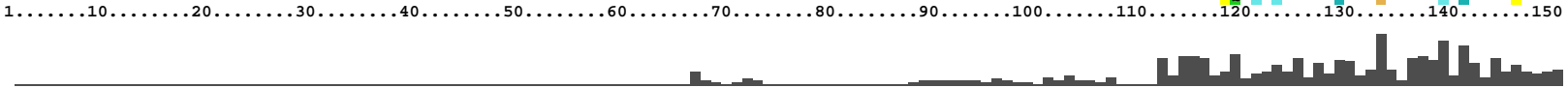
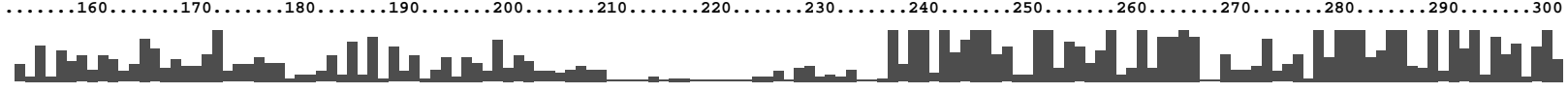


gi | 6753374 | ref | NP\_033994.1 | ... MGARCRS ... F ALLLLLQVSSWLCQELPEPS ... CSPGFSSEVYTFPVPERHLERGHVLRGRVFEGETGRPRIT 68  
gi | 13786164 | ref | NP\_112624.1 | ... MGARCRS ... F ALLLLLQVSSWLCQEPESSDS ... CRPGFSSEVYTFVPERHLERGHVLRGRVFEGETGRPRIT 70  
gi | 4757960 | ref | NP\_004351.1 | ... MGPPWRS ... L S ALLLLLQVSSWLCQEPPEP ... CHPGFDAESYTFVPRHLERGRVLRGRVFEGETGRQRT 66  
gi | 114663332 | ref | XP\_001168150.1 | ... MGPPWRS ... L S ALLLLLQVSSWLCQEPPEP ... CHPGFDAESYTFVPRHLERGRVLRGRVFEGETGRQRT 66  
gi | 73957458 | ref | XP\_536807.2 | ... MALFGIKAARFVHVECCSRSSQAARGAGPRGSPGGRTPRPSVASGAAGTCDNRKSCRLAPPRAARRLAPGSRPPAMPGRYGGAPALLPLLLLQVSSGLCQEPPEP ... CRPGFGADSYTFVPRHLERGRVLRGRVFEGETGLPRIT 146  
gi | 50582555 | ref | NP\_001002763.1 | ... MGPPWRS ... L S ALLLLLQVSSWLCQEPPEP ... CIPGFGAESYTFVPRHLERGRVLRGRVFEGETGLPRIT 66  
gi | 86129428 | ref | NP\_001034347.1 | ... MGPPWRS ... L S ALLLLLQVSSWLCQEPPEP ... CIPGFGAESYTFVPRHLERGRVLRGRVFEGETGLPRIT 66  
gi | 292616322 | ref | XP\_002662973.1 | ... MGRRWGSPALQR ... FFVLVLLLLLQVGRRCDEAAP ... CQPGFAAFTFVSPVDFVAAGRELGRVFAACSGRPWA 73  
gi | 292616318 | ref | XP\_002662972.1 | ... --MYRVLDTOTCQEQDPLHLNKKPMLD ... EAAQQQKANRQLIKILSCGFABESPCTPGFESKLLLVVVKHDKHLKGERLGRVVFSTCDGRTGI 89  
gi | 292616316 | ref | XP\_001331428.3 | ... MCIQDSVT ... DAAIHQWRRLNACVLSGLAESPCTPGFESNLLVFKVHKDHLKGERLGRVVFSTCDRRTV 71  
gi | 18858397 | ref | NP\_571895.1 | ... MACVITVG ... LGVIFLFR ... VFSGGYTHMSTCTPGLEEFVFKVHRNHLHSGKRLGKVFSTFNCDDGRT 67  
gi | 292616334 | ref | XP\_695998.4 | ... MPILVIEETHNRITG ... IFVDMTVEHTL 29



gi | 6753374 | ref | NP\_033994.1 | ... AFFSEDSRFKVAIDGVIIVKRHLKLEKLETSFLVLRARDSSHRELSTKVTILKSMGHHHRHHRDPAESNPPELLMFPVYVPG ... LRRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NRDKEIKVFYITGGADKPPVGVFIERETGW 215  
gi | 13786164 | ref | NP\_112624.1 | ... AFFSEDSRFKVAIDGVIIVKRHLKLEKLETSFLVLRARDSSHRELSTKVTILKSMGHHHRHHRDPAESNPPELLMFPVYVPG ... LRRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NRDKEIKVFYITGGADKPPVGVFIERETGW 217  
gi | 4757960 | ref | NP\_004351.1 | ... AFVSLDTRFKVGDGVIIVKRPLRFHNPDIHFLVYAWDSTYRKFTSTKVTILNTVGHHRPPPPQASVSGIQAEELLTFNNSSPG ... LRRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NKDKGKVFYITGGADTPPVGVFIERETGW 213  
gi | 114663332 | ref | XP\_001168150.1 | ... AFVSLDTRFKVGDGVIIVKRPLRFHNPDIHFLVYAWDSTYRKFTSTKVTILNTVGHHRPPPPQASVSGIQAEELLTFNNSSPG ... LRRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NKDKGKVFYITGGADTPPVGVFIERETGW 213  
gi | 73957458 | ref | XP\_536807.2 | ... AVVSDTRFKVGDGVIIVKRPLQLHKPISFLVLRARDSSRRLKSTKVTILKAAATHHHHHH--HDAPSKTQTEVLTFFPSSQHG ... LRRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NRDKEIKVFYITGGADAPPVGVFIERETGW 291  
gi | 50582555 | ref | NP\_001002763.1 | ... VVVSDTRFKVGDGVIIVKRPLVHLRPELSFLVLRARDSSRRLKSTKVTILEVAHHHHHSHDPSGCTQTEVLTFFPSPHG ... LRRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NRDKEIKVFYITGGADAPPVGVFIERETGW 213  
gi | 86129428 | ref | NP\_001034347.1 | ... VVVPDTRFKVNGDGVVSTKRPDLTYGRKISFTIYAQDAMGKRHSARVTVG--RHRHRRHHRHNLQDTPAVLTFPKHPDGLRQKRWDWVIPPISCPENKGEFFPKNLVQIKS ... NKDKESKVFYITGGADSPVGVFIERETGW 219  
gi | 292616322 | ref | XP\_002662973.1 | ... LFQSIDKRFELNDGVTILKRRQVTLHEGKHFVSVHAWDSSGKMKHTASVRRVPAQTKSLSDLL ... LIPKSSSLGLN ... RAKRCWILPPLTLHEGKGFPPMRLFOIKS ... DSASPTPAYKITEGADQDPKGIQIDRLSGW 181  
gi | 292616318 | ref | XP\_002662972.1 | ... DFQSDIQEIDLNMDDGLMMRRSVTLHEGKHFVSVHAWDSSGKMKHTASVRRVPAQTKSLSDLL ... HDSSSLGLN ... RAKRCWILPPLTLHEGKGFPPMRLFOIKS ... DSASPTPAYKITEGADQDPKGIQIDRLSGW 218  
gi | 292616316 | ref | XP\_001331428.3 | ... LFQSIDKRFELNDGVTILKRRQVTLHEGKHFVSVHAWDSSGKMKHTASVRRVPAQTKSLSDLL ... DLVL ... LIPKSSSLGLN ... RAKRCWILPPLTLHEGKGFPPMRLFOIKS ... DSASPTPAYKITEGADQDPKGIQIDRLSGW 206  
gi | 18858397 | ref | NP\_571895.1 | ... LFQSIDKRFELNDGVTILKRRQVTLHEGKHFVSVHAWDSSGKMKHTASVRRVPAQTKSLSDLL ... SSSDVLTKNKKVKGWIIIPISVSESKGFFMRLFOIKS ... DYALTRLAYKITEGADLPKGIQIDRLSGW 199  
gi | 292616334 | ref | XP\_695998.4 | ... TIISIHDEKRR-REATLHGRSSITLTK-VRKCTIDSDTFSN---LLVEEFQSSSE---GRR---RRKREWAIPFTVLENDKALPKILFKLANLDGVPEDIRYSITGEGADQPPVGVFIERTVMSGI 147



gi | 6753374 | ref | NP\_033994.1 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 365  
gi | 13786164 | ref | NP\_112624.1 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 367  
gi | 4757960 | ref | NP\_004351.1 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 363  
gi | 114663332 | ref | XP\_001168150.1 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 363  
gi | 73957458 | ref | XP\_536807.2 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 441  
gi | 50582555 | ref | NP\_001002763.1 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 363  
gi | 86129428 | ref | NP\_001034347.1 | ... LKVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 369  
gi | 292616322 | ref | XP\_002662973.1 | ... VSVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 331  
gi | 292616318 | ref | XP\_002662972.1 | ... VSVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 368  
gi | 292616316 | ref | XP\_001331428.3 | ... VSVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 356  
gi | 18858397 | ref | NP\_571895.1 | ... VSVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 349  
gi | 292616334 | ref | XP\_695998.4 | ... VSVTQPLDREAIKALYLLSHAVSSNGEAVDPEMELIIVTVDONDNKPEFTQEVFGKASALLEGALPSTVMQVTAADDDAVNTYAAIAVYITLSQDPPELPHKMFVNRNDGVIISVLTSLGDRSFPYITLVVQAADLQEGGLSTTAKAVI 295



gi | 6753374 | ref | NP\_033994.1 | ... TVKDIINDAPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DPDQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 514  
gi | 13786164 | ref | NP\_112624.1 | ... TVKDIINDAPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DPDQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 516  
gi | 4757960 | ref | NP\_004351.1 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DDGGQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 512  
gi | 114663332 | ref | XP\_001168150.1 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DDGGQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 512  
gi | 73957458 | ref | XP\_536807.2 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--NNNDQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 590  
gi | 50582555 | ref | NP\_001002763.1 | ... TVLDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--BNEKQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 512  
gi | 86129428 | ref | NP\_001034347.1 | ... EVDIANDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DPDQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 519  
gi | 292616322 | ref | XP\_002662973.1 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DDGGQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 481  
gi | 292616318 | ref | XP\_002662972.1 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DDGGQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 518  
gi | 292616316 | ref | XP\_001331428.3 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--NNNDQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 506  
gi | 18858397 | ref | NP\_571895.1 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--BNEKQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 499  
gi | 292616334 | ref | XP\_695998.4 | ... TVTDINDNPPVFNSTYQGVPEVNEVARIATLTKVTDADDAPNTPAWKAIVTVN--DDGGQFVTVVDP--TNDGILKAKGLDFEAKQYLLHVRVNEEPPFEGSLVPTSTAVTVVDDVVDNEAPIFMPAERRVEVPEDEFGVQEIISYTAQE 445



