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                                                  :* *** **: **  *:*:*  * :* :...****  *.:** :::********.  *.  *  *: : :*.****  .:*.* *        **: :  :.* :*::** ***:  : :   :: :
gi|24663672|ref|NP_524053.2|      ---------------------MARGPKKHLKRLAAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLLIFLRNRLKYALNGAEVTKIVMQRLVKVDGKVRTDPTYPAGYM--------DVITLEKTGEFFRLVYDVKGRFVIHRISAEEAKY   121
gi|158286707|ref|XP_308886.4|     ---------------------MARGPKKHLKRLNAPRGWMLDKTGGTFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRHVKIDGKVRTDPNYPAGFM--------DVINIHKTGEYFRLIYDVKGRFTVHRITSEEAKY   121
gi|114689109|ref|XP_001138805.1|  ---------------------MARGPKKHLKRVAAPKHWMLDKLTGVFAPRPSTGPHKLRECLPLIIFLRNRLKYALTGDEVKKICMQRFIKIDGKVRTDITYPAGFMVTGYCLISDVISIDKTGENFRLIYDTKGRFAVHRITPEEAKY   129
gi|56090273|ref|NP_001007601.1|   ---------------------MARGPKKHLKRVAAPKHWMLDKLTGVFAPRPSTGPHKLRECLPLIIFLRNRLKYALTGDEVKKICMQRFIKIDGKVRTDITYPAGFM--------DVISIDKTGENFRLIYDTKGRFAVHRITPEEAKY   121
gi|4506725|ref|NP_000998.1|       ---------------------MARGPKKHLKRVAAPKHWMLDKLTGVFAPRPSTGPHKLRECLPLIIFLRNRLKYALTGDEVKKICMQRFIKIDGKVRTDITYPAGFM--------DVISIDKTGENFRLIYDTKGRFAVHRITPEEAKY   121
gi|78369408|ref|NP_001030522.1|   ---------------------MARGPKKHLKRVAAPKHWMLDKLTGVFAPRPSTGPHKLRECLPLIIFLRNRLKYALTGDEVKKICMQRFIKIDGKVRTDITYPAGFM--------DVISIDKTGENFRLIYDTKGRFAVHRITPEEAKY   121
gi|6677805|ref|NP_033120.1|       ---------------------MARGPKKHLKRVAAPKHWMLDKLTGVFAPRPSTGPHKLRECLPLIIFLRNRLKYALTGDEVKKICMQRFIKIDGKVRTDITYPAGFM--------DVISIDKTGENFRLIYDTKGRFAVHRITPEEAKY   121
gi|57090063|ref|XP_537399.1|      ---------------------MARGPKKHLKRVAAPKHWMLDKLTGVFAPRPTTGPHKLRECLPLIIFLRNRLKYALTGDEVKKICMQRFIKIDGKVRTDITYPAGFM--------DVISIDKTGENFRLIYDTKGRFAVHRITPEEAKY   121
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gi|19113142|ref|NP_596350.1|      ---------------------MVRGPKKHLKRVAAPHHWLLDKLSGTYAPKPSPGPHKARECLPLIVFLRNRLKYALNGREVKAILMQRLIKVDGKVRTDSTFPTGFM--------DVISVEKTGEHFRLVYDIKGRFTVHRITAEEAKY   121
gi|19112469|ref|NP_595677.1|      ---------------------MVRGPKKHLKRVAAPHHWLLDKLSGTYAPKPSPGPHKARECLPLIVFLRNRLKYALNGREVKAILMQRLIQVDGKVRTDSTFPTGFM--------DVISVEKTGEHFRLVYDIKGRFTVHRITAEEAKY   121
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gi|164429760|ref|XP_964251.2|     ---------------------MGRGPKKHQKRLSAPSHWLLDKLSGVYAPRPSAGPHKLRECMPLIVFVRNRLKYALNYRETKAIMMQRLIKVDGKVRTDITYPAGFM--------DVITIEKTGENFRLIYDTKGRFTVHRIQDEEAKY   121
gi|6321997|ref|NP_012073.1|       ---------------------MARGPKKHLKRLAAPHHWLLDKLSGCYAPRPSAGPHKLRESLPLIVFLRNRLKYALNGREVKAILMQRHVKVDGKVRTDTTYPAGFM--------DVITLDATNENFRLVYDVKGRFAVHRITDEEASY   121
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gi|45187482|ref|NP_983705.1|      ---------------------MARGPKKHLKRLAAPHHWLLDKLSGCYAPRPSAGPHKLRESLPLIVFLRNRLKYALNGREVKAILMQRHVKVDGKVRTDTTYPAGFM--------DVITLEATNENFRLVYDVKGRFAVHRITDEEATY   121
gi|50303511|ref|XP_451697.1|      ---------------------MARGPKKHLKRLAAPHHWLLDKLSGCYAPRPSAGPHKLRESLPLIVFLRNRLKYALNGREVKAILMQRHVKVDGKVRTDTTFPAGFM--------DVITLEATNENFRLVYDVKGRFAVHRITDEEASY   121
gi|18415395|ref|NP_568179.1|      ---------------------MARGLKKHLKRLNAPKHWMLDKLGGAFAPKPSSGPHKSRECLPLVLIIRNRLKYALTYREVISILMQRHIQVDGKVRTDKTYPAGFM--------DVVSIPKTNENFRLLYDTKGRFRLHSIKDEEAKF   121
gi|15237195|ref|NP_200650.1|      ---------------------MARGLKKHLKRLNAPKHWMLDKLGGAFAPKPSSGPHKSRECLPLVLIIRNRLKYALTYREVISILMQRHIQVDGKVRTDKTYPAGFM--------DVVSIPKTNENFRLLYDTKGRFRLHSIKDEEAKF   121
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gi|115436514|ref|NP_001043015.1|  ---------------------MARGLKKHLKRLNAPKHWMLDKLGGAFAPKPSSGPHKSRECLPLILIIRNRLKYALTYREVISILMQRHVLVDGKVRTDKTYPAGFM--------DVISIPKTGENYRLLYDTKGRFRLQSVKDEDAKF   121
gi|115443689|ref|NP_001045624.1|  ---------------------MARGLKKHLKRLNAPKHWMLDKLGGAFAPKPSSGPHKSRECLPLILIIRNRLKYALTYREVISILMQRHVLVDGKVRTDKTYPAGFM--------DVISIPKTGENYRLLYDTKGRFRLQSVKDEDAKF   121
gi|115463485|ref|NP_001055342.1|  ---------------------MARGLKKHLKRLNAPSHWMLDKLGGAFAPKPSSGPHKARECLPLILILRNRLKYALTYREVISILMQRHVMVDGKVRTDKTYPAGFM--------DVVSIAKTGENFRLLYDTKGRFRLHSIKDEDAKF   121
gi|17543386|ref|NP_501103.1|      ---------------------MRGPKKHLKRLAAPSHWMLDKLGGVFAVRPNPGPHKLRESLPLSLFLRNRLKYALNYTEAKKILTQRVVRVDGKVRTCHKFPTGFM--------DVVAIERTNEYFRMLYDTKGRYVVHRIQAAEADF   120
gi|124803509|ref|XP_001347741.1|  MICLRCFFLPDFAIIFFFFLLNGKGIKKHLKRVNAPSHWMLNKMGGQYAPKTSSGPHKLLESIPLVILLRNRLKYALTFDEVKMILIQKIVKVDNKVRTDCTFPVGLM--------DVIHITKSNEYFRLLYDIKGRFVPHRITNEESKY   142
                                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|24663672|ref|NP_524053.2|      KLCKVKKTQLGAKGVPFLVTHDGRTIRYPDPLIHANDSVQVDIASGKITDYIKFDSGNLCMITGGRNLGRVGTVVNRERHPGSFDIVHIKDSQGHVFATRLTNVFIIGKGNKPYISLPKGKGVKLSIAEERDRLAAKTH------   261
gi|158286707|ref|XP_308886.4|     KLLKVKRVQIGPKRVPFLLTHDGRTIRYPDPQIHQHDSIQYDIATGKVLDVLKFEPGNLCMITGGRNLGRCGTVILREKHPGSFEIVHVKDTTGHVFATRLSNVFIIGKSTKAYISLPKGKGVKLTIAEERDRRLANKAAQ-----   262
gi|114689109|ref|XP_001138805.1|  KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNRERHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSG----   271
gi|56090273|ref|NP_001007601.1|   KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNRERHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSG----   263
gi|4506725|ref|NP_000998.1|       KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNRERHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSG----   263
gi|78369408|ref|NP_001030522.1|   KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNRERHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSG----   263
gi|6677805|ref|NP_033120.1|       KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNRERHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSG----   263
gi|57090063|ref|XP_537399.1|      KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNREKHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSGQNGP   267
gi|46048780|ref|NP_990439.1|      KLCKVRKIFVGTKGIPHLVTHDARTIRYPDPLIKVNDTIQIDLETGKITDFIKFDTGNLCMVTGGANLGRIGVITNRERHPGSFDVVHVKDANGNSFATRLSNIFVIGKGNKPWISLPRGKGIRLTIAEERDKRLAAKQSSG----   263
gi|53933236|ref|NP_001005589.1|   KLCKVRKILIGTKGIPHLVTHDARTIRYPDPLIKVNDTIRIDLDTGKITDFIKFETGNMCMVTGGANLGRIGVITNREKHPGSFDVVHVKDSIGNSFATRLSNIFVIGKGNKPWVSLPRGKGVRLTIAEERDKRLAAKQSSS----   263
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gi|19113142|ref|NP_596350.1|      KLCKVKRVQLGAKGVPFLVTHDGRTIRYPDPLIKVNDTIKLNLETNKIESFIKFDTSAQVMVTGGRNMGRVGTIVHREHHLGSFEIIHVKDALDREFATRLSNVFVIGETGKSWISLPKGKGVKLSITEERDRRRALKGLA-----   262
gi|19112469|ref|NP_595677.1|      KLCKVKRVQLGAKGVPFLVTHDGRTIRYPDPLIKVNDTIKLNLETNKIESFIKFDTSAQVMVTGGRNMGRVGTIVHREHHLGSFEIIHVKDALDREFATRLSNVFVIGEAGKSWISLPKGKGVKLSITEERDRRRALKGLA-----   262
gi|145610060|ref|XP_366671.2|     KLGKVKRVQLGRGGIPFLVTHDARTIRYPDPLIKVNDTVKINLDTGKITDFIKFDTGALAMVTAGNNMGRVGVITHRERHDGGFNIVHLKDAIDNTFTTRESNVFVIGTE-KPWISLPKGKGVKLTIAEERDRRRAQTIAGH----   262
gi|164429760|ref|XP_964251.2|     KLGKVKRVQLGKGGIPFLVTHDARTIRYPDPLIKVNDTVKINLETGKIEDFVKFDTGAIAMVTGGRNMGRVGVITHRERHDGGFNIIHVKDALDNTFATRESNVFVIGSE-KPWISLPKGKGVKLSIAEERDRRRANALAH-----   261
gi|6321997|ref|NP_012073.1|       KLGKVKKVQLGKKGVPYVVTHDGRTIRYPDPNIKVNDTVKIDLASGKITDFIKFDAGKLVYVTGGRNLGRIGTIVHKERHDGGFDLVHIKDSLDNTFVTRLNNVFVIGEQGKPYISLPKGKGIKLSIAEERDRRRAQQGL------   261
gi|6322605|ref|NP_012679.1|       KLGKVKKVQLGKKGVPYVVTHDGRTIRYPDPNIKVNDTVKIDLASGKITDFIKFDAGKLVYVTGGRNLGRIGTIVHKERHDGGFDLVHIKDSLDNTFVTRLNNVFVIGEQGKPYISLPKGKGIKLSIAEERDRRRAQQGL------   261
gi|45187482|ref|NP_983705.1|      KLGKVKRVQLGKKGVPYVVTHDGRTIRYPDPNIKVNDTVKVDLATGKITDFIKFDTGKLVYVTGGRNLGRIGVITHRERHEGGFDLVHIKDSLENTFVTRLNNVFVIGEQGRPWISLPRGKGIKLSIAEERDRRRAQQGL------   261
gi|50303511|ref|XP_451697.1|      KLAKVKKVQLGKKGIPYVVTHDGRTIRYPDPNIKVNDTVKVDLATGTITDFIKFDTGKLVYVTGGRNLGRVGTIVHRERHEGGFDLVHIKDSLENTFVTRLNNVFVIGEPGRPWISLPKGKGIKLTISEERDRRRAQHGL------   261
gi|18415395|ref|NP_568179.1|      KLCKVRSIQFGQKGIPYLNTYDGRTIRYPDPLIKPNDTIKLDLEENKIVEFIKFDVGNVVMVTGGRNRGRVGVIKNREKHKGSFETIHIQDSTGHEFATRLGNVYTIGKGTKPWVSLPKGKGIKLTIIEEARKRLASQQAA-----   262
gi|15237195|ref|NP_200650.1|      KLCKVRSIQFGQKGIPYLNTYDGRTIRYPDPLIKPNDTIKLDLEANKIVEFIKFDVGNVVMVTGGRNRGRVGVIKNREKHKGSFETIHIQDSTGHEFATRLGNVYTIGKGTKPWVSLPKGKGIKLTIIEEARKRLASQQAA-----   262
gi|18398393|ref|NP_565414.1|      KLCKVRSIQFGQKGIPYLNTYDGRTIRYPDPLIKPNDTIKLDLEENKIVEFIKFDVGNVVMVTGGRNRGRVGVIKNREKHKGSFETIHIQDSTGHEFATRLGNVYTIGKGTKPWVSLPKGKGIKLTIIEEARKRLSAQQA------   261
gi|115436514|ref|NP_001043015.1|  KLCKVRSVQFGQKGIPYLNTYDGRTIRYPDPLIKANDTIKIDLETNKIVDFIKFDVGNVVMVTGGRNTGRVGVIKNREKHKGSFETIHVEDALGHAFATRLGNVFTIGKGNKPWVSLPKGKGIKLSIIEEQRKRDAAAQAAANA--   265
gi|115443689|ref|NP_001045624.1|  KLCKVRSVQFGQKGIPYLNTYDGRTIRYPDPIIKANDTIKIDLETNKIVDFIKFDVGNVVMVTGGRNTGRVGVIKNREKHKGSFETIHVEDALGHQFATRLGNVFTIGKGNKPWVSLPKGKGIKLSIIEEQRKRDAAAQAAANA--   265
gi|115463485|ref|NP_001055342.1|  KLCKVRSVQFGQKGIPFLNTNDGRTIRYPDPLIKANDTIKIDLETNKIVDFIKFDVGNIVMVTGGRNTGRVGVIKSREKHKGSFETIHVEDALGHQFATRMGNVFTIGKERKPWVSLPKGKGIKLSIIEEARKRNAEAAAEA----   263
gi|17543386|ref|NP_501103.1|      KLCKVKSVRTVNKGVPVLTTTDGRTIRYPDPHVKVNDTIVFNISTQKITDSVKFEPGNLAYVTGGRNVGRVGIIGHRERLPGASDIIHIKDSAGHSFATRISNVFVIGKGNKALVSLPTGAGIRLSIAEERDKRMAQKH-------   259
gi|124803509|ref|XP_001347741.1|  KLCKVKKILLRKGRLSIAVTHDGRSIPYIHPDVKVNDTVRLDLETGKVLEHLKFQVGSLVMVTAGHSVGRVGVISSIDKNMGTYDIIHVKDSRNKVFATRLSNVFVIGDNTKPYISLPREKGIKLDIIEERRNRLKALNN------   282
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