

gi	31543330	ref	NP_032736.2	-----MAHLKTVVAGCCCPFLSNLGS-----	SKVLPGRKDFVR	MLRTH	ALWCKSPVKPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	91
gi	61557127	ref	NP_001013175.1	-----MAHLKTVVTCCLCPVSNLGS-----	CKVLPGRKDFLR	IFRTH	ALWCKSPAKPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	91
gi	122939153	ref	NP_892022.2	-----MANLLKTVVTCCLPFLSNLGS-----	CKGLRVKDDFLR	IFYTH	DELWCKAPVVKPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	91
gi	114600390	ref	XP_001134902.1	-----MANLLKTVVTCCLPFLSNLGS-----	CKGLRVKDDFLR	IFYTH	DELWCKAPVVKPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	91
gi	27806831	ref	NP_776368.1	-----MANLLKTVVTCCLPFLSNLGS-----	CKVLPGRKNFLR	IFHTH	RILWCSAPVVKPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	91
gi	73953777	ref	XP_867928.1	-----MANLLKTVVTCCLPFLSNLGS-----	CKVLPGRKDFLR	IFHTH	ALWCKAPVVKPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	91
gi	47550793	ref	NP_999921.1	-----MASLLRVVASCSPFLSGLQ-----	ARTV--KKPCVR	FFRTH	ALNRLI--SPGIPYKQLTVGVPKEIFON	NEKRVALSPAGVQALVKQGFN	87
gi	158291348	ref	XP_312859.4	-----MIRGRVLRCCLOQDALLQ-----	KKPVLEPLFSG	IVKLL	KDKGKPAVAVKGVYQNLVGVPKERWAN	NEKRVALSPAGVQALVKQGFN	89
gi	17550456	ref	NP_509028.1	-----MVI-----	LRSKITRLYWR	LFSNG	IKK-----IEYSKLKVAVPKEIFPGEKRV	ELSPNGVALLKKNGIS	63
gi	39972475	ref	XP_367628.1	MLWTVVRRPAALAHGHGPGLSGLPALSVLDGASSPVTIHRQRQRWHTNLSNKHRAIASRHSIALVAVPKRQPIRHAIVLPTVPALPAAGVTKVNSASTKVVVPTT	IPYTELTVGVPKEIFON	NEKRVALTPQNALLKKGFKRVLV	150		
gi	32412306	ref	XP_326633.1	-----MWSW-----GLRP-----	SLVLDNATLSLSPSRIIAR	LVALPTKN	YSIGATAPVPTTVPYKQLTVGVPKEIFON	NEKRVALTPQNALLKKGFKRVLV	97



gi	31543330	ref	NP_032736.2	ESGAGEASKFPDDLYRAAGACIQCMK-EVLA-	DLVVKVRAPMVNPLGVAHEADFLKPSGTLIS	FIYPAONPDLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANISGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	239
gi	61557127	ref	NP_001013175.1	ESGAGEASKFPDDLYRAAGACIQCTR-EVLA-	DLVVKVRAPMVNPLGVAHEADFLKPSGTLIS	FIYPAONPDLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANISGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	239
gi	122939153	ref	NP_892022.2	ESGAGEASKFDDHYRAAGACIQGAK-EVLA-	DLVVKVRAPMVNPLGVAHEADLLKTSGLTIS	FIYPAONPELLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	239
gi	114600390	ref	XP_001134902.1	ESGAGEASKFDDHYRAAGACIQGAK-EVLA-	DLVVKVRAPMVNPLGVAHEADLLKTSGLTIS	FIYPAONPELLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	239
gi	27806831	ref	NP_776368.1	ESGAGEASKFDDHYRAAGACIQGAK-EVLA-	DLVVKVRAPMPLNPLGVAHEADLLKTSGLTIS	FIYPAONPELLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	239
gi	73953777	ref	XP_867928.1	ESGAGEASKFDDHYRAAGACIQGVK-EVMA-	DLVVKVRAPMVNPLGVAHEADLLKTSGLTIS	FIYPAONPELLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	239
gi	47550793	ref	NP_999921.1	ESGAGESAKFDDMYTKAGATIRDVK-DVFS-	DVLLKVRAPMPLNPLGVAHEASLMSEGA	LVSFYIYPAONPELMDTLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	235
gi	158291348	ref	XP_312859.4	ESGAGLNAKFRDADYEAGASIVDGR-KAFET	DIVLKVROPIEP	ETPQLRDASTLISFIYPAONKELIDKLA	RRKINAFAMDAPRISRAQVFDALSSMANISGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	231
gi	17550456	ref	NP_509028.1	ENAGVLAGYSNBEYVRSGADVQKHN-EVFNIT	DIIMLKVRPPTE	EVSKLKSGLTISFIYPAONPELLNKLSEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	GQITAAAGKVPVPAKILIVGGGVAG	205
gi	39972475	ref	XP_367628.1	ERAGAQADFPDEYERAGAEIVDQ-TVWA	TDLILMKVRGPSLT	EAEGMKTGQITISFLQPAONKDLVQKLS	SEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	293
gi	32412306	ref	XP_326633.1	EKAGAEAEFHDSAVATAGATLVESASD	VWNNADIVLVRGPSVA	EAEMLKEGQITISFLQPAONKDLVQKLS	SEKRTITVLAMDQVPRVITIAQ	GYDALSSMANIAGYKAVVLAANHFGRFFT	241



gi	31543330	ref	NP_032736.2	LASAGAASKSMGAVVRGFDTRAALAEQFKSLGAEP	LEVDLKESEGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	389	
gi	61557127	ref	NP_001013175.1	LASAGAASKSMGAVVRGFDTRAALAEQFKSLGAEP	LEVDLKESEGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	389	
gi	122939153	ref	NP_892022.2	LASAGAASKSMGAVVRGFDTRAALAEQFKSLGAEP	LEVDLKESEGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	389	
gi	114600390	ref	XP_001134902.1	LASAGAASKSMGAVVRGFDTRAALAEQFKSLGAEP	LEVDLKESEGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	389	
gi	27806831	ref	NP_776368.1	LASAGAASKSMGAVVRGFDTRAALAEQFKSLGAEP	LEVDLKESEGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	389	
gi	73953777	ref	XP_867928.1	LASAGAASKSMGAVVRGFDTRAALAEQFKSLGAEP	LEVDLKESEGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	389	
gi	47550793	ref	NP_999921.1	LAAAGSARAMGAVVRGFDTRAALAEQFKSLGAEP	LEVDIKESGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDLII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	385	
gi	158291348	ref	XP_312859.4	LAAIQARGMGAVVRGFDTRPVVKEQVESMGAE	FLTINIS	EDGSTAGGVSKEMSKFEI	EAEMALFADQCKEVDVII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	381
gi	17550456	ref	NP_509028.1	LSAIGTSRGMGAVVRGFDTRAAVKEHVESLGA	QFLTVNVKEDGEGGGYAKEMSKFEI	EAEMKLFADQCKEVDVII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	355	
gi	39972475	ref	XP_367628.1	LSAIATARRMGAVVRGFDTRPAITRE	QVSLGAEFIEVDVQ	EDGSGAGGYAKEMSKFEI	EAEMKLFADQCKEVDVII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	443
gi	32412306	ref	XP_326633.1	LSAIATARRMGAVVRGFDTRSAARE	QVSLGAEFIEVDVQ	EDGSGAGGYAKEMSKFEI	EAEMKLFADQCKEVDVII	STALIPGKKAPVLF	SKEMIESMKEG	SVVVDLAAEAGGNFET	TKPGELYVHKGIT	HIGYIDLPSRMA	QASTLYS	391



gi	31543330	ref	NP_032736.2	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	539																																				
gi	61557127	ref	NP_001013175.1	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	539																																				
gi	122939153	ref	NP_892022.2	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	539																																				
gi	114600390	ref	XP_001134902.1	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	539																																				
gi	27806831	ref	NP_776368.1	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	539																																				
gi	73953777	ref	XP_867928.1	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	539																																				
gi	47550793	ref	NP_999921.1	NNITKLLKAI	SPDKDNFHFV	EVDKDDFDG	TMSHVIRGT	VVMKDGKVI	FPAPTPKNI	PEEAPVVKPKVAE	LEAEKAGT	VSMTYKLLT	ASVYSAGL	GLMGLG	IVAPNFAF	SQMVT	TFGLAGI	IYH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	535																																				
gi	158291348	ref	XP_312859.4	NNISKFLLSMG	-EKDHFHIN	EEDE	-----	VVRGSMVL	GGNLMWPPV	IPVSAK	PPPAVA	AKPAIA	EALPAD	PFKE	LRBS	LMY	TGGL	GTL	GLG	VAPN	AAFT	MTMT	T	FAM	SG	IVG	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	522																												
gi	17550456	ref	NP_509028.1	NNIAKFLLL	HLGKDR	-TFVNEE	DE	-----	VVRGALVVR	DGQMKW	PPPP	-----	INFP	PPPA	AAK	DKP	SE	NTAL	AN	QLL	SG	LS	GV	SL	YH	YH	VWGV	TPALH	SP	PLMS	VTNAI	SGLTA	493																													
gi	39972475	ref	XP_367628.1	NNITKLLLSMA	PVEKE	FGIDLS	DE	-----	VVRGAI	IVT	QKEV	LP	PP	APR	-----	PAP	PPA	AAK	PVT	-	KEA	EV	VAL	TP	QK	Q	RE	V	AG	GM	GA	AL	AK	GL	IG	-	PA	FM	GN	MF	T	GL	AS	LI	GY	RA	V	V	N	V	AP	AL	H	SP	PL	MS	VT	NAI	SG	MT	579	
gi	32412306	ref	XP_326633.1	NNITKFLLSMA	PNQEF	FGIDL	DE	-----	VVRGAI	IV	NK	GN	IL	PP	APR	-----	PAP	PPA	AAK	PVT	-	KEA	EV	VAL	TP	QK	Q	RE	V	AG	GM	GA	AL	AK	GL	IG	-	PA	FM	GN	MF	T	GL	AS	LI	GY	RA	V	V	N	V	AP	AL	H	SP	PL	MS	VT	NAI	SG	MT	528



