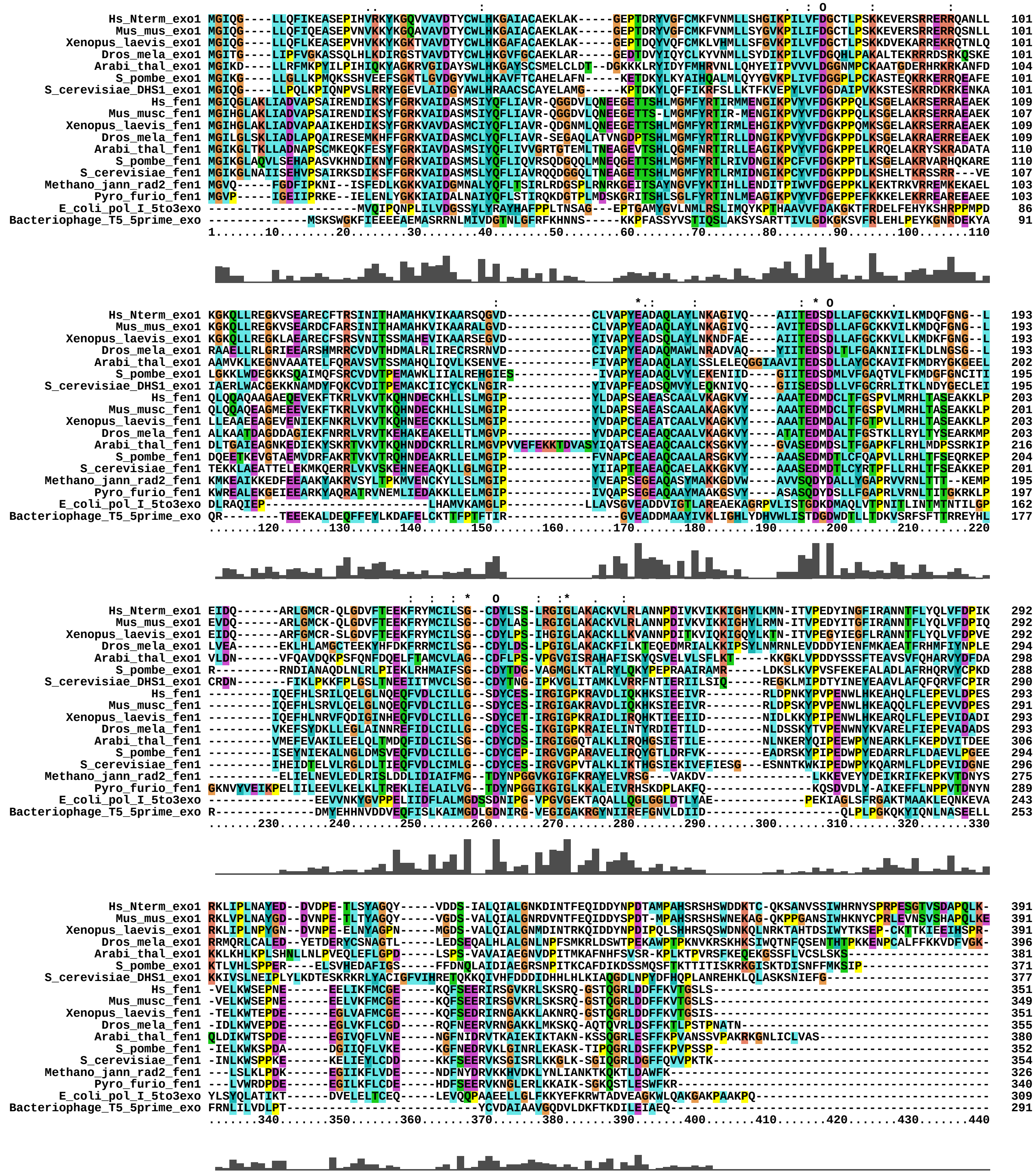

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                                                  ..               :                                         .  : O      :          :
              Hs_Nterm_exo1 MGIQG----LLQFIKEASEPIHVRKYKGQVVAVDTYCWLHKGAIACAEKLAK-----GEPTDRYVGFCMKFVNMLLSHGIKPILVFDGCTLPSKKEVERSRRERRQANLL   101
               Mus_mus_exo1 MGIQG----LLQFIQEASEPVNVKKYKGQAVAVDTYCWLHKGAIACAEKLAK-----GEPTDRYVGFCMKFVNMLLSYGVKPILIFDGCTLPSKKEVERSRRERRQSNLL   101
        Xenopus_laevis_exo1 MGIQG----LLQFLKEASEPVHVKKYKGKTVAVDTYCWLHKGAFACAEKLAK-----GEPTDQYVQFCMKLVHMLLSFGVKPILVFDGCTLPSKKDVEKARREKRQTNLQ   101
             Dros_mela_exo1 MGITG----LIPFVGKASSQLHLKDIRGSTVAVDTYCWLHKGVFGCAEKLAR-----GEDTDVYIQYCLKYVNMLLSYDIKPILVFDGQHLPAKALTEKRRRDSRKQSKE   101
            Arabi_thal_exo1 MGIKD----LLRFMKPYILPIHIQKYAGKRVGIDAYSWLHKGAYSCSMELCLDT--DGKKKLRYIDYFMHRVNLLQHYEIIPVVVLDGGNMPCKAATGDERHRKRKANFD   104
               S_pombe_exo1 MGIKG----LLGLLKPMQKSSHVEEFSGKTLGVDGYVWLHKAVFTCAHELAFN-----KETDKYLKYAIHQALMLQYYGVKPLIVFDGGPLPCKASTEQKRKERRQEAFE   101
     S_cerevisiae_DHS1_exo1 MGIQG----LLPQLKPIQNPVSLRRYEGEVLAIDGYAWLHRAACSCAYELAMG-----KPTDKYLQFFIKRFSLLKTFKVEPYLVFDGDAIPVKKSTESKRRDKRKENKA   101
                    Hs_fen1 MGIQGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVR-QGGDVLQNEEGETTSHLMGMFYRTIRMMENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEK   109
              Mus_musc_fen1 MGIHGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVR-QGGDVLQNEEGETTS-LMGMFYRTIR-MENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEK   107
        Xenopus_laevis_fen1 MGIHGLAKLIADVAPAAIKEHDIKSYFGRKVAVDASMCIYQFLIAVR-QDGNMLQNEEGETTSHLMGMFYRTIRMLEHGIKPVYVFDGKPPQMKSGELAKRSERRAEAEK   109
             Dros_mela_fen1 MGILGLSKLIADLAPQAIRESEMKHFFGRKVAIDASMCLYQFLIAVR-SEGAQLATVNGDPTSHLMGMFYRTIRLLDNGIKPVYVFDGKPPDLKSGELAKRAERREEAEK   109
            Arabi_thal_fen1 MGIKGLTKLLADNAPSCMKEQKFESYFGRKIAVDASMSIYQFLIVVGRTGTEMLTNEAGEVTSHLQGMFNRTIRLLEAGIKPVYVFDGKPPELKRQELAKRYSKRADATA   110
               S_pombe_fen1 MGIKGLAQVLSEHAPASVKHNDIKNYFGRKVAIDASMSLYQFLIQVRSQDGQQLMNEQGETTSHLMGMFYRTLRIVDNGIKPCFVFDGKPPTLKSGELAKRVARHQKARE   110
          S_cerevisiae_fen1 MGIKGLNAIISEHVPSAIRKSDIKSFFGRKVAIDASMSLYQFLIAVRQQDGGQLTNEAGETTSHLMGMFYRTLRMIDNGIKPCYVFDGKPPDLKSHELTKRSSRR---VE   107
     Methano_jann_rad2_fen1 MGVQ-----FGDFIPKNI--ISFEDLKGKKVAIDGMNALYQFLTSIRLRDGSPLRNRKGEITSAYNGVFYKTIHLLENDITPIWVFDGEPPKLKEKTRKVRREMKEKAEL   103
            Pyro_furio_fen1 MGVP-----IGEIIPRKE--IELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTINLMEAGIKPVYVFDGEPPEFKKKELEKRREAREEAEE   103
       E_coli_pol_I_5to3exo ---------------------MVQIPQNPLILVDGSSYLYRAYHAFPPLTNSAG---EPTGAMYGVLNMLRSLIMQYKPTHAAVVFDAKGKTFRDELFEHYKSHRPPMPD    86
Bacteriophage_T5_5prime_exo --------------MSKSWGKFIEEEEAEMASRRNLMIVDGTNLGFRFKHNNS-----KKPFASSYVSTIQSLAKSYSARTTIVLGDKGKSVFRLEHLPEYKGNRDEKYA    91
                            1.......10........20........30........40........50........60........70........80........90.......100.......110
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              Hs_Nterm_exo1 KGKQLLREGKVSEARECFTRSINITHAMAHKVIKAARSQGVD------------CLVAPYEADAQLAYLNKAGIVQ----AIITEDSDLLAFGCKKVILKMDQFGNG--L   193
               Mus_mus_exo1 KGKQLLREGKVSEARDCFARSINITHAMAHKVIKAARALGVD------------CLVAPYEADAQLAYLNKAGIVQ----AVITEDSDLLAFGCKKVILKMDQFGNG--L   193
        Xenopus_laevis_exo1 KGKQLLREGKLAEARECFSRSVNITSSMAHEVIKAARSEGVD------------YIVAPYEADSQLAYLNKNDFAE----AIITEDSDLLAFGCKKVLLKMDKFGNG--L   193
             Dros_mela_exo1 RAAELLRLGRIEEARSHMRRCVDVTHDMALRLIRECRSRNVD------------CIVAPYEADAQMAWLNRADVAQ----YIITEDSDLTLFGAKNIIFKLDLNGSG--L   193
            Arabi_thal_exo1 AAMVKLKEGNVAAATELFQRAVSVTSSMAHQLIQVLKSENVE------------FIVAPYEADAQLAYLSSLELEQGGIAAVITEDSDLLAYGCKAVIFKMDRYGKGEEL   202
               S_pombe_exo1 LGKKLWDEGKKSQAIMQFSRCVDVTPEMAWKLIIALREHGIES------------IVAPYEADAQLVYLEKENIID----GIITEDSDMLVFGAQTVLFKMDGFGNCITI   195
     S_cerevisiae_DHS1_exo1 IAERLWACGEKKNAMDYFQKCVDITPEMAKCIICYCKLNGIR------------YIVAPFEADSQMVYLEQKNIVQ----GIISEDSDLLVFGCRRLITKLNDYGECLEI   195
                    Hs_fen1 QLQQAQAAGAEQEVEKFTKRLVKVTKQHNDECKHLLSLMGIP------------YLDAPSEAEASCAALVKAGKVY----AAATEDMDCLTFGSPVLMRHLTASEAKKLP   203
              Mus_musc_fen1 QLQQAQEAGMEEEVEKFTKRLVKVTKQHNDECKHLLSLMGIP------------YLDAPSEAEASCAALAKAGKVY----AAATEDMDCLTFGSPVLMRHLTASEAKKLP   201
        Xenopus_laevis_fen1 LLEAAEEAGEVENIEKFNKRLVKVTKQHNEECKKLLSLMGIP------------YVDAPCEAEATCAALVKAGKVY----AAATEDMDALTFGTPVLLRHLTASEAKKLP   203
             Dros_mela_fen1 ALKAATDAGDDAGIEKFNRRLVRVTKEHAKEAKELLTLMGVP------------YVDAPCEAEAQCAALVKAGKVY----ATATEDMDALTFGSTKLLRYLTYSEARKMP   203
            Arabi_thal_fen1 DLTGAIEAGNKEDIEKYSKRTVKVTKQHNDDCKRLLRLMGVPVVEFEKKTDVASYIQATSEAEAQCAALCKSGKVY----GVASEDMDSLTFGAPKFLRHLMDPSSRKIP   216
               S_pombe_fen1 DQEETKEVGTAEMVDRFAKRTVKVTRQHNDEAKRLLELMGIP------------FVNAPCEAEAQCAALARSGKVY----AAASEDMDTLCFQAPVLLRHLTFSEQRKEP   204
          S_cerevisiae_fen1 TEKKLAEATTELEKMKQERRLVKVSKEHNEEAQKLLGLMGIP------------YIIAPTEAEAQCAELAKKGKVY----AAASEDMDTLCYRTPFLLRHLTFSEAKKEP   201
     Methano_jann_rad2_fen1 KMKEAIKKEDFEEAAKYAKRVSYLTPKMVENCKYLLSLMGIP------------YVEAPSEGEAQASYMAKKGDVW----AVVSQDYDALLYGAPRVVRNLTTT--KEMP   195
            Pyro_furio_fen1 KWREALEKGEIEEARKYAQRATRVNEMLIEDAKKLLELMGIP------------IVQAPSEGEAQAAYMAAKGSVY----ASASQDYDSLLFGAPRLVRNLTITGKRKLP   197
       E_coli_pol_I_5to3exo DLRAQIEP-----------------------LHAMVKAMGLP-----------LLAVSGVEADDVIGTLAREAEKAGRPVLISTGDKDMAQLVTPNITLINTMTNTILGP   162
Bacteriophage_T5_5prime_exo QR--------TEEEKALDEQFFEYLKDAFELCKTTFPTFTIR----------------GVEADDMAAYIVKLIGHLYDHVWLISTDGDWDTLLTDKVSRFSFTTRREYHL   177
                            .......120.......130.......140.......150.......160.......170.......180.......190.......200.......210.......220
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              Hs_Nterm_exo1 EIDQ------ARLGMCR-QLGDVFTEEKFRYMCILSG--CDYLSS-LRGIGLAKACKVLRLANNPDIVKVIKKIGHYLKMN-ITVPEDYINGFIRANNTFLYQLVFDPIK   292
               Mus_mus_exo1 EVDQ------ARLGMCK-QLGDVFTEEKFRYMCILSG--CDYLAS-LRGIGLAKACKVLRLANNPDIVKVIKKIGHYLRMN-ITVPEDYITGFIRANNTFLYQLVFDPIQ   292
        Xenopus_laevis_exo1 EIDQ------ARFGMCR-SLGDVFTEEKFRYMCILSG--CDYLPS-IHGIGLAKACKLLKVANNPDITKVIQKIGQYLKTN-ITVPEGYIEGFLRANNTFLYQLVFDPVE   292
             Dros_mela_exo1 LVEA------EKLHLAMGCTEEKYHFDKFRRMCILSG--CDYLDS-LPGIGLAKACKFILKTEQEDMRIALKKIPSYLNMRNLEVDDDYIENFMKAEATFRHMFIYNPLE   294
            Arabi_thal_exo1 VLDN------VFQAVDQKPSFQNFDQELFTAMCVLAG--CDFLPS-VPGVGISRAHAFISKYQSVELVLSFLKT-----KKGKLVPDDYSSSFTEAVSVFQHARVYDFDA   298
               S_pombe_exo1 R---------RNDIANAQDLNLRLPIEKLRHMAIFSG--CDYTDG-VAGMGLKTALRYLQKYPEPRAAIRAMR-----LDKSLKVPVSFEKEFALADLAFRHQRVYCPKD   288
     S_cerevisiae_DHS1_exo1 CRDN-------FIKLPKKFPLGSLTNEEIITMVCLSG--CDYTNG-IPKVGLITAMKLVRRFNTIERIILSIQ-----REGKLMIPDTYINEYEAAVLAFQFQRVFCPIR   290
                    Hs_fen1 ---------IQEFHLSRILQELGLNQEQFVDLCILLG--SDYCES-IRGIGPKRAVDLIQKHKSIEEIVR--------RLDPNKYPVPENWLHKEAHQLFLEPEVLDPES   293
              Mus_musc_fen1 ---------IQEFHLSRVLQELGLNQEQFVDLCILLG--SDYCES-IRGIGAKRAVDLIQKHKSIEEIVR--------RLDPSKYPVPENWLHKEAQQLFLEPEVVDPES   291
        Xenopus_laevis_fen1 ---------IQEFHLNRVFQDIGINHEQFVDLCILLG--SDYCET-IRGIGPKRAIDLIRQHKTIEEIID--------NIDLKKYPIPENWLHKEARQLFLEPEVIDADI   293
             Dros_mela_fen1 ---------VKEFSYDKLLEGLAINNREFIDLCILLG--CDYCES-IKGIGPKRAIELINTYRDIETILD--------NLDSSKYTVPENWNYKVARELFIEPEVADADS   293
            Arabi_thal_fen1 ---------VMEFEVAKILEELQLTMDQFIDLCILSG--CDYCDS-IRGIGGQTALKLIRQHGSIETILE--------NLNKERYQIPEEWPYNEARKLFKEPDVITDEE   306
               S_pombe_fen1 ---------ISEYNIEKALNGLDMSVEQFVDLCILLG--CDYCEP-IRGVGPARAVELIRQYGTLDRFVK--------EADRSKYPIPEDWPYEDARRLFLDAEVLPGEE   294
          S_cerevisiae_fen1 ---------IHEIDTELVLRGLDLTIEQFVDLCIMLG--CDYCES-IRGVGPVTALKLIKTHGSIEKIVEFIESG---ESNNTKWKIPEDWPYKQARMLFLDPEVIDGNE   296
     Methano_jann_rad2_fen1 ----------ELIELNEVLEDLRISLDDLIDIAIFMG--TDYNPGGVKGIGFKRAYELVRSG---VAKDV---------------LKKEVEYYDEIKRIFKEPKVTDNYS   275
            Pyro_furio_fen1 GKNVYVEIKPELIILEEVLKELKLTREKLIELAILVG--TDYNPGGIKGIGLKKALEIVRHSKDPLAKFQ---------------KQSDVDLY-AIKEFFLNPPVTDNYN   289
       E_coli_pol_I_5to3exo ---------------EEVVNKYGVPPELIIDFLALMGDSSDNIPG-VPGVGEKTAQALLQGLGGLDTLYAE-------------PEKIAGLSFRGAKTMAAKLEQNKEVA   243
Bacteriophage_T5_5prime_exo R--------------DMYEHHNVDDVEQFISLKAIMGDLGDNIRG-VEGIGAKRGYNIIREFGNVLDIID-------------------QLPLPGKQKYIQNLNASEELL   253
                            .......230.......240.......250.......260.......270.......280.......290.......300.......310.......320.......330
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              Hs_Nterm_exo1 RKLIPLNAYED--DVDPE-TLSYAGQY-----VDDS-IALQIALGNKDINTFEQIDDYNPDTAMPAHSRSHSWDDKTC-QKSANVSSIWHRNYSPRPESGTVSDAPQLK-   391
               Mus_mus_exo1 RKLVPLNAYGD--DVNPE-TLTYAGQY-----VGDS-VALQIALGNRDVNTFEQIDDYSPDT-MPAHSRSHSWNEKAG-QKPPGANSIWHKNYCPRLEVNSVSHAPQLKE   391
        Xenopus_laevis_exo1 RKLIPLNPYGN--DVNPE-ELNYAGPN-----MGDS-VALQIALGNMDINTRKQIDDYNPDIPQLSHHRSQSWDNKQLNRKTAHTDSIWYTKSEP-CKTTKIEEIHSPR-   391
             Dros_mela_exo1 RRMQRLCALED--YETDERYCSNAGTL-----LEDSEQALHLALGNLNPFSMKRLDSWTPEKAWPTPKNVKRSKHKSIWQTNFQSENTHTPKKENPCALFFKKVDFVGK-   396
            Arabi_thal_exo1 KKLKHLKPLSHNLLNLPVEQLEFLGPD-----LSPS-VAVAIAEGNVDPITMKAFNHFSVSR-KPLKTPVRSFKEQEKGSSFLVCSLSKS--------------------   381
               S_pombe_exo1 KTLVHLSPPER----ELSVHEDAFIGS-----FFDNQLAIDIAEGRSNPITKCAFDIKDSSMQSFTKTTITISKRKGISKTDISNFFMKSIP------------------   371
     S_cerevisiae_DHS1_exo1 KKIVSLNEIPLYLKDTESKRKRLYACIGFVIHRETQKKQIVHFDDDIDHHLHLKIAQGDLNPYDFHQPLANREHKLQLASKSNIEFG-----------------------   377
                    Hs_fen1 -VELKWSEPNE------EELIKFMCGE-----KQFSEERIRSGVKRLSKSRQ-GSTQGRLDDFFKVTGSLS---------------------------------------   351
              Mus_musc_fen1 -VELKWSEPNE------EELVKFMCGE-----KQFSEERIRSGVKRLSKSRQ-GSTQGRLDDFFKVTGSLS---------------------------------------   349
        Xenopus_laevis_fen1 -TELKWTEPDE------EGLVAFMCGE-----KQFSEDRIRNGAKKLAKNRQ-GSTQGRLDDFFKVTGSIS---------------------------------------   351
             Dros_mela_fen1 -IDLKWVEPDE------EGLVKFLCGD-----RQFNEERVRNGAKKLMKSKQ-AQTQVRLDSFFKTLPSTPNATN-----------------------------------   355
            Arabi_thal_fen1 QLDIKWTSPDE------EGIVQFLVNE-----NGFNIDRVTKAIEKIKTAKN-KSSQGRLESFFKPVANSSVPAKRKGNLICLVAS------------------------   380
               S_pombe_fen1 -IELKWKSPDA------DGIIQFLVKE-----KGFNEDRVKLGINRLEKASK-TIPQGRLDSFFKPVPSSP---------------------------------------   352
          S_cerevisiae_fen1 -INLKWSPPKE------KELIEYLCDD-----KKFSEERVKSGISRLKKGLK-SGIQGRLDGFFQVVPKTK---------------------------------------   354
     Methano_jann_rad2_fen1 ---LSLKLPDK------EGIIKFLVDE-----NDFNYDRVKKHVDKLYNLIANKTKQKTLDAWFK---------------------------------------------   326
            Pyro_furio_fen1 ---LVWRDPDE------EGILKFLCDE-----HDFSEERVKNGLERLKKAIK-SGKQSTLESWFKR--------------------------------------------   340
       E_coli_pol_I_5to3exo YLSYQLATIKT------DVELELTCEQ-----LEVQQPAAEELLGLFKKYEFKRWTADVEAGKWLQAKGAKPAAKPQ---------------------------------   309
Bacteriophage_T5_5prime_exo FRNLILVDLPT---------------------------YCVDAIAAVGQDVLDKFTKDILEIAEQ---------------------------------------------   291
                            .......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440
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