

**Table S1** Primers used for quantitative PCR.

Name	Sequence (5'-3')
<i>estG</i> FP	CTTTTGTCTCCAGGCTCC
<i>estG</i> RP	GCGCGAGGCGATATTCAAAGC
<i>xcpR</i> FP	GCGATAGCAGGGACTAATGC
<i>xcpR</i> RP	TCTGCTGAAGGCACATCAAG

**Table S2** The information for the transcriptomic sample.

Nam	Detailed description	Sampling time
CK	Mono-culture of ZM05 with DPrP as the sole carbon source	18h
CD	Mono-culture of ZM05 with DPrP as the sole carbon source under Cd (II) stress	48 h
CO	Coculture of ZM05 and ZM06 with DPrP as the sole carbon source under Cd (II) stress	48 h

**Table S3** Gene involved in the stress response of strain ZM05 annotated by KEGG

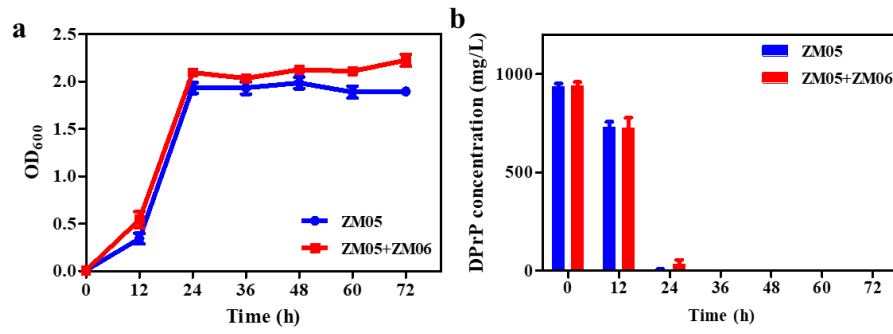
database

<b>Gene</b>	<b>Gene annotation</b>	<b>CD vs. CK</b>	<b>CO vs. CD</b>
<i>cspA</i>	cold shock protein	2.03	-
<i>trxB, TRR</i>	thioredoxin reductase (NADPH)	2.1	-
<i>ribH</i>	Riboflavin synthase, alpha subunit	2.62	-
<i>ribE</i>	Riboflavin synthase, alpha subunit	2.36	-

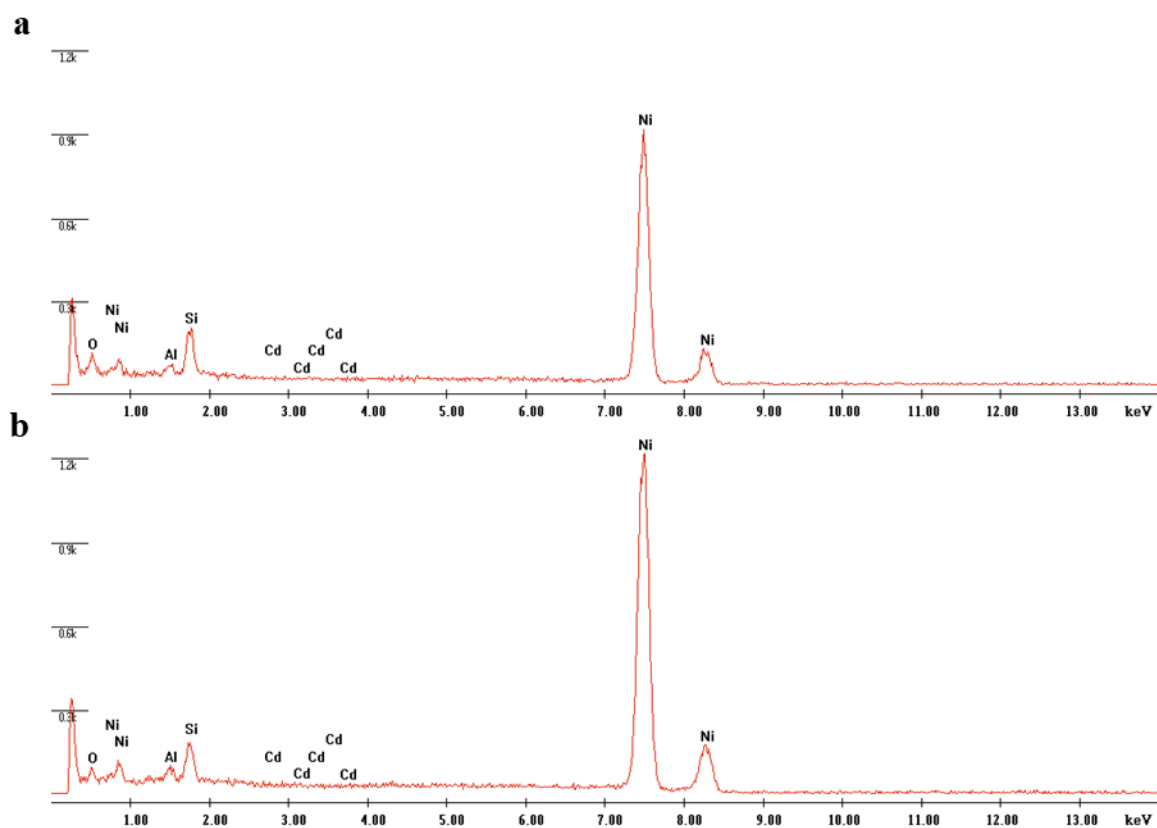
“-” means no significant change.

**Table S4** Degradation gene of strain ZM05 annotated by KEGG database

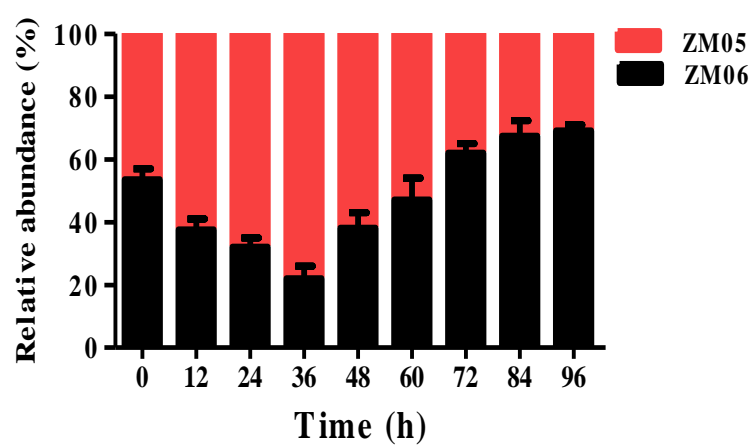
<b>Gene</b>	<b>Gene annotation</b>	<b>CD vs. CK</b>	<b>CO vs. CD</b>
<i>catE</i>	catechol 2,3-dioxygenase	-1.16	1.09
<i>catA</i>	catechol 1,2-dioxygenase	-2.65	2.02
<i>yvaK</i>	carboxylesterase	-0.01	0.05
<i>K06999</i>	carboxylesterase	-2.83	1.31
<i>pcaC</i>	4-carboxymuconolactone decarboxylase	3.63	-1.90
<i>pcaD</i>	3-oxoadipate enol-lactonase	3.36	-1.31
<i>pcaB</i>	3-carboxy-cis,cis-muconate cycloisomerase	3.17	-0.79
<i>pcaG</i>	protocatechuate 3,4-dioxygenase, alpha subunit	4.78	-0.72
<i>pcaH</i>	protocatechuate 3,4-dioxygenase, beta subunit	4.93	-0.67
<i>pobA</i>	p-hydroxybenzoate 3-monooxygenase	4.75	-1.89
<i>pcaI</i>	3-oxoadipate CoA-transferase	2.94	-3.08
<i>pcaJ</i>	pca regulon regulatory protein	3.14	-3.44
<i>pcaR</i>	pca regulon regulatory protein	2.52	-2.61



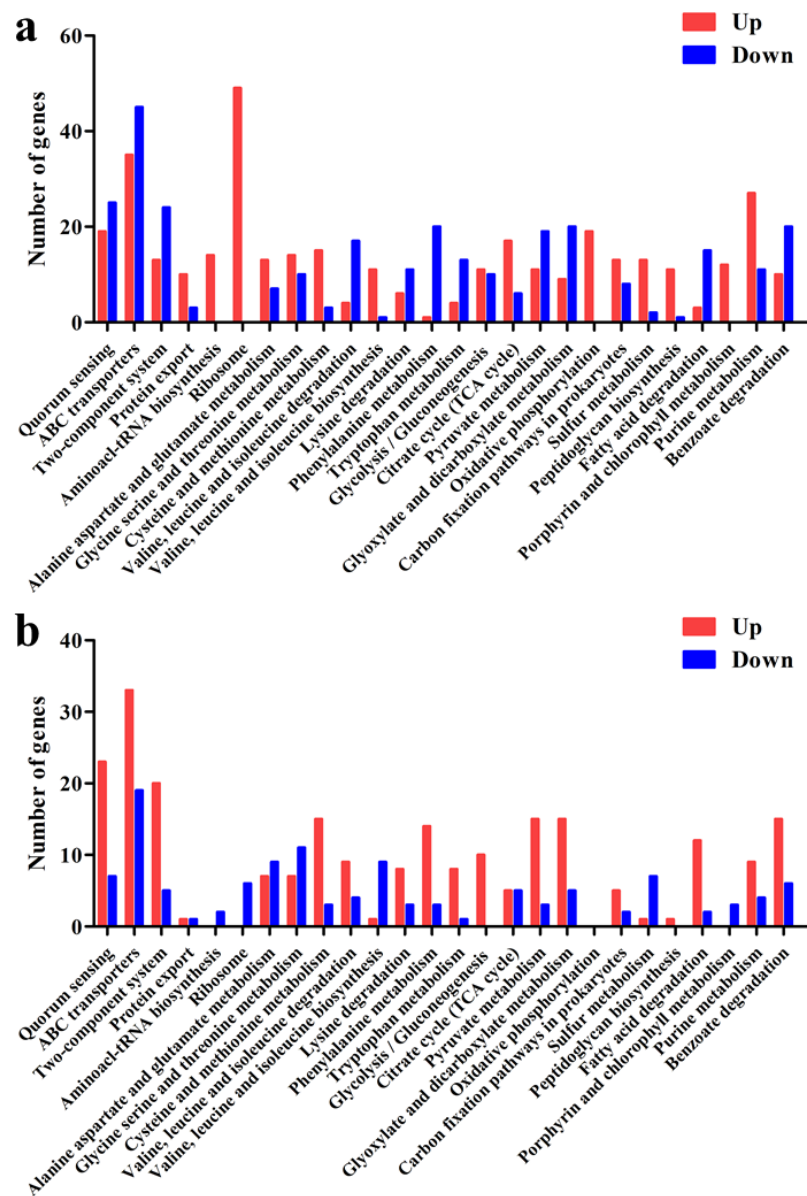
**Fig. S1.** Growth curve (a) and DPrP degradation behavior (b) in monoculture and coculture under optimum conditions. All data are presented as the mean  $\pm$  SE. The blue line (column) represents the monoculture of strain ZM05; the red line (column) represents the coculture of strains ZM05 and ZM06. \*\*\* $p < 0.001$ , \*\* $p < 0.01$ , \* $p < 0.05$ .



**Fig.S2.** Energy dispersive spectrum (EDS) analysis of strain ZM05 (a) and ZM06 (b) under Cd (II) stress.



**Fig.S3.** Relative abundances of strain ZM05 and strain ZM06 in coculture system under Cd (II) stress. All data are presented as the mean  $\pm$  SE.



**Fig. S4.** Metabolism pathway (KEGG) analyses of DEGs from strain ZM05 with or without Cd (II) stress (a) and strain ZM05 in mono-culture system or coculture system under Cd (II) stress (b).