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Scc1_Hs_HR21spA_KIA0078 MLHGLQRALAKT-------------------------GAESISLLELCR-----------------------NTNR--KQAAAKFYSFLVLKKQQAIELTQE---------EP----YSDIIA   562
        Rec8_Hs_HR21spB EAVHRAVALELQ-------------------------ANREPDFSSLVS-----------------------PLSPR--RMAARVFYLLLVLSAQQILHVKQE---------KP----YGRLLI   479
                Scc1_Dm AAHLFIDVRAHF-------------------------IAKDSLELSQLTS-----------------------GNSR--KQAAQKFYSLLVLKKFKVLHIDQS---------AP----YADITI   643
        Rec8_Dm_Mei-910 VMMSLLSIWRNNPK----------------------ITGIDAIDFIKTFD-------------------------SR--IKASLAFLHLLYLVRDHFIEISKR---------ANSLEMY-QITL   485
      Scc1_Ce_A_K08A8_3 LLQNIATKLEN----------------------QNGQVELDEMLK-----------------------KGTSR--KVAAAKFYSLLCLKKNQCIDIEQK---------EP----YGDIMI   526
      Rec8_Ce_B_W02A2_6 RLNIHKELLNEAE----------------------ARYPEWVNFNEFTA-----------------------DHDR--KKAATAFEGLLLSLKNMKVEAKQE---------DP----YFPILV   710
          Scc1_Sp_Rad21 AKDSLRNKWDPY-----------------------TEGEKVSFQTLSA-----------------------GCNR--EEAVQLFFDVLVLATKDVISVKQD---------VA---IQNEITL   555
                Rec8_Sp FYEYAKTAIYE--------------------------NNGRITFSSLLP-----------------------NDLKR--PVVAQAFSHLLSLATKSAFLVKQD---------KP----YSEISV   491
        Scc1_Sc_YDL003w AIVQMAKILRKEL----------------------SEEKEVIFTDVLKSQ------------------ANTEPENITKREASRGFFDILSLATEGCIGLSQT---------EA----FGNIKI   483
   Rec8_Sc_YPR007c_Spo69 RKMLLVDIIPSRM----------------------GEAQTGANFDDVER-----------------------GVSR--QIAASAFLSLLNLATKGMVKLNEY---------PV----ADAVTK   603
        Scc1_Leishmania VQQTLERIRMELSLRAARDHK-------KSRTQSAASLVGASCALREVCR-----------------------GLRR--RNAARTFVDVLALASKQYVSAQQA---------LG----SDEVQV   482
              Scc1_At_A LKQRSSSSPTTSS-----------------------HPSGDLSLSEILA-----------------------GKTR--KLAARMFFETLVLKSRGLIDMQQD---------RP----YGDIAL   619
           Rec8_At_SYN1 IKSHLKTHFETP-------------------------GAPQVESLNKLAV-----------------------GMDR--NAAAKLFFQSCVLATRGVIKVNQA---------EP----YGDILI   550
        Scc1_E_cuniculi EEIVMESYLDIE-----------------------KLPRTFVFNEIAG-----------------------GHNR--YEKGRLFLSLLNLLGSGVVQGRQK---------NP----YSDIEC   295
               Ctds1_Hs GDQLVSRFPQL-------------------------NEWCPFAELVA-----------------------GQPA--FEVCRSMLASLQLANDYTVEITQQ---------PG----L-EMAV   521
               Ctds1_At IQEYGDRIINKLTV----------------------EESGNVETFTDLMK-----------------------DQEK--HEVARAFSALLQLVNNGDVDLEKP---------GN---STNEPMC   524
     Ctds1_Dm_CG14685-PB IKDLGTEILDICK-----------------------AGNRTATLADVMA-----------------------DKDP--SIMCRYMLASLVLTNHGNVSLDF----------ENR-DKSKPIDM   809
        Ctds1_Ce_C29E4_2 VGRAVIGQYDI--------------------------EGGTKRLLDLVM--------------------------DRPWYEISRYFLSCLFMCNVGNVMVSE----------------DMELPL   833
        Ctds1_Plasm_falc LDLYKKNIINYTI----------------------NNGENILFTKLIK-----------------------NKDK--FEISRNFLTTLMLINADILNIKKINKHKKSNNISN----Y-EIHI   679
 Ctds1_Cryptosporidium_1 IHEEGKMIIERMKK--------------------FNIMEQPIRFEEVTN-----------------------GFSK--WQVCRSFLATLMLSNNREIDILQ----------EN----QNAIEE   571
         scpA_B_subtilis IEARMNEIVHSLK-----------------------SRGTRINFMDLFP-----------------------YEQK--EHLVVTFLAVLELMKNQLVLIEQE---------HN----FSDIYI   180
         scpA_Thermotoga VEEMMERILDE--------------------------IDGEIEILRLLS-----------------------RAENV--YELIVRLLAILELVKIGKLILVG----------------DDRIRR   163
    DHFR_scpA_Mycoplasma IEQVQAEILATIK----------------------QFGYHSVSLKRVLLK----------------------VNHHISLMYFITAFVALLVLINNQIIDIEQT---------SF----DDELYI   344
        scpA_Pseudomonas TRERMSEVLERL-----------------------KGGAFVPFIQLFT-----------------------LEEGK--LGVVVTFMAILELVKEQMVELVQN---------EA----FGAIHV   165
      scpA_Chloroflexus VAEVAERIRARL-----------------------ERTAWFDFTDLLS-----------------------NDPTT--EEVIVSFWAMLELLKRRAIVVEQT---------ML----FGPILI   169
        scpA_Pyrococcus LYEIVKEIYNE--------------------------TGKPIRFWDLVF-----------------------DVDP--KIIARTFLYLLFLENMGKVEMIQE---------EP----FGEILV   153
      scpA_Methanococcus ISDIIAELLDDL----------------------MKEGIIVYQEKFK--------------------------TR--EDRVRYFIPSLYLANDGKAELIQE---------KL----FGELII   162
scpA_Thermosynechococcus MARDVESLLREMA----------------------PEGTWLDFQKLLQ--------------------------RK--PDAVGVFWALLFLAAQSKVDLQQT---------DF----YQPLQV   180
         scpA_Cytophaga IELQKEYIINKV-----------------------SRGQRISFTEIIN-----------------------DIPV-KMAVIYNFLSILELLALQKIQLHLG---------EG----FNNFWI   182
      scpA_Mycobacterium QAEHLLAMLKAR----------------------GSGQWASFSELVA-----------------------DCTAP--IEIVGRFLALLELYRTRAVAFEQS---------EP----LGALQV   199
        scpA_Treponema VNEKLTLLSELL-----------------------GVRGRCVFTELIK-----------------------QPSR--ADVVCAFVAILEAAKTHLVHISQP---------EF----FGPITL   176
          scpA_Aquifex FEEVLEELWNSFKE---------------------LEVGTRLSFFNFLS--------------------------K--KDLVPQFMALLYLDYESKVRLFQE---------KP----FEDITV   139
      scpA_Fusobacterium IKEVMDNILMKV--------------------------YFKKWPIDDLFL-----------------------EAENK--LHLIYIFLAILELYKDAKINIDN----------------GEITK   167
       scpA_Thermoplasma IEKTYRAIIES-----------------------GKQKVFMSEIWG-----------------------NTR---RERAVFFLYSMFLFRDGRISLSQE---------EP----NGDILI   187
    scpA_Prochlorococcus TTAALGVFLNDWE----------------------QALHWVDFEQLVGQW------------------EQVSTADLDTDRVGVFWALLFLCSQGKVELAQE--------GSL----YAPLRL   203
      scpA_Archaeoglobus IARVEREVFEAL-----------------------RKKDTVTLFSLVK-----------------------SWDV--PTLVDYYVSVLHLAFRKKVEIRQE---------EF----YGDVEI   160
     scpA_Rhodospirillum VENAIRRIGALLG----------------------GLADWTPIRNFLPPG------------------LEDPLVRR--SAVAATFVATLELAKQGVLDLRQD---------GG---VYAPITV   154
          Barren_Encepha IKKLKDSVLDSV--------------------------KGGSTSLLSIFEGIPK---------------VYNGEESKD--ISVHLCFISLLHLANEKNIQLKAV----------------GNDIEV   369
                Barren_At LKETLWECLQESHQPPIQNLI--------VQDEEHQQEPPESRSFKVLLASFPD--------------DCQAAERTQD--ISPHLCFICLLHLANEHNLSLIGS---------QN----LDDLTI   613
             Barren_Dm_B LKKSCNSLIQKQLLNAVPEETI-----PSHPKKKGEHYSKGFASFQQVYQKLPD---------------LLTTKMSDS--LSPSVAFYAVLHLANDLKLRLIPQ---------ED----LEDFQI   641
          Barren_Plasm_f IKKILCDIVKPNEEQKSNTNDSLCEYQTEKDNQIVTYTAEKTTTFEEIVKEVKHNEYNKDKNIYNTTTAKLNESEASS--TSIHMLFVCLLYTCNDQELLLEKI---------PN----QNNFYV   909
                Barren_Hs LKQSMWSLLTALSGKEADAEANH----REAGKEAALAEVADEKMLSGLTKDLQR---------------SLPPVMAQN--LSIPLAFACLLHLANEKNLKLEGT---------ED----LSDVLV   652
                Barren_Sc LKKNVWRSINNLIQEHDSRKNREQ--SSNDSETHTEDESTKELKFSDIIQGISK---------------MYSDDTLKD--ISTSFCFICLLHLANEHGLQITHT---------EN----YNDLIV   623
                Barren_Sp LKEKLWKCLDLENTIKENSINSH----IEGSEMESEETNMPVKSFFSTVNQLEE---------------TYEKKELKD--ISTSFAFICVLHLANEHNLELTSN---------ED----FSDVFI   635
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