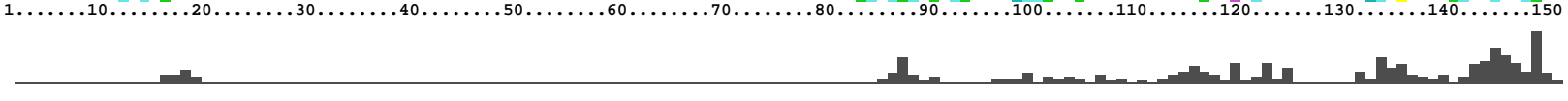


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gi |145611046|ref |XP_368561.2|  --MNLIASSEKRNMDDEKRRSGDMLGWTHTFLRKSSWVTVGRATTVIGRCNEEALVGVALLLYICGAKGQPCGLRHNFFILVFLLCWDFPKSTVFLKMLVRSAAIGRSNRITLLHFQISPR-----AIVSDACAS-VSILELRNSN 141
gi |85113895|ref |XP_964601.1|  -----MKPASR-----LFVLSLFWLWSP-----EAQCKSDSE-----CAISPK-----AIVSDACAS-VSILELRNSN 52
gi |19075813|ref |NP_588313.1|  -----MFMWMTAKAG-----LVGLLLILYKN-----VCQVLCCKSGSSVKSQSPWSIKNDGK-----SIIDHTLNSYSIDENLNSR 65
gi |7657067|ref |NP_056589.1|  -----MGRA-----WGLLVGL-----LGVVWLLRLGHGEERRPETAQRFCFCQVS-----GYLDDCTCD-VETIDKFN 59
gi |19924061|ref |NP_612537.1|  -----MGRA-----WGLLVGL-----LGVVWLLRLGHGEERRPETAQRFCFCQVS-----GYLDDCTCD-VETIDKFN 59
gi |7657069|ref |NP_055399.1|  -----MGRG-----WGLFVGL-----LGAVWLLSSGHGEEOPPEAAQRFCFCQVS-----GYLDDCTCD-VETIDKFN 59
gi |114653045|ref |XP_509950.2|  -----MGRG-----WGLFVGL-----LGAVWLLSSGHGEEOPPEAAQRFCFCQVS-----GYLDDCTCD-VETIDKFN 59
gi |73963815|ref |XP_547813.2|  -----MGRR-----WGLFVGL-----VGAWLLGPHGHEORPETAQRFCFCQVS-----GYLDDCTCD-VETIDKFN 59
gi |157074206|ref |NP_001096818.1|  -----MGRR-----WGLFVGL-----LVAVGLLGLGHGEEOPPEAAQRFCFCQVS-----GYLDDCTCD-VETIDKFN 59
gi |118092359|ref |XP_421473.2|  -----MAAG-----GALLRALG-----FAALLLPALPRGS-----PGSAERRCFQCVT-----GHLDDCTCD-VETIDAFN 57
gi |41054814|ref |NP_956644.1|  -----MET-----CVLLGLF-----LTSVHVHTA-----GSAHRFCQVIT-----GHLDDCACD-VETIDKFN 51
gi |71993035|ref |NP_001021704.1|  -----MREP-----LLQLTVLS-----LIIIVVNTQFE-----SGRLCFCKGF-----EAVSPCCSKPOTIDKLN 53
gi |42571127|ref |NP_973637.1|  MAEIDVGSVVKGKKGSGKR-----WILLIGAIAAVLLAVVVAVFNTNONSISEFTGKINCRCQAEQOKYIGIVEDCCCDYFIVVNLNTE 85
gi |50307077|ref |XP_453517.1|  -----MVKVLQLC-----FLSAILVQALNSIVDQKDEAKVDINTVFDNDSINFCRMDK-----EAGIALCDVIFHEINEVN-N 69
gi |45187524|ref |NP_983747.1|  -----MQLNKL-----MLGFMLCASALADDGQAAEF-----HSANFKIKDK-----QQVGSICDIIFHEINEVN-E 58
gi |6323505|ref |NP_013576.1|  -----MRLRLAIA-----LCLLAFISAISNNSIADQIQN-----AFNDLHFCKVDRN-----DIVVESCNVLPNELNAIN-E 64

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gi |145611046|ref |XP_368561.2|  LKPAIDDVTRSDFFSHYRLNLFNKICPPWNDEGMCGNIACAVETLDNEEDLPEVWRAS---ELGKLEGLVEHPNKAQREPEKPLRQKLGEDVGS CVVEYDDECDERDYCVPEDESASAKGDVSLLRNPERFICYAGGAGAAV 287
gi |85113895|ref |XP_964601.1|  IKPALEDLRTTDFFSHYRLNLFNKICPPWNDEGMCGNIACAVETLDNEEDLPEVWRAS---ELGKLEGLPRAKHPGKSVKPEPKRPLQKLGEDVGS CVVEYDDECDERDYCVPEDESASAKGDVSLLRNPERFICYAGGAGAAV 198
gi |19075813|ref |NP_588313.1|  VSPLLFDLLEKSDVMFRYRLNLFNKICPPWNDEGMCGNIACAVETLDNEEDLPEVWRAS---SLGKLEGLFPELSRQIVEIDRS---VMEHVDKISGSCLLERLDD-EAHQYCVVDNEDLSG-CVVVSLLENPERFICYAGGAGAAV 204
gi |7657067|ref |NP_056589.1|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIN-CCGRRDCAVKPCCHSDEVDPDGKS-----ASYKYSKEAN-LLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDSFCEIDDIQSPDAEYVLLNPERYTYGKGPDAWKI 198
gi |19924061|ref |NP_612537.1|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIN-CCGRRDCAVKPCCHSDEVDPDGKS-----ASYKYSKEAN-LLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDSFCEIDDIQSPDAEYVLLNPERYTYGKGPDAWKI 198
gi |7657069|ref |NP_055399.1|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIS-CCGRRDCAVKPCQSDEVDPDGKS-----ASYKYSBEANNLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDNFCEADDIQSPDAEYVLLNPERYTYGKGPDAWKI 199
gi |114653045|ref |XP_509950.2|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIS-CCGRRDCAVKPCQSDEVDPDGKS-----ASYKYSBEANNLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDNFCEADDIQSPDAEYVLLNPERYTYGKGPDAWKI 199
gi |73963815|ref |XP_547813.2|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIS-CCGRRDCAVKPCQSDEVDPDGKS-----ASYKYSBEANNLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDNFCEADDIQSPDAEYVLLNPERYTYGKGPDAWKI 199
gi |157074206|ref |NP_001096818.1|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIN-CCGRRDCAVKPCCHSDEVDPDGKS-----ASYKYSBEANNLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDNFCEADDIQSPDAEYVLLNPERYTYGKGPDAWKI 199
gi |118092359|ref |XP_421473.2|  RLFPRQLKLESDYFRYKVNLR-KPCPPWINDIS-CCGRRDCAVKPCCHSDEVDPDGKS-----AGYKYSBEANNLIECECAER-LGAVDESLSSEETQKAVLQWTKHDD-SDSFCEADDIQSPDAEYVLLNPERYTYGKGPDAWKI 197
gi |41054814|ref |NP_956644.1|  KTFPKLQKLESDYFRYKVNLR-KPCPPWINDIS-CCGLKYCAVKPCSPDEVDPDGKS-----SSYKYSKASHDIEECECAER-LGAVDESLSSEETQKAVLQWTKHDD-ESDRFCMLDDESDPDAEYVLLNPERYTYGKGPDAWKI 191
gi |71993035|ref |NP_001021704.1|  RIYEKVKLKKDFRFRYKVNLR-KTCPPWADDR-CCGTNCGIACFD-DEVPAGLRRRNVNMEAAAVKKEEEDDADKCADAGNNDIPMDRLHDDDEKRLQDAMDHDDGLEDKFCETEDDES DMHVVLDLKNPERYTYGAGKSPQRV 200
gi |42571127|ref |NP_973637.1|  VLNPLLDLVKTPFRYKVKVLR-CDCPPWDDG-MCRLRDCSVCECPSESEPEVFKK-----PLSQVNPVQEGKP-QAIVDRITDIT--RAFRGWVITDN---PWISDDEDDNDEMIVNLRNPERYTYGIPSAARI 212
gi |50307077|ref |XP_453517.1|  NLRPQLLSLVQSDFFKFKLDLY-KCCPFWSDDNGYCVNRACAVDVEDWDSLPEYVQFP-----EILGNENAITDIT---DDECSFLDELCDKPRFEAKED---IEYCDINDFNSQHSVLVLDLTPANPERFICYGGGQSAHI 199
gi |45187524|ref |NP_983747.1|  QIRPQLARLVKIDFFRFRYKLDLY-KCCPFWSDDNGYCVNRACAVDVEDWDSLPEYVQFP-----EVLGGLDEDSVKSSEGGSEDECSFLNELGRRREFARPEPL---LIDYCDVDFNTKLSVLVLDLTPANPERFICYGGGQSAHI 194
gi |6323505|ref |NP_013576.1|  NIRDDLSALLKSDFFKFKLDLY-KCCPFWDANDGLCLNRACSVDDVEDWDSLPEYVQFP-----EILGSFNNDIMKEADSDDECKFLDLCLTSKKPFVIED---LNYCDVDFNFKNAVLIDLTPANPERFICYGGGQSAHI 199

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gi |145611046|ref |XP_368561.2|  *. ** : * : : : : : : * * : : : : : * * : : : : * * : : : : * * : : : : * 141
gi |85113895|ref |XP_964601.1|  WDAIYRENCFSRSFFNPAPKPPPALGGGLSSNSKNPAAAMDFRSVLEAAGROQVLRERRAEEFNTPFVAKTGLEDEDECLEKRVFYRVISGMHSAISITHLCDW-----FLNQTTGQWQPNLACVNIHLR-----FPERISNLY 326
gi |19075813|ref |NP_588313.1|  WDAIYRENCFSRSFFNPAPKPPPALGGGLSSNSKNPAAAMDFRSVLEAAGROQVLRERRAEEFNTPFVAKTGLEDEDECLEKRVFYRVISGMHSAISITHLCDW-----FLNQTTGQWQPNLACVNIHLR-----FPERISNLY 326
gi |7657067|ref |NP_056589.1|  WEMIVNQCIPDSS-----APITIDFPALFMQ-----PLAPPKPOEQLKERMDAWTLEQRVFRVRLSGMHSSISITHLCHG-----YLNQRNGVWGNLQCFQEKVNL-----YPERLENLY 306
gi |19924061|ref |NP_612537.1|  WSVIYEENCFKPQIQR-----PLASGRGKENTFYSWLEGLCVEKRAFVRLISGLHASINVHLSAR-----YLLQDTWLEK-KWGHNVTEFOORFDGILTEGEGPRLRNLNY 301
gi |7657069|ref |NP_055399.1|  WSVIYEENCFKPQIQR-----PLASGQGHKENTFYSWLEGLCVEKRAFVRLISGLHASINVHLSAR-----YLLQDTWLEK-KWGHNVTEFOORFDGILTEGEGPRLRNLNY 301
gi |114653045|ref |XP_509950.2|  WNVIYEENCFKPQIKRPP-----LNPLASGQGTSEENTFYSWLEGLCVEKRAFVRLISGLHASINVHLSAR-----YLLQDTWLEK-KWGHNVTEFOORFDGILTEGEGPRLRNLNY 305
gi |73963815|ref |XP_547813.2|  WNVIYEENCFKPQIKRPP-----LNPLASGQGTSEENTFYSWLEGLCVEKRAFVRLISGLHASINVHLSAR-----YLLQDTWLEK-KWGHNVTEFOORFDGILTEGEGPRLRNLNY 305
gi |157074206|ref |NP_001096818.1|  WNVIYEENCFKPQIKRPP-----LNPLASGQGTSEENTFYSWLEGLCVEKRAFVRLISGLHASINVHLSAR-----YLLQDTWLEK-KWGHNVTEFOORFDGILTEGEGPRLRNLNY 305
gi |118092359|ref |XP_421473.2|  WNSIYEENCFKPQNVKR-----PLTSGRQDDCGQMPFYKWLKGVCEKRAFVRLISGLHASINVHLSAR-----YLLQDTWSEK-KWGPNVTEFOORFDVVRGEGPRLRNLNY 300
gi |41054814|ref |NP_956644.1|  WNSIYEENCFKPYEVNRP-----LNPLASNSGDD-GQGFYRWLEGLCVEKRAFVRLISGLHASINVHLSAR-----YLLDENWFEM-KWGHNVTEFOORFDEDLTKGEGPRLRNLNY 296
gi |71993035|ref |NP_001021704.1|  WKSIIYENCFKPKD-----PKFDRNFLNPSNE-----GMCLEKRVFYRVISGLHASITISIAAYNKRPPPLSGQFGSOMGTWFRNTEMFAGRFGTKWS-WEGPQRRLNRY 300
gi |42571127|ref |NP_973637.1|  WEAIYSENCFKHTE-----EGSQBEKILYKLVLSGLHSSISVHIASD-----YLLDEATNL---WGQNTLLIDYRVL-----RYPDRVNLNY 286
gi |50307077|ref |XP_453517.1|  WSSIIYKENCFSLGD-----ENQCLAKDAFVRLISGLHASITHLSDN-----HLNTEGKWEPLNLEFMTRVGN-----FPDRVNLNY 272
gi |45187524|ref |NP_983747.1|  WSAIYKENCFTLGE-----CGFCLAKDVFYRLISGLHASIATHLSDN-----YLDTKTKGWPNLELFMARVGN-----HDDRVANLY 267
gi |6323505|ref |NP_013576.1|  WSIYIYDNCFTIGE-----TGESLAKDAFVRLISGLHASITHLSEKE-----YLNKTKGWEPLNLEFMARIGN-----FPDRVNLNY 272

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