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gi|5454086|ref|NP_006298.1|  -MGSPARRPALLLLLP LLLLLLLRVPSPRSFPGSGDSPLEDDEVGYS--HPRYKDTWPCSP I KVKYGDVYCRAPGGYKKTALGTRCDIRCKQGYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPANGGFKCVDGAFNSRCEYY 150
gi|94966791|ref|NP_001035579.1| -MGSPALRPALLLLLP-----LLLRVPPSRGFPGSGDSPLEDDEVVYS--DAKYKDIWPCSP I KVKYGDVYCRAPGGYKKTALGTRCDIRCKQGYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPVNGGFKCIDGAFNSRCEYY 150
gi|8394362|ref|NP_058607.1|  -MGSPGLRPELLLPQVLLP LLLALLHLVLPSPGFPGSGDSPLEDDGVWYS--HSLYKDTWPCSP I KVKYGDVYCRAPPGGYKKTALGTRCDIRCKRKYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPANGGFKCVDGAFNSRCEYY 150
gi|11993952|ref|NP_071969.1|  -MGSPGLRPTLLLPQVLLP LLLALLHLVLPSPGFPGSGDSPLEDDGVWYS--HSLYKDTWPCSP I KVKYGDVYCRAPPGGYKKTALGTRCDIRCKRKYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPANGGFKCVDGAFNSRCEYY 150
gi|114688164|ref|XP_521003.2|  ---MPSHYTSQATPLG-----PQDTSHSGSGDSPLEDDEVGYS--HPRYKDTWPCSP I KVKYGDVYCRAPGGYKKTALGTRCDIRCKQGYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPANGGFKCVDGAFNSRCEYY 150
gi|74007287|ref|XP_548948.2|  MAHAPRSRTAQPGR-----QPGSRRRGLLFSALGSLLPALGSGSAPHRLCDTPWPCSP I KVKYGDVYCRAPGGYKKTALGTRCDIRCKRKYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPANGGFKCVDGAFNSRCEYY 150
gi|118084013|ref|XP_416781.2|  -----MPLSCIQE-----GRETWPCSP I KVKYGNVYCRAPPGGYKKTALGTRCDIRCKQGYELHGSLLIQCQSNKRWSDKVICQKRCPTLAMPANGGFKCIDGAFNSRCEYY 150
gi|62122833|ref|NP_001014348.1|  ---MDTWMCVYMIYV-----TQLSGSFAYVPGSYWYPTDDE-----DVRTYTGVPWCAPVVYKKGHVGCQTPRGERIKYVNLGARCIRCKTGYELHGSSEIVCMASKQWGNACREVRCPKLNLPANGGFKCIDGAFNSRCEYY 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|5454086|ref|NP_006298.1|  CSPGYTLKGERIVT CMDNKAWSGRPAS CVDMEPPRIKCP SVKERIAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCGKLNAPENGYMKCSSDGDNYGATCFEFCIGGY 300
gi|94966791|ref|NP_001035579.1| CSPGYTLKGEQIVR CMDNKAWSGQPAT CVDLEPPRIKCP SVKERVAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCGKLNAPENGYMKCSSDGDNYGATCFEFCIGGY 300
gi|8394362|ref|NP_058607.1|  CSPGYTLKGERIVT CMDNKAWSGRPAS CVDLEPPRIKCP SVKERIAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCGKLNAPENGYMKCSSDGDNYGATCFEFCIGGY 300
gi|11993952|ref|NP_071969.1|  CSPGYTLKGERIVT CMDNKAWSGRPAS CVDMEPPRIKCP SVKERIAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCGKLNAPENGYMKCSSDGDNYGATCFEFCIGGY 300
gi|114688164|ref|XP_521003.2|  CSPGYTLKGERIVT CMDNKAWSGRPAS CVDMEPPRIKCP SVKERIAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCGKLNAPENGYMKCSSDGDNYGATCFEFCIGGY 300
gi|74007287|ref|XP_548948.2|  CSPGYTLKGERIVT CMDNKAWSGRPAS CVDMEPPRIKCP SVKERIAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCGKLNAPENGYMKCSSDGDNYGATCFEFCIGGY 300
gi|118084013|ref|XP_416781.2|  CSPGYTLKGERIVT CMDNKAWSGRPAS CVDTEPPRIKCP SVKEKIAEPNKLTVRVSWETPEGRD TADGIL TDVILKGLPPGSHFP EGDHKI QYTVYDRAENKGTCKFRVKVR--VRCVKLVPDNGYIKCSGDGNYGATCFEFCIGGY 300
gi|62122833|ref|NP_001014348.1| CSPGYTLTGDHSAICQSSRTWSGGNSV CNDVDPVVIKCP NVKEKTAEPGKLTARVTDWTEPGKDAADGIL TDVILKGLPPGSHFP EGNHKLSTVTFDRAENKATCRFNVVR--VRCVPLSVFDNGWMKCDAGDNYGATCFEFCIGGY 300
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gi|5454086|ref|NP_006298.1|  ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLOLGMLQQAQCGLDLRHIVVELVGVFPFLIGRIGAKIMPALALQRLLLRIPLYSFSMVLVDKHHGMDKERYVSLVMPVAFNLIDT 450
gi|94966791|ref|NP_001035579.1| ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLOLGMLQQAQCGLDLRHIVVELVGVFPFLIGRIGAKIMPALALQRLLLRIPLYSFSIVVLDKHHGMDKERYVSLVTPVAFNLIDT 450
gi|8394362|ref|NP_058607.1|  ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLOLGMLQQAQCGLDLRHIVVELVGVFPFLIGRIRAKIMPALALQRLLLRIPLYSFSMVLVDKHHGMDKERYVSLVTPMALFNLIDT 450
gi|11993952|ref|NP_071969.1|  ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLOLGMLQQAQCGLDLRHIVVELVGVFPFLIGRIRAKIMPALALQRLLLRIPLYSFSMVLVDKHHGMDKERYVSLVTPMALFNLIDT 450
gi|114688164|ref|XP_521003.2|  ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLOLGMLQQAQCGLDLRHIVVELVGVFPFLIGRIGAKIMPALALQRLLLRIPLYSFSMVLVDKHHGMDKERYVSLVMPVAFNLIDT 450
gi|74007287|ref|XP_548948.2|  ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTARNLLYRLOLGMLQQAQCGLDLRHIVVELVGVFPFLIGRIGAKIMPALALQRLLLRIPLYSFSIVVLDKHHGMDKERYVSLVMPVAFNLIDT 450
gi|118084013|ref|XP_416781.2|  ELQGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTAANFFYRMLQGMQPAQCGLDLRHIVVELVGVFPFLIGRIGAKIMPALALQRLLLRIPLYSFSMVLVDKHHGMDKERYVSLVMPVAFNLIDT 450
gi|62122833|ref|NP_001014348.1| DLKGSARVCQSNLAWSGTEPTCAAMNVNVGVRTAAALLDQFYEKRRLLIVSTPTAANFFYRMLQGMQPAQCGLDLRHIVVELVGVFPFLIGRIRHRIIAPLALQRLLLRIPLYSFSMVLVDKHHGMDKERYVSLVMPVAFNLIDT 450
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gi|5454086|ref|NP_006298.1|  FPLRKEEMVLQAEMSGTCNT 470
gi|94966791|ref|NP_001035579.1| FPLRKEEMVLQAEMSGTCNT 470
gi|8394362|ref|NP_058607.1|  FPLRKEEMVLQAEMSGTCNV 470
gi|11993952|ref|NP_071969.1|  FPLRKEEMVLQAEMSGTCNT 470
gi|114688164|ref|XP_521003.2|  FPLRKEEMVLQAEMSGTCNT 470
gi|74007287|ref|XP_548948.2|  FPLRKEEMVLQAEMSGTCNT 470
gi|118084013|ref|XP_416781.2|  FPLRKEEMVLQAEMSGTCNT 470
gi|62122833|ref|NP_001014348.1| IPLRTEEMVLQAEMSGTCNT 470
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