

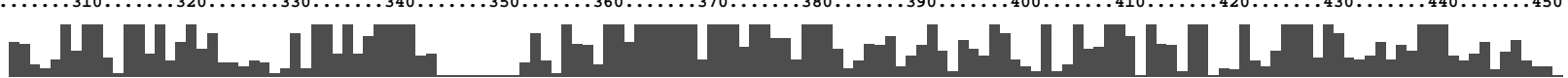
gi	45331202	ref	NP_034619.2	-----MRAGLGPITLALVL-----EVAWAGELKPTAPPIFTGRPFVVAWVPTQECAPRHKVPLD-----LRAFVDVKAIPNEGFFNONITTFYDRDLGLVPRFDAAGTSTVHGGVPPONGSLCA	150
gi	25282397	ref	NP_742037.1	-----MRAGLGPITLALVL-----EVAWASELKPITAPPIFTGRPFVVAWVPTQECAPRHKVPLD-----LRAFVDVKAIPNEGFFNONITTFYDRDLGLVPRFDAAGTSTVHGGVPPONGSLCA	150
gi	15022801	ref	NP_003764.3	-----MRAGLGPITLALVL-----AVSWAMELKPITAPPIFTGRPFVVAWVPTQDCGPRKLVPLD-----LNAFDVQASPNEGFVNQNTITFYDRDLGLVPRFDSAGRSVHGGVPPONVSLWA	150
gi	114587028	ref	XP_001168504.1	-----MRAGLGPITLALVL-----AVAWAMELKPITAPPIFTGRPFVVAWVPTQDCGPRKLVPLD-----LNAFDVQASPNEGFVNQNTITFYDRDLGLVPRFDSAGRSVHGGVPPONVSLWA	150
gi	73985708	ref	XP_541876.2	-----MWAGLGPITLALVL-----VVAWAAALKPTAPPIFTGRPFVVAWVPTQDCGPRKLVPLD-----LKAFDVQASPNEGFVNQNTITFYDRDLGLVPRFSSVGRSVHGGVPPONGSLWA	150
gi	27805929	ref	NP_776772.1	-----VVAWATELKPITAPPIFTGRPFVVAWVPTQDCGPRKLVPLD-----LKAFDVQASPNEGFVNQNTITFYDRDLGLVPRFSSVGRSVHGGVPPONGSLWA	150
gi	118112383	ref	XP_414258.2	-----MWAGLGPITLALVL-----VVAWATELKPITAPPIFTGRPFVVAWVPTQDCGPRKLVPLD-----LKAFDVQASPNEGFVNQNTITFYDRDLGLVPRFSSVGRSVHGGVPPONGSLWA	150
gi	292615274	ref	XP_002662593.1	-----MRGGCAAVLALVPALPNLWPAVLAVLARQSPKPKSAAPLLLRPFVVAWVPTQDCGPRKLVPLD-----LKAFDVQASPNEGFVNQNTITFYDRDLGLVPRFSSVGRSVHGGVPPONGSLWA	150
gi	189518440	ref	XP_696268.3	-----MAHWIRLYWRICLLVHLL-----AEDLKPTRWPLYQKPLVLVWVAPTEDCRPRHKVHFQ-----LDQFQIVASPNQGFKONLITFYKDRDLGLVPRFSSVGRSVHGGVPPONGSLWA	150
gi	125850030	ref	XP_687640.2	MSERTGVLNGFSPQIRSEMKNITHLSTRTIQRASLWQLVLLMLLFWI-----CLKAQDLKNTRWPLYQKPLVLVWVAPTEDCRPRHKVHFQ-----LDQFQIVASPNQGFKONLITFYKDRDLGLVPRFSSVGRSVHGGVPPONGSLWA	150



gi	45331202	ref	NP_034619.2	HLPLMLKESVVERIYIQTQEPGGLAVIDWEEWRPVVWRNWKQKDVYRQSRQLVASRHPDWPDDRVMKQAAQYEFFAARQFMLNLTLYVKAVRPHLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	25282397	ref	NP_742037.1	HLPLMLKESVVERIYIQTQEPAGLAVIDWEEWRPVVWRNWKQKDVYRQSRQLVASRHPDWPDDRIVKQAAQYEFFAARQFMLNLTLYVKAVRPHLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	15022801	ref	NP_003764.3	HRKMLQKRVEHYIRTQESAGLAVIDWEDWRPVVWRNWKQKDVYRRLSRQLVASRHPDWPDDRIVKQAAQYEFFAAQFMLETLRYVKAVRPHLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	114587028	ref	XP_001168504.1	HRKMLQKRVEHYIRTQESAGLAVIDWEDWRPVVWRNWKQKDVYRRLSRQLVASRHPDWPDDRIVKQAAQYEFFAAQFMLETLRYVKAVRPHLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	73985708	ref	XP_541876.2	HLKMLQEHVEHYIRSQEPAGLAVIDWEDWRPVVWRNWKQKDVYRQSRQLVAVRHPDWPADRIVKQAAQYEFFAARQFMLETLRFVKAFRPRHLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	27805929	ref	NP_776772.1	HLKMLQEHVEHYIRTQEPAGLAVIDWEDWRPVVWRNWKQKDVYRRLSRQLVAVRHPDWPADRIVKQAAQYEFFAARQFMLETLRFVKAFRPRHLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	118112383	ref	XP_414258.2	HLMLRQENIGKYIRSATSEGLAVIDWEEWRPILWIRNWKQKDVYQEVSRRELVEQRPWFSPSEKVNKQAVFEPFESAARHFMTLYRYAKSRPRQLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	292615274	ref	XP_002662593.1	HLEKMPGIEKYYIRDLPLAKGLAVIDWEEWRPLWIRNWEAKEIYKRSKHLVSKQNPDTWSSQISKTAQMEFELSRRKFMQETLRLAKSLRPHQLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	189518440	ref	XP_696268.3	HLEKMPGIEKYYIRDLPLAKGLAVIDWEEWRPLWIRNWEAKEIYKRSKHLVSKQNPDTWSSQISKTAQMEFELSRRKFMQETLRLAKSLRPHQLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300
gi	125850030	ref	XP_687640.2	HLEKMPDGLKYYIKDQAVKGLAVIDWEEWRPLWIRNWEAKEIYKRSKHLVSKQNPDTWSSQISKTAQMEFELSRRKFMQETLRLAKSLRPHQLWGFYLFPCYNHDYVQNWESYTGRCPDVEVARNDQLAWLWAEISTALFPPSVYLDDEL	300



gi	45331202	ref	NP_034619.2	ASSVHSRNFVSRFRVQEARVAHHTHANHALPYYVFTTRPTYSR-----GLTGLSOVDLISTIGESAALGAGVIFWGDSEDASSMETCCOYLKNYLLQLLVPIVNVSWATQYCSWTCCHGHGRCVRRNPSASTFHLHLNASSFRLVPG-	450
gi	25282397	ref	NP_742037.1	ASSKHRSRNFVSRFRVQEARVAHHTHANHALPYYVFTTRPTYSR-----RLTELNQMDLISTIGESAALGAGVIFWGDSEVASSMENCONLKKYLLQTLVPIVNVSWATQYCSWTCCHGHGRCVRRNPSASTFHLHLNASSFRLVPG-	450
gi	15022801	ref	NP_003764.3	ASSRHGRNFVSRFRVQEARVAHHTHANHALPYYVFTTRPTYSR-----RLTGLSEMDLISTIGESAALGAGVILWGDAGYTTSTETCCOYLKDYLRLLVPIVNVSWATQYCSRAQCHGHGRCVRRNPSASTFHLHLNASSFRLVPG-	450
gi	114587028	ref	XP_001168504.1	ASSRHGRNFVSRFRVQEARVAHHTHANHALPYYVFTTRPTYSR-----RLTGLSEMDLISTIGESAALGAGVILWGDAGYTTSTETCCOYLKDYLRLLVPIVNVSWATQYCSRAQCHGHGRCVRRNPSASTFHLHLNASSFRLVPG-	450
gi	73985708	ref	XP_541876.2	ASSTHGRNFVSRFRVQEARVAHHTHANHALPYYVFTTRPTYSR-----RLTGLSEMDLISTIGESAALGAGVILWGDAGYTTSTETCCOYLKDYLRLLVPIVNVSWAAQYCSWAQCHGHGRCVRRNPSASTFHLHLNASSFRLVPS-	450
gi	27805929	ref	NP_776772.1	ASSTHGRNFVSRFRVQEARVADVHHANHALPYYVFTTRPTYSR-----GLTGLSEMDLISTIGESAALGAGVILWGDAGYTTSTETCRRLKDYLRSLVPIVNVSWAAQYCSWAQCHGHGRCVRRNPSASTFHLHLNASSFRLVPS-	450
gi	118112383	ref	XP_414258.2	ASTPSNRKFRVRRVMEAMRISQHHHEGYSLPVFFVTRPTYSR-----KMDVLSQPDLISTIGESAALGAGVIFWGDSEVETKKNRSCCTIKDYMEGDLGRYIVNVMAAQHCSITLCHGQGRCKRRNSASTFHLHLNASSFRLVPG-	450
gi	292615274	ref	XP_002662593.1	RSTSFGRQFVRRNVEGMRLASVGGG-LARPVFVYSRPTIYAN-----ELEVLTETDLVSTIGESVALGAGVILWGDAAASSNASCSSINQYLRGPLGQYLLNVSTAAEQCSGFLCSSHGRCLRRHADTDTYHLHLPKTHITVGG-	450
gi	189518440	ref	XP_696268.3	RSTSFGRQFVRRNVEGMRLASVGGG-LARPVFVYSRPTIYAN-----ELEVLTETDLVSTIGESVALGAGVILWGDAAASSNASCSSINQYLRGPLGQYLLNVSTAAEQCSGFLCSSHGRCLRRHADTDTYHLHLPKTHITVGG-	450
gi	125850030	ref	XP_687640.2	KDNPKGRQFVRRNVEGMRLASVGGG-SARPVFVYSRPTIYANMTSSNPAAELLLTETDLVSTIGESVALGAGVILWGDSTVASSQAQCSSLNEYLRGPLGRYLLNVSTAAEQCSRNLCGFRGCLRRKQNTDTYHLHLNASSFRLVPG-	450



gi	45331202	ref	NP_034619.2	-HTPSEPQLRPEGELSEADLNLYLQKHFRCCOYLWGGGECORNYKGAAGNASRAWAGSHLSLLGLVAVALTWTL	525
gi	25282397	ref	NP_742037.1	-RTPSEPQLRPEGELSEADLNLYLQKHFRCCOYLWGGGECORNYKGAAGNASRAWAGSHLSLLGLVAVALTWTL	525
gi	15022801	ref	NP_003764.3	-HAPGEPQLRPVGELESWADIDHLQTHFRCCOYLWGSGECCQWDHRRQAAGGASAWAGSHLSLLALAALAFWTWL	525
gi	114587028	ref	XP_001168504.1	-HAPGEPQLRPVGELESWADIDHLQTHFRCCOYLWGSGECCQWDHRRQAAGGASAWAGSHLSLLALAALAFWTWL	525
gi	73985708	ref	XP_541876.2	-HVPGEPQLRPEGELSWADLNHLQTHFRCCOYLWGGGECQWDHTRAAAGGARAWAGSHLTGPLAVAVALTWTL	525
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gi	118112383	ref	XP_414258.2	EQQPORPLIWKAGHLSHTDVFHLOTHFRCHCQGGQGNSSQSS-AGPHGSAPGLPAMGLVLLVFWMWC	525
gi	292615274	ref	XP_002662593.1	-----GSEMRVRGDLVVEEHRRTKDFCCOCCPSGVQGERCDLEDPQQRGHGNTLKALWIYPLSPLLLHLTL	525
gi	189518440	ref	XP_696268.3	-----GSEMRVRGDLVVEEHRRTKDFCCOCCPSGVQGERCDLEDPQQRGHGNTLKALWIYPLSPLLLHLTL	525
gi	125850030	ref	XP_687640.2	-----ANTLKLTCQMSSEELGRLRDDFCOCCNGYSGDDCSIKD-NGNRAALWLSALQVWVLPILLMGLFLH	525

