ACCSCIENCE PUBLISHING

Asian Journal of Water, Environment and Pollution

ORIGINAL RESEARCH ARTICLE

Transcriptomic and proteomic profiling of antibiotic resistance gene expression in bacteria exposed to uranium stress

Supplementary Files

Table S1. Spearman correlation parameters and statistical summary of gene–protein expression discordant pairs

Strain	Uranium concentration (mg/L)	Spearman ρ	*p*-value	Total gene–protein expression discordant pairs
Escherichia coli	0.05	0.42	<0.001	51
Escherichia coli	5	0.45	<0.001	76
Bacillus subtilis	0.05	0.28	<0.01	98
Bacillus subtilis	5	0.39	<0.001	121

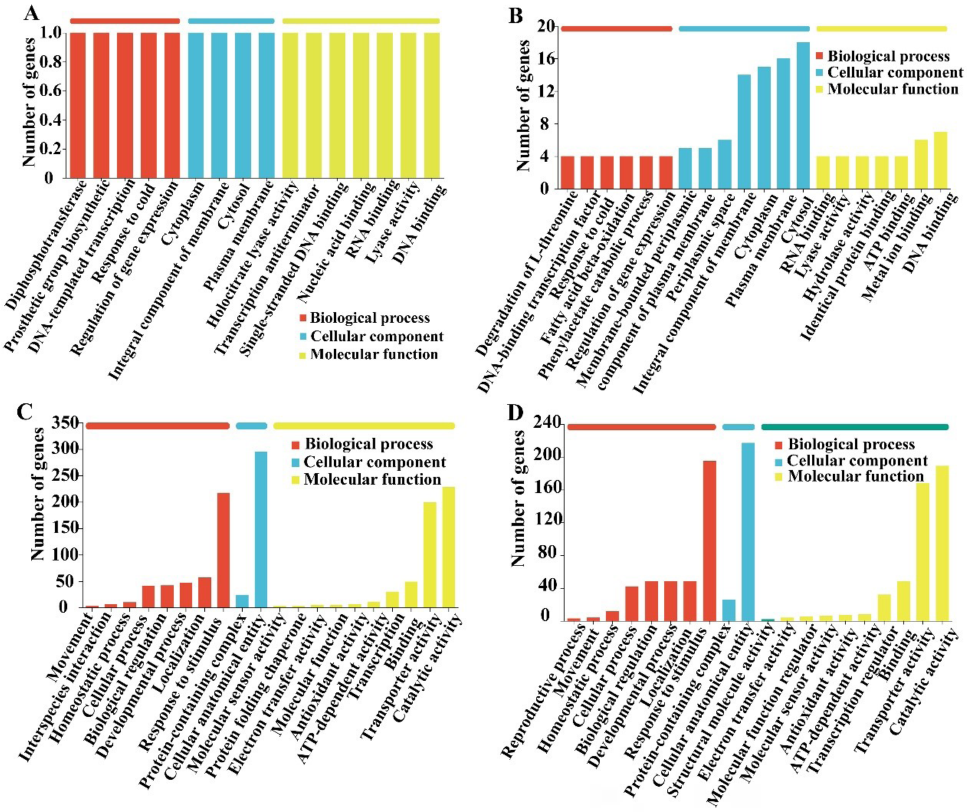

Figure S1. Gene Ontology (GO) functional annotation of differentially expressed genes under uranium (U) stress. (A–B) GO classification of differentially expressed genes in *Escherichia coli*: (A) 0.05 mg/L U. (B) 5 mg/L U. (C–D) GO classification of differentially expressed genes in *Bacillus subtilis*: (C) 0.05 mg/L U. (D) 5 mg/L U. Data are from three biological replicates.

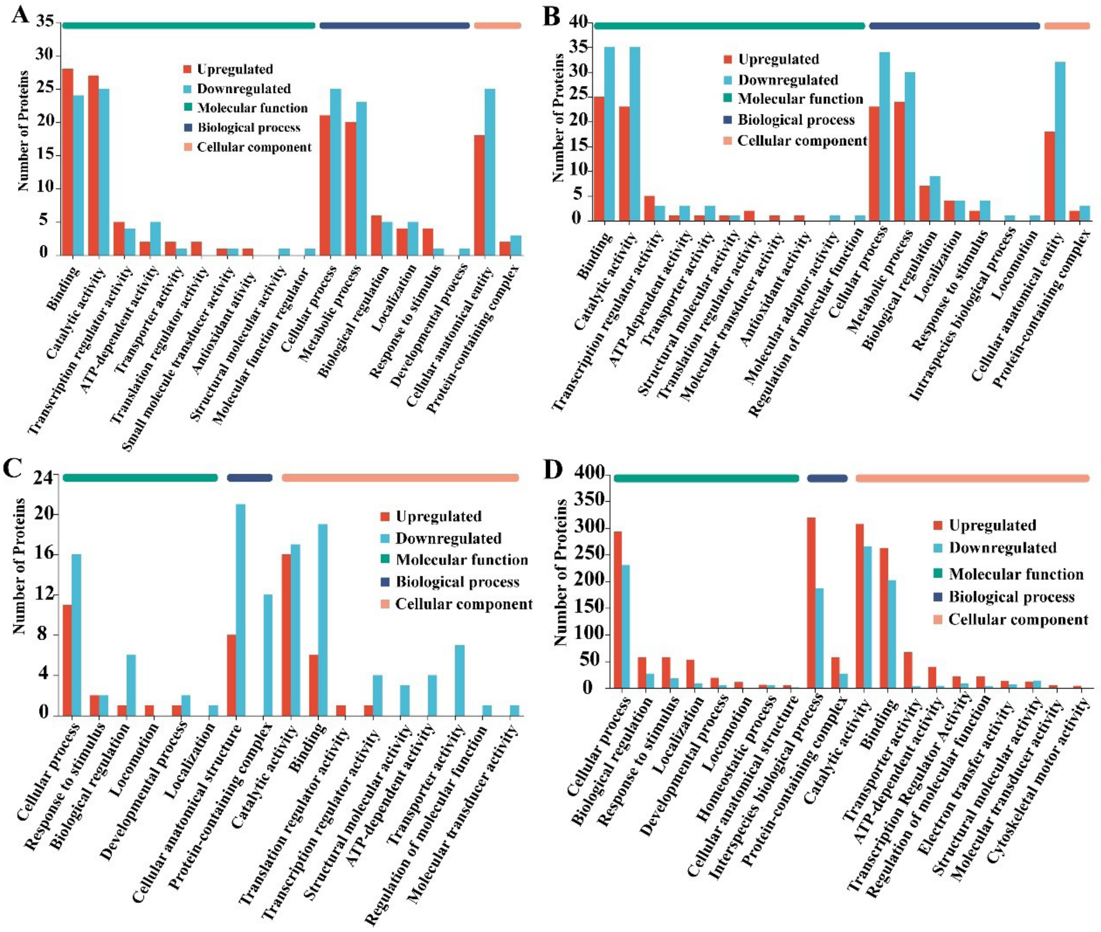

Figure S2. Gene Ontology (GO) functional annotation of differentially expressed proteins under uranium (U) stress. (A–B) GO classification of differentially expressed proteins in *Escherichia coli*: (A) 0.05 mg/L U. (B) 5 mg/L U. (C–D) GO classification of differentially expressed proteins in *Bacillus subtilis:* (C) 0.05 mg/L U. (D) 5 mg/L U. Data are from three biological replicates.