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                                 * ::.*.*****.* *:*:*  : ** :****.: * : ..*      *:.*:   . :* :***:*  ::  :*. .:: * .::*::*** : *:: **  :::** ..* ** *. ..* *  *  **  :*:.* ...      *:
gi|124486706|ref|NP_032304.2|    MHVNGKVALVTGAAQGIGKAFAEALLLHGAKVALVDWNLEAGVKCKAALDEQFEPQKTLFVQCDVADQKQLRDTFRKVVDHFGRLDILVNNAGVNNEKNWEQTLQINLVSVISGTYLGLDYMSKQNGGEGGIIINMSSLAGLMPVAQQPV   150
gi|40538858|ref|NP_077366.2|     MHVNGKVALVTGAAQGIGKAFTEALLLHGAKVALVDWNLETGVKCKAALDEQFEPQKTLFIQCDVADQKQLRDTFRKVVDHFGRLDILVNNAGVNNEKNWEQTLQINLVSVISGTYLGLDYMSKQNGGEGGIIINISSIAGLMPVAQQPV   150
gi|31542939|ref|NP_000851.2|     MHVNGKVALVTGAAQGIGRAFAEALLLKGAKVALVDWNLEAGVQCKAALDEQFEPQKTLFIQCDVADQQQLRDTFRKVVDHFGRLDILVNNAGVNNEKNWEKTLQINLVSVISGTYLGLDYMSKQNGGEGGIIINMSSLAGLMPVAQQPV   150
gi|114596929|ref|XP_001157531.1| MHVNGKVALVTGAAQGIGRAFAEALLLKGAKVALVDWNLEAGVQCKAALDEQFEPQKTLFIQCDVADQQQLRDTFRKVVDHFGRLDILVNNAGVNNEKNWEKTLQINLVSVISGTYLGLDYMSKQNGGEGGIIINMSSLAGLMPVAQQPV   150
gi|77735793|ref|NP_001029591.1|  MHVNGKVALVTGAAQGIGRAFAEALLLKGAKVALVDWNLEAGVKCKAALDEQFEPQKTLFIQCDVADQEQLRDTFRKVVDHFGKLDILVNNAGVNNEKNWEKTLQINLVSVISGTYLGLDYMSKQNGGEGGININMSSLAGLMPVAQQPV   150
gi|57105210|ref|XP_543199.1|     MHVNGKVALVTGAAQGIGRASAEALLHKGAKVALVDWNLEAGVKCKAALDEQFEPQKTLFIQCDVADQGQLRDTFRKVVDHFGRLDILVNNAGVNNEKNWEKTVQINLVSVISGTYLGLDYMSKQNGGEGGIIINMSSLAGLMPVAQQPV   150
gi|50746505|ref|XP_420526.1|     MHVNGKVALVTGGAQGIGRAFVQALLGKGAKVALLDRNPEAGQQSKAALDEQFEAQRTVFIQCDVTDTEQLKGAFKKVIEHFGRLDIVVNNAGVNNEKDWESTIQINLTSVIRGTYLGLEYMRKGNGGDGGVIINISSLAGLMPAAFQPV   150
gi|189514903|ref|XP_694331.3|    MSLHGKTALVTGGAQGIGRAVVEELLQNGAKVALVDLNQSVGEECKSDLDDQFGEDNCIFIQCDVTDGEKLGDAFRNTVDRFGRLDIVINNAGINNEKNWEKTIEVNLTSVIKGTYLALEHMSKEYGKQGGAIINVSSMAAFLHSPHQPV   150
gi|158301663|ref|XP_321329.4|    MDLKNKVALVTGAATGLGRAFSEELLKHGAKVVICDLDSDAGELTVEELEKQYG-ARVLFCHCDVTDYIQFEEAFEYTVNMFKEVNIVINNAEIMNDNFWELEVDVNLNGAIRGTLLAQKFMDKSKGKGGGVLVNIGSGVSVTPQLSTPI   149
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 * *:*:.::*:::: . .  .  : .**  . **. :..   .: .::. *.   .    :.        :.   :*. :: :: : : .* :  :* .:  :   *.
gi|124486706|ref|NP_032304.2|    YCASKHGIIGFTRSAAMAANLMKSGVRLNVICPGFVDTPILESIEKEENMGQYIEYKDQIKAMMKFYGVLHPSTIANGLINLIEDDALNGAIMKITASKGIHFQDYDISPLLVKAPLTS   269
gi|40538858|ref|NP_077366.2|     YCASKHGIIGFTRSAAMAANLMKSGVRLNVICPGFVKTPILESIEKEENMGQYIEYTDQIKAMMKFYGILDPSAIANGLINLIEDDALNGAIMKITASKGIHFQDYDLFPSFSKAP---   266
gi|31542939|ref|NP_000851.2|     YCASKHGIVGFTRSAALAANLMNSGVRLNAICPGFVNTAILESIEKEENMGQYIEYKDHIKDMIKYYGILDPPLIANGLITLIEDDALNGAIMKITTSKGIHFQDYDTTPFQAKTQ---   266
gi|114596929|ref|XP_001157531.1| YCASKHGIVGFTRSAALAANLMNSGVRLNAICPGFVNTAILESIEKEENMGQYIEYKDHIKDMIKYYGILDPPLIANGLITLIEDDALNGAIMKITTSKGIHFQDYDTTPFQAKTQ---   266
gi|77735793|ref|NP_001029591.1|  YCASKHGIVGFTRSAAMAANLMNSGVRLNAICPGFVDTPILKSIEKEENMGKYIEYMGPIKDMMKYYGILDPSMIANGLITLIEDDALNGAIMKITTSKGIHFQDYDTTPFHMKMQ---   266
gi|57105210|ref|XP_543199.1|     YCASKHGIIGFTRSAAMAANLMNSGVRLNAICPGFVNTPILESIEKEENMGQYIEYKDHIKDMMKFYGILDPSMIASGLITLIEDDALNGAIMKITTSKGIHFQDYETTPFHAKTQ---   266
gi|50746505|ref|XP_420526.1|     YCATKHGVIGFTRSIALAANMENYGVRLNTICPGFVNTPILQSIDKEENMGQYYSYKDEIKNMMQFYGVMDPSIIAEGLITIIEDDTLNGEVMKITASQGIHFQEYSQTPYTSKR----   265
gi|189514903|ref|XP_694331.3|    YTATKYGVIGFSRAMADASEQGNYGVRINALCPAFVDTQLLQTVEHEETMGKFVKYKDDFKQRMDKYGVLKPSLIAEGMLRLITDESLNGAVMKITCSKGIHFHTYEPLSA--------   261
gi|158301663|ref|XP_321329.4|    YTATKHAILGLTKACGDPFHHANTNVRAFAYCPGPIEN---SSSHNKRFMSPAYEKAKELDTAGVQLQRMEH--VAKELIPLLKN-APTGSIWLVTGGKPAKEIPYSSI---------   252
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260........
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