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                                 **      ******** *********** .**:********* ..    .***:*********:*** *:***:********* ***:: ********:*****:**:*.*.****.:.*:***:*:* ** ***:* ::**********
gi|6753380|ref|NP_034000.1|      MAATR---YEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGAAGGGLPVSTVREVALLRRLEAFEHPNVVRLMDVCATSRTDRDIKVTLVFEHIDQDLRTYLDKAPPPGLPVETIKDLMRQFLSGLDFLHANCIVHRDLKPENIL   150
gi|16758944|ref|NP_446045.1|      MATTR---YEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGAAGGGLPVSTVREVALLRRLEAFEHPNVVRLMDVCATSRTDRDIKVTLVFEHIDQDLRTYLDKAPPPGLPVETIKDLMRQFLSGLDFLHANCIVHRDLKPENIL   150
gi|4502735|ref|NP_000066.1|      MATSR---YEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGGLPISTVREVALLRRLEAFEHPNVVRLMDVCATSRTDREIKVTLVFEHVDQDLRTYLDKAPPPGLPAETIKDLMRQFLRGLDFLHANCIVHRDLKPENIL   150
gi|114644117|ref|XP_509173.2|    MATSR---YEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGGLPISTVREVALLRRLEAFEHPNVVRLMDVCATSRTDREIKVTLVFEHVDQDLRTYLDKAPPPGLPAETIKDLMRQFLRGLDFLHANCIVHRDLKPENIL   150
gi|57092583|ref|XP_538252.1|     MATPR---YEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGAGGGLPISTVREVALLRRLEAFEHPNVVRLMDVCATARTDRETKVTLVFEHVDQDLRTYLDKAPPPGLPVETIKDLMRQFLRGLDFLHANCIVHRDLKPENIL   150
gi|83035065|ref|NP_001032683.1|  MATSR---YEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGAGGGLPISTVREVALLRRLEAFEHPNVVRLMDVCATARTDRETKVTLVFEHVDQDLRTYLDKAPPPGLPVETIKDLMRQFLRGLDFLHANCIVHRDLKPENIL   150
gi|118150570|ref|NP_001071245.1| MAQEVGLQYEPVAEIGGGAYGTVYKARDRDSGQFVALKSVRVQTNQ---DGLPLSTVREVALLKRLEQFDHPNIVRLMDVCATLRTDQETKVTLVFEHVDQDLRAYLEKVPAPGLPVDKIRDLMQQLLCGLAFLHTNRVLHRDLKPENIL   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 *** * ************* :**************:***************:**.****************:********** :****.**:** :*:*.:  *.*:.***:   **:: *.**:***:****:* *****:.**:*.:: :
gi|6753380|ref|NP_034000.1|      VTSNGTVKLADFGLARIYSYQMALTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPREVSLPRGAFAPRGPRPVQSVVPEMEESGAQLLLEMLTFNPHKRISAFRALQHSYLHK   300
gi|16758944|ref|NP_446045.1|      VTSNGTVKLADFGLARIYSYQMALTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPREVSLPRGAFSPRGPRPVQSVVPEMEESGAQLLLEMLTFNPLKRISAFRALQHSYLHK   300
gi|4502735|ref|NP_000066.1|      VTSGGTVKLADFGLARIYSYQMALTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPRDVSLPRGAFPPRGPRPVQSVVPEMEESGAQLLLEMLTFNPHKRISAFRALQHSYLHK   300
gi|114644117|ref|XP_509173.2|    VTSGGTVKLADFGLARIYSYQMALTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPRDVSLPRGAFPPRGPRPVQSVVPEMEESGAQLLLEMLTFNPHKRISAFRALQHSYLHK   300
gi|57092583|ref|XP_538252.1|     VTSGGTVKLADFGLARIYSYQMALTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPRDVSLPRGAFSPRGPRPVQTVVPEMEESGAQLLLEMLTFNPHKRISAFRALQHSYLQK   300
gi|83035065|ref|NP_001032683.1|  VTSGGTVKLADFGLARIYSYQMALTPVVVTLWYRAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPRDVSLPRGAFSPRGPRPVQSVVPELEESGAQLLLEMLTFNPHKRISAFRALQHSYLHK   300
gi|118150570|ref|NP_001071245.1| VTSRGQVKLADFGLARIYSCHMALTPVVVTLWYRSPEVLLQSTYATPVDIWSTGCIFAEMFRRKPLFCGDSEADQLGKIFAVIGLPAEDQWPTDVTLSHHNFSPQSPRPITDCVPDITEKGAELLLKMLTFDPLKRISALNALDHPFFSE   300
                                 .......160........170........180........190........200........210........220........230........240........250........260........270........280........290........300
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gi|6753380|ref|NP_034000.1|      EESDAE   306
gi|16758944|ref|NP_446045.1|     EESDPE   306
gi|4502735|ref|NP_000066.1|      DEGNPE   306
gi|114644117|ref|XP_509173.2|    DEGNPE   306
gi|57092583|ref|XP_538252.1|     AEGNPE   306
gi|83035065|ref|NP_001032683.1|  AEGDAE   306
gi|118150570|ref|NP_001071245.1| ------   306
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