

gi | 31981160 | ref | NP_080116.2 | MNKHQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 92
gi | 19705527 | ref | NP_599229.1 | MNKHQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 92
gi | 7661744 | ref | NP_054757.1 | MNKHQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 92
gi | 73975929 | ref | XP_532484.2 | MNKHQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 92
gi | 194666218 | ref | XP_584557.4 | MNKHQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 92
gi | 114612501 | ref | XP_518982.2 | MCSIALAFWGVORPQVVAETGAVREAGLRVPCVYVNVSEVLHSSIVCRRCCCCCCCCRCRCTNRRSPQPCASSLPPR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 150
gi | 57530697 | ref | NP_001006358.1 | MNKHQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 92
gi | 41055484 | ref | NP_957212.1 | MNTGKQKQKPVLTG QRFKTRKR DEKEKFEPTVFRDILVQGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDLILVAGSMLAPGGTRIDDDGDKTK 94
gi | 18421544 | ref | NP_568534.1 | MSSKEKPLGG TRIKTRKR NIAAPLDPAAFSDAVVQIYHDNAGDELVAKSIESS--DLNFRYGDIFFEVIFIGGRIQPGTVKSD---GE 87
gi | 18408228 | ref | NP_564845.1 | MSSKEKPLGG TRIKTRKR NIAAPLDPAAFSDAVVQIYHDNAGDELVAKSIESS--DLNFRYGDIFFEVIFIGGRIQPGTVKSD---GE 87
gi | 115485233 | ref | NP_001067760.1 | MSSKEKPLGG QRIKTRKR NIAAPLDPAAFSDAVVQIYHDNAGDELVAKSIESS--DLNFRYGDIFFEVIFIGGRIQPGTVKSD---GE 88
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 31981160 | ref | NP_080116.2 | MTNHCVFSANEDHETIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLGN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 239
gi | 19705527 | ref | NP_599229.1 | MTNHCVFSANEDHETIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLGN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 239
gi | 7661744 | ref | NP_054757.1 | MTNHCVFSANEDHETIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLGN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 239
gi | 73975929 | ref | XP_532484.2 | MTNHCVFSANEDHETIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLGN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 239
gi | 194666218 | ref | XP_584557.4 | MTNHCVFSANEDHETIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLGN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 239
gi | 114612501 | ref | XP_518982.2 | MTNHCVFSANEDHETIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLGN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 297
gi | 57530697 | ref | NP_001006358.1 | MTRHCVFFAEDHDAIRNYA QVFNKLIIRRYKYLEKAFEDMKL LLLFLKAFSEAEQTKLAML SGILLAN GILPATILTSLFTDSLVEKIGIAASFAVKLFKAWMAEKDANSVTSALRKANLDKRLLLELFPVNRQSVDFHFAKYFDDAGL 239
gi | 41055484 | ref | NP_957212.1 | VTHQCVFNAEENHTIRNSYA QVFNKLIIRRYKYLEKAFEEBTK LLLLLKGFTESEQTKLAML TGVLLAN GILPPPILTSLFTSDNLVKEGISAFAVKMFKAWEKDNANVTALRKANLDKRLLLELFPANKQNVHFTRKFFTEAGL 241
gi | 18421544 | ref | NP_568534.1 | RHTVSVIDCEPKREAILPSVVIYQKILRRKFLIKNENLVTRRFLOSLLEFENERRKLAIFALAFSQKLSGLPETVFPQLKDLVAKGIVLNFVDFEFNYLVNSLDDLIILRRGKMDNLMDFLPPRRSAESFAEHFNEGL 237
gi | 18408228 | ref | NP_564845.1 | RHPYSIIDCEPKREAILPSVVIYQKILRRKFLIKNENLVTRRFLOSLLEFENERRKLAIFALAFSQKLSGLPETVFPQLKDLVAKGIVLNFVDFEFNYLVNSLDDLIILRRGKMDNLMDFLPPRRSAESFAEHFNEGL 237
gi | 115485233 | ref | NP_001067760.1 | RHPYSVLDCAQRRAILPSVVIYQKILRRRPFILKNLNVTRRFLOSLLEFENERRKLAIFALAFSQKLSGLPETVFPQLKDLVAKGIVLNFVDFEFNYLVNSLDDLIILRRGKMDNLMDFLPPRRSAESFAEHFNEGL 238
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 31981160 | ref | NP_080116.2 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 388
gi | 19705527 | ref | NP_599229.1 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 388
gi | 7661744 | ref | NP_054757.1 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 388
gi | 73975929 | ref | XP_532484.2 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 388
gi | 194666218 | ref | XP_584557.4 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 388
gi | 114612501 | ref | XP_518982.2 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 446
gi | 57530697 | ref | NP_001006358.1 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVAEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 388
gi | 41055484 | ref | NP_957212.1 | KELSDFLRVQOQLGTRKELQKELQERLSQEQPIKEVVLVYKKEEMKRNLDLPETAVIGLLWTCIMNAVEWN KKEELVTEQALKHLKQYAPLLAVFSSQGOSELVLLQVQYCYDNIHFMKAFQKIVVLFYKADVLSSEAILKWKYKAHAA 390
gi | 18421544 | ref | NP_568534.1 | TDLVEYHSKMFVVKLEIKTILTSKVTESNVDEVIESVKQIKDAKLPDIEVVRVVDGLMDAVQNSGKNQOQNANSVLRQVKTWAPLLNFCISGKLELELMYKVMQCYEDAKLMKVFPEVVRSLYELDLVAEDTILHWFRKGTN 387
gi | 18408228 | ref | NP_564845.1 | TALVEYNERKIFEVKLEIKTILTSKVTESNVDEVIESVKQIKDAKLPDIEVVRVVDGLMDAVQNSGKNQOQNANSVLRQVKTWAPLLNFCISGKLELELMYKVMQCYEDAKLMKVFPEVVRSLYELDLVAEDTILHWFRKGTN 387
gi | 115485233 | ref | NP_001067760.1 | TSLVEYNEKMFVVKLEIKLTLTTMINEAEISVTEAVKQVQKDAKLPDIEVVRVVDGLMEAVQNSGKNQOQNANSVLRQVKTWAPLLNFCISGRLLELELYKVMQCYEDAKLMKVFPEVVRSLYELDLVAEDTILHWFRKGTN 388
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 31981160 | ref | NP_080116.2 | KGKSVFLDOMKKFVWELQNAEESESEGEES 419
gi | 19705527 | ref | NP_599229.1 | KGKSVFLDOMKKFVWELQNAEESESEGEES 419
gi | 7661744 | ref | NP_054757.1 | KGKSVFLDOMKKFVWELQNAEESESEGEEN 419
gi | 73975929 | ref | XP_532484.2 | KGKSVFLDOMKKFVWELQNAEESESEGEEN 419
gi | 194666218 | ref | XP_584557.4 | KGKSVFLDOMKKFVWELQNAEESESEGEEN 419
gi | 114612501 | ref | XP_518982.2 | KGKSVFLDOMKKFVWELQNAEESESEGEEN 477
gi | 57530697 | ref | NP_001006358.1 | KGKSVFLDOMKKFVWELQNAEESESEFRI---- 414
gi | 41055484 | ref | NP_957212.1 | KGKSVFLDOMKKFVWELQNAEESESEGEED 421
gi | 18421544 | ref | NP_568534.1 | KGRQTFVKSLEFPFNWLEEAEBEE----- 411
gi | 18408228 | ref | NP_564845.1 | KGRQTFVKSLEFPFNWLEEAEBEE----- 411
gi | 115485233 | ref | NP_001067760.1 | KGRQSFVKALEFPFNWLEEAEBEE----- 412
.....460.....470.....480.....

