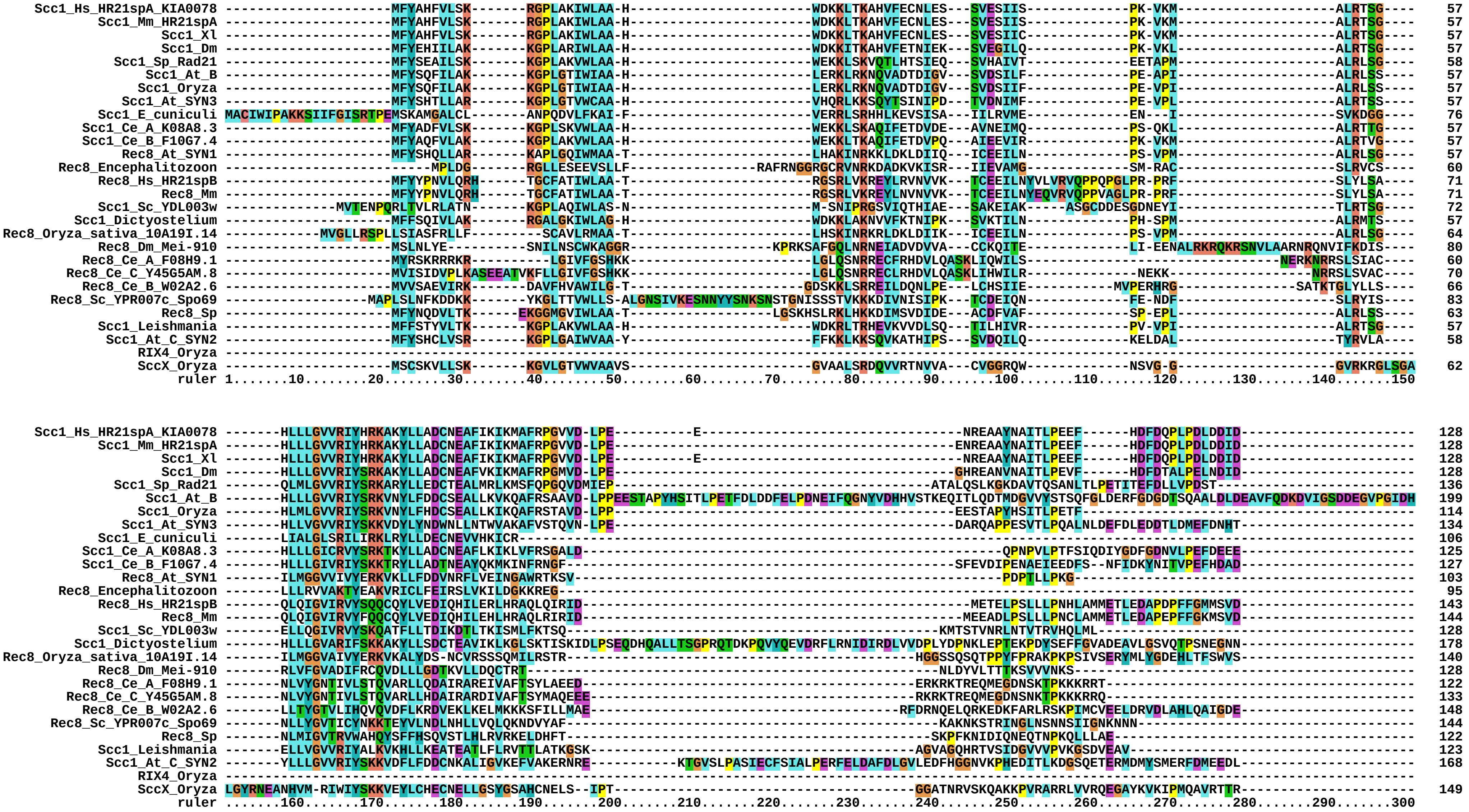

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    Scc1_Hs_HR21spA_KIA0078 ---------------------MFYAHFVLSK-------RGPLAKIWLAA-H-----------------------WDKKLTKAHVFECNLES---SVESIIS-------------PK-VKM--------------------ALRTSG----   57
            Scc1_Mm_HR21spA ---------------------MFYAHFVLSK-------RGPLAKIWLAA-H-----------------------WDKKLTKAHVFECNLES---SVESIIS-------------PK-VKM--------------------ALRTSG----   57
                    Scc1_Xl ---------------------MFYAHFVLSK-------RGPLAKIWLAA-H-----------------------WDKKLTKAHVFECNLES---SVESIIC-------------PK-VKM--------------------ALRTSG----   57
                    Scc1_Dm ---------------------MFYEHIILAK-------KGPLARIWLAA-H-----------------------WDKKITKAHVFETNIEK---SVEGILQ-------------PK-VKL--------------------ALRTSG----   57
              Scc1_Sp_Rad21 ---------------------MFYSEAILSK-------KGPLAKVWLAA-H-----------------------WEKKLSKVQTLHTSIEQ---SVHAIVT-------------EETAPM--------------------ALRLSG----   58
                  Scc1_At_B ---------------------MFYSQFILAK-------KGPLGTIWIAA-H-----------------------LERKLRKNQVADTDIGV---SVDSILF-------------PE-API--------------------ALRLSS----   57
                 Scc1_Oryza ---------------------MFYSQFILAK-------KGPLGTIWIAA-H-----------------------LERKLRKNQVADTDIGV---SVDSIIF-------------PE-VPI--------------------ALRLSS----   57
               Scc1_At_SYN3 ---------------------MFYSHTLLAR-------KGPLGTVWCAA-H-----------------------VHQRLKKSQYTSINIPD---TVDNIMF-------------PE-VPL--------------------ALRTSS----   57
            Scc1_E_cuniculi MACIWIPAKKSIIFGISRTPEMSKAMGALCL-------ANPQDVLFKAI-F-----------------------VERRLSRHHLKEVSISA---IILRVME-------------EN---I--------------------SVKDGG----   76
          Scc1_Ce_A_K08A8.3 ---------------------MFYADFVLSK-------KGPLSKVWLAA-H-----------------------WEKKLSKAQIFETDVDE---AVNEIMQ-------------PS-QKL--------------------ALRTTG----   57
          Scc1_Ce_B_F10G7.4 ---------------------MFYAQFVLAK-------KGPLAKVWLAA-H-----------------------WEKKLTKAQIFETDVPQ---AIEEVIR-------------PK-VKM--------------------ALRTVG----   57
               Rec8_At_SYN1 ---------------------MFYSHQLLAR-------KAPLGQIWMAA-T-----------------------LHAKINRKKLDKLDIIQ---ICEEILN-------------PS-VPM--------------------ALRLSG----   57
       Rec8_Encephalitozoon --------------------------MPLDG-------RGLLESEEVSLLF----------------RAFRNGGRGCRVNRKDADKVKISR---IIEVAMG-------------SM-RAC--------------------SLRVCS----   60
            Rec8_Hs_HR21spB ---------------------MFYYPNVLQRH------TGCFATIWLAA-T-----------------------RGSRLVKREYLRVNVVK---TCEEILNYVLVRVQPPQPGLPR-PRF--------------------SLYLSA----   71
                    Rec8_Mm ---------------------MFYYPNVLQRH------TGCFATIWLAA-T-----------------------RGSRLVKREYLNVNVVK---TCEEILNYEQVRVQPPVAGLPR-PRF--------------------SLYLSA----   71
            Scc1_Sc_YDL003w --------------MVTENPQRLTVLRLATN-------KGPLAQIWLAS-N-----------------------M-SNIPRGSVIQTHIAE---SAKEIAK-----ASGCDDESGDNEYI--------------------TLRTSG----   72
         Scc1_Dictyostelium ---------------------MFFSQIVLAK-------RGALGKIWLAG-H-----------------------WDKKLAKNVVFKTNIPK---SVKTILN-------------PH-SPM--------------------ALRMTS----   57
Rec8_Oryza_sativa_10A19I.14 ------------MVGLLRSPLLSIASFRLLF---------SCAVLRMAA-T-----------------------LHSKINRKRLDKLDIIK---ICEEILN-------------PS-VPM--------------------ALRLSG----   64
            Rec8_Dm_Mei-910 ---------------------MSLNLYE----------SNILNSCWKAGGR------------------KPRKSAFGQLNRNEIADVDVVA---CCKQITE-------------LI-EENALRKRQKRSNVLAARNRQNVIFKDIS----   80
          Rec8_Ce_A_F08H9.1 ---------------------MYRSKRRRKR----------LGIVFGSHKK-----------------------LGLQSNRRECFRHDVLQASKLIQWILS--------------------------------NERKNRRSLSIAC----   60
        Rec8_Ce_C_Y45G5AM.8 ---------------------MVISIDVPLKASEEATVKFLLGIVFGSHKK-----------------------LGLQSNRRECLRHDVLQASKLIHWILR--------------NEKK------------------NRRSLSVAC----   70
          Rec8_Ce_B_W02A2.6 ---------------------MVVSAEVIRK-------DAVFHVAWILG-T----------------------GDSKKLSRREILDQNLPE---LCHSIIE-----------MVPERHRG---------------SATKTGLYLLS----   66
      Rec8_Sc_YPR007c_Spo69 ------------------MAPLSLNFKDDKK-------YKGLTTVWLLS-ALGNSIVKESNNYYSNKSNSTGNISSSTVKKKDIVNISIPK---TCDEIQN-------------FE-NDF--------------------SLRYIS----   83
                    Rec8_Sp ---------------------MFYNQDVLTK------EKGGMGVIWLAA-T------------------LGSKHSLRKLHKKDIMSVDIDE---ACDFVAF-------------SP-EPL--------------------ALRLSS----   63
            Scc1_Leishmania ---------------------MFFSTYVLTK-------KGPLAKVWLAA-H-----------------------WDKRLTRHEVKVVDLSQ---TILHIVR-------------PV-VPI--------------------ALRTSG----   57
             Scc1_At_C_SYN2 ---------------------MFYSHCLVSR-------KGPLGAIWVAA-Y-----------------------FFKKLKKSQVKATHIPS---SVDQILQ-------------KELDAL--------------------TYRVLA----   58
                 RIX4_Oryza ------------------------------------------------------------------------------------------------------------------------------------------------------
                 SccX_Oryza ---------------------MSCSKVLLSK-------KGVLGTVWVAAVS-----------------------GVAALSRDQVVRTNVVA---CVGGRQW-------------NSVG-G--------------------GVRKRGLSGA   62
                      ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

    Scc1_Hs_HR21spA_KIA0078 -------HLLLGVVRIYHRKAKYLLADCNEAFIKIKMAFRPGVVD-LPE----------E---------------------------------NREAAYNAITLPEEF------HDFDQPLPDLDDID----------------------  128
            Scc1_Mm_HR21spA -------HLLLGVVRIYHRKAKYLLADCNEAFIKIKMAFRPGVVD-LPE-------------------------------------------ENREAAYNAITLPEEF------HDFDQPLPDLDDID----------------------  128
                    Scc1_Xl -------HLLLGVVRIYHRKAKYLLADCNEAFIKIKMAFRPGVVD-LPE----------E---------------------------------NREAAYNAITLPEEF------HDFDQPLPDLDDID----------------------  128
                    Scc1_Dm -------HLLLGVVRIYSRKAKYLLADCNEAFVKIKMAFRPGMVD-LPE-------------------------------------------GHREANVNAITLPEVF------HDFDTALPELNDID----------------------  128
              Scc1_Sp_Rad21 -------QLMLGVVRIYSRKARYLLEDCTEALMRLKMSFQPGQVDMIEP----------------------------------------ATALQSLKGKDAVTQSANLTLPETITEFDLLVPDST-------------------------  136
                  Scc1_At_B -------HLLLGVVRIYSRKVNYLFDDCSEALLKVKQAFRSAAVD-LPPEESTAPYHSITLPETFDLDDFELPDNEIFQGNYVDHHVSTKEQITLQDTMDGVVYSTSQFGLDERFGDGDTSQAALDLDEAVFQDKDVIGSDDEGVPGIDH  199
                 Scc1_Oryza -------HLMLGVVRIYSRKVNYLFHDCSEALLKIKQAFRSTAVD-LPP-------------------------------------------EESTAPYHSITLPETF------------------------------------------  114
               Scc1_At_SYN3 -------HLLVGVVRIYSKKVDYLYNDWNLLNTWVAKAFVSTQVN-LPE-------------------------------------------DARQAPPESVTLPQALNLDEFDLEDDTLDMEFDNHT----------------------  134
            Scc1_E_cuniculi -------LIALGLSRILIRKLRYLLDECNEVVHKICR-----------------------------------------------------------------------------------------------------------------  106
          Scc1_Ce_A_K08A8.3 -------HLLLGICRVYSRKTKYLLADCNEAFLKIKLVFRSGALD-----------------------------------------------------QPNPVLPTFSIQDIYGDFGDNVLPEFDEEE----------------------  125
          Scc1_Ce_B_F10G7.4 -------HLLLGIVRIYSKKTRYLLADTNEAYQKMKINFRNGF-------------------------------------------------SFEVDIPENAEIEEDFS--NFIDKYNITVPEFHDAD----------------------  127
               Rec8_At_SYN1 -------ILMGGVVIVYERKVKLLFDDVNRFLVEINGAWRTKSV------------------------------------------------------PDPTLLPKG-------------------------------------------  103
       Rec8_Encephalitozoon -------LLLRVVAKTYEAKVRICLFEIRSLVKILDGKKREG------------------------------------------------------------------------------------------------------------   95
            Rec8_Hs_HR21spB -------QLQIGVIRVYSQQCQYLVEDIQHILERLHRAQLQIRID-------------------------------------------------METELPSLLLPNHLAMMETLEDAPDPFFGMMSVD----------------------  143
                    Rec8_Mm -------QLQIGVIRVYFQQCQYLVEDIQHILEHLHRAQLRIRID------------------------------------------------MEEADLPSLLLPNCLAMMETLEDAPEPFFGKMSVD----------------------  144
            Scc1_Sc_YDL003w -------ELLQGIVRVYSKQATFLLTDIKDTLTKISMLFKTSQ-----------------------------------------------KMTSTVNRLNTVTRVHQLML----------------------------------------  128
         Scc1_Dictyostelium -------HLLLGVARIFSKKAKYLLSDCTEAVIKLKGLSKTISKIDLPSEQDHQALLTSGPRQTDKPQVYQEVDRFLRNIDIRDLVVDPLYDPNKLEPTEKPDYSEFFGVADEAVLGSVQTPSNEGNN----------------------  178
Rec8_Oryza_sativa_10A19I.14 -------ILMGGVAIVYERKVKALYDS-NCVRSSSQMILRSTR--------------------------------------------HGGSSQSQTPPYFPRAKPKPSIVSERYMLYGDEHLTFSWVS----------------------  140
            Rec8_Dm_Mei-910 -------RLVFGVADIFRCQVDLLLGDTKVLLDQCTRT----------------------------------------------------NLDYVLTTTKSVVVNKS-------------------------------------------  128
          Rec8_Ce_A_F08H9.1 -------NLVYGNTIVLSTQVARLLQDAIRAREIVAFTSYLAEED------------------------------------------ERKRKTREQMEGDNSKTPKKKRRT---------------------------------------  122
        Rec8_Ce_C_Y45G5AM.8 -------NLVYGNTIVLSTQVARLLHDAIRARDIVAFTSYMAQEEE-----------------------------------------RKRKTREQMEGDNSNKTPKKKRRQ---------------------------------------  133
          Rec8_Ce_B_W02A2.6 -------LLTYGTVLIHQVQVDFLKRDVEKLKELMKKKSFILLMAE---------------------------------------RFDRNQELQRKEDKFARLRSKPIMCVEELDRVDLAHLQAIGDE----------------------  148
      Rec8_Sc_YPR007c_Spo69 -------NLLYGVTICYNKKTEYVLNDLNHLLVQLQKNDVYAF-----------------------------------------------KAKNKSTRINGLNSNNSIIGNKNNN-----------------------------------  144
                    Rec8_Sp -------NLMIGVTRVWAHQYSFFHSQVSTLHLRVRKELDHFT----------------------------------------------SKPFKNIDIQNEQTNPKQLLLAE--------------------------------------  122
            Scc1_Leishmania -------ELLVGVVRIYALKVKHLLKEATEATLFLRVTTLATKGSK-----------------------------------------AGVAGQHRTVSIDGVVVPVKGSDVEAV------------------------------------  123
             Scc1_At_C_SYN2 -------YLLLGVVRIYSKKVDFLFDDCNKALIGVKEFVAKERNRE-----------KTGVSLPASIECFSIALPERFELDAFDLGVLEDFHGGNVKPHEDITLKDGSQETERMDMYSMERFDMEEDL----------------------  168
                 RIX4_Oryza ------------------------------------------------------------------------------------------------------------------------------------------------------
                 SccX_Oryza LGYRNEANHVM-RIWIYSKKVEYLCHECNELLGSYGSAHCNELS--IPT--------------------------------------GGATNRVSKQAKKPVRARRLVVRQEGAYKVKIPMQAVRTTR----------------------  149
                      ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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    Scc1_Hs_HR21spA_KIA0078 --------------------------------------------------------------------------------------------------------VAQQFSLNQSRVEEITMREEVGNISILQENDFGDFGMDDREIMREG   174
            Scc1_Mm_HR21spA --------------------------------------------------------------------------------------------------------VAQQFSLNQSRVEEITMREEVGNISILQENDFGDFGMDDREIMREG   174
                    Scc1_Xl --------------------------------------------------------------------------------------------------------VAQQFSLNQSRVEEITMREEVSNINILQDNDFGDFGMDDREMMREG   174
                    Scc1_Dm --------------------------------------------------------------------------------------------------------IEAQFSINQSRADEITMREDYGSLSLSLQDD-GFGDIGFEAETPEI   173
              Scc1_Sp_Rad21 --------------------------------------------------------------------------------------------------------FDFQWSQLLRTPSRSSNTLELHSLPISSSPSFPSSQLSIEAGRNAQ   182
                  Scc1_At_B NAYLDAAAPGIKDSMEGVSEAMPMDFNEEQVEDLAMNNEFIEDAQAPQTPGLVEVPNSSSVREQMACDDHMDVEDLNAEEGIKSSGELNANEMPKRGEDLSSEYNAPESAVTPVEVDKSQIDENVNTQNEPEEERAEHVHVTSPCCSHIT   349
                 Scc1_Oryza ----------------------------------------------------------------------------------------------------------------------------------------------------HL   116
               Scc1_At_SYN3 -------------------------------------------------------------------------------------------------RSEEDITLTDQIPTGIDPYVAVTFDEDIISESIPMDVDQSTEPVSRHTGEIDV   187
            Scc1_E_cuniculi -----------------------------------------------------------------------------------------------------------------------------------------------KDMDRER   113
          Scc1_Ce_A_K08A8.3 ---------------------------------------------------------------------------------------------------------LNHAPICQSRLDDITLKEDIPQK---FTYNYGEPLEDDDFGEIAA   167
          Scc1_Ce_B_F10G7.4 -------------------------------------------------------------------------------------------------------YNEQLIMANVSRREDITMKETV-NFNVEFNIDADFDGFGDEGESWQL   173
               Rec8_At_SYN1 --------------------------------------------------------------------------------------------------------------KTHARKEAVTLPEN-------EEADFGDFEQTRNVPKFGN   136
       Rec8_Encephalitozoon -----------------------------------------------------------------------------------------------------------------------------------------------PWRRKER   102
            Rec8_Hs_HR21spB --------------------------------------------------------------------------------------------------------------PRLPSPFDIPQIRHLLEAAIPERVEEIPPEVPTEPREPER   183
                    Rec8_Mm -------------------------------------------------------------------------------------------------------------PRLPSPFDIPQIRHLLEAATPEKTRKETLPEATPDPRKPDR   185
            Scc1_Sc_YDL003w -------------------------------------------------------------------------------------------------------------------EDAVTEREVLVTPGLEFLDDTTIPVGLMAQENSME   163
         Scc1_Dictyostelium ------------------------------------------------------------------------------------------------------NLVFDGTTTVTPQSDRRFKSDELREAEYNTMVSTPDTGLPFGQGKTPK   226
Rec8_Oryza_sativa_10A19I.14 ------------------------------------------------------------------------------------------------------VTGAKGAGLRAVWYEAVTLPENIMDMDVEQPMLFSEADTTRFRGMIVS   188
            Rec8_Dm_Mei-910 -----------------------------------------------------------------------------------------------------------EIRIQRKGKRVITKKSKVTVSKRPRLQESDL--LDEFSHEYYE   169
          Rec8_Ce_A_F08H9.1 --------------------------------------------------------------------------------------------------------MVEEFPLTPTPI-SVALKQNITMPDVLSLHKNDQINVEDDLAAPTM   167
        Rec8_Ce_C_Y45G5AM.8 ---------------------------------------------------------------------------------------------------------AEEFPLAPTPI-SVALRQNITMPDVLSVHKNDQINVEDDLAAPTM   177
          Rec8_Ce_B_W02A2.6 ---------------------------------------------------------------------------------------------LGINGNPGDFIMMDALPNMNQWIDNNSELNAIYGCVEPYLREKEITMHSTFVEGNGS   205
      Rec8_Sc_YPR007c_Spo69 ------------------------------------------------------------------------------------------------------YTWEECVFFDDDPLYDITKVPALEFLNTTLQDNVSFIEEAKSIRRQDY   192
                    Rec8_Sp ---------------------------------------------------------------------------------------------------------------DPAFIPEVSLYDAFNLPSVDLHVDMSSFTQPKENPNISV   161
            Scc1_Leishmania --------------------------------------------------------------------------------------------------------------TFDWNADVAAKHGAVADAAEALGEGRFNAIADLLGNSHRI   163
             Scc1_At_C_SYN2 ------------------------------------------------LFTFHETFSTNHNENKHESFAHDMELDSENVRDTTEEASVRVVEAEPLDSNEPSRDHQNASRHREDPESDDILLEPQMSEDIRIAQEEDTVRETICTIVQRL   270
                 RIX4_Oryza ----------------------------------------------------------------------------------------------------------------------------------------MDEEISVDPSQGNN    14
                 SccX_Oryza ---------------------------------------------------------------------------------------------AETRATSQITEVRDTHATPDLPTFTIPKRFELDSFDLGIPEDRDDDDVDHHQLPHQG   206
                      ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450


    Scc1_Hs_HR21spA_KIA0078 SAFEDDDMLVSTTTSNLLLESEQSTSNLNEKINHLEYEDQYKDDNFGEGNDGGILDDKLISNNDGGIFDDPPALSEAGVMLPEQPAHDDMDEDDNVSMGGPDSPDSVDPVEPMPTMTDQTTLV---------------------------   297
            Scc1_Mm_HR21spA SAFEDDDMLVSTSASNLLLEPEQSTSNLNEKMNHLEYEDQYKDDNFGEGNDGGILDDKLISNNDGGIFDDPPALSEAGVMLPEQPAHDDMDEDDNGSLGGPDSPDSVDPVEPMPTMTDQTTLV---------------------------   297
                    Scc1_Xl SAFEDD--MLTTNASNLKLEPEQSTSQLNEKSNHLEYDDQYKDDNFGEGNEGGILDDKLLSNDAGGIFDDPPAMPEEGVAMPEQPVHDDLDDDDNVSMGAPDSPDSVDPVEPLPTMTDQTTLV---------------------------   295
                    Scc1_Dm IRCSIPSNINDKIFDNDVLENIESLDPHSLDAHADMPGSRLDGDGFGDSFGQPALFEDDLFGDPSQPVEQITKESTT-VLNADDSDEDAIDNIHNVPSPATSLVNSIEDEKEENNLNGHASVS---------------------------   295
              Scc1_Sp_Rad21 VESGFSLGESFAHVGNDM-QFHLPISNSGAATPRSVHSDNQSQISIEVGRDAPAAAATDLSGIIGPQMTKSPASSVTHFSTPSMLPIGGTSLDDELLAPVDDLNLDLGLDDLLGDEQGANAPA------------------------IEA   307
                  Scc1_At_B TEMEDPGQVMNEAGANVVPDKPDAVPPL-ETPGEENRDHFAIATEVNQETDSSLQGDEQAYSRPDGQLNNAHETDEQLGNLTGFTDSDFPPPEKVLAVPNRQGDGNDFMVESTPDKEDPGTCNDDAGNNNITGKKRTFTESTLTAESLNS   498
                 Scc1_Oryza DDFELPEAAFQGDIDHHVSTKEQITLQDNPEKTGYSTSQFGLDERFGDGNSSHIG-----------------------------------------------------------------------------------------------   171
               Scc1_At_SYN3 ETAHETGPDNEPRDSNIAFD----TGTYSPRNVTEEFTEVQDPRQSNLTEERIPNSERNDATSPGTVPEIERMRDAAHDLSPTSHPSFAAQQQDVRVERTESLDETLNEKEPTIPSIDEEMLN--------------------SGRHSAF   313
            Scc1_E_cuniculi SFKQPSSRGITLGLDLESLYVDDQMIDPEEFTILPEEEDPGDGQDPGDASFGGL---------------------------------DDISYIEEARLGGEDSTRISTTTEVTQISLGE-------------------------------   199
          Scc1_Ce_A_K08A8.3 GVGPEDYYRLMEDVNKMDLEMELARDAATTSDNLFGREREPTPFLNDAHAPGNAIFGDEDFAGGDMDDDDHNVQGSSGFTDNNAMHMEDMDYESGNTMMRGETPLRSDTPNTFRAPSPAPSIA---------------------------   290
          Scc1_Ce_B_F10G7.4 DHLYGSVEPLSLRPTPQPESLMEVERDRDVAANGTEISRIDADSVI--FSEGPTRPNLIFDNQEGGNFMPEMNLKVENQTLENDGGVGPADMFSSMIHPVREHAVADVQNDDGMDFDYQPF-----------------------------   292
               Rec8_At_SYN1 YMDFQQTFISMRLDESHVNNNPEPEDLGQQFHQADAENITLFEYHGSFQTNNETYDRFERFDIEGDDETQMNSNPREGAEIPTTLIPSPPRHHDIPEGVNPTSPQRQEQQENRRDGFAEQM-----------------------------   257
       Rec8_Encephalitozoon NMLSMDTGLVSNGYSSEFNDTHHTDSLMLSYSEALDPADILQCSPRRRCRN---------------VFDKVMVLSTSGMIIP-------------------DTSRGGKEMEALEPAKEEAFVI---------------------------   191
            Rec8_Hs_HR21spB IPVTVLPPEAITILEAEPIRMLEIEGERELPEVSRRELDLLIAEEEEAILLEIPRLPPPAPAEVEGIGEALGPEELRLTGWEPGALLMEVTPPEELRLPAPPSPERRPPVPP--------------------------------------   295
                    Rec8_Mm TLATVQSPEVITLQEAEPIRMLQIEGEQDLPEISRGDLELLIAEKDDAILLEERQRGRLLRQRRASLPLDESREEPRALEGAGLVSALSPPAPAQVEGIQEALPGQVFPPEVQKMTGWEPGAL---------------------------   308
            Scc1_Sc_YDL003w RKVQGAAPWDTSLEVGRRFSPDEDFEHNNLSSMNLDFDIEEGPITSKSWEEGTRQSSRNFDTHENYIQDDDFPLDDAGTIGWDLGITEKNDQNNDDDDNSVEQGRRLGESIMSEEPTDFGFDL---------------------------   286
         Scc1_Dictyostelium TPDSVKSNIDILISDNQNPLFNYSATTPLPKSQRELMEDAGMVTFDEGMNMPPQDDGGGDDQQHVDIGMRHGDDDYPAYTGPETHDDDQQPHQEQFDENGRPITPAKSVTTDKTGEEDTTTTT--------------------------A   350
Rec8_Oryza_sativa_10A19I.14 IPLKSVMHVQRLEDLDDQYINVNLDDDDFSRAENHHQENITLADNFGSGLGETDVFNRFERFDITDDDATFNVTPDGHPQVPSNLVPSPPRQEDSPQQQENHHAASSPLHEEAQQGQFKHM-----------------------------   309
            Rec8_Dm_Mei-910 KMLSECQMWQTECTQQVVEDLNESIEQPRSCTQSKSYHSITITEEIELPEDHSLIMPSNGFGEAEGADLTIFQE-----LYPKDGTRNSLKRHSIAQDPTDILPDKMPRLDDCDVFQADNAIM---------------------------   287
          Rec8_Ce_A_F08H9.1 EQLEMMYGMLESENRNTAIDLT-FIDRYSSNDCRQNVHNLNLETDFQRPSDDFIRSQLMTPTKSIPQEEEFQPATHLKEMLLFRQLPITLDETERRRSMEEEMEEARNSGINTEFIPPQQM-----------------------------   287
        Rec8_Ce_C_Y45G5AM.8 EQLEMMYGMLESENRNTAIDLTFIDRYSFNDARQNVHNLNLNMETDFQRPSDDFIRSQLMTPTKSIPQEEEVFQPATHLKDVLRFAHLPIALDETERRRSMDEEMEEARNSGINTEFLTPQQM---------------------------   300
          Rec8_Ce_B_W02A2.6 NEHNKERRNDAVIADFSQLLFPEIPEITLGEKFPIDVDSRKRSAILQEEQEEALQLPKEASEIVQEEPTKFVSIALLPSETVEQPAPQEPIQEPIQPIIEEPAPQLELPQPELPPQLDAIDLV------------------TIPASQQDM   337
      Rec8_Sc_YPR007c_Spo69 INELSNSNRFELHGDMTNSDAQSNLGSNVRNSFPLDEIPVDVDFNLDLDDIVSHQGTPLGSHSSSQKDGNDFKFNYQGDELVLNFENDNENNSNGGEDTSVENEGPVANLKDYELGLEAQA-----------------------------   313
                    Rec8_Sp LETLPDSTSYLINTSQNYSLRNNVSSFVYEDSRAFSTEE---PLDFEFDENGDIQELTKGTINSDPSLQAASQHSNLGSVQREYNSEEQESRIHMFEIDEDVLPLPVPLQSVMDSEHNEN------------------------------   278
            Scc1_Leishmania DVSDTDKEDALLASAWYTVQPTSQAAGDGLHTTQQDYDEIAKMRADLMAFGERASGSASTSKSKSSLSSMEKGRGSVAVDVDGMAFPAVGDELDIGVPLPDELPPGFPALEGQVPAGMIPT-----------------------------   284
             Scc1_At_C_SYN2 VDSHESSGDNLHRDGHTENLESEKTSKKTSCEKMQHDRALSSECGIPEAIHGIEDQPSGATRINGEKEIPEMSTLEKPEPVSVTGSRDLQEGVEKCRDHNEAEMADFELFHGSHKEQSETSEV-------------NLHGSEKGFLSDMT   407
                 RIX4_Oryza SEAVNTSNINQADKAPDLPEIMREAPFEGPELNLPDIDEVNND-PMDVTEESSPFVSKNITPPALERTISPGQGGLSGTSIPNARGSTSTTYDNIEDVIPMDIGMPDFRIEPSPPRVQDEMNA---------------------------   136
                 SccX_Oryza TMLEDENHHTSCLFESYKMMTCSYADLDSACIMP-----VRVTIPTEMMSVISEVNSLLCLSSIGGEPENHNAESACFTPVKDILPPEMVDMMAEVNDPSDKSTRGKKPQRELNRDENGNSAC---------------------------   324
                      ruler .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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                                                                                             .
    Scc1_Hs_HR21spA_KIA0078 ------------PNEEEAFALEPIDITV------------------------KETKAKRKRKLIVDSVK-ELDSK--TIRAQLSDYSDIVTTLDLAPP-T-KKLMMWKETGGVEKLFSLPAQPL--------------------------   380
            Scc1_Mm_HR21spA ------------PNEEEAFALEPIDITV--------------------KETKA----KRKRKLIVDSVK-ELDSK--TIRAQLSDYSDIVTTLDLAPP-T-KKLMMWKETGGVEKLFSLPAQPLWNNRLL--------------------   386
                    Scc1_Xl ------------PNEEEAFALEPIDITV------------------------KETKAKRKRKLIVDSVK-ELDSK--TIRAQLSDYSDIVTTLDLAPP-T-KKLMMWKETGGVEKLFSLPAQPLWNTRLL--------------------   384
                    Scc1_Dm -ENVPMNEITLVQNEDEGFALAPLDVSM----------------------YKGVTKAKRKRKLIIDEIK-NISGE--EMKAQLADTSDILTTLDLAPP--TKRLMYWKETGGVEKLFSLPSRSIPARALFGNYNRQLFSHSTFFEDFSSV   417
              Scc1_Sp_Rad21 DEQAETSSIHLPSDIMEDDSSRPAAAGV-------EEGQVVESATAPQQEKINPQKTVRRQRAIIDPVT-ELSSK--QMKKQLADTSSITSP----------------------------------------------------------   389
                  Scc1_At_B VESVGLIQSKRTADSVPDDDDLLSSILVGKSSFLKMRPTPVLEPATTKRLRSAPRSTATKRKVLMDDPM-VLHGD--IIRQQLTNTEDIRRVRKKAPC-TVPEIVMLQRQALEDGLFKEPIFTGMSVELVSLHTEPYDLRGIMIIENDDR   644
                 Scc1_Oryza ----------------------------------------------------------------LDLEE--------VISANISFLQKFIEM----------------------------------------------------------   191
               Scc1_At_SYN3 ELRSGSPGSAAGSEEERADFVHPSPQLV------------------LQPSPPPQPQRRARKRKNFDGVT-VLTNK--NISERLKDPSDTLRKRKKMPS-SKLKFWRMNNQSRKDQNFNEPLFTGFSDDLRNVFEKDYVASKPHLAVSDET   441
            Scc1_E_cuniculi -------------------------------------------------------RKEKKRRIAEDTEL-EFDSQ--VFRVNLRNTRDIIHK----------------------------------------------------------   233
          Scc1_Ce_A_K08A8.3 -PSVATSVSAMEHDTIESYYER-------------------------QAQKRAMQKEQNMRKRRVDDVK-MITGE--EMKGNMADFSDILTRLDLAPP--SRKLMMGKKRSHAEYMHHNPGMIGFSKN----------------------   387
          Scc1_Ce_B_F10G7.4 ---EPENVEPSRPQSPESFALEPLDV---------------------EHMEGRKKRQRKARKLIVDAET-MISND--AFREQQEDFSDTMRVVEMAPP-T-RKMFNLCVSGDLQHLSREPGCKMFNR-----------------------   390
               Rec8_At_SYN1 -------EEQNIPDKEEHDRPQP-----------------------------AKKRARKTATSAMDYEQTIIAGH--VYQSWLQDTSDILCR-------GEKRKVRGTIRPDMESFKRANMPPTQLFEKDSSYPPQLYQLWSKNTQVLQT   362
       Rec8_Encephalitozoon ---------------------------------------------------------REARRTIPDA-----------------------------------------------------------------------------------   201
            Rec8_Hs_HR21spB ----------------------------------------------------PPRRRRRRRLLFWDKET-QISPE--KFQEQLQTRAHCWEC---------------PMVQPPERTIRGPAELFRTPTLSGWLPPELLGLWTH-------   368
                    Rec8_Mm LTEVTPPQELRLPAPPSTEKRLPS------------------------LQRPLPRRHRRRQLLFWDKET-QISRE--KFEEQLQTGAHCWE---------------YPVAQPPKRMLTSPAELFRTPTLSGWLPPELLGLWTH-------   409
            Scc1_Sc_YDL003w DIEKEAPAGNIDTITDAMTESQPK-----------------------QTGTRRNSKLLNTKSIQIDEET--------------ENSESIASS------------NTYKEERSNNLLTPQPT-----------------------------   358
         Scc1_Dictyostelium SVGGATTDNNVATEEKTEFEIQQLQQQL---------LLEKQKEEQVQKDKPKTRRSRVLGSTLSDKDI-----------RKFKNTRSLVVERSLLPS-SLNLVITKSKEIPAKQQMLTAIRKNISNTFHRMYGDLLDNRYPKVINKDED   479
Rec8_Oryza_sativa_10A19I.14 -------------------GQQP-------------------------AKSSKRKKRRKDDEVMMDNDQIMIPGN--VYQTWLKDPSSLITKRHRINS-KVNLIRSIKIRDLMDLPLVSLISSLEKSPLEFYYPKELMQLWKECTEVKSP   412
            Rec8_Dm_Mei-910 ---TQIFPHNIEPAEVTQIVCEPSLPSV----------------LNSFGEITFSHPKNRKRKLIVDK--------------RIEYTRE--------------QLVKHRQKYMEEYLSRNVIVP---------------------------   363
          Rec8_Ce_A_F08H9.1 DVPRLVSENMDLDDEVSIPIRIP------------------------KVPLSATKKQTSENEGAEEGIN---------YKIPLREMHHIMED------------YSSLHFKDPEPLYRKTSKVMNLKELLNPIPYFL-------------   379
        Rec8_Ce_C_Y45G5AM.8 NVPRIASEILELDDEVLIPRTIP------------------------KAPHSATKNQMAENEGAEEGIN---------YKIPLRDMHHLMED------------YSSLHFKDVEPLCRKTSKVMNLKDLLNPIPYYL-------------   392
          Rec8_Ce_B_W02A2.6 VVEYLQLINDLPDDENSRLPPLPKDLEL-------FEDVILPPPAKKSKVEEEEDALERARRRPSSRPVTPIN------QTDLTDLHSTVRP--EDPSFAIDSQIHDVLPQRKKSKRNLPIIHSDDLEIDEAVQKVLQADYSSLVRKKED   472
      Rec8_Sc_YPR007c_Spo69 -------------SEEENDLQQKLNTRM--------------------QRGHRADVGGQFSKVQFDAKT-SYPNE--VLKFNHGNYSHLMEK---------NRIRKLTGQNFLTSNISSLVRSCGEEEFFSTNWLSIFNDFSNIKTSEWD   418
                    Rec8_Sp -------------------------------------------------EPRALKRRKVQKLLEPDE----------NIELSTRTLSQWRKN-------YVERMIALEATKYVRRRGASSAKKKELNKFFDW------------------   344
            Scc1_Leishmania --DPFLLPDMMNMDEEAAAAAQ---------------------------RSRPGRRMRPVNVCDLDSTT--LSRE--AFEKCMADRSDILN--------------------------SEPRRGPYDAQ----------------------   353
             Scc1_At_C_SYN2 VSKDPSSEFNATDTPVTVTPKTPSRLKI------SEGGTSPQFSIIPTPAAKESSRVSRKRKCLIDDEV-IIPNK--VMKEMIEDSSKLLAKRRNVPH-TDCPERRTKRFANPFRSFLEPLIQYGSSDLQSLFCQPIKLKNWATTGTPKD   547
                 RIX4_Oryza ---QPVQGEMNAQPVQDEMNAQPV------------------------QDEMNAHPAQDKRRIRYDNEI-VFSNAYMKRQIDGGELHRLVGKRRKLPQ-AAVDVWKFNRIRQKDGFLLDPLVHGMCATLRQTYERTFPHVIDPEAESGSV   257
                 SccX_Oryza HIPLSGSKEVQIPENIVENVTFPSRDA----------------NCPTIEESENGSLHGTNTNPSCDG-----------FEEPGSLEQPTLRC--------KTKLINELSPSTPEPMTEGGTGLPCSPKFMVTTPAKKEKHRVTRKRRRGL   439
                      ruler .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750


    Scc1_Hs_HR21spA_KIA0078 ---------------------------------------------------------------------------WNNRLLKLFTRCLTPLVPEDLRKRRKGGEADNLDEFLKEFENPEVPREDQQQQHQQRDVIDEPIIEEPSRLQESV   455
            Scc1_Mm_HR21spA -----------------------------------------------------------------------------KLFTRCLTPLVPEDLRKRRKGGEADNLDEFLKEFENPEVPREEQQPQQQQPQPQRDVIDEPIIEEPSRLQDSV   459
                    Scc1_Xl -----------------------------------------------------------------------------KLFTRCLTPLVLDDLRKRRKGGEADNLDEFLKEFENPEVPREELRPQDVIDQPILEEASHLQESLMEGSRTHL   457
                    Scc1_Dm VPMEILA----------------------------------------------------------------------LEFYTKENENALIIFNKKGRKRKNDNMSNLFLDHVPDSVVQSLEAPEVLRANHKSLGVSTVSVEIVSKEQESI   497
              Scc1_Sp_Rad21 -----------------------------------------------------------------------------LCLNTSSIVFNATVNFTRNGKFNTSIFSSNLNPKVNELLQADFKQAILRKRKNESPEEVEPAKHQRTDTSTEN   462
                  Scc1_At_B HASVGAVEDNECSVTAVEENKTEESSDPQAHPNDCEEQPGTAHTHPQEEQTINQQEELKDDNELAEKSDLEVLKE-GNGAADEVNLVVIDDVSQIPSEEKLDRVEDLQVEESHENHDGEGGQDVCADPNEKSCTDVIEIAEGDTDINPIF   793
                 Scc1_Oryza ------------------------------------------------------------------------------------------------------------------------------------------------------   191
               Scc1_At_SYN3 LPEPA------------------------------------------------------------------------SVSPTREAEVEINPVSPIPDSTNPDSTVQLSPAQQTEDVLDSAGPRPAHAESVATEAQSPRTFDNDDMGIEHL   519
            Scc1_E_cuniculi -----------------------------------------------------------------------------------------------------------------------ESALDIRNELASRLSIAPEILSRIGCREIHP   264
          Scc1_Ce_A_K08A8.3 --------------------------------------------------------------------------------------------------------KQFIRKYQSYLVVTKHDDVDEKNEWIKNALGLREIGEEELQQQQQE   433
          Scc1_Ce_B_F10G7.4 ---------------------------------------------------------------------------------------------------------ELLQRYRRCLVTREFDLNYTMQELSDSSSFTPSMEAQAEPWEDLN   435
               Rec8_At_SYN1 SSSES------------------------------------------------------------------------RHPDLRAEQSPGFVQERMHNHHQTDHHERSDTSSQNLDSPAEILRTVRTGKGASVESMMAGSRASPETINRQA   440
       Rec8_Encephalitozoon --------------------------------------------------------------------------------------------------------------------------QSIEVEYSEVSTFGSVERGRSSSVHSTR   229
            Rec8_Hs_HR21spB --------------------------------------------------------------------------------------------------------------------CAQPPPKALRRELPEEAAAEEERRKIEVPSEIEV   402
                    Rec8_Mm ------------------------------------------------------------------------------------------------------------CAQVPQRMLRQRPQLETEETVEEERAADEEERRKTEALSEIE   451
            Scc1_Sc_YDL003w -----------------------------------------------------------------------------NFTTKRLWSEITESMSYLPDPILKNFLSYESLKKRKIHNGREGSIEEPELNVSLNLTDDVISNAGTNDNSFNE   431
         Scc1_Dictyostelium PYFSFLRSRLMYG---------------------------------------------------------------RMLKNEELSMSMAADGVSSLDLGIPNFEDLELVDDENQERKVEEAFLKSINNRVITESGNLIAPSERKKLKTQP   566
Rec8_Oryza_sativa_10A19I.14 KAPSS------------------------------------------------------------------------GYYTICSFLSPFWITKGTVAIFFKGGQQSSSPEQQQRNLPPQAFPTQPQVDNDREMGFHPVDFADDIEKLRGN   490
            Rec8_Dm_Mei-910 ------------------------------------------------------------------------------------------------------KSSDLRKPPKELLCKLVSFLALHNHSGPKLSNEEKEFEAENTLRTIFG   411
          Rec8_Ce_A_F08H9.1 ------------------------------------------------------------------------------------RKGCNTDMWDLFKVKTRKFDSTIGHDVSDTEEEDEDEETERRNRLKAELEPLETIDLSQMKFMTTP   445
        Rec8_Ce_C_Y45G5AM.8 -------------------------------------------------------------------------------------RKGCNTDMWDLFKVKTRKFDSTIGRHDVSDTEDEDEEAERRNRREAERELLETIDLSQMKFMATP   457
          Rec8_Ce_B_W02A2.6 VIAKIPPKTDAVAV---------------------------------------------------------------LMNLPEPVFSIGYRLPPEVRDMFKACYNQAVGSPVSDDEEDEDEEEEEEYKYAKVCLLSPNRIVEDTLLLEEQ   559
      Rec8_Sc_YPR007c_Spo69 LYPQGFSSV--------------------------------------------------------------------ERGRKRAHSLVSTQSSSSTRSHEYGRKSFRNNKNDNYSSDMENDNLLLNLEQINEDLEDGHYIEENSQGNILD   500
                    Rec8_Sp -----------------------------------------------------------------------------------------ESFHPLLKPWIEKLKPSNNTPSEIDDVLRNIDTSEVEVGRDVQGELGLNIPWNTSSRSNSA   405
            Scc1_Leishmania ---------------------------------------------------------------------------------EEADRYTVTGSANAANALATNPALDAAPLSGVLNPALRLTYAKALRQSAEEAVAMAAQAFRESMARRSE   422
             Scc1_At_C_SYN2 AKIARHKEKSS------------------------------------------------------------------LDTVRSPGVILSSDQTENTQEIMETPQAAALAGLKVTAGNSNVVSVEMGASSTTSGTAHQTENAAETPVKPSV   631
                 RIX4_Oryza EHTPGV-----------------------------------------------------------------------------ANDSIQDTHDHQLSPKSPGNTDAQPEHQFNQQAPRNSDGQPEPELNPKSQAKQARSHFDDMPEIPRF   330
                 SccX_Oryza YNKDYIPTDRG------------------------------------------------------------------DKRKIFKAQGKVLTLRNTIEDASDLVQQRRKAPHTCLYTWKEGKIRSLPVTFMDPLILYPTSVYVRHTITADT   523
                      ruler .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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    Scc1_Hs_HR21spA_KIA0078 MEASRTNIDESAMPPPPPQGVKRKAGQIDPEPVMPPQQVEQMEIPPVELPPEEPPNICQLIPELELLPEKEKEKEKEKEDDEEEEDEDASGGD---------------------------------------------------------   548
            Scc1_Mm_HR21spA MEASRTTIEESAMPPPPPQGVKRKAGQIDPEPSIPPQQVEQMEIPPVELPPEEPPNICQLIPELELLPEKEKEKEKEKEEEEEEDEDASGG----------------------------------------------------------D   551
                    Scc1_Xl DDTIMPPPPPKQGVKRDSLQMEPEPMPMMQEAEPQIEMPPPPLPPPLELPPEEPQSISDLIPELNLLPEKEKEKDEEEEEEEEDTTGT-------------------------------------------------------------E   546
                    Scc1_Dm SCQNELTFFDNMRSPDLLSLNEMEQFSSINELPLTPRNMNHEMGDDFNQGDSTPAGLDHGHATPQHGNIGEMDHDSVIPTKKTAVILNESVG---------------TSVLSDNGVSKRTNNILKGWDNYEIPSFVGQNHGDEQMENETD   632
              Scc1_Sp_Rad21 QETAEVLDPEEIAAAELANITEAAIATLPQETVVQPEGEAPELGSPMGFPVTALESADDSLFDAPPVMLDEADLLGSERLDSSVSEALPS------------------------------------------------------------   552
                  Scc1_At_B NEMDLKVEDELPHEDEKTDASAEVSELGRDDQTPCDNTVGSTETGCLEAGDLSNMALENCNEPLVEANSDGLNPETESYNKYEPHNEMSNEEASMQNALDGEHTSRDGLMGDNDEMDTMENAHDTGFLNVDDDEVDEDHEEDDIQYDDET   943
                 Scc1_Oryza ------------------------------------------------------------------------------------------------------------------------------------------------------   191
               Scc1_At_SYN3 RDGGFPVYMPSPPPRSSPFRTDDFTTQSGNWETESYRTEPSTSTVPEDLPGQRNLGLSPVSERTDEELYFLEVGGNSPVGTPASQDSAALTG----------------------------------------------------RARALA   617
            Scc1_E_cuniculi RESIESIRDATIVESYGDISFGEHAAESQASEEIVMESYLDIEKLP--------------------------------------------------------------------------------------------------------   310
          Scc1_Ce_A_K08A8.3 MDMHVQDDSSYVDDFDEVPPLDFDQLDMMD----MPQSMDDINMVDDDVPQRNPLSPFAPMVEDEEMSPSEKRKKRDEEKEEPETD----------------------------------------------------------------   515
          Scc1_Ce_B_F10G7.4 LNEDIQEDIQAQGPAVDEFFNDVRMDDDDDRQPAQEMDFGDNFDFPQEVEHQECAPIPIQSGFAGENKENEDAEDWSDPFGSSNSSRRGQLEA-------------------------------------------------YGFGNTST   536
               Rec8_At_SYN1 ADINVTPFYSGDDVRSMPSTPSARGAASINNIEISSKSRMPNRKRPNSSPRRGLEPVAEERPWEHREYEFEFSMLPEKRFTADKEILFETA------------------------------------------------------STQTQ   536
       Rec8_Encephalitozoon YDFSDPISDEGILDLSHSILDFDEH-----------------------------------------------------------------------------------------------------------------------------   254
            Rec8_Hs_HR21spB PREALEPSVPLMVSLEISLEAAEEEKSRISLIPPEERWAWPEVEAPEAPALPVVPELPEVPMEMPLVLPPELELLSLEAVHRAVALELQA------------------------------------------------------------   492
                    Rec8_Mm VLREAQEPSGPLMLSSELSLEAAEDEKSRTSLIPPEWWAWSEEGQPEPPALPMLPELPEVPMEMPPRPELSSEAVLRAVALKLQAN----------------------------------------------------------------   537
            Scc1_Sc_YDL003w LTDNMSDFVPIDAGLNEAPFPEENIIDAKTRNEQTTIQTEKVRPTPGEVASKA---IVQMAKILRKELSEEKEVIFTDVLKSQANTEP--------------------------------------------------------------   516
         Scc1_Dictyostelium LTDDDKDLINRLRTEFDDRSKNRKSLFYKPDINQTLRGMGAFGGGDGG-GEKSIGSPDGSTDFLKRAKEKEEEEERLRREEGDMGQHFMHGGDDDH-----------QGIGLGYDQEEQPGFVHPGDLGDVPEYSFESAQRPNQQAYQRE   704
Rec8_Oryza_sativa_10A19I.14 TSGEYGRDYDAFHSDHSVTPGSPGLSRRSASSSGGSGRGFTQLDPEVQLPSGRSKRQHSSGKSFGNLDPVEEEFPFEQELRDFKMRRLSDVGPT-------------------------------------------PDLLEEIEPTQTP   597
            Rec8_Dm_Mei-910 CEFTENLSKEIFVRPSQATKCRDKAAHIYQPEPLEVEDCVQPQLQPRDDVNQNYHNEMNEHGIYREDNHDDTYSVMMSLLSIWRNNPKITG-----------------------------------------------------------   502
          Rec8_Ce_A_F08H9.1 LKDKSPILTPVHRPEEIEFREELELPRFEQFEPMNVNPISPKFQMEEPALFEDNWNSKPTWSNTSSENIADALTIRGNIIRQLDDKSPF-------------------------------------------------------------   534
        Rec8_Ce_C_Y45G5AM.8 LKEKSPIMTPAHRPEEIEFREELEVPRLEQFEPMNVNPISPRMDEPALL--EENWNSKPTWSNPISENIADALTIRANIIHKLNSECPYEV-----------------------------------------------------------   546
          Rec8_Ce_B_W02A2.6 PRQPEEFPSTDNINPPRQLQENPVFENLEYEAPPHPIRTARTPTPIKDLKYSVISLFPTPEKRRETSIIAELNLDPIPVEEIDPLLTMRTEEELEN----------VRRRQKSSLGVQFMRTDDLEEDTRRNRLFEDEERTRDAREDELF   699
      Rec8_Sc_YPR007c_Spo69 FNLNLPPSSFGRSHTRNSTRSSGFNEDIVGALRRRVGPSEQNFAEEDDSSNSCFSDGSQQNLQQDKTNFQDVILDYQTKKFYDYIKERSIV---------------------------------------------------------VG   593
                    Rec8_Sp INSKSHSQTGSEHSTPLLDTKYRKRLPHSPSMPSRVEFLPALESSQFHETLNSELSLQLSDDFVLYKNTQEENAHLMLSMEKECANFYEYA-----------------------------------------------------------   496
            Scc1_Leishmania VPAGGGGALEADDAQVAAADLDGSAMLVPEAEVAQQRRKRGRDDGDGVDDSTMTAGVSASVQQTLERIRMELSLRAARDHKKSRTQSAAS------------------------------------------------------------   512
             Scc1_At_C_SYN2 IAPETPVRTSEQTAIAPETPVVSEQVEIAPETPVRESMSKRFFKDPGTCYKKSRPASPFTSFEEHPSVYYVENRDLDTILMNDEVNADER------------------------------------------------------------   721
                 RIX4_Oryza SPQNIPSPIRDDNSPFKTPGAGGTPKSRLGETPASGTPADMSYMSPGQDSDPQVSPFPFNDELDGDLPEIPSLMSTPGVISTAGTGTTGLG-----------------------------------------------------------   421
                 SccX_Oryza PENSCRESVKSRRRLSLELSESNNICDDAKNVEGESIPDEPRKRKLDELTDSVQATVGCYTESAQYHNDEDYRFNDDTVKEKDFSIGGHES-------------------HSTELQERLNALKSKNPQLDEALDADIDSMEEDTHMDEQH   654
                      ruler .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050

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    Scc1_Hs_HR21spA_KIA0078 QDQEERRWNKRTQQMLHGLQRALA-----KTGAESISLLELC-RNTNRKQAAAKFYSFLVLKKQQAIELTQEE-PYSDIIATPGPRFHII---------------------------    631
            Scc1_Mm_HR21spA QDQEERRWNKRTQQMLHGLQRALA-----KTGAESISLLELC-RNTNRKQAAAKFYSFLVLKKQQAIELTQEE-PYSDIIATPGPRFHII---------------------------    634
                    Scc1_Xl QDQEERRWNKRTQQMLHGLQRVLA-----KTGAESISLLDLC-RNTNRKQAAAKFYSFLVLKKQQAIELTQRE-PYSDIVATPGPRFHTV---------------------------    629
                    Scc1_Dm EQFEERVLNKRAAHLFIDVRAHF-------IAKDSLELSQLT-SGNSRKQAAQKFYSLLVLKKFKVLHIDQSA-PYADITITRGPTFENP-KI------------------------    715
              Scc1_Sp_Rad21 --------SQTAKDSLRNKWDPY-------TEGEKVSFQTLS-AGCNREEAVQLFFDVLVLATKDVISVKQDV-AIQNEITLTAKRGMLLSSL------------------------    628
                  Scc1_At_B RLLENSGWSSRTRAVAKYLQTLFD--KETENGKNVLVADKLL-AGKTRKEASRMFFETLVLKTRDYIQVEQGK-PYESIIIKPRPKLTKS-IF------------------------   1031
                 Scc1_Oryza --------------------------------FVVFILHYLV-------CAVWIFFYHLSLLR---------------IIIDVLPE-------------------------------    223
               Scc1_At_SYN3 QYLKQRSSSSPTTSSHP---------------SGDLSLSEIL-AGKTRKLAARMFFETLVLKSRGLIDMQQDR-PYGDIALKLMPALFSK-VQT-----------------------    693
            Scc1_E_cuniculi ---------------------------------RTFVFNEIA-GGHNRYEKGRLFLSLLNLLGSGVVQGRQKN-PYSDIECTVIQ--------------------------------    360
          Scc1_Ce_A_K08A8.3 ---EDNRWSKRTHALLQNIATKLE-----NQNGQVELDEMLK-KGTSRKVAAAKFYSLLCLKKNQCIDIEQKE-PYGDIMIKAGPNININTI-------------------------    597
          Scc1_Ce_B_F10G7.4 YKEDDGKWAKRAKHILKKVSADI------ETSGQADFSSVTA-TAKNRKQAAEQFYSLLTLAKSQAISVDQSE-PYGEIVIRPGANFKEACPLSSPKPMGLGNTMENSTMRTPMRPV    645
               Rec8_At_SYN1 KPVCNQSDEMITDSIKSHLKTHFE----TPGAPQVESLNKLA-VGMDRNAAAKLFFQSCVLATRGVIKVNQAE-PYGDILIARGPNM------------------------------    617
       Rec8_Encephalitozoon -------------------------------------------AVGSRQRRARIFYRMLELSSRGCVIPIQKQ-AYGKIVLIRADWPGDG-F-------------------------    301
            Rec8_Hs_HR21spB -------------------------------NREPDFSSLVS-PLSPRRMAARVFYLLLVLSAQQILHVKQEK-PYGRLLIQPGPRFH-----------------------------    547
                    Rec8_Mm --------------------------------KELDFSSLVPPLSPRKLASRVFYLLLVLSTQKILLVEQQK-PYGPLLIRPGPKFP------------------------------    591
            Scc1_Sc_YDL003w -------------------------------------------ENITKREASRGFFDILSLATEGCIGLSQTE-AFGNIKIDAKPALFER-FINA----------------------    566
         Scc1_Dictyostelium HEEEKKILSQKTANMHSILSDHFEKKETINFLQDIVRPQQAQNPNNTRLVAACYFYELLVLKTKVLVNLEQPE---NDTETYPDIKISKTSQFGNIEQFTIVKNAD-----------    807
Rec8_Oryza_sativa_10A19I.14 YEKKSNPIDQVTQSIHSYLKLHFD----TPGASQSESLSQLA-HGMTTAKAARLFYQACVLREENKCAIA----LFPELDKWATPSLLSHRQMLENLEEVPWKFNHCSHV-------    698
            Rec8_Dm_Mei-910 -----------------------------------IDAIDFIKTFDSRIKASLAFLHLLYLVRDHFIEISKRANSLEMYQITLGKESAKLIDNLMLSETL-----------------    567
          Rec8_Ce_A_F08H9.1 ---------------------------------EVTLDSMIPVAATSRREAARTFYTVLELLKERKIKATQRA-PYENIDLLLSTDDSEDIDDLAMADF------------------    599
        Rec8_Ce_C_Y45G5AM.8 ----------------------------------TLDSIIPL-AATSRREAARTFYTVLELLKEREIKAIQRD-PYGNIDLLLSTDDIEDIDELAMADF------------------    609
          Rec8_Ce_B_W02A2.6 FYSSGSLLPNNRLNIHKELLNEAE-----ARYPEWVNFNEFT-ADHDRKKAATAFEGLLLSLKNMKVEAKQED-PYFPILVRHISHEEM----------------------------    781
      Rec8_Sc_YPR007c_Spo69 RTTRSNPPFKRKMLLVDIIPSRM------GEAQTGANFDDVE-RGVSRQIAASAFLSLLNLATKGMVKLNEYP-VADAVTKDLKLRREDEIIVYA----------------------    680
                    Rec8_Sp ----------KTAIY--------------ENNGRITFSSLLP-NDLKRPVVAQAFSHLLSLATKSAFLVKQDK-PYSEISVSLNLKSTDA-I-------------------------    561
            Scc1_Leishmania ------------------------------LVGASCALREVC-RGLRRRNAARTFVDVLALASKQYVSAQQAL-GSDEVQVTLNESALRLLAAA-----------------------    574
             Scc1_At_C_SYN2 QDLQQETWSSRTRNVAKFLEKTFL-EQREREEEEKVSLLQLC-RGRTQKESARLFYETLVLKTKGYLEVKQNH-PYSDVFLMRVSRPQKA-C-------------------------    809
                 RIX4_Oryza ------SMSARTRAVAQYFKDQMA-SATSDDQPGKFILNRIL-EGRHRKQAARMFFETLVLKSYDYIDVEQEA-AYGDIAVSVKPSLSGAQFQCLDPHIISFDPREGALVGFAEMA-    528
                 SccX_Oryza ARDEGLLRSTRTRTVARYFHQLLV-DQKCQQRNNSVCLGQAL-EGTKRKTSARFFYETLILKSGSLIEVNQEQ-TYGDIIVSATPRLEAA-LRSSEKQ-------------------    748
                      ruler ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160.......
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