

gi	145605417	ref	XP_364448.2	-----MSTPSSGR--TRSSQSAIPPSRNAARNAAGPNSAAEDQEPASSVVRGTPRGPROGQLASSPMFYQ--FSPANG--RTQEPSSPLRQMHQSTARRSNAIPSSPLRQDSDQDPERFRASG--SGLIGESPIRYESS	132
gi	32422589	ref	XP_331738.1	-----MSSPAKRRTTRSSQSAIP--RTTRSSQAGPS-----SALPTROTRAQLASSPLFYEPSSPANG--AAPVSSPLRQMSNTQSTAHQGNA--PSSPLRQDETQSDADRTFRANGRSOLIGDSSPIRYASS	118
gi	63054428	ref	NP_588004.2	-----MSSSQQSQ--RANLRLRP-----GRANS--SREAVDSSPLFFPASSPST-----RLITPRTTARTPLA--SSPLLFESSSPG--PNIPTQSSR--SHLLSQRNDLFDSS	91
gi	6325276	ref	NP_015344.1	-----MSSQSSSPTKEDNNSSPVVP-----NPDVVPQLSSPALFYS--SSSQG--DIYGRNNSQNLSSQGNIRAAG--SSPLNFPSSSQRNSVDFQSQGRQGRIRSSASASGRSR	105
gi	45187848	ref	NP_984071.1	-----MTSSPQR-----PQEASSPALFYNPSSSQP--DTYER-----GQONAGNMIG--SSPFHYPSSSQSQN-----RNRNGGAFSSQGVF	71
gi	50306041	ref	XP_452982.1	-----MSSPQAQ-----QPSNPLFYDPSFP--HGTQD-----GQASQDRGVG--SSPFHYPSSSNATQELARAAPPSSSGLREN-----	69
gi	42569072	ref	NP_179236.3	-----MADSSSLG-----MNDGPPSPGENVSSPIEN-----TYSSPAALHRRRRGRSSTPTFAFPFP-----PSSLASNS--	64
gi	17137242	ref	NP_477185.1	-----MSSPARSPS--VGGATPKQGARFTRGLAS--QDVTFMRMGPGR-----AVRSPDNISLFPSPGNISLPAFSPARGIGAN	73
gi	58386786	ref	XP_315054.2	-----MSSPARSTRRRRGDSSQENSQRTPMKSTSNSETETPMRIGSSMPNGASVAIESDQVTVPTSPAVDQPVLQASIFYGRAAG	84
gi	33469919	ref	NP_005905.2	-----MSSPA--STPSRRGRRRGRAPQAQTPRSEDARSSPQRRRGEDSTS--TGELOPMPSTSPGVLDQSPAADVLFSPPQMHSSAI	80
gi	114620052	ref	XP_528129.2	-----MSSPA--STPSRRGRRRGRAPQAQTPRSEDARSSPQRRRGEDSTS--TGELOPMPSTSPGVLDQSPAADVLFSPPQMHSSAI	80
gi	31982197	ref	NP_032591.2	-----MSSPA--STPSRRGRRRGRVTPQSLRSESRSSPNRRRGEDS--S--TGELLPMPSTSPGADLQSPAQNALFSSPPQMHSLAI	79
gi	34870013	ref	XP_344049.1	-----MSSPA--STPSRRGRRRGRVTPQSLRSESRSSPNRRRGEDS--S--TGELLPMPSTSPGADLQSPAQNALFSSPPQMHSLAI	79
gi	73999288	ref	XP_535063.2	MKRLADCRMCRGRRCRWREISSAYFVRESEPAQAFREPRGRVCGEGASRRYAAGTRFVLGGTPEAMSSPA--STPSRRGRRRGRVTPQSLRSESRSSPNRRRGEDSTS--TGELOPMPSTSPGADLQSPAADLALFSSPAQIQPSAI	146
gi	115495629	ref	NP_001068626.1	-----MSSPA--STPSRRGRRR--AAPA--PR--QDPL--SGEPQLPSSPQGAEPF-----TPSRAPPAAV	53
gi	118086936	ref	XP_424376.2	-----MSSPA--STPSRRGRRRGRG--NPPF--QDARSPFPQRRRPDQSA--TGELOPMPSTSP--PABQ--SPRADLALFSSPPQFRRSAI	77
gi	38707991	ref	NP_944595.1	-----MSSPS--QQRKR--DPPTPAS--EDPLSPQGRSRAHD--STELQPMPTSP-----AQDASLFSPPMAPRSVI	62
gi	17508417	ref	NP_490962.1	-----MGRNNDPAEPOSE--MPP--NDPAEPOSE--ADLFAEPSSQ-----HSSMRSGSEQVAGNMS	40
gi	124513100	ref	XP_001349906.1	-----MGTFRRLRGGQNNNNNSP-----FALSSSNIFGSSNNEIFGNSFMHTPMSRRRTKNSKSLNLSMLNESRYLQNSA	70



gi	145605417	ref	XP_364448.2	s-PGRAFNPDLTIRSESSGIFVGS-RSGSARNRRGDINPDALLR--SRPFRVVDLPSGNVTVV--GSDAPSFRTVNDP--SEANALGGDSSGLIWTIVSIDD--FASFKDFARNFTRKRLWSDGMTE--AETQRDDAESRPVMSAMET	276
gi	32422589	ref	XP_331738.1	SSSPGRQLQQSD--LRSESSQLFVSSQSRVAGRSRRRDINGDPLRTPAQIPRRRIILDGGRVIRDAPGSDANSFVNNPN--SEADALGGQSQGLVWGTITSLDD--FSAFKDFLRFNTRKRMWADGADE--AETIGHPPDADSKPVWALEAN	265
gi	63054428	ref	NP_588004.2	SQRTPRSRRRGD-----IHSSVQMSIPSRRRREVDQ--RPGVSTPSSLLFS--GSDALTFQAHF-----SEVADTVRVIVWTVNSIQEIASFRFLRGFKKKYRPSYR-----NELMPPDADQLVYIEALRN	209
gi	6325276	ref	NP_015344.1	YHSDLR--DRALPT--SS--SLGRNQNRVHMRRNDLHTS-----DLSSPRRIVDFD-----TRSGVNTLDTSS--SAPPSEASEFLRIIWGTIVNSIQEICTTNRNFKLMSFKYKFRKILD--ER--EFLINN--TDEELYYIKQLN	232
gi	45187848	ref	NP_984071.1	-----RERSYAG-----SSLPGTAR--RLQHYGR--DIHAS-----DLSSPRRNVFN-----SPS-----TLSSDPPSENDEPMRIWGTIVNSIQEIVACTFNFLMTFKYKFRKILD--EQ--ELFINE--TDEELYYVQLNH	186
gi	50306041	ref	XP_452982.1	-----NLRSDLLNYS-----SLSSAREGRHS--RSRRGEINAS-----DLSSPRRIVTFN-----NLSSDNGFSS--SRPSEAADQLKIWGTIVNSIQEIGNSFRFLMSFKLKRKELD--DQ--EIFINE--TDOELYYVQLN	193
gi	42569072	ref	NP_179236.3	-----PPTSRP--AAR-----KGRNGHGGGGGGGGGGDGF--TPMSTDEPLPSSD-----DGEDGGDDTTPFVWGTIVNSIQDVKSAIEMFVKHFRARENSD-----LFRGKVMYSIRK	166
gi	17137242	ref	NP_477185.1	MSEIDLSSPLNYGT--PSSMGSIRTPRS--GIRGTP--LRARPDIR--DKRIR--VAIGGG--SGLLEPIPKGSET--DPVSESSQAPQLVWGTIVNVVSGCKSKFIMRFIDPSAEQDEISEN-----IDVNGPLVLOKLE	202
gi	58386786	ref	XP_315054.2	MSQIDISSPLNYGT--PSSMGSIRTPRS--GVRGTP--MRQRPDLRVKLP--ROVNVVSGSD--AAHLDP--IQEES--QASAGDIP--SSGPRLVVWGTIVNVVTECMKSFQFILRYIDPNAADDELTEG-----INLNEPLVMORLGE	212
gi	33469919	ref	NP_005905.2	PLDFDVSSPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--AAAEDIVASEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	199
gi	114620052	ref	XP_528129.2	PLDFDVSSPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--AAAEDIVASEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	199
gi	31982197	ref	NP_032591.2	PLDFDVSSPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--AAAEDIVASEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	198
gi	34870013	ref	XP_344049.1	PLDFDVSSPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--AAAEDIVASEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	198
gi	73999288	ref	XP_535063.2	PLDFDVSSPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--AAAEDIVASEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	265
gi	115495629	ref	NP_001068626.1	PLDLDMSPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--AAAEDIVASEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	172
gi	118086936	ref	XP_424376.2	PLDFDISPLTYGT--PSSR--VEGT--PRSGVRGTP--VRQRPDLGSAQKGLQVDLQSDG--PABDLVTAEC-----SLGQKLVWGTIVNVVATCKENFQRFQRFIDPLA--KEEENVG--IDITEPLYMORLGE	181
gi	38707991	ref	NP_944595.1	QSEIDASSPLMYGT--PSSR--VEGT--PRSGIRGTP--ARQRADLGSVRKAPQVDMHSEF--ASGDAAVAGDQ--GAGQRLVWGTIVNVVGTCKEKFQRFQRFIDPLA--KEEENAG--LDLNEPLVMORLGE	195
gi	17508417	ref	NP_490962.1	PRSSASALQYGS--EMGSVSS--MSAS--TLRRG--GPRGDLGIAADVHR--VQIRG--MEDEMGADD--GQPRVYVWGTIVNVVATCKEKFQRFQRFIDPLA--KEEENAG--LDLNEPLVMORLGE	163
gi	124513100	ref	XP_001349906.1	GSQFIKYGHPLAIR--RIKCARADIGDVGREAFMEDVESRLPHFIDSNLEQIKELFN--QFFDEFNINYSVDVLD--TDEDRSISEYLLHRRDNLKVLAYG--WKMIKFI--ETGRQNECLRN--TNYEDDENNENSEGI	205



gi	145605417	ref	XP_364448.2	MLLLTGTSRLYVLDRLDKAVPRTIKLWHQIQAMVQELVPIIMDQALTNMMEDELAQAEVMR--RSQSSAGARATPMAA--PSSEPOYASSEFGG--PATPRPGAEPENDLEQVAQTTVAIRPFGLKLTNLRDLNPSDDMDKLVTKGVLVIRITPV	425
gi	32422589	ref	XP_331738.1	MLLLTGTLKLYLDRDLKAVPRTIKLWHQIAHQYPTIILPVMQCVHDCMMELAQKEMASQR--ASONSRTAPGAQO--HSEPNFPSSERSEPPTPRPAQTAARTEDQVQSMVAVVRVMDGDKITNLRDLNPSDDMDKLVTKGVLVIRITPV	412
gi	63054428	ref	NP_588004.2	MRIMGLEILLNLDVQDLKHVPTTKLKHOLYSPOEIIIPIMDQIKDVMVLDLGG--NPPEDVLDLIELKIKRIFPNLEKICINMRDLNPGDIDKLVTKGVLVIRITPV	315
gi	6325276	ref	NP_015344.1	MRELGTNLDARNLLAYKQTEDLHQLLNVPOEVISIMDQIKDVMVLDLGG--LDYVLDLIEETKFKVFRVYVNSGCKGMRELNPNDIDKLVTKGVLVIRITPV	338
gi	45187848	ref	NP_984071.1	MRLQGTGNLNLDRNLLSFGTEKLYHOLLNVPOEVISIMDQAVKDCMVQLAVDIDG--AEGENLIEESKIKRIPYVNSGCKGMRELNPNDIDKLVTKGVLVIRITPV	295
gi	50306041	ref	XP_452982.1	MRLQGTGNLNLDRNLLAVKHTKLFHQLYVPEIITAIMDQIKDVMVSLALDNG--LESVLINEIESKIKRIPYVNSGCKGMRELNPNDIDKLVTKGVLVIRITPV	269
gi	42569072	ref	NP_179236.3	VTEIEGEWIDVDAFDVFDYD--DLNKMVRVPLEVLAIFDIVLMDLVS--INLRLEKHHVQVRFVFNRLTSTSMRNLNPSDIEKMLISGKMLIRSSSI	290
gi	17137242	ref	NP_477185.1	IHTLEEPVNLNCAHLKIFDQD--LYRQLICYPOEVIIPGFDMAINEMFFER--YPAALLEHQLQVRFNADKTRNMRSLNPEDDMDLITISGMVIRTSNI	298
gi	58386786	ref	XP_315054.2	IHTLEEPVNLNCAHLKIFDQD--LYRQLICYPOEVIIPGFDMAINEMFFER--YPAALLEHQLQVRFNADKTRNMRSLNPEDDMDLITISGMVIRTSNI	308
gi	33469919	ref	NP_005905.2	INVIQEPFLNVNCEHIKSFQDN--LYRQLISYPOEVIPTFDMAVNEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	295
gi	114620052	ref	XP_528129.2	INVIQEPFLNVNCEHIKSFQDN--LYRQLISYPOEVIPTFDMAVNEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	295
gi	31982197	ref	NP_032591.2	INVIQEPFLNVNCEHIKSFQDN--LYRQLISYPOEVIPTFDMAVNEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	294
gi	34870013	ref	XP_344049.1	INVIQEPFLNVNCEHIKSFQDN--LYRQLISYPOEVIPTFDMAVNEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	294
gi	73999288	ref	XP_535063.2	INVIQEPFLNVNCEHIKSFQDN--LYRQLISYPOEVIPTFDMAVNEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	361
gi	115495629	ref	NP_001068626.1	INVIQEPFLNVNCEHIKSFQDN--LYRQLISYPOEVIPTFDMAVNEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	268
gi	118086936	ref	XP_424376.2	INNVGEPFLNVNCDHLRAFEN--LYRQLICYPOEVIPTFDMAANEIFFDR--YPSILEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	291
gi	38707991	ref	NP_944595.1	ISVVGEPVNLNCTHIQTFDAD--LYRQLICYPOEVIPTFDMSVNEIFFDR--FNSVLEHQLQVRFNALKTKSMRNLNPEDDIDOLITISGMVIRTSNI	277
gi	17508417	ref	NP_490962.1	CNDAEVTIINLNLKHLNFASEA--LYRKVIAYPADVIYPLDIVVNEVFAER--FNR--HLAQSIELRPFNAQIKRNRNLNPEDDIDOLITISGMVIRTSNI	258
gi	124513100	ref	XP_001349906.1	RNLEHIKSFEEIDLTHIFFNKK--LYKLLIEYPSDCISEIDKILSTKNSLLALVLEG--DTRS--SSDKYPLS--KQDYCRVRFNKKKHDTPRKLGNQIETLVCKVGVIRITPV	318



gi|145605417|ref|XP\_364448.2|...  
gi|32422589|ref|XP\_331738.1|...  
gi|63054428|ref|NP\_588004.2|...  
gi|6325276|ref|NP\_015344.1|...  
gi|45187848|ref|NP\_984071.1|...  
gi|50306041|ref|XP\_452982.1|...  
gi|42569072|ref|NP\_179236.3|...  
gi|17137242|ref|NP\_477185.1|...  
gi|58386786|ref|XP\_315054.2|...  
gi|33469919|ref|NP\_005905.2|...  
gi|114620052|ref|XP\_528129.2|...  
gi|31982197|ref|NP\_032591.2|...  
gi|34870013|ref|XP\_344049.1|...  
gi|73999288|ref|XP\_535063.2|...  
gi|115495629|ref|NP\_001068626.1|...  
gi|118086936|ref|XP\_424376.2|...  
gi|38707991|ref|NP\_944595.1|...  
gi|17508417|ref|NP\_490962.1|...  
gi|124513100|ref|XP\_001349906.1|...  
...460...470...480...490...500...510...520...530...540...550...560...570...580...590...600



gi|145605417|ref|XP\_364448.2|...  
gi|32422589|ref|XP\_331738.1|...  
gi|63054428|ref|NP\_588004.2|...  
gi|6325276|ref|NP\_015344.1|...  
gi|45187848|ref|NP\_984071.1|...  
gi|50306041|ref|XP\_452982.1|...  
gi|42569072|ref|NP\_179236.3|...  
gi|17137242|ref|NP\_477185.1|...  
gi|58386786|ref|XP\_315054.2|...  
gi|33469919|ref|NP\_005905.2|...  
gi|114620052|ref|XP\_528129.2|...  
gi|31982197|ref|NP\_032591.2|...  
gi|34870013|ref|XP\_344049.1|...  
gi|73999288|ref|XP\_535063.2|...  
gi|115495629|ref|NP\_001068626.1|...  
gi|118086936|ref|XP\_424376.2|...  
gi|38707991|ref|NP\_944595.1|...  
gi|17508417|ref|NP\_490962.1|...  
gi|124513100|ref|XP\_001349906.1|...  
...610...620...630...640...650...660...670...680...690...700...710...720...730...740...750



gi|145605417|ref|XP\_364448.2|...  
gi|32422589|ref|XP\_331738.1|...  
gi|63054428|ref|NP\_588004.2|...  
gi|6325276|ref|NP\_015344.1|...  
gi|45187848|ref|NP\_984071.1|...  
gi|50306041|ref|XP\_452982.1|...  
gi|42569072|ref|NP\_179236.3|...  
gi|17137242|ref|NP\_477185.1|...  
gi|58386786|ref|XP\_315054.2|...  
gi|33469919|ref|NP\_005905.2|...  
gi|114620052|ref|XP\_528129.2|...  
gi|31982197|ref|NP\_032591.2|...  
gi|34870013|ref|XP\_344049.1|...  
gi|73999288|ref|XP\_535063.2|...  
gi|115495629|ref|NP\_001068626.1|...  
gi|118086936|ref|XP\_424376.2|...  
gi|38707991|ref|NP\_944595.1|...  
gi|17508417|ref|NP\_490962.1|...  
gi|124513100|ref|XP\_001349906.1|...  
...760...770...780...790...800...810...820...830...840...850...860...870...880...890...900



gi		145605417		ref		XP_364448.2		-----EILPVEFLTSYISYARANIHPITIQEAAARELVDAVEMRKLGEDVRSAEKRIITATTTROLESMIRLSEAHAKMRLATEVVSASDVREANRLIKSAL	927
gi		32422589		ref		XP_331738.1		-----DVLPEVEFLTSYISYARSHIHPALTPBAGRELVDAVEMRKLGDVRAAEKRIITATTTROLESMIRLSEAHAKMRLAQTVTRDDVREAVRLIKSAL	911
gi		63054428		ref		NP_588004.2		-----EVPFVEFLTSYITTYARNINPVISBEAAKELVNAYVGMRKLGEDVRAAEKRIITATTTROLESMIRLSEAHAKMRLRNVEVGDVLEAARLIKTAI	810
gi		6325276		ref		NP_015344.1		-----DVLPEVEFLTMYISYAKEHIHPITTEAAKTELVRAYVGMRKMGDDSRSDPKRIITATTTROLESMIRLSEAHAKMRLKLNVELEDVQEAVRLIRSAI	833
gi		45187848		ref		NP_984071.1		-----DILPVEHFLTMYINYAKQHHPVITTEGAKTELVRAYVNMRSMDGDDSRADPKRIITATTTROLESMIRLSEAHAKMRLRQVVEVSDVQEAVRLIKSAI	788
gi		50306041		ref		XP_452982.1		-----DILPVEFLTAYINYAKQNIHPVITTESAKTELVRAYVGMRKMGDDSRSDPKRIITATTTROLESMIRLSEAHAKMRLSERVELEDVQEAVRLIKSAI	792
gi		42569072		ref		NP_179236.3		-----EADITTLTITVYSYARKNIHPKLEDEAAEELTRGYVELRKKAGKFASSKKVITATPTROLESIRLSEAHAKMRLRFEWVEKHDVDEAFRLIRVAM	748
gi		17137242		ref		NP_477185.1		-----MFDMSVLRDYLAYAREHLSPTLDEAQQRLIAYVDMRKVG---AGRGQISAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	771
gi		58386786		ref		XP_315054.2		-----LVDMVLRDYLAYAKEHINPVLSEEAQRLIAYVDMRKVG---AGRGQISAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	781
gi		33469919		ref		NP_005905.2		-----LLDMAVLKDYIAYAHSTIMPRLSEEAQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	769
gi		114620052		ref		XP_528129.2		-----LLDMAVLKDYIAYAHSTIMPRLSEEAQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	769
gi		31982197		ref		NP_032591.2		-----FLDMAVLKDYIAYAHSTIMPRLSEEAQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	768
gi		34870013		ref		XP_344049.1		-----FLDMAVLKDYIAYAHSTIMPRLSEEAQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	768
gi		73999288		ref		XP_535063.2		-----FMDMAVLKDYIAYAHSMVMPRLSQEASQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	835
gi		115495629		ref		NP_001068626.1		-----GMDMAVLKDYIAYAHSTIMPRLSQDASQALIEAYVDMRKVG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	742
gi		118086936		ref		XP_424376.2		-----YMDMAVLKDYIAYAHSTIMPRLSEEAQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	765
gi		38707991		ref		NP_944595.1		-----HLDMAVLKDYIAYAHSTIMPRLSEEAQALIEAYVDMRKIG---SSRGMVSAAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	747
gi		17508417		ref		NP_490962.1		-----HYDMNLKDYIAYAKANIHPKLESEEAQALIEAYVDMRKAG---AQHGQITAYPROLESIRLSEAHAKMRLRQVVELLDVBEAARLHREAL	729
gi		124513100		ref		XP_001349906.1		NERENYVNDGNDNDDDDISNYLNDSDAONKRGSWANVNISEYDEYNNSSNKKTKSKNYLIDSNLALYIAYCRITCNPIISLESKKIIEEYIKMRCKEG---TKSPASPROLEGLVRLSGLAKMKLKRVSPEANEAARLNMNTA	908



gi		145605417		ref		XP_364448.2		KTAATD-AQGRIDMSLLTEGTSAAERRRREDLKAAVLGL-LDEMTAGGHQVRVSEVARKLSEGA---SVPEASDFAEICIRALEMDGAVTISGEGPRKQIRRITAQV	1029
gi		32422589		ref		XP_331738.1		KTAATD-SQGRIDMSLLTEGTSAAERRRREDLKAAVLGL-LDEMTAGGHQVRVSEVARKLSEGA---SVPEASDFAEICIRALEMDGAVTISGEGPRKQIRRITAQV	1013
gi		63054428		ref		NP_588004.2		KDYADPAAGKISLDLIVNE--RETLVPEDMVKELANL-LSNLTVGGKTMVLSOLLTRFREQS---STRLDASDFEACLGALERRRGRKVTISAGHRIVRSIAQTD	911
gi		6325276		ref		NP_015344.1		KDYADPAAGKISLDLIVNE--RETLVPEDMVKELANL-LSNLTVGGKTMVLSOLLTRFREQS---STRLDASDFEACLGALERRRGRKVTISAGHRIVRSIAQTD	933
gi		45187848		ref		NP_984071.1		KDYADPAAGKISLDLIVNE--RETLVPEDMVKELANL-LSNLTVGGKTMVLSOLLTRFREQS---STRLDASDFEACLGALERRRGRKVTISAGHRIVRSIAQTD	888
gi		50306041		ref		XP_452982.1		KDYADPAAGKISLDLIVNE--RETLVPEDMVKELANL-LSNLTVGGKTMVLSOLLTRFREQS---STRLDASDFEACLGALERRRGRKVTISAGHRIVRSIAQTD	892
gi		42569072		ref		NP_179236.3		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	847
gi		17137242		ref		NP_477185.1		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	866
gi		58386786		ref		XP_315054.2		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	876
gi		33469919		ref		NP_005905.2		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	863
gi		114620052		ref		XP_528129.2		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	863
gi		31982197		ref		NP_032591.2		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	862
gi		34870013		ref		XP_344049.1		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	862
gi		73999288		ref		XP_535063.2		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	929
gi		115495629		ref		NP_001068626.1		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	836
gi		118086936		ref		XP_424376.2		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	859
gi		38707991		ref		NP_944595.1		QOSATDPRGIVDISILTTGMSATSRKRKEELAEALRKL--ILSKGKTPALKYQOLFEDIRGOS---DIAITKDMFEEALRALADDDFLVTVGK--TVRLL-----	750
gi		17508417		ref		NP_490962.1		QOSAVDPSTGRVDVAILASGMSASGRKAVEAMCEAVLQO--LKTAKG--FVTSKALFHTLKS-A---DKTCQREVFDEANINELSKKESARSQD-RIRFQTEA	823
gi		124513100		ref		XP_001349906.1		FQSLIDPLSGRIDFDQVNLGQISQHKKSDSLIKDIIMNALVLKNMTEDELLTTCHEIIMNDPQH---TTSMDRKSFEAFYDLEKSQETIRLCSGLYKKK-----	1005

