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gi|6679683|ref|NP_031976.1|      -METLPASW-      VLALLLCL-      GSHLLQAV 150
gi|11078689|ref|NP_067721.1|    -METFPAAW-      VLALLLCL-      GSHLLQAV 150
gi|4557567|ref|NP_001423.1|      MTAGR-      RMEML-      CAGR-      VPALLLCL-      GFHLLQAV 150
gi|114594256|ref|XP_001155238.1|  MTAGR-      RMEML-      CAGR-      VPALLLCL-      GFHLLQAV 150
gi|73975403|ref|XP_854760.1|    MHLVRAPPPHPDPRRDGEVRRERSAARCEAAFRPRALRAFQGRMILGRPRHAPARCETRGSPHLAPPGWARGWRLLDGLG--RNAFPPKCLDRGVLHPAQLVSGAHSGLCGSSGRRRSKRTCAPALLRLEASRFPPPESPPPAAPGFHLLHAV 150
gi|47575887|ref|NP_001001203.1|  -MNAGGPQ-      -RSLLLFLG-      -VLLQAV-      VLLQAV 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|6679683|ref|NP_031976.1|    ISTTVVIPSCIPGESEDNCTALVQIEDDPRVAQVLITKCSSDMDGYCLHGQCIVLVDMREKFCRCEVGYTGLRCEHFFLTVHOPLSKEYVALVILILFLIITAGCIVYFCRWYKNRKSKSREEYERVTSGDPVLPQV 289
gi|11078689|ref|NP_067721.1|    ISTTVVIPSCIPEESEDNCTALVQIEDDPRVAQVLITKCSSDMDGYCLHGHCIVLVDMSEKYCRCEVGYTGLRCEHFFLTVHOPLSREYVALVILVFLFLIVTAGSMYFCRWYRNRKSKSREEYERVTSGGPGLPQV 289
gi|4557567|ref|NP_001423.1|      LSTTVVIPSCIPGESSDNCTALVQIEDNPRVAQVSITKCSSDMNGYCLHGQCIVLVDMSQNYCRCEVGYTGVRCEHFLTVHOPLSKEYVALVILILFLIIVVGSTYFCRWYRNRKSKEPKEYERVTSGDPELPQV 289
gi|114594256|ref|XP_001155238.1|  LSTTVVIPSCIPGESSDNCTALVQIEDNPRVAQVSITKCSSDMNGYCLHGQCIVLVDMSQNYCRCEVGYTGVRCEHFLTVHOPLSKEYVALVILILFLIIVVGSTYFCRWYRNRKSKEPKEYERVTSGDPELPQV 289
gi|73975403|ref|XP_854760.1|      LSTTVVIPSCMPGESEDNCTALVQIEDNPRVAQVSITKCSSDMNGYCLHGQCIVLVDMSQTYCRCEVGYTGVRCEHFLTVHOPLSKEYVALVILILFLIIVAGSLYFCRWYRNRKSKEPKEYERVTSGDPALPQV 289
gi|47575887|ref|NP_001001203.1|  MGTTVIVILCAPEMENCTALVQIEDNSPRVAQVGITRCKPEMKDYCFHGQCVVIVDLDEHYCRCDVGFSGVRCVHSEL-VROPLSTEYVALVILVLLFLIAISIVGYICRRYRSKRRHTNASEYKEVG--AL-- 289
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....

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