

gi	21704104	ref	NP_663535.1												
gi	109499624	ref	XP_223359.4	MAVIALKAWVA--GRAARRCAREVTHPARTEP 31											
gi	156151386	ref	NP_079363.2												
gi	114594913	ref	XP_517303.2	MRRPGLKIAIVGFAFAPRGLRPLGQRWSRCSRSRVPTWQS--SRDACPLRRPVRPLGLAPRRQRRGPEAPEAAQRAQVAPGLARLWQARLVGKGRADRPHPA--SVRQVQOLAGAHLAG 117											
gi	73975266	ref	XP_539262.2												
gi	194667872	ref	XP_001253517.2												
gi	118090529	ref	XP_420716.2												
gi	50303095	ref	XP_451485.1	MVIRSGSIVIAWHTVCAASAFIAALVVGVTLHFVHKIVANAWRYYPDEWFPVSVAIGDRYPERSIFQILIALTALPRFLLLFTHYYLNR----SLFTLLVGVIVRITTCGGVVYITSTDDHDAHDVFMI--SYIVLTI 131											
gi	45190564	ref	NP_984818.1	MISVNGKHIVHLHSFPASAFCICALVVGYQLHFHFKIVRNAHYGYDPDEWFPVSVAIGDRYPERSIFQILIALTAFPRFLLLMHWVR--ER----SALGVMAFGTRTMTTCGGVVYITSTDDHDAHDVFMI--SYIVLTI 131											
gi	10383785	ref	NP_009943.2	MIIINGKTIIPIAHTICAFSAFAAALVTGYSLHFHFKIVRNAHYTYPDDEWFPVSVAIGDRYPERSIFQILIALTAFPRFLLLMGHYYLNO----SKVCFLVGVLRITVCGGVVYITSTDDHDAHDVFMI--SYIVLTI 131											
gi	145608108	ref	XP_360833.2	MASRLHRPG--IGPTGCDMTVAQLDLAQQLAIEALPTG--QIVQNEWGYCPDEWFPVSVAIGDKYPERSEFMMLIAITSGPRFALVGLWYLLRRNGQALPKFVAITGCVRITLTCGGVYITSTDDHWHDLMTSYIVFTI 139											
gi	32410539	ref	XP_325750.1	MASRYKDKDAGVVSFNGQWISWHTVVAAYAAFLSALITICGALHYHKIVKNEWGYDPDEWFPVSVAIGDRYPERSIFMIFATITSGPRFALVGLWYLLAKPGRVLPAKAIISGVIRITLTCGGWYITSTDDHWHDLMTSYIVFTI 150											
gi	63054589	ref	NP_594060.2	MTEKISSLVESAQYVVLVETICSAFAAFILPILALALYTHYYQVVKNEFYGYPEWFPVSVAIGWYPERSEFQWLIALTPRRLVLLWLLTSG--ISRSPVITITALGVLRITLTCGGVVYITSTDDHWHDLMTSYIVLISNA 142											
1102030405060708090100110120130140150

gi	21704104	ref	NP_663535.1											
gi	109499624	ref	XP_223359.4	MPGLWR										
gi	156151386	ref	NP_079363.2	AASDLLRDTEQTRADPTGS--AERLRGEGIVLVAFLVAAMPESLWR 6										
gi	114594913	ref	XP_517303.2	MPSLWR 77										
gi	73975266	ref	XP_539262.2	RNEGGRRPQRTRRRREPGGAGLQQRARPARLSWKALPLAAMPESLWR 6										
gi	194667872	ref	XP_001253517.2	MSWNRN--KKDDLCK 13										
gi	118090529	ref	XP_420716.2	MSPWR 6										
gi	50303095	ref	XP_451485.1	MANASVKKCSLKEITMLCVIWS 22										
gi	45190564	ref	NP_984818.1	PWDWMIKHSQY--KEWKK--ILMTAFFGLIPLIYWFIOHQVHRRAG--AYSIVYAFWESLIVLDIAFDALACQDFEQIKISVSDWSAIEDENIVVPIEYIVEIEEQVDIIIVIEVEEKLNDS 251										
gi	10383785	ref	NP_009943.2	PWCVEVVRHATHNRALRK--VVGGAFFGTLIPLIYWFIOHQVHRRAG--AYSIVYAFWESLIIILDLDFDLSYADMEDLTIITFGQGRSPS--GVLVSKITLILLSSAGKGLGGCAM 242										
gi	145608108	ref	XP_360833.2	PWDIMIDRYSPNLSKNGK--LIDATIFFGLTFPMIYWFIOHQVQORAG--AYSIVYAFWESLILLDLDFADAFADFKKIDIVLAFNEKPGN--SFFQIRDSSPINYGE--KSE 240										
gi	32410539	ref	XP_325750.1	PWTAGCIASPPNAKAIKRYKYLCSAFFGTLVPLIYFYIQKKVHRVAG--AYTIYAFWESLILDFDVFDAVIALDFDSEPELLIKVHVASQ--GN 232										
gi	63054589	ref	NP_594060.2	PWTTCIASPPNAKAIKRYKYLCSAFFGTLVPLIYFYIQKKVHRVAGGFRPYLEMILLRTOQYVNLTFAPMRR--AYTVYAFFEWALILFDVAFDAVIALDFDSEPEVVKVDVKGASK--GAN 269										
gi	63054589	ref	NP_594060.2	PWFILVSKCSFVNSMASRIRNIGSALFVLLIPPLIYWFIOHQKFKHIP--AYTVYAFFEWLILDLDFDLSALYDFWDFKPFVFNLHTSKTYSN--PSSFATRKEKGEH 246										
.....160170180190200210220230240250260270280290300

gi	21704104	ref	NP_663535.1	ATAETLLGLYVSWLYHGLSPMIYYFPLQTLLETGLEFFCVAFSLPILLTIPPWLVKNKKWLSLRLRIVTVGSIASFEAPNAKLRMLVLAGVSSSLI 105										
gi	109499624	ref	XP_223359.4	ATAETLLGLYISWSLYHGLGPMIYYFPLQTLLETGLEVFGVAFSLPILLTIPPWLVKNKRALLRLRIITVGSVASFEAPNAKLRMLVLAGVSSSLI 176										
gi	156151386	ref	NP_079363.2	EILLESLLGCYSWSLYHDLGPMIYYFPLQTLLETGLEGFSAFLSPIFLTTPFWLVKNKKWMLLRLRIITGSIASFQAPNAKLRMLVLAGVSSSLI 105										
gi	114594913	ref	XP_517303.2	EILLESLLGCYSWSLYHDLGPMIYYFPLQTLLETGLEGFSAFLSPIFLTTPFWLVKNKKWMLLRLRIITGSIASFQAPNAKLRMLVLAGVSSSLI 114										
gi	73975266	ref	XP_539262.2	VLAQGLARRVVSLSLCHLGLGPMIYYFPLQTLLETGLEGFSAFLSPIFLTTPFWLVKNKRALLRLRIITVGSVASFOASNAKLRMLVLAGVSSSLI 262										
gi	194667872	ref	XP_001253517.2	EVLLESLLGLYVSWLYHDLGPMIYYFPLQTLLETGLEGFSAFLSPIFLTTPFWLVKNKKWMLLRLRIITVGSIASFOAPNAKLRMLVLAGVSSSLI 105										
gi	118090529	ref	XP_420716.2	FLSFFVSQYISWSLYHALPMMIYYFPLQTLLETGLEVFAVAFSLPVLFIIGPCWRLANNKYILALLRLITVGSIASYQAFNASIRLFLILAAGVSSSLI 121										
gi	50303095	ref	XP_451485.1	EELSDDENIQEHSRLLE--SNDNEITILLKEEDIMYPNLDPVPPSQDSFMYIVVNFNFSFMFWTVTSLPCMWHFPLWYMGISGYEAIVLISLSPVFLIIPVLTVVVDVYG--MLLANVFSIGAIFIDPETRLLIVVALAHALIVMTEF 398										
gi	45190564	ref	NP_984818.1	EEMLEEVITQEHKELYL--LPDEPII--NQASLFYIVVSIFDSDFMFWNTLALLCMWFFPLWYMGISGYEAIVAAVLSVPLLIVPFPPFLIQOYQ--PLLANVIGIGAYIVPEFWRMLMVAVALGSLTMMNF 370										
gi	10383785	ref	NP_009943.2	LQKSGEKKVKEKQVARS--ATGSYFR--FDSFFYLLINFGFVFNVSLLCSLWHPFLWYMGISGYEAAILGYPFLFYLPVSEAFTQYQ--VLLGGITAIGAYIVOMPRLRISVAVGSLIIVATEF 367										
gi	145608108	ref	XP_360833.2	VSPQKAAVLEKEKQKATAGLMHQKVF--PSGMLDIAADVHGDFVWILTSGLVTLWYFPLWYMGISGYEAALVMSVSPVLLIGISPPRWLTTRORFFHLLSLGVLVAFLIKPFIQRLIYAVGFLGMQCCLAW 362										
gi	32410539	ref	XP_325750.1	ASVPAAVLEKEKQKATAGVYSAGFN--LGPALDIAADVHGDFVWILTSGLVTLWYFPLWYMGISGYEAALVMSVSPVLLIGIRPRLSLTVNNQRLRFLVSLAGLLAYKVHDFVVRLETVGFGVMQCCLAW 399										
gi	63054589	ref	NP_594060.2	LSVAAAVGTCANIKKDSNVKCSK--KQILFSLLYFSSEVYLSEVFWVLSLGLLVVWYFPLWYMGISGYEACILFELSPFLIGIPRLRFASKVPVIFLFLNVIGIAAVKLEPVRRLRFTAFVCCCECLAW 379										
.....310320330340350360370380390400410420430440450

gi	21704104	ref	NP_663535.1	VQTVVWWSGSGLRYLKIWFILGHVLLLVLRWIYTSLNPVWWSYQMSNRVILLSAVALDRICDGDYRNPQEKKPRE----VATGRITLSWLLPGAAGFSLFLTHWIFGCVSLVSRWAVS--GHPHP--GPDNPPFGGAVLLGFS 246										
gi	109499624	ref	XP_223359.4	VQTVVWWSGSGLRYLKIWFILGHVLLLVLRWIYTSLNPVWWSYQMSNRVILLSAVALDRICDGDYRNPQEKKPRE----VATGRITLSWLLPGAAGFSLFLTHWIFGCVSLVSRWAVS--GHPHP--GPDNPPFGGAVLLGFA 317										
gi	156151386	ref	NP_079363.2	VQAVTWWSGSHLQRYLRIWGFILGQVLLVLRWIYTSLNPVWWSYQMSNKKVILLSAIAALDRICDGDYRNPQEKKPRE----VATGRITLSWLLPGAAGFSLFLTHWIFGCVSLVSRWAVS--GHPHP--GPDNPPFGGAVLLCLA 246										
gi	114594913	ref	XP_517303.2	VQAVTWWSGSHLQRYLRIWGFILGQVLLVLRWIYTSLNPVWWSYQMSNKKVILLSAIAALDRICDGDYRNPQEKKPRE----VATGRITLSWLLPGAAGFSLFLTHWIFGCVSLVSRWAVS--GHPHP--GPDNPPFGGAVLLCLA 405										
gi	73975266	ref	XP_539262.2	VQAVTWWSGSGLRFLRIWGFILGQILLVLRWIYTSLNPVWWSYQMSNRVILLSVAIALDRICDGDGNKPEEKRPGE----AAKGTASRPRAWLGAAGFSLVFLTHWIFGCVSLVSRWAVS--GHPHP--GPDNPPFGGAVLLGLA 253										
gi	194667872	ref	XP_001253517.2	VHAVTWWTNGLQRYFRIWGFILGQILLVLRWIYTSLNPVWWSYQMSNRVILLSVAIALDRICDGDYRNPQEKKPRE----VATGRITLSWLLPGAAGFSLVFLTHWIFGCVSLVSRWAVS--GHPHP--GPDNPPFGGAVLLGLA 246										
gi	118090529	ref	XP_420716.2	VQTVVWWSGSHLQRYLRIWGFILGQVLLVLRWIYTSLNPVWWSYQMSNTVLLIIGLVAEAERIYVDVERQKGANATGN--VTRKAVSPQNWLSGMAFGSLMFLVTVIFGCVSLVSRWAVS--GHPHT--GPDNPPFGGAVLLGLA 262										
gi	50303095	ref	XP_451485.1	ALNLSLNSSS--SIGKFSITWIMGLLSVVKMGVFNINPVLWAMNENGGNLLIPGLVSTLFAITPPTNSCHLWN--SKITLRLPFKRLKLV--VGFGLVFAFHQSLTDAVSTLIVWCWEGWNS--HKGPLAWPAGLVCVAMI 538										
gi	45190564	ref	NP_984818.1	AVTLKSVIKDNARVAQFAITWISGLVAVVLMKAFYNNPLWPMKEENGWYKTLGLAATAFAMITPVVNRCHYARKKSEPSGQTYITILPLVKRALASVGFALVFAIHQSLTSSITLIVWCWEGWNSQSAKMPLAWPFTGLTCVAMI 520										
gi	10383785	ref	NP_009943.2	VNLRVINA--ETSFSFALTWLLGLVASVILKMGVFNINPVLWILDERNGYKTLGLVTLVFLGMLSPVYNSINFEGKR--NAQAKSASLIGKFLVAFGFSLLFCGIHQLLTDSSTIYWAWEGWNS--HGPLEWPWGALTCVMI 509										
gi	145608108	ref	XP_360833.2	VATLHSEVHVEGRLELRIWAVGLLSSIVKFACTRIINPITWPMRATGGWNTGLFLGLLAWRFRTRGFLNLDGV----QIKSGSFLAECISGGLFFALHSLLSLDSIMILVWVWDCGFFIR--GFTSNTAFYATTFAMI 498										
gi	32410539	ref	XP_325750.1	AATVSDVHPSRLESRIWAVGLLSSIAKFAFYNNPILWPMRATGGWNTGLVLVILAVALFRTRRGPPLNSVGV----QOKNGSLLSAGTIGGLFFAHSLLDSIMILVWVWDCGFFIR--GFTSNTAFYATTFAMI 536										
gi	63054589	ref	NP_594060.2	SLFVNISPENLAEKIK--VFLGLLASSIAFYSPFSNNPWVILNBTNGGKQIPALIVIGIACILFAIFRFGOTTAN--AVEHFKRKTIKTAASLGLVFLFCDSITVLMTWVWDCGFFIR--GPDYHPHGAVSIWVTEF 520										
.....460470480490500510520530540550560570580590600

gi	21704104	ref	NP_663535.1	SGLMLSGSSWLHDAGLAWWMTGAAASAMGLLYLRTWAAAVSGCVLAVFTGSMWPOVLGHLVNGKNSGEAMATGMILVLTQFFCAWCTAFKFPVGGVYARERSDVLVLTIMVITGLSMLFPGPK	391
gi	109499624	ref	XP_223359.4	SGLMLSGSSWLCDTGLAWWMTGATSAMGLLYLRTWAAAVSGCALAVFTGSMWPOVLGHLVNGTNPGGAMTGMISLVLVQVFFCAWCTAFKFPVGGVYARERSDVLVLTIMVITGLSMLFRPK	462
gi	156151386	ref	NP_079363.2	SGLMLPSCCLWFRGTGLLWVWTGASAAGLLYLHTWAAAVSGCVFAIFTASMWPOVLGHLINSGTNPGRKMTIAMIFVYLLIEFFCAWCTAFKFPVGGVYARERSDVLVLTIMVITGLSMLFPGPK	391
gi	114594913	ref	XP_517303.2	SGLMLPSCCLWFRGTGLLWVWTGASAAGLLYLHTWAAAVSGCVFAIFTASMWPOVLGHLINSGTNPGRKMTIAMIFVYLLIEFFCAWCTAFKFPVGGVYARERSDVLVLTIMVITGLSMLFPGPK	550
gi	73975266	ref	XP_539262.2	SGLMLSTCPWFPGSGLLWVWTGAAASAGLLYLPTWAAAVSGCVLALFTASMWPOVLHLLISGSSPGKAMTAMIFVYLLIEFFCAWCTAFKFPVGGVYARERSDVLVLTIMVITGLSMLFPGPK	397
gi	194667872	ref	XP_001253517.2	SGLMLSSCSWFPGSSLLWVITGATSAGLLYLPTWAAAVSGCVLALFTASVWPOVLGHLISGSSPGKAMTAMIFVYLLIEFFCAWCTAFKFPVGGVYARERSDVLVLTIMVITGLSMLFPGPK	391
gi	118090529	ref	XP_420716.2	HGLMLSFWSWSSVAFWGLTIGASAGLLYLPTWAAAVSNILAVFTMCIWVPLAGRFVYG-CLHPGKAMTAMFTVYLLIEFFCAWCTAFKFPVGGVYARERSHLLLGFTIMLCIGLFTIGSK	406
gi	50303095	ref	XP_451485.1	GGALFGKQSERITSMG---LAISTLALAVPQVKEFRVFPVGLPYVVSIIWIPSYFELVNIYIQSPGFLYSPFFIIVLFLAHVWTVAYAVFVYGVWILLREKLLQVLCFS	676
gi	45190564	ref	NP_984818.1	VGVHLSKRFAESPGSSTRWLVVALSTAGLSLSTHIGGWYKFGPGGLPYAGSIVMVIIPNYFITM-NKASYFSLGGSPGCGYILLTLSHVWTCAYAFVFPFVWVLRERLHWLVTAS	652
gi	10383785	ref	NP_009943.2	FASLSSVKFMGKPLVP-CLLILLISAVLSARSISQWPXYIFGGLLYAIAMLVVPSYFSALQVQNIWVYVLSFSVYIIFVLAHVWVYAYAFVPMGWVLRKIEITVLAFASS	645
gi	145608108	ref	XP_360833.2	AGVLTG---AVKPGLASLVTSYFICGCVGAGMYYIYHPWKGYGYLLTYLMAVAVPLLRDAAKRSPGLVFLGCFIIFVLAHVWVYAYAFVPMGWVLRKIEITVLAFASS	642
gi	32410539	ref	XP_325750.1	CGLLTIG---VFRPGMINTWATYGVACVGAAMLILYEQWGYCYGALILTYLMAVAVPLLRDAAKRSPGLVFLGCFIIFVLAHVWVYAYAFVPMGWVLRKIEITVLAFASS	678
gi	63054589	ref	NP_594060.2	CAVLVAVLYLQSGAFLMIG-FVLACGFSYFMYLIEVGGGLLIFTSYVLIYSPAFIRISFYSPAKVWGGAFVLYLILVLAHVWVYAYAFVPMGWVLRKIEITVLAFASS	669



gi	21704104	ref	NP_663535.1	YMKLILWLVGVGLLGLLRHRIYERQLGRGAPAVTVVSAALWPPFRFGYDNEGWPNLERSAQLLKEIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	540
gi	109499624	ref	XP_223359.4	YMKLILWLVGVGLLGLLRHRIYERKLGKGGAPADVVSAALWPPFRFGYDNEGWPNLERSAQLLKEIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	611
gi	156151386	ref	NP_079363.2	YMKLFLWLLVGVGLLGLLRHKAAYERKLGKGVAPTEVSAALWPPFRFGYDNEGWSLERSAQLLNQIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	540
gi	114594913	ref	XP_517303.2	YMKLFLWLLVGVGLLGLLRHKAAYERKLGKGVAPTEVSAALWPPFRFGYDNEGWSLERSAQLLNQIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	699
gi	73975266	ref	XP_539262.2	YMKLFLWLLVGVGLLGLLRHKAAYENKLGKGVAPTEVSAALWPPFRFGYDNEGWSLERSAQLLNQIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	546
gi	194667872	ref	XP_001253517.2	VVKLFLWLLVGVGLLGLLRHKAAYERKLGKGVAPTEVSAALWPPFRFGYDNEGWSLERSAQLLNQIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	540
gi	118090529	ref	XP_420716.2	YTKLILLWLVGVGLLGLLRHRIYERKLGKGGAPADVVSAALWPPFRFGYDNEGWSLERSAQLLNQIGADFTIILESDASKPYIGNNDLIMWLGEKLGFTDFGPPSTRDHWGIMVLSRYP	555
gi	50303095	ref	XP_451485.1	KIRVVAVGLLLTIFITQYR-PTLVPEPYHPEANLITAGIWTIHFGLDNDLWASEDRMIDILKMDQLDIVGELLEDTQRITIGNRDLAKMAHDLGMYADFGPPGNKH	818
gi	45190564	ref	NP_984818.1	RVTIVLVGMVAIAVSVQQLK-PTGVPOYPHEDANLITAGIWTIHFGLDNDLWASEDRMIDILKMDQLDIVGELLEDTQRITIGNRDLAKMAHDLGMYADFGPPGNKH	800
gi	10383785	ref	NP_009943.2	VYVFFAVALLSLTARFYDIR-PTGVPQYPHEDSOLITAGIWTIHFGLDNDLWASEDRMIDILKMDQLDIVGELLEDTQRITIGNRDLAKMAHDLGMYADFGPPGNKH	794
gi	145608108	ref	XP_360833.2	KHYIIVLGAINVAFVLAAYLRFPINDYKPYHAPDRVITAGIWTIHFGLDNDLWASEDRMIDILKMDQLDIVGELLEDTQRITIGNRDLAKMAHDLGMYADFGPPGNKH	791
gi	32410539	ref	XP_325750.1	KHYVGIILGLLNLPLVANFLRFPISYDKPYHAEDRLITAGIWTIHFGLDNDLWASEDRMIDILKMDQLDIVGELLEDTQRITIGNRDLAKMAHDLGMYADFGPPGNKH	827
gi	63054589	ref	NP_594060.2	KKSLLTGFCALMALMKAFAIQMPPDYTPYHNEKLFITAGIWTIHFGLDFMVASENRIRDAVDRMELLDVGLLESDFQRLIMGFRDLQVLAHDLGMYADFGPPGNKH	818



gi	21704104	ref	NP_663535.1	LVDFVVTG-FGNHEDDLDRKLQAIAVSKLLKNC--SNQVIFLGYITSEPGSRDYTLQIKH-GNVKIDIDSSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	677
gi	109499624	ref	XP_223359.4	LVDFVVTG-FGNHEDDLDRKLQAIAVSKLLKNC--SNQVIFLGYITSEPGSRDYTLQIKH-GHVKIDIDSSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	748
gi	156151386	ref	NP_079363.2	LVDFVVTG-FGNHEDDLDRKLQAIAVSKLLKSS--SNQVIFLGYITSEPGSRDYTLQIKH-GNVKIDIDSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	677
gi	114594913	ref	XP_517303.2	LVDFVVTG-FGNHEDDLDRKLQAIAVSKLLKSS--SNQVIFLGYITSEPGSRDYTLQIKH-GNVKIDIDSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	836
gi	73975266	ref	XP_539262.2	LVDFVVTG-FGNHEDDLDRKLQAIAVSKLLKSS--SNQVIFLGYITSEPGSRDYTLQIKH-GNVKIDIDSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	683
gi	194667872	ref	XP_001253517.2	PVDFVVTG-FGNHEDDLDRKLQAIAVSKLLKNS--SEQVIFLGYITSEPGSRDYTLQIKH-GNVKIDIDSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	677
gi	118090529	ref	XP_420716.2	LIDFVVAH-FGNEEDDLDRKLQAIAVSKLLKFS--SKQVIFLGYITSEPGSRDYTELIEH-GNVQIDIDSDGRDWCYIIMYRGLIRLGYARISHAELSDSEIOMAKFRIPD	692
gi	50303095	ref	XP_451485.1	LVDFVVTG-SQGEDEEDDRRLQSEAMAEIMGST--DRPSILLSVLVKKPQDNVNIYVSDKSCMYDIDPDEDRCWCYIILYKLLKRAVYRSTRITIDTELOVAKFQVLP	960
gi	45190564	ref	NP_984818.1	LVDFVVTG-SQGEDEEDDRRLQSEALRDMIGAR--DRPGILLSVLVKKPQDNVNIYVSEASGMQIDPDEDRCWCYIILYKLLKRTGFARVSTRITIDTELOVAKFQVLP	936
gi	10383785	ref	NP_009943.2	LVDFVVTG-SQGEDEEDDRRLQSNYMAKLMGNT--TRPALLSVLVVPEGNVNTYVSEASGMQIDPDEDRCWCYIILYKLLKRTGFARVSTRITIDTELOVAKFQVLP	936
gi	145608108	ref	XP_360833.2	MVDVVFVH-SQGEDEEDDRRLQSEYMLRMGST--NRPSVLLSVLVTRPLEGNVNTYVSEASGMQIDPDEDRCWCYIILYKLLKRTGFARVSTRITIDTELOVAKFQVLP	938
gi	32410539	ref	XP_325750.1	LVDFVVTG-SQGEDEEDDRRLQSEYLAKLMGSIADRPALLSVLVTRPLEGNVNTYVSDISGMQIDPDEDRCWCYIILYKLLKRTGFARVSTRITIDTELOVAKFQVLP	975
gi	63054589	ref	NP_594060.2	LIDVVTG-SQGEDEEDDRRLQSTELARLMRES--PRPLVFLGYVTVNVGQ-EPQITLIRDTGMLDIEPADYDRWCYIILYKLLKRTGFARVSTRITIDTELOVAKFQVLP	951



gi	21704104	ref	NP_663535.1	YKEGHNEN-IHHFHMNTPKYFY--	699
gi	109499624	ref	XP_223359.4	YKEGHNEN-NHHFHMNTPKYFY--	770
gi	156151386	ref	NP_079363.2	YKEGHNEN-NHHFHMNTPKYFL--	699
gi	114594913	ref	XP_517303.2	YKEGHNEN-NHHFHMNTPKYFL--	858
gi	73975266	ref	XP_539262.2	YKEGHNEN-NHHFHMSTPKYFL--	705
gi	194667872	ref	XP_001253517.2	YKEGHNEN-NHHFHMSTPKYFL--	699
gi	118090529	ref	XP_420716.2	YKDGHNEN-IHHFHMSTPKYFKQTN	718
gi	50303095	ref	XP_451485.1	GERGHHVH-----VFDEPRYFN--	977
gi	45190564	ref	NP_984818.1	GVRGHRVH-----VFNEPRYFN--	953
gi	10383785	ref	NP_009943.2	GERGHRVH-----VFDEPRYFL--	953
gi	145608108	ref	XP_360833.2	GVRGHRVH-----VFDEPRYFN--	956
gi	32410539	ref	XP_325750.1	GVRGHHVH-----VFDEPRYFYF--	994
gi	63054589	ref	NP_594060.2	GVNGHYDN-----NLVVHEFWYD--	971

