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gi|4503433|ref|NP_001940.1| MRKGIQPALEQYLVTAGGGEGAAVVAAAAAASMDKRALLASPGFAAAAAAAGAYIQILTTNTSTTSCSSSLOS GAVAA GPLLPSAPGAEQTAGSLLYTTPHGPSRAGLLQPPALGRGSGGGGGPPAKRRLLELGE SGHQYLS DGL 150
gi|76663083|ref|XP_614932.2| MRKGIQPALEQYLVTAGGGEGAAVVAAAAAASMDKRALLASPGFP--AAAAAPSAIYIILTTNTSTTSCSSSLOS GAVAA GPLLPSAPGVEQTAGSLIYTPHGPSRAGLLQPPALGRGSGGGGGPPAKRRLLELGE SGHQYLS DGL 148
gi|83523736|ref|NP_034223.1| MRKGIQPALEQYLVTAGGGEGAAVVAAAAAASMDKRALLASPGFA--AAAAPGTIYIILTTNPSTTSCATSLQSGALTAGPLLSPVPGTEP--AASLYTTPQGPSRVLQPPAPGRGG--GGGPPAKRRLLELGE SGHQYLS DGL 142
gi|109504877|ref|XP_214476.4| -----MDS-----SGTHFDLCLTEIVN----- 23
gi|118086362|ref|XP_418915.2| MGGGIAATANC---AATGATQAQIQTIPHMDMTNHMAVG---AATAPGTSQSIRDTDTADQIATGATAFTIYVQTITSVTHITTNQMAMGATARATNQKAMGAATATDP--AAGGAALATDKTAKRRLLELGE SGHQYLS AEL 139
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|4503433|ref|NP_001940.1| KTPKGGRAALRSPD SPKTPKSPSEKTRYDTSLSGLLTKKFIQLLSQSPDGVLDLNRAAEVLKVKRRIYDITNVLEGIHLIKKSKNNVQWMCGLSEDDGMLAQCGLSKEVTELSQEEKKLDELIO SCTLDLKLLTEDSENORLAVVT 300
gi|76663083|ref|XP_614932.2| KTPKGGRAALRSPD SPKTPKSPSEKTRYDTSLSGLLTKKFIQLLSQSPDGVLDLNRAAEVLKVKRRIYDITNVLEGIHLIKKSKNNVQWMCGLSEDDGMLAQCGLSKEVTELSQEEKKLDELIO SCTLDLKLLTEDSENORLAVVT 298
gi|83523736|ref|NP_034223.1| KTPKGGRAALRSPD SPKTPKSPSEKTRYDTSLSGLLTKKFIQLLSQSPDGVLDLNRAAEVLKVKRRIYDITNVLEGIHLIKKSKNNVQWMCGLSEDDGMLAQCGLSKEVTELSQEEKKLDELIO SCTLDLKLLTEDSENORLAVVT 292
gi|109504877|ref|XP_214476.4| QMP-----STPVYVPRDAS-----IR-----GCSLSEDDGMLAQCGLSKEVTELSQEEKKLDELIO SCTLDLKLLTEDSENORLAVVT 98
gi|118086362|ref|XP_418915.2| KTPKGGRAALRSPD SPKTPKSPSEKTRYDTSLSGLLTKKFIQLLSQSPDGVLDLNRAAEVLKVKRRIYDITNVLEGIHLIKKSKNNI QWMCGLSEDDGMMARQGLTKEVTELTQEEKKLDELIO SCTLDLKLLTEDSENORLAVVT 289
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|4503433|ref|NP_001940.1| YDIRKISGLKDOTVIVVKAPPETRLVDPDIESLQIHLASTQGPIEVYLCPEETEHRPMTNNDHNGNIPKPTSKDLASTNSGHSDCSVSMANLSPLASPANLLQOTEDQIPSNLEGPFFVNLPPLLQEDYLLSLGEEEGISDLFDA 450
gi|76663083|ref|XP_614932.2| YDIRKISGLKDOTVIVVKAPPETRLVDPDIESLQIHLASTQGPIEVYLCPEETEHRPMTNNDHNGNIPKPTSKDLASTNSGHSDCSVSMANLSPLASPANLLQOTEDQIPSNLEGPFFVNLPPLLQEDYLLSLGEEEGISDLFDA 448
gi|83523736|ref|NP_034223.1| YDIRKISGLKDOTVIVVKAPPETRLVDPDIESLQIHLASTQGPIEVYLCPEETEHRPMTNNDHNGNIPKPTSKDLASTNSGHSDCSVSMANLSPLASPANLLQOTEDQIPSNLEGPFFVNLPPLLQEDYLLSLGEEEGISDLFDA 442
gi|109504877|ref|XP_214476.4| YDIRKISGLKDOTVIVVKAPPETRLVDPDIESLQIHLASTQGPIEVYLCPEETEHRPMTNNDHNGNIPKPTSKDLASTNSGHSDCSVSMANLSPLASPANLLQOTEDQIPSNLEGPFFVNLPPLLQEDYLLSLGEEEGISDLFDA 248
gi|118086362|ref|XP_418915.2| YDIRKISGLKDOTVIVVKAPPETRLVDPDIEVALIHLSSSTQGPIEVYLCPEENDALSPMKTYSQDHNGNISKITISKEVASVNSGQDCSVNMATISPLASPANLLQOTEDQIPSNLEGPFFVNLPPLLQEDYLLSLGEEEGISDLFDA 439
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|4503433|ref|NP_001940.1| YDLEKLP-LVEDFMCS 465
gi|76663083|ref|XP_614932.2| YDLEKLP-LVEDFMCS 463
gi|83523736|ref|NP_034223.1| YDLEKLP-LVEDFMCS 457
gi|109504877|ref|XP_214476.4| YDLEKLP-LVEDFMCS 263
gi|118086362|ref|XP_418915.2| YDLEKLP-LVDEFIYS 455
.....460.....

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