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gi|31543509|ref|NP_032949.2| MASPE---CFHSEDESLKGCCEMIVQKHGICQVLKCEIVHLVCAKPRDRPLRFLREHFELKEEENRQILAROKSNSQCDSDHDEEISPTPPNPVVKARRRRGGVSAEVYTEEDAVSYVRKVIIPKDYKMTALAKAISKNVLFSHLDDNE 145
gi|76096308|ref|NP_001028851.1| -MSPQ---IMCV---SVCGEGMGWDVVEISQSHAEG---CAQTTG-----LEENRQILAROKSNSQCDSDHDEEISPTPPNPVVKARRRRGGVSAEVYTEEDAVSYVRKVIIPKDYKMTALAKAISKNVLFSHLDDNE 122
gi|38257139|ref|NP_002726.1| MASPE---ACPSSEDESLKGCCELVVQLHGICQVLKDCIVHLVCIKPERPMKFLREHFELKEEENRQILAROKSNSQSDSHDDEISPTPPNPVVKARRRRGGVSAEVYTEEDAVSYVRKVIIPKDYKMTALAKAISKNVLFPAHLDDNE 145
gi|50755469|ref|XP_414754.1| MAAS---SCSVEEESLKGCELVQKHNIQQLKCEIVNLCIAKPRPMKFLREHFELKEEENRQILAROKSSQSDSHDDEISPPPPNPVVKARRRRGGVSAEVYTEEDAVSYVRKVIIPKDYKMTALAKAISKNVLFPAHLDDNE 145
gi|115495407|ref|NP_001070091.1| -MATS---SSNLEEESLKGCEVQKHNIQQLKCEIVNLCIAKPERPMKFLREHFELKEEENRQIMAROKSNSQSDSHDDEISPPPPNPVVKARRRRGGVSAEVYTEEDAVSYVRKVIIPKDYKMTALAKAISKNVLFPAHLDDNE 144
gi|73958238|ref|XP_856004.1| MASQS---SYQVEEESLKECELVQKHGICQVLKDCIVHLVCIKPRPMKFLREHFELKEEENRQITGGRS-AVPPSDSHDDEISPTPPNPVVKARRRRGGVSAEVYTEEDAVSYVRKVIIPKDYKMTALAKAISKNVLFPAHLDDNE 144
gi|133901990|ref|NP_001076771.1| MNYSGLDVFMSGGNEEDQLAQCQAVVQRHNIQQLVKEAIVVLCIHKPDNPVLFKDHFEKLENEQRAE---GGNPDAAADDDIIVEPPK---RSGGRRRTGISAEPIKEDD-TEYKVVVTPKDADARRSLESAMRKNLLFAHLEED 140
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|31543509|ref|NP_032949.2| RSDIFDAMFPVTHIGGETVIQQNEGDNFYVIDQGEVDVYVNGEWWNIIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYEEFLSKVSILESLEKWERLTVADALEPVQFEDGEKIVVQGEPGDDFFYII 295
gi|76096308|ref|NP_001028851.1| RSDIFDAMFPVTHIGGETVIQQNEGDNFYVIDQGEVDVYVNGEWWNIIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYEEFLSKVSILESLEKWERLTVADALEPVQFEDGEKIVVQGEPGDDFFYII 272
gi|38257139|ref|NP_002726.1| RSDIFDAMFPVTHIGGETVIQQNEGDNFYVIDQGEVDVYVNGEWWNIIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYEEFLSKVSILESLEKWERLTVADALEPVQFEDGEKIVVQGEPGDDFFYII 295
gi|50755469|ref|XP_414754.1| RSDIFDAMFPVTHIGGETVIQQDEGDNFYVIDQGEVDVYVNGEWWTSIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYEEFLSKVSILESLEKWERLTVADALEPVQFEDGEKIVVQGEPGDDFFYII 295
gi|115495407|ref|NP_001070091.1| RSDIFDAMFPVTHIGGETVIQQDEGDNFYVIDQGEVDVYVNGEWWTSIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYEEFLSKVSILESLEKWERLTVADALEPVQFEDGEKIVVQGEPGDDFFYII 294
gi|73958238|ref|XP_856004.1| RSDIFDAMFPVTHIGGETVIQQDEGDNFYVIDQGEVDVYVNGEWWTSIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYEEFLSKVSILESLEKWERLTVADALEPVQFEDGEKIVVQGEPGDDFFYII 294
gi|133901990|ref|NP_001076771.1| QKTMVDAMFPVEKSAGETIIEQGEEDNFYVIDKGTVDVYVNGEYVLTINIEGGSFGEALALIYGT PRAATVKAATDLKLGIDRDSYRRILMGSTLRKRKMYDEFLSKVQILADLDQWERANVADALERCDFEPGTHVVEQGPGEFFYII 290
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|31543509|ref|NP_032949.2| TEGTASVLQRRSPNEEYVEVGRGLGSDYFGEIALLLRPRAATVVARGPLKCKVLDLDRPRFRERVLGPCPEIILKRNIIQRYSFISLTV 381
gi|76096308|ref|NP_001028851.1| TEGTASVLQRRSPNEEYVEVGRGLGSDYFGEIALLLRPRAATVVARGPLKCKVLDLDRPRFRERVLGPCSEIILKRNIIQRYSFISLTV 358
gi|38257139|ref|NP_002726.1| TEGTASVLQRRSPNEEYVEVGRGLGSDYFGEIALLLRPRAATVVARGPLKCKVLDLDRPRFRERVLGPCSEIILKRNIIQRYSFISLTV 381
gi|50755469|ref|XP_414754.1| TEGTASVLQRRSDNEEYVEVGRGLGSDYFGEIALLLRPRAATVVARGPLKCKVLDLDRPRFRERVLGPCSEIILKRNIIQRYSFISLTV 381
gi|115495407|ref|NP_001070091.1| TEGTASVLQRRSDNEEYVEVGRGLGSDYFGEIALLLRPRAATVVARGPLKCKVLDLDRPRFRERVLGPCSEIILKRNIIQRYSFISLTV 380
gi|73958238|ref|XP_856004.1| TEGTASVLQRRSPNEEYVEVGRGLGSDYFGEIALLLRPRAATVVARGPLKCKVLDLDRPRFRERVLGPCSEIILKRNIIQRYSFISLTV 380
gi|133901990|ref|NP_001076771.1| LEGEANVLQKRSDDAFVGVHLGMSDYFGEIALLLRPRAATVVARVTHLKCITLDRNFRERVMGPRVEIILKRDVSNVNSYVRLMT 376
.....310.....320.....330.....340.....350.....360.....370.....380.....

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