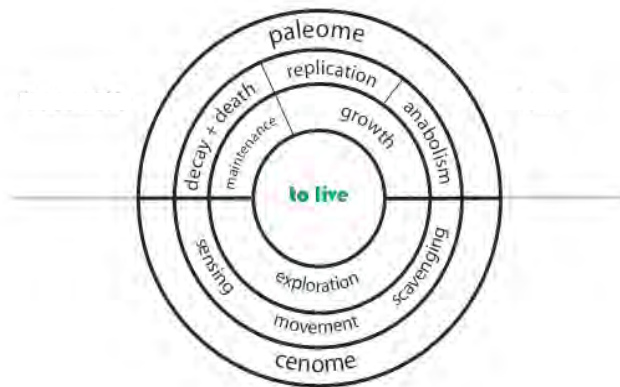


# phyloprofile : co-evolution differs in different clades

the functional paleome is ubiquitous; the structural paleome is not

for example degradosomes differ in firmicutes, gamma-proteobacteria and alpha-proteobacteria



Genomic Object Editor: BSU29250  
*Bacillus subtilis* 168 - chromosome BSU

5/3' | TrEMBL alignments | SwissProt alignments | **PhyloProfile** | PubM |d | KEGG | BRENDA | MicroCyc

MaGe curated annotation | Status: **finished** | Annotator: ebelda

Genes sharing similar phylogenetic profile (900)

Label	Gene	Product	EC number	MCC rank	MCC	Distance rank	Distance	Rank	Correlation score	NbOrigins
BSU28580	muSB	putative DNA mismatch repair enzyme	—	1	1.000	1597	0.940	2	0.884	1
BSU28950	thrS	threonyl-tRNA synthetase	6.1.1.3	12	0.867	196	0.983	3	0.830	56
BSU27950	ysxB	conserved hypothetical protein	—	26	0.828	1	1.000	4	0.828	1
BSU16980	my	endonuclease Y	—	4	0.936	196	0.983	5	0.814	0
BSU25580	comEB	putative enzyme associated to DNA transport (competence)	3.5.4.12	3	0.936	563	0.978	6	0.805	0
BSU01750	ybbP	putative enzyme with DAC domain protein	—	5	0.899	196	0.983	7	0.782	0
BSU25630	yzeK	putative hydrolase	—	6	0.895	196	0.983	8	0.778	0
BSU15970	ybM	conserved hypothetical protein	—	7	0.893	563	0.978	9	0.768	0
BSU22350	dnaD	DNA-remodelling primosomal protein	—	11	0.873	196	0.983	10	0.759	0
BSU23050	fmmP	FMN permease	—	13	0.867	471	0.981	11	0.751	0
BSU15060	ybM	conserved hypothetical protein	—	15	0.862	196	0.983	12	0.750	0
BSU18090	parE	subunit B of DNA topoisomerase IV	5.99.1.-	31	0.820	1	1.000	13	0.738	0
BSU34750	whiA	putative morphogen	—	34	0.818	1	1.000	14	0.736	0

s engelen, d vallenet, c médigue, a danchin  
 distinct co-evolution patterns of genes associated to dna polymerase iii dnae and polc  
*bmc genomics* (2012) [in press]



# linking RNA, lipid and sulfur metabolism

