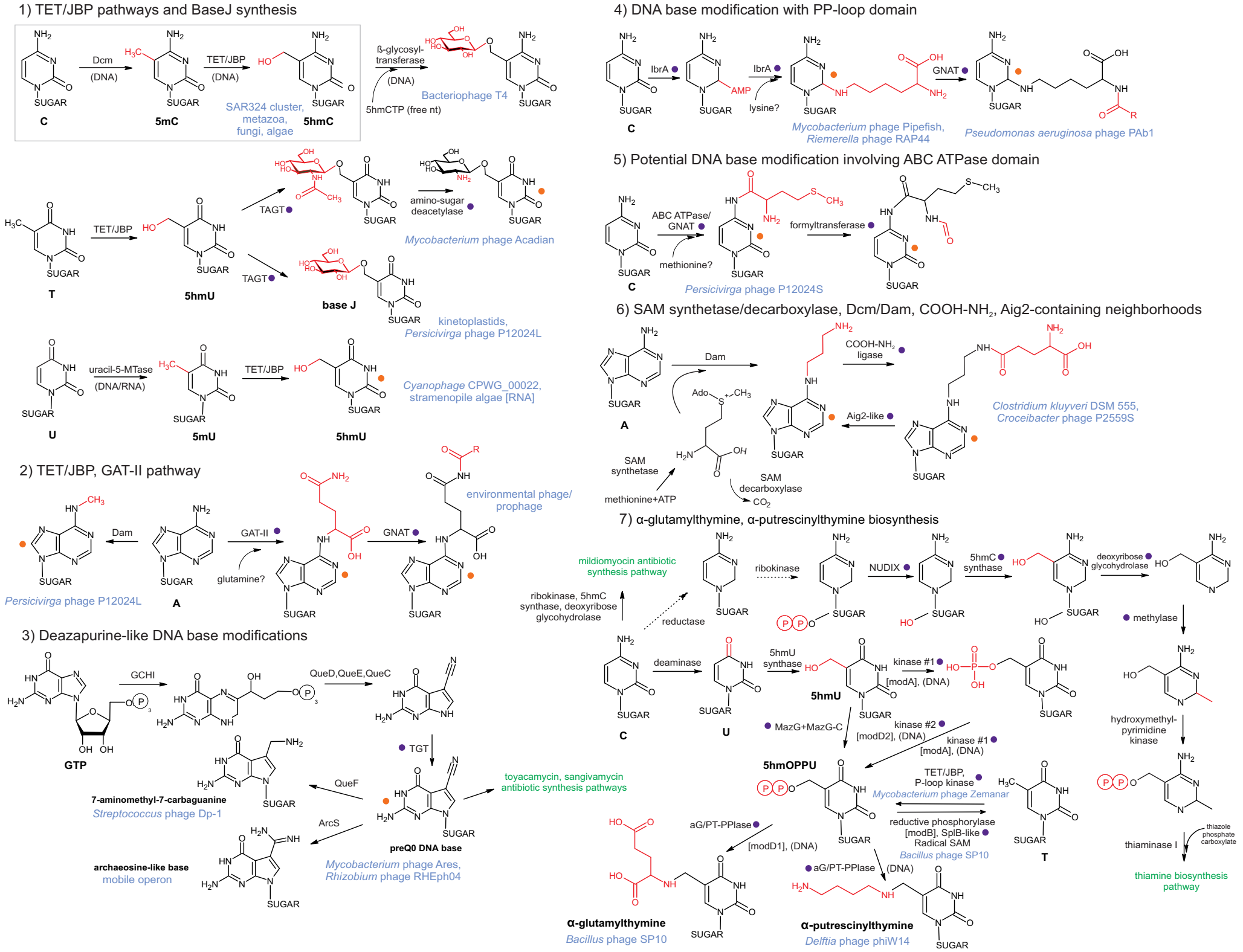
1) TET/JBP pathways and BaseJ synthesis
Dcm
(DNA)
TET/JBP
(DNA)
C
5mC
5hmC
SAR324 cluster, metazoa, fungi, algae
ß-glycosyl-transferase
(DNA)
5hmCTP (free nt)
Bacteriophage T4
T
5hmU
TET/JBP
TAGT
amino-sugar deacetylase
Mycobacterium phage Acadian
base J
kinetoplastids, Persicivirga phage P12024L
U
uracil-5-MTase
(DNA/RNA)
5mU
5hmU
Cyanophage CPWG_00022, stramenopile algae [RNA]
2) TET/JBP, GAT-II pathway
Dam
GAT-II
glutamine?
GNAT
environmental phage/ prophage
Persicivirga phage P12024L
A
3) Deazapurine-like DNA base modifications
GCHI
QueD,QueE,QueC
GTP
TGT
QueF
ArcS
7-aminomethyl-7-carbaguanine
Streptococcus phage Dp-1
toyacamycin, sangivamycin antibiotic synthesis pathways
preQ0 DNA base
Mycobacterium phage Ares, Rhizobium phage RHEph04
archaeosine-like base
mobile operon
4) DNA base modification with PP-loop domain
IbrA
AMP
lysine?
GNAT
Mycobacterium phage Pipefish, Riemerella phage RAP44
Pseudomonas aeruginosa phage PAb1
5) Potential DNA base modification involving ABC ATPase domain
ABC ATPase/ GNAT
methionine?
formyltransferase
Persicivirga phage P12024S
6) SAM synthetase/decarboxylase, Dcm/Dam, COOH-NH2, Aig2-containing neighborhoods
Dam
COOH-NH2 ligase
Aig2-like
SAM synthetase
methionine+ATP
SAM decarboxylase
Clostridium kluyveri DSM 555, Croceibacter phage P2559S
7) α-glutamylthymine, α-putrescinylthymine biosynthesis
mildiomycin antibiotic synthesis pathway
ribokinase, 5hmC synthase, deoxyribose glycohydrolase
reductase
ribokinase
NUDIX
5hmC synthase
deoxyribose glycohydrolase
methylase
deaminase
5hmU synthase
kinase #1 [modA], (DNA)
kinase #2 [modD2], (DNA)
MazG+MazG-C
5hmOPPU
TET/JBP, P-loop kinase
Mycobacterium phage Zemanar
reductive phosphorylase [modB], SplB-like Radical SAM
Bacillus phage SP10
hydroxymethyl-pyrimidine kinase
thiaminase I
thiazole phosphate carboxylate
thiamine biosynthesis pathway
aG/PT-PPlase
[modD1], (DNA)
α-glutamylthymine
Bacillus phage SP10
α-putrescinylthymine
Delftia phage phiW14