFCAETEKELSKWKNSSLLKDAIRDNCIDLSPRSLSGSPSSIEVTRICIEKITEKDFTOFYDCITKSIIPYKTS--LESLSNSNSGVGG 1157
gi|114682866|ref|XP_514753.2| RIRLPRKATKTKKNYKDLNS--ESECEQEPFSHSFKENIPVKEENIHSRMKIVKLPKQKQKVFCAETEKELSKWKNSSLLKDAIRDNCIDLSPRSLSGSPSSIEVTRICIEKITEKDFTOFYDCITKSIIPYKTS--LESLSNSNSGVGG 1157
gi|73992653|ref|XP_534470.2| RIRLPRKATKTKKNYKDLNS--ESECEQEPFSHSFKENIPVKEENIHSRMKIVKLPKQKQKVFCAETEKELSKWKNSSLLKDAIRDNCIDLSPRSLSGSPSSIEVTRICIEKITEKDFTOFYDCITKSIIPYKTS--LESLSNSNSGVGG 1175
gi|109689713|ref|NP_796165.2| RIRLPRKATKTKKNYKDLNS--ESECEQEPFSHSFKENIPVKEENIHSRMKIVKLPKQKQKVFCAETEKELSKWKNSSLLKDAIRDNCIDLSPRSLSGSPSSIEVTRICIEKITEKDFTOFYDCITKSIIPYKTS--LESLSNSNSGVGG 1136
gi|18543333|ref|NP_570091.1| RIRLPRKATKTKKNYKDLNS--ESECEQEPFSHSFKENIPVKEENIHSRMKIVKLPKQKQKVFCAETEKELSKWKNSSLLKDAIRDNCIDLSPRSLSGSPSSIEVTRICIEKITEKDFTOFYDCITKSIIPYKTS--LESLSNSNSGVGG 1142
gi|118100648|ref|XP_417396.2| TRPKRQRAVQPKNYKDPSSSESESEYS--ACHYKREKSKVQKCVNEKNDGNQKDLNLEVPKTKVATCVNKAFIKSKNSTEQE-----IEMSPESPETEIMRCAERISECVTQDHTSSEGGPGLQKSPKENEISPFKGIS 511
gi|189535810|ref|XP_685048.3| QIQNRNDKQKQVSSPERLKVNKISWDRKKEAWARLSSLPASSPEKMSIEKLAIDLNSNITPLRSLSPITADSPLEPLIPKATQTSLSLCKIPRSKSAVIPSPLSITVSKTSRGSKSLPAVQVLSVPHVLSQSQPLSISKE 1087
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi|38373673|ref|NP_055073.2| TIKSPKNNKCNFLCASECSPIPRPLFLPRHTPKSNTIVNRKISSLVLTETQNSNSYSDVSSYSSSEERFMETESPHINENYIQSK-----REESHLSLSLSSSEGREKTWFDMPDCDATHVSGPTQHLRKRKIYIEDN--LSNS 1297
gi|114682866|ref|XP_514753.2| TIKSPKNNKCNFLCASECSPIPRPLFLPRHTPKSNTIVNRKISSLVLTETQNSNSYSDVSSYSSSEERFMETESPHINENYIQSK-----REESHLSLSLSSSEGREKTWFDMPDCDATHVSGPTQHLRKRKIYIEDN--LSNS 1297
gi|73992653|ref|XP_534470.2| PIKSPINSDK-KLCARESLSLIPQSLFLGNRS-----TSPLMSSEGRECIWCDMPDSTHVSDSIPIHICKRMYVEDN--LSSA 1252
gi|109689713|ref|NP_796165.2| RQSPRISETSAMCVKRSYSPASGPPFSPRHTPKSNTIVNRKISSLVLTETQNSNSYSDVSSYSSSEERFMETESPHINENYIQSK-----REGNHAASPLSLSSSEKIKEMWFDMPSENTHVSGPSQRGSKRMYLDEBDELNS 1277
gi|18543333|ref|NP_570091.1| HGKSPRISETSAMCVKRSYSPASGPPFSPRHTPKSNTIVNRKISSLVLTETQNSNSYSDVSSYSSSEERFMETESPHINENYIQSK-----REGNHAASPLSLSSSEKIKEMWFDMPSENTHVSGPSQRGSKRMYLDEBDELNS 1282
gi|118100648|ref|XP_417396.2| SNLCLKQKNTQNNYLNLSFMSVKKLIPGNKSFSPVLAAYLLNLSAVPHETCYCKNTEGVSSTHDAENLDFRHFQDKISTEGKQODIKPVIKNGEELSPVLSSESEVSWNQPCCGTHESGPTSHVFLKRRYKQCDT--ESH 660
gi|189535810|ref|XP_685048.3| TLNSPDLQHEQRAVKNKLSPASFERRSVNSLTIQSHKSLNMAALDELKLTPECKQKSDERAERFKSPSVIHTIIPCHIDDE-----DSEEDKENKAPSPSLKMKPRKLFVFNKYIWTTPSKGRNSKPLMKTQSSSE 1228
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi|38373673|ref|NP_055073.2| NEVEMEEKGER---RANLLPKKCLKIEDADHIIHKMSESVSSLSINDFSIPWETWQNEFAGIEMTYETVRLNSEFKRRNRIHMKLSYFTTQSWKTAQOHLRIMNHSSQDSRIKKLDKFOFIIIELENFKEDSQSLKDLKKEKFDVDF 1443
gi|114682866|ref|XP_514753.2| NEVEMEEKGER---RANLLPKKCLKIEDADHIIHKMSESVSSLSINDFSIPWETWQNEFAGIEMTYETVRLNSEFKRRNRIHMKLSYFTTQSWKTAQOHLRIMNHSSQDSRIKKLDKFOFIIIELENFKEDSQSLKDLKKEKFDVDF 1443
gi|73992653|ref|XP_534470.2| DEVELKEEGER---RVCLIPKRRKSNEDSVHHTYEVSGSISPLSINDFSIHGESWENELS-----EVMCSLSLAEFRFRKFTVRSQKIMDYFTKQSWKTAQOHLRIMNHSSQDSRIKKLDKFOFIIIELENFKEDSQSLKDLKKEKFDVDF 1393
gi|109689713|ref|NP_796165.2| NEAEVBAEAE---REHLLSKRCQWNSQHTFKTS-----LSVDFSVR-KDWQQLQG-----AGMFYDINSIDYKRRKTFDSQKIMDYFTKQSWKTAQOHLRIMNHSSQDSRIKKLDKFOFIIIELENFKEDSQSLKDLKKEKFDVDF 1413
gi|18543333|ref|NP_570091.1| SEAEVBAEAE---REHLLSKKLCORRHFFQHTSET---LSVDFSVR-KDWQQLQG-----AGMFYDINSIDYKRRKTFDTQKIMDYFTKQSWKTAQOHLRIMNHSSQDSRIKKLDKFOFIIIELENFKEDSQSLKDLKKEKFDVDF 1418
gi|118100648|ref|XP_417396.2| DEVEKKEEKKRRTKLPKRLKTDVAVTYRGYEN---LSVDFSVRPAALDWDIWEPSCSIDICQKIQKQKTEKIKKISRRKMRFAKQSLRAANQHLTIVNRLLCQRVQLDRFHFVLIQIELENFKEDSQSLKDLKKEKFDVDF-- 803
gi|189535810|ref|XP_685048.3| EEDIVVAENKR---RKKSVHSLNRRKFTISLIEVEVETLSCTRSCRHVSVADDLTQPAQEMRICHQFSDELKSKIKNRGRMMDLYTSQSLKIQHMSVHVQVHYSQRLEKQVLLSEIQSDVDVLRGMEELMAW 1375
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi		38373673		ref		NP_055073.2		EKIFQKFSAYQKSEQRLHLLKTSLAKSVFCNTDS	---	EEVFTSEMC	-----	LMKEDMKVLQDRLLK	---	DMLEEELLNVR	-----	ELMSVFM	SHERNANV	---	1530	
gi		114682866		ref		XP_514753.2		EKIFQKFSAYQKILLRLLHLLKTSLAKSVFCNTDN	---	EEVFTSEMC	-----	LMKEDMKVLQDRLLK	---	DMLEEELLNVR	-----	ELMSVFM	SHERNANV	---	1530	
gi		73992653		ref		XP_534470.2		EKIFQKFSAYQKSEQRPPLLLSEGCVSGQSSSERSPVYLD	---	EEVFTSEMC	-----	LMKEDMKVLQDRLLK	---	DMLEEELLNVR	-----	ELMSVFM	SHERNANV	---	1529	
gi		109689713		ref		NP_796165.2		EKLQKMRAYHRCEERERFRVLKSLDKSFLVYNSVY	---	EEVFTSEMC	-----	LMKANMKMLQDKLLK	---	EMHEEVLNIRR	-----	GLQSLFK	AHEGND	---	1500	
gi		18543333		ref		NP_570091.1		EKIVHKMRAFHQSERERFRALKTSLDKSLLVYNSVY	---	EENVLTSEMC	-----	LMKANMKMLQDKLLK	---	EMHEEVLNIRR	-----	GLQSLFK	AHEGND	---	1505	
gi		118100648		ref		XP_417396.2		-----	-----	-----	-----	-----	-----	EEELINVRR	-----	GLQTLFL	AEDGKF	---	825	
gi		189535810		ref		XP_685048.3		EKQTSAFHTYQEKRRRLQKFKSTIQNDVCDLKY	---	EEQIFLEMS	-----	SMKKNMKSVQERFFK	---	EMQDEDL	SVRR	-----	GLQAMFF	PASRF	---	1460
							1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....												

