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gi|33859624|ref|NP_035441.1| MA---RPLEEALDVIVSTFHKYSGKEGDKFKLNKTELKELLTRELPSFLGKRTDEAAFQKVMNSLDSNRDNEVDFQEYCVFLSCIAMMCNEFFEGCPDKEPRKK 104
gi|6981326|ref|NP_036750.1| MA---RPLEEALDVIVSTFHKYSGNEGDKFKLNKTELKELLTRELPSFLGKRTDEAAFQKLMNNLDSNRDNEVDFQEYCVFLSCIAMMCNEFFEGCPDKEPRKK 104
gi|4506765|ref|NP_002952.1| MA---CPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAAFQKLMNSLDSNRDNEVDFQEYCVFLSCIAMMCNEFFEGFPDKQPRKK 104
gi|114559718|ref|XP_001138744.1| MA---CPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAAFQKLMNSLDSNRDNEVDFQEYCVFLSCIAMMCNEFFEGFPDKQPRKK 104
gi|55741496|ref|NP_001003161.1| MT---FPLEKALDVMVSTFHKYSGKEGDKFKLNRSSELKELLMRELPSFLGKRTDEAAFQKLMNSLDSNRDNEVDFQEYCVFLSCVAMMCNEFFEGFPDKQPRKK 104
gi|27807075|ref|NP_777020.1| MA---YPLEKALDVMVSTFHKYSGKEGDKFKLNKSELKELLTRELPSFLGKRTDEAFQKLMNSLDCNKDNEVDFQEYCVFLSCIAMMCNEFFEGFPDKQPRKK 104
gi|47086523|ref|NP_997926.1| MA---SDTQKAMAMLIATFHKYSGKEGDKLTLKSGELKELLSAELGDFGKTTDKAALDKIFKDLDAADGSVDFQEYITLIACITMLCNEFFT-----GKK 104
gi|130494223|ref|NP_001076426.1| MSGKMSDTQKAMAMLIATFHKYSGKEGDKLTLKSGELKELLSAEMSDVFGKTTDKASLDNIFKDLDAADGSVDFQEYITLIACITMLCNEFFQ-----KGK 104
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100....

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