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                                                  :.:..********:**.*****.***** :. ****..*** .*****:**:****************************************:************************
gi|19923198|ref|NP_001745.2|      MASDSIFESFPSYPQCFMRECILGMNPSRDVHDASTSRRFTPPSTALSPGKMSEALPLGAPDA-GAALAGKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATA   150
gi|114684019|ref|XP_001168297.1|  MASDSIFESFPSYPQCFMRECILGMNPSRDVHDASTSRRFTPPSTALSPGKMSEALPLGAPDA-GAALAGKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATA   150
gi|76608443|ref|XP_870864.1|      MASDSMFESFPSYPQCFMRECVHGMNPSRDVHDASTSRRFTPPSTALSPGKMSEALPLGAPDA-GAALAGKLRSGDRSMVDVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATA   150
gi|8392900|ref|NP_059021.1|       ---------------------------MRIPVDASTSRRFTPPSTALSPGKMSEALPLGAPDG-GAALASKLRSGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATA   150
gi|74001231|ref|XP_544871.2|      ---------------------------MRIPVDASTSRRFTPPSTALSPGKMSEALPLGAPDA-GAALAGKLRTGDRSMVEVLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATA   150
gi|18859331|ref|NP_571678.1|      -----------------------MVFLWDAKYEPAPGRRFTPPSTTLSSGKMSEGLPLGAQESTGAALVGKLRMADRSMVEVLSDHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDIPDGTLVTVMAGNDENYSAELRNATA   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                  *:****************************************:****************** *: .***:*:***     ****:*** **** .*:**.*.:** :..*..  .:**: *:**:*.**.***:*** ***.*:: :***:
gi|19923198|ref|NP_001745.2|      AMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRRHRQKLDDQTKPGSLSFSERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPQPQSQMQDTRQIQPSPPWSYDQSYQYLGSIASPSVHPA   300
gi|114684019|ref|XP_001168297.1|  AMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRRHRQKLDDQTKPGSLSFSERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPQPQSQMQDTRQIQPSPPWSYDQSYQYLGSIASPSVHPA   300
gi|76608443|ref|XP_870864.1|      AMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRRHRQKLDDQTKPGSLSFSERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPQPQSQMQDTRQIQPSPPWSYDQSYQYLGSIASPSVHPA   300
gi|8392900|ref|NP_059021.1|       AMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRRHRQKLDDQTKPGSLSFSERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPQPQSQMQDARQIQPSPPWSYDQSYQYLGSITS-SVHPA   300
gi|74001231|ref|XP_544871.2|      AMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRRHRQKLDDQTKPGSLSFSERLSELEQLRRTAMRVSPHHPAPTPNPRASLNHSTAFNPQPQSQMQDTRQIQPSPPWSYDQSYQYLGSIASPSVHPA   300
gi|18859331|ref|NP_571678.1|      AIKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYQRAIKITVDGPREPRRHRQKPDEAVKPGALAFSE------QLRRSAMRCSPHH-GPAPNTRPTLN-TPPFGSPAHSQIPDSRQMQTSPSWSYEQSYPYLGPISTPAVHPT   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                  *****.*::                                        ..:**** **     *.**:***:.*     **: ** *****:* ****.********.* : ********.** ******.*.**:.*..**
gi|19923198|ref|NP_001745.2|      TPISPGRASGMTTLS------AELSSRLS-------------------------TAPDLTAFSDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSGIGIGMSAMGS-ATRYHTYLPPPYP-GSSQAQGGPFQASSPSYH   450
gi|114684019|ref|XP_001168297.1|  TPISPGRASGMTTLS------AELSSRLS-------------------------TAPDLTAFSDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSGIGIGMSAMGS-ATRYHTYLPPPYP-GSSQAQGGPFQASSPSYH   450
gi|76608443|ref|XP_870864.1|      TPISPGRASGMTTLS------AELSSRLS-------------------------TASDLTAFGDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSGIGIGMSAMSS-ATRYHTYLPPPYP-GSSQAQGGPFQASSPSYH   450
gi|8392900|ref|NP_059021.1|       TPISPGRASGMTSLS------AELSSRLS-------------------------TAPDLTAFGDP-----RQFPTLPSISD-----PRMHYP-GAFTYSP-PVTSGIGIGMSAMSS-TSRYHTYLPPPYP-GSSQAQAGPFQTGSPSYH   450
gi|74001231|ref|XP_544871.2|      TPISPGRASGMTTLSGIPGRLSGLKPAFSPGRAWPRSLPPHALFSPVPPPPPTPAAAPDLTAFGDP-----RQFPALPSISD-----PRMHYP-GAFTYSPTPVTSGIGIGMSAMSS-ATRYHTYLPPPYP-GSSQAQGGPFQASSPSYH   450
gi|18859331|ref|NP_571678.1|      TPISPNRTALH-----------------------------------------CPELTAFTDPRVGLERSFPSLPSLPDGRFSDPRVPYPTGAFTYTPTPVTSAIGIGMSAMSSPAGRYHTYLPPAYPAGSSQAQAGAFQASSSPYH   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                  ***.::********:       ********** *******:***:****.**: ***:*****.***.*.      *******
gi|19923198|ref|NP_001745.2|      LYYGASAGSYQFSMVG------GERSPPRILPPCTNASTGSALLNPSLPNQSD-VVEAEGSHSNSPTNMAPSARLEEAVWRPY   533
gi|114684019|ref|XP_001168297.1|  LYYGASAGSYQFSMVG------GERSPPRILPPCTNASTGSALLNPSLPNQSD-VVEAEGSHSNSPTNMAPSARLEEAVWRPY   533
gi|76608443|ref|XP_870864.1|      LYYGASAGSYQFSMVS------GERSPPRILPPCTNASTGSALLNPSLPNQSD-VVEAEGSHSNSPTNMAPAARLEEAVWRPY   533
gi|8392900|ref|NP_059021.1|       LYYGTSAGSYQFSMVG------GERSPPRILPPCTNASTGAALLNPSLPSQSD-VVETEGSHSNSPTNMPP-ARLEEAVWRPY   533
gi|74001231|ref|XP_544871.2|      LYYGASAGSYQFSMVG------GERSPPRILPPCTNASTGSALLNPSLPNQSD-VVEAEGSHSNSPTNMAPAARLEEAVWRPY   533
gi|18859331|ref|NP_571678.1|      LYYSSAAGSYQFSMMPSGGAAAGERSPPRILP-CTNASTGSALLHPSLPNQSEGVVEAEGSHSSSPTSMSV-----EAVWRPY   533
                                  .......460.......470.......480.......490.......500.......510.......520.......530...
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