

gi	241896898	ref	NP_060035.2	MPGLRRDRLLLLLLGALLSADLYFHLWPOV--QRQLRPRERPRGCPCTGRASLARDSA--AAASDPCTIVHNFSTRTEPRTEPAGGSHSGSSSKLQALFAHPLVNPPEPPLLAGEDSLLASQEAALRYRKRVARWNRHKMYREOMNLT	150
gi	114670175	ref	XP_511648.2	-----MRFGGDRHFN-----HIP-----WRHKMYREOMNLT	150
gi	24418883	ref	NP_722477.1	MPGLRRDRLLALLLLGALFADLYFHLWPOV--QRQLRPGERPAACPCSGRAPASLHSA--AASRDLCGASHNFSGALPRVEHPSRGGHPAPRSKALQALFAHSLVQVLEDPPLLGPEDWLLASQEAALRYRKRVARWNRHKIYKEOFNLT	150
gi	109489283	ref	XP_573215.2	MPGLRRDRLLALLLLGALFADLYFHLWPOV--QRQLGPGERPAACPCSGRAPSTSLHSA--AASRDPCGASHNFSGALPRVEHPSRGGHPAPRSKALQALFAHSLVQVLEDPPLLGPEDWLLASQEAALRYRKRVARWNRHRIYKEOFNLT	150
gi	73965423	ref	XP_537576.2	-----MDMGVQVLLQEFK-----VMDSEFK-----NFSKNKPPPPPHHRP-----QRRHKMYKEQNLNT	150
gi	194675732	ref	XP_599356.4	-----MAFVKLPVQREGERDAESQPG--DREVRSILIRYSEGKNIGKEAHLHQLVQ--LWVRLWQGL--SYSPESPESPPKDDRYRLALFSSLKGSIFPCHLFVHLS--SFLRRRHKMYKEQNLNT	150
gi	118099783	ref	XP_415690.2	MPGPRRDRPALLLQALFVADLYFHLWPSA--RRRLAPASARAASSSSSSAS--SPMRR--FAHPLYRAA-----APGPAEPLLAGAREAL-----YYRRKAARWNRHKLKLYRQELNT	150
gi	195546800	ref	NP_001124252.1	---MRRDRLLVAVTVLLAADLHFLILLRSLWSYFLPRSCSCGDSNGSVDAMMWSQWLAVSTIEKGS--KLRLERFRLHPLNIRLDPDLADELLERQELIN-----YYQRKVSWEWEMKFKYVMEAAAAS	150



gi	241896898	ref	NP_060035.2	SL---DPLQLRLEASWVQFHLGINRHGLYSRSSPVVSKLLDMRHFPTISADYSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	114670175	ref	XP_511648.2	SL---DPLQLRLEASWVQFHLGINRHGLYSRSSPVVSKLLDMRHFPTISADYSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	24418883	ref	NP_722477.1	SL---DPLQFRPEASWVQFHLGINRHGLYSRSSLAISKLLHDMRHFPTISADYSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	109489283	ref	XP_573215.2	SL---DPPVQFRPEASWVQFHLGINRHGLYSRSSPVVSKLLHDMRHFPTISADHSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	73965423	ref	XP_537576.2	SL---DAPLQLRQEAASWVQFHLGISRRLGLYSRSSPVVSKLLDMRHFPTISADYSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	194675732	ref	XP_599356.4	SP---EPPVQLRQEAASWVQFHLGINRHGLYPRSSPVVSKLLDMRHFPTISADYSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	118099783	ref	XP_415690.2	AS---AALLPLRPEASWVQFHLGISRMDGLYPRSSPAVSRLLRDMHFATISADYSODEKALLGACDCQIVKPSGVHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRLVNVTKEILE	300
gi	195546800	ref	NP_001124252.1	NTSISDRVSKPKDASWVQFHLGIRYALYNREDSVDTLLDMQITVINAFTODEKALLGACDCQIVKPSGLHLKLVLRFSDFGKAMFKPMRQORDEETPVDFYFIDFQRHNAEIAAFHLLDRILDFFRRVPPVIGRFLVNVTKEILE	300



gi	241896898	ref	NP_060035.2	VTKNEILQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	114670175	ref	XP_511648.2	VTKNEILQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	24418883	ref	NP_722477.1	VTKNEILQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	109489283	ref	XP_573215.2	VTKNEILQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	73965423	ref	XP_537576.2	VTKNEILQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	194675732	ref	XP_599356.4	VTRNEVLQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	118099783	ref	XP_415690.2	VTRNEVLQSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450
gi	195546800	ref	NP_001124252.1	ITVHNEELRSVFFVSPANVCFFAKCPYMCKTEYAVCGNPHLLEGSLSAFLPSLNLAPRLSVPNPWIRSYTLAGKEEWEVNPVLYCDIVKQIYPYNSQRLLNVIDMAIFDFLIGNMDRHHYEMFTKFGDDGFLIHLDNARGFGRHSHDEIS	450



gi	241896898	ref	NP_060035.2	ILSPLSQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	114670175	ref	XP_511648.2	ILSPLSQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	24418883	ref	NP_722477.1	ILAPLQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	109489283	ref	XP_573215.2	ILAPLQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	73965423	ref	XP_537576.2	ILSPLSQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	194675732	ref	XP_599356.4	ILAPLQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	118099783	ref	XP_415690.2	ILAPLQCCM-----IKKKLLHLQLLAQADYRLSDVMRESLLEDQLSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558
gi	195546800	ref	NP_001124252.1	ILAPLQCCISAGGVINCSRIKRSITLFLRKLSSSEYLLSDVMRESLSDALSPVLTPEHLLALDRRLQIILRTVEGCIVAHQOQSVIVDGPVEQLAPDSGOANLTS	558

