

gi|4505861|ref|NP_000921.1|MDAMKRGKLCVLLLCGAVFVSPSE 150
gi|114619965|ref|XP_528120.2| MESCITKAVFTGQKCLTQEGGRSGESCDAMAGGMLAPRPCVYSLGPFKGLMPESEPRRPPAALHFTKKRKLKPKITEGQRCLEBPTIGAPPTADPTGVGWRENLCSEREGASREFKGRCEALMDAMKRGKLCVLLLCGAVFVSPSE 150
gi|6679375|ref|NP_032898.1|MKRELLCVLLLCGLFAFLPDCG 150
gi|42476137|ref|NP_037283.2|MKGELLCVLLLCGVAFTLPDCG 150
gi|88853808|ref|NP_776571.2|MMSAMKTEFLCVLLLCGAVFTSPSE 150
gi|73979159|ref|XP_539955.2|MGRATGVRFPLASGAGRCQGERA 150
gi|50806276|ref|XP_424404.1|MWKILRMKGLLSLILLVGVTKTQCCG 150
gi|189522957|ref|XP_001921433.1|MNLILLNLLLSALSCAADTE 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|4505861|ref|NP_000921.1|IHFARFRRGARSYQVICRDEKIQMIYQOHQSWLRPVLRSNRVEYWCNS-GRACCHSVVPVKSCEPRCFNGGTCCOALYFSD-FVCCPEGFAGKCCCEIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGL 300
gi|114619965|ref|XP_528120.2|IHFARFRRGARSYQVICRDEKIQMIYQOHQSWLRPVLRSNRVEYWCNS-GRACCHSVVPVKSCEPRCFNGGTCCOALYFSD-FVCCPEGFAGKCCCEIDTRATCYEDQGISYRGTWSTAESGAECTNWNSSVLAQKPYSGRRPDAIRLGL 300
gi|6679375|ref|NP_032898.1|IHGRFRRGARSYRATCRDEPTQITTYQOHQSWLRPMLRSRVEYCRCNS-GLVQCHSVVPVRSCEPRCFNGGTCCOALYFSD-FVCCPDGPFVGRKCDIDTRATCFEEOGITVYRGTWSTAESGAECTNWNSSVLSKPYNARRPNAIKLGL 300
gi|42476137|ref|NP_037283.2|IHRFRFRRGARSYRATCRDEPTQITTYQOHQSWLRPMLRGNRVEYCRCNS-GLAACHSVVPVRSCEPRCFNGGTCCOALYFSD-FVCCPDGPFVGRKCDIDTRATCFEEOGITVYRGTWSTAESGAECTNWNSSALSQKPYARRPNAIKLGL 300
gi|88853808|ref|NP_776571.2|IYRRLRRGARSYKVTCRDGTQMTYRQHDQSWLRPMLRGNVVEHWCWDG-GRACCHSVVPVRSCEPWCNNGTCCOALYFSD-FVCCPEGFAGKCCCEIDATATCYKDGVAIYRGTWSTAESGAECTNWNSSALAMKPYSGRRPNAIRLGL 300
gi|73979159|ref|XP_539955.2|LQRCARPVAFTG--ICRDEKIQMIYQOHQSWLRPMLRGNRVEYCRCAG-GRPQCHSVVPVRSCEPRCFNGGTCCOALYFSD-FVCCPEGFAGKCCCEIDATATCYKDGVAIYRGTWSTAESGAECTNWNSSALAMKPYARRPNAIRLGL 300
gi|50806276|ref|XP_424404.1|IHMRYKRGARQ-AICTDYSGGQIYRQHSWLR--LSGSRLEYCRCDR-GWSYCHTIVPRACTRNKCYLNGQCSQAYSPOLFI CRCHHGFSGKCCCEIDTEVKCYKNAIVYRGTWSTAESGAECTNWNSSALAMKPYSGRRPNAIRLGL 300
gi|189522957|ref|XP_001921433.1|LHDQKRGTRNYREACVDSNSAAVRDIGNVWLR--WGLKLVFECRCALGRARCHEVPTTKCFVSKCYNGGCKEALYSDF-FCQCPGFGTQCEINTLERCRRGGLGYRGSWSVSSGMECTNWNSSALRQKFTARRPNAIRLGL 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|4505861|ref|NP_000921.1|GNHNYCRNPDRLSPKWCYVFKAGKYSEFCSTPACSEGN--DCYFGNGSAYRGTHTSLTEGASCLPWNMILIGVYTAQNPSAALGLGKHNYCRNPDGAKPCHVKNRRLTWEYCDVPSCTCGLROYK---PQFRKGGFLFA 450
gi|114619965|ref|XP_528120.2|GNHNYCRNPDRLSPKWCYVFKAGKYSEFCSTPACSEGN--DCYFGNGSAYRGTHTSLTEGASCLPWNMILIGVYTAQNPSAALGLGKHNYCRNPDGAKPCHVKNRRLTWEYCDVPSCTCGLROYK---PQFRKGGFLFA 450
gi|6679375|ref|NP_032898.1|GNHNYCRNPDRLSPKWCYVFKAGKYTEFCSTPACPKGKSE--DCYVGVKVTYRGTHTSLTTPASCLPWNMILVMGKSYTAWRINSQALGLARHNYCRNPDGAKPCHVKNRRLTWEYCDVPSCTCGLROYK---PQFRKGGFLFA 450
gi|42476137|ref|NP_037283.2|GNHNYCRNPDRLSPKWCYVFKAGKYTEFCSTPACPKGKTE--DCYVGVKVTYRGTHTSLTTPASCLPWNMILVMGKSYTAWRINSQALGLARHNYCRNPDGAKPCHVKNRRLTWEYCDVPSCTCGLROYK---PQFRKGGFLFA 450
gi|88853808|ref|NP_776571.2|GNHNYCRNPDQSLPKWCYVFKAGKYTEFCSTPACAKVAEEDGDCYTGNGLAIRGTRSTKSGASCLPWNMILVFTSKIYTAWNSAPALGLGKHNYCRNPDGAKPCHVKNRRLTWEYCDVPSCTCGLROYK---PQFRKGGFLFA 450
gi|73979159|ref|XP_539955.2|GSHNYCRNPDGDLRPWCYVFKAGKYTEFCSTPACPKKNE--DCYFGKGLAYRGTYSFTTSGTCLPWNMILVAGKRYTAWRINSQALGLGSHNYCRNPDGAKPCHVKNRRLTWEYCDVPSCTCGLROYK---PQFRKGGFLFA 450
gi|50806276|ref|XP_424404.1|GNHNYCRNPDQSLPKWCYVFKAGKYTEFCSTPACPKKNE--INCKVGRGTDYRGSHTVITSGAICLWNSQIIVSKLYTAWRINSQALGLGSHNYCRNPDQSLPKWCYVFKAGKYTEFCSTCGLROYK---PQFRKGGFLFA 450
gi|189522957|ref|XP_001921433.1|GNHNYCRNPDGSLPKWCYVFKAGKYSEFCSTPACPKKNE--ECAQRSGQTYRGTHTSLTTPASCLPWNMILVAGKRYTAWRINSQALGLGSHNYCRNPDGDLRPWCYVFKAGKYTEFCSTCGLROYK---PQFRKGGFLFA 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|4505861|ref|NP_000921.1|DIASHPWQAAIFAKHRRSPGERFLCGGILLISCWVLSAAHCFQERYPPHLLTVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|114619965|ref|XP_528120.2|DIASHPWQAAIFAKHRRSPGERFLCGGILLISCWVLSAAHCFQERYPPHLLTVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|6679375|ref|NP_032898.1|DITSHPWQAAIFVKNRSPGERFLCGGVLISCWVLSAAHCFERFPPHLLKVVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|42476137|ref|NP_037283.2|DITSHPWQAAIFVKNRSPGERFLCGGVLISCWVLSAAHCFERFPPHLLKVVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|88853808|ref|NP_776571.2|DITSHPWQAAIFVKNRSPGERFLCGGILLISCWVLSAAHCFQERYPPHLLKVVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|73979159|ref|XP_539955.2|DITSHPWQAAIFVKNRSPGERFLCGGILLISCWVLSAAHCFQERYPPHLLKVVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|50806276|ref|XP_424404.1|DIEAHPWQAAIFVKNRSPGERFLCGGILLISCWVLSAAHCFQERYPPHLLKVVILGRTYRVPVPEEKEKFEVEKYIVHKEFDDDDTYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
gi|189522957|ref|XP_001921433.1|DIREQPWQAAITVYLRSPKTHNFLCGGVLISCWVLSAAHCFQERYEESRLVVLGRITFRLQNSSEKIFDVEKYIWHQYDDETYDNDIALLQLKSDSRLCARESSVVRIVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAH 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|4505861|ref|NP_000921.1|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|114619965|ref|XP_528120.2|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|6679375|ref|NP_032898.1|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|42476137|ref|NP_037283.2|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|88853808|ref|NP_776571.2|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|73979159|ref|XP_539955.2|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|50806276|ref|XP_424404.1|VRLYPSSRCTSQHLNRTVINDMLCAGDTRSGGPPQANLHDACGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
gi|189522957|ref|XP_001921433.1|VRLWPQDQVPEKLSGRLVINDMLCAGDTRG-----LDDACKGDSGGPLVLCNDGRMLVGIISWGLGCGKQDVPVGYTKVINYLDWIRDNMRP- 696
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....

