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BpsA      1  -----MAFILLSIGTSLPAYNVNQEKAAEFARYM
SrsA      1  -----MTRIAAVHGALPPHRHTQREVTDLVART
Pks18     1  -MNVSAESGAPRRAGQRHEVGLAQLPPAPPTTVAVLEGLATGTPRRVNVQSDAADRVAEL
ArsC      1  -----MNDMAHPNSAVLADFIPVQLAKPVPQRITLLETAYGFARAHCLSNGITDEEGFVQ
CHS       1  MVSVSEIRKAQRAEG-----PATLLAIGTANPANCVEQSTYPDFYFKI

BpsA      29  FQHSFK--DIDRLLSSFKNQIHSRQFVKPIEW-----YKEGHSFEEKNQIYIEETL
SrsA      29  CLPPGA--DRRVLDRLENARVRARHTVLPDGL-----YRALDGFGLTNDVVFIRSAV
Pks18     60  FLDPGQ--RERIPRVYQKSRIITRRMAVDPLDAKFD--VFRREPATIRDRMHLEFYEHAV
ArsC      56  VYKTVKEKFDKYAVSPAQIKQRQLVYFPKLTDIRFGDGNFDIADPEPDQAHLRLEFDIKKD
CHS       44  TNSEHKTELKEKFQRMCDKSMIKRRYMYLTEEILKENPNVCEYMAPSLDARQDMVVVEVP

BpsA      79  KHSRAAVRECLSHPEFF-----QEAIPYEKVEAVFFVSSTGLSTPSIEARLMNELPFSPL
SrsA      79  DLGARAVRGALRS-----AGLRPTDVDLLMFTSVTGIAAPSVDARLVTRLCMRS
Pks18     115  PLAVDVSKRALAG-----LPYRAAEIGLLVLATSTGFIAPGVDVAIVKELGLSLP
ArsC      116  PRGADLKRTHESYAKVVGKGLEQMFEGTLEAPDDLIVHTCSCYLAPSPAERMVADRGWFE
CHS       104  RLCKEAAVKAIKE-----WGQPKSKITHLIVCTTSGVDMPGADYQLTKLLGLRP

BpsA      133  YTKRIPIWGLGCAGGASGLARAAEYCK-----AYPEAFVLVVISAEELCSLTFQ-PEDKTK
SrsA      128  DVKRLPVFGLGCVAGAAGTARLHDYLL-----GRPDDVAVLLSVELCSLTFQ-RHDASP
Pks18     164  SISRVVVFNMGCAAAMNALGTATNYVR-----AHPAMKALVVCIELCSVNAV-FADDIN
ArsC      176  TTVTHSYN-MGCYGAFFPAIKMAHGMLASAQWGATPKTRVDIAHTELMSAHNN-IAESRV
CHS       153  YVKRYMMYQQGCFAGGTVLRRLAKDLAE-----NNKGARVLVVCSEVTAVTFRGPSTHLL
          *

BpsA      186  SNLIGTSLFGDGIAAALLCGEKADRRVSKLKLAPKIMDAQSVLTKQSEDVMGWDFTDQGF
SrsA      181  ANLVATALFGDGAALVALGGR-----RAVSGPEIVATRSRMYPDTEHVMGWVVGSTGF
Pks18     217  -DVVIHSLFGDGCALVIGASQVQEK--LEPGKVVRSSFSQLDNTEDGIVLGVNHNGLI
ArsC      234  DNIISATLFSDELKIKYSVYPEDELRR--QGLRGLRILAMSEHLLPDSADTMTGVPGSHQF
CHS       207  DSLVGOALFGDGAALIVGSDPVP--EIEKPIFEMVWTAQTIAPDSEGAIDGHLREAGL

BpsA      246  KVIFSRDIPTLVEKWLKTNVQIFLDKHKLSF--HDISVFLAHPGGKKVIDAYIKSLGLS
SrsA      235  RVVLDPAVPDVRQYLADDVREFLDEHGLKP--KDVAVHWVCHPGGPKVLEAVTEVLDLP
Pks18     274  TCENLSENLPGYIFSGVAPVVTMLWDNGLQI--SDIDLWAIHPGGPKIIEQSVRSGLGIS
ArsC      292  VMTLSPLVPPIIKRHVRAFAVDLRRRAGMDFERDKDALSFAIHPGGPKIVDHVQEELGLA
CHS       264  TFHLLKDVPGIVSKNITKALVEAFEPLGISD--YNSIFWIAHPGGPAILDQVEQKLALK
          *

BpsA      303  SEKLSSAQSILOKHGNMSSATILYVIKDHLQNGH-----KKEAERGLIGALGPGFSSE
SrsA      292  DGALDVTWRSLADVGNLSSSVLHVLRDTIEQRR-----PEPGTPLLAMGPGFCCE
Pks18     331  AELAAQSWDVLARFGNMLSVSLIFVLETMVQQAES-----AKAISTGVAFAGPGVTVVE
ArsC      352  EDQVAISKSVFLENGNMSSSTIPHILKAYLEEAT-----VGTRIACLGFGPGLTAA
CHS       321  PEKMNATREVLSEYGNMSSACVLFILDEMRKKSTQNGLKTTEGLEWGVLFVFGPGPLTIE
          *

BpsA      356  LLIFSWEKGA
SrsA      345  LVLWRW----
Pks18     385  GMLFDIIRR-
ArsC      403  GLVLEKI---
CHS       381  TVVLRVVAI-

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Fig. S1. Nakano et al.