A

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AfsA      1 -----MPEAAVLIDPVPTMDAEAEVVHPVGIEMVHRTRPEDAFPRNWVRLGRDRFAVEAVLPHDHPFFAPVGDDLHDPLL    75
ScbA      1 -----MPEAVVLINSASDANSIEQTALPVPMALVHRTRVQDAFPVSWIPKGGDRFSVTAVLPHDHPFFAPVHGDRHDPLL    75
BarX      1 -----------MTSTVPR-------------ELVHRAAVAEVFLTGWSRTAENRFALTAQWPRAHSYFTPVN-GCYDPLL    55
FarX      1 -------------------------------MVHRTSTAQVLLTDWQRLDDARFSVTARWPLSHAFFTPVGDGYYDPLM    48
JadW1     1 ------------MHTTSRG------------EFVHRADPADIIPTDWTQLRQNRFSVSARVACLRSLLLSRAGARHDPML    56
AvaA      1 MSVVLDDSRTMKAPSMGATVEVLSFLQPVTRELVHRSSIAEVFVTDGVRTGENAFSVGAQWPRDHALYHPDENGLNDPLL    80
                                          . ***   .  .  .  .  .    .*.. *  .  .  .  ..     **..

AfsA     76 VAEAMRQAAMLAFHAGYGIPLGYHFLLTELDYV-CHPEHLGVGGEPTEIGLEVFCSDLKWRAGLPAQGRVGWAVHRGDRL   154
ScbA     76 IAETLRQAAMLVFHAGYGVPVGYHFLMATLDYT-CHLDHLGVSGEVAELEVEVACSQLKFRGGQPVQGQVDWAVRRAGRL   154
BarX     56 ASETIRQVGTLLSHAEFGVSFGDQFLMWDLHHS-VRPEQAGVGAAPADLELDVICSDIRRRGRRLAGMRYEVTLYCGGQV   134
FarX     49 CAETIRQIAYLLGHAEFAVPFGHQFVLWDLSVSVVRPELLRVGLVPATVDLAITCVEIKRRAGRLSGLGYEAVVRRDGQV   128
JadW1    57 VAETIPETSMLVAHAELGVPLDEQFVMWDLSYS-ADSEALTVDGLSSDVTVDVVCSDITRRGSRLRNLRTTVVLTRDDRL   135
AvaA     81 FAETLRQAHFYGAHTYFGVPVGSRFIGQDVSFEITDPTALRVGAAPLAVVLNGTWTEERDRRGRPAGARLDVTLTVDGRP   160
             .*. ..   .  *.  ... .  *   ..      .. . *.  .    . . ..    * ..    .      . ..

AfsA    155 AATGVAATRFSTPKAYRRMRGD-VPVEG----ISLPETAPVPASPAGRARVEDVVLSGTGREGVWELRVDTRHPTLFQRP   229
ScbA    155 AATGTATTRFTSPQVYRRMRGD-FATPT----ASVPGTAPVPAARAGRTRDEDVVLSASSQQDTWRLRVDTSHPTLFQRP   229
BarX    135 IATGGAAFDCTSPAVYQRLRGDRVGATGV---RPLP--QPLAPASVGRFLTTDVVLSATERPLEWQLRVDEQHPVLFDHP   209
FarX    129 VATGRASVTCTSPAVYQRIRPEHVLTPEH---RPLPLTAPAAPQSVARLSPTDVVLSPLDRENRWQLRVDTNHPVLFDHW   205
JadW1   136 LATGSGTARCTSALAYRRMRGERMEALG----RPVPLIPGVHPRLVGRARTEDVVLAPGNRPDQWQLRVNTAHTTLFRRP   211
AvaA    161 CGRGHTRGLMLDDRRYRLLRGRPAASGEVSPPRPAPDARIARPNRVGRLRWKDCVLERDRPDQDWRLRVDRDHAVLFDHP   240
             ..* .    ...  *.. *.           .. *   .  .  ..* .  *.**.   .   * ***.. *. **  .

AfsA    230 NDHVPGMLLLEAARQAACLVA--------GPAGIVPVEARTRFHRYSEFGSPCWIGAVVQPGA-DED-TVTVRVTGHQDG   299
ScbA    230 NDHVPGMLLLEAARQAACLVT--------GPAPFVPSIGGTRFVRYAEFDSPCWIQATVRPGP-AAG-LTTVRVTGHQDG   299
BarX    210 VDHVPGMVLMESARQAAQAID--------PSRPFLPTTMRSEFSRYAELDRPCWIQAEPLPAA-DNG-DRQVRVTGHQDD   279
FarX    206 VDHVPGMVLMEAARQAAASAL--------GRPSFMPLGVAGEFKRYVELDAPCVIESERLFQD-VPGAEEVVRVTGHQNG   276
JadW1   212 NDHVPGMVLLEAARQAATATT--------GSAAYLPTDLSVSFLRYVELDSPCWIEAESVPTP-DPS-TTTIRVTGHQDG   281
AvaA    241 TDHVPLMVMLEGFRQLGHLTVHEASRRTLGDRAFALAGLSLDCAAFGELGETILLSLEKGPSEGVPTEECALRVAAHQGE   320
             ****.*...*..**..            .   . .      . .. *.. .... ..  .          .**..**..

AfsA    300 ETVFSTVLSGP-------------RAHG                                                      314
ScbA    300 SLVFLTTLSGP-------------AFSG                                                      314
BarX    280 TTVFSCLIGTR-------------GAAE                                                      294
FarX    277 ELTFVGTVTAS-------------SYGY                                                      291
JadW1   282 SPVFRCTLTSPSRELSVATAGLDTRLAG                                                      309
AvaA    321 RLLARADMTWKCVG----SRAPWSRFASW                                                     345
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B

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AfsA/19-102      EVVHPVGIEMVHRTRPEDAFPRNWVRLGRDRFAVEAVLPHDHPFFAPVGDDLHDPLLVAEAMRQAAMLAFHAGYGIPLGYH-FLL
ScbA/19-102      QTALPVPMALVHRTRVQDAFPVSWIPKGGDRFSVTAVLPHDHPFFAPVHGDRHDPLLIAETLRQAAMLVFHAGYGVPVGYH-FLM
BarX/1-82        -MTSTVPRELVHRAAVAEVFLTGWSRTAENRFALTAQWPRAHSYFTPV-NGCYDPLLASETIRQVGTLLSHAEFGVSFGDQ-FLM
FarX/1-75        ---------MVHRTSTAQVLLTDWQRLDDARFSVTARWPLSHAFFTPVGDGYYDPLMCAETIRQIAYLLGHAEFAVPFGHQ-FVL
JadW1/1-83       -MHTTSRGEFVHRADPADIIPTDWTQLRQNRFSVSARVACLRSLLLSRAGARHDPMLVAETIPETSMLVAHAELGVPLDEQ-FVM
AvaA/24-107      SFLQPVTRELVHRSSIAEVFVTDGVRTGENAFSVGAQWPRDHALYHPDENGLNDPLLFAETLRQAHFYGAHTYFGVPVGSR-FIG
                      .  . ***   .  .  .  .  .    .*.. *  .  .  .  .      **.. .*. ..   .  *.  ... .   *
AfsA/185-264     PETAPVPASPAGRARVEDVVLSGTGREGVWELRVDT----RHPTLFQRPNDHVPGMLLLEAARQAACLVAGPAGIVPVEAR-TRF
ScbA/185-264     PGTAPVPAARAGRTRDEDVVLSASSQQDTWRLRVDT----SHPTLFQRPNDHVPGMLLLEAARQAACLVTGPAPFVPSIGG-TRF
BarX/165-244     PLPQPLAPASVGRFLTTDVVLSATERPLEWQLRVDE----QHPVLFDHPVDHVPGMVLMESARQAAQAIDPSRPFLPTTMR-SEF
FarX/161-240     PLTAPAAPQSVARLSPTDVVLSPLDRENRWQLRVDT----NHPVLFDHWVDHVPGMVLMEAARQAAASALGRPSFMPLGVA-GEF
JadW1/167-246    PLIPGVHPRLVGRARTEDVVLAPGNRPDQWQLRVNT----AHTTLFRRPNDHVPGMVLLEAARQAATATTGSAAYLPTDLS-VSF
AvaA/196-276     PDARIARPNRVGRLRWKDCVLERDRPDQDWRLRVDR----DHAVLFDHPTDHVPLMVMLEGFRQLGHLTVHEASRRTLGDRAFAL
                 *   .     ..*    *.**.       * ***..     *. **   . ****.*...*..**..    .     .      .
PKS/1046-1122    -------RQLVHKDYDHNVLLARLSRADENTVLAEMVQDPAHPFFYEHPKDHVPGLYLVEAARQLVTALSHVYHGVAMGKA-FIL
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