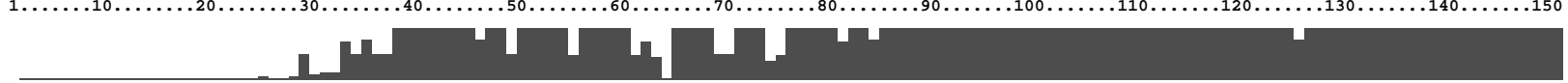
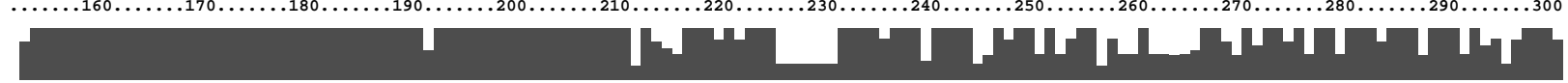


gi|19923198|ref|NP_001745.2| MASDSIFESFPSYPOCFMRECLGMNPSRDVHDASTSRRFPPPTALSPGKMSALPLGAPDA-GAALAGKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVVALGDPVDPGTLVTVMAGNDENYSAELRNATA 149
gi|114684025|ref|XP_001168376.1| MASDSIFESFPSYPOCFMRECLGMNPSRDVHDASTSRRFPPPTALSPGKMSALPLGAPDA-GAALAGKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVVALGDPVDPGTLVTVMAGNDENYSAELRNATA 149
gi|76608443|ref|XP_870864.1| MASDSMFESFPSYPOCFMRECVHGMNPSRDVHDASTSRRFPPPTALSPGKMSALPLGAPDA-GAALAGKLRSGDRSMVDVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVVALGDPVDPGTLVTVMAGNDENYSAELRNATA 149
gi|8392900|ref|NP_059021.1| -----MRIPVDASTSRRFPPPTALSPGKMSALPLGAPD-GAALASKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVVALGDPVDPGTLVTVMAGNDENYSAELRNATA 122
gi|74001231|ref|XP_544871.2| -----MRIPVDASTSRRFPPPTALSPGKMSALPLGAPDA-GAALAGKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVVALGDPVDPGTLVTVMAGNDENYSAELRNATA 122
gi|18859331|ref|NP_571678.1| -----MVFLWDAKYEPAAGRRFPPTSTLSSGKMSGLPLGAQESLGAALVGLKLRMADRSMVEVLSLHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVVALGDIIPDGTILVTVMAGNDENYSAELRNATA 127



gi|19923198|ref|NP_001745.2| AMKNQVARFNDLRFVGRSGRGKSFLLTIIVFNPPQVATYHRAIKIIVDGPREFRRHRQKLDLQKPGSLFSEERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPOPOSQMODTRQIQSPFPWSYDQSYQVLGSIASPSVHPA 299
gi|114684025|ref|XP_001168376.1| AMKNQVARFNDLRFVGRSGRGKSFLLTIIVFNPPQVATYHRAIKIIVDGPREFRRHRQKLDLQKPGSLFSEERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPOPOSQMODTRQIQSPFPWSYDQSYQVLGSIASPSVHPA 299
gi|76608443|ref|XP_870864.1| AMKNQVARFNDLRFVGRSGRGKSFLLTIIVFNPPQVATYHRAIKIIVDGPREFRRHRQKLDLQKPGSLFSEERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPOPOSQMODTRQIQSPFPWSYDQSYQVLGSIASPSVHPA 299
gi|8392900|ref|NP_059021.1| AMKNQVARFNDLRFVGRSGRGKSFLLTIIVFNPPQVATYHRAIKIIVDGPREFRRHRQKLDLQKPGSLFSEERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPOPOSQMODARQIQSPFPWSYDQSYQVLGSIASPSVHPA 271
gi|74001231|ref|XP_544871.2| AMKNQVARFNDLRFVGRSGRGKSFLLTIIVFNPPQVATYHRAIKIIVDGPREFRRHRQKLDLQKPGSLFSEERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPOPOSQMODTRQIQSPFPWSYDQSYQVLGSIASPSVHPA 272
gi|18859331|ref|NP_571678.1| AIKNQVARFNDLRFVGRSGRGKSFLLTIIVFNPPQVATYQRAIKIIVDGPREFRRHRQKDEAVKPGALAFSE-----QLRRSAMRCSPHH-GPAPNTRPTLN-IPFGSPAHSQIPDSRQMTSPSWSYEQSYPLGPISTPAVHPA 269



gi|19923198|ref|NP_001745.2| TPISPGRASGMTLS-----AELSSRLS-----TAPDLTAFSDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSIGIGMSAMGS-ATRYHTYLPFPYP-GSSQAQGGFFQASSPSYH 404
gi|114684025|ref|XP_001168376.1| TPISPGRASGMTLS-----AELSSRLS-----TAPDLTAFSDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSIGIGMSAMGS-ATRYHTYLPFPYP-GSSQAQGGFFQASSPSYH 404
gi|76608443|ref|XP_870864.1| TPISPGRASGMTLS-----AELSSRLS-----TASDLTAFGDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSIGIGMSAMSS-ATRYHTYLPFPYP-GSSQAQGGFFQASSPSYH 404
gi|8392900|ref|NP_059021.1| TPISPGRASGMTLS-----AELSSRLS-----TAPDLTAFGDP-----RQFPALPSISD-----PRMHYP-GAFTYSP-PTVTSIGIGMSAMSS-TSRYHTYLPFPYP-GSSQAQGGFFQASSPSYH 375
gi|74001231|ref|XP_544871.2| TPISPGRASGMTLSGIPGRLSGLKPAFSPGRAWPRSLPPHALFSPVPPPPPAPAAAPDLTAFGDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSIGIGMSAMSS-ATRYHTYLPFPYP-GSSQAQGGFFQASSPSYH 409
gi|18859331|ref|NP_571678.1| TPISPNRHALH-----CPBLTAFITDPRVGLERSFPLSLPDPGRFDPVVPVPTGAFTYTPTPVTSIGIGMSAMSSPAGRYHTYLPFPYPAGSSQAQAGAFQASSPSYH 374



gi|19923198|ref|NP_001745.2| LYYGASAGSYQFSMVG-----GERSPPRILPCTNASTGSAALLNPSLNPQSD-VVEAEGSHSNSTNMAPSARLEAVWRPY 480
gi|114684025|ref|XP_001168376.1| LYYGASAGSYQFSMVG-----GERSPPRILPCTNASTGSAALLNPSLNPQSD-VVEAEGSHSNSTNMAPSARLEAVWRPY 480
gi|76608443|ref|XP_870864.1| LYYGASAGSYQFSMVS-----GERSPPRILPCTNASTGSAALLNPSLNPQSD-VVEAEGSHSNSTNMAPSARLEAVWRPY 480
gi|8392900|ref|NP_059021.1| LYYGTSAGSYQFSMVG-----GERSPPRILPCTNASTGSAALLNPSLNPQSD-VVETEGSHSNSTNMP-ARLEAVWRPY 450
gi|74001231|ref|XP_544871.2| LYYGASAGSYQFSMVG-----GERSPPRILPCTNASTGSAALLNPSLNPQSD-VVEAEGSHSNSTNMAPSARLEAVWRPY 485
gi|18859331|ref|NP_571678.1| LYYSSAAGSYQFSMMPGGAAAGERSPPRILPCTNASTGSAALLHPSLNPQSEGVVEAEGSHSNSTNMP-ARLEAVWRPY 451

