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gi|5031741|ref|NP_005871.1|ALCGFQFTFKHLDGRQIVVKYPPGKVIIEPCVVRVVRGEGMPQYRNPFKGDLYIKFDVQFPENNWINPKLSELEDLLPSRPEVPIIIG--ETEEVELQEFD---STRGSGGGQRREAYNDSDEESS--HHGPGVCAHQ 412
gi|114662436|ref|XP_528644.2|ALCGFQFTFKHLDGRQIVVKYPPGKVIIEPCVVRVVRGEGMPQYRNPFKGDLYIKFDVQFPENNWINPKLSELEDLLPSRPEVPIIIG--ETEEVELQEFD---STRGSGGGQRREAYNDSDEESS--HHGPGVCAHQ 519
gi|9789937|ref|NP_062768.1|ALCGFQFTFKHLDARQIVVKYPPGKVIIEPCVVRVVRGEGMPQYRNPFKGDLYIKFDVQFPENNWINPKLSELEDLLPSRPEVPIIIG--ETEEVELQEFD---STRGSGGGQRREAYNDSDEESS--HHGPGVCAHQ 412
gi|56799412|ref|NP_114468.2|ALCGFQFTFKHLDARQIVVKYPPGKVIIEPCVVRVVRGEGMPQYRNPFKGDLYIKFDVQFPENNWINPKLSELEDLLPSRPEVPIIIG--ETEEVELQEFD---STRGSGGGQRREAYNDSDEESS--HHGPGVCAHQ 412
gi|95147672|ref|NP_001035581.1|ALCGFQFTFKHLDGRQIVVKYPPGKVIIEPCVVRVVRGEGMPQYRNPFKGDLYIKFDVQFPENNWINPKLSELEDLLPSRPEVPIIIG--DTEEVELQEFD---STRGSGGGQRREAYNDSDEESS--HHGPGVCAHQ 412
gi|57524857|ref|NP_001005841.1|ALCGFQFTFKHLDGRQIVVKYPPGKVIIEPCVVRVVRGEGMPQYRNPFKGDLYIKFDVQFPENNWINPKLSELEDLLPSRPEVPIIIG--DAEEVDLQEFD---TTRGSGGGQRREAYNDSDEESS--HHGPGVCAHQ 411
gi|17563890|ref|NP_504452.1|ALCGYNFLIKHLDGHLVLSKQGDVVKPGVIRGVLGKGMPPKYPPELKGNLVFEVEFEVPEKHFLLDDEKAYAVLKSCTPTSKVNVVTP--AAAEVSLMEVD---EKKYVRG--RGGDAYNEDSDEEQQGGHHQGVRCQH 439
gi|18420428|ref|NP_568412.1|ALCGFQFVLTHLDRQLLIRKSKPGEVVKPDSYKAIISDEGMPYIQRPFMKGKLYIHFTVEFPDSLEPDTKALEAVLPPKPTKAAISDMEID--ECBEITLHDVN--IEDEMRR--KAQAQREAYDDDDDDHDP--GGAQRVCAHQ 419
gi|15229874|ref|NP_189997.1|ALCGFQFVLTHLDRQLLIRKSKPGEVVKPDSYKAIISDEGMPYIQRPFMKGKLYIHFTVEFPDSLEPDTKALEAVLPPKPTKAAISDMEID--ECBEITLHDVN--IEDEMRR--KAQAQREAYDDDDDDHDP--GGAQRVCAHQ 420
gi|115454357|ref|NP_001050779.1|ALCGFQFVLTHLDRQLLIRKSKPGEVVKPDSYKAIISDEGMPYIQRPFMKGKLYIHFTVEFPDSLEPDTKALEAVLPPKPTKAAISDMEID--ECBEITLHDVN--IEDEMRR--KAQAQREAYDDDDDDHDP--GGAQRVCAHQ 417
gi|115455793|ref|NP_001051497.1|ALCGFQFVLTHLDRQLLIRKSKPGEVVKPDSYKAIISDEGMPYIQRPFMKGKLYIHFTVEFPDSLEPDTKALEAVLPPKPTKAAISDMEID--ECBEITLHDVN--IEDEMRR--KAQAQREAYDDDDDDHDP--GGAQRVCAHQ 417
gi|145603119|ref|XP_362017.2|ALAGGTIFVEHLDERWLSVLIQPGEAIAIPNSVKMIRGQGMPSYRHHDY--GNMVIQFSVRFPEKNTQDPAAFEALRKYLPAPAVVNVPP-----DAMTEPALELDVEGNGAGRGFSNSGFMEDDEPQAE---R--VCCASG 399
gi|85090435|ref|XP_958415.1|ALAGGTIFVEHLDERWLSVLIQPGEAIAIPNSVKMIRGQGMPSYRHHDY--GNMVIQFSVRFPEKNTQDPAAFEALRKYLPAPAVVNVPP-----DAMTEPALELDVEGNGAGRGFSNSGFMEDDEPQAE---R--VCCASG 414
gi|19112220|ref|NP_595428.1|ALAGGQIVVHLDLDRWLILPIIPGECIRPNELKVLPGQMLSRHHQY--GNLYIRFHVDFPEPFFAT--PEQLALLEKALPPRKIESAPKNAHTBECVLATVDPTEKVRIDNNVDPTTALSMDEDEDEEGG---HPGVCAHQ 407
gi|50310423|ref|XP_455231.1|ALAGGQFAVKHVSGEYLKVEIVPGEVISPGSVKVIIEGKGMPIPKYGGY--GNLLIKFNIRKPPAHTD--DELLKLEETLPPRNVPSTIPADAIVEDCVLADFPDS--SKHGARAGGNRGSVSDSDDEDEGHHG---AEGVCAHQ 409
gi|45187616|ref|NP_983839.1|ALAGGQFALEHVSQDWLKIIDIVPGEVIAPGMVKVIEGKGMPIQYGSY--GDLLIKFNIRKPKSHPAD--EALKKLEETLPPKTLPRIPNAEVEECVLADFPDS--AKHDSRSG--NGRGSVSDSDEEBAHT---EGVCAHQ 410

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