

gi|31560812|ref|NP_033894.2| MDLSAVQIQEVONVLHAMQKILECPICLEELIKEPSTKCDHIFCKFCMLKLLN-QKKGPSQCPLCKNEITKRSLOQSTRFSOLAPELLRIMAFAELDTGMOLTINGFSFSK--RNNSCELNNEASIIQVGYRNRVRRLPQVEGNAIL 147
gi|6978573|ref|NP_036646.1| MDLSAVRIQEVONVLHAMQKILECPICLEELIKEPSTKCDHIFCKFCMLKLLN-QKKGPSQCPLCKNEITKRSLOQSTRFSOLAPELLRIDAFELDTGMOCANGFSFSK--KNSSELLENDASIIQVGYRNRVKLQIHSGSAIL 147
gi|6552315|ref|NP_009233.1| MDLSALRVVEEVONVINAMQKILECPICLEELIKEPSTKCDHIFCKFCMLKLLN-QKKGPSQCPLCKNDITKRSLOESTRFSOLVEELLKIIICAFQDITGLLEYANSYNFYAK--ENNSPEHLKDEVSIQSMGYRNRKRRLLOSEPENPSL 147
gi|114667024|ref|XP_001157352.1| MDLSALRVVEEVONVINAMQKILECPICLEELIKEPSTKCDHIFCKFCMLKLLN-QKKGPSQCPLCKNDITKRSLOESTRFSOLVEELLKIIICAFQDITGLLEYANSYNFYAK--ENNSPEHLKDEVSIQSMGYRNRKRRLLOSEPENPSL 147
gi|61740517|ref|NP_001013434.1| MDLSADRVVEEVONVLNAMQKILECPICLEELIKEPSTKCDHIFCKFCMLKLLN-QKKGPSQCPLCKNDITKRSLOESTRFSOLVEELLKIIHAFELDTGLQFADSYNFYSK--ENNSPEHLKDEVSIQSMGYRNRKRRLROSEPENPSL 147
gi|30466260|ref|NP_848668.1| MDLSADHVVEEVONVLNAMQKILECPICLEELIKEPSTKCDHIFCKFCMLKLLN-QKKGPSQCPLCKNDITKRSLOESTRFSOLVEELLKIIHAFELDTGLQFANSYNFYSK--EDNSPEHLKDEVSIQSMGYRNRKRRLROSEPENPSL 147
gi|45383782|ref|NP_989500.1| MDLSVIAIGDVONVLSAMQKILECPICLEELIKEPSTKCDHVFCRFKMLKLLSRKKKGVICPLCKTETVTKRSLEKNSRFKOLTEGLLEAISAFELDTGVKFLSRFYPKTISEVAIAELLGNNSVIGSKGFRNRKRKAKENRQDSCIL 150



gi|31560812|ref|NP_033894.2| -KDSLGLVQLSNLGIIVRSVKNNRITQPRKKSIVYIELDSDSSEETVTKPGDCSVRDQELLOIAPQEAAGDEKGLHSAEAAECDFSE-GIRNIEHHQCD-DLNPTENHATERHPEKCSISISNVCEVPCGDAHASSLOPE-----T 284
gi|6978573|ref|NP_036646.1| -KDSLGLVQLSNLGIIVRSVKNNRITQPRKKSIVYIALESDDSSEERVNAPDGCVSRDQELFQIAPGGAGDEKGLNSAKKAACDFSE-GIRNIEHHQCDKDLNPTENHATERHPEKCPRIISVANVHVEPCGIDARASSLOLRG-----T 285
gi|6552315|ref|NP_009233.1| QETSLSVQLSNLGIIVRILRTRKRIQPKKTSVYIEL-----AACFSEITDVNTEHHQPNNDLNTTEKRAAERHPEKYOGSSVSNLHVPCGINTHASSLOHE-----N 246
gi|114667024|ref|XP_001157352.1| -ETSLSVQLSNLGIIVRILRTRKRIQPKKTSVYIEL-----ETSLSVQLSNLGIIVRILRTRKRIQPKKTSVYIEL-----AACFSEITDVNTEHHQPNNDLNTTEKRAAERHPEKYOGSSVSNLHVPCGINTHASSLOHE-----N 245
gi|61740517|ref|NP_001013434.1| -ETSLSVQLSNLGIIVRILRTRKRIQPKKTSVYIELGSDSEDVTKKASSCSVGDDE-LEIISQARABEASLNPAPKAAECDFSG-DITNIEHHOSNKDLITTEKHAATKPKPEKYOGISVSNLHVPCGINTHASSLOHE-----N 284
gi|30466260|ref|NP_848668.1| -ETSLSVQLSNLGIIVRILRTRKRIQPKKTSVYIELGSDSEDVTKKASYFVSGDHELLEITPQAKAKTNLNPAPKAAECDFSEKDDITNIEHHQSLIKDLITTEKHAATETHEPEKYOGISVSNLHVPCGINTHASSLOHE-----N 287
gi|45383782|ref|NP_989500.1| EAVNDFQLTDNRVKGSSVRSKPKCKCKIEKGVLLIELGTDSSEEHFILASSIGLEDEKLEELPEKSAEKYSSCNIQPLKLGAKETILNPVIGETDFLKEALDKKSMNLNTEHKCNQVNTIEGQSSPLNVFADALLTGQRDGIGNASPLKND 300



gi|31560812|ref|NP_033894.2| SSSLLLIEDRMNAEKAIEFCNKKSQPLAVSQSRRWAASKGTCDNRQVPSITGEKVGPNADSLSDREK-WTHPQLSCLPENSAGAITDVPWITLNSVQKVNWFERSRTGEMLTSDSASARRHESNAEAAVLEVSNEVDGGFSSSRKIDLVAPPD 433
gi|6978573|ref|NP_036646.1| RLLLEIETDRLDAEKAIEFCNKKSQPLAVSQSRRWAASKGTCDNRQVPSITGEKADPNVDSLGRKQ-WNHPKSLCPENSAGAITDVPWITLNSIIOKVNWFERSRTGEMLTSDSNASDRRPAENAEAAVLEVSNEVDGCFSSSKKIDLVPAPD 434
gi|6552315|ref|NP_009233.1| SSSLLITKDRMNVKAIEFCNKKSQPLAVSQSRRWAASKGTCDNRRTPTSEKKVVDLADLPCRKE-WNKQKLPCEENPRDTEVPWITLNSIIOKVNWFERSRDELLGSDSDHDGSESNAKVADVLDVLEVEDEYSSSEKIDLLASDP 395
gi|114667024|ref|XP_001157352.1| SSSLLITKDRMNVKAIEFCNKKSQPLAVSQSRRWAASKGTCDNRRTPTSEKKVVDLADLPCRKE-WNKQKLPCEENPRDTEVPWITLNSIIOKVNWFERSRDELLGSDSDHDGSESNAKVADVLDVLEVEDEYSSSEKIDLLASDP 394
gi|61740517|ref|NP_001013434.1| SSSLLITKDRMNVKAIEFCNKKSQPLAVSQSRRWAASKGTCDNRQVPSITGEKVVVNDLPCRKE-LNKQKPPSDSPRSDQVPWITLNSIIRKVNWFERSRDELLGSDSDHDGSELTAVGVGAVEVPEVGEYSSSEKIDLLASDP 433
gi|30466260|ref|NP_848668.1| SSSLLITENRLNVEKAIEFCNKKSQPLAVSQSRRWAASKGTCDNRQVPSITGEKIVLNTDPLRKE-LRKKQKALCPDSDPSPQVVPWITLNSIIOKVNWFERSRDEILLGSDSDHDGSEENVEGAVETPNKVDGYSSEKIDLLASDP 436
gi|45383782|ref|NP_989500.1| TDFLKNAREMDVETQCSHKQKQELDLLEDSEGRLLDKIKKEDICVPSVEDVEMEPDSDSLLEKPEKPLQPKIPHCPTLNEVSTKGLNQSIQKVNWFERSRDEILLGSDSDHDGSEENVEGAVETPNKVDGYSSEKIDLLASDP 447



gi|31560812|ref|NP_033894.2| HHTLMCKSGRDFSKPVENIDSKIFGKSYQR--KGSRPHLNHVTE--IIGTFTTPEPIIQEOPFNKLRKR--STLQPEDFIKKADLSAGVORTPDNINGDTLMEPNEQAVSITSNQCENKIAGSNLOKEKSAHPTESLRKEPASTAG 577
gi|6978573|ref|NP_036646.1| DNAMVCTSGRDFSKPVENINDKIFGKTYQR--KGSRPHLNHVTE--IIGTFTTPEPIIQEOPFNKLRKR--STLCHPEDFIKKADLTVVQRISENINGDTQMEPNDQAMSIISNGQENRATGNDLORGNAPHPTESLRKEPASTAG 578
gi|6552315|ref|NP_009233.1| HEALICKSERVHKSQVSNIEDKIFGKTYQR--KASLPNLSHVTEENLIIGAFVTEPIIQERPLNKLKRRRPTSLGLHPEDFIKKADL-AVOKTPEMINQGTNQTQNGQVMNINSNGHENKTRGDSIONKKNPNPESLEKESAFKTK 542
gi|114667024|ref|XP_001157352.1| HEALICKSERVHKSQVSNIEDKIFGKTYQR--KASLPNLSHVTEENLIIGAFVTEPIIQERPLNKLKRRRPTSLGLHPEDFIKKADL-AVOKTPEMINQGTNQTQNGQVMNINSNGHENKTRGDSIONKKNPNPESLEKESAFKTK 541
gi|61740517|ref|NP_001013434.1| QDAFICESERVHTKPVGGNIEDKIFGKTYQR--KASLPKVSHTTEVLITIGACAIEPDMQTPFLMKAHEKRRTTSLGLHPEDFIKKVELGIVFKTPEKLIIEGINIKKRDGHVINIINNGPEIETEDDYVQKKNANPESLEKESAFKTK 581
gi|30466260|ref|NP_848668.1| HGTLIH--ERVHKSQVSNIEDKIFGKTYQR--KASLPNFSHIADLILGAFVTEPIIQEOPFNKLRKR--STLQPEDFIKKADLIVPKTPEKMTGDTQTEKQCHGMNISDGHENKTRKRDYVQKKNANPESLEKESAFKTK 582
gi|45383782|ref|NP_989500.1| VFAVIERNRKRWTKQTYSIEDKIFGKTYERGRKSNPSTILRDILPATKKEDAABEGGLNNSRKRDRKRRKRSACTLQPEDFIKKKLEEDRCPQGIKSSLDGAEKE-----KCDENSADVNKPLLEKRRKSTLAEPKRGLOWNA 591



gi|31560812|ref|NP_033894.2| AKSISNSVSDLEVELNVHSSKAPKKNLRRKSSIRICALP--LEPIS-RNPSPTCAELQIDSCSSSEETKKNHNSQOPAGHLREPOLIEDTEPAADAK-KNEPNEHIRKRRASDAFPEEKLKMKAGLLTSCSSPRKSGPVPNPSPORTG 722
gi|6978573|ref|NP_036646.1| AKSISNSISDLEVELNVHSSKAPKKNLRRKSS-TRCVLP--LEPIS-RNPSPTCAELQIDSCSSSEETKKNNSNOPAGHIREPOLIEDTEPAADAK-KNEPNEHIRKRRASDAFPEEKLKMKAGLLTSCSSPRKSGPVPNPSPERKG 722
gi|6552315|ref|NP_009233.1| AEPISSSISNMELELNTHNSKAPKKNLRRKSSRHHIHA--LELVVSRNLSPNCTELQIDSCSSSEETKKNNSNOPMPVRHNSRNLQLMDEKPEPATGVKKSNNKPEQTSKRHSDTFPELKLNTNAPGSFTNCSNTSELKEFVNPSPRREEK 690
gi|114667024|ref|XP_001157352.1| AEPISSSISNMELELNTHNSKAPKKNLRRKSSRHHIHA--LELVVSRNLSPNCTELQIDSCSSSEETKKNNSNOPMPVRHNSRNLQLMDEKPEPATGVKKSNNKPEQTSKRHSDTFPELKLNTNAPGSFTNCSNTSELKEFVNPSPRREEK 689
gi|61740517|ref|NP_001013434.1| TEPMSRRIISNMELELNTHNSKAPKKNLRRKSSARHTCA--LEFVNRNLNPPDHSLELQIDSCSSSEETKKNNSNOPMPVRHNTLQLMDEKPEPATGVKKSNNKPEQTSKRHSDTFPELKLNTNAPGSFTNCSNTSELKEFVNPSPRREEK 729
gi|30466260|ref|NP_848668.1| AEPISISNMELELNTHNSKAPK--NLRKRSSTKPIE--LELVVSRNLSPNCTELQIDSCSSSEETKKNNSNOPMPVRHNSRNLQLMDEKPEPATGVKKSNNKPEQTSKRHSDTFPELKLNTNAPGSFTNCSNTSELKEFVNPSPRREEK 723
gi|45383782|ref|NP_989500.1| AEKVSCKSDGQLELNSDQKSTKNACSTKACCRHSTIRCAIHLVDRPGSFDLAEPLINSEYPNNEPISKADCCRRQRRLQLLEBEITKETGKMRVIKAEKNSDSGPEGSVFG-VERVNLVHNSQCKDLRQKQDILLSVMSLADR 740



gi	31560812	ref	NP_033894.2	TEQLETRMSDPAKELGDRVLGGEPSGKTKDRSEESTSVSLVPTDIDYDTONSVSLDAHTVRYARTGSQAOCMTQFVASENPKELVHGSS-NNAGSGTEGLKPLRLHNLN-LSOEK-VEMEDSELDIYQYLVNTFVQVSKROSQSFALFSEKPRSPC	869
gi	6978573	ref	NP_036646.1	IEQLEMCMPDNNKELGDLVLGGEPSGKTEPESEESTSVSLVPTDIDYDTONSVSILEANTVRYARTGSVQCMTQFVASENPKELVHGSS-NNAGSGSECFKPLRLHNLN-HNQET-IEMEDSELDIYQYLVNTFVQVSKROSQSFALFSEKLRSPC	869
gi	6552315	ref	NP_009233.1	EKLETKVKNNAEDPKDLMLSGE-RVLQTERSVESISSLVPTDYDGTQESISLLLEVSTLTKAKTEPNKCVSQCAAFENPKGLIHGCKDNRNDTEGFKYPLGHEVNI-HSRETSIEMESELDAQYLVNTFKVSKROSQSFALFSPNPGNAE	838
gi	114667024	ref	XP_001157352.1	EKLETKVKNNAEDPKDLMLSGE-RVLQTERSVESISSLVPTDYDGTQESISLLLEVSTLTKAKTEPNKCVSQCAAFENPKGLIHGCKDTRNDTEGFKYPLGHEVNI-HSRETSIEMESELDAQYLVNTFKVSKROSQSFALFSPNPGNP	837
gi	61740517	ref	NP_001013434.1	ESRRMTQVSDSTRDKPVELVLSGG-RGLQTERSVESISSLVLDIDYDGTQESISLLLEVSTLTKAKTEPNKCVSQCAAFENPKGLIHGCKDTRNDTEGFKYPLGHEVNI-HSRETSIEMESELDAQYLVNTFKVSKROSQSFALFSPNPGNP	877
gi	30466260	ref	NP_848668.1	EENLGIQVNSTKDKDLILREG-KALQTERSVESISSLVPTDYDGTQESISLLLEVSTLTKAKTEPNKCVSQCAAFENPKGLIHGCKDTRNDTEGFKYPLGHEVNI-HSRETSIEMESELDAQYLVNTFKVSKROSQSFALFSPNPGNP	872
gi	45383782	ref	NP_989500.1	GADLEANGIQISKNSDDMAKNRNFNFPTFSQCLSNFNFPSSKAGSQEGEMLQKLPQPSKTLVLAASILTTEKRSWQCTVFSQDQCCSRNPKDFRTGKSPMAK-NASFTMEARDESLEMDIYQYLVNTFKVSKROSQSFALFSPNPGNP	886



gi	31560812	ref	NP_033894.2	KDC----AHSVPSKELSPKVLAKGKQKER-QLQEEFEIISHVQAAVAVGLVPPVPCQEGK-LAADIMCDR--GCRLLCPSSHVRSYRSGENGLSATAKSGISQSHFKQSVSPVRSIKIDNRKPLTEGRFRHTS--TEMAVGNENLQSTVHTV	1011
gi	6978573	ref	NP_036646.1	KDCILVGGARVPSREPPKVTSRGEQKER-QLQEEFEIISHVQAAVAVGLVPPVPCQEGK-PGAVTMCAD--VSRLLCPSSHVRSYRSGENGLNITKSGISQSHFKQSVSPVRSIKIDNRKPLTEGRFRHHT--BERGMGNLAVQSTIHTS	1012
gi	6552315	ref	NP_009233.1	EBCATFSAHGSLKQSPKVFCEQKQENKQKNESNIKIPQVTVNIAGPVPVQKDK-PVDNAKCSIKGGRFCLSSQFRGNTEGLITPNKHGLLONPPIRIPPLFPFKSVKCKCKNLEENFEHMSPEREMGNB-NIPSTVSTIS	986
gi	114667024	ref	XP_001157352.1	EBCATFSAHCRSLKQSPKVFEREQENKQKNESNIKIPVOTVNIAGPVPVQKDK-PVDYAKCSIKGGRFCLSSQFRGNTEGLITPNKHGLLONPPIRIPPLFPFKSVKCKCKNLEENFEHMSPEREMGNB-NIPSTVSTIS	985
gi	61740517	ref	NP_001013434.1	EDCVTVCPRSGAFKQGPVTLCEGQKESQKKKESERIRHVOAVHINAGSAVSOAKAKPQGFARCSIKGGRFCLSSQFRGNTEGLITPNKHGLLONPPIRIPPLFPFKSVKCKCKNLEENFEHMSPEREMGNB-NIPSTVSTIS	1027
gi	30466260	ref	NP_848668.1	KECATVFHAGSGLRQSPRDPKCRQKEDSQKSEKSKQHVOAICTIVHFVVAQDQDRTPGDDAKCSAKEVTRVCSQSSLRGKTELVEVANKQGVSEKPNLIPSLSPIKSIVKTI CKKSPSE-KFEEVPT--PEKTLGSEIISQAVSTIS	1021
gi	45383782	ref	NP_989500.1	KACTLDDVASEKLNTPDQVEERNSKYLKTENLKEETLAEGLNSVCEKFEPCSEAC-----VSPFVCFVSSAAVHIVENQDVSKVANGLNLTLLRLTCAARNEDGNPKGQGEKLNSTGIGVSEKLRLSVPRVN	1021



gi	31560812	ref	NP_033894.2	LNN-RGNACQEAES-----SIIHEVCSIGDSFPGQLGRNRGPKVNVPPVLDSPQGVCCQSVPVV-DKYLEIKKC-----EGEAVCADFPSPCLFSDHLEQSMG-KVFCVCSLTPDPLL-DVEIQGHTSFGEGDIMER	1137
gi	6978573	ref	NP_036646.1	LNN-RGDACLKAESS-----GSVIEVHSTGENVQGLDRNRGPKVNVTVLLDSDTOPGVSKQSAFV-DKYLEIKC-----ESKAVSADFSPCLFSDHLEKPMRDKTFQVCSLTPDPLL-DVEIQENASFGEGDITEK	1138
gi	6552315	ref	NP_009233.1	RNNIRENVEKEASSNNINEVGSSTNEVGSSSINIEVSSDENIQAELGRNRGPKVNLNMLRGLVLPVYKQSLPGSNCKHPKIKQ--EYEEVVTVNTDFSPCLISDNLQPMGSSHASQVCSLTPDPLL-DGEIKEDTFAENDIKES	1133
gi	114667024	ref	XP_001157352.1	RNNIRENVEKEASSNNINEVGSSTNEVGSSSINIEVSSDENIQAELGRNRGPKVNLNMLRGLVLPVYKQSLPGSNCKHPKIKQ--EYEEVVTVNTDFSPCLISDNLQPMGSSHASQVCSLTPDPLL-DGEIKEDTFAENDIKES	1132
gi	61740517	ref	NP_001013434.1	QNNIRECASKEVGSNVVNEVGSSTNEVGSSSINIEVSSDENIQAELGRNRGPKVNLNMLRGLVLPVYKQSLPGSNCKHPKIKQ--EYEEVVTVNTDFSPCLISDNLQPMGSSHASQVCSLTPDPLL-DGKIKGKVFASDIKES	1175
gi	30466260	ref	NP_848668.1	QNNIQESLFKEVSSNSVNEVGSSTNEVGSSSINIEVSSDENIQAELGRNRGPKVNLNMLRGLVLPVYKQSLPGSNCKHPKIKQ--EYEEVVTVNTDFSPCLISDNLQPMGSSHASQVCSLTPDPLL-DDEIKENHFAESDRIKES	1169
gi	45383782	ref	NP_989500.1	RSQEDQSNTEHAFQRGLNAVTEYFYSNESNQEKAEVVDKGLMTHQFQPSMLPCTACQNPFAFNCETLTKKIITRRERSLVKNEERVIQTVSTGLSEFVSREALVESLKGHSDFDLSLTPDGLLCSNDNTEASAFVYTNRKTDS	1171



gi	31560812	ref	NP_033894.2	AVFNGSILRRSSRSPVPVTHASKS---SILHRSRLKLESSESDSTEDEDLPQFOHLLS-RISNTP-ELTRCNAVTVTQMPEKAGTQAAPWKGSSSDCNEVIMIEASQEHQFSEDPRCPSGSMFSSQHSAAQGSANANSQDSNFP	1280
gi	6978573	ref	NP_036646.1	AIFNGSVLRRSSRSPVPVTHASKS---RSLHRGRSLKLESSESDSTEDEDLPQFOHLLS-RVSNTP-ELTRCNAVTVTQVPEKAGTQAAPRKSISSDCNEVILGEASQEVQFSEDQKCGSMFSSQHSAAQGSANANSQDPPDFNP	1281
gi	6552315	ref	NP_009233.1	AVFKSVQKQELSRSPVPTHTHLA---CGYRRGAKKLESSEENLSSEDEELPQFOHLLFGKVVNIIPSQSTRHSTVAIECLSKNTEENLLSKNLSLDCSNQVILAKASQEHHLSEETKCSASFSSQCSLEEDLANTNTODPFLIG	1278
gi	114667024	ref	XP_001157352.1	AVFKSVQKQELSRSPVPTHTHLA---CGYRRGAKKLESSEENLSSEDEELPQFOHLLFGKVVNIIPSQSTRHSTVAIECLSKNTEENLLSKNLSLDCSNQVILAKASQEHHLSEETKCSASFSSQCSLEEDLANTNTODPFLIG	1277
gi	61740517	ref	NP_001013434.1	AVFKSVQKQELSRSPVPTHTHLA---CGYRRGAKKLESSEENLSSEDEELPQFOHLLFGKVVNIIPSQSTRHSTVAIECLSKNTEENLLSKNLSLDCSNQVILAKASQEHHLSEETKCSASFSSQCSLEEDLANTNTODPFLIG	1321
gi	30466260	ref	NP_848668.1	AVFSEVQKQELSRSPVPTHTHLA---CGYRRGAGKLES--EETVSEDEDELPCQQLLFGKVVNIPSPETGICNTVATIEGLKPEKELGNLSEKLSGLNDCSGVSAKVSQEHHLNIEARCSGLFSSQCSLEEDLANTNTODPFLMF	1314
gi	45383782	ref	NP_989500.1	AVFVKRSQAQVVKEVNDSVSCPRREGIQRFRRRQKLOSSEES--DDEDLPSPQELMFGKVSVPFLQVTKQVTVSVVSSANP-TLPCSECLNE--NNEQKTEAALNENCASPSQSESECVVNLFSSQSNMSESVDGAEKQKTLQV	1319



gi	31560812	ref	NP_033894.2	-PSKQRSKCCNEEAFSLDKELISDNE-EMACLEEDNDQEEDESIIPDS--EASGYESENLSDECSS--OSDILTQORAMKYNLIKLOQEMAHLEAVLEQRGNPSPGHSPSLPADPCALEDLDPPELNNSGAAILTSKININENPV	1422
gi	6978573	ref	NP_036646.1	-PSKQRRHOAENEAFSLDKELISDNE-DMACLEEASDQEEDESIIPDS--VASGYEENLSDECSS--OSDILTQORAMKNDLIKLOQEMAELEAVLEQHGSPSPGHSPCLPADPCALEDLDPPELNNRSGTALLTSKININENPV	1423
gi	6552315	ref	NP_009233.1	-SSKQMRHSESQCVGLSDDKELVSDDE-ERGTGLEENN-QEESMDNLGEEAAGCESSETVSEDSCGLSSQSDILTQORDIMQNLIKLOQEMAELEAVLEQHGSPNSYPSIISDSSALEDLRNPQSTSEKAVLTSQKSEYPIS	1425
gi	114667024	ref	XP_001157352.1	-SSKQMRHSESQCVGLSDDKELVSDDE-ERGTGLEENN-QEESMDNLGEEAAGCESSETVSEDSCGLSSQSDILTQORDIMQNLIKLOQEMAELEAVLEQHGSPNSYPSIISDSSALEDLRNPQSTSEKAVLTSQKSEYPIS	1424
gi	61740517	ref	NP_001013434.1	PTSKQVRHSENLDV-LNDKELVSDDEEREPGLEEDSPQEESVSDLGEVAGVSETLSEDCSGLSSQSDILTQORDIMQNLIKLOQEMAELEAVLEQHGSPNSYPSIISDSSALEDLRNPQSTSEKAVLTSQKSEYPIS	1469
gi	30466260	ref	NP_848668.1	RPSKQV-NQSEEEV-LSDKELVSDDE-ERREGLEEDSCQEESVSDLGEVAGVSETLSEDCSGLSSQSDILTQORDIMQNLIKLOQEMAELEAVLEHRSQNSYPSIISDSSALEDLRNPQSTSEKAVLTSQKSEYPIS	1461
gi	45383782	ref	NP_989500.1	SNVKKSKQAPQSCSGGLKRLKNNLN-----DEYQEDPNMGANLGE-EASGSDSTLRVDESHFQEGEILLTQOKNAMONNLKLOQEMAELEAVLKHGSDAEVLE-----LCRELTYCGIGGLEKMRMRDT--	1444



gi | 31560812 | ref | NP_033894.2 | ONLKEACDDKFLQHLGEPFSGDDESGMGRPFPFKSPPLAGSRGSAHCCSRHLKRRSPQEBELLQAPAGSEAS---EPEHNSFGQCLPRRELEGTPTPLGSGILFSS--RDPESESPKPAHIGTTPASTSALKIPIQGGVA--FRSAA 1563
gi | 6978573 | ref | NP_036646.1 | ONPKRACDDKSPQPPDGLPSGDKESGMRRPFPFKSPPLTSSRCSARGHSRSLQNRNSTQEBELLQAPAXLEKS---CEPHNLTGRCLPRODLEGTPTPLGSGILFSS--RDPDESSEPKVSAALVCTAPASTSALKISOGVAGSCRSPA 1566
gi | 6552315 | ref | NP_009233.1 | ONPEGLSADKFVVS--ADSSTSKNKEPGVERSSPSKCPSLDDRWMHSCSGSLQNRNYPQEBELIKVVVDVEEQLEESGPHDLTETSYLPRODLEGTPTPLGSGILFSDDDPESDPSEDRAPESARVGNIPSSSTSALKVPOPKVAESAQSPA 1574
gi | 114667024 | ref | XP_001157352.1 | ONPEGLSADKFVVS--ADSSTSKNKEPGVERSSPSKCPSLDDRWMHSCSGSLQNTNYPQEBELIKVVVDVEEQLEESGPHDLTETSYLPRODLEGTPTPLGSGILFSDDDPESDPSEDKAPESAHVGNIPSSSTSALKVPOPKVAESAQSPA 1573
gi | 61740517 | ref | NP_001013434.1 | ONPELSLTDKFCVF--LDSSTSKNKEPGMIRSSPSQSRLLDTRWVHSCPRSLQDTNCPQKELIKVVSMEEQPTESSEARDLMEQSYLSRPLDLEGAPVLESGILFSDDDPESDPSHRASELAHVSSMPTSTSALKLPOFQVEESAQSTA 1618
gi | 30466260 | ref | NP_848668.1 | ONPELSLADKFPVQ--LDSSTSKNKEPGMERSSASKFQLSYNRWYHSS--RSLQDRNCPQKELINVDAMEEQOLAKREAQDLMG--SFLPRODQEGTPTPLGSGILFSEHEPESDPSEDRAAEPAHVSSMPPASALKLSQFRVEESTKNSA 1608
gi | 45383782 | ref | NP_989500.1 | -----ENVSEHDSKTKLTKASVLPVLCGNVTKPNPSSFSVHKPCQIABANDSVAAGDNKSNVIVCKSKRSVCFPTSLVHNVAG----- 1526
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi | 31560812 | ref | NP_033894.2 | AAGAD----KAVVGIIVSKIKPELTSSEERARDRISMVVSGLTPKEVMTVQKFAEKYRLTLDAITEETHVVIKTDAEFVCERTLKYLFLGIAGGKWIVSYSWVVRVIEERRLLNVHEFEVKGDVVTGRNHQGPRRSRESREK-----L 1702
gi | 6978573 | ref | NP_036646.1 | AGGAD----TAVVVIIVSKIKPEVTSPEKERAERDISMVVSGLTPKEVMTVQKFAEKYRLALDVIDEETHVVIKTDAEFVCERTLKYLFLGIAGGKWIVSYSWVVIKIQERKLLSVHEFEVKGDVVTGRNHQGPRRSRESREK-----L 1705
gi | 6552315 | ref | NP_009233.1 | AAHTTDTAGYNAMESVSREKPELTAETERNKRMMSMVVSGLTPEEFMLVYKFAKHHITLNLITEETHVVMKTDAEFVCERTLKYLFLGIAGGKWIVSYFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQR-----KI 1719
gi | 114667024 | ref | XP_001157352.1 | AAHTTDTAGYNAMESVSREKPELTAETERNKRMMSMVVSGLTPEEFMLVYKFAKHHITLNLITEETHVVMKTDAEFVCERTLKYLFLGIAGGKWIVSYFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQR-----KI 1718
gi | 61740517 | ref | NP_001013434.1 | AVHIASDTAGYNKSEDSVGIKPEVTSSTRGVNKRISMVASGLTPKEFMLVHKFAKHHITLNLITEETHVIMKTDAEFVCERTLKYLFLGIAGGKWIVSYFWVTQSIKERKMLDEHDFEVRGDVVNGRNHQGPKRARESQR-----KI 1768
gi | 30466260 | ref | NP_848668.1 | AAHIANTTRCNLRBESMSKEKPEVTSSTRSRRKRLSMVASGLTPKELMLVQKFAKHHITLNLITEETHVIMKTDPEFVCERTLKYLFLGIAGGKWIVSYFWVTQSIKEGKMLDEHDFEVRGDVVNGRNHQGPKRARESQR-----KI 1753
gi | 45383782 | ref | NP_989500.1 | -----KENAASSTTCRTMSIVASGLNQSEHLMVQKFAKTKQSTFSNHTDGTETHVIMKTDPELVCEERTLKYLFLGIAGGKWIVSYQWITIQSFKEGRILDEHDFEVRGDVVNGRNHQGPKRARESQR-----I 1651
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800



gi | 31560812 | ref | NP_033894.2 | FKGLQVYCEPFTNMPKDELERMLQLCGASVVKELPSLTHDGAHLVIVQPSAWTEDNSCPDIGQLCKARLVMMWDVWVLDLSLRYRCDLDAVLVQNTIC--DSSEPODSND 1812
gi | 6978573 | ref | NP_036646.1 | FEGLQIYCEPFTNMPKDELERMLQLCGASVVKELPLLTRDGAHPIVLVQPSAWTEDNDCPDIGQLCKARLVMMWDVWVLDLSLRYRCDLDAVLVQNTICGRDSEPODSND 1817
gi | 6552315 | ref | NP_009233.1 | FRGLEICCYGPFNTNMPKDELEWVQLCGASVVKELSSFTLGTGVHPVIVVQPDADWEDNGFHAIGOMCEAPVVTREWVLDLSVALYCCOELDTYLIPOIPHSHY----- 1822
gi | 114667024 | ref | XP_001157352.1 | FRGLEICCYGPFNTNMPKDELEWVQLCGASVVKELSSFTLGTGVHPVIVVQPDADWEDNGFHAIGOMCEAPVVTREWVLDLSVALYCCOELDTYLIPOIPHSHY----- 1821
gi | 61740517 | ref | NP_001013434.1 | FRGLEICCYGPFNTNMPKDELEWVQLCGASVVKELSSFTLGTGVHPVIVVQPDADWEDSGFHAIGOMCEAPVVTREWVLDLSVALYCCOELDTYLIPOIPHSHY----- 1878
gi | 30466260 | ref | NP_848668.1 | FKGLEICCYGPFNTNMPKDELEWVQLCGASVVKELSSFTDQGTHTPVVVQPDADWEDAGFHVIGOMCEAPVVTREWVLDLSVALYCCOELDTYLVLP----- 1849
gi | 45383782 | ref | NP_989500.1 | FKDFEICCYGPFNTNMPKDELEWVQLCGASVVKELHFLTHKVNSTAVVVQPDADWEGTSTYAIQRKNNVAVVTREWVLDLSVACFECOELDAVLVSD----- 1749
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910..

