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        scpA_B_subtilis ------------------------------------------------------------------------------------------------------------------------------------------------------
           scpA_Xylella ------------------------------------------------------------------------------MLQATPHRIPEKFQCDTKTSTGSKPRPAIAPSDINTMNSERAQIANPPTQTPVPQQQEIPLAMVHGQPVLQI     72
  scpA_Ralstonia_metall -------------------------------------------------------MPCCGTRPRSIWRSALAPTRRAWPRSRTCTPPRTDLPAGTPPMHPSDPQEQAAQEKLSLPVELPSVAGAGSATSAADMVDGLAFARLYGEPLFKL     95
         scpA_Geobacter -----------------------------------------------------------------------------------MQEAPGRVPGPDPCPLPGTPRRTHRKAGARGRNPCRRGGPCRNRGRANHGRGAGRPQSMSNGGNLDL     67
        scpA_Oenococcus ------------------------------------------------------------------------------------------------------------------------------------------------------
 scpA_Lactobacillus_g ------------------------------------------------------------------------------------------------------------------------------------------------------
  scpA_Clostridium_therm ------------------------------------------------------------------------------------------------------------------------------------------------------
scpA_Desulfitobact_haf3 ---------------------------------------------------------------------------------------------------------------------------------------------MSNGSSVS-      8
       scpA_Leuconostoc ------------------------------------------------------------------------------------------------------------------------------------------------------
        scpA_Thermotoga ------------------------------------------------------------------------------------------------------------------------------------------------------
  DHFR_scpA_Mycoplasma_p MITLIWCQDKHFGIGRDNTIPWKLTEANQHFYNTTKNQTVVMGYNTFQELGDKLTDHNVVVLSKKHFEELQNNTNIKVFNSIEKLLQHHFNRDLYVIGGKQIFHHFIELADRLIISVLPVDFKCNLRLKLGLDSFELMQEQQHSQFKVQY    150
       scpA_Deinococcus -------------------------------------------------------------------------------------------------------------------------------------------------MIAGK      5
        scpA_Pyrococcus ------------------------------------------------------------------------------------------------------------------------------------------------------
     scpA_Methanococcus ------------------------------------------------------------------------------------------------------------------------------------------------------
  scpA_Methanosarcina_a ------------------------------------------------------------------------------------------------------------------------------------MAELIDHADHAALNISGL     18
 scpA_Archaeoglobus_ful ------------------------------------------------------------------------------------------------------------------------------------------------------
   scpA_Thermosynec_el ------------------------------------------------------------------------------------------------------------------------------------------------------
     scpA_Trichodesmium ------------------------------------------------------------------------------------------------------------------------------------------------------
scpA_Prochloroccc_marin ------------------------------------------------------------------------------------------------------------------------------------------------------
      scpA_Ferroplasma -------------------------------------------------------------------------------------------------------------------------------MRGLERDEILKALITQDVGEDLS     23
 scpA_Thermoplasma_volc -----------------------------------------------------------------------------------------------------------------------------------MRVEDILDQLVMQSRDQDG     19
     scpA_Halobacterium -------------------------------------------------------------------------------------------------------------------------------------------------MTDRD      5
           scpA_Aquifex ------------------------------------------------------------------------------------------------------------------------------------------------------
   scpA_Bifidobact_lon -------------------------------------------------------------------------------------------------------------------------MNETSLSRLPSLREAGSRSETEGSSAEAE     29
        scpA_Ureaplasma ---------------------------------------------------------------------------------------------------------------------------------------------------MNR      3
     scpA_Fusobacterium ------------------------------------------------------------------------------------------------------------------------------------------------------
  scpA_Rhodopseudomonas ------------------------------------------------------------------------MRRRPALQRQARRDAPGGGRDSGASGQGADTRRGGAGRPPCPTAVRPRCGAGRTRRIDRPRKGGRMTAEILQFETGRP     78
   scpA_Mycoplasma_pulm ------------------------------------------------------------------------------------------------------------------------------------------------------
 scpA_Mycobacterium_tub ------------------------------------------------------------------------------------------------------------------------------------------MNGLQNSLANGG     12
     scpA_Chloroflexus ------------------------------------------------------------------------------------------------------------------------------------------------------
       scpA_Leptospira ------------------------------------------------------------------------------------------------------------------------------------------------------
        scpA_Cytophaga ------------------------------------------------------------------------------------------------------------------------------------------------------
     scpA_Streptoc_pn ------------------------------------------------------------------------------------------------------------------------------------------------------
         scpA_Treponema ------------------------------------------------------------------------------------------------------------------------------------------------------
   scpA_Clostridium_perf ------------------------------------------------------------------------------------------------------------------------------------------------------
scpA_Desulfitobact_hafn ------------------------------------------------------------------------------------------------------------------------------------------------------
scpA_Rhodospirillum_rubr ------------------------------------------------------------------------------------------------------------------------------------------------------
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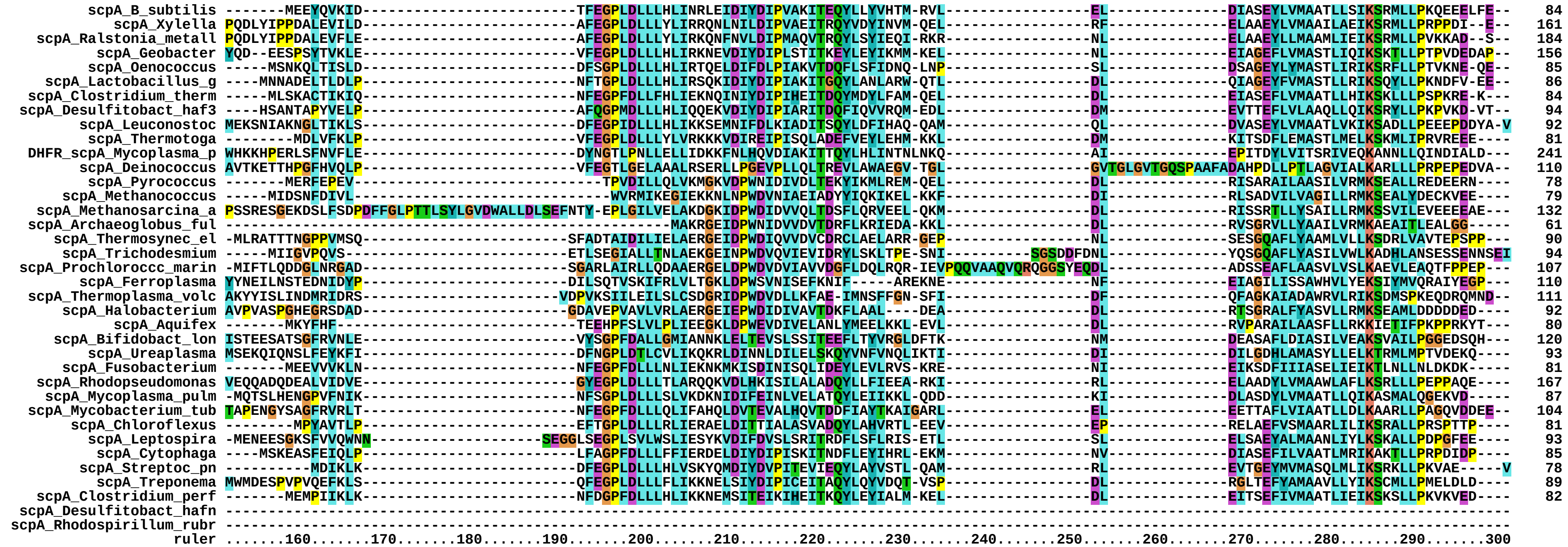

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         scpA_B_subtilis -------MEEYQVKID-------------------------TFEGPLDLLLHLINRLEIDIYDIPVAKITEQYLLYVHTM-RVL-----------------EL--------------DIASEYLVMAATLLSIKSRMLLPKQEEELFE--    84
            scpA_Xylella PQDLYIPPDALEVILD-------------------------AFEGPLDLLLYLIRRQNLNILDIPVAEITRQYVDYINVM-QEL-----------------RF--------------ELAAEYLVMAAILAEIKSRMLLPRPPDI--E--   161
   scpA_Ralstonia_metall PQDLYIPPDALEVFLE-------------------------AFEGPLDLLLYLIRKQNFNVLDIPMAQVTRQYLSYIEQI-RKR-----------------NL--------------ELAAEYLLMAAMLIEIKSRMLLPVKKAD--S--   184
          scpA_Geobacter YQD--EESPSYTVKLE-------------------------VFEGPLDLLLHLIRKNEVDIYDIPLSTITKEYLEYIKMM-KEL-----------------NL--------------EIAGEFLVMASTLIQIKSKTLLPTPVDEDAP--   156
         scpA_Oenococcus -----MSNKQLTISLD-------------------------DFSGPLDLLLHLIRTQELDIFDLPIAKVTDQFLSFIDNQ-LNP-----------------SL--------------DSAGEYLYMASTLIRIKSRFLLPTVKNE-QE--    85
    scpA_Lactobacillus_g ----MNNADELTLDLP-------------------------NFTGPLDLLLHLIRSQKIDIYDIPIAKITGQYLANLARW-QTL-----------------DL--------------QIAGEYFVMASTLLRIKSQYLLPKNDFV-EE--    86
  scpA_Clostridium_therm -----MLSKACTIKIQ-------------------------NFEGPFDLLFHLIEKNQINIYDIPIHEITDQYMDYLFAM-QEL-----------------DL--------------EIASEFLVMAATLLHIKSKLLLPSPKRE-K---    84
 scpA_Desulfitobact_haf3 ----HSANTAPYVELP-------------------------AFQGPMDLLLHLIQQEKVDIYDIPIARITDQFIQVVRQM-EDL-----------------DM--------------EVTTEFLVLAAQLLQIKSRYLLPKPVKD-VT--    94
        scpA_Leuconostoc MEKSNIAKNGLTIKLS-------------------------DFEGPIDLLLHLIKKSEMNIFDLKIADITSQYLDFIHAQ-QAM-----------------QL--------------DVASEYLVMAATLVKIKSADLLPEEEPDDYA-V    92
         scpA_Thermotoga --------MDLVFKLP-------------------------VFEGPLDLLLYLVRKKKVDIREIPISQLADEFVEYLEHM-KKL-----------------DM--------------KITSDFLEMASTLMELKSKMLIPRVREEE----    81
  DHFR_scpA_Mycoplasma_p WHKKHPERLSFNVFLE-------------------------DYNGTLPNLLELLIDKKFNLHQVDIAKITTQYLHLINTNLNKQ-----------------AI--------------EPITDYLVITSRIVEQKANNLLQINDIALD---   241
        scpA_Deinococcus AVTKETTHPGFHVQLP-------------------------VFEGTLGELAAALRSERLLPGEVPLLQLTREVLAWAEGV-TGL-----------------GVTGLGVTGQSPAAFADAHPDLLPTLAGVIALKARLLLPRPEPEDVA--   110
         scpA_Pyrococcus -------MERFEPEV-----------------------------TPVDILLQLVKMGKVDPWNIDIVDLTEKYIKMLREM-QEL-----------------DL--------------RISARAILAASILVRMKSEALLREDEERN----    78
      scpA_Methanococcus -----MIDSNFDIVL------------------------------WVRMIKEGIEKKNLNPWDVNIAEIADYYIQKIKEL-KKF-----------------DI--------------RLSADVILVAGILLRMKSEALYDECKVEE----    79
   scpA_Methanosarcina_a PSSRESGEKDSLFSDPDFFGLPTTLSYLGVDWALLDLSEFNTY-EPLGILVELAKDGKIDPWDIDVVQLTDSFLQRVEEL-QKM-----------------DL--------------RISSRTLLYSAILLRMKSSVILEVEEEEAE---   132
  scpA_Archaeoglobus_ful ----------------------------------------------------MAKRGEIDPWNIDVVDVTDRFLKRIEDA-KKL-----------------DL--------------RVSGRVLLYAAILVRMKAEAITLEALGG-----    61
     scpA_Thermosynec_el -MLRATTTNGPPVMSQ------------------------SFADTAIDILIELAERGEIDPWDIQVVDVCDRCLAELARR-GEP-----------------NL--------------SESGQAFLYAAMLVLLKSDRLVAVTEPSPP---    90
      scpA_Trichodesmium -----MIIGVPQVS--------------------------ETLSEGIALLTNLAEKGEINPWDVQVIEVIDRYLSKLTPE-SNI----------SGSDDFDNL--------------YQSGQAFLYASILVWLKADHLANSESSENNSEI    94
 scpA_Prochloroccc_marin -MIFTLQDDGLNRGAD------------------------SGARLAIRLLQDAAERGELDPWDVDVIAVVDGFLDQLRQR-IEVPQQVAAQVQRQGGSYEQDL--------------ADSSEAFLAASVLVSLKAEVLEAQTFPPEP---   107
        scpA_Ferroplasma YYNEILNSTEDNIDYP------------------------DILSQTVSKIFRLVLTGKLDPWSVNISEFKNIF-----AREKNE-----------------NF--------------EIAGILISSAWHVLYEKSIYMVQRAIYEGP---   110
  scpA_Thermoplasma_volc AKYYISLINDMRIDRS-----------------------VDPVKSIILEILSLCSDGRIDPWDVDLLKFAE-IMNSFFGN-SFI-----------------DF--------------QFAGKAIADAWRVLRIKSDMSPKEQDRQMND--   111
      scpA_Halobacterium AVPVASPGHEGRSDAD------------------------GDAVEPVAVLVRLAERGEIEPWDIDIVAVTDKFLAAL----DEA-----------------DL--------------RTSGRALFYASVLLRMKSEAMLDDDDDED----    92
            scpA_Aquifex -------MKYFHF----------------------------TEEHPFSLVLPLIEEGKLDPWEVDIVELANLYMEELKKL-EVL-----------------DL--------------RVPARAILAASFLLRKKIETIFPKPPRKYT---    80
     scpA_Bifidobact_lon ISTEESATSGFRVNLE-------------------------VYSGPFDALLGMIANNKLELTEVSLSSITEEFLTYVRGLDFTK-----------------NM--------------DEASAFLDIASILVEAKSVAILPGGEDSQH---   120
         scpA_Ureaplasma MSEKQIQNSLFEYKFI-------------------------DFNGPLDTLCVLIKQKRLDINNLDILELSKQYVNFVNQLIKTI-----------------DI--------------DILGDHLAMASYLLELKTRMLMPTVDEKQ----    93
      scpA_Fusobacterium -------MEEVVVKLN-------------------------NFEGPFDLLLNLIEKNKMKISDINISQLIDEYLEVLRVS-KRE-----------------NI--------------EIKSDFIIIASELIEIKTLNLLNLDKDK-----    81
   scpA_Rhodopseudomonas VEQQADQDEALVIDVE-------------------------GYEGPLDLLLTLARQQKVDLHKISILALADQYLLFIEEA-RKI-----------------RL--------------ELAADYLVMAAWLAFLKSRLLLPEPPAQE----   167
    scpA_Mycoplasma_pulm -MQTSLHENGPVFNIK-------------------------NFSGPLDLLLSLVKDKNIDIFEINLVELATQYLEIIKKL-QDD-----------------KI--------------DLASDYLVMAATLLQIKASMALQGEKVD-----    87
  scpA_Mycobacterium_tub TAPENGYSAGFRVRLT-------------------------NFEGPFDLLLQLIFAHQLDVTEVALHQVTDDFIAYTKAIGARL-----------------EL--------------EETTAFLVIAATLLDLKAARLLPAGQVDDEE--   104
       scpA_Chloroflexus --------MPYAVTLP-------------------------EFTGPLDLLLRLIERAELDITTIALASVADQYLAHVRTL-EEV-----------------EP--------------RELAEFVSMAARLILIKSRALLPRSPTTP----    81
         scpA_Leptospira -MENEESGKSFVVQWNN--------------------SEGGLSEGPLSVLWSLIESYKVDIFDVSLSRITRDFLSFLRIS-ETL-----------------SL--------------ELSAEYALMAANLIYLKSKALLPDPGFEE----    93
          scpA_Cytophaga ----MSKEASFEIQLP-------------------------LFAGPFDLLLFFIERDELDIYDIPISKITNDFLEYIHRL-EKM-----------------NV--------------DIASEFILVAATLMRIKAKTLLPRPDIDP----    85
        scpA_Streptoc_pn ----------MDIKLK-------------------------DFEGPLDLLLHLVSKYQMDIYDVPITEVIEQYLAYVSTL-QAM-----------------RL--------------EVTGEYMVMASQLMLIKSRKLLPKVAE-----V    78
          scpA_Treponema MWMDESPVPVQEFKLS-------------------------QFEGPLDLLLFLIKKNELSIYDIPICEITAQYLQYVDQT-VSP-----------------DL--------------RGLTEFYAMAAVLLYIKSCMLLPMELDLD----    89
   scpA_Clostridium_perf -------MEMPIIKLK-------------------------NFDGPFDLLLHLIKKNEMSITEIKIHEITKQYLEYIALM-KEL-----------------DL--------------EITSEFIVMAATLIEIKSKSLLPKVKVED----    82
 scpA_Desulfitobact_hafn ------------------------------------------------------------------------------------------------------------------------------------------------------
scpA_Rhodospirillum_rubr ------------------------------------------------------------------------------------------------------------------------------------------------------
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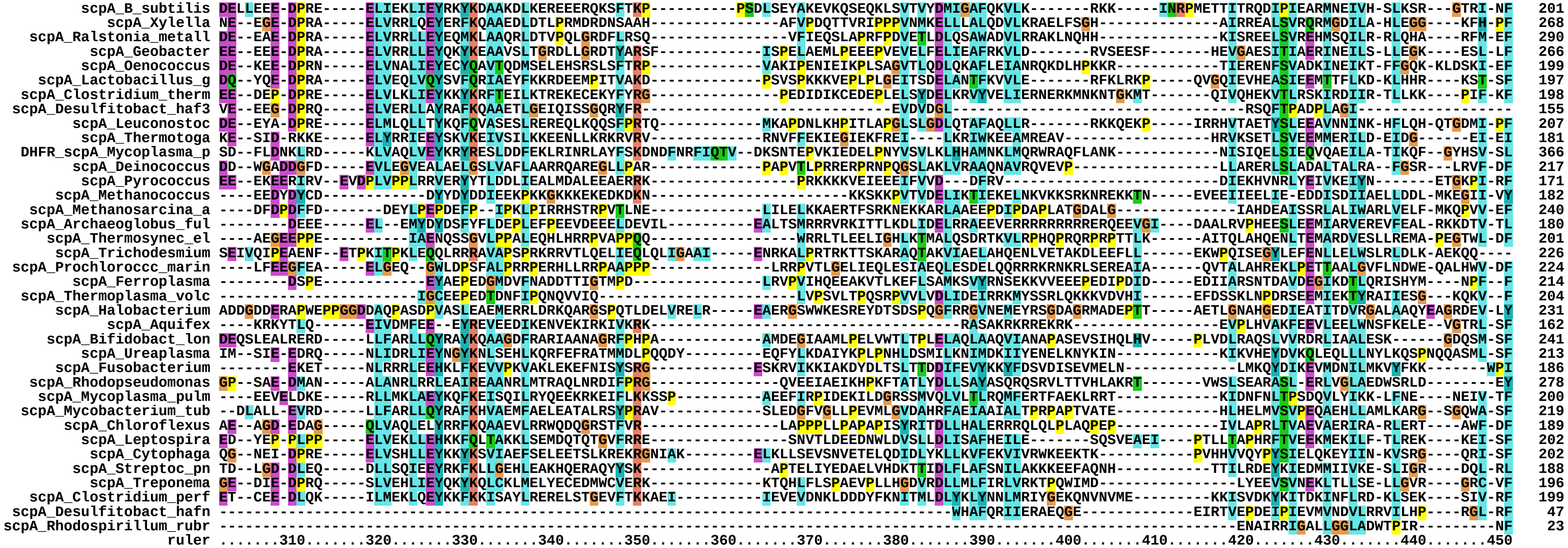

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            scpA_B_subtilis DELLEEE-DPRE-----ELIEKLIEYRKYKDAAKDLKEREEERQKSFTKP----------PSDLSEYAKEVKQSEQKLSVTVYDMIGAFQKVLK-------RKK-----INRPMETTITRQDIPIEARMNEIVH-SLKSR---GTRI-NF   201
               scpA_Xylella NE--EGE-DPRA-----ELVRRLQEYERFKQAAEDLDTLPRMDRDNSAAH---------------AFVPDQTTVRIPPPVNMKELLLALQDVLKRAELFSGH--------------AIRREALSVRQRMGDILA-HLEGG----KFH-PF   268
      scpA_Ralstonia_metall DE--EAE-DPRA-----ELVRRLLEYEQMKLAAQRLDTVPQLGRDFLRSQ----------------VFIEQSLAPRFPDVETLDLQSAWADVLRRAKLNQHH--------------KISREELSVREHMSQILR-RLQHA----RFM-EF   290
             scpA_Geobacter EE--EEE-DPRA-----ELVRRLLEYQKYKEAAVSLTGRDLLGRDTYARSF------------ISPELAEMLPEEEPVEVELFELIEAFRKVLD-------RVSEESF-------HEVGAESITIAERINEILS-LLEGK----ESL-LF   266
            scpA_Oenococcus DE--KEE-DPRN-----ELVNALIEYECYQAVTQDMSELEHSRSLSFTRP-------------VAKIPENIEIKPLSAGVTLQDLQKAFLEIANRQKDLHPKKR------------TIERENFSVADKINEIKT-FFGQK-KLDSKI-EF   199
      scpA_Lactobacillus_g DQ--YQE-DPRA-----ELVEQLVQYSVFQRIAEYFKKRDEEMPITVAKD-------------PSVSPKKKVEPLPLGEITSDELANTFKVVLE-------RFKLRKP-----QVGQIEVHEASIEEMTTFLKD-KLHHR----KST-SF   197
     scpA_Clostridium_therm EE--DEP-DPRE-----ELVLKLIEYKKYKRFTEILKTREKECEKYFYRG---------------PEDIDIKCEDEPLELSYDELKRVYVELIERNERKMNKNTGKMT-------QIVQHEKVTLRSKIRDIIR-TLLKK----PIF-KF   198
   scpA_Desulfitobact_haf3 VE--EEG-DPRQ-----ELVERLLAYRAFKQAAETLGEIQISSGQRYFR-----------------------------EVDVDGL----------------------------------RSQFTPADPLAGI------------------   155
           scpA_Leuconostoc DE--EYA-DPRE-----ELMLQLLTYKQFQVASESLREREQLKQQSFPRTQ------------MKAPDNLKHPITLAPGLSLGDLQTAFAQLLR-------RKKQEKP-----IRRHVTAETYSLEEAVNNINK-HFLQH-QTGDMI-PF   207
            scpA_Thermotoga KE--SID-RKKE-----ELYRRIEEYSKVKEIVSILKKEENLLKRKRVRV-------------RNVFFEKIEGIEKFREI----LKRIWKEEAMREAV-----------------HRVKSETLSVEEMMERILD-EIDG------EI-EI   181
     DHFR_scpA_Mycoplasma_p SD--FLDNKLRD-----KLVAQLVEYKRYRESLDDFEKLRINRLAYFSKDNDFNRFIQTV--DKSNTEPVKIEDELPNYVSVLKLHHAMNKLMQRWRAQFLANK------------NISIQELSIEQVQAEILA-TIKQF--GYHSV-SL   366
          scpA_Deinococcus DD--WGADDGFD-----EVLEGVEALAELGSLVAFLAARRQAREGLLPAR-------------PAPVTLPRRERPRNPQGSLAKLVRAAQNAVRQVEVP-----------------LLARERLSLADALTALRA--FGSR---LRVF-DF   217
           scpA_Pyrococcus EE--EKEERIRV--EVDPLVPPLRRVERYYTLDDLIEALMDALEEAERRK-----------------PRKKKKVEIEEEIFVVD---DFRV-------------------------DIEKHVNRLYEIVKEIYN-------ETGKPI-RF   171
         scpA_Methanococcus ----EEDYDYCD------------DYYDYDDIEEKPKKGKKKEKEDKDKN-----------------------KKSKKPVTVDELIKTIEKELNKVKKSRKNREKKTN-----EVEEIIEELIE-EDDISDIIAELLDDL-MKEGII-VY   182
     scpA_Methanosarcina_a ----DFDPDFFD-------DEYLPEPDEFP--IPKLPIRRHSTRPVTLNE-------------LILELKKAERTFSRKNEKKARLAAEEPDIPDAPLATGDALG--------------IAHDEAISSRLALIWARLVELF-MKQPVV-EF   240
     scpA_Archaeoglobus_ful --------DEEE-----EL--EMYDYDSFYFLDEPLEFPEEVDEEELDEVIL----------EALTSMRRRVRKITTLKDLIDELRRAEEVERRRRRRRRRERQEEVGI----DAALRVPHEESLEEMIARVEREVFEAL-RKKDTV-TL   180
      scpA_Thermosynec_el ----AEGEEPPE----------IAENQSSGVLPPALEQHLHRRPVAPPQQ-----------------WRRLTLEELIGHLKTMALQSDRTKVLRPHQPRQRPRPTTLK------AITQLAHQENLTEMARDVESLLREMA-PEGTWL-DF   201
        scpA_Trichodesmium SEIVQIPEAENF--ETPKITPKLEQQLRRRAVAPSPRKRRVTLQELIEQLQLIGAAI-----ENRKALPRTRKTTSKARAQTAKVIAELAHQENLVETAKDLEEFLL------EKWPQISEGYLEFENLLELWSLRLDLK-AEKQQ----   226
   scpA_Prochloroccc_marin ----LFEEGFEA-----ELGEQ--GWLDPSFALPRRPERHLLRRPAAPPP--------------LRRPVTLGELIEQLESIAEQLESDELQQRRRKRNKRLSEREAIA------QVTALAHREKLPETTAALGVFLNDWE-QALHWV-DF   224
           scpA_Ferroplasma --------DSPE------------EYAEPEDGMDVFNADDTTIGTMPD---------------LRVPVIHQEEAKVTLKEFLSAMKSVYRNSEKKVVEEEPEDIPDID-----EDIIARSNTDAVDEGIKDTLQRISHYM----NPF--F   214
     scpA_Thermoplasma_volc -----------------------IGCEEPEDTDNFIPQNQVVIQ-----------------------LVPSVLTPQSRPVVLVDLIDEIRRKMYSSRLQKKKVDVHI------EFDSSKLNPDRSEEMIEKTYRAIIESG---KQKV--F   204
        scpA_Halobacterium ADDGDDERAPWEPPGGDDAQPASDPVASLEAEMERRLDRKQARGSPQTLDELVRELR-----EAERGSWWKESREYDTSDSPQGFRRGVNEMEYRSGDAGRMADEPTT-----AETLGNAHGEDIEATITDVRGALAAQYEAGRDEV-LY   231
              scpA_Aquifex ----KRKYTLQ------EIVDMFEE--EYREVEEDIKENVEKIRKIVKRK------------------------------------RASAKRKRREKRK-----------------EVPLHVAKFEEVLEELWNSFKELE--VGTRL-SF   162
      scpA_Bifidobact_lon DEQSLEALRERD-----LLFARLLQYRAYKQAAGDFRARIAANAGRFPHPA------------AMDEGIAAMLPELVWTLTPLELAQLAAQVIANAPASEVSIHQLHV-----PLVDLRAQSLVVRDRLIAALESK------GDQSM-SF   241
          scpA_Ureaplasma IM--SIE-EDRQ-----NLIDRLIEYNGYKNLSEHLKQRFEFRATMMDLPQQDY---------EQFYLKDAIYKPLPNHLDSMILKNIMDKIIYENELKNYKIN------------KIKVHEYDVKQLEQLLLNYLKQSPNQQASML-SF   213
       scpA_Fusobacterium --------EKET-----NLRRRLEEHKLFKEVVPKVAKLEKEFNISYSRG------------ESKRVIKKIAKDYDLTSLTTDDIFEVYKKYFDSVDISEVMELN-------------LMKQYDIKEVMDNILMKVYFKK-------WPI   186
    scpA_Rhodopseudomonas GP--SAE-DMAN-----ALANRLRRLEAIREAANRLMTRAQLNRDIFPRG---------------QVEEIAEIKHPKFTATLYDLLSAYASQRQSRVLTTVHLAKRT-------VWSLSEARASL-ERLVGLAEDWSRLD--------EY   278
     scpA_Mycoplasma_pulm ----EEVELDKE-----RLLMKLAEYKQFKEISQILRYQEEKRKEIFLKKSSP----------AEEFIRPIDEKILDGRSSMVQLVLTLRQMFERTFAEKLRRT------------KIDNFNLTPSDQVLYIKK-LFNE----NEIV-TF   200
    scpA_Mycobacterium_tub --DLALL-EVRD-----LLFARLLQYRAFKHVAEMFAELEATALRSYPRAV------------SLEDGFVGLLPEVMLGVDAHRFAEIAAIALTPRPAPTVATE------------HLHELMVSVPEQAEHLLAMLKARG--SGQWA-SF   219
        scpA_Chloroflexus AE--AGD-EDAG-----QLVAQLELYRRFKQAAEVLRRWQDQGRSTFVR----------------LAPPPLLPAPAPISYRITDLLHALERRRQLQLPLAQPEP------------IVLAPRLTVAEVAERIRA-RLERT----AWF-DF   189
         scpA_Leptospira ED--YEP-PLPP-----ELVEKLLEHKKFQLTAKKLSEMDQTQTGVFRRE----------------SNVTLDEEDNWLDVSLLDLISAFHEILE-------SQSVEAEI----PTLLTAPHRFTVEEKMEKILF-TLREK----KEI-SF   202
          scpA_Cytophaga QG--NEI-DPRE-----ELVSHLLEYKKYKSVIAEFSELEETSLKREKRGNIAK--------ELKLLSEVSNVETELQDIDLYKLLKVFEKVIVRWKEEKTK-----------PVHHVVQYPYSIELQKEYIIN-KVSRG----QRI-SF   202
       scpA_Streptoc_pn TD--LGD-DLEQ-----DLLSQIEEYRKFKLLGEHLEAKHQERAQYYSK---------------APTELIYEDAELVHDKTTIDLFLAFSNILAKKKEEFAQNH-----------TTILRDEYKIEDMMIIVKE-SLIGR----DQL-RL   188
          scpA_Treponema GE--DIE-DPRQ-----SLVEHLIEYQKYKQLCKLMELYECEDMWCVERK-------------KTQHLFLSPAEVPLLHGDVRDLLMLFIRLVRKTPQWIMD----------------LYEEVSVNEKLTLLSE-LLGVR----GRC-VF   196
     scpA_Clostridium_perf ET--CEE-DLQK-----ILMEKLQEYKKFKKISAYLRERELSTGEVFTKKAEI----------IEVEVDNKLDDDYFKNITMLDLYKLYNNLMRIYGEKQNVNVME---------KKISVDKYKITDKINFLRD-KLSEK----SIV-RF   199
   scpA_Desulfitobact_hafn -------------------------------------------------------------------------------------WHAFQRIIERAEQGE-------------EIRTVEPDEIPIEVMVNDVLRRVILHP----RGL-RF    47
  scpA_Rhodospirillum_rubr ----------------------------------------------------------------------------------------------------------------------ENAIRRIGALLGGLADWTPIR---------NF    23
                      ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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         scpA_B_subtilis MDLFP-------YEQKEHLVVTFLAVLELMKNQLVLIEQ-EH-NFSDIYITGSESIHGA--------------------------------------------------------------------------------------  251
            scpA_Xylella TALFTAE------EGKLGVLVTFLAILELAKEQLLDIVQ-EA-SLGPIYIKSLATHHTNGALQLSSDFDNSPSTHVPP-------------------------------------------------------------------  338
   scpA_Ralstonia_metall SELFEDA--IRSGKGVPVVVVNFIAMLELSRESLVEITQ-AE-PFAPIYVRLAYTPA----------------------------------------------------------------------------------------  343
          scpA_Geobacter DELFP------EHFNRDFLIATFLAVLELCKLKMVKVVQ-AN-RYGSIWIQPAVMDGEGSLVDAES-------------------------------------------------------------------------------  324
         scpA_Oenococcus QYLFK------LSSSNDEMITTFLAILELAKDHFILLSQ-ND-E-QQIFLTKGEMNA----------------------------------------------------------------------------------------  247
    scpA_Lactobacillus_g FDCIK------NFQDLDQVIGLFLAVLELCRDHKILVKQ-NR-DFGDLELEKVETNGK---------------------------------------------------------------------------------------  247
  scpA_Clostridium_therm SELFS-----PKTRSRLEIVTGFLAILELAKLKKITLIQ-PK-PFADITVCKCEDTNLEDIDDENVAAEN---------------------------------------------------------------------------  261
 scpA_Desulfitobact_haf3 -----------HSEALWHAIQR---IIERAEQGE------------EIRTGGAGMNPH---------------------------------------------------------------------------------------  187
        scpA_Leuconostoc ASFFD------DIYEREHLVVTFLALLEMAKDKRLKLHQ-EH-QQQEIYVEIEAFGEDE--------------------------------------------------------------------------------------  258
         scpA_Thermotoga LRLLS------RAENVYELIVRLLAILELVKIGKLILVG-DD-RIRRYTNAAQGRY-----------------------------------------------------------------------------------------  229
  DHFR_scpA_Mycoplasma_p KRVLLKV---NHHISLMYFITAFVALLVLINNQIIDIEQ-TS-FDDELYICLLDSSRIEQLQETPEAMVERAVKQRQEAQELARQVAREKAIANAQKREAYLKAKYGKDYLTREQFLKLSPEERAAHVAKMKQLKLVKNDNGRDN  506
        scpA_Deinococcus WTV--------HADDWGERTTYFAALLEGVKEGSFQVEQ-PE-MYGDIRVHAAQAETKEETGGEVPSPVS---------------------------------------------------------------------------  277
         scpA_Pyrococcus WDLVF-------DVDPKIIARTFLYLLFLENMGKVEMIQ-EE-PFGEILVVPVKIS-----------------------------------------------------------------------------------------  218
      scpA_Methanococcus QEKF---------KTREDRVRYFIPSLYLANDGKAELIQ-EK-LFGELIIKLKSF------------------------------------------------------------------------------------------  226
   scpA_Methanosarcina_a SELL---------RMSEDRVMDYLSLLFLASSRKVWLFQ-SE-MFGELYIYPGEESGFSTEGNPPLFHQMKQGLIEDVSAPELSRREKFAGSKPQVEGMDRAPDEAVYPEVLSFEPEHIDINSPVDSPEETR-------------  361
  scpA_Archaeoglobus_ful FSLVK-------SWDVPTLVDYYVSVLHLAFRKKVEIRQ-EE-FYGDVEIQKF--------------------------------------------------------------------------------------------  224
     scpA_Thermosynec_el QKLL---------QRKPDAVGVFWALLFLAAQSKVDLQQ-TD-FYQPLQVRTCLPDAIPLEDLG---------------------------------------------------------------------------------  254
      scpA_Trichodesmium NEQI-------NVQVKSDRVGAFWALLLLSAQSKIELSQ-EE-FYQEIKIHTISSHSQEQKVLDDKI------------------------------------------------------------------------------  284
 scpA_Prochloroccc_marin EQLVGQWEQVSTADLDTDRVGVFWALLFLCSQGKVELAQ-EGSLYAPLRLKRLLAPGTIAQLPLTSLNVPAATPAEVVNAA----------------------------------------------------------------  304
        scpA_Ferroplasma VEDYW-------GNTKYERANFILFLLFLERGGKVTLNQ-EE-PFGNIEVIKLF-------------------------------------------------------------------------------------------  259
  scpA_Thermoplasma_volc MSEIW-------GNTRRERAVFFLYSMFLFRDGRISLSQ-EE-PNGDILIETNVI------------------------------------------------------------------------------------------  250
      scpA_Halobacterium AEI---------AAAGPSRVETFLAVLFLAHRGAVTLAQ-DE-LFGDLWVQATEEFPAQAATVPPA-------------------------------------------------------------------------------  286
            scpA_Aquifex FNF----------LSKKDLVPQFMALLYLDYESKVRLFQ-EK-PFEDITVEILKT------------------------------------------------------------------------------------------  205
     scpA_Bifidobact_lon SELTR------DCTSRIEVVARFMAVLVFFKQGVLQYQQ-DG-PFAELHLRWVSGVDETMNDVNISEGDFA--------------------------------------------------------------------------  304
         scpA_Ureaplasma FDIQAV-----IDKNKRFFAIMFLIILILINRNEILFEELDNDYLLKINIERVVDDYNSSSVEQAKNLTSNLTKDTIINFKGEDNE-----------------------------------------------------------  294
      scpA_Fusobacterium DDLFL------EAENKLHLIYIFLAILELYKDAKINIDN------GEITKC----------------------------------------------------------------------------------------------  225
   scpA_Rhodopseudomonas LLRYMP----DPTQRATVLASSFAAALELVREGEVELHQ-SG-PLAPLYFRKRPPSPAMEAAALPDTPVG---------------------------------------------------------------------------  342
    scpA_Mycoplasma_pulm EMIFS-------LPSLSHFVITLIALLDLSRRQELLIYQ-DQ-QFGTIRIEKGPNYEE---------------------------------------------------------------------------------------  249
  scpA_Mycobacterium_tub SELVA------DCTAPIEIVGRFLALLELYRTRAVAFEQ-SE-PLGALQVSWTGDDAERSDEKERRL------------------------------------------------------------------------------  278
       scpA_Chloroflexus TDLLS------NDPTTEEVIVSFWAMLELLKRRAIVVEQ-TM-LFGPILIGRGTAPIVTEPADEDEL------------------------------------------------------------------------------  248
         scpA_Leptospira PELFER-----EKPEKAEIVATFLALLELSKQRILRAKQ-HK-LFGEIRLFLVEGHWNGTEQQSKD-------------------------------------------------------------------------------  261
          scpA_Cytophaga TEIIN------DIPVKMAVIYNFLSILELLALQKIQLHL-GE-GFNNFWIAQYDGEHAAVNEYANDIE-----------------------------------------------------------------------------  262
        scpA_Streptoc_pn QDLFK------EAQNVQEVITLFLATLELIKTQELILVQ-EE-SFGDIYLMEKKEESQVPQS-----------------------------------------------------------------------------------  242
          scpA_Treponema TELIK------Q-PSRADVVCAFVAILEAAKTHLVHISQ-PE-FFGPITLYAREVSPKVQDVCHA--------------------------------------------------------------------------------  252
   scpA_Clostridium_perf SEFIP------QCECKLEVVVTFMAMLELIKRSEIKVVQ-YE-NFGEIMMEKVIVNE----------------------------------------------------------------------------------------  248
 scpA_Desulfitobact_hafn SQLI-------RGTKRMEIIVSFLALLELLKSGKVHCEQ-SS-QNEEIFVFPTEKAWEFTEGE----------------------------------------------------------------------------------  101
scpA_Rhodospirillum_rubr LPPGLE----DPLVRRSAVAATFVATLELAKQGVLDLRQ-DGGVYAPITVRPVAAGNRTGVAP----------------------------------------------------------------------------------   81
                   ruler .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.....
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