

gi|31560511|ref|NP_036142.2| 150
gi|109498236|ref|XP_222932.4| 150
gi|39995071|ref|NP_006018.3| 150
gi|114573428|ref|XP_001160902.1| 150
gi|73960745|ref|XP_547491.2| 150
gi|119908266|ref|XP_582828.3| 150
gi|118088152|ref|XP_419550.2| 150
gi|47087335|ref|NP_998634.1| 150
gi|17137168|ref|NP_477145.1| 150
gi|158292249|ref|XP_313789.4| 150



gi|31560511|ref|NP_036142.2| 298
gi|109498236|ref|XP_222932.4| 298
gi|39995071|ref|NP_006018.3| 298
gi|114573428|ref|XP_001160902.1| 298
gi|73960745|ref|XP_547491.2| 298
gi|119908266|ref|XP_582828.3| 298
gi|118088152|ref|XP_419550.2| 298
gi|47087335|ref|NP_998634.1| 298
gi|17137168|ref|NP_477145.1| 300
gi|158292249|ref|XP_313789.4| 300



gi|31560511|ref|NP_036142.2| 440
gi|109498236|ref|XP_222932.4| 440
gi|39995071|ref|NP_006018.3| 442
gi|114573428|ref|XP_001160902.1| 442
gi|73960745|ref|XP_547491.2| 442
gi|119908266|ref|XP_582828.3| 442
gi|118088152|ref|XP_419550.2| 439
gi|47087335|ref|NP_998634.1| 444
gi|17137168|ref|NP_477145.1| 437
gi|158292249|ref|XP_313789.4| 434



gi|31560511|ref|NP_036142.2| 580
gi|109498236|ref|XP_222932.4| 580
gi|39995071|ref|NP_006018.3| 589
gi|114573428|ref|XP_001160902.1| 589
gi|73960745|ref|XP_547491.2| 577
gi|119908266|ref|XP_582828.3| 577
gi|118088152|ref|XP_419550.2| 546
gi|47087335|ref|NP_998634.1| 558
gi|17137168|ref|NP_477145.1| 507
gi|158292249|ref|XP_313789.4| 548



gi	31560511	ref	NP_036142.2	TSKLLGAMSPPLGTLRSCFSWSGTLREFSRTPSPASTLTLQ	FRRKSDPPACLP	PEASAVV	DRCDKSEMLGE-T	QPLHELGCSSRSQESMDS	CG-LNT	SLSQPSSRDS	GSSESDCNKSLDN	GEQNE	-KQHLPHFSK--	KDGL	724												
gi	109498236	ref	XP_222932.4	TSKFLGTMSPPTLGLRSCFSWSGTLGFEFSRTPSPSTRSTLQ	FRRKSEPPACLP	PEACAVT	DVCDKSGTLGD	KSQSLHELDWSSRSQESIDSTCS	LNT	SLSQPSSKDS	DSSESDCNKSLDN	GSQNE	-KQHLPHFPK--	KDIL	723												
gi	39995071	ref	NP_006018.3	SSKFTRTISPPPTLGLRSCFSWSGGLGDFSRTPSPSPSTALQ	FRRKSDSPTSLPEN	NMS	DVSQLKSEESDDDESHPLREGACSSQESG	GFSLQSSNASKLSCSSKDS	DSSESDCNKLLDS	QSDQTE	-KLCLSHFSK--	KDTP	733														
gi	114573428	ref	XP_001160902.1	SSKFTRTISPPPTLGLRSCFSWSGGLGDFSRTPSPSPSTALQ	FRRKSDSPTSLPEN	NMS	DVSQLKSEESDDDESHPLREGACSSQESG	GFSLQSSNASKLSCSSKDS	DSSESDCNKLLDS	QSDQTE	-KLRLSHFSK--	KDTP	733														
gi	73960745	ref	XP_547491.2	TSKFLRTISPPPTLGLRSCFSWSGGLGDFSRTPSPSPSTALQ	FRRRTPPTLDRREVS	SMSQSRSD	ESGD	EAPP	SRLAAWSP	QSESTALSPHNLNASKLSPSSKDS	DSSESDCNMKSFDLGNPK	-KPHLSQFLK--	KDTL	721													
gi	119908266	ref	XP_582828.3	TSFTFRTISPPPTLGLRSCFSWSGGLDISRTPSPSPSTALQ	FRRKSDSPTSLPEN	TEKS	DIAPLKSDESD	ESHPLHDVGCSSQESM	LDLSPHNLNASKLSPSSKDS	DSSESDCNFKSLDK	GNQKE	-KLHLPHFSK--	KDTP	721													
gi	118088152	ref	XP_419550.2	EKKTKTVSSLP	EE-RPRSCFQWLSILGNHSGNPGPSHIVFSQ	SHQQR	SNCMESQ	ADDNNGVAESGAVCG	ESDE	ESSPLIEPQCF	SQSKVVEPPQCS	LRSSKILLV	NNNDIKESDS	SKLFDN	GTDR	VEFSAVQ	DR	KNMV	692								
gi	47087335	ref	NP_998634.1	PASPCSSRPASVGLG	--VFSWSGTLKELNKVSHPARDS	TER	--RSSSP	PGGLSTLQQ	FHRNKARISWAGPGLSL	SSPV	EGS	EDAGNS	PGSP	QDSAYF	QSS	SI	ASVEN	HLV	EDNSDKEKERDSV	VNS	SS	FLDRL	KFAV	703			
gi	17137168	ref	NP_477145.1	FAKEQVQ	IRSRFFATQDEQ	-----	TRLQREHLRDT	ENDDM	QK	-----	LSHSG	-----	HKKLRLVCKDIP	PKNPIRQRC	SQI	DGETD	DDTAS	LESQDKGV	PS	LES	EDLNNSQ	QIP	TEGNTN	624			
gi	158292249	ref	XP_313789.4	ISKDEPKVISRFFC	IQNKSQSRT	DTSKG	SNIAKTS	EDDMK	DIKSKRDS	HALKATAIYL	SSPEARL	OSRGDRTP	EKRKR	VQIP	PPES	GESSNSV	LGRFDS	GIAMSENN	NEDEG	LE	CSGTGL	SS	QKENDD	VVMHP	VEMECS	DLKP	697



gi	31560511	ref	NP_036142.2	RRNKVPLGCRSSS	MSFSTTKIKPLV	PARVSGLSKKS	GSMG	TRKHHD	VENKPGLO	TKISELWKN	FGFKDSEKLP	SCKKP--	LSPVKDN	-IQLTPETE	DEIFN	KPECVRA	QRAIFH	837																																									
gi	109498236	ref	XP_222932.4	GRNKVPLGCRSSS	MSLSAATKIKPLV	PARVSGLSKKGSI	QKRKHDAEN	KPGLO	TKISELWKN	FGFKDSEKLP	SCKKP--	LSPVKDN	-IQLTPETE	DEIFN	KPECARA	QRAIFH	836																																										
gi	39995071	ref	NP_006018.3	LRNKVPGLYKSSS	ADSLSTTKIKPL	PARASGLSKKP	ASIQKRKHNAEN	KPGLO	IKLNLWKN	FGFKDSEKLP	PPCKKP--	LSPVRDN	-IQLTPEA	EEDIFN	KPECGRV	QRAIFQ	846																																										
gi	114573428	ref	XP_001160902.1	LRNKVPGLYKSSS	ADSLSTTKIKPL	PARASGLSKKP	ASIQKRKHNAEN	KPGLO	IKLNLWKN	FGFKDSEKLP	PPCKKP--	LSPVRDN	-IQLTPEA	EEDIFN	KPECGRV	QRAIFQ	846																																										
gi	73960745	ref	XP_547491.2	LRNKVPGLYKSSS	VDSLSTTKIKPL	PARASGLSKKPSI	QKRKHDAEN	RPGLQ	IKINELWKN	FGFKDSEKLP	SCKKPDPL	SPVKDN	-IQLTPEA	EEDIFN	KPECIHV	QRAIFQ	836																																										
gi	119908266	ref	XP_582828.3	LRNKIPGLYKSSS	VDSLSTTKIKPL	PARASGLSKKPP	SVHKRNHNAEN	KPGLO	IKINELWKN	FGFKDSEKLP	SCKKPDPL	SPVKDN	-IQLTPE	EEDIFN	NSCMLV	QRAIFQ	835																																										
gi	118088152	ref	XP_419550.2	ARIKVPGLRKSSS	VGSHIVKLLKPL	I	PARVSGLSKKL	SPVKRNHDAEN	KLGLQ	ATIGELNR	NFQFRDY	EKLP	SCKKSDPL	SPVKDN	-IQLTPE	EEEIFN	HLEHA	VQRAIFQ	807																																								
gi	47087335	ref	NP_998634.1	NRTKVSGLSRKGA	CCQKGGKI	ETSAPARAS	GLRKKPS	---	GKNV	NNEN	SPGLQ	ATISGLW	GF	FKKDP	PKLSA	T	KGPE	MP	VG	EN	V	MT	T	ADKEIF	IIAE	-----	806																																
gi	17137168	ref	NP_477145.1	TTIRIKSLDLLENS	PEPTQES	DRNNDAI	ILLDDSC	SSDQ	RAS	TSSSSQ	RQNF	LPT	KRRVGL	SKPS	TAKKG	T	PKSR	TNG	KL	GAV	Q	NQ	IKL	SM	FG	Q	TK	PK	VLK	-----	732																												
gi	158292249	ref	XP_313789.4	RNARLALFERR	PAKQLSQ	LES	KDN	TEEL	AI	VLD	DDSS	DEDT	KRT	A	QAIS	AEK	S	KAR	SS	CKR	PGL	INR	Q	S	V	P	K	T	D	N	I	N	L	G	L	T	---	Q	T	R	L	S	M	F	G	F	Q	K	V	G	F	P	T	V	N	N	G	---	808

