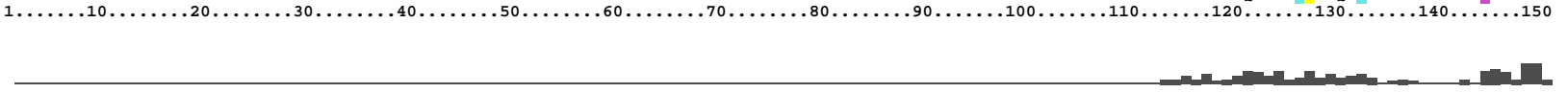


gi	21703722	ref	NP_663333.1	-----MSSCVSSQPTSDRAVPQDELGSGGGR--EGQKPC	36
gi	13786172	ref	NP_112628.1	-----MSSCVSSQPTSDRAAPQDELGSGGGR--ESQKPC	36
gi	73995188	ref	XP_543388.2	-----MSSCVSSQPTSDPAALQDELGGGGSS--EGQKPC	35
gi	115495061	ref	NP_001068858.1	-----MSSCISQSSSDRAAPQDELGGGGSSSEEGQKPC	38
gi	27437015	ref	NP_006540.3	-----MSSCVSSQPTSDRAAPQDELGG--RGSSSEEGQKPC	37
gi	118098481	ref	XP_415134.2	-----MPSCI--PGSPPAPQ-----PSHRRGG	21
gi	189525837	ref	XP_688971.3	-----MADTA	6
gi	116007870	ref	NP_001036633.1	MDLTDPLLITKSOQVNSQEVDFQKKTEDIFPSKFKHKKASCGLLAVNESRCTDHQLQCEENVIGLSLELQIAENSSINVSRELKPHDHTFPKDKQTFKQIDELRKSVEINIKVQNLKKSQVVENFEKCSINLANKCLYINLNTSPKER	150
gi	158284861	ref	XP_307935.4	-----MTQHKILPKTQSLDLADN--DDMLASNRSE	30



gi	21703722	ref	NP_663333.1	RGLSSLSIHLGMEFIVVTECEPGRGVDLNLARDQPPADQQLPLLEA-----DPESRSLSGRKMSLOEPGOGGPASSNSLDMNGRCICPISLSPASSPSSSPRMPRR--PTVESHHSITGLQDCVOLNQYTLKDEIGK	173
gi	13786172	ref	NP_112628.1	RGLSSLSIHLGMEFIVVTECEPGRGVDLNLARDQPLLEADQQLPLDAS-----EPESRSLSSGKMSLOERSOGGPASSS--LDMNGRCICPISLSPASSPSSSPRMPRR--PTVESHHSITGLQDCVOLNQYTLKDEIGK	172
gi	73995188	ref	XP_543388.2	QGLSSLSIRLGMESFIVVTECEPGCAVDRLGSRDRPRRAEGRKVPDASA-----SGQARPQLCSRKLSLOERSQ-----LDANGRCVHPVLPSPVSPSSPRLPRR--PTVESHHSITGLQDCVOLNQYTLKDEIGK	165
gi	115495061	ref	NP_001068858.1	RGLSSLSIRLGMESFIVVTECEPQCAVDHGLRDRPLRAHGGIITLDAS-----GQARPPLSGRKLLOERSL-----LDANGRCVYPALPSPVSPSSPRLPRR--PTVESHHSITGLQDCVOLNQYTLKDEIGK	166
gi	27437015	ref	NP_006540.3	RGLSSLSIHLGMEFIVVTECEPQCAVDLGLARDRPLLEADQVEVPLDTS-----GQARPPLSGRKLLOERSGGLAAGG--LDMNGRCICPISLSPVSPSSPRLPRR--PTVESHHSITGLQDCVOLNQYTLKDEIGK	173
gi	118098481	ref	XP_415134.2	PGLPLSAGRPAEMLIVVTECEAT-----ASEEMSGVAIVES-----REPRAKLNLGSRKLSLOERSHPVRS--GDSERFIPLSPVSPVTSPPHSPRRLPRR--PTVENRYSITGLQDCVOLNQYTLKDEIGK	145
gi	189525837	ref	XP_688971.3	SRLLDLDYHAELADMVA-----AMVAATRITPPNGY-----RTPHRLNLSDRKLLOERS-----CONGGPRMRR--PTIESKRYSITGDDCVOLNQYTLKDEIGK	101
gi	116007870	ref	NP_001036633.1	NALDKQAMFIRKHFLELCTDKVCSLHFNHCTDTHKCVVDSESNKPNMKKCLDYESVKRYPCKVSNPEPPPHNASKPILME-----TRPIMPVNPVYFSPYTPFSPRPSRSPKPAFREARRISIDKSSGFLQNLQYLRIMEIGK	291
gi	158284861	ref	XP_307935.4	SOLETSAAAGTGGAGGLR-----GRVLPKQLLEQT-----TRPIMPVNPVYFSPYTPFSPRPSRSGRRRTPLRESRRVIEQSSGFLQNLQYLRIMEIGK	118



gi	21703722	ref	NP_663333.1	GSYGVVKLAYNENDNTYAMKVLKSKKLLRQAGFPRRPPPR--GARPAPGGCIPRGPIEQVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	320
gi	13786172	ref	NP_112628.1	GSYGVVKLAYNENDNTYAMKVLKSKKLLRQAGFPRRPPPR--GTRPAPGGCIPRGPIEQVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	319
gi	73995188	ref	XP_543388.2	GSYGVVKLAYNENDNTYAMKVLKSKKLLRQAGFPRRPPPR--GTRPAPGGCIPRGPIEQVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	312
gi	115495061	ref	NP_001068858.1	GSYGVVKLAYNENDNTYAMKVLKSKKLLRQAGFPRRPPPR--GTRPAPGGCIPRGPIEQVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	313
gi	27437015	ref	NP_006540.3	GSYGVVKLAYNENDNTYAMKVLKSKKLLRQAGFPRRPPPR--GTRPAPGGCIPRGPIEQVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	320
gi	118098481	ref	XP_415134.2	GSYGVVKLAYNENDNTYAMKVLKSKKLLRQAGFPRRPPPR--GARGASEGLCPRGPIEQVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	292
gi	189525837	ref	XP_688971.3	GSYGVVKLAYNEDDDQYAMKVLKSKKLLRQAGFRRRPPSRNSGVSQENLLKPSGLLDRVYQEIAILKKLDHPNVVKLVLEVLDDPNEHLVMVFLVNGPVMVEVPLKPLSEDAARFYFODLIGIEYLHYQKLIHRDIKPSNLLV	251
gi	116007870	ref	NP_001036633.1	GSYGLVKLAYSEEDSTHYAMKILSKRKLRLRQAGLMRRGPGRK-----ATSLDRVRYREIAVLKKLDHPNVVKLVLEVLDDPLEDSLVLVFLVNGPVEVLSIPETPLSEERAWNVRDVLGVEYLHYQRIIHGDLKPA	427
gi	158284861	ref	XP_307935.4	GSYGLVKLAYSEEDSTHYAMKILSKRKLRLRQAGLMRRGPGRK-----GTSPLDRVRYREIAVLKKLDHPNVVKLVLEVLDDPLEDSLVLVFLVNGPVEVLSIPETPLSEERAWNVRDVLGVEYLHYQRIIHGDLKPA	254



gi	21703722	ref	NP_663333.1	GEDGHKIIDPFGVSNFEGKSDALLSN--FVGTAFMAPESLSETRKIFSGKALDVWAMGVTLICFVFGQCFPFMDERIMCLHSKIKSQALEFPDD--PDIAEDLKDILTRLMDKNPESRIVVPEIK	441
gi	13786172	ref	NP_112628.1	GEDGHKIIDPFGVSNFEGKSDALLSN--FVGTAFMAPESLSETRKIFSGKALDVWAMGVTLICFVFGQCFPFMDERIMCLHSKIKSQALEFPDD--PDIAEDLKDILTRLMDKNPESRIVVPEIK	440
gi	73995188	ref	XP_543388.2	GEDGHKIIDPFGVSNFEGKSDALLSN--FVGTAFMAPESLSETRKIFSGKALDVWAMGVTLICFVFGQCFPFMDERIMCLHSKIKSQALEFPDD--PDIAEDLKDILTRLMDKNPESRIVVPEIK	433
gi	115495061	ref	NP_001068858.1	GEDGHKIIDPFGVSNFEGKSDALLSN--FVGTAFMAPESLSETRKIFSGKALDVWAMGVTLICFVFGQCFPFMDERIMCLHSKIKSQALEFPDD--PDIAEDLKDILTRLMDKNPESRIVVPEIK	434
gi	27437015	ref	NP_006540.3	GEDGHKIIDPFGVSNFEGKSDALLSN--FVGTAFMAPESLSETRKIFSGKALDVWAMGVTLICFVFGQCFPFMDERIMCLHSKIKSQALEFPDD--PDIAEDLKDILTRLMDKNPESRIVVPEIK	441
gi	118098481	ref	XP_415134.2	GEDGHVKIADPFGVSNFEGKADALLTN--FVGTAFMAPETLSETRKIFSGKALDVWAMGITLICFVFGQCFPFMDERILSLHNKIKTQTLLEFPDD--PEVDFLKDILTRLMDKNPESRISVPEIKASTIQQLQPLARDFWPFAPAGTW	434
gi	189525837	ref	XP_688971.3	GDDGHVKIADPFGVSNFEGKSDALLSN--SAGTAFMAPETLTDQDQRFSGKALDIWAMGVTLICFVFGKCFPHDDYILGLHEKIRISMSVEFPDK--PEISEQLKDILTRLMDKNPESRITLAEIK	372
gi	116007870	ref	NP_001036633.1	TDFGHVKIADLGVCFNEFLGDDAISNGSTIAGTAFAPRAPETLIPGQNEYCGRAADVWALGATLISLIFGNVFLFSDIYELKIQDSVDFKPFEN--HKVTENLKDLCIVQMLEKNTQRTITLPEIK	550
gi	158284861	ref	XP_307935.4	SDSGSVKVAIDGVCFNEFLGDDAAMNNGSTIAGTAFAPRAPETLIPGQHNYNGKAADIWALGATLISLIFGNVFLFSDIYELKIQDSVDFKPFEN--RSNSAPGYSYHMSTARQPSDILLPISLMEHCS	383



gi	21703722	ref	NP_663333.1	LHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKQGS--EDSPRGPPEAPVQ	535
gi	13786172	ref	NP_112628.1	LHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKPPTREWELSEPKEARQRRQPPGPRGCGGGGSSALVGGPCVESCAGAPAPGPPRPQPQ	578
gi	73995188	ref	XP_543388.2	LHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKPPTREWELSEPKEARQRRQPPGPRGCGGGGSSALVGGPCVESCAGAPAPGPPRPQPQ	571
gi	115495061	ref	NP_001068858.1	LHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKPPTREWELSEPKEARQRRQPPGPRGCGGGGSSALVGGPCVESCAGAPAPGPPRPQPQ	572
gi	27437015	ref	NP_006540.3	LHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKPPTREWELSEPKEARQRRQPPGPRGCGGGGSSALVGGPCVESCAGAPAPGPPRPQPQ	579
gi	118098481	ref	XP_415134.2	KGREAEKMEKLEHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKPPTREWELSEPKEARQRRQPPGPRGCGGGGSSALVGGPCVESCAGAPAPGPPRPQPQ	579
gi	189525837	ref	XP_688971.3	LHPWVTRHGAEPLPSEDENCILVEVT EEEVENSVKHIPSLSLAIVILVKMIRKRSFSGNPFEG--SRREERSLSAPGNLLTKPPTREWELSEPKEARQRRQPPGPRGCGGGGSSALVGGPCVESCAGAPAPGPPRPQPQ	539
gi	116007870	ref	NP_001036633.1	SKWVSDGQYPLPPEEENCILVDDDEDIDSVVRSIPKLDLILIKMLKKEHFGNPFVKGCSTSS--LACCSRIERFIRAG--RSNSAPGYSYHMSTARQPSDILLPISLMEHCS	468
gi	158284861	ref	XP_307935.4	EHVPMKGGTVLPLPEEENCILVDDDEDIDSVVRSIPKLDLILIKMLKKEHFGNPFVKGCSTSS--LACCSRIERFIRAG--RSNSAPGYSYHMSTARQPSDILLPISLMEHCS	666



gi	21703722	ref	NP_663333.1	-EEVLL---	541
gi	13786172	ref	NP_112628.1	QPEEAMEPE-	587
gi	73995188	ref	XP_543388.2	RPDEAME---	578
gi	115495061	ref	NP_001068858.1	RPDEVME---	579
gi	27437015	ref	NP_006540.3	RPEEAMEPE-	588
gi	118098481	ref	XP_415134.2	-EEVLS---	545
gi	189525837	ref	XP_688971.3	IEDEIFP---	475
gi	116007870	ref	NP_001036633.1	CNEGTHSFDY	676
gi	158284861	ref	XP_307935.4	-----	479
				.....760	

