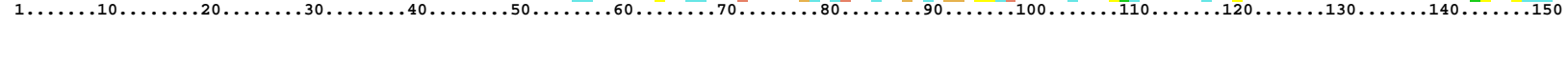


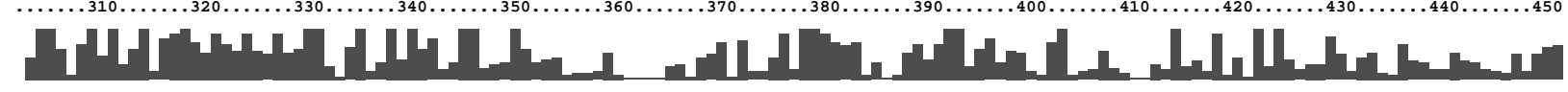
gi | 24662962 | ref | NP\_524030.2 | ---MASFQTHQDMSNKENPGIKTIPAGVKN---TKQPLAVITGGKAEKNALAPRANFAVLNGNINVPFPAKGVQVFRDVRNLNVDENVBYGAKSKSNVVPVVEQFKTFSVYEDNNITQVAPSGSKSLALVLDKENHDKVKGAGQOKELVDVLDLS 150  
gi | 158300141 | ref | XP\_320142.3 | ---RSAP-----LQELKHAELLE 150  
gi | 4502613 | ref | NP\_001228.1 | ---MLGNSAPGAPATREAGSALLALQOTALG---EDQENINPEKAAPVQOPRTRAALAVLKSNGRGLAQQRPKTRRVAFLKDLPLVNDHEVTVVPP-WKANSKQPAFTTHVDEAEKEAQKPAES-QKTEREDALAFN 150  
gi | 55623156 | ref | XP\_517420.1 | ---MLGNSAPGAPATREAGSALLALQOTALG---EDQENINPEKAAPVQOPRTRAALAVLKSNGRGLAQQRPKTRRVAFLKDLPLVNDHEVTVVPP-WKANSKQPAFTTHVDEAEKEAQKPAES-QKTEREDALAFN 150  
gi | 73983960 | ref | XP\_540965.2 | ---MLGSSAPGAPATREAGSALLALQOTALG---EDQENINPEKAAPVQOPRTRAALAVLKSNGRGLAQQRPKTRRVAFLKDLPLVNDHEVTVVPP-WKANSKQPAFTTHVDEAEKEAQKPAES-QKTEREDALAFN 150  
gi | 115497582 | ref | NP\_001068591.1 | ---MLGSSAPGAPATREAGSALLALQOTALG---EDQENINPEKAAPVQOPRTRAALAVLKSNGRGLAQQRPKTRRVAFLKDLPLVNDHEVTVVPP-WKANSKQPAFTTHVDEAEKEAQKPAES-QKTEREDALAFN 150  
gi | 6753308 | ref | NP\_033958.1 | ---MPGTSRHS---GRDAGSALLSLHG---EDQENINPEKLAQOPR---AQAFLKAGNVRGPAQOQKLRIRRVAPLKLDPINDEHVTVVPP-SWKAQKQPAFTTHVDEAEKEAQKPAES-QKTEREDALAFN 150  
gi | 61097935 | ref | NP\_446154.1 | ---MSTQGSVAVHDSIHNQENMLSRLRGAARNRVENRNVNPNKAAANRNLVLEELNSQRRLG---LRGAKGSSGQPIIACKPEENARSFGERPNSRQPAFAFQIHLNDPEPDGAGSKKAPLQ-RSTMDCSPLT 150  
gi | 45382585 | ref | NP\_990575.1 | ---MSTQGSVAVHDSIHNQENMLSRLRGAARNRVENRNVNPNKAAANRNLVLEELNSQRRLG---LRGAKGSSGQPIIACKPEENARSFGERPNSRQPAFAFQIHLNDPEPDGAGSKKAPLQ-RSTMDCSPLT 150  
gi | 23308637 | ref | NP\_694481.1 | ---MSTQGSVAVHDSIHNQENMLSRLRGAARNRVENRNVNPNKAAANRNLVLEELNSQRRLG---LRGAKGSSGQPIIACKPEENARSFGERPNSRQPAFAFQIHLNDPEPDGAGSKKAPLQ-RSTMDCSPLT 150  
gi | 30694019 | ref | NP\_564499.3 | ---MSTQGSVAVHDSIHNQENMLSRLRGAARNRVENRNVNPNKAAANRNLVLEELNSQRRLG---LRGAKGSSGQPIIACKPEENARSFGERPNSRQPAFAFQIHLNDPEPDGAGSKKAPLQ-RSTMDCSPLT 150  
gi | 15239172 | ref | NP\_199122.1 | ---MADEKEN---CVMRTR---AAAKRKASMEAAIDKERINK-KRVVLGELNLSN---IK---VNLLAN---KSRKATIK 150  
gi | 42571785 | ref | NP\_973983.1 | ---MAENQN---CARMTR---AAAKRKAS---SMALDENPVS-KRVVLGELNLSN---VVAVE---NQEREITK 150  
gi | 15220145 | ref | NP\_175155.1 | ---MVS---KDKKIHSQDNPDQASPVEW-AEIRKLLAFQEN---IO--- 150  
gi | 115454079 | ref | NP\_001050640.1 | ---MAGKEN---AAAQPLRTR---AARAAAV---AVAVAAKRKRVALSELPLSN---AVVAVRR--- 150  
gi | 115489300 | ref | NP\_001067137.1 | ---MADKENSTPASAARLTRSSAAAGCAQAKRSAAAGVADGGAPAKRKRVALSDELPLSN---AVVAVRR--- 150  
1 .....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 24662962 | ref | NP\_524030.2 | TPMSVTDVSPMSVDRSILGVIQSLSISVGTETGVSPTGRVKELPPRRNDQRFLVVOVQMDIHLVFPFRESKKKK---RPKPLYMR-RQKDISHNMSRILDLVLVEVEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMYIAA 300  
gi | 158300141 | ref | XP\_320142.3 | TPMSVGENFSPMSIDKSLIIVEGGPI-----PRNDRERFVEVEYQEDILLVLEAEKRN-RPKPYML-KQTDITISMRILVLDWLVSEVEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMYIAA 300  
gi | 4502613 | ref | NP\_001228.1 | SAISLPGPRKPLVPLDYPMGSESPHTMDSI---VLEDEKPVSVNEVPDYHEDIHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 55623156 | ref | XP\_517420.1 | SAISLPGPRKPLVPLDYPMGSESPHTMDSI---VLEDEKPVSVNEVPDYHEDIHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 73983960 | ref | XP\_540965.2 | SAISLPGPRKPLVPLDYPMGSESPHTMDSI---VLEDEKPVSVNEVPDYHEDIHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 115497582 | ref | NP\_001068591.1 | SAVTLPGPRKPLVPLDYPMGSESPHTMEMSV---VLEDEKPVSVNEVPDYHEDIHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 6753308 | ref | NP\_033958.1 | AAVSLPAARKPLVPLDYPMGSESPHTMEMSV---VLED-KPVNVNEVPDYHEDIHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 61097935 | ref | NP\_446154.1 | YDLTVETR-----DVESPHAMDSI---VLEDEKPVSVNEVPDYHEDIHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 45382585 | ref | NP\_990575.1 | AALGVGERPLAPLGNAMELSLDSPSINDIIV---MSEAEERFNVNVPDVSIDHYTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 23308637 | ref | NP\_694481.1 | LNPLVTRLRQPLATIDPLVLEASFDSE---MDMSV---IDCEERTVNNVSEYAAIEHTLREMEVCK---KPKVGYMK-KOPDITNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 30694019 | ref | NP\_564499.3 | PKRNLKPPKPKIKSAPVAIIDLKSSDIDS---RSDDPQMGCGPVVADIEYLRLEVEPKQRPDIYIEKVRQDVTNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 15239172 | ref | NP\_199122.1 | QKK-----KSVSITPIELN-SDID---RSDDPQMCGPVVTSIFEYLRLEVEPK---RPLVDYIEKIKQDVTNSMRAILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 42571785 | ref | NP\_973983.1 | AKLSVN-----TSKRQMKKALMIPEASVLIIE---RSVDPQMCGPFASDICAFLREMEGPKRHPPLDYIEKVSQDLTPHMRVAVLDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 15220145 | ref | NP\_175155.1 | AKLSVN-----TSKRQMKKALMIPEASVLIIE---RSVDPQMCGPFASDICAFLREMEGPKRHPPLDYIEKVSQDLTPHMRVAVLDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 115454079 | ref | NP\_001050640.1 | AASHAAEPKKPAPPAP---AVVVVVDDDDE---GGEDPQLCAPYASDINLYLRSMVQAQRRAADYIETVQVVDVTANMRGILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
gi | 115489300 | ref | NP\_001067137.1 | PSSKQEPAAEAASGGGGSPVSASLST---ASPSGWDPPQYASDIYLYRSMVQARRSAADYIEAVQVVDVTANMRGILVDWLVVEGEEYKLDTEFTLVLVSLVDFLDRFLQMVAVRSKLLQVGTAAAMLIA 300  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 24662962 | ref | NP\_524030.2 | KVEEIPPEVGEFVFLDDSSYTKAQVLRMEQVILKILSFDLCTPTAIVFINTNAVLCD---MPEKLYMTLVISELSMEGETLQVPLSLMSSAVALARHILGM---FMWTPRLIEIITTKLEDLKTVVLHCHTKTKAKELNTOAM 450  
gi | 158300141 | ref | XP\_320142.3 | KVEEIPPEVGEFVFLDDSSYTKAQVLRMEQVILKILSFDLCTPTAIVFINTNAVLCD---MPEKLYMTLVISELSMEGETLQVPLSLMSSAVALARHILGM---FMWTPRLIEIITTKLEDLKTVVLHCHTKTKAKELNTOAM 450  
gi | 4502613 | ref | NP\_001228.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 55623156 | ref | XP\_517420.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 73983960 | ref | XP\_540965.2 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 115497582 | ref | NP\_001068591.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 6753308 | ref | NP\_033958.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 61097935 | ref | NP\_446154.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 45382585 | ref | NP\_990575.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 23308637 | ref | NP\_694481.1 | KFEIIPPEVAEAFYIITDDYTKKQVLRMEHLVLKVLTFDLAAPTIVNQFLTOYFLHQIP---ANCKVESLAMEFLGELSLIDADPVLKYLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 30694019 | ref | NP\_564499.3 | KVEEISPPKVDYFCYITDNTFSSKQDVVKMEADILLALQFELGRPTINTFMRRFTRVAQDDFVPHLQLEPLCCVLSLSILDYK---TVKFLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 15239172 | ref | NP\_199122.1 | KVEEIPPNVDDYFCYITDNTYTKQEVKMEADILLALQFELGRPTINTFMRRFTRVAQDDFEMSHLOMEFLCCVLSLSMLDYQ---SVKFLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 42571785 | ref | NP\_973983.1 | KVEEIPPKVEDYFCYITDNTFTKQEVVSMOEDILLALQFELGRPTIKTFLRRFTRVAQEDFDKSQLQTEFLCCVLSLSMLDYT---CVMRTRPNSLIIASAVFLARFIIRPKHPNWNMEEYTRVKAADLQVCGTIHDLVLSRGGALBAI 450  
gi | 15220145 | ref | NP\_175155.1 | KVEEIKRRPKVEDYFCYITDNTYTKQDVLMKMEADILLALQFELGRPTINTFMRRFTRVAQEDFVPHLQLEPLCCVLSLSMLDYS---CVKFLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 115454079 | ref | NP\_001050640.1 | KVEEISPPNVEDYFCYITDNTYTKQEVVSMOEDILLALQFELGRPTIKTFLRRFTRVAQEDDKYPSLPLEFMCVLAELSLLEYG---CVRLPSSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
gi | 115489300 | ref | NP\_001067137.1 | KVEEISPPHVEDYFCYITDNTYTKQEVVSMOEDILLALQFELGRPTIKTFLRRFTRVAQEDDKYPSLPLEFMCVLAELSLLEYG---CLRFLPSVIAAGAAFHALALYVTG---QSWPESLIRKTYTLESKPCMLDLHQTYLKAPOHAQCSI 450  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



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gi|24662962|ref|NP_524030.2|REKYNRDIYKKVAMMESVEMSKDDFDLCEATNCK-----QKEDHQQPDINTKENVNLFYKF 515
gi|158300141|ref|XP_320142.3|QEKYKSKTYHEVASLPATEIITKESFDKICATLCNSAAATLLLSNTDSKLLKEMGRENPENLLLFV- 515
gi|4502613|ref|NP_001228.1|REKYKNSKYHGVSLLNPPETLNL----- 515
gi|55623156|ref|XP_517420.1|REKYKNSKYHGVSLLNPPETLNL----- 515
gi|73983960|ref|XP_540965.2|REKYKNSKYHGVSLLNPPETLNV----- 515
gi|115497582|ref|NP_001068591.1|REKYKNSKYHGVSLLNPPETLNV----- 515
gi|6753308|ref|NP_033958.1|REKYKHSKYHSVSLLNPPETLSV----- 515
gi|61097935|ref|NP_446154.1|REKYKHSKYHSVSLLNPPETLNV----- 515
gi|45382585|ref|NP_990575.1|REKYKSTKYHAVSLIDAPEITLDEL----- 515
gi|23308637|ref|NP_694481.1|REKYKGSKYHEVSLIEPPEKMLLN----- 515
gi|30694019|ref|NP_564499.3|REKYKHHKFQCVATMPVSPPELPLVTFWEDVTI----- 515
gi|15239172|ref|NP_199122.1|REKYKQHKFKCVATMPVSPPELPLVTFWEDVNI----- 515
gi|42571785|ref|NP_973983.1|RNKYKQHKYKCVATMPVSPPELPLVAFEDITIRGMA----- 515
gi|15220145|ref|NP_175155.1|REKYKQHKFQYVAIIPVYQELPLVTFWEDVVTI----- 515
gi|115454079|ref|NP_001050640.1|RDKYKQHRFKGVSTLLPPVEIPASYFDLNE----- 515
gi|115489300|ref|NP_001067137.1|RDKYKQHKFKCVSTLLPPVDIPASYLQDLTE----- 515

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