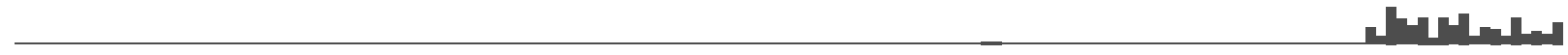


gi | 21450061 | ref | NP_659099.1 |MVLKRMHRPRCCSYQLVFE 19
gi | 11067419 | ref | NP_067722.1 |MVLKRMHRPRCCSYQLVFE 19
gi | 148747859 | ref | NP_001092001.1 |MKVGVWPGEGSCWVGLAVEDSPALGAPRVGALPDVVPEGLLLMVLRRMHRPRCCSYQLLLE 61
gi | 114645065 | ref | XP_522596.2 |MVLRRMHRPRCCSYQLLLE 19
gi | 73997018 | ref | XP_543717.2 | MGVRRSRISSGSRRESIASCWEVAGIIPWRPRAVGGAEVQRGPGRKADVGRPAGRPRAPDRQAPVKVFLSLPRLLAALQHLRLTSPEDCEEVVGWPGESRWVGLAVEDSPALGASVGGGLPDVVPEGLLLMVLKRMHRPRCCSYQLLLE 150
gi | 122692463 | ref | NP_001073771.1 |MKVGVWPGEGRWVGLAVEGDSILGAPPLGGLPDVVPEGLLLMVLRRMHRPRCCSYQLLLE 61
gi | 125852968 | ref | XP_001343240.1 |MTERFTWPGSADSVSGHTLSKMLLMEN-----AEVSDQTGWITVDVASFWTEKIG--SILH 56
gi | 118129647 | ref | XP_424494.2 |MPGCREPREEDEEE-----DEEEEGVQEGQLGMEGPEFCRAPSQR 44



gi | 21450061 | ref | NP_659099.1 | HR-RPSCIOGLRWTPPLNSGSLDFRVSLAQAT---TEHVHKAGKLLHRHLLATYPTLIRDRKYHLRLYRHCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWTFQDRDAQFYRFPGPEPEP---AGTQDVEEEL 159
gi | 11067419 | ref | NP_067722.1 | HR-RPSCIOGLRWTPPLNSGSLDFRVSLAQAT---TEHVHKAGKLLHRHLLATYPTLIRDRKYHLRLYRHCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWTFQDRDAQFYRFPGPEPEP---AGTQDVEEEL 159
gi | 148747859 | ref | NP_001092001.1 | HQ-RPSCIOGLRWTPPLNSGSLDFRVSLAQAS---TERVLRAGROLHRHLLACPNLIRDRKYHLRLYRCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWAFQDRDAQFYRFPGPEPEP---VGHMEBEEL 201
gi | 114645065 | ref | XP_522596.2 | HQ-RPSCIOGLRWTPPLNSGSLDFRVSLAQAS---TERVLRAGROLHRHLLACPNLIRDRKYHLRLYRCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWAFQDRDAQFYRFPGPEPEP---VGHMEBEEL 159
gi | 73997018 | ref | XP_543717.2 | HQ-RPSRIIOGLRWTPPLNSGSLDFRVSLAQAS---TERVLRAGROLHRHLLASPTLIRDRKYHLRLYRCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWTFQDRDQFYRFPGPEPEP---AGVHEBEEL 290
gi | 122692463 | ref | NP_001073771.1 | HQ-RPSCIOGLRWTPPLNSGSLDFRVSLAQAS---AERVLRAGROLHRHLLACPNLIRDRKYHLRLYRCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWAFQDRDQFYRFPGPEPEP---VGHMEBEEL 201
gi | 125852968 | ref | XP_001343240.1 | GS-EGNYITVDRAGOGASKKGQTSPPSATSTLNKSLFDRILKAARVVVSTLMEGNPLIRDRKHHLKTYRCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWAFQDRDQFYRFPGPEPEP---VGHMEBEEL 205
gi | 118129647 | ref | XP_424494.2 | PPPAPVCTRRCCQPLLDASSISLDYGHSLITQIWN---RAGKLLTYLTSISPLIRDRKHHLRHRCCS GRELVG DILALGLGVHSRSQAVGICQVLLDEGALCHVKHDWAFQDRDQFYRFPGPEPEP---PRVGLRDAEEL 182



gi | 21450061 | ref | NP_659099.1 | VEAMALLSQRGPDALLVALRKPPGQRTDEELDLIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 309
gi | 11067419 | ref | NP_067722.1 | VEAMALLSQRGPDALLVALRKSPGQRTDEELDLIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 309
gi | 148747859 | ref | NP_001092001.1 | AEAVALLSQRGPDALLVALRKPPGQRTDEELDLIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 351
gi | 114645065 | ref | XP_522596.2 | AEAVALLSQRGPDALLVALRKPPGQRTDEELDLIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 309
gi | 73997018 | ref | XP_543717.2 | VEAVALLSQRGPDALLVALRKPPGQRTDEELDLIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 440
gi | 122692463 | ref | NP_001073771.1 | VEALALLSQRGPDALLVALRKPPGQRTDEELDLIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 351
gi | 125852968 | ref | XP_001343240.1 | QESLSLLIQMGPDALLMILIRKCPSPRTPEDELEVIYBEELHIIKAVAHLSVSKRELASVLFESHAKAGTVLFSQGDGKTSWYIWRGVSNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 355
gi | 118129647 | ref | XP_424494.2 | LEAVTFLAQLGPDALLMALARKPPAQRTEDELELIFEELHIIKAVAHLSNSVKRELAAVLLFEPHSHKAGTVLFSQGDGKTSWYIWKGSVNVVTHGKGLVTLHEGDDFGQLALVNDAPRAAIIILRENNCHFLRVKQDFNRIIKDVEA 332



gi | 21450061 | ref | NP_659099.1 | KIMRLEEKGKVVVLVLERISQAGPSRPPTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEPADPAGGSEQEHSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 459
gi | 11067419 | ref | NP_067722.1 | KIMRLEEKGKVVVLVLERISQAGPSRPPTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEPEPAGGSEQERSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 459
gi | 148747859 | ref | NP_001092001.1 | KIMRLEEKGKVVVLVLERASQAGPSRPPTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEP---AGGSEQERSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 498
gi | 114645065 | ref | XP_522596.2 | KIMRLEEKGKVVVLVLERASQAGPSRPPTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEP---AGGSEQERSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 456
gi | 73997018 | ref | XP_543717.2 | KIMRLEEKGKVVVLVLERASQAGPSRPPTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEP---AGGSEQERSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 587
gi | 122692463 | ref | NP_001073771.1 | KIMRLEEKGKVVVLVLERISQAGPSRPPTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEP---AGGSEQERSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 498
gi | 125852968 | ref | XP_001343240.1 | NIVRLLEEKGKVVVLVLEK---AQDTPGRRNYTVMSGTPEKILELLEAMRPDSSAHDPTETFLSDFLLTHSVFMPCTOLFALLHHFHFVEP---AGGSEQERSTYICNKROQILRLVGRWVALVSPMLHSDPVATSFLOKLSDLVG 496
gi | 118129647 | ref | XP_424494.2 | NIMRLEEKGKVVVLVLEK---LQGG---SEGSDELEKAAVALNTRKRVVVLVCHWVALVSPMLHSDPVATSFLOKLSDLVG 361



gi | 21450061 | ref | NP_659099.1 | RDARLSNLLREQYVERRRHRLLENGCGNVSPQTKARNAPVWLPNQDEPLPSSAGAIRVGDVYDICTRPHDSVLTLLHLPVTAASVREVMAALAHEDHWKGGVQVVKVNSAGDAIGLQPDARGVATSLGLNERLRFVVPQEVHELTPHPEQL 609
gi | 11067419 | ref | NP_067722.1 | RDTRLSNLLREQYVERRRHRLLENGCGNVSPQTKARNAPVWLPNQDEPLPSSAGAIRVGDVYDICTRPHDSVLTLLHLPVTAASVREVMAALAHEDHWKGGVQVVKVNSAGDAIGLQPDARGVATSLGLNERLRFVVPQEVHELTPHPEQL 609
gi | 148747859 | ref | NP_001092001.1 | RDTRLSNLLREQVWERRRHRLLENGCGNASPMKARNLPVWLPNQDEPLPSSAGAIRVGDVYDICTRPHDSVLTLLHLPVTAASVREVMAALAHEDGWKGGVQVVKVNSAGDAIGLQPDARGVATSLGLNERLRFVVPQEVHELTPHPEQL 648
gi | 114645065 | ref | XP_522596.2 | RDTRLSNLLREQVWERRRHRLLENGCGNASPMKARNLPVWLPNQDEPLPSSAGAIRVGDVYDICTRPHDSVLTLLHLPVTAASVREVMAALAHEDGWKGGVQVVKVNSAGDAIGLQPDARGVATSLGLNERLRFVVPQEVHELTPHPEQL 606
gi | 73997018 | ref | XP_543717.2 | RDTRLCILNLLREQVWERRRHRLLENGCGNASPMKARNLPVWLPNQDQPLCSNRAIRVGDVYDICTRPHDSVLTLLHLPVTAASVREVMAALAHEDGWKGGVQVVKVNSAGDAIGLQPDARGVATSLGLNERLRFVVPQEVHELTPHPEQL 737
gi | 122692463 | ref | NP_001073771.1 | RDTRLSNLLREQVWERRRHRLLENGCGNASPMKARNLPVWLPNQDEPLPSSAGAIRVGDVYDICTRPHDSVLTLLHLPVTAASVREVMAALAHEDGWKGGVQVVKVNSAGDAIGLQPDARGVATSLGLNERLRFVVPQEVHELTPHPEQL 648
gi | 125852968 | ref | XP_001343240.1 | ADSRLSSMLRQLRDRRKTIMENGCHTLL---KLNQKFDWFSAYEPPVG-KLRSIKAQDKVLYEIFRPDHEKAVTVMLPDAVNDILITLVDPP---RNIVLVKMNSSGDRVQLKLETTAVSASLGNERLRFVVPQEVHELTPHPEQL 639
gi | 118129647 | ref | XP_424494.2 |RSSRMENGDGSISSPKRSSMSWLSQDEAALSSSCALRAHDKVPEVYRADHSCLVTVLPVNASVRRVQLSLPQLGWDGEHLLVKNVNSAGDKVGLQLDVAVFTSLGLNERLRFVVPQEVHELTPHPEQL 494



