

gi | 7305031 | ref | NP_038841.1 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 150
gi | 16758808 | ref | NP_446379.1 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 145
gi | 32490572 | ref | NP_036439.2 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 142
gi | 114672351 | ref | XP_512036.2 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 142
gi | 194678110 | ref | XP_870774.3 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 144
gi | 118086838 | ref | XP_419142.2 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 144
gi | 73961950 | ref | XP_537321.2 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 144
gi | 51571933 | ref | NP_001003987.1 | MTTESGSDSESKPDQEAEPQEAAGPQQAAGAPGPEPAGGNSLNGEKQPALEQFPEAAAHSTPVKREIGDKDRDFAAAAKOLEYQOFEDDKLSQRSSSSKLSRSPKIVKRPKSMOCKVILLDGEYCDVDKRSRGQVLFDKVCEH 122
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 7305031 | ref | NP_038841.1 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 300
gi | 16758808 | ref | NP_446379.1 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 295
gi | 32490572 | ref | NP_036439.2 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 292
gi | 114672351 | ref | XP_512036.2 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 292
gi | 194678110 | ref | XP_870774.3 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 294
gi | 118086838 | ref | XP_419142.2 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 294
gi | 73961950 | ref | XP_537321.2 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 294
gi | 51571933 | ref | NP_001003987.1 | LNLLEKDYFGLTYRDAENCKNWLDPKAEIKKQIRSGAWHFSFNVKFYPPDPAQLSEDIIRYYLCLQLRDDIVSGLRPLCSFVTLALLGYSYVQSELGDYDPPDECNDYIS EFRFAPNHTKLEDKVIELHKSHRGMTPAEAMHFL ENAKK 272
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 7305031 | ref | NP_038841.1 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 450
gi | 16758808 | ref | NP_446379.1 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 445
gi | 32490572 | ref | NP_036439.2 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 442
gi | 114672351 | ref | XP_512036.2 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 442
gi | 194678110 | ref | XP_870774.3 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 444
gi | 118086838 | ref | XP_419142.2 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 441
gi | 73961950 | ref | XP_537321.2 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 444
gi | 51571933 | ref | NP_001003987.1 | LSMYGVDLHHAADS EGV EIMLGV CAS GLLIYRDLRLINRFAPWKVLKISYKRNNFYIKIRPGEFEQFESTIGFKLPNHRRAAKRLWKVCVEHHTFFRLLLEPAPPKFFLTLGSKFRYSGRTOAOTRRASALIDRPAPYFERSSSKRYITMSR 422
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 7305031 | ref | NP_038841.1 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 528
gi | 16758808 | ref | NP_446379.1 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 588
gi | 32490572 | ref | NP_036439.2 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 572
gi | 114672351 | ref | XP_512036.2 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 572
gi | 194678110 | ref | XP_870774.3 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 575
gi | 118086838 | ref | XP_419142.2 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 273
gi | 73961950 | ref | XP_537321.2 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 593
gi | 51571933 | ref | NP_001003987.1 | SLDGASVNEHHEIYMKDVSAAE VGTGOYATTKGISQTNLIITVPEKKAEEERDEEEDRRKKAEEATPVIALRHEGK-----RASPGSAVPRAELSESDAQGKAYLGDQDVA 481
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 7305031 | ref | NP_038841.1 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 561
gi | 16758808 | ref | NP_446379.1 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 738
gi | 32490572 | ref | NP_036439.2 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 722
gi | 114672351 | ref | XP_512036.2 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 722
gi | 194678110 | ref | XP_870774.3 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 725
gi | 118086838 | ref | XP_419142.2 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 423
gi | 73961950 | ref | XP_537321.2 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 743
gi | 51571933 | ref | NP_001003987.1 | FSYRQTPAGKGTILF SFSLQLPESFPLSLLDDGYSFPNLSLSENLNLLPQSLQHYLPIRSPSLVPCFLFIFFFLLSASFVVPYALTLSPFLALCLCYLEPKAASLSASLDNDPSSSEETDSERDTAAGGETTATESDQ EEDAELKADLD 554
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



