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                                  ******:********.:*:**.**.:**** *.:* *  *.  . . ...**                    ..*:            **:   ....:* *                          *** .:  .
gi|7304901|ref|NP_038504.1|       MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREAIQNPGPRHPEAANIAPPGA---------------CLQQR------QETSPRRRRRQQH-TEDGSPQAHIRGPTGYLALEEEQQPSQQQAASEGHPESSCLPEPGAATAPGKGLPQQ   150
gi|6978535|ref|NP_036634.1|       MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREAIQNPGPRHPEAASIAPPGA---------------CLQQR------QETSPRRRRRQQH-PEDGSPQAHIRGTTGYLALEEEQQPSQQQSASEGHPESGCLPEPGAATAPGKGLPQQ   150
gi|50978706|ref|NP_001003053.1|   MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREVIQNPGPRHPEAVSAAPPGA---------------HLQQQQQQQQQQETSPRQQQQQQQ-GDDGSPQAQSRGPTGYLALDEEQQPSQQRSASKGHPESACVPEPGVTSATGKGLQQQ   150
gi|194680525|ref|XP_001253943.2|  MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVCEVIQNPLPRHPEASSAAPSGA---------------RLQQQ------QETSPRQQQQQQQQRREDGSPQVQSRGPTGYLALEEEQQPSQHHSAPEGHPESGCVPEPRAASAAGKGLQQP   150
gi|21322252|ref|NP_000035.2|      MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREVIQNPGPRHPEAASAAPPGASLLLLQQQQQQQQQQQQQQQQQQQQQQQQETSPRQQQQQQG--EDGSPQAHRRGPTGYLVLDEEQQPSQPQSALECHPERGCVPEPGAAVAASKGLPQQ   150
gi|91680856|ref|NP_001035179.1|   MEVQLGIGRVYPRPPGRTFRGVFQTFFQSVCEAFQAP--RDEPGPGLPAPGA-----------------------------PCPQ------------SPRPPPVASPAFLPL---------------------PEPRAAARP-------   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|7304901|ref|NP_038504.1|       PPAPPDQDDSAAPSTLSLLGPTFPGLSSCSADIKDILNEAGTMQLLQQQ-QQQQQHQQQHQQHQQQQ--EVISEGSS-ARAREATGAPSSSKDSYLGGNSTISDSAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYASLLGGPPAVR   300
gi|6978535|ref|NP_036634.1|       PPAPPDQDDSAAPSTLSLLGPTFPGLSSCSADIKDILSEAGTMQLLQQQ-QQQQQQQQQQQQQQQQQQQQQ--EVISEGSSSVRAREATGAPSSSKDSYLGGNSTISDSAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYASLLGGPPAVR   300
gi|50978706|ref|NP_001003053.1|   QPAPPDENDSAAPSTLSLLGPTFPGLSSCSTDLKDILSEAGTMQLLQQQRQQQQQQQQQQQQQQQQQQQEVVSEGSSSGRAREAAGASTSSKDSYLGGSSTISDSAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGGPPAVR   300
gi|194680525|ref|XP_001253943.2|  PPAPLDEDDSAAPSTLSLLGPTFPGLSSCSTDLKDILSEAGTMQLLQQQ---------------QQQQQEAVSEGSS-GRAREATGAPISSKDSYLGGSSTISDSAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGPPAAVR   300
gi|21322252|ref|NP_000035.2|      LPAPPDEDDSAAPSTLSLLGPTFPGLSSCSADLKDILSEASTMQLLQQQ-----------------QQEAVSEGSSSGRAREASGAPTSSKDNYLGGTSTISDNAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVR   300
gi|91680856|ref|NP_001035179.1|   ----------------AMGSPFP----GAGDLKELLGEPGVLPLLPPE-----------------------------AEPGAGRAEPALKEDFLG------DSAKELCKAVSASMGLAVETLEAPRE-PPPREDCMFALPGGPPRAPR   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                   .. *                   :.  :.**.                 . *  .: ::*:*: *.**:  ..   *  ..   ** : :*              * :*****.* :                          .*   .  ***   .
gi|7304901|ref|NP_038504.1|       PTPCAPLPECKGLPLDEGPGKSTEETAEYSSFKGGYAKGLEGESLGCSGSSEAGSSGTLEIPSSLSLYKSGALDEAAAYQNRDYYNFPLALSGPPHPPPPTHPHARIKLENPLDYGSAWAAAAAQCRYGDLGSLHGGSVAGPSTGSPPAT   450
gi|6978535|ref|NP_036634.1|       PTPCAPLAECKGLSLDEGPGKGTEETAEYSSFKGGYAKGLEGESLGCSGSSEAGSSGTLEIPSSLSLYKSGAVDEAAAYQNRDYYNFPLALSGPPHPPPPTHPHARIKLENPSDYGSAWAAAAAQCRYGDLASLHGGSVAGPSTGSPPAT   450
gi|50978706|ref|NP_001003053.1|   --PCAPLAECKGSLLDDGPGKGTEETAEYSPFKAGYAKGLDGDSLGCSSSSEAGGSGTLEMPSTLSLYKSGALDEAAAYQSRDYYNFPLSLGGPPPHPPPPHPHTRIKLENPLDYGSAWAAAAAQCRYGDLASLHGAGAAGPSSGSPSAT   450
gi|194680525|ref|XP_001253943.2|  PTPCAPLAECKGSLLDDGPSKGTEETAEYSPFKAGYTKGLDTESLSCSGSGEAGGSGTLELPSTLSLYKSGALDEVAAYQTRDYYNFPLALAGPPPPPPPPHPHARIKLENPLDYGSAWVAAAAQCRYGDLASLHGGGAAGPGSGSPSAA   450
gi|21322252|ref|NP_000035.2|      PTPCAPLAECKGSLLDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLELPSTLSLYKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPHPHARIKLENPLDYGSAWAAAAAQCRYGDLASLHGAGAAGPGSGSPSAA   450
gi|91680856|ref|NP_001035179.1|   PDAAEPP----------------EPPTPAAFKG----------------SGAEAALAVEVPAGLPLYRVSPPPEEPP--GRDCFVLP--------------PPARIKLESPPEP----------------------AAVGAWGSP--V   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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gi|7304901|ref|NP_038504.1|       TSSSWHTLFTAEEGQLYGP--GGGGGSSSPS------------DAGPVAPYGYTRPPQGLTSQESDYSASEVWYPGGVVNRVPYPSP-NCVKSEMGPWMENYSGPYGDMRLDSTRDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS   600
gi|6978535|ref|NP_036634.1|       ASSSWHTLFTAEEGQLYGP--GGGGGSSSPS------------DAGPVAPYGYTRPPQGLASQEGDFSASEVWYPGGVVNRVPYPSP-SCVKSEMGPWMENYSGPYGDMRLDSTRDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS   600
gi|50978706|ref|NP_001003053.1|   TSSSWHTLFTAEEGQLYGP--CGGSGGGSAG------------DGGSVAPYGYTRPPQGLAGQEGDFPPPDVWYPGGVVSRVPFPSP-SCVKSEMGSWMESYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS   600
gi|194680525|ref|XP_001253943.2|  ASSSWHTLFTAEEGQLYGPAVCGGGGGGSAG------------EAGAVAPYGYTRPPQGLAGQEGDFSPPDVWYPGGVVSRVPYPSP-SCVKSEMGPWMENYSGPYGDMRLETTRDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS   600
gi|21322252|ref|NP_000035.2|      ASSSWHTLFTAEEGQLYGPCGGGGGGGGGGGGGGGGGGGGGGEAGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSP-TCVKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS   600
gi|91680856|ref|NP_001035179.1|   PAPPWPSFF-ADEGQLYGP-----CAEPPPG-----------------AFGCGRP------ENADFAA-DAWHP---MARAPYAAPGSCIKSELGPWAEGYAGAYGDVRLEAGREHILPIDYYFPPQKTCLICGDEASGCHYGALTCGS   600
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

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gi|7304901|ref|NP_038504.1|       CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGENSNAGSPTEDPSQKMTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNL   750
gi|6978535|ref|NP_036634.1|       CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGENSSAGSPTEDPSQKMTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNL   750
gi|50978706|ref|NP_001003053.1|   CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASNVTSPTEEPTQKLTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNL   750
gi|194680525|ref|XP_001253943.2|  CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSATSPTEEPAQKLTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNL   750
gi|21322252|ref|NP_000035.2|      CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETTQKLTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNL   750
gi|91680856|ref|NP_001035179.1|   CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGSLKTQDEAEAASSSSPTEEQAPKMVMTHVNGFECQPIFLNVLEAIEPAVVCAGHDNSQPDSFSNLLSSLNELGERQLVYVVKWAKALPGFRNL   750
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

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gi|7304901|ref|NP_038504.1|       HVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF   900
gi|6978535|ref|NP_036634.1|       HVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF   900
gi|50978706|ref|NP_001003053.1|   HVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF   900
gi|194680525|ref|XP_001253943.2|  HVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF   900
gi|21322252|ref|NP_000035.2|      HVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF   900
gi|91680856|ref|NP_001035179.1|   HVDDQMSIIQYSWMGLMIFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRQLSQEFGWLQITPQEFLCMKALLFFSIIPVDGLKNQKLFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKVLDSVHPIAKDLHQFTF   900
                                  .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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                                  *****:******:*************************::
gi|7304901|ref|NP_038504.1|       DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ   941
gi|6978535|ref|NP_036634.1|       DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ   941
gi|50978706|ref|NP_001003053.1|   DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ   941
gi|194680525|ref|XP_001253943.2|  DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ   941
gi|21322252|ref|NP_000035.2|      DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ   941
gi|91680856|ref|NP_001035179.1|   DLLIKAHMVSVDYPEMMAEIISVQVPKILSGKVKPIYFHAE   941
                                  .......910.......920.......930.......940.
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[redacted]