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                                                  *****:* ..*:*.* *****:******  ********** **.***:******************:*:   ********::**.*.***** *****:**.******
gi|22547182|ref|NP_003403.2|  MLLDAGPQYPAIGVTTFGASRHHSAGDVAERDVGLGINPFADGMGAFKLNPSSHELASAGQTAFTSQAPGYAAAAALGHHHHPGHVGSYSSAAFNSTRDFLFRNRGFGDAAAAASAQHSLFAASAGGFGGPHGHTDAAGHLLFPGLHEQA   150
gi|114589701|ref|XP_516806.2|  ----------------------------------------MGAFKLNPSSHELASAGQTAFTSQAPGYAAAAALGHHHHPGHVGSYSSAAFNSTRDFLFRNRGFGDAAAAASAQHSLFAASAGGFGGPHGHTDAAGHLLFPGLHEQA   150
gi|42476265|ref|NP_033599.2|  MLLDAGPQYPAIGVTTFGASRHHSAGDVAERDVGLGINPFADGMGAFKLNPSSHELASAGQTAFTSQAPGYAAAAALGHHHHPGHVGSYSSAAFNSTRDFLFRNRGFGDAAAAASAQHSLFAASAGGFGGPHGHTDAAGHLLFSGLHEQA   150
gi|12083617|ref|NP_073168.1|  MLLDAGPQYPAIGVTTFGASRHHSAGDVAERDVGLGINPFADGMGAFKLNPSSHELASAGQTAFTSQAPGYAAAAALGHHHHPGHVGSYSSAAFNSTRDFLFRNRGFGDAAAAASAQHSLFAASAGGFGGPHGHTDAAGHLLFSGLHEQA   150
gi|45383626|ref|NP_989585.1|  MLLDAGPQYPAIGVTTFGSSRHHSAADVTDREVGLGINPFADGMGAFKLNPGGHELASAGQTAFTSQAPGY--AAALGHHHHPPHVGSYSSAAFNSTRDFLFRNRGFGEAAAA-SAQHSLFASAAGGFGGPHGHGDAAGHILFPGLHEQA   150
gi|18859577|ref|NP_571008.1|  MLLDAGPQYPTIGVTTFGSTRHHSTGEVTDREVALGINPFADGMGAFKINHSSHDLGS-GQTAFSSQAPGYA-AAALGHHHHPTHVSSYSTAAFNSTRDFLFRNRGFGDAT---SAQHSLFASAAGSFAGPHGHSDAAGHLLFPGLHEQA   150
gi|76661198|ref|XP_594986.2|  MLLDAGPQYPAIGVTTFGASRHHSAGDVAERDVGLGINPFADGMGAFKLNPSSHELASAGQTAFTSQAPGYAAAAALGHHHHPGHVGSYSSAAFNSTRDFLFRNRGFGDAAAAASAQHSLFAASAGSFGGPHGHTDAAGHLLFPGLHEQA   150
                              1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                              * ***.****.*********** *.****:*:********:.****** **:*********************************:*******************:******************** ************************
gi|22547182|ref|NP_003403.2|  AGHASPNVVNGQMRLGFSGDMYPRPEQYGQVTSPRSEHYAAPQLHGYGPMNVNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEK   300
gi|114589701|ref|XP_516806.2|  AGHASPNVVNGQMRLGFSGDMYPRPEQYGQVTSPRSEHYAAPQLHGYGPMNVNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEK   300
gi|42476265|ref|NP_033599.2|  AGHASPNVVNGQMRLGFSGDMYPRPEQYGQVTSPRSEHYAAPQLHGYGPMNVNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEK   300
gi|12083617|ref|NP_073168.1|  AGHASPNVVNGQMRLGFSGDMYPRPEQYGQVTSPRSEHYAAPQLHGYGPMNVNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEK   300
gi|45383626|ref|NP_989585.1|  AGHASPNVVNGQMRLGFSGDMYGRAEQYGQVTSPRSEHYASSQLHGYGHMNMNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEK   300
gi|18859577|ref|NP_571008.1|  ATHASSNVVNSQMRLGFSGDMYGRAEQYGHVASPRSEHYASTQLHGYGPMNMNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLTNPKKSCNKTFSTMHELVTHLTVEHVGGPEQSNHICFWEECGREGKPFKAKYKLVNHIRVHTGEK   300
gi|76661198|ref|XP_594986.2|  AGHASPNVVNGQMRLGFSGDMYPRPEQYGQVTSPRSEHYAAPQLHGYGPMNVNMAAHHGAGAFFRYMRQPIKQELICKWIEPEQLANPKKSCNKTFSTMHELVTHVTVEHVGGPEQSNHICFWEECPREGKPFKAKYKLVNHIRVHTGEK   300
                              .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|22547182|ref|NP_003403.2|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHESSSQ--------------------GSQPSPAASSGYESS--------------TPPTIVSPST   450
gi|114589701|ref|XP_516806.2|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHESSSQ--------------------GSQPSPAASSGYESS--------------TPPTIVSPST   450
gi|42476265|ref|NP_033599.2|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHESSSQ--------------------GSQPSPAASSGYESS--------------TPPTIVSPTT   450
gi|12083617|ref|NP_073168.1|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHESSSQ--------------------GSQPSPAASSGYESS--------------TPPTIVSPTT   450
gi|45383626|ref|NP_989585.1|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHESSSQ--------------------GSQPSPAASSGYESS--------------TPPTIVSPST   450
gi|18859577|ref|NP_571008.1|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVHESSSQ--------------------GSQPSPAASSGYESS--------------TPPTIVSPST   450
gi|76661198|ref|XP_594986.2|  PFPCPFPGCGKVFARSENLKIHKRTHTGEKPFKCEFEGCDRRFANSSDRKKHMHVHTSDKPYLCKMCDKSYTHPSSLRKHMKVIAALSPPALEPGALAALRPGSGGEWQLGCGRSRQRRKGHDSSLQTAQKGRGLEKGMWVPKALLNLLF   450
                              .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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gi|22547182|ref|NP_003403.2|  DNPTTSSLSPSSS-----------AVHHTAGHSALSSNFNEWYV---------   503
gi|114589701|ref|XP_516806.2|  DNPTTSSLSPSSS-----------AVHHTAGHSALSSNFNEWYV---------   503
gi|42476265|ref|NP_033599.2|  DNPTTSSMSPSSS-----------AVHHTAGHSALSSNFNEWYV---------   503
gi|12083617|ref|NP_073168.1|  DNPTTSSMSPSSS-----------AVHHTAGHSALSSNFNEWYV---------   503
gi|45383626|ref|NP_989585.1|  ENQTASSLSPSSS-----------AGHHTASHSTLTSNFNEWYV---------   503
gi|18859577|ref|NP_571008.1|  ENQSSSSISPASS-----------TVHHTSSHSTLSSNFNEWYV---------   503
gi|76661198|ref|XP_594986.2|  NNESQKKRAEAATEGEPGQSRLDDAAEAAASAAWLAAPARSWGLARGPECWLT   503
                              .......460.......470.......480.......490.......500...
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