

gi	110347402	ref	NP_034196.3	-----MPARTAPARVPALASGASLDPHVRRRLKDLERDGLTEKECVKELNLLHFLQTEIKSQCDDLETKLHKEELSEEGYLAKVKSLLNK	88
gi	29789295	ref	NP_445806.1	-----MPARTAPARVPALASGASLDPHVRRRLKDLERDGLTEKECVKELNLLHFLQTEIKSQCDDLETKLHKEELSEEGYLAKVKSLLNK	88
gi	195927037	ref	NP_001124295.1	-----MPARTAPARVPTLAVPAISLDDVRRRLKDLERDGLTEKECVKELNLLHFLQTEIKNQCDDLETKLHKEELSEEGYLAKVKSLLNK	88
gi	114675304	ref	XP_001163764.1	MAGSVPSFCTGYRLSPFGTSPPPRPDWGRRRLRSSLPLIGFRAKSRGACAAATAASAAS	150
gi	73986989	ref	XP_533919.2	-----MVHAASARRPSPVARKARAASAAAASAAVSAAS	122
gi	32880212	ref	NP_872592.1	-----MPARTAPARVPALASRAFSLPDDVRRRLKDLERDGLTEKECVKELNLLHFLQTEIKNQCDDLETKLHKEELSEEGYLAKVKSLLNK	88
gi	118122152	ref	XP_001235520.1	-----	
gi	40538748	ref	NP_571264.1	-----MPTKTSLSLPEDEVKERLQVLDDEGDSLSDEFCVKEKLRLLQEFLLADTQDDKLNEDKLRSSSELTEVVMSEVKAIVLKK	79
gi	15236676	ref	NP_192638.1	-----METKVGKDKKR---SVDSNDVSKERRPKRAAACRNFKKLRISDKSETVEAKKEQVVEEIVAIQLTSSLESNDPFRNRRITDF	84
gi	15236413	ref	NP_193150.1	-----MEMETKAGKDKKR---SVDSDDVSKERRPKRAAACNFKKESLRISDKSETVEAKKEQILAEETVAIQLTSSLESNDPFRNRRITDF	86
gi	15236318	ref	NP_193097.1	-----MKTAKGDKKR---SVDSDDVSRERRPKRATSGNFKKESLRFSKSEKIVETVEAKKEQ	54
gi	15239810	ref	NP_199727.1	-----MVENGAKAAKRRKRLPEIQEVEDVPRTRRRRAAACISFKKESIRVCEKSATIEVKKQQIVVEEFLALRLT-ALETVDVEDRPTRRINDF	89
gi	115455937	ref	NP_001051569.1		
gi	115470907	ref	NP_001059052.1		

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



gi	110347402	ref	NP_034196.3	DLSENGHTLTKAN--GCPANGSRP---TWRAEMADSNRSRPRPKPRGPRRSKSDSDILF-----ETSPSSVALTRRTROTITIAHFHKGPTKRRKPEESEEGNAEASAEERDQDKRRVVDVESGAAAA--VE	214
gi	29789295	ref	NP_445806.1	DLCLENGHLSITKAN--GCPANGSRP---TWKAEMADSNRSRPRPKPRGPRRSKSDSEIMI-----EASSSVATRRITROTITISHP-KGPAKRKPKDESEKGNANESAEERDQDKRRVAGVRESRFRAGSVE	216
gi	195927037	ref	NP_001124295.1	DLSENGAHANREVN--GRLENGQARREARRVGMADANSPPKPLSKPRTPRRSKSDGAKRSRDPASASQVVTGIRAEFSPPRITRKRSTROTITISHPFAKGPAKRKPQESERAKDESIKEEDKDQDEKRRRVSRRERVARPLPAE	236
gi	114675304	ref	XP_001163764.1	DLSENGAHANREVN--GRLENGQARREARRVGMADANSPPKPLSKPRTPRRSKSDGAEAK-----PEPSPPRITRKRSTROTITISHPFAKGPAKRKPQESERAKDESIKEEDKDQDEKRRRVSRRERVARPLPAE	282
gi	73986989	ref	XP_533919.2	DLSENGAHAFSREMN--GCLENGQTSGEDRRVGMANKSPKPKVSKLCTPRRSKSDGETKS-----EASSSPRITRROTITITISHPFARGPAKRKPEEPEPKAKSDDLEEE--NDQEEKRRRVSREQGARALPAE	254
gi	32880212	ref	NP_872592.1	DLSENGAHAFSREAN--GCLENGQTSGEDCRVVMKEKGPFPVSRLYTPRRRSKSDGETKS-----EVSS--PRITRKTROTITITISHPFARGPAKRKPEEPEPKAKSDDVDEE--KDQEEKRRRVSRRERVAGLLPAE	219
gi	118122152	ref	XP_001235520.1		
gi	40538748	ref	NP_571264.1	ALGVGKEGDGVEQNGHSNGFSENGSHKDNGEQEGAMDTPQDEGDAIKSPAPKGRGRRSKADSEF-----KKSPPASRVTRNTGKQIVVMSFR--VPKRKSDELNGEP--ANGDTF	188
gi	15236676	ref	NP_192638.1	VLHNSDGVPPQVEMLELGDIFLEGVVL--PLGDDKNEKKGVRVQSFGRVENWNISGYEDGSPVIWIS-----TALADYDCRKPASKYKLYDYFFEKACACVEVFKLSK---NPDTSLDELLAAVARSMS--GSKIFSSGGA	215
gi	15236413	ref	NP_193150.1	VLHDSGVPQVEMLELGDIFIEGVVL--PLGDDKNEKKGVRVQSFGRVENWNISGYEDGSPVIWIS-----TALADYDCRKPASKYKLYDYFFEKACACVEVFKLSK---NPDTSLDELLAAVARSMS--GSKIFSSGGA	217
gi	15236318	ref	NP_193097.1	-----IVDDKEKKGVRVQSFGRVENWNTISGYEDGSPVIWIS-----TVIADYDCRKPASKYKLYDYFFEKACACVEVCKNLSL---NPDTSLDELLAAVARSMS--GRKIFSSGGV	158
gi	15239810	ref	NP_199727.1	VLFDSDGVPPQVEMLELHDIFVSGAILPFDVCTDKEKKGVRVQSFGRVEHWSISGYEDGSPVIWIS-----TELADYDCRKPAAASYRKYDYIFYEKARASVAVYKLSKSGGDPDIGLELLAAVARSMS--GSKIFSSGGA	227
gi	115455937	ref	NP_001051569.1		
gi	115470907	ref	NP_001059052.1		

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



gi	110347402	ref	NP_034196.3	KLEEVTAQTGLGPEEPCQEDDNRSLRRHRELSSLRRKSKEDDPREARPEHLDEDEDGKDKRSSRPRSPQRPDPAKRRRPEAEPEQVAPETPEDRDEDEEREKRRRTTRKKLESHTVPSVRSERKAAQSKS-VIPKINSPKCPECG	363
gi	29789295	ref	NP_445806.1	KPERVRPQTGLCQEEQGEEDDRR-PRRQTRERLARRKSRREDDPREARPEHLDDVDDDEKDKRSSRPRSPQRPDLAKRRRPEAEPEQVAPETPEDRDEDEEREKRRRTTRKKLEPELSTVPSVRSERKASQKASAIPLKLNPPQCECG	364
gi	195927037	ref	NP_001124295.1	EPERAKSCTRTEKEEERDEKEEKR-LRSQTKETPKQKLKEEPDREARAGVQADEDED-GDEKDEKRRSPQKDLAARRRPEEKEPEKVNQVISEKDEDEKEEKRRTTPKEP-----TEKKMARAKTVMNSKHPPKCIQCGQ	374
gi	114675304	ref	XP_001163764.1	EPERAKSCTRTEKEEERDEKEEKR-LRSQTKETPKQKLKEEPDREARAGVQADEDED-GDEKDEKRRSPQKDLAARRRPEEKEPEKVNQVISEKDEDEKEEKRRTTPKEP-----TEKKMARAKTVMNSKHPPKCIQCGQ	420
gi	73986989	ref	XP_533919.2	EPERVQPGTHMDEEEREKEEKR-LRSQTKETPKPKSKEEPDREGRTG-LQEMD--GDEKDEKRRSPQKDLAARRRPEEKEPEKVNQVISEKDEDEKEEKRRTTPKEP-----TEKKMARAKTVVSSKHPLRCVQCGQ	390
gi	32880212	ref	NP_872592.1	EPGRVPRGTHMDEEG-RDDKEEKR-LRSQTKETPKHKAKEEPDRDVRPQGAQEMNE-GEDKDEKRRSPQKDLAARRRPEEKEPEKVNQVISEKDEDEKEEKRRTTPREL-----TEKKMTRAKIAVSKINPPKCTECLQ	356
gi	118122152	ref	XP_001235520.1	-----EEEELEKEQDEKR-IKIEIKEGE-----IKTEITTEVREKR-IKTEDEKPE-----IKDEITQVKTSTPAKTPPKCVDCRQ	98
gi	40538748	ref	NP_571264.1	-----IKTEITTEVREKR-IKTEDEKPE-----VALRIDESQLVKSDDLHVDGAEEDVRYAKLIG-----AENAANLKPVSTAKTPPKCPCDRQ	238
gi	15236676	ref	NP_192638.1	IQEFVISQGEFIYNLAGLDETAKNHEFCFVENRVLVSLRDHESKTHKALS-----VALRIDESQVVTSDHLVDGAEEDVRYAKLIG-----EEEEYRISMERSRNKRSSTTS-ASNKF	325
gi	15236413	ref	NP_193150.1	IQEFVISQGEFIYNLAGLDETAKNHEFCFVENRVLVSLRDHESKTHKALS-----VALRIDESQVVTSDHLVDGAEEDVRYAKLIG-----VALRIDESQVVTSDHLVDGAEEDVRYAKLIG-----EEEEYRISMERSRNKRSSTTSGGSSRF	328
gi	15236318	ref	NP_193097.1	IQEFVISQGEFIYNLAGLDETAKNHEFCFVDRVSLRD-ESRKHKALFSN-----VALRIDESQVVTSDLMGGEEDLKYAKLIG-----EEEEYRISMERSRNKRSSTTS-APNKF	267
gi	15239810	ref	NP_199727.1	IIDFVISQGEFIYNLAGLDETAKNHEFCFVDRVSLRD-ESRKHKALFSN-----VALRIDESQVVTSDLMGGEEDLKYAKLIG-----DEENKSMQER-KNESSSGS-ASNMF	345
gi	115455937	ref	NP_001051569.1		
gi	115470907	ref	NP_001059052.1		

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



gi|110347402|ref|NP\_034196.3|... 497  
gi|29789295|ref|NP\_445806.1|... 498  
gi|195927037|ref|NP\_001124295.1|... 508  
gi|114675304|ref|XP\_001163764.1|... 554  
gi|73986989|ref|XP\_533919.2|... 524  
gi|32880212|ref|NP\_872592.1|... 490  
gi|118122152|ref|XP\_001235520.1|... 222  
gi|40538748|ref|NP\_571264.1|... 373  
gi|15236676|ref|NP\_192638.1|... 472  
gi|15236413|ref|NP\_193150.1|... 475  
gi|15236318|ref|NP\_193097.1|... 378  
gi|15239810|ref|NP\_199727.1|... 491  
gi|115455937|ref|NP\_001051569.1|  
gi|115470907|ref|NP\_001059052.1|

.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|110347402|ref|NP\_034196.3|... 643  
gi|29789295|ref|NP\_445806.1|... 645  
gi|195927037|ref|NP\_001124295.1|... 657  
gi|114675304|ref|XP\_001163764.1|... 703  
gi|73986989|ref|XP\_533919.2|... 672  
gi|32880212|ref|NP\_872592.1|... 638  
gi|118122152|ref|XP\_001235520.1|... 222  
gi|40538748|ref|NP\_571264.1|... 521  
gi|15236676|ref|NP\_192638.1|... 600  
gi|15236413|ref|NP\_193150.1|... 603  
gi|15236318|ref|NP\_193097.1|... 506  
gi|15239810|ref|NP\_199727.1|... 618  
gi|115455937|ref|NP\_001051569.1|  
gi|115470907|ref|NP\_001059052.1|

.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|110347402|ref|NP\_034196.3|... 790  
gi|29789295|ref|NP\_445806.1|... 792  
gi|195927037|ref|NP\_001124295.1|... 804  
gi|114675304|ref|XP\_001163764.1|... 850  
gi|73986989|ref|XP\_533919.2|... 819  
gi|32880212|ref|NP\_872592.1|... 785  
gi|118122152|ref|XP\_001235520.1|... 222  
gi|40538748|ref|NP\_571264.1|... 667  
gi|15236676|ref|NP\_192638.1|... 740  
gi|15236413|ref|NP\_193150.1|... 748  
gi|15236318|ref|NP\_193097.1|... 647  
gi|15239810|ref|NP\_199727.1|... 768  
gi|115455937|ref|NP\_001051569.1|  
gi|115470907|ref|NP\_001059052.1|

.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi	110347402	ref	NP_034196.3		QMMFHAHWFCAGTDTVLGATSDPLELFLVDECEENMOLSYIHSKVKVIYKAPSENWAMEGGTDEPETLPGAEDGKTYFFQLWYDQYARFESPPKTOPEDNKKHKFCLSCIRLAELRQKEMPKVLEGLEEVGDG--RVYCSSITKNGVVYRL	938
gi	29789295	ref	NP_445806.1		-QMFHAHWFCAGTDTVLGATSDPLELFLVDECEENMOLSYIHSKVKVIYRGPSPNWAMEGGMDPEAMLPGAEDGKTYFFQLWYDQYARFESPPKTOPAEDNKKHKFCLSCIRLAELRQKEMPKVLEGLEEVGDG--RVYCSSITKNGVVYRL	939
gi	195927037	ref	NP_001124295.1		QMFHAHWFCAGTDTVLGATSDPLELFLVDECEENMOLSYIHSKVKVIYKAPSENWAMEGGMDPEESLLE-GDDGKTYFFQLWYDQYARFESPPKTOPEDNKKHKFCLSCIRLAELRQKEMPKVLEGLEEDLDS--RVLYYSATKNGILYRV	951
gi	114675304	ref	XP_001163764.1		QMFHAHWFCAGTDTVLGATSDPLELFLVDECEENMOLSYIHSKVKVIYKAPSENWAMEGGMDPEESLLE-GDDGKTYFFQLWYDQYARFESPPKTOPEDNKKHKFCLSCIRLAELRQKEMPKVLEGLEEDLDS--RVLYYSATKNGILYRV	997
gi	73986989	ref	XP_533919.2		QMFHAHWFCAGTDTVLGATSDPLELFLVDECEENMOLSYIHSKVKVIYKAPSENWALEGGMDPEALIT-EDDGKTYFFQLWYDQYARFESPPKTOPEDNKKYKFCVSCARLAEMRQKEIPRVLEGLEEDLDS--RVLYYSATKNGIQYRV	966
gi	32880212	ref	NP_872592.1		QMFHAHWFCAGTDTVLGATSDPLELFLVDECEENMOLSYIHSKVKVIYKAPSENWAMEGGMDPEALMS-EDDGKTYFFQLWYDQYARFESPPKTOPEDNKKYKFCVSCARLAEMRQKEIPRVLEGLEEDLDS--RVLYYSATKNGIQYRV	932
gi	118122152	ref	XP_001235520.1		-----	222
gi	40538748	ref	NP_571264.1		-KMFHAHWFCRGTDTVLGATSDPLELFLVDECEENMOLSFHIGKVNVIYKAPSENWAMEGGMDPEALMS-EDDGKTYFFQLWYDQYARFESPPKTOPEDNKKYKFCVSCARLAEMRQKEIPRVLEGLEEDLDS--RVLYYSATKNGIQYRV	815
gi	15236676	ref	NP_192638.1		CKMLHGKLLQRGSETVIGLAANERELFLNECLTVHLKDIKGTVSLDIRSRPWGHQYRKENLVVDKLDRAAEERKANGLPTEYYCKSLYSPERGGFFSLPRNDIGLGSFCSSCKIKKEEERESKTKLNI-----KIGVFSNGIEYVN	885
gi	15236413	ref	NP_193150.1		SKMLHGKLLQRGSETVIGLAANERELFLNECLTVHLKDIKGTVSLDIRSRPWGHQYRKENLVVDKLDRAAEERKANGLPTEYYCKSLYSPERGGFFSLPRNDIGLGSFCSSCKIKKEEERESKTKLNI-----KIGVFSNGIEYVN	893
gi	15236318	ref	NP_193097.1		SKMLHGKLLQRGSETVIGLAANERELFLNECLTVHLKDIKGTVSLDIRSRPWGHQYRKENLVVDKLDRAAEERKANGLPTEYYCKSLYSPERGGFFSLPRNDIGLGSFCSSCKIKKEEERESKTKLNI-----KIGVFSNGIEYVN	792
gi	15239810	ref	NP_199727.1		CKMLHGKLLQRGSETVIGLAANERELFLNECLTVHLKDIKGTVSLDIRSRPWGHQYRKENLVVDKLDRAAEERKANGLPTEYYCKSLYSPERGGFFSLPRNDIGLGSFCSSCKIKKEEERESKTKLNI-----KIGVFSNGIEYVN	913
gi	115455937	ref	NP_001051569.1		-----	
gi	115470907	ref	NP_001059052.1		-----	

.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi	110347402	ref	NP_034196.3		GDSVYLPPAEFTFNKIVASPVKR-PKKDPVNE---TLYP-EHYRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	1082
gi	29789295	ref	NP_445806.1		GDSVYLPPAEFTFNKIVASPMKR-SKRDPVNE---NPVPRDTRRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	1085
gi	195927037	ref	NP_001124295.1		GDSVYLPPAEFTFNKIVASPVKR-PRKEPVDE---DLYP-EHYRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	1096
gi	114675304	ref	XP_001163764.1		GDSVYLPPAEFTFNKIVASPVKR-PRKEPVDE---DLYP-EHYRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	1142
gi	73986989	ref	XP_533919.2		GDSVYLPPAEFTFNKIVASPVKR-PRKEPVDE---DLYP-EHYRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	1111
gi	32880212	ref	NP_872592.1		GDSVYLPPAEFTFNKIVASPVKR-PRKEPVDE---DLYP-EHYRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	1077
gi	118122152	ref	XP_001235520.1		-----	222
gi	40538748	ref	NP_571264.1		GDSVYLPPAEFTFNKIVASPVKR-SHRKDDVDE---DLYP-EHYRKYSDYIKGNSLDAPEPYRIGRIKEIHCCKKKG-KVNEADIKLRLYKFRPENTHRSYNGSYHDIINMLYWSDEEAVVNFSDVQGRCTVEYGEDLLESIDYSGGGP	961
gi	15236676	ref	NP_192638.1		GDFVYVLPNYITKDKLKKGTSRRTILKCGRNVGLKA-----FVVCQLLDVIVLEESRKAASFQVKLTRFYRPEDISE--EKAYASDIQELYSQDTYILPPEALGKCEVRKKSMDPLCREYPIILD--	1006
gi	15236413	ref	NP_193150.1		GDFVYVLPNYITKDKLKKGTSRRTILKCGRNVGLKA-----FVVCQLLDVIVLEESRKAASFQVKLTRFYRPEDISE--EKAYASDIQELYSQDTYILPPEALGKCEVRKKSMDPLCREYPIILD--	1013
gi	15236318	ref	NP_193097.1		GDFVYVLPNYITKDKLKKGTSRRTILKCGRNVGLKA-----FVVCQLLDVIVLEESRKAASFQVKLTRFYRPEDISE--EKAYASDIQELYSQDTYILPPEALGKCEVRKKSMDPLCREYPIILD--	909
gi	15239810	ref	NP_199727.1		GDFVYVLPNYITKDKLKKGTSRRTILKCGRNVGLKA-----FVVCQLLDVIVLEESRKAASFQVKLTRFYRPEDISE--EKAYASDIQELYSQDTYILPPEALGKCEVRKKSMDPLCREYPIILD--	1029
gi	115455937	ref	NP_001051569.1		EDFVYVLPNYITKDKLKKGTSRRTILKCGRNVGLKA-----FVVCQLLDVIVLEESRKAASFQVKLTRFYRPEDISE--EKAYASDIQELYSQDTYILPPEALGKCEVRKKSMDPLCREYPIILD--	
gi	115470907	ref	NP_001059052.1		-----	

.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi	110347402	ref	NP_034196.3		DRFYFLEAYNAKSKTGFEDPPN---HARSPGNKGGKGGKGGKGGKGVSEPKK---PEAAIKLPKLRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1198
gi	29789295	ref	NP_445806.1		DRFYFLEAYNAKSKTGFEDPPN---HARSPGNKGGKGGKGGKGGKGVSEPKK---PEAAIKLPKLRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1201
gi	195927037	ref	NP_001124295.1		NRFYFLEAYNAKSKTGFEDPPN---HARSPGNKGGKGGKGGKGGKGVSEPKK---PEAAIKLPKLRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1212
gi	114675304	ref	XP_001163764.1		NRFYFLEAYNAKSKTGFEDPPN---HARSPGNKGGKGGKGGKGGKGVSEPKK---PEAAIKLPKLRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1258
gi	73986989	ref	XP_533919.2		DRFYFLEAYNAKSKTGFEDPPN---HARSPGNKGGKGGKGGKGGKGVSEPKK---PEAAIKLPKLRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1227
gi	32880212	ref	NP_872592.1		DRFYFLEAYNAKSKTGFEDPPN---HARSPGNKGGKGGKGGKGGKGVSEPKK---PEAAIKLPKLRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1193
gi	118122152	ref	XP_001235520.1		-----	222
gi	40538748	ref	NP_571264.1		DRFYFLEAYNAKSKTGFEDPPN---HARSAVNGKGGKGGKGGKGGKQSRRTTGSQAQEPVVPKLRRLDVFSGCGGLSEGFGHAGISETLWAIEMWDPAAQAFRLNPNPGTIVFTEDCNVLLK	1079
gi	15236676	ref	NP_192638.1		HIFFCVDFYDSSITGYLKQFPANMKLKFSTIKDETLLREKKGKGVETGTSSGMLMKPDEVPKPKLATLDIFAGCGGLSHGLEKAGVSDIKWAIYEPEPAGHAFKQNHPEAVTFVDCNVIL-----RAIMEKCGDVDDCVSTVE	1145
gi	15236413	ref	NP_193150.1		HIFFCVDFYDSSITGYLKQFPANMKLKFSTIKDETLLREKKGKGVETGTSSGMLMKPDEVPKPKLATLDIFAGCGGLSHGLEKAGVSDIKWAIYEPEPAGHAFKQNHPEAVTFVDCNVIL-----RAIMEKCGDVDDCVSTVE	1152
gi	15236318	ref	NP_193097.1		HIFFCVDFYDSSITGYLKQFPANMKLKFSTIKDETLLREKKGKGVETGTSSGMLMKPDEVPKPKLATLDIFAGCGGLSHGLEKAGVSDIKWAIYEPEPAGHAFKQNHPEAVTFVDCNVIL-----RAIMEKCGDVDDCVSTVE	1054
gi	15239810	ref	NP_199727.1		HIFFCVDFYDSSITGYLKQFPANMKLKFSTIKDETLLREKKGKGVETGTSSGMLMKPDEVPKPKLATLDIFAGCGGLSHGLEKAGVSDIKWAIYEPEPAGHAFKQNHPEAVTFVDCNVIL-----RAIMEKCGDVDDCVSTVE	1167
gi	115455937	ref	NP_001051569.1		-----	
gi	115470907	ref	NP_001059052.1		-----	

.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi	110347402	ref	NP_034196.3		-LVMAGEVINSLGRLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1347
gi	29789295	ref	NP_445806.1		-LVMAGEVINSLGRLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1350
gi	195927037	ref	NP_001124295.1		-LVMAGETTNSRGRLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1361
gi	114675304	ref	XP_001163764.1		-LVMAGETTNSRGRLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1407
gi	73986989	ref	XP_533919.2		-LVMAGEATNSRGKRLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRYFLLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1376
gi	32880212	ref	NP_872592.1		-LVMAGEVINSRGKLLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRYFLLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1342
gi	118122152	ref	XP_001235520.1		-----	222
gi	40538748	ref	NP_571264.1		-LVMSEKIKNSLGGKRLPKGQDVEMLCGGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRKFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1228
gi	15236676	ref	NP_192638.1		AAELVAKLDENQKSTLPLPGQADFISSGPPCGGFGMNRFDGSSWSKVQCEMILAFSLFADYFRPKYFLLLENVKKFVYTKNGRTFQLTMASLLEIGYQVRFGLLEAGTYGVSQPRKRVI IWAASPEEVLPEWPEPMHVFDPNGSKISLPR	1295
gi	15236413	ref	NP_193150.1		AAELAALKLDENQKSTLPLPGQVDFINSGPPCGGFGMNRFSHGSSWSKVQCEMILAFSLFADYFRPKYFLLLENVKKFVYTKNGRTFQLTMASLLEMGYQVRFGLLEAGTYGVSQPRKRVI IWAASPEEVLPEWPEPMHVFDPNGSKISLPR	1302
gi	15236318	ref	NP_193097.1		AAELATKLDENQKSTLPLPGQVDFISGPPCGGFGMNRFRNSRYSKFKNSLVVSVLSYCDYRPRFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1204
gi	15239810	ref	NP_199727.1		ANELAALKLIEQKSTLPLPGQVDFINSGPPCGGFGMNRFSHGSSWSKVQCEMILAFSLFADYFRPKYFLLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	1317
gi	115455937	ref	NP_001051569.1		AAERAALKLSEDKIKNLPVPGVEVEFINSGPPCGGFGMNRFSHGSSWSKVQCEMILAFSLFADYFRPKYFLLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	202
gi	115470907	ref	NP_001059052.1		AAEQAAKFSQDNIMNLPVPGVEVEFINSGPPCGGFGMNRFSHGSSWSKVQCEMILAFSLFAEYFRPRFFLLENVNRNFSVFRKSMVLKLLRCLVLRMGYQCTFGVLQAGQYVVAQTRRRRAIILAAAPGKELPLFPPEPLHVFAPRACQLSVVV	233



gi	110347402	ref	NP_034196.3		DDKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKACDPSRQFNTL	1496
gi	29789295	ref	NP_445806.1		DDKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKICDPSRQFNTL	1499
gi	195927037	ref	NP_001124295.1		DDKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKICDPSRQFNTL	1511
gi	114675304	ref	XP_001163764.1		DDKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKICDPSRQFNTL	1557
gi	73986989	ref	XP_533919.2		DDKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKICDPSRQFNTL	1526
gi	32880212	ref	NP_872592.1		DDKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKICDPSRQFNTL	1491
gi	118122152	ref	XP_001235520.1		-----	222
gi	40538748	ref	NP_571264.1		DEKKFVSNITRLSSGPFRTITVRDITMSDLPEIRNGASNEIPIYNGEPLSFWFQRLRGSYQYPIILRDHICKDMSALVAARMRHIPFPGSDWRDLPIQVRLDGDVIAHKLOYTFHDVKNYSSSTGALRGVCSCAE-GKICDPSRQFNTL	1377
gi	15236676	ref	NP_192638.1		G-LHYDVRNITKFGAPFRSITVRDITGDLPLVENGESKINKEYRTTPVSWFKKIRGN--MSVLDTHICKGLNELNLRCKKIPKRPAGDWRDLDPDENVTLSN-----GLVEKL	1401
gi	15236413	ref	NP_193150.1		G-LRYDAGCNTKFGAPFRSITVRDITGDLPLVENGESKINKEYRTTPVSWFKKIRGN--MSVLDTHICKGLNELNLRCKKIPKRPAGDWRDLDPDENVTLSN-----GLVEKL	1408
gi	15236318	ref	NP_193097.1		G-LHYAAVQSKTKFGAPFRSITVRDITGDLPLVENGESKINKEYRTTPVSWFKKIRGN--MSVLDTHICKGLNELNLRCKKIPKRPAGDWRDLDPDENVTLSN-----GLVEKL	1299
gi	15239810	ref	NP_199727.1		G-LHYAAVRSITKFGAPFRSITVRDITGDLPLVENGESKINKEYRTTPVSWFKKIRGN--MSVLDTHICKGLNELNLRCKKIPKRPAGDWRDLDPDENVTLSN-----GLVEKL	1423
gi	115455937	ref	NP_001051569.1		G-KFYAAVRSITKFGAPFRSITVRDITGDLPLVENGESKINKEYRTTPVSWFKKIRGN--MSVLDTHICKGLNELNLRCKKIPKRPAGDWRDLDPDENVTLSN-----GLVEKL	308
gi	115470907	ref	NP_001059052.1		G-KFYAAAKSTAGGAPFRSITVRDITGDLPLVENGESKINKEYRTTPVSWFKKIRGN--MSVLDTHICKGLNELNLRCKKIPKRPAGDWRDLDPDENVTLSN-----GLVEKL	339



gi	110347402	ref	NP_034196.3		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEAAKTD	1619
gi	29789295	ref	NP_445806.1		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEETTID	1622
gi	195927037	ref	NP_001124295.1		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEAAKTD	1632
gi	114675304	ref	XP_001163764.1		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEAAKTD	1678
gi	73986989	ref	XP_533919.2		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEAAKTD	1645
gi	32880212	ref	NP_872592.1		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEAAKTD	1611
gi	118122152	ref	XP_001235520.1		-----	222
gi	40538748	ref	NP_571264.1		IPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVINPEPMGKQGRVLHPEQHRVSVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAKAIGLEIKLCLLSARESSASA AVKAKEEAAKTD	1499
gi	15236676	ref	NP_192638.1		RPLALSKTAKNHNHWAGLYGRLDWQGNLPISTIDPQPMGKVGCMCFHPEODRIITVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAFALGRKLEALYKSSSQHQS-----	1512
gi	15236413	ref	NP_193150.1		RPLALSKTAKNHNHWAGLYGRLDWQGNLPISTIDPQPMGKVGCMCFHPEODRIITVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAFALGRKLEALYKSSSQHQS-----	1519
gi	15236318	ref	NP_193097.1		VENLLNK-AKDHNGYKGLYGRLDWQGNLPISTIDPQPMGKVGCMCFHPEODRIITVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAFALGRKLEALYKSSSQHQS-----	1404
gi	15239810	ref	NP_199727.1		IPFCLPNTAERHNHWAGLYGRLDWQGNLPISTIDPQPMGKVGCMCFHPEODRIITVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAFALGRKLEALYKSSSQHQS-----	1534
gi	115455937	ref	NP_001051569.1		IPWCLPNTAKRHNHWAGLYGRLDWQGNLPISTIDPQPMGKVGCMCFHPEODRIITVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAFALGRKLEALYKSSSQHQS-----	413
gi	115470907	ref	NP_001059052.1		IPWCLPNTAKRHNHWAGLYGRLDWQGNLPISTIDPQPMGKVGCMCFHPEODRIITVRECARSGGFPDYSYRFFGNILDRHRVGVNAVPPPLAFALGRKLEALYKSSSQHQS-----	445

