

gi	4757828	ref	NP_004767.1	-----		
gi	114682590	ref	XP_001167173.1	-----		
gi	73992567	ref	XP_543044.2	-----		
gi	119906072	ref	XP_586129.3	-----		
gi	118100919	ref	XP_417519.2	-----		
gi	116089306	ref	NP_062809.2	-----		
gi	109469265	ref	XP_342585.3	-----		
gi	113673319	ref	NP_001038797.1	-----		
gi	17536691	ref	NP_496449.1	-----		
				MPMCSKATSDFLFPLSLCVPECCLDLILRPSLYAPGCPGVLRLSPVVPWSSLVLGCHHRLSQNPDKVPPQGHYCLPCCQLWHSEATAQRPQHRARVWGSRRLSQGHLCFPGEAIGENRARGGRRTSSFAEHSQOHALQRPPEFAAGSRSA	150	
				-----MLVMLAAPPLSPSPDLKPPG-----		
				-----GRC-----	25	
				1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150		

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gi	73992567	ref	XP_543044.2	-----		
gi	119906072	ref	XP_586129.3	-----		
gi	118100919	ref	XP_417519.2	-----		
gi	116089306	ref	NP_062809.2	-----		
gi	109469265	ref	XP_342585.3	-----		
gi	113673319	ref	NP_001038797.1	-----		
gi	17536691	ref	NP_496449.1	-----		
				-----MRARRGLLRLP-----RRSLLAALFFFLSSSLLYFVYVAPG-----IVNTYLFMMQAQGILIRDNVRTIGAQVVEQVLR-SAYAKRNSNVNDSYPLD	88	
				-----MRARRGLLRLP-----RRSLLAALFFFLSSSLLYFVYVAPG-----IVNTYLFMMQAQGILIRDNVRTIGAQVVEQVLR-SAYAKRNSNVNDSYPLD	88	
				-----MNEGKVVYAAPLCPQSPFLSQWATNRVRCRRP-----LGSRAGGALARIRPAL-----ERRSPRAGAVAAPEEGLSPFSDVPCGSPLRGGRRTGVNTYLFMMQAQGILIRDNMRTIGAQVVEQVLR-SAYAKRNSNVNDSYPLD	134	
				-----MNMNTYLFMMQAQGILIRDNMRTIGAQVVEQVLR-SAYAKRNSNVNDSYPLD	52	
				-----SPRPAPPRAVAVAPSCCGVGRCRWLGAAVAQRFPPGLGACERQGGGTSAMRWPRGPRGAWRLLRPRRLLAVLFLFLSSSFLYFVYVAPG-----IVNTYLFMMQAQGMIRENMRRTIGAQVVEQVLR-SAYAKRNSNVNDSYPLD	290	
				-----MRARRGLLRLP-----RRSLLAALFFFLSSSLLYFVYVAPG-----IVNTYLFMMQAQGILIRDNVRTIGAQVVEQVLR-SAYAKRNSNVNDSYPLD	88	
				-----GQRGGGARSPEGGDRPGGEPERRRERGPRPSSRRRLSMRARRGLLRLP-----RRSLLAALFFFLSSSLLYFVYVAPG-----IVDQMLMVKGGGGLKKEVLR---IYEQAAGTWYHRTNQCGSGESLIER	148	
				-----MPTHLRFR-----RRSFLGLLFLFLSLSALYFIYVAPG-----IVNTYLFMMQAQARGIQIRVNRNMGAVLEQVLR-SAYS---INCTEYTYE	80	
				-----MRTSHCIIR-----SFSFKRLIIFVAASTLIYVMLLRNS-----LNDERRIAATEEQVRSVIVNVQSKNSGVAER-LHDIKDFVELETARQTLT	85	
			160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300		



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gi	113673319	ref	NP_001038797.1	-----		
gi	17536691	ref	NP_496449.1	-----		
				LNHSET-FLOTTTF---LPEDFYFANHTCPERLPSMKGPIIDINMSEIGMDYIHELFSK-DPTIKLGGHWKPSDCMPRWKVAIILPFRNRHEHLPVLFRRHLLPMLQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	233	
				LNHSET-FLOTTTF---LPEDFYFANHTCPERLPSMKGPIIDINMSEIGMDYIHELFSK-DPTIKLGGHWKPSDCMPRWKVAIILPFRNRHEHLPVLFRRHLLPMLQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	233	
				LNHSET-FLOTTTF---LPEDFYFANHTCPERLPSMKGPIIDINMSEIAMDDIHELFSK-DPAIKLGGHWKPSDCLPRWKVAIILPFRNRHEHLPVLLRHLIPMLQRQLRFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	279	
				LNHSET-FLOTTTF---LPEDFYFANHTCPERLPSMKGPIIDINMSEIGMDAIHELFSK-DPTIKLGGHWKPSDCMPRWKVAIILVPPFRNRHEHLPVLLRHLIPMLQRQLRFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	197	
				LNHSET-FLOTTTF---LPEDFYFANHTCPERLPSMKGPIIDINMSEIAMDDIHELFSK-DPAIKLGGHWKPSDCLPRWKVAIILPFRNRHEHLPVLLRHLIPMLQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	435	
				LNHSEA-FPPPTTF---LPEDFYFANHTCPERLPSMKGPIIDINMSEIAMDDIHELFSK-DPAIKLGGHWKPSDCMPRWKVAIILPFRNRHEHLPVLLRHLIPMLQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	233	
				SRHTEPGCAPIVSEFVXLPTWYNFRSKHDCPERLPSKGGPIIDINMSEIAMDDIHELFSK-DPAIKLGGHWKPSDCMPRWKVAIILPFRNRHEHLPVLLRHLIPMLQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	297	
				FNFSEI-DASPTPE---LPEGFIVKPEQVCEKPLPSMKGRIKVMSEIALDEVEKLLKLNDEPLSGGGHWKPSDCMPRWKVAIILPFRNRHEHLPVLLRHLIPALQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	226	
				FLNMEEAVTKPKPP---VKIAEEDGSCPIVEKIPDLGALPQATLLIQNLQEGEVHAI-HPELGPGGHWKPSDCMPRWKVAIILPFRNRHEHLPVLLRHLIPALQRQLQFAFYVVEQVGTQPPNRAMLNVGFOEAMKDLWDWCLIFH	229	
			310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450		



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gi	116089306	ref	NP_062809.2	-----		
gi	109469265	ref	XP_342585.3	-----		
gi	113673319	ref	NP_001038797.1	-----		
gi	17536691	ref	NP_496449.1	-----		
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	381	
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	381	
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	427	
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	345	
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	583	
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	381	
				DVDHIPESDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	443	
				DVDHILENDRNYYCGGMPRHFAFKLDKYMVLLPYTEFFGGVSGLTVEQFRKINGFPNFAFWGGEDDLDLWNRVONAGYVSRPEGDTGKYKSIPIHHRGEVQFLGRYALLRKSKEKROGLDGLNLLNYFAN--ITYDALYKNIIVNLTPE	374	
				DVDMPFDDRRNPSYSCPPGPRHLGAFVSNLGVQLWYKKEIVGGVLAVMADYRAVNGYSNQFWAGGEGDDMGQRILSLNLTIERPNPEIGRYSMKLVKVKRRTAPKLIYKLLGNSANRVAVDGLNETDKWTIRKVIIRPLVHYLVVDVGV	379	
			460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600		



gi	4757828	ref	NP_004767.1	LACVNEY-	388
gi	114682590	ref	XP_001167173.1	LACVNEY-	388
gi	73992567	ref	XP_543044.2	LACVNEY-	434
gi	119906072	ref	XP_586129.3	LACVNEY-	352
gi	118100919	ref	XP_417519.2	LALVNEY-	590
gi	116089306	ref	NP_062809.2	LACVNEY-	388
gi	109469265	ref	XP_342585.3	LACVNEY-	450
gi	113673319	ref	NP_001038797.1	LAPVADY-	381
gi	17536691	ref	NP_496449.1	PEEWQAKA	387

