Systems with Ligases of more than one fold

Cyanophycin Biosynthesis

- * Cyanophycinase | ATPgrasp+ Mur_ligase
  16330482 (Synechocystis sp.)
- Amidohydrolase_TIM | Cyanophycinase | ATPgrasp+ Mur_ligase | ATPgrasp+ Mur_ligase
  71281643 (Colwellia psychrerythraea)
- Cyanophycinase | Asparaginase_NTN | ATPgrasp+ Mur_ligase
  149173091 (Planctomyces maris)

Cyanophycin synthetase like

- N_synthetase | GNAT+ATPgrasp | M42peptidase
  15598656 (PA3460) (Pseudomonas aeruginosa)

Systems combining ATP-grasp COOH-NH2 ligases or Fem/MurM peptide ligases

- ab_hydrolase | ATPgrasp | CP_ATPgrasp | GCS2 | acylACP_synthase
  148656737 (RoseRS_2616) (Roseiflexus sp.)
- GCS2+ CP_ATPgrasp | N_synthetase | ab_hydrolase | ? | GNAT
  158314125 (Frankia sp.)
- Phytolike_transglut | ATPgrasp | GCS2
  162451860 (Sorangium cellulosum)
- GCS2 | CP_ATPgrasp | GAT-II
  162450526 (Sorangium cellulosum)
- ATPgrasp | CP_ATPgrasp | GAT-I | GCS2
  226226766 (Gemmatimonas aurantiaca)
- GGT_NTN | GCS2+ M20_peptidase
  226363571 (Rhodococcus opacus)
- LON_protease | ab_hydrolase | ATPgrasp | Fem/MurM
  86606555 (Synechococcus sp.)

Phage associated

- COOH_NH2_ligase | ? | COOH_NH2_ligase_phage | GAT-II_F6PAT | ? | ? | ATPgrasp
  167583639 (Enterobacteria phage phiEco32)
- CotE | ? | ATPgrasp_YheD | COOH_NH2_ligase | ATPgrasp_YheD
  218290134 (Alicyclobacillus acidocaldarius)

RimK-like ATP-grasp N-terminal domain (RLAN) associated

- papain protease | RLAN+ ATPgrasp_RimK | GCS2 | M20_peptidase
  74317472 (Thiobacillus denitrificans)
- RLAN | ATPgrasp_RimK | GCS2 | 4Fe-4S ferredoxin
  45358000 (Methanococcus maripaludis)
- RLAN | ATPgrasp_RimK | metal-sulfur cluster protein | GCS2
  116754981 (Methanosaeta thermophila)
- GNAT+ papain | RLAN+ ATPgrasp_RimK
  15597140 (PA1944) (Pseudomonas aeruginosa PAO1)

Systems with multiple ATPgrasp ligases

YheC/D-like systems

- YheA | Membrane Protein | ATPgrasp_YheD | ATPgrasp_YheD | YheE | SspB
  221308815 (Bacillus subtilis)
- Membrane Protein | ATPgrasp_YheD | ATPgrasp_YheD | ATPgrasp_YheD | ATPgrasp_YheD
  124522400 (Bacillus coagulans)
- ATPgrasp_YheD +Mur_ligase | ATPgrasp | Mur_ligase | Mur_ligase
  126650748 (Bacillus sp.)
- PP2A | PP2A | ATPgrasp_YheD | ATPgrasp_YheD
  169185234 (Paenibacillus sp.)

Myxococcus MXAN_4097-like systems with ATP-grasp, D-aminopeptidase and other peptidases

- 2xATPgrasp_DaDalike | Daminopeptidase
  108757010 (MXAN_4097) (Myxococcus xanthus)
- ATPgrasp_DaDalike | GGT_NTN | M20_peptidase
  163783735 (Hydrogenivirga sp.)
- GGT_NTN | ATPgrasp_DaDalike+M20 | M20_peptidase
  163763164 (Bacillus selenitireducens)

Systems with a single ligase and peptidase

Putrescine utilization system

- * PuuC_Ald_dehydrogenase | HTH | PuuD_GAT-I | GS_PuuA | permease
  89108143 (Escherichia coli)

FluG-like

- PuuD_GAT-I | Glutamine_synthetase | Amidohydrolase_TIM | APG_permease
  191637324 (Lactobacillus casei)

Systems with an inactive peptide formyl-glycine synthesizing enzyme

- GCS2 | DinB+Clectin | GAT-II | methylase
  15610840 (Mycobacterium tuberculosis)
- COOH_NH2_ligase | DinB+Clectin+ Methylase
  109899965 (Pseudoalteromonas atlantica)

Systems with a COOH-NH2 ligase associated with an AIG2 or GAT-I

- COOH_NH2_ligase | AIG2 | NLPC+M23
  89897292 (Desulfitobacterium hafniense)
- COOH_NH2_ligase+AIG2 | NLPC+M23
  160941832 (Clostridium bolteae)
- COOH_NH2_ligase | GAT-I
  114766840 (Roseovarius sp.)

Systems associated with a novel 7-TM

- Pepsinlike | inactransglut + 7TM | ATPgrasp_RimK
  15596963 (Pseudomonas aeruginosa)

Systems involved in polysaccharide/sugar modifications

Teichuronopeptide biosynthesis

- Glycosyl transferase | Glycosyl transferase | ATPgrasp_TupA | ATPgrasp_CyaS +acyl ptase | ATPgrasp_CyaS +acyl ptase | ATPgrasp_CyaS +acyl ptase
  15616217 (Bacillus halodurans)
- ATPgrasp_CyaS + a/a toroid | SET | acyl ptase+ a/a toroid
  126437616 (Mycobacterium sp. JLS)

O-Antigen biosynthesis

- RfbD/glF | wfdf | ATPgrasp_TupA | Glyco2 | wzy | Glyco1
  187880528 (Escherichia coli)
- ATPgrasp_TupA | ATPgrasp_TupA | ATPgrasp_CF | Glyco1 | Glyco1 | Glyco2
  167753436 (Alistipes putredinis)

Peptide synthesis/Protein tagging systems

Systems involved in Cell Wall synthesis D-Ala-D-Ala like

- * FtsW | MurG | MurC | ATPgrasp_DaDa | FtsQ | FtsA | FtsZ
  15799776 (Escherichia coli)
- * ATPgrasp_DaDa | VanY | acyltransf+ A_racemase | A_racemase
  145954476 (Clostridium difficile)
- ATPgrasp_DaDa | ab_hydrolase | ? | Mur_ligase
  32265630 (Helicobacter hepaticus)

Glutathione biosynthesis systems

- GCS1 | LuxS
  16130600 (Escherichia coli)
- ATPgrasp_GS | M20+Zincin
  37675691 (Vibrio vulnificus)
- NH3_transporter | GCS1 | ATPgrasp_GS
  107023796 (Burkholderia cenocepacia)
- GGT_NTN | GCS1 | ATPgrasp_CyaS
  45657677 (Leptospira interrogans)

Pupylation system

- * PAC2 | ? | Peptidase_M50 | ? | Proteasomal_AAA | PafA | PUP | Proteasomal_NTN_B | Proteasomal_NTN_A | PafA
  163840780 (Renibacterium salmoninarum)

Novel peptide synthesis system

- CP_ATPgrasp | alphaE | transglut
  15609548 (Rv2411c) (Mycobacterium tuberculosis H37Rv)
- GAT1 | CP_ATPgrasp | alphaE | transglut | Proteasome_peptidase
  15596927 (Pseudomonas aeruginosa) (Anbu)
- transglut+ permuted_GS | CP_ATPgraspi+ alphaE | transglut | ZnR+Zincin
  118473643 (Mycobacterium smegmatis)
- CP_ATPgrasp | alphaE | transglut | transglut+ permuted_GS | CP_ATPgraspi+ alphaE | transglut
  53721536 (Burkholderia pseudomallei)
- CP_ATPgrasp | transglut | alphaE
  15898151 (Sulfolobus solfataricus)

Siderophore and cofactor modifying systems

Siderophore biosynthesis

- PP_sidBP | ATPgrasp_PvsA | PvsB_D_kinase | sid_transporter | PvsB_D_kinase
  226357235 (Deinococcus deserti)

MptN

- ATPgrasp_RimK | M20_peptidase
  20092084 (Methanosarcina acetivorans)
- M20_peptidase | Pepsinlike | ATPgrasp_RimK | Succ_E_desuc
  15642279 (Vibrio cholerae)

MptN-like

- GHMP_kinase | dehydrogenase | ATPgrasp | Cyclohydrolase | ATPgrasp_RimK | phosphoribosyl transferase | FAE
  170743848 (Methylobacterium sp.)

CofF-like

- Peptidase_M50 | ATPgrasp_RimK | Mur_ligase
  163799948 (Methanococcus voltae)

Complex peptide derived metabolites

Friulimicin Biosynthesis like systems

- * Cys_synthase DabA | Arg_lyase DabB | ATPgrasp_DabC | NR_peptide_synthetase | GHMP_kinase
  126635114 (Actinoplanes friuliensis)
- GHMP_kinase | Cys_synthase | ATPgrasp_DabC +Arg_lyase
  134293847 (Burkholderia vietnamiensis)
- NR_peptide_synthetase | ? | Arg_lyase | PLPDE+ ATPgrasp_DabC | T_aldolase | NR_peptide_synthetase | GHMP_kinase
  226871503 (Actinosynnema mirum)
- Arg_lyase | Cys_synthase | ATPgrasp_DabC | T_aldolase
  226314775 (Brevibacillus brevis)
- T_aldolase | MFS | ATPgrasp | ATPgrasp
  56421297 (Geobacillus kaustophilus)
- HisRS | ATPgrasp | ATPgrasp
  150389826 (Alkaliphilus metalliredigens)

Friulimicin Biosynthesis-like systems with a circularly permuted ATP-grasp ligase

- 2-oxoacid_aldolase | PqqC | PLPDE_amino transferase | CP_ATPgrasp | Menaquinone_methylase
  111224051 (Frankia alni)
- PLPDE_amino transferase | Rossmann_redox | M24_amino peptidase | CP_ATPgrasp
  197784306 (Streptomyces sviceus)
- PqqC+Aminot +CP_ATPgrasp | E1 | 2OGFeDO | acetylase
  37526105 (Photorhabdus luminescens)

Bacilysin biosynthesis

- transporter | BacA | BacB | BacC | ATPgrasp_BacD | ? | PLPDE_amino transferase
  154687889 (Bacillus amyloliquefaciens)

Ribosomal peptide-metabolite biosynthesis systems

- ABC_ATPase | GNAT | ATPgrasp_RimK | ATPgrasp_RimK | Marinostatin_Microviridin | Marinostatin_Microviridin
  183206718 (Planktothrix agardhii)
- Papain+ABC_mem +ABC_ATPase | ? | Marinostatin_Microviridin | Marinostatin_Microviridin | ATPgrasp_RimK | ATPgrasp_RimK
  124009446 (Cyanothece sp.)
- TM_protein | Streptomyces_peptide | ATPgrasp_RimK
  21219223 (Streptomyces coelicolor)
- Actinomycete_peptide | ATPgrasp_RimK | Aspartyl-O-methylase
  21221320 (Streptomyces coelicolor)
- Bacteroidetes_peptide | Bacteroidetes_peptide | ATPgrasp_RimK | Dictinct_peptide | SAM_radical
  163753842 (Kordia algicida)

Butirosin biosynthesis-like systems

- ACP | ATPgrasp_Btr1 | Rossmann_redox | MurG
  226865117 (Actinosynnema mirum)
- Gly_C_acetyltfase_PLPDE | CP_ATPgrasp | Acyl_ACP_synthase | CP_ATPgrasp | MFS | GST
  78066459 (Burkholderia sp.)

Classical Butirosin biosynthesis system

- btrA | PLPDE | btrC | btrD | btrE | btrF | btrG_Aig2 | BtrH_papain | ACP | ATPgrasp_Btr1 | BtrK_PLPDE_decarboxylase | monooxygenase | PGmutase | BtrV | BtrQ | BtrW | BtrW
  70720850 (Bacillus circulans)