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gi | 8051631 | ref | NP_057951.1 | MSLKLGASNVTKNDPKSINSRVFIGNLNTALVKKSDVETIFISKYGRVAGCSVHKGYAFVQYSNERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAASAIYSGYIFDYDYRDDFYDRLFDYRGRLSFPVPVPRAVPVKRPV 150
gi | 114681541 | ref | XP_514591.2 | MSLKLGASNVTKNDPKSINSRVFIGNLNTALVKKSDVETIFISKYGRVAGCSVHKGYAFVQYSNERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAASAIYSGYIFDYDYRDDFYDRLFDYRGRLSFPVPVPRAVPVKRPV 150
gi | 12963505 | ref | NP_075619.1 | MSLKIQTSNVTNKNDPKSINSRVFIGNLNTAVVKKSDVETIFISKYGRVAGCSVHKGYAFVQYANERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAATAIY-----RLFDYRGRLSFPVPVPRAVPVKRPV 134
gi | 58865494 | ref | NP_001011958.1 | MSLKIQTSNVTNKNDPKSINSRVFIGNLNTAVVKKSDVETIFISKYGRVAGCSVHKGYAFVQYANERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAATAIY-----RLFDYRGRLSFPVPVPRAVPVKRPV 134
gi | 62460386 | ref | NP_001014847.1 | MSLKIQTSNVTNKNDPKSINSRVFIGNLNTAVVKKSDVETIFISKYGRVAGCSVHKGYAFVQYANERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAASAIY-----RLFDYRGRLSFPVPVPRAVPVKRPV 134
gi | 73992250 | ref | XP_542969.2 | MSLKIQTSNVTNKNDPKSINSRVFIGNLNTAVVKKSDVETIFISKYGRVAGCSVHKGYAFVQYANERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAASVIYSGYDFDYDYRDDFYDRLFDYRGRLSFPVPVPRAVPVKRPV 150
gi | 118100477 | ref | XP_417332.2 | MSLKLVQTSNITNKNDPKSINSRVFIGNLNTAVVKKSDVETIFISKYGRVAGCSVHKGYAFVQYANERHARAAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAASTLYSGYDFDYDYRDDFYDRLFDYRGRVSE--PVPRAVPVKRPV 148
gi | 45387647 | ref | NP_991173.1 | MSLKLVQTSNITNKNDPKSINSRVFIGNLNTAVVKKSDVETIFISKYGRVAGCSVHKGYAFVQYANERHARGAVLGENGRVLAGOTLDINMAGEPKPDRPKGLKRAASTLYSGYDFDYDYRDDFYDRLFDYRGRVSE--PVPRAVPVKRPV 148
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 8051631 | ref | NP_057951.1 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 292
gi | 114681541 | ref | XP_514591.2 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 293
gi | 12963505 | ref | NP_075619.1 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 282
gi | 58865494 | ref | NP_001011958.1 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 281
gi | 62460386 | ref | NP_001014847.1 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 269
gi | 73992250 | ref | XP_542969.2 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 279
gi | 118100477 | ref | XP_417332.2 | TVPLVRRVKTIPVVKLFARSTAVITSSAKIKLKSSELOAIKTELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 266
gi | 45387647 | ref | NP_991173.1 | AVPVVRRVKS-LPVKLLTRSAILPNSVVKHKLKSTELQAIKSELTOIKSNIDALLSRLEQIAAEQKANPDGKKKGDDGGA- GGGGGGGGGGGGGGGGGGGGG-----SSRPPAPOENTTSEAGLPQGEARTRDDGDEEGLLT-HSEEEEL 260
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 8051631 | ref | NP_057951.1 | EHSQD TDADDGALQ 306
gi | 114681541 | ref | XP_514591.2 | EHSQD TDADDGALQ 307
gi | 12963505 | ref | NP_075619.1 | EHSQD TDAEDGALQ 296
gi | 58865494 | ref | NP_001011958.1 | EHSQD TDAEDGALQ 295
gi | 62460386 | ref | NP_001014847.1 | EHSQD TDVEDGALQ 283
gi | 73992250 | ref | XP_542969.2 | EHSQD TDAEDGALQ 293
gi | 118100477 | ref | XP_417332.2 | ENNHY TDMDARLQ 280
gi | 45387647 | ref | NP_991173.1 | ENNHIE EMDP-ILQ 273
.....310.....

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