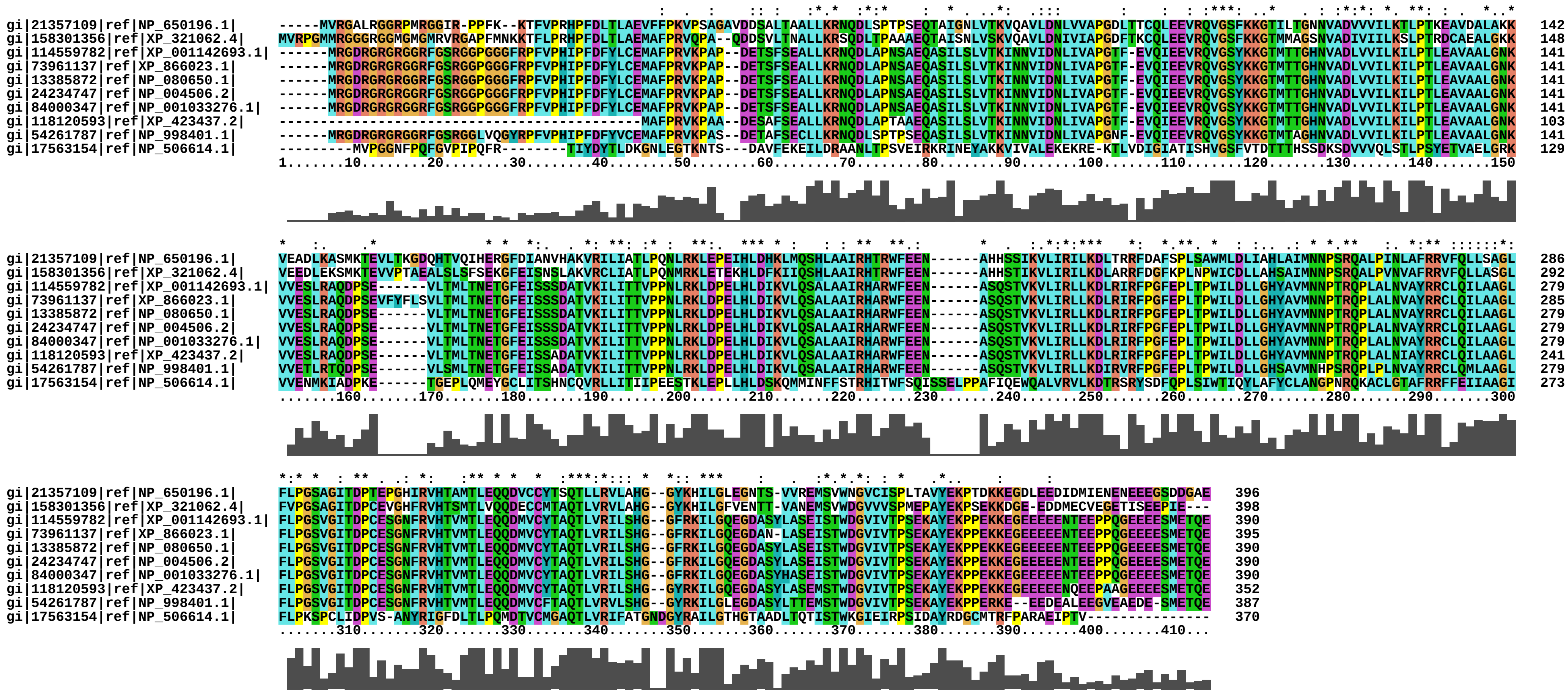
: . :   :: :   :*.* :*:*   : * . ..*:   .:::   :   : : :***: ..*   . : :*:*: *. **: : .   *..*
gi|21357109|ref|NP_650196.1| -----MVRGALRGGRPMRGGIR-PPFK--KTFVPRHPFDLTLAEVFFPKVPSAGAVDDSALTAALLKRNQDLSPTPSEQTAIGNLVTKVQAVLDNLVVAPGDLTTCQLEEVRQVGSFKKGTILTGNNVADVVVILKTLPTKEAVDALAKK 142
gi|158301356|ref|XP_321062.4| MVRPGMMRGGGRGGMGMGMRVRGAPFMNKKTFLPRHPFDLTLAEMAFPRVQPA--QDDSVLTNALLKRSQDLTPAAAEQTAISNLVSKVQAVLDNIVIAPGDFTKCQLEEVRQVGSFKKGTMMAGSNVADIVIILKSLPTRDCAEALGKK 148
gi|114559782|ref|XP_001142693.1| ------MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAP--DETSFSEALLKRNQDLAPNSAEQASILSLVTKINNVIDNLIVAPGTF-EVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNK 141
gi|73961137|ref|XP_866023.1| ------MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAP--DETSFSEALLKRNQDLAPNSAEQASILSLVTKINNVIDNLIVAPGTF-EVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNK 141
gi|13385872|ref|NP_080650.1| ------MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAP--DETSFSEALLKRNQDLAPNSAEQASILSLVTKINNVIDNLIVAPGTF-EVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNK 141
gi|24234747|ref|NP_004506.2| ------MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAP--DETSFSEALLKRNQDLAPNSAEQASILSLVTKINNVIDNLIVAPGTF-EVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNK 141
gi|84000347|ref|NP_001033276.1| ------MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAP--DETSFSEALLKRNQDLAPNSAEQASILSLVTKINNVIDNLIVAPGTF-EVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNK 141
gi|118120593|ref|XP_423437.2| --MAFPRVKPAA--DESAFSEALLKRNQDLAPTAAEQASILSLVTKINNVIDNLIVAPGTF-EVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNK 103
gi|54261787|ref|NP_998401.1| ------MRGDRGRGRGGRFGSRGGLVQGYRPFVPHIPFDFYVCEMAFPRVKPAS--DETAFSECLLKRNQDLSPTPSEQASILSLVTKINNVIDNLIVAPGNF-EVQIEEVRQVGSYKKGTMTAGHNVADLVVILKILPTLEAVAALGNK 141
gi|17563154|ref|NP_506614.1| ---------MVPGGNFPQFGVPIPQFR--------TIYDYTLDKGNLEGTKNTS---DAVFEKEILDRAANLTPSVEIRKRINEYAKKVIVALEKEKRE-KTLVDIGIATISHVGSFVTDTTTHSSDKSDVVVQLSTLPSYETVAELGRK 129
1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
*   :.   .*   * *   *:.   . *: **: :* :   **:.   *** * :   : : **   **.:   *   .   :.*:*:***   *:   *.**. *   : :.. .: * *.**   :. *:** ::::::*:
gi|21357109|ref|NP_650196.1| VEADLKASMKTEVLTKGDQHTVQIHERGFDIANVHAKVRILIATLPQNLRKLEPEIHLDHKLMQSHLAAIRHTRWFEEN------AHHSSIKVLIRILKDLTRRFDAFSPLSAWMLDLIAHLAIMNNPSRQALPINLAFRRVFQLLSAGL 286
gi|158301356|ref|XP_321062.4| VEEDLEKSMKTEVVPTAEALSLSFSEKGFEISNSLAKVRCLIATLPQNMRKLETEKHLDFKIIQSHLAAIRHTRWFEEN------AHHSTIKVLIRILKDLARRFDGFKPLNPWICDLLAHSAIMNNPSRQALPVNVAFRRVFQLLASGL 292
gi|114559782|ref|XP_001142693.1| VVESLRAQDPSE------VLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGL 279
gi|73961137|ref|XP_866023.1| VVESLRAQDPSEVFYFLSVLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGL 285
gi|13385872|ref|NP_080650.1| VVESLRAQDPSE------VLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGL 279
gi|24234747|ref|NP_004506.2| VVESLRAQDPSE------VLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGL 279
gi|84000347|ref|NP_001033276.1| VVESLRAQDPSE------VLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGL 279
gi|118120593|ref|XP_423437.2| VVESLRAQDPSE------VLTMLTNETGFEISSADATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNIAYRRCLQILAAGL 241
gi|54261787|ref|NP_998401.1| VVETLRTQDPSE------VLSMLTNETGFEISSADATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEEN------ASQSTVKVLIRLLKDIRVRFPGFEPLTPWILDLLGHSAVMNHPSRQPLPLNVAYRRCLQMLAAGL 279
gi|17563154|ref|NP_506614.1| VVENMKIADPKE------TGEPLQMEYGCLITSHNCQVRLLITIIPEESTKLEPLLHLDSKQMMINFFSTRHITWFSQISSELPPAFIQEWQALVRVLKDTRSRYSDFQPLSIWTIQYLAFYCLANGPNRQKACLGTAFRRFFEIIAAGI 273
.......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
: * : ** . .: *:   :** * * * :***:*::: * *:: ***   :   .   :*.*.*: : *   .*..   :   :
gi|21357109|ref|NP_650196.1| FLPGSAGITDPTEPGHIRVHTAMTLEQQDVCCYTSQTLLRVLAHG--GYKHILGLEGNTS-VVREMSVWNGVCISPLTAVYEKPTDKKEGDLEEDIDMIENENEEEGSDDGAE 396
gi|158301356|ref|XP_321062.4| FVPGSAGITDPCEVGHFRVHTSMTLVQQDECCMTAQTLVRVLAHG--GYKHILGFVENTT-VANEMSVWDGVVVSPMEPAYEKPSEKKDGE-EDDMECVEGETISEEPIE--- 398
gi|114559782|ref|XP_001142693.1| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCYTAQTLVRILSHG--GFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTEEPPQGEEEESMETQE 390
gi|73961137|ref|XP_866023.1| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCYTAQTLVRILSHG--GFRKILGQEGDAN-LASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTEEPPQGEEEESMETQE 395
gi|13385872|ref|NP_080650.1| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCYTAQTLVRILSHG--GFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTEEPPQGEEEESMETQE 390
gi|24234747|ref|NP_004506.2| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCYTAQTLVRILSHG--GFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTEEPPQGEEEESMETQE 390
gi|84000347|ref|NP_001033276.1| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCYTAQTLVRILSHG--GFRKILGQEGDASYHASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTEEPPQGEEEESMETQE 390
gi|118120593|ref|XP_423437.2| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCYTAQTLVRILSHG--GYRKILGQEGDASYLASEMSTWDGVIVTPSEKAYEKPPEKKEGEEEEENQEEPAAGEEEESMETQE 352
gi|54261787|ref|NP_998401.1| FLPGSVGITDPCESGNFRVHTVMTLEQQDMVCFTAQTLVRVLSHG--GYRKILGLEGDASYLTTEMSTWDGVIVTPSEKAYEKPPERKE--EEDEALEEGVEAEDE-SMETQE 387
gi|17563154|ref|NP_506614.1| FLPKSPCLIDPVS-ANYRIGFDLTLPQMDTVCMGAQTLVRIFATGNDGYRAILGTHGTAADLTQTISTWKGIEIRPSIDAYRDGCMTRFPARAEIPTV--------------- 370
.......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410...