

gi | 115298678 | ref | NP_000055.2 | GQSEDRQVPVPGQOMTLKIEGDHGRVAVLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTPGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVQLTEKRMKDVGVKYPKE-LRKCCEEDGMRE-NPMRFSCORRR 712
gi | 114674922 | ref | XP_512318.2 | RRKEGRREKGEOR--KEERRRGGKGGGRGR-KGKEDRKRKRKRPMIWDVVEKADIGCTPGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLLTEKRMKDVGVKYPKE-LRKCCEEDGMRE-NPMRFSCORRR 458
gi | 126518317 | ref | NP_033908.2 | DPRDN-HLAPGQOITLRIEIGNQGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTPGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVQLMERRMDKAGQYTDKGLRKCCEEDGMRE-IPMRFSCORRR 712
gi | 8393024 | ref | NP_058690.1 | DPRDNQAPAGHQITLRIEIGNQGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTPGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVQLMERRMDKAGQYTDKGLRKCCEEDGMRE-IPMRFSCORRR 712
gi | 99028969 | ref | NP_001035559.2 | GQSEDRQVPVPGQOMTLKIEGDHGRVAVLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTPGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVQLTEKRMKDVGVKYPKE-LRKCCEEDGMRE-NPMRFSCORRR 710
gi | 73987236 | ref | XP_533932.2 | SGKEQRSHLPGQOITLRIEIGNQGDGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTAGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLLTEKRMKDVGVKYPKE-LRKCCEEDGMRE-NPMRFSCORRR 711
gi | 118113407 | ref | XP_001236914.1 | SEADNRVHEPRTMRLHIEGDHKAHVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTPGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVRLKHKGKMAEYSDKNLKRKCCEEDGMRE-NLMGYSCERRA 428
gi | 82524272 | ref | NP_571318.1 | VKEKNTYETGNDVNLHITGDPGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTGGGKDSMGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLQITITTLAGQYTE-KIRPCCYDGMRE-NRIGYTCERRA 708
gi | 189546565 | ref | XP_001920029.1 | VKEKNTYETGNDVNLHITGDPGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTGGGKDSMGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLQITITTLAGQYTE-KIRPCCYDGMRE-NRIGYTCERRA 708
gi | 82524318 | ref | NP_001032313.1 | VTEKQKVFYETGNEVNLQISGDPGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTGGGKDSMGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLQITITTLAGQYTE-KIRPCCYDGMRE-NRIGYTCERRA 708
gi | 189546569 | ref | XP_001920074.1 | VTKQNNYNTGEEVNLQISGDPGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTAGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLQITITTLAGQYTE-KIRPCCYDGMRE-NRIGYTCERRA 707
gi | 189546571 | ref | XP_695351.3 | VXD-MLFPGDGLSLKITGDPGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTAGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLQITITTLAGQYTE-KIRPCCYDGMRE-NRIGYTCERRA 686
gi | 189546573 | ref | XP_696246.3 | VDFVEVVEPEGEELRITGDPGARVGLVAVDKGVFVNLKKNLTKOSKIWDVVEKADIGCTAGSGKDYAGVFS DAGLFTSSGQQQTAORAELOCPQPAARRRR---SVLQITITTLAGQYTE-KIRPCCYDGMRE-NRIGYTCERRA 700
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi | 115298678 | ref | NP_000055.2 | FISL--GEACKKVFLDCCNIIELRRQHARASHLGLARSLNLD---DIIAENIVSRSEFPESWLWN-VEDLKEPP---KNGISTKLMNIFLKDSITITWEILAVSLSDKKGICVADPFEVTVMOFFIDLRLPYSVVRNEQVEIRAVLY 852
gi | 114674922 | ref | XP_512318.2 | FISL--GEACKKVFLDCCNIIELRRHARAHLGLSLVRSDDLDE---DIIAENIVSRSEFPESWLWN-VEDLKEPP---KNGISTKLMNIFLKDSITITWEILAVSLSDKKGICVADPFEVTVMOFFIDLRLPYSVVRNEQVEIRAVLY 598
gi | 126518317 | ref | NP_033908.2 | LITQ--GENCIAKAFIDCCNIIKLRQHRDRHVLGLARSELDE---DIIPBEDIISRSHFPESWLWT-IEBELKEPE---KNGISTKLMNIFLKDSITITWEILAVSLSDKKGICVADPFEVTVMOFFIDLRLPYSVVRNEQVEIRAVLY 852
gi | 8393024 | ref | NP_058690.1 | LITQ--GESCILKAFMDCCNIIKLRQHRDRHVLGLARSELDE---DIIPBEDIISRSHFPESWLWT-IEBELKEPE---KNGISTKLMNIFLKDSITITWEILAVSLSDKKGICVADPFEVTVMOFFIDLRLPYSVVRNEQVEIRAVLY 852
gi | 99028969 | ref | NP_001035559.2 | FILQ--GDACVKAFLDCCNIIQLRQHARDGALELARIDLDD---DIIPBEDIISRSHFPESWLWT-IEBELKEPE---KNGISTKLMNIFLKDSITITWEILAVSLSDKKGICVADPFEVTVMOFFIDLRLPYSVVRNEQVEIRAVLY 851
gi | 73987236 | ref | XP_533932.2 | FVSRSEESHCVKAFLDCCNIIQLRLNYSRMDNLGLARSELDE---DIFLEBEDIVSRSHFPESWLWT-IEBELKEPE---KNGISTKLMNIFLKDSITITWEILAVSLSDKKGICVADPFEVTVMOFFIDLRLPYSVVRNEQVEIRAVLY 853
gi | 118113407 | ref | XP_001236914.1 | VVLD--GKACTEAFSLCCLIKGIRDEE-RELVQELARSDMDE---AFLSDEEDITSRLFPESWLWV-VEELTEPEPN---EQGISMKTIPLFKDSITITWEILAVSLSENK 529
gi | 82524272 | ref | NP_571318.1 | VVID--GEECVKAFHLCKEVEKNHKEKEEELILARSDDE---EGDYKDYDDITSRTQFPESWLWEEFDLCKDCS---KPSKDK-VIYLKDSITITWQILAISSLPTHGICVAEPEEIVVFKSFFIDLKVPYSAVRGEQVEIKAIH 848
gi | 189546565 | ref | XP_001920029.1 | VVID--GEECVKAFHLCKEVEKNHKEKEEELILARSDDE---EGDYKDYDDITSRTQFPESWLWEEFDLCKDCS---KPSKDK-VIYLKDSITITWQILAISSLPTHGICVAEPEEIVVFKSFFIDLKVPYSAVRGEQVEIKAIH 848
gi | 82524318 | ref | NP_001032313.1 | VVID--GEECVKAFHLCKEVEKNHKEKEEELILARSDDE---EGDYKDYDDITSRTQFPESWLWEEFDLCKDCS---KPSKDK-VIYLKDSITITWQILAISSLPTHGICVAEPEEIVVFKSFFIDLKVPYSAVRGEQVEIKAIH 848
gi | 189546569 | ref | XP_001920074.1 | YIGD--GPECVKAFLHCCDEMCKRKNKIEEEMILARSDDDD---DYIYDSEIIVSRQFPESWLWEEFDLCKDCS---ASAMEK-AMYLKDSITITWQILAISSLPTHGICVAEPEEIVVFKSFFIDLKVPYSAVRGEQVEIKAIH 846
gi | 189546571 | ref | XP_695351.3 | FISD--TQECIKAFVRCCKLIEHRVKYNAEKELFLRSDEDD---FDSDMDLIVRTQFPESWLWEEITLPAFLPNCITETSTLRT-GIYLKDSITITWQILAISSLPTHGICVAEPEEIVVFKSFFIDLKVPYSAVRGEQVEIKAIH 829
gi | 189546573 | ref | XP_696246.3 | FILD--GKECRDAFLDCCNIIELRR-EPAAEEIFLGRSEDE---FVNSDDIVSRILFPESWLWEEVMLPKCLGNRCQTITLPLKDWLWLDKDSITITWEILAVSLNTHGICVADVHEMIVAKNFFIDLKVPYSAVRGEQVEIKAIH 842
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi | 115298678 | ref | NP_000055.2 | NYRNOELKVRVELLHNPAPCSLAIKRRHQQTIVIPPKSSLSVPVIVPLKGLDEVVKAAVVHHFISDGVRRKSLKVVPEGIRMNKIVAVRILDPERLGRGVKEDIPPADLSDVDPDTESETRILLOGTVAQMTEDAVDAERLKH 1002
gi | 114674922 | ref | XP_512318.2 | NYRNOELKVRVELLHNPAPCSLAIKRRHQQTIVIPPKSSLSVPVIVPLKGLDEVVKAAVVHHFISDGVRRKSLKVVPEGIRMNKIVAVRILDPERLGRGVKEDIPPADLSDVDPDTESETRILLOGTVAQMTEDAVDAERLKH 748
gi | 126518317 | ref | NP_033908.2 | NYRQEKLVKRVVELLHNPAPCSMATAKNRYFTIIPPKSSVAVPVIVPLKIGLDEVVKAAVVHHFISDGVRRKSLKVVPEGIRMNKIVAVRILDPERLGRGVKEDIPPADLSDVDPDTESETRILLOGTVAQMTEDAVDAERLKH 1002
gi | 8393024 | ref | NP_058690.1 | NYRQEKLVKRVVELLHNPAPCSMATAKNRYFTIIPPKSSVAVPVIVPLKIGLDEVVKAAVVHHFISDGVRRKSLKVVPEGIRMNKIVAVRILDPERLGRGVKEDIPPADLSDVDPDTESETRILLOGTVAQMTEDAVDAERLKH 1002
gi | 99028969 | ref | NP_001035559.2 | NYRBAENLKVRVELLHNPAPCSLAIKRRHQQTIVIPPKSSVAVPVIVPLKIGLDEVVKAAVVHHFISDGVRRKSLKVVPEGIRMNKIVAVRILDPERLGRGVKEDIPPADLSDVDPDTESETRILLOGTVAQMTEDAVDAERLKH 1001
gi | 73987236 | ref | XP_533932.2 | NYQEREDLKVVELLHNPAPCSLAIKSKSYQITVNIIPAKSSVAVPVIVPLKIGLDEVVKAAVVHHFISDGVRRKSLKVVPEGIRMNKIVAVRILDPERLGRGVKEDIPPADLSDVDPDTESETRILLOGTVAQMTEDAVDAERLKH 1003
gi | 118113407 | ref | XP_001236914.1 | NYTPKHLKVRVEFLETAGVCSAASKKGYRITVNVNDRKSSVAVSFVIVPMTLESQHIEVKAASIID--YDGVRRKSLKVVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 529
gi | 82524272 | ref | NP_571318.1 | NYTPKHLKVRVEFLETAGVCSAASKKGYRITVNVNDRKSSVAVSFVIVPMTLESQHIEVKAASIID--YDGVRRKSLKVVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 933
gi | 189546565 | ref | XP_001920029.1 | NYTPKHLKVRVEFLETAGVCSAASKKGYRITVNVNDRKSSVAVSFVIVPMTLESQHIEVKAASIID--YDGVRRKSLKVVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 907
gi | 82524318 | ref | NP_001032313.1 | NYTPKHLKVRVEFLETAGVCSAASKKGYRITVNVNDRKSSVAVSFVIVPMTLESQHIEVKAASIID--YDGVRRKSLKVVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 933
gi | 189546569 | ref | XP_001920074.1 | NYTP--DKRKRVEFLETAGVCSAASKKGYRITVNIIPPKSSVAVPVIVPMTLGNHMIKAAVDAVYDGVRRKSLKVVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 992
gi | 189546571 | ref | XP_695351.3 | NYSN--QKLVNVRFKTSEADICSSAGKKTGRLRVSDVLMSSRAVPLIIPMDADEWIEVEAXXSSNRKDIRKSLKVVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 977
gi | 189546573 | ref | XP_696246.3 | NLYS--KAVKVRVELKEKDKICSPASNKGYAVVIVVASKSSVVPVIVPLALGRHAEVKAASAGR--GNDGVKDLVLLVSEGVLKFRTRKLELNPQKK---GKPLVLRSGIPADVPGTVPVNIYITVTGEEISQIEQAINSGSFMGE 985
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 115298678 | ref | NP_000055.2 | LIVTPSGCGEONMIGMPTVIAVHYLDETEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFVKRAPSTWLAAYVVKVFLAVNLIAIDSVLQCGAVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1152
gi | 114674922 | ref | XP_512318.2 | LIVTPSGCGEONMIGMPTVIAVHYLDETEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFVKRAPSTWLAAYVVKVFLAVNLIAIDSVLQCGAVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 898
gi | 126518317 | ref | NP_033908.2 | LIVTPAGCGEONMIGMPTVIAVHYLDQTEQWEKFGLEKRGALRELKKGYTQQLAFKQPSAFAAFNRPSTWLAAYVVKVFLAVNLIAIDSVLQCGAVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1152
gi | 8393024 | ref | NP_058690.1 | LIVTPSGCGEONMIGMPTVIAVHYLDQTEQWEKFGLEKRGALRELKKGYTQQLAFKQPSAFAAFNRPSTWLAAYVVKVFLAVNLIAIDSVLQCGAVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1152
gi | 99028969 | ref | NP_001035559.2 | LIQTPSGCGEONMIGMPTVIAVHYLDSDEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFQYRPPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1151
gi | 73987236 | ref | XP_533932.2 | LIVTPSGCGEONMIGMPTVIAVHYLDQTEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFQYRPPSTWLAAYVVKVFLAVNLIAIDSVLQCGAVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1153
gi | 118113407 | ref | XP_001236914.1 | LIQTPSGCGEONMIGMPTVIAVHYLDQTEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFQYRPPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 629
gi | 82524272 | ref | NP_571318.1 | LIQTPSGCGEONMIGMPTVIAVHYLDQTEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFQYRPPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1142
gi | 189546565 | ref | XP_001920029.1 | LIQTPSGCGEONMIGMPTVIAVHYLDQTEQWEKFGLEKRGALRELKKGYTQQLAFRQPSAFAAFQYRPPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 907
gi | 82524318 | ref | NP_001032313.1 | LKRPGGCGEONMAMMLPVAATHYLDNINQWESVIGIDRRKVAINHIIKTYGEGOLKRYRPGDSYAIWNTSPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1142
gi | 189546569 | ref | XP_001920074.1 | LIVQPHGCGEONMIFMLPVIATHYLDNINQWESVIGIDRRKVAINHIIKTYGEGOLKRYRPGDSYAIWNTSPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1141
gi | 189546571 | ref | XP_695351.3 | LIVLPHGCGEONMILMLPVIATHYLDNINQWESVIGIDRRKVAINHIIKTYGEGOLKRYRPGDSYAIWNTSPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1126
gi | 189546573 | ref | XP_696246.3 | LIQTPSGCGEONMGLMMPVIAATHYLDNINQWHTVRAGLRTAEVIRKGYNPGDSYAAWNTSPSTWLAAYVVKVFLAVNLIAIDSKDLCEVVKWLILEKQKPDGVFOEDAPVIHOEMIGGLRNNNEKDMALTAFLVLSLQ 1134
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi | 115298678 | ref | NP_000055.2 | EAKDICEE... 1302
gi | 114674922 | ref | XP_512318.2 | EAKDICEE... 1048
gi | 126518317 | ref | NP_033908.2 | EARDICEE... 1302
gi | 8393024 | ref | NP_058690.1 | EARDICEE... 1302
gi | 99028969 | ref | NP_001035559.2 | EAKDICEA... 1301
gi | 73987236 | ref | XP_533932.2 | EAEDICI... 1303
gi | 118113407 | ref | XP_001236914.1 | ES... 689
gi | 82524272 | ref | NP_571318.1 | EGKEIC... 1292
gi | 189546565 | ref | XP_001920029.1 | EGKEIC... 907
gi | 82524318 | ref | NP_001032313.1 | EGKEIC... 1292
gi | 189546569 | ref | XP_001920074.1 | EGRELC... 1291
gi | 189546571 | ref | XP_695351.3 | EGSCICA... 1273
gi | 189546573 | ref | XP_696246.3 | EGSRRC... 1280
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi | 115298678 | ref | NP_000055.2 | RSSKITH... 1451
gi | 114674922 | ref | XP_512318.2 | RSSKITH... 1139
gi | 126518317 | ref | NP_033908.2 | RSSATTF... 1451
gi | 8393024 | ref | NP_058690.1 | RSSPTV... 1451
gi | 99028969 | ref | NP_001035559.2 | RNSAVR... 1449
gi | 73987236 | ref | XP_533932.2 | RST... 1452
gi | 118113407 | ref | XP_001236914.1 | R... 703
gi | 82524272 | ref | NP_571318.1 | RRKTRD... 1440
gi | 189546565 | ref | XP_001920029.1 | RRKTRD... 907
gi | 82524318 | ref | NP_001032313.1 | RRKTRD... 1440
gi | 189546569 | ref | XP_001920074.1 | RSKPSR... 1438
gi | 189546571 | ref | XP_695351.3 | RSEKTK... 1418
gi | 189546573 | ref | XP_696246.3 | -VRPTV... 1428
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi | 115298678 | ref | NP_000055.2 | SHSEDD... 1601
gi | 114674922 | ref | XP_512318.2 | SHTEED... 1139
gi | 126518317 | ref | NP_033908.2 | SHTEED... 1601
gi | 8393024 | ref | NP_058690.1 | SHTEED... 1601
gi | 99028969 | ref | NP_001035559.2 | SHTEED... 1599
gi | 73987236 | ref | XP_533932.2 | SHNQED... 1549
gi | 118113407 | ref | XP_001236914.1 | SH... 703
gi | 82524272 | ref | NP_571318.1 | SHKES... 1589
gi | 189546565 | ref | XP_001920029.1 | SHEVSE... 907
gi | 82524318 | ref | NP_001032313.1 | SHEVSE... 1589
gi | 189546569 | ref | XP_001920074.1 | SNKES... 1586
gi | 189546571 | ref | XP_695351.3 | SNKEK... 1567
gi | 189546573 | ref | XP_696246.3 | SHTRK... 1577
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi | 115298678 | ref | NP_000055.2 | YLMWGL... 1663
gi | 114674922 | ref | XP_512318.2 | YLMWGL... 1139
gi | 126518317 | ref | NP_033908.2 | YLMWGL... 1663
gi | 8393024 | ref | NP_058690.1 | YLMWGL... 1663
gi | 99028969 | ref | NP_001035559.2 | YLVWGV... 1661
gi | 73987236 | ref | XP_533932.2 | YLVWGV... 1549
gi | 118113407 | ref | XP_001236914.1 | YL... 703
gi | 82524272 | ref | NP_571318.1 | YLIMGN... 1651
gi | 189546565 | ref | XP_001920029.1 | YLIMGN... 907
gi | 82524318 | ref | NP_001032313.1 | YLIMGN... 1651
gi | 189546569 | ref | XP_001920074.1 | YLIMGN... 1648
gi | 189546571 | ref | XP_695351.3 | YLIMGN... 1629
gi | 189546573 | ref | XP_696246.3 | YLIMGN... 1638
.....1660.....1670.....1680.....1690.....1700.....1710...

