

ORIGINAL RESEARCH ARTICLE

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

Supplementary file

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
<i>Escherichia coli</i>	0.05	0.42	<0.001	51
<i>Escherichia coli</i>	5	0.45	<0.001	76
<i>Bacillus subtilis</i>	0.05	0.28	<0.01	98
<i>Bacillus subtilis</i>	5	0.39	<0.001	121

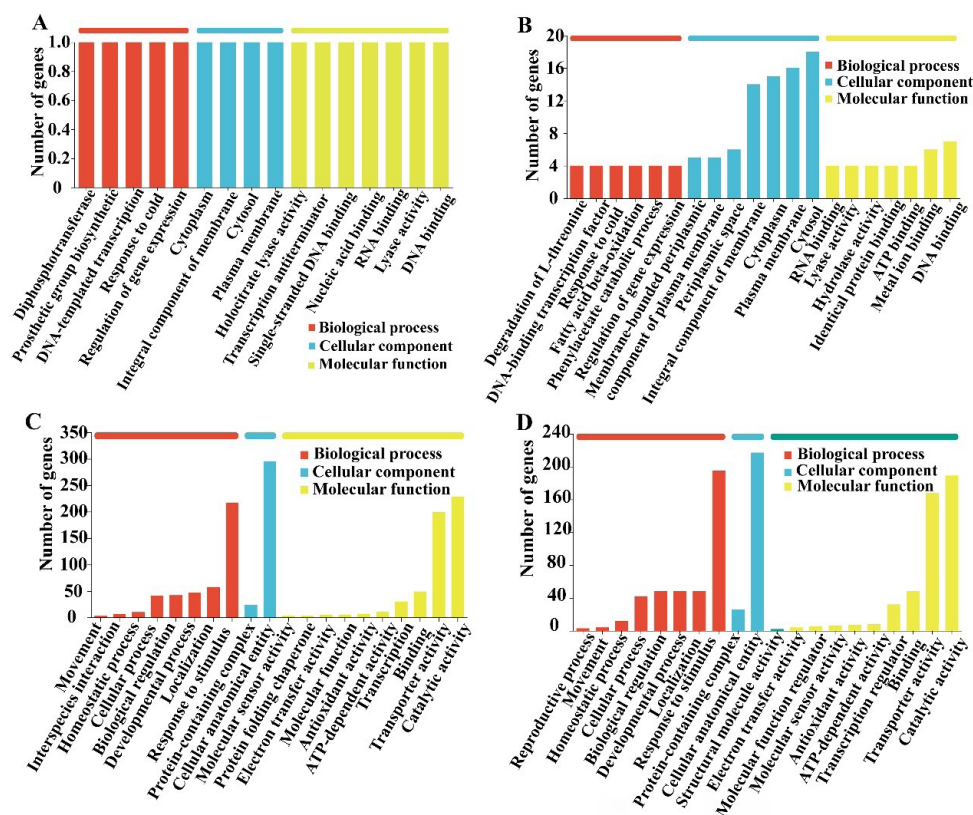


Figure S1. Gene Ontology (GO) functional annotation of differentially expressed genes under uranium (U) stress. (A–B) GO classification of differentially expressed genes in *Escherichia coli*: (A) 0.05 mg/L U. (B) 5 mg/L U. (C–D) GO classification of differentially expressed genes in *Bacillus subtilis*: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

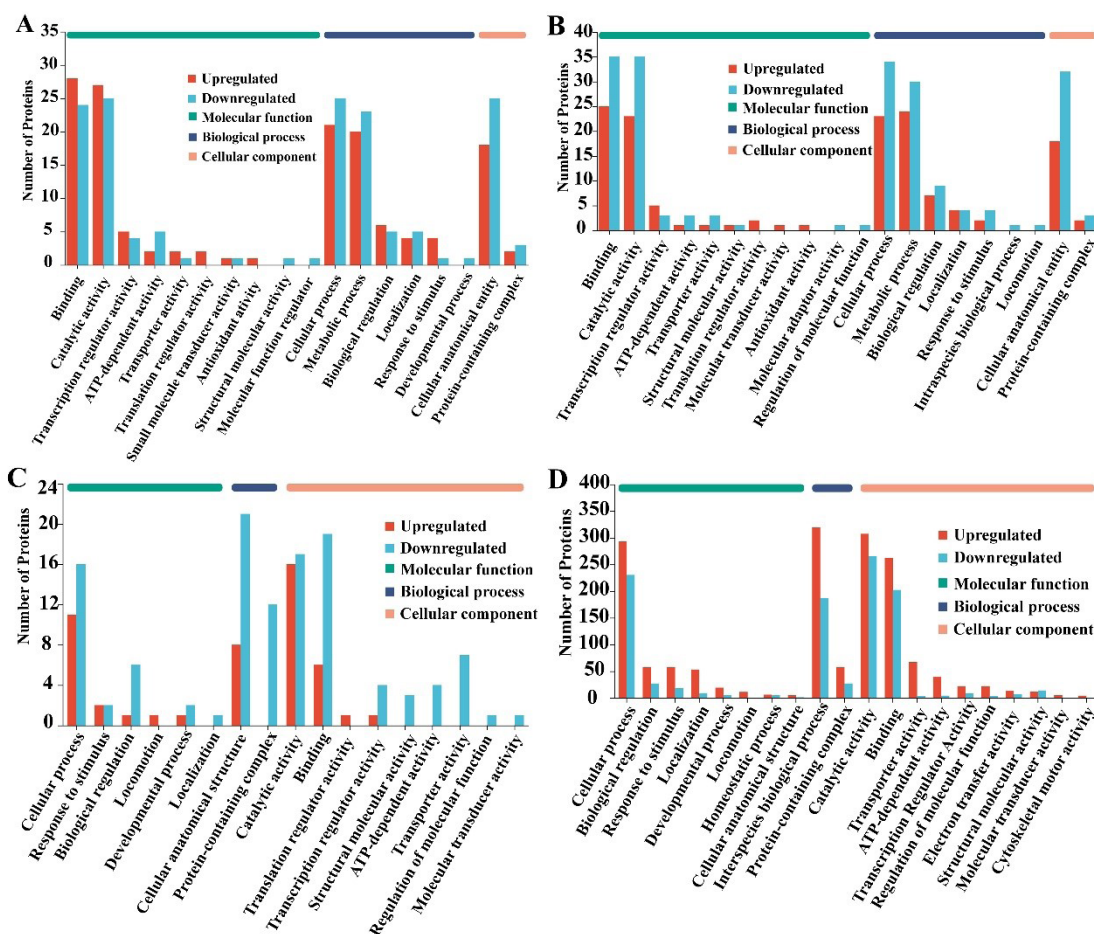


Figure S2. Gene Ontology (GO) functional annotation of differentially expressed proteins under uranium (U) stress. (A–B) GO classification of differentially expressed proteins in *Escherichia coli*: (A) 0.05 mg/L U. (B) 5 mg/L U. (C–D) GO classification of differentially expressed proteins in *Bacillus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