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gi | 111955033 | ref | NP_034940.2 | -----MAAMQTLTLCFVCLLPGH-----LALPLSQEAGDVSAHQ-WEQAQNYLRKFYPHDS-----KTKKVNSLVDNLKEMOKFFGLPMTGKLSPYIMEIMQKPRCGVPD 94
gi | 6981214 | ref | NP_036996.1 | -----MAAMRLLTFRIVCLLPGC-----LALPLSQEAGEVVALQ-WEQAQNYLRKFYLDH-----KTKKATSAVDKLRKEMOKFFGLPETGKLSPRVMEIMQKPRCGVPD 94
gi | 4505219 | ref | NP_002414.1 | -----MRLTTLCAVCLLPGS-----LALPLPQEAGGMSLEQ-WEQAQDYLLKRFYLYDS-----ETKNANSLEAKLKEMOKFFGLPITGMLNSRVVEIMQKPRCGVPD 91
gi | 114640081 | ref | XP_508721.2 | -----MRLTTLCAVCLLPGS-----LALPLPREAGGMSLEQ-WEQAQDYLLKRFYLYDS-----ETKNANSLEAKLKEMOKFFGLPITGMLNSRVVEIMQKPRCGVPD 91
gi | 73955234 | ref | XP_546550.2 | -----MWPVAVLCALCLLPGS-----LALPLPREAGGMSLEQ-WKQAQDYLLKRFYLYDS-----KTRDADSEFKTKLKEMOKFFRLPVTGILNSRTIEIMQKPRCGVPD 91
gi | 115496540 | ref | NP_001068598.1 | -----MRLVLLCAACLLPGS-----PALPLGPGGGEGDPR-WQLAQDYLLKRFYSSDS-----KIKNANSLEVRLKRMGGFFHLPIITGILSPRIIEIMEKPRSGVPD 91
gi | 57529313 | ref | NP_001006278.1 | -----MQVLLLCAAILLPGS-----LPPFVPLKPAWLNAD-LDIIVTLYLNKFFPLE-----KHP-AVSLSEERIKEMOKFFHLITITGKLNATKTIIMQKPRCGVPD 90
gi | 15235820 | ref | NP_193397.1 | -----MERNLIYRRNRALCFVILPCFFYRFGARNTPEAEQSTAKATQLIHVSNSITWDESRLLVDVQIGSHVSGVSELKRYLHRFGYVNDGSEIFSDVFDGPLESAISLYQENLGLPIITGRDLDSTVTWLSLPRCGVSDTHMIMINDPLHTI 147
gi | 115483382 | ref | NP_001065361.1 | -----MVVVLGLPVVHGHC-----GVAVHSFKQLLDAGRCSHVTVGLAELKRYLARFGYMAKPGRDITDAFDEHLEVAVRRYQTRFSLPVTIGRLDNATLDQIMSRCRCVGDVDVERFVVALSPGAF 116
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 111955033 | ref | NP_034940.2 | -----VAEYSLMPNSPKWHSR-----IVTYRIVS-----YTSDDLPRIVDQIVKRALRMWSMQLPLNFKRVS-WGTADIIIGFARRDHDGDSFPFDGPGNTLGHAFAPGPG-----LGGDAHFKDEYWDGEDAGVNFLEAATHEFGHSLGLSHSSVP 231
gi | 6981214 | ref | NP_036996.1 | -----VAEYSLMPNSPKWHSR-----IVTYRIVS-----YTTDLPRFLVDQIVKRALRMWSMQLPLNFKRVS-WGTADIIIGFARGDHDGDNFPPFDGPGNTLGHAFAPGPG-----LGGDAHFKDEYWDGEDSGVNFLEAATHEFGHSLGLSHSSVP 231
gi | 4505219 | ref | NP_002414.1 | -----VAEYSLFPNSPKWTSK-----VVTYRIVS-----YTRDLPHTITVDRLVSKALNMWQKEIPLHFRKVV-WGTADIMIGFARGAHDGDSYPPFDGPGNTLAHAFAPGTG-----LGGDAHFDDEDERWTDGSSLGINFLYAATHEFGHSLGMGHSSDP 228
gi | 114640081 | ref | XP_508721.2 | -----VAEYSLFPNSPKWTSK-----VVTYRIVS-----YTRDLPHTITVDRLVSKALNMWQKEIPLHFRKVV-WGTADIMIGFARGAHDGDSYPPFDGPGNTLAHAFAPGTG-----LGGDAHFDDEDERWTDGSSLGINFLYAATHEFGHSLGMGHSSDP 228
gi | 73955234 | ref | XP_546550.2 | -----VAHFSLFPNPKWTSK-----VITYRIAS-----YTPDLPRFRVNLQVAKALAMWSKEIPLSFRVVP-RGTADIMIGFARGAHDGDSYPPFDGPGNTLAHAFAPGPD-----LGGDAHFDDEDERWTDGSSLGINFLYAATHEFGHSLGLGHSSDP 228
gi | 115496540 | ref | NP_001068598.1 | -----VAEYSLFPNPKWTSK-----VVTYRIMS-----YTSDDLPHITVNQLVAKAFKIWEALPLTFKRLR-WGTADIMIGFARRAHDGDPYPPFDGPGNTLAHAFAPGPG-----LGGDAHFDDEDERWTDGSLGINFLYAATHEFGHSLGLSHSSDP 228
gi | 57529313 | ref | NP_001006278.1 | -----VANVQIFYGSPRWNRK-----VLYTYKLVN-----YTPDLPREYVDDAIRRALMWSNVTPPLRFKRYT-SGQADIMIKFARRAHDGDPYPPFDGPGNTLAHAFAPGEG-----LGGDAHFDDEDERWTS-KYNQGVNLFVAATHEFGHSLGLSHSNVR 226
gi | 15235820 | ref | NP_193397.1 | -----AHYTYFNGKPKWNRD-----LLTYALSK-----YTKLDYLTSEDVKTVFRRAFSQWSVPIPVSEFEVDDFTADLLKIGFYAGDHDGDLFPDGLGTLAHAFAPENGRLLHDAETWIVDDDLKSSSEVAVDLESVAHEIGHLLGLGHSSQE 289
gi | 115483382 | ref | NP_001065361.1 | -----GGVVSRFIFFKGEPRWIRSDPPVIVLSYAVSPHAAVGYLPPAAVRAVQRAFARWARTIPVGVVEVDDYEAADIKVGFYAGNHDGCVFPDGLGTLGHAFSPKNGRLLHLDASEHWAVDFVD-AIASAIDLESVAHEIGHVGLGHSSASE 265
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 111955033 | ref | NP_034940.2 | -----GIVMYPYQRDYSEDFSLTKDDIAGIQLYGRKNTL----- 267
gi | 6981214 | ref | NP_036996.1 | -----SSVMYPYQGDHSEDFSLTKDDIAGIQLYGRKNTL----- 267
gi | 4505219 | ref | NP_002414.1 | -----NAVVMYPYGNQDPPNFKLSQDDIKGIQLYGRKNSRKK----- 267
gi | 114640081 | ref | XP_508721.2 | -----NAVVMYPYGNQDPPNFKLSQDDIKGIQLYGRKNSRKK----- 267
gi | 73955234 | ref | XP_546550.2 | -----DAVMYPYSIRDKSNFKLSQDDIEGIGKLYG-----GNRI----- 263
gi | 115496540 | ref | NP_001068598.1 | -----NAVVMYPYSKEDSKNFKLSQDDINGIQLYGRKNSRKK----- 267
gi | 57529313 | ref | NP_001006278.1 | -----GALMYPVLSYVNPETFTLHWDDRRGIQLYGRNSANS----- 263
gi | 15235820 | ref | NP_193397.1 | -----SAVMYPSLR-PRKVKVDLTVDDVAGVILKLYGPNKRLDLSLQSEDIKNGTVSHRFLSGNFVGLLVVGLILFL 364
gi | 115483382 | ref | NP_001065361.1 | -----RAVMYPSIK-PRKVKVRLVDDVEGVAALYGSNPQFSLSSLEQGTSSSS-----PRRLLAGSARLLCTVLLVILVQL 337
.....310.....320.....330.....340.....350.....360.....370.....

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