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                                  ***: .***:.*** **:**********:***:***.***:*:*:****:**:*: *:**:************.*.******** ****::* **:**:*******.:*.**: *** **::::::  *::::********: *****
gi|225543097|ref|NP_001139411.1| MSGE-ENPASKPTPVQDVQGDGRWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDGTQHVLWRLENGELEHIRPKIVVVWVGTNNHGHTAEQVTGGIKAIVQLVNERQPQARVVVLGLLPRGQHPNPLR   150
gi|114677535|ref|XP_001154079.1| MSGE-ENPASKPTPVQDVQGDGRWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDGTQHVLWRLENGELEHIRPKIVVVWVGTNNHGHTAEQVTGGIKAIVQLVNERQPQARVVVLGLLPRGQHPNPLR   150
gi|27807201|ref|NP_777090.1|     MSGD-ENPASKPTPVQDVQGDGRWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDSTQHVLWRLENGELEHIRPKIVVVWVGTNNHGHTAEQVTGGIKAIVQLVNERQPQARVVVLGLLPRGQHPNPLR   150
gi|6679201|ref|NP_032802.1|      MSGEGENPASKPTPVQDVQGDGRWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDSTQHVLWRLENGELEHIRPKIVVVWVGTNNHSHTAEQVTGGIKAIVQLVNKLQPQARVVVLGLLPRGQHPNPLR   150
gi|16758470|ref|NP_446106.1|     MSGEGENPASKPTPVQDVQGDGRWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDSTQHVLWRLENGELEHIRPKIVVVWVGTNNHSHTAEQVTGGIKAIVQLVNKLQPQARVVVLGLLPRGQHPNPLR   150
gi|57036489|ref|XP_533656.1|     MSGE-ENPASKPTPVQDVQGDGRWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGSDSTQHVLWRLENGELEHIRPKIVVVWVGTNNHGHTAEQVTGGIKAIVQLVNQRQPQARVVVLGLLPRGQHPNPLR   150
gi|41055008|ref|NP_957352.1|     MSGD-SNPAATPTPCQDIQGDGRWMSLHNRFVSDSKGKEPDVLFVGDSLIQLLHEFEVWRKLFSPLHALNFGIGGDATQHVLWRLINGELDYISPKVVVLWVGTNNHGQTPEQICGGIMAIINVIHQKLPNSHTLVLGLLPRGKSPNPLR   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                  *:*  ** **:* :*. .:. **: *********:*:*:********:  .*  **..**. *  ** :.      *
gi|225543097|ref|NP_001139411.1| EKNRQVNELVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLLAQDQGQG-APLLEPAP-----   238
gi|114677535|ref|XP_001154079.1| EKNRQVNELVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLLAQDQGQG-APLLEPAP-----   238
gi|27807201|ref|NP_777090.1|     EKNRRVNELVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLLTQDQGQGGAPLPEPSP-----   238
gi|6679201|ref|NP_032802.1|      EKNRQVNELVRAALAGYPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLLAQDQGQG-IPLPETAS-----   238
gi|16758470|ref|NP_446106.1|     EKNRQVNELVRAALAGYPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLLAQDQGQG-IPLPETAP-----   238
gi|57036489|ref|XP_533656.1|     EKNRRVNELVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLLAQDQGQG-IPLPEATP-----   238
gi|41055008|ref|NP_957352.1|     ERNASVNALVQAEVASLSHVSFLNMDPGFVHSDGSIAHQDMYDYLHLTPHAYQRVCEPLHEHLKSLLEKH-----AP----------   238
                                  .......160.......170.......180.......190.......200.......210.......220.......230........
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