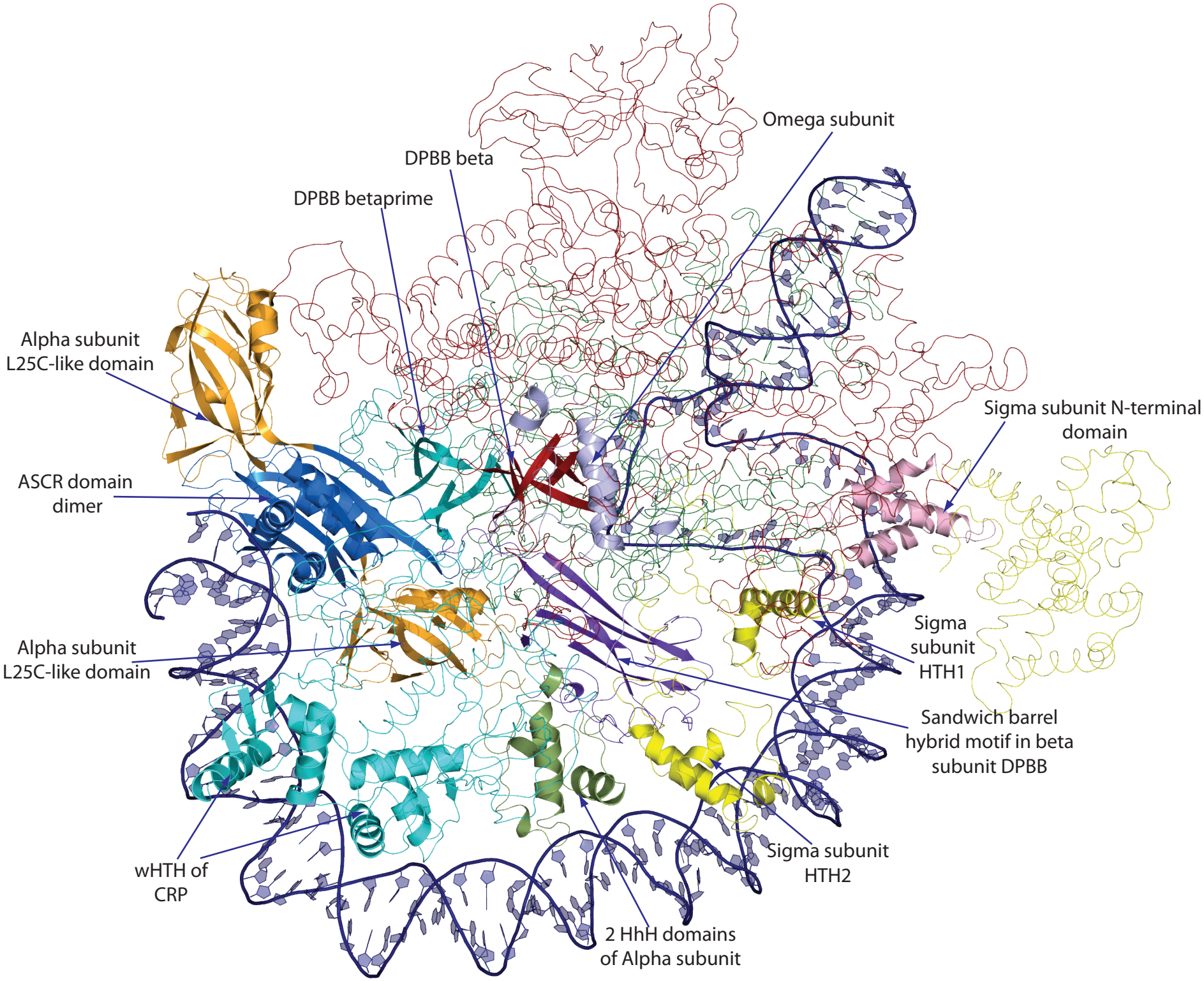
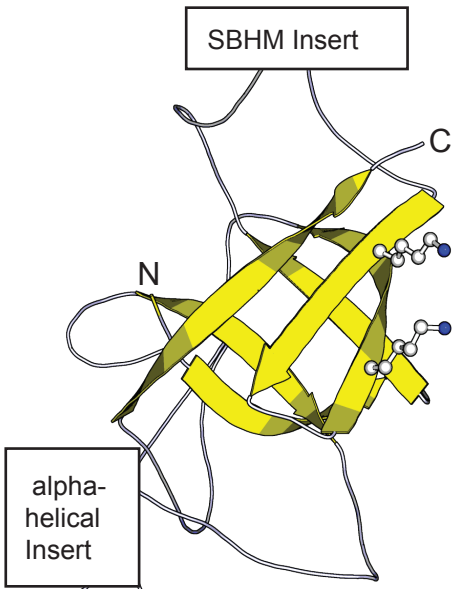
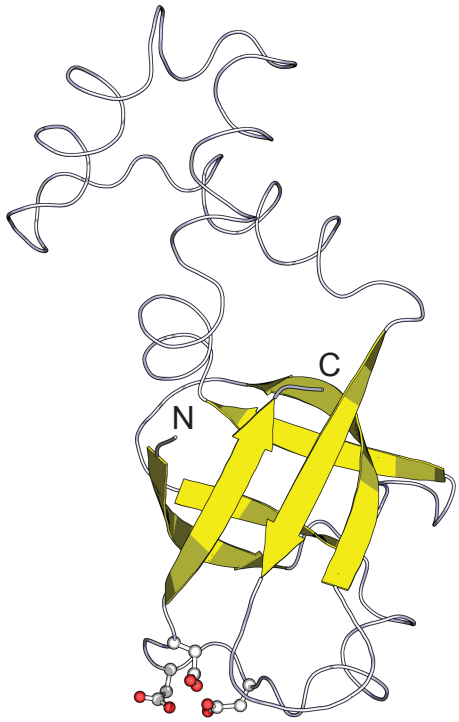
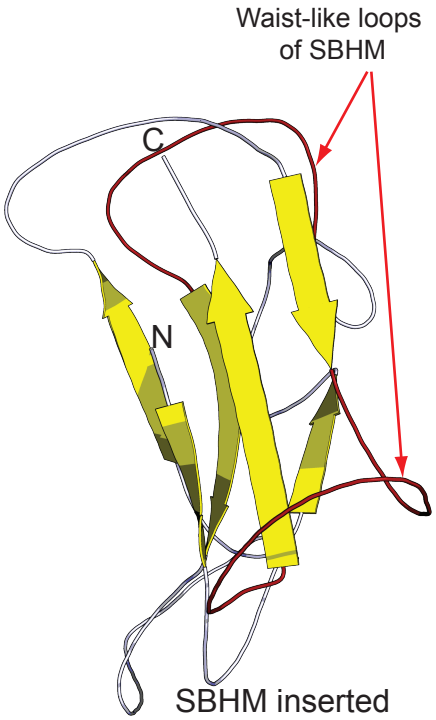

Omega subunit
DPBB beta
DPBB betaprime
Alpha subunit
L25C-like domain
Sigma subunit N-terminal
domain
ASCR domain
dimer
Sigma
subunit
HTH1
Alpha subunit
L25C-like domain
Sandwich barrel
hybrid motif in beta
subunit DPBB
wHTH of
CRP
Sigma subunit
HTH2
2 HhH domains
of Alpha subunit



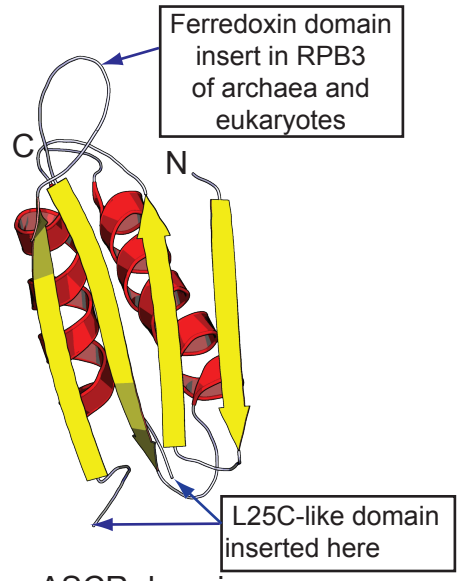
DPBB
β subunit
(PDB: 1iw7C)



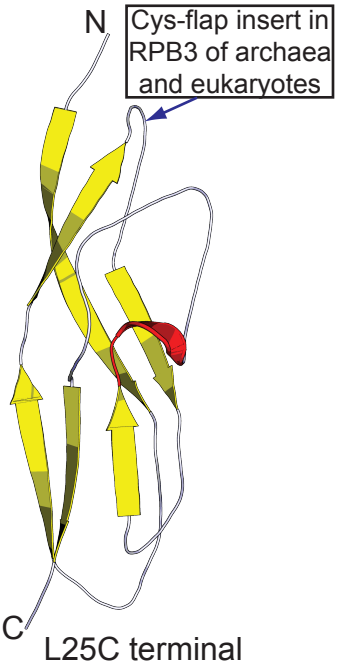
DPBB
β' subunit
(PDB: 1iw7D)



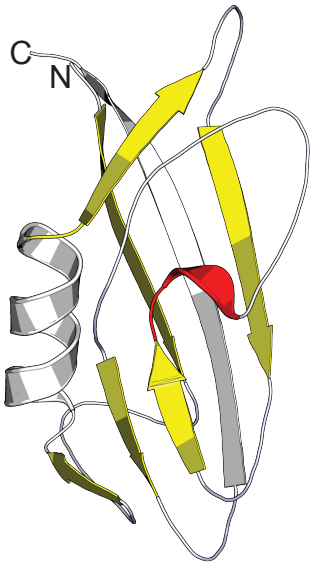
SBHM inserted
in DBPP
β subunit
(PDB: 1iw7C)



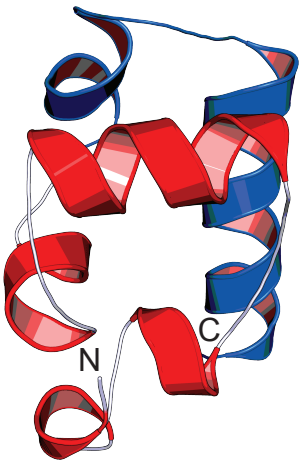
ASCR domain
α subunit
(PDB: 1iw7A)



L25C terminal
domain
(PDB: 1feu)

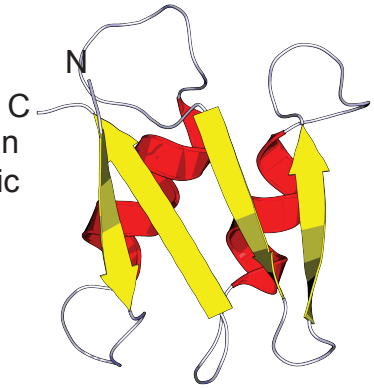


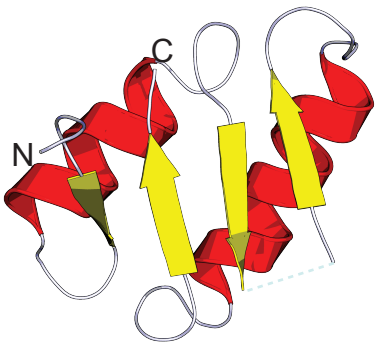
L25C-like
domain in α subunit
ASCR(PDB: 1iw7A)



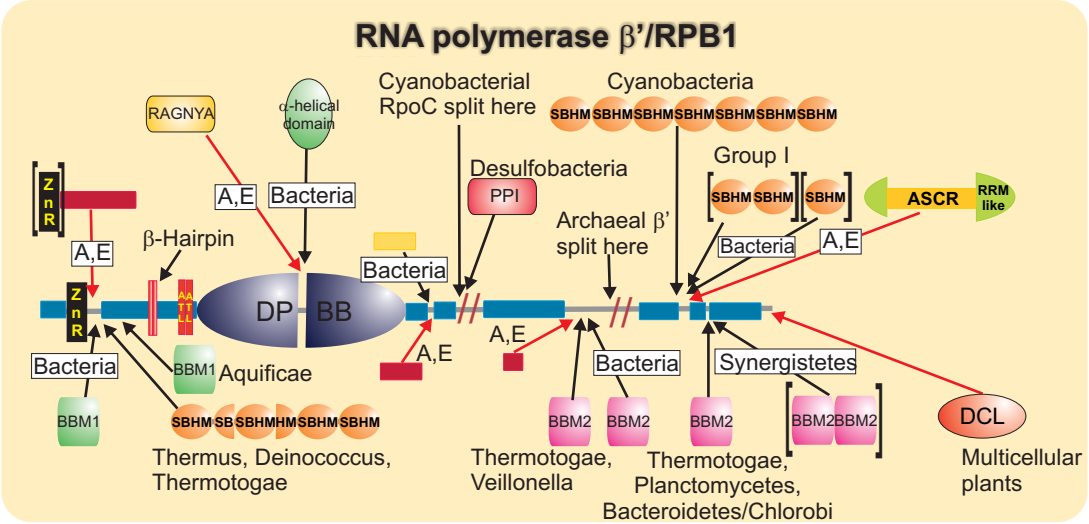
Helix-hairpin-Heix
domain in α subunit
(PDB: 1lb2B)

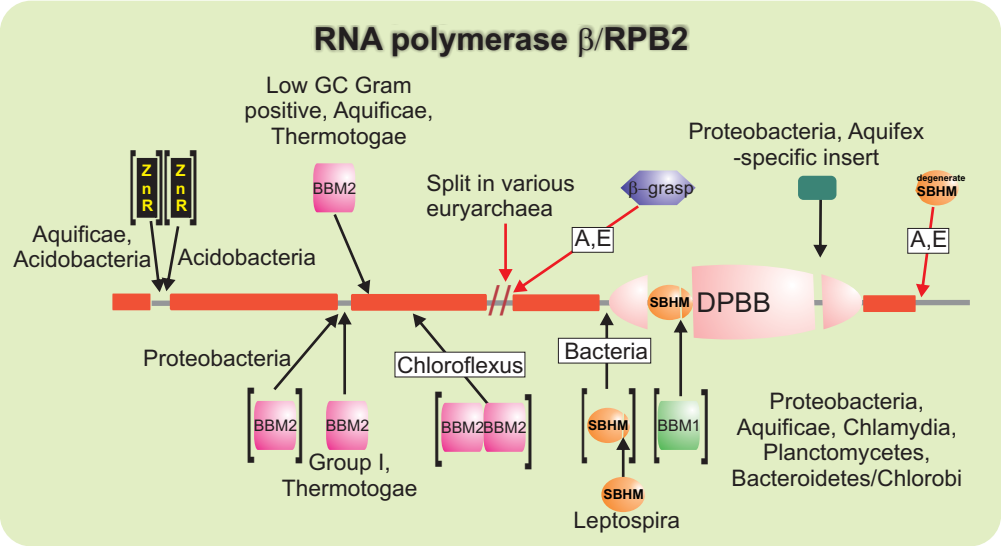
RAGNYA fold domain
in archaeo-eukaryotic
beta subunit
(RPO1N /RPB2,
PDB: 2waqA)

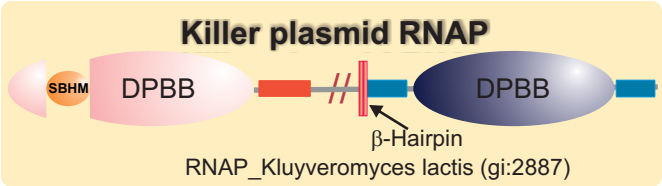


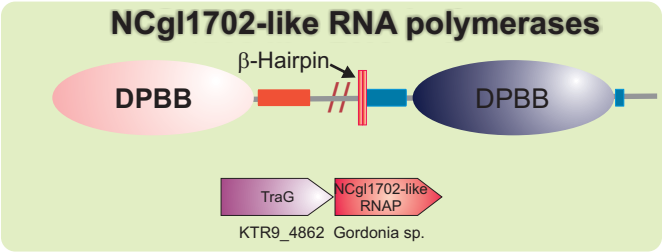


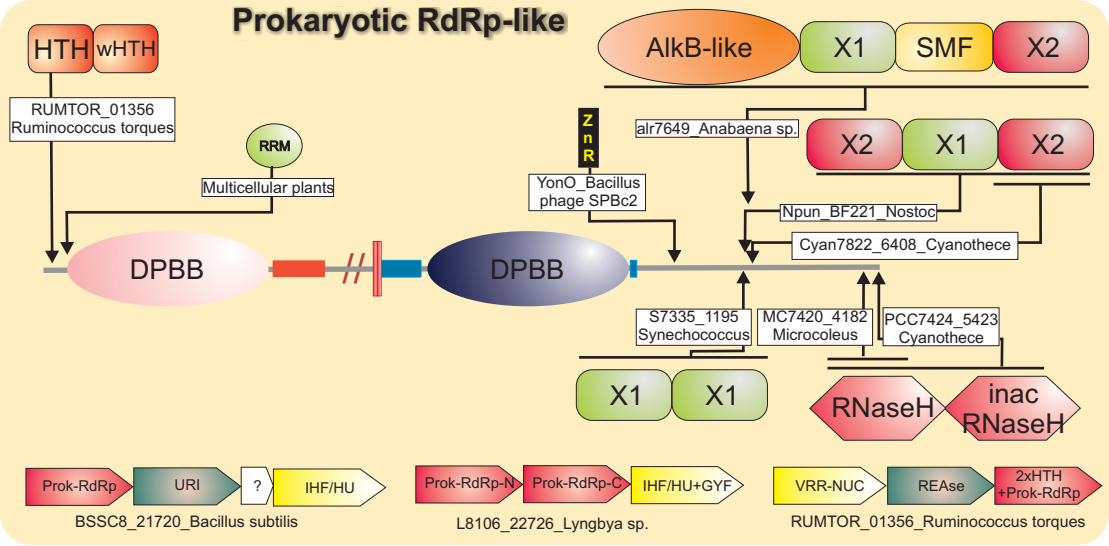
Mycobacterium
Rv2411c-like ATP-
grasp RAGNYA
subdomain
(PDB: 3n6xA)

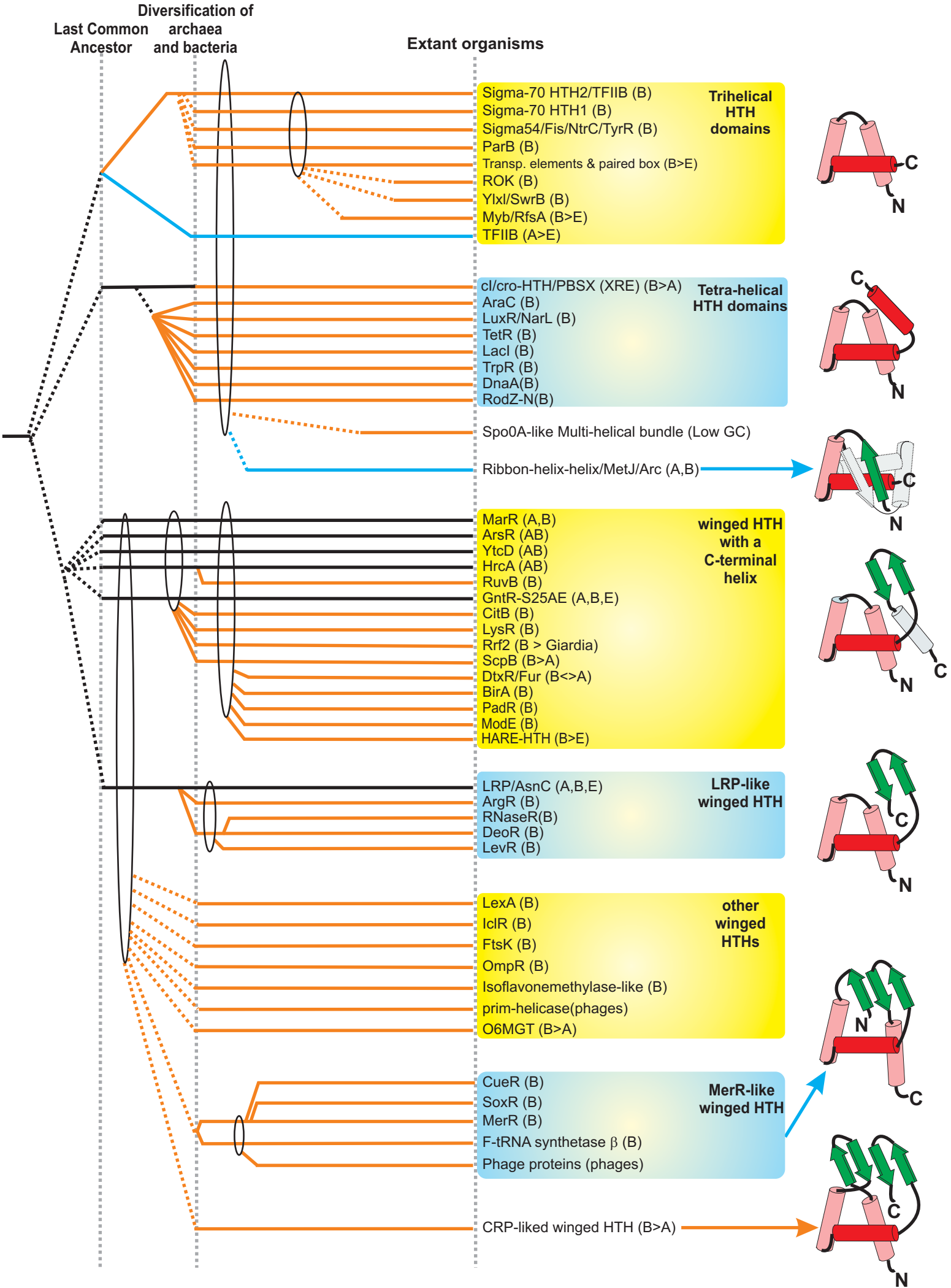

RNA polymerase β'/RPB1
RAGNYA
α-helical domain
Cyanobacterial RpoC split here
Cyanobacteria
SBHM SBHM SBHM SBHM SBHM SBHM SBHM
Group I
Desulfobacteria
PPI
ASCR
RRM like
ZnR
A,E
Bacteria
β-Hairpin
Archaeal β' split here
DP
BB
AA TT
BBM1
Aquificae
SBHM SB SBHM HM SBHM SBHM
Thermus, Deinococcus, Thermotogae
BBM2
Thermotogae, Veillonella
Thermotogae, Planctomycetes, Bacteroidetes/Chlorobi
Synergistetes
DCL
Multicellular plants

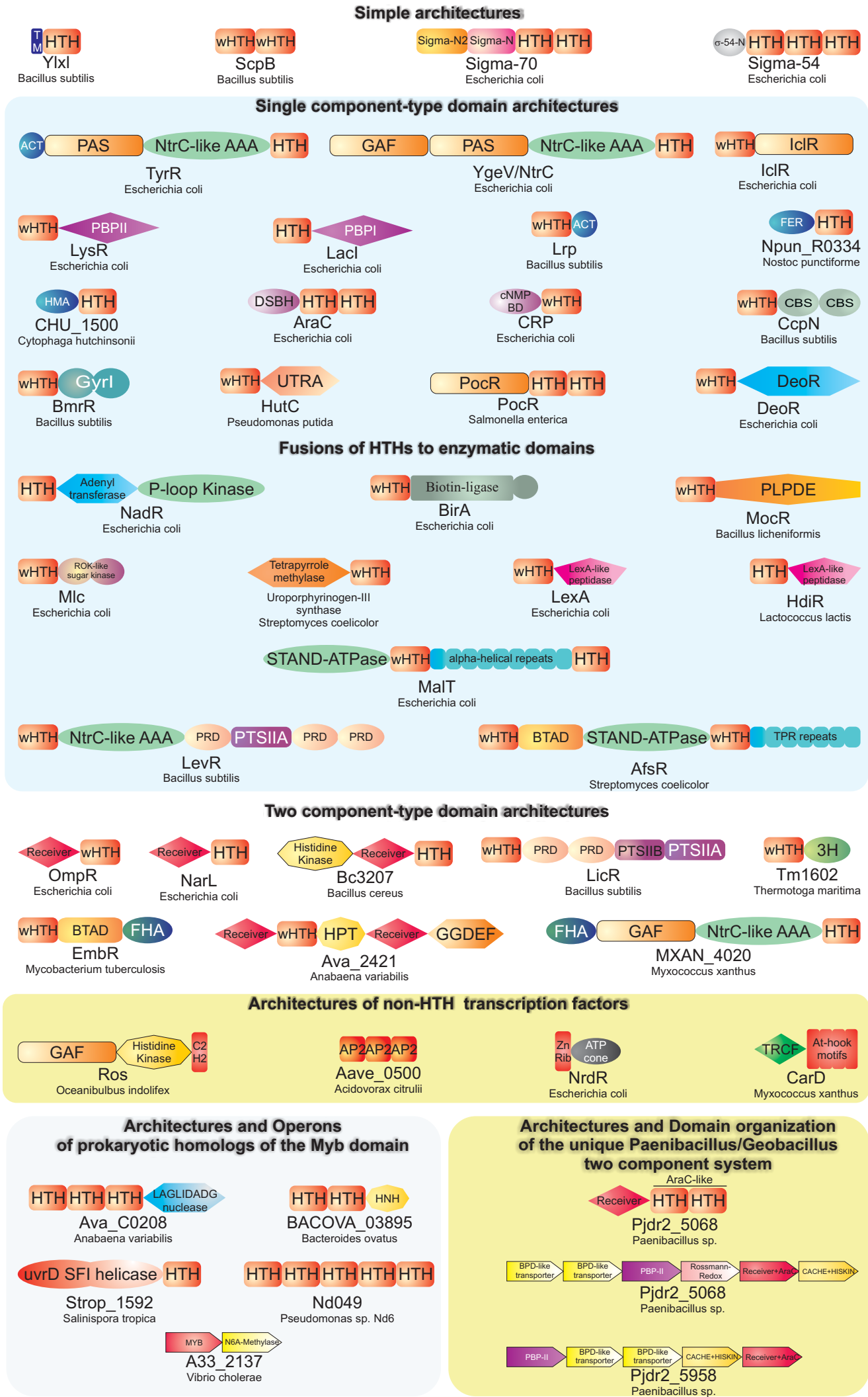

RNA polymerase β/RPB2
Low GC Gram positive, Aquificae, Thermotogae
Proteobacteria, Aquifex -specific insert
ZnR
BBM2
Split in various euryarchaea
β–grasp
degenerate SBHM
Aquificae, Acidobacteria
Acidobacteria
A,E
SBHM
DPBB
Proteobacteria
Chloroflexus
Bacteria
BBM1
Group I, Thermotogae
Proteobacteria, Aquificae, Chlamydia, Planctomycetes, Bacteroidetes/Chlorobi
Leptospira

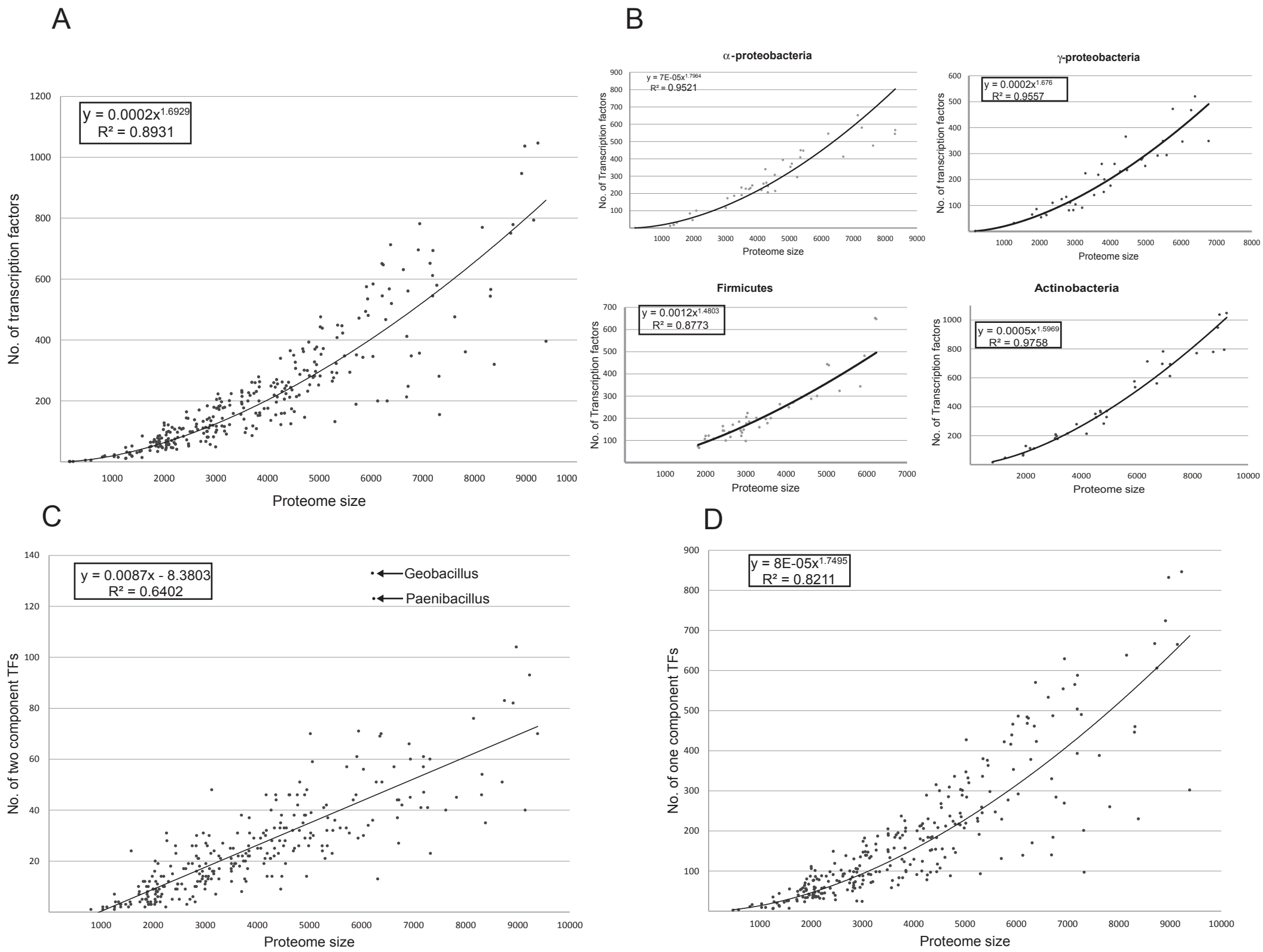

Killer plasmid RNAP
SBHM
DPBB
β-Hairpin
RNAP_Kluyveromyces lactis (gi:2887)


NCgl1702-like RNA polymerases
β-Hairpin
DPBB
TraG
NCgl1702-like RNAP
KTR9_4862 Gordonia sp.


Prokaryotic RdRp-like
HTH
wHTH
RUMTOR_01356 Ruminococcus torques
RRM
Multicellular plants
AlkB-like
X1
SMF
X2
alr7649_Anabaena sp.
ZnR
YonO_Bacillus phage SPBc2
Npun_BF221_Nostoc
Cyan7822_6408_Cyanothece
DPBB
S7335_1195 Synechococcus
MC7420_4182 Microcoleus
PCC7424_5423 Cyanothece
RNaseH
inac RNaseH
Prok-RdRp
URI
?
IHF/HU
BSSC8_21720_Bacillus subtilis
Prok-RdRp-N
Prok-RdRp-C
IHF/HU+GYF
L8106_22726_Lyngbya sp.
VRR-NUC
REAse
2xHTH +Prok-RdRp
RUMTOR_01356_Ruminococcus torques


Last Common Ancestor
Diversification of archaea and bacteria
Extant organisms
Sigma-70 HTH2/TFIIB (B)
Sigma-70 HTH1 (B)
Sigma54/Fis/NtrC/TyrR (B)
ParB (B)
Transp. elements & paired box (B>E)
ROK (B)
YlxI/SwrB (B)
Myb/RfsA (B>E)
TFIIB (A>E)
Trihelical HTH domains
C
N
cI/cro-HTH/PBSX (XRE) (B>A)
AraC (B)
LuxR/NarL (B)
TetR (B)
LacI (B)
TrpR (B)
DnaA(B)
RodZ-N(B)
Tetra-helical HTH domains
C
N
Spo0A-like Multi-helical bundle (Low GC)
Ribbon-helix-helix/MetJ/Arc (A,B)
C
N
MarR (A,B)
ArsR (AB)
YtcD (AB)
HrcA (AB)
RuvB (B)
GntR-S25AE (A,B,E)
CitB (B)
LysR (B)
Rrf2 (B > Giardia)
ScpB (B>A)
DtxR/Fur (B<>A)
BirA (B)
PadR (B)
ModE (B)
HARE-HTH (B>E)
winged HTH with a C-terminal helix
C
N
LRP/AsnC (A,B,E)
ArgR (B)
RNaseR(B)
DeoR (B)
LevR (B)
LRP-like winged HTH
C
N
LexA (B)
IclR (B)
FtsK (B)
OmpR (B)
Isoflavonemethylase-like (B)
prim-helicase(phages)
O6MGT (B>A)
other winged HTHs
N
C
CueR (B)
SoxR (B)
MerR (B)
F-tRNA synthetase β (B)
Phage proteins (phages)
MerR-like winged HTH
CRP-liked winged HTH (B>A)
C
N


Simple architectures
TM HTH
YlxI
Bacillus subtilis
wHTH wHTH
ScpB
Bacillus subtilis
Sigma-N2 Sigma-N HTH HTH
Sigma-70
Escherichia coli
σ-54-N HTH HTH HTH
Sigma-54
Escherichia coli
Single component-type domain architectures
ACT PAS NtrC-like AAA HTH
TyrR
Escherichia coli
GAF PAS NtrC-like AAA HTH
YgeV/NtrC
Escherichia coli
wHTH IclR
IclR
Escherichia coli
wHTH PBPII
LysR
Escherichia coli
HTH PBPI
LacI
Escherichia coli
wHTH ACT
Lrp
Bacillus subtilis
FER HTH
Npun_R0334
Nostoc punctiforme
HMA HTH
CHU_1500
Cytophaga hutchinsonii
DSBH HTH HTH
AraC
Escherichia coli
cNMP BD wHTH
CRP
Escherichia coli
wHTH CBS CBS
CcpN
Bacillus subtilis
wHTH GyrI
BmrR
Bacillus subtilis
wHTH UTRA
HutC
Pseudomonas putida
PocR HTH HTH
PocR
Salmonella enterica
wHTH DeoR
DeoR
Escherichia coli
Fusions of HTHs to enzymatic domains
HTH Adenyl transferase P-loop Kinase
NadR
Escherichia coli
wHTH Biotin-ligase
BirA
Escherichia coli
wHTH PLPDE
MocR
Bacillus licheniformis
wHTH ROK-like sugar kinase
Mlc
Escherichia coli
Tetrapyrrole methylase wHTH
Uroporphyrinogen-III synthase
Streptomyces coelicolor
wHTH LexA-like peptidase
LexA
Escherichia coli
HTH LexA-like peptidase
HdiR
Lactococcus lactis
STAND-ATPase wHTH alpha-helical repeats HTH
MalT
Escherichia coli
wHTH NtrC-like AAA PRD PTSIIA PRD PRD
LevR
Bacillus subtilis
wHTH BTAD STAND-ATPase wHTH TPR repeats
AfsR
Streptomyces coelicolor
Two component-type domain architectures
Receiver wHTH
OmpR
Escherichia coli
Receiver HTH
NarL
Escherichia coli
Histidine Kinase Receiver HTH
Bc3207
Bacillus cereus
wHTH PRD PRD PTSIIB PTSIIA
LicR
Bacillus subtilis
wHTH 3H
Tm1602
Thermotoga maritima
wHTH BTAD FHA
EmbR
Mycobacterium tuberculosis
Receiver wHTH HPT Receiver GGDEF
Ava_2421
Anabaena variabilis
FHA GAF NtrC-like AAA HTH
MXAN_4020
Myxococcus xanthus
Architectures of non-HTH transcription factors
GAF Histidine Kinase C2 H2
Ros
Oceanibulbus indolifex
AP2 AP2 AP2
Aave_0500
Acidovorax citrulii
Zn Rib ATP cone
NrdR
Escherichia coli
TRCF At-hook motifs
CarD
Myxococcus xanthus
Architectures and Operons of prokaryotic homologs of the Myb domain
HTH HTH HTH LAGLIDADG nuclease
Ava_C0208
Anabaena variabilis
HTH HTH HNH
BACOVA_03895
Bacteroides ovatus
uvrD SFI helicase HTH
Strop_1592
Salinispora tropica
HTH HTH HTH HTH HTH
Nd049
Pseudomonas sp. Nd6
MYB N6A-Methylase
A33_2137
Vibrio cholerae
Architectures and Domain organization of the unique Paenibacillus/Geobacillus two component system
AraC-like
Receiver HTH HTH
Pjdr2_5068
Paenibacillus sp.
BPD-like transporter BPD-like transporter PBP-II Rossmann-Redox Receiver+AraC CACHE+HISKIN
Pjdr2_5068
Paenibacillus sp.
PBP-II BPD-like transporter BPD-like transporter CACHE+HISKIN Receiver+AraC
Pjdr2_5958
Paenibacillus sp.


A
y = 0.0002x^1.6929
R² = 0.8931
No. of transcription factors
Proteome size
B
α-proteobacteria
y = 7E-05x^1.7964
R² = 0.9521
γ-proteobacteria
y = 0.0002x^1.676
R² = 0.9557
Firmicutes
y = 0.0012x^1.4803
R² = 0.8773
Actinobacteria
y = 0.0005x^1.5969
R² = 0.9758
No. of Transcription factors
Proteome size
C
y = 0.0087x - 8.3803
R² = 0.6402
Geobacillus
Paenibacillus
No. of two component TFs
Proteome size
D
y = 8E-05x^1.7495
R² = 0.8211
No. of one component TFs
Proteome size