Systems analogous to the Butirosin biosynthesis
SWIM
COOH_NH2_ ligase
182625462 (Clostridium perfringens)
COOH_NH2_ ligase
Aig2
160941832 (Clostridium bolteae)
Systems prototyped by Friulimicin and Bacilysin biosynthesis
ATPgrasp_DabC
Arg_lyase
226871503 (Actinosynnema mirum)
PLPDE
ATPgrasp_DabC
134293847 (Burkholderia vietnamiensis)
PqqC
PLPDE_ aminotransferase
CP_ATPgrasp
37526105 (Photorhabdus luminescens)
Novel peptide synthesis/protein tagging system
CP_ATPgrasp_inact
alpha_E
alpha_E
118473643 (Mycobacterium smegmatis)
transglutaminase
permuted COOH _NH2_ligase
15609703 (Mycobacterium tuberculosis)
alpha_E
alpha_E
transglutaminase
3136019 (Mycobacterium leprae)
Novel systems which combine ligases of more than one fold
GNAT
RLAN
ATPgrasp_RimK
218150664 (Desulfovibrio salexigens)
GNAT
ATPgrasp_CyaS
15598656 (Pseudomonas aeruginosa)
GCS2
CP_ATPgrasp
183984988 (Mycobacterium marinum)
ATPgrasp_YheD
Mur_ligase
126650748 (Bacillus sp.)
GCS1
ATPgrasp_CyaS
22537960 (Streptococcus agalactiae)
ATPgrasp_CyaS
Mur_ligase
20141408 (Synechocystis sp.)
(Cyanophycin synthetase)
Systems combining a ligase and a peptidase/amidase
GCS2
M20_peptidase
226363571 (Rhodococcus opacus)
ATPgrasp_DaDalike
M20_peptidase
150391473 (Alkaliphilus metalliredigens)
Amidohydrolase_TIM
COOH_NH2_ ligase
585147 (Emericella nidulans)
NlpC/p60
CP_ATPgrasp_GlutSS
16130888 (Escherichia coli) (glutathionyl-spermidine synthetase)
GNAT
papain
90022556 (Saccharophagus degradans)
Systems with multiple ATP-grasp ligases
ATPgrasp_DaDalike
ATPgrasp_DaDalike
108757010 (Myxococcus xanthus)
ATPgrasp_DaDalike
ATPgrasp_DaDalike
D_aminopeptidase
162449160 (Sorangium cellulosum)
ATPgrasp_CPS_LS
HTH
HTH
ATPgrasp_CPS_LS
MGS
16128027 (Escherichia coli) (carbamoyl phosphate synthetase)
Miscellaneous
X
SET
ATPgrasp_TTL
11056036 (Homo sapiens)
2OGFeDO
ATPgrasp_TTL
224818354 (Thioalkalivibrio sp.)
Fem/MurM
Lysyl_tRNAsynthetase
15608778 (Mycobacterium tuberculosis)
YEATS
COOH_NH2_ ligase
223997528 (Thalassiosira pseudonana)
ATPgrasp_PurD
GarC
16131835 (Escherichia coli)
CofE
Nitro_reductase
46401596 (Streptomyces aureofaciens)
N_synthetase
CofE
237672647 (Brachybacterium faecium)
RLAN
ATPgrasp_RimK
15597140 (Saccharophagus degradans)
Systems involved in polysaccharide/sugar modifications
ATPgrasp_CyaS
Acyl ptase
15616215 (Bacillus halodurans)
alpha/alpha toroid
ATPgrasp_CyaS
126437616 (Mycobacterium sp.)
acyl tfase
ATPgrasp_CF
29348352 (Bacteroides thetaiotaomicron)
alpha/alpha toroid
Mur_ligase
PP2A
119870782 (Mycobacterium sp. KMS)
ATPgrasp_CF
Acyl ptase
alpha/alpha toroid
ATPgrasp_TupA
126437614 (Mycobacterium sp. JLS)
TPR
TPR
TPR
Fam1 Glycosyl transferase
ATPgrasp_TupA
225197477 (Desulfonatronospira thiodismutans)
Fam2 Glycosyl transferase
ATPgrasp_TupA
218563042 (Campylobacter jejuni)