

Table 3. Mean mRNA half-life by gene functional class

Gene class	No. of genes in category	Mean half-life
Amino acid synthesis	96	3.8*
Macromolecule synthesis	206	4.4*
Nucleotide biosynthesis	30	4.6
Synthesis of cofactors/carriers	106	4.8
Cell division	37	5.0
Macromolecule degradation	60	5.0
Global regulatory functions	49	5.1
Fatty acid synthesis	20	5.1
Adaptation	25	5.1
Ribosome constituents	50	5.4
Central intermediary metabolism	170	5.6
Protection responses	44	6.0
Transport/binding proteins	393	6.2**
Energy metabolism, carbon	173	6.3**
Degradation of small molecules	150	6.3**
Cell envelope	109	6.4**

A mean half-life in M9 + glucose medium was calculated for each functional class of genes. As described in *Results*, a one-way ANOVA indicated a significant between-groups difference: $P < 0.001$. Post-hoc analysis identified a subset of functional classes with significantly shorter mean half-lives indicated by * and a subset with significantly longer mean half-lives indicated by **, $P < 0.05$.