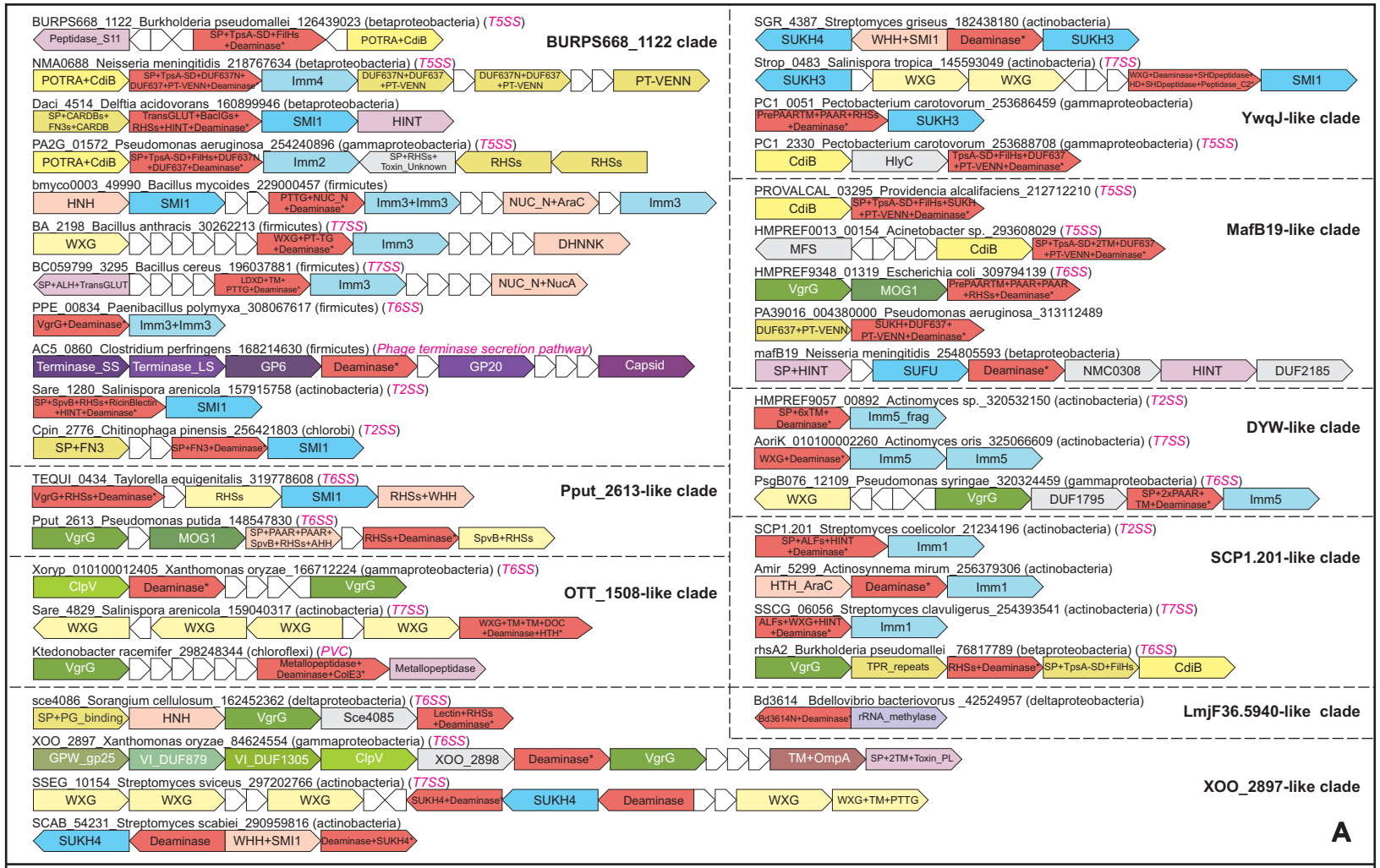
BURPS668_1122 clade
BURPS668_1122_Burkholderia pseudomallei_126439023 (betaproteobacteria) (T5SS)
Peptidase_S11
SP+TpsA-SD+FilHs +Deaminase*
POTRA+CdiB
NMA0688_Neisseria meningitidis_218767634 (betaproteobacteria) (T5SS)
POTRA+CdiB
SP+TpsA-SD+DUF637N+ DUF637+PT-VENN+Deaminase*
Imm4
DUF637N+DUF637 +PT-VENN
DUF637N+DUF637 +PT-VENN
PT-VENN
Daci_4514_Delftia acidovorans_160899946 (betaproteobacteria)
SP+CARDBs+ FN3s+CARDB
TransGLUT+BacIGs+ RHSs+HINT+Deaminase*
SMI1
HINT
PA2G_01572_Pseudomonas aeruginosa_254240896 (gammaproteobacteria) (T5SS)
POTRA+CdiB
SP+TpsA-SD+FilHs+DUF637N +DUF637+Deaminase*
Imm2
SP+RHSs+ Toxin_Unknown
RHSs
RHSs
bmyco0003_49990_Bacillus mycoides_229000457 (firmicutes)
HNH
SMI1
PTTG+NUC_N +Deaminase*
Imm3+Imm3
NUC_N+AraC
Imm3
BA_2198_Bacillus anthracis_30262213 (firmicutes) (T7SS)
WXG
WXG+PT-TG +Deaminase*
Imm3
DHNNK
BC059799_3295_Bacillus cereus_196037881 (firmicutes) (T7SS)
SP+ALH+TransGLUT
LDXD+TM+ PTTG+Deaminase*
Imm3
NUC_N+NucA
PPE_00834_Paenibacillus polymyxa_308067617 (firmicutes) (T6SS)
VgrG+Deaminase*
Imm3+Imm3
AC5_0860_Clostridium perfringens_168214630 (firmicutes) (Phage terminase secretion pathway)
Terminase_SS
Terminase_LS
GP6
Deaminase*
GP20
Capsid
Sare_1280_Salinispora arenicola_157915758 (actinobacteria) (T2SS)
SP+SpvB+RHSs+RicinBlectin +HINT+Deaminase*
SMI1
Cpin_2776_Chitinophaga pinensis_256421803 (chlorobi) (T2SS)
SP+FN3
SP+FN3+Deaminase*
SMI1
Pput_2613-like clade
TEQUI_0434_Taylorella equigenitalis_319778608 (T6SS)
VgrG+RHSs+Deaminase*
RHSs
SMI1
RHSs+WHH
Pput_2613_Pseudomonas putida_148547830 (T6SS)
VgrG
MOG1
SP+PAAR+PAAR+ SpvB+RHSs+AHH
RHSs+Deaminase*
SpvB+RHSs
OTT_1508-like clade
Xoryp_010100012405_Xanthomonas oryzae_166712224 (gammaproteobacteria) (T6SS)
ClpV
Deaminase*
VgrG
Sare_4829_Salinispora arenicola_159040317 (actinobacteria) (T7SS)
WXG
WXG
WXG
WXG
WXG+TM+TM+DOC +Deaminase+HTH*
Ktedonobacter racemifer_298248344 (chloroflexi) (PVC)
VgrG
Metallopeptidase+ Deaminase+ColE3*
Metallopeptidase
sce4086_Sorangium cellulosum_162452362 (deltaproteobacteria) (T6SS)
SP+PG_binding
HNH
VgrG
Sce4085
Lectin+RHSs +Deaminase*
XOO_2897_Xanthomonas oryzae_84624554 (gammaproteobacteria) (T6SS)
GPW_gp25
VI_DUF879
VI_DUF1305
ClpV
XOO_2898
Deaminase*
VgrG
TM+OmpA
SP+2TM+Toxin_PL
SSEG_10154_Streptomyces sviceus_297202766 (actinobacteria) (T7SS)
WXG
WXG
WXG
SUKH4+Deaminase
SUKH4
Deaminase
WXG
WXG+TM+PTTG
SCAB_54231_Streptomyces scabiei_290959816 (actinobacteria)
SUKH4
Deaminase
WHH+SMI1
Deaminase+SUKH4*
YwqJ-like clade
SGR_4387_Streptomyces griseus_182438180 (actinobacteria)
SUKH4
WHH+SMI1
Deaminase*
SUKH3
Strop_0483_Salinispora tropica_145593049 (actinobacteria) (T7SS)
SUKH3
WXG
WXG
WXG+Deaminase+SHDpeptidase+ HD+SHDpeptidase+Peptidase_C2*
SMI1
PC1_0051_Pectobacterium carotovorum_253686459 (gammaproteobacteria)
PrePAARTM+PAAR+RHSs +Deaminase*
SUKH3
PC1_2330_Pectobacterium carotovorum_253688708 (gammaproteobacteria) (T5SS)
CdiB
HlyC
TpsA-SD+FilHs+DUF637 +PT-VENN+Deaminase*
MafB19-like clade
PROVALCAL_03295_Providencia alcalifaciens_212712210 (T5SS)
CdiB
SP+TpsA-SD+FilHs+SUKH +PT-VENN+Deaminase*
HMPREF0013_00154_Acinetobacter sp._293608029 (T5SS)
MFS
CdiB
SP+TpsA-SD+2TM+DUF637 +PT-VENN+Deaminase*
HMPREF9348_01319_Escherichia coli_309794139 (T6SS)
VgrG
MOG1
PrePAARTM+PAAR+PAAR +RHSs+Deaminase*
PA39016_004380000_Pseudomonas aeruginosa_313112489
DUF637+PT-VENN
SUKH+DUF637+ PT-VENN+Deaminase*
mafB19_Neisseria meningitidis_254805593 (betaproteobacteria)
SP+HINT
SUFU
Deaminase*
NMC0308
HINT
DUF2185
DYW-like clade
HMPREF9057_00892_Actinomyces sp._320532150 (actinobacteria) (T2SS)
SP+6xTM+ Deaminase*
Imm5_frag
AoriK_010100002260_Actinomyces oris_325066609 (actinobacteria) (T7SS)
WXG+Deaminase*
Imm5
Imm5
PsgB076_12109_Pseudomonas syringae_320324459 (gammaproteobacteria) (T6SS)
WXG
VgrG
DUF1795
SP+2xPAAR+ TM+Deaminase*
Imm5
SCP1.201-like clade
SCP1.201_Streptomyces coelicolor_21234196 (actinobacteria) (T2SS)
SP+ALFs+HINT +Deaminase*
Imm1
Amir_5299_Actinosynnema mirum_256379306 (actinobacteria)
HTH_AraC
Deaminase*
Imm1
SSCG_06056_Streptomyces clavuligerus_254393541 (actinobacteria) (T7SS)
ALFs+WXG+HINT +Deaminase*
Imm1
rhsA2_Burkholderia pseudomallei_76817789 (betaproteobacteria) (T6SS)
VgrG
TPR_repeats
RHSs+Deaminase*
SP+TpsA-SD+FilHs
CdiB
LmjF36.5940-like clade
Bd3614_Bdellovibrio bacteriovorus_42524957 (deltaproteobacteria)
Bd3614N+Deaminase*
rRNA_methylase
XOO_2897-like clade
A
B
PVC
Terminase pathway
T6SS
T7SS
T2SS
T5SS
PVC-AAA
ColE3
MYND
Metallopeptidase
Terminase_SS
Terminase_LS
XOO_2898
Deaminase_7
FBOX
DOC
TPR
GP6
VI_DUF1305
ClpV
TGT
HNH
HTH
SIR2
sce4085
VI_DUF879
VgrG
AHH
Pput_2614
GPW_gp25
MOG1
Deaminase_11
LamG
Transglu
SpvB
Deaminase_8
PG_binding
RHS
beta-propeller
LDXD
LxG
WXG
LINKER
NUC-N
BactIG
PT-TG
PrePAARTM
PAAR
FN3
HINT
ALF
BicinB-lectin
FilH
DUF637
PT-VENN
DUF637N
SP
TM
PseudoN
NTalpha
TPSASD
CdiB
HlyC
PPR
CdiAC
ANK
Deaminase_5
Deaminase_3
Toxin_PL
HD
Peptidase_C2
LF
CCCH
Deaminase_9
SAM
Tu
Deaminase_10
AT-hook
SET
Deaminase_12
Bd3614N
THT
dsRBD
Deaminase_13
Imm2
Imm4
Imm3
Imm1
Imm5
Deaminase_1
Deaminase_6
Deaminase_2
SUKH4
HTH_AraC
SMI1
SUKH3
NMC0308
Deaminase_4
SUFU
Deaminase_1: BURPS668_1122-like
Deaminase_2: SCP1.201-like
Deaminase_3: YwqJ-like
Deaminase_4: MafB19-like
Deaminase_5: DYW-like
Deaminase_6: XOO_2897-like
Deaminase_7: OTT_1508-like
Deaminase_8: B3gp45-like
Deaminase_9: CDD-like
Deaminase_10: AID/APOBEC-like
Deaminase_11: Pput_2613-like
Deaminase_12: Tad2-like
Deaminase_13: Tad1/ADAR-like