

Table 2. Distribution of methionine synthase genes in bacterial genomes

Bacterial class	Organism	Genome size (Mb)	<i>metE</i>	<i>metH</i>	No. of Cobalamin biosynthesis genes
γ-Proteobacteria	<i>Pseudomonas</i>	6.26	+	+	22
	<i>Salmonella</i>	4.86	+	+	19
	<i>Escherichia</i>	4.64	+	+	5
	<i>Haemophilus</i>	1.83	+	+	0
	<i>Blochmannia</i>	0.71	+	-	0
	<i>Baumannia</i>	0.69	+	-	0
	<i>Buchnera</i>	0.64	+	-	0
α-Proteobacteria	<i>Bradyrhizobium</i>	9.11	+	+	21
	<i>Mesorhizobium</i>	7.04	+	+	21
	<i>Agrobacterium</i>	4.92	+	+	20
	<i>Sinorhizobium</i>	3.65	-	+	20
	<i>Brucella</i>	3.29	-	+	21
	<i>Rickettsia</i>	1.11	-	-	0
	<i>Hodgkinia</i>	0.14	-	+	13

Distribution of methionine synthase genes in bacterial genomes. The bacterial genomes are listed in order of decreasing genome size within each class. Cobalamin-independent methionine synthase, *metE*; cobalamin-dependent methionine synthase, *metH*.