

gi	31543127	ref	NP_038614.2	-----	150
gi	62647663	ref	XP_232107.3	-----	150
gi	14211943	ref	NP_115992.1	-----	150
gi	114578309	ref	XP_001161407.1	-----	150
gi	119903231	ref	XP_869640.2	-----	150
gi	73980442	ref	XP_540217.2	-----	150
gi	224589092	ref	NP_001139156.1	-----	150
gi	118090925	ref	XP_423667.2	-----	150

MPVWIKGKEEAEWPRYPGAEGLVWVPAFVPRQDALLCARERLRGA AAAAGPFGAAVCHGAERDGDPAEGRGGVGPVPSVPA AAAAVQRSRRESCAVVRGCGVPEWLYPFRGISPPQRLRAGSRGCSVRAGVGGGPGHGCGAGRAGEG

.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi	31543127	ref	NP_038614.2	-----	300
gi	62647663	ref	XP_232107.3	-----	300
gi	14211943	ref	NP_115992.1	-----	300
gi	114578309	ref	XP_001161407.1	-----	300
gi	119903231	ref	XP_869640.2	-----	300
gi	73980442	ref	XP_540217.2	-----	300
gi	224589092	ref	NP_001139156.1	-----	300
gi	118090925	ref	XP_423667.2	-----	300

-----MRAVSVWYCCPWGLLLHLLCLCFVSGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCRGTE

-----MRAVNVVYCCPWRLLHLLHLLCLCFVSGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCKGTE

-----MRPVSVWWSWPWG-LLLCLLCLCSCLGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCSGTE

-----MRPVSVWWSWPWG-LLLCLLCLCSCLGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCSGTE

-----MRPVSVWWSWPWG-LLLCLLCLCSCLGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCSGTE

-----MRPVSVWWSWPWG-LLLCLLCLCSCLGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCSGTE

-----MRPVSVWWSWPWG-LLLCLLCLCSCLGS-PSPSTDPPEKKVGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFTEATGWTHSAKYGGPTGRIWLDNLSCSGTE

-----MELHWCCHHIVFLNINWVSCFAQVTPPARSS-PTP--TPQTADNPDSLKFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLANAHVLCRQLGFVSAATGWTHSAKYGGPTGRIWLDNLSCSGTE

AAQRSSAPGSSALGRIDGVSALAAAYPRRERERAMGRCTRARWQELLVLLGGLMWMWGSQAQPPSPSTSSVPLKFRLAGFPRKPYEGRVEIQRAGEWGTICDDDFLQAAHVLCRELGFVSAATGWTHSAKYGGPTGRIWLDNLSVAGN

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi	31543127	ref	NP_038614.2	-----	450
gi	62647663	ref	XP_232107.3	-----	450
gi	14211943	ref	NP_115992.1	-----	450
gi	114578309	ref	XP_001161407.1	-----	450
gi	119903231	ref	XP_869640.2	-----	450
gi	73980442	ref	XP_540217.2	-----	450
gi	224589092	ref	NP_001139156.1	-----	450
gi	118090925	ref	XP_423667.2	-----	450

GSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-QLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPEGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----MLAKKQHSFGLHSVACVGTETEA

GSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-QLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPEGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----MLAKKQHSFGLHSVACVGTETEA

QSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

QSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

RSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

QSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

RSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

RSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

RSVTECASRGWNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LLAQROOHSFGLHGVACVGTETEA

KAIRDCKHRGWNSDCSHEBDAGVICKDQRLPGFSDSNVIEVEH-HLQVEEVLRLPAVEWGRRLPVTVEGLVEVRLPDGWSQVCDKGSVAHNSHVCGMLGFPGEKRVNMAFYR-----LFAERQOLNRLHLSVACVGTETEA

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi	31543127	ref	NP_038614.2	-----	600
gi	62647663	ref	XP_232107.3	-----	600
gi	14211943	ref	NP_115992.1	-----	600
gi	114578309	ref	XP_001161407.1	-----	600
gi	119903231	ref	XP_869640.2	-----	600
gi	73980442	ref	XP_540217.2	-----	600
gi	224589092	ref	NP_001139156.1	-----	600
gi	118090925	ref	XP_423667.2	-----	600

HLSLCSLEFYRANDTTRCSPGPAVAVSCVPLGPLYATFGQKKQOHSKPOGE---ARVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HLSLCSLEFYRANDTTRCAGGSPAVVSCMLGPLYATSTGQKKQOHSKPOGE---ASVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HLSLCSLEFYRANDTARCPGGAPAVVSCVPLGPLYAASGQKKQOHSKPOGE---ARVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HLSLCSLEFYRANDTARCPGGAPAVVSCVPLGPLYAASGQKKQOHSKPOGEVETARVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HLSLCSLEFYRANDTTRCAGGSPAVVSCVPLGPLYAASGQKKQOHSKPOGE---ARVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HLAAQPLEFNYNATESCPGGAPAVVSCVPLGPLYAASGQKKQOHSKPOGE---ARVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HLAAQPLEFNYNATESCPGGAPAVVSCVPLGPLYAASGQKKQOHSKPOGE---ARVRLKGGAHQGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

HISMCTFQFVRCNSAACSCTGMPAVVSCVPLGPLYAASGQKKQOHSKPOGE---PRVRLKGGAKAGEGRVEVLKAGTWGTVCDRWDLQAASVVCRELGFGTAREALSARMGQGMGAIHLSVRCVSGOEPSLWRCPSKNIITAEDCSHS

EDAAVRCNIPVMGYENLIRLSGGRSRFEGRVEVAVGAAGDEPRWGLVCGEGWGLEAMVACRQLGLGFANHGLO

.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi	31543127	ref	NP_038614.2	-----	750
gi	62647663	ref	XP_232107.3	-----	750
gi	14211943	ref	NP_115992.1	-----	750
gi	114578309	ref	XP_001161407.1	-----	750
gi	119903231	ref	XP_869640.2	-----	750
gi	73980442	ref	XP_540217.2	-----	750
gi	224589092	ref	NP_001139156.1	-----	750
gi	118090925	ref	XP_423667.2	-----	750

QDAGVRCNLPYTGVEIKIRLSGGRSRYEGRVEVQIGIP--GHLRWGLICGDDWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

QDAAVRCNLPYTGVEIKIRLSGGRSRYEGRVEVQIGIP--GHLRWGLICGDDWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

QDAGVRCNLPYTGAEIRIRLSGGRSQHEGRVEVQIGGP--GPLRWGLICGDDWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

QDAGVRCNLPYTGAEIRIRLSGGRSQHEGRVEVQIGGP--GPLRWGLICGDDWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

QDAGVRCNLPYTGVEIKIRLSGGRSRHEGRVEVQIGGP--GSLRWGLICGDDWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

QDAGVRCNLPYTGVEIKIRLSGGRSRHEGRVEVQIGGL--GPLRWGLICGDDWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

EDASVRCNIPVMGYEKTIVRILGGRTRYEGRVEVLRHEAD--GTLRWGLICGEGWGLEAMVACRQLGLGFANHGLOVRLSGGRSRFEGRVEVQIGRPVCGRWSVCEGWSIKAEAMVLCRQLGLGFANHGLO

EDAAVRCNIPVMGYENLIRLSGGRSRFEGRVEVAVGAAGDEPRWGLVCGEGWGLEAMVACRQLGLGFANHGLO-----ETIYWDSGNVIEVVMGVRCTGS

.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi |31543127|ref|NP_038614.2| ELSLNQCAHSSSHITCKRTGTRFTAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |62647663|ref|XP_232107.3| ELSLNQCAHNTHTVCKRTGTRFTAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |14211943|ref|NP_115992.1| ELSLDCCAHHGTHITCKRTGTRFTAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |114578309|ref|XP_001161407.1| ELSLDCCAHHGTHITCKRTGTRFTAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |119903231|ref|XP_869640.2| ELSLDCCAHHGTHITCKRTGSRFTAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |73980442|ref|XP_540217.2| ELSLDCCAHHGTHVACKRTGTRFTAGVICSETASDLLLHLSALVQETAYIEDRPLHMLYCAAEENCLARSARSANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |224589092|ref|NP_001139156.1| EMSISQCHHRT-VNCKAAARFAAGVICSETASDLVLNAPLVQETTYIEDRPLHMLYCAAEEDCLSKSAASANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECQ 900
gi |118090925|ref|XP_423667.2| ELSLSHCQHGSSLNCRNTGTRFAAGVICSETASDLLLHAPLVQETAYIEDRPLHMLYCAAEENCLSSARHANWPYGHRRLLRFSSQIHNLRADFRPKAGRHSWVWHECHRHGHYHSMDFTHYDILTPNGTKVAEGHKASFCLDTECF 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi |31543127|ref|NP_038614.2| EDVSKRYECANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAESDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEANRRFERYPGQTSNQIV 1008
gi |62647663|ref|XP_232107.3| EDVSKRYECANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAESDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEANRRFERYPGQTSNQIV 1008
gi |14211943|ref|NP_115992.1| EDVSKRYECANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAESDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEANRRFERYPGQTSNQII 1008
gi |114578309|ref|XP_001161407.1| EDVSKRYECANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAESDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEANRRFERYPGQTSNQII 1008
gi |119903231|ref|XP_869640.2| EDVSKRYECANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAESDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEANRRFERYPGQTSNQII 1008
gi |73980442|ref|XP_540217.2| EDVSKRYECANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAESDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEANRRFERYPGQTSNQII 1008
gi |224589092|ref|NP_001139156.1| EGVSKRYKCANFGEQGITVGCWDLRYRHDIDCQWIDITDVKPGNYILQVVINPNFEVSEDFTNAMKCNCKYDGHRIWVHNCBIGDAFSEAEKKFERYPGQLNNQIS 1008
gi |118090925|ref|XP_423667.2| EGSVSCYVCPPL----- 1008
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....

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