

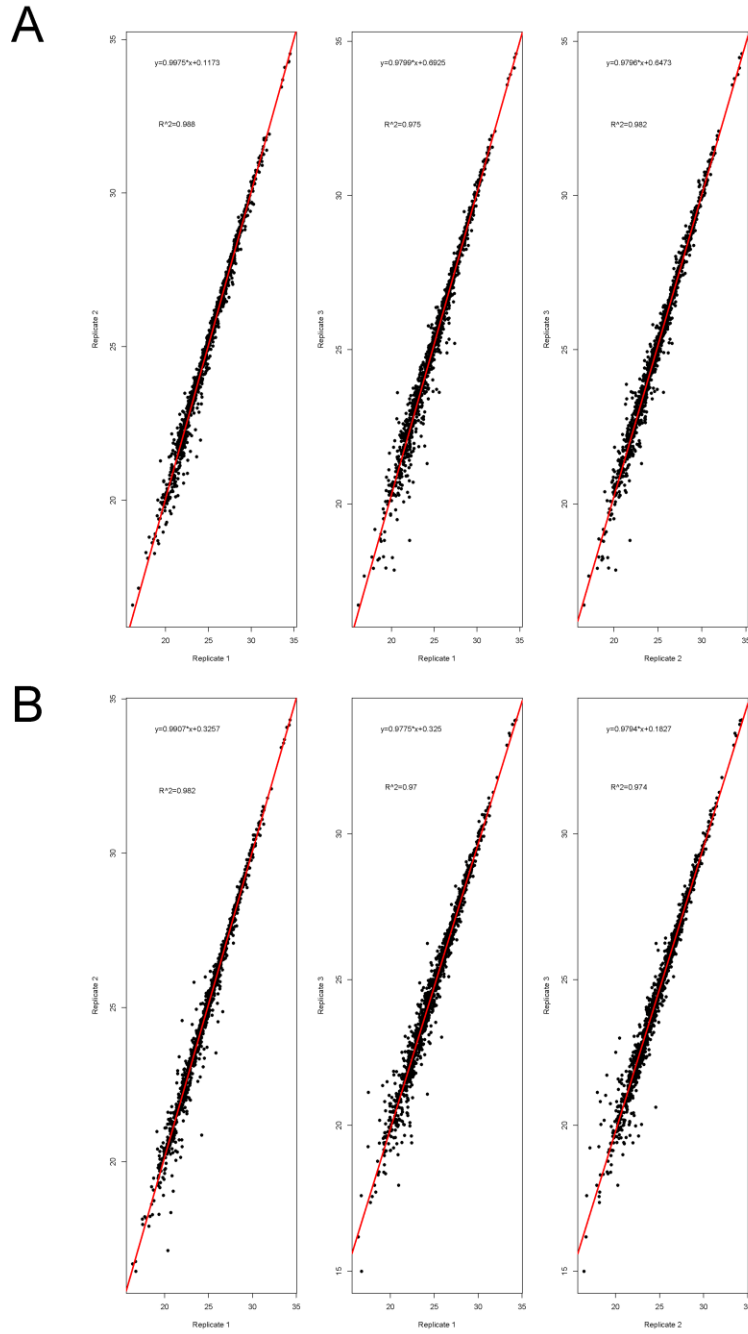
**Quantitative proteomics approach to investigate the antibacterial  
response of *Helicobacter pylori* to daphnetin, a traditional Chinese  
medicine monomer.**

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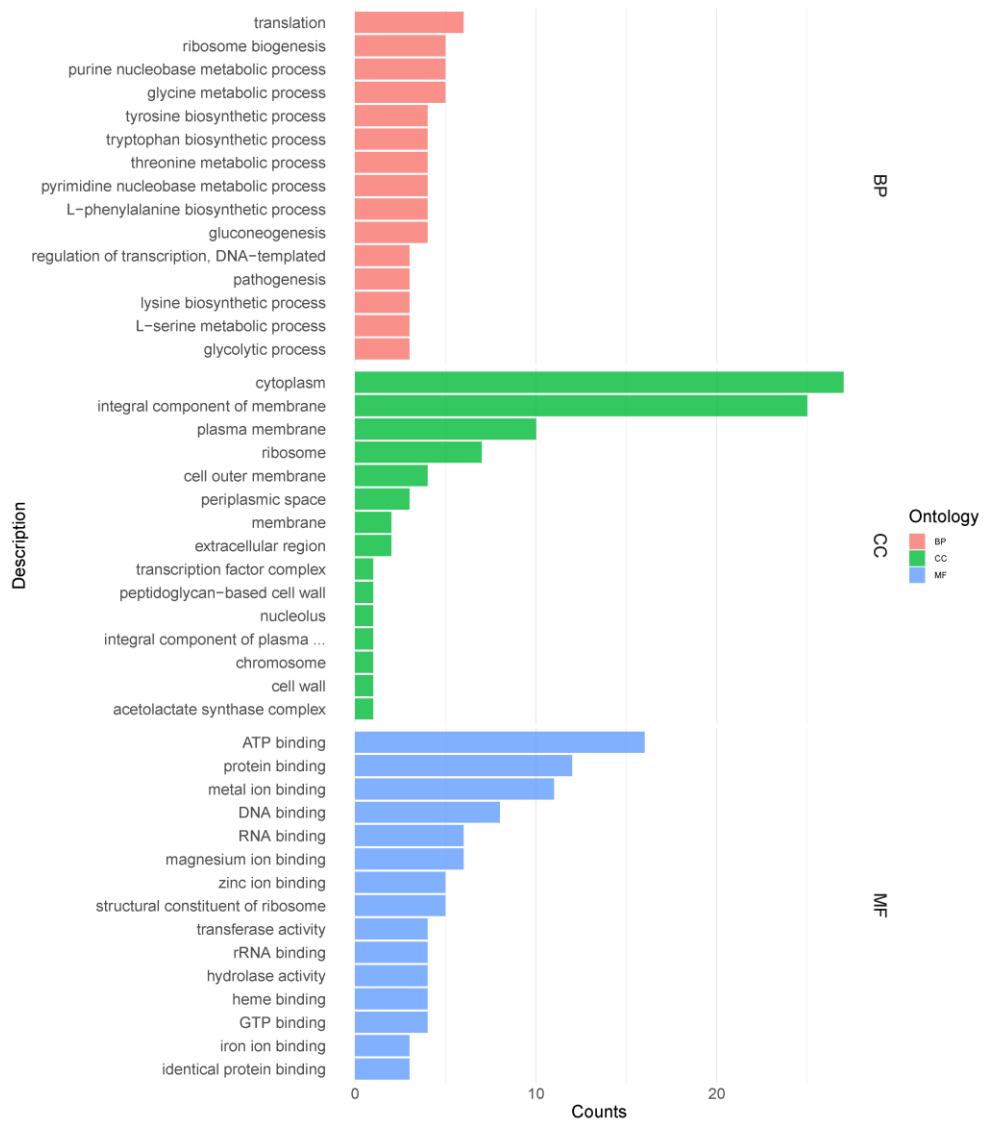
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**Supplementary figures and tables**

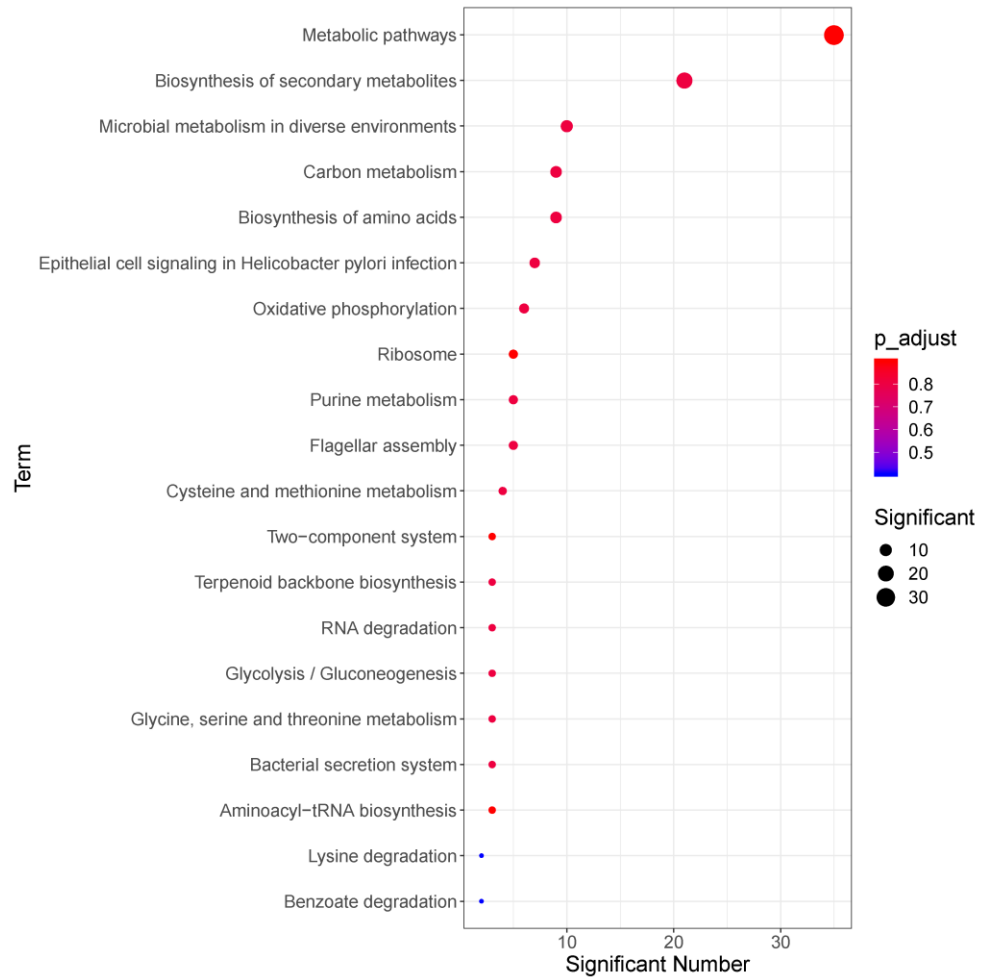
Figure S1 Linear correlation curves of replicates from two groups. A) Control group; B) Daphnetin treated group.



**Figure S2 GO annotation enrichment analysis in biological process(BP), cellular component(CC) and molecular function(MF).**



**Figure S3 Dotplot map of the top 20 KEGG pathways sequenced by protein counts derived from the differentially expressed proteins treated with daphnetin.**



**Table S1 The list of partial significantly differentially expressed proteins under daphnetin pressure (filtered by  $p < 0.05$ , fold change  $> 1.5$ ).**

Uniprot ID ( <i>H. pylori</i> ATCC43504)	Gene name	Protein name	Fold.Chan ge	Uniprot ID of homolog ous protein in H. <i>pylori</i> ATCC266 95
<b>Hub proteins in String network</b>				
IOZBQ4	purA HP_0255	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	0.55	P56137
IOZBS6	HP_0277	Ferredoxin	2.89	O25054
IOZBT0	tgt HP_0281	Queueine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	0.66	O08314
IOZC78	tsf HP_1555	Elongation factor Ts (EF-Ts)	1.76	P55975
IOZE10	purD HP_1218	Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	2.01	O25817
IOZE23	COG0690 Preprotein translocase subunit SecE	Preprotein translocase subunit SecE	1.65	
IOZE29	rpoBC HP_1198	Bifunctional DNA-directed RNA polymerase subunit beta-beta' (EC 2.7.7.6) [Includes: DNA-directed RNA polymerase subunit beta (RNA polymerase subunit beta) (Transcriptase subunit beta); DNA-directed RNA polymerase subunit beta' (RNA polymerase subunit beta') (Transcriptase subunit beta')]	0.43	O25806
IOZF18	dnaJ HP_1332	Chaperone protein DnaJ	1.53	O25890
IOZF92	frr HP_1256	Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	0.33	P56398
IOZFE3	infA HP_1298	Translation initiation factor IF-1	1.86	P65108
IOZFH0	rpsR HP_1244	30S ribosomal protein S18	0.66	P66459
IOZFP7	folE HP_0928	GTP cyclohydrolase 1 (EC 3.5.4.16) (GTP	1.58	P56462

		cyclohydrolase I) (GTP-CH-I)		
IOZFS0	recR HP_0925	Recombination protein RecR	1.53	P56214
IOZFS2	htpX HP_0927	Protease HtpX homolog (EC 3.4.24.-)	0.33	O25582
IOZFT3	dnaK HP_0109	Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	4.85	P55994
IOZGR5	tyrS HP_0774	Tyrosine--tRNA ligase (EC 6.1.1.1) (Tyrosyl-tRNA synthetase) (TyrRS)	2.22	P56417
IOZGT4	rpsT HP_0076	30S ribosomal protein S20	0.19	P56027
IOZHC3	dnaN HP_0500	Beta sliding clamp (Beta clamp) (Sliding clamp) (Beta-clamp processivity factor) (DNA polymerase III beta sliding clamp subunit) (DNA polymerase III subunit beta)	2.98	O25242
IOZHE1	pheT HP_0402	Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit) (PheRS)	0.29	P56145
IOZI68	rpmF HP_0200	50S ribosomal protein L32	0.22	P56054
IOZIK8	gyrA HP_0701	DNA gyrase subunit A (EC 5.6.2.2)	0.10	P48370
IOZI88	HP_0221	Nitrogen fixation protein NifU	0.12	O25009
IOZEZ6	hugZ HP_0318	Heme oxygenase HugZ (EC 1.14.99.-)	3.21	O25087
IOZEP5	queA HP_1062	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	0.49	O25702
IOZDP0	HP_1182	ATP_bind_3 domain-containing protein	0.58	O25794
IOZE14	pnp HP_1213	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	0.24	O25812
IOZF96	HP_1269	NADH-quinone oxidoreductase subunit J (EC 7.1.1.-)	0.35	O25859
IOZGU4	rpoD HP_0088	RNA polymerase sigma factor RpoD (Sigma-70)	1.60	P55993
IOZE21	tuf tufA HP_1205	Elongation factor Tu (EF-Tu)	0.02	P56003
IOZB68	rpsU HP_0562	30S ribosomal protein S21	0.63	P56028
IOZBZ4	icd HP_0027	Isocitrate dehydrogenase [NADP] (IDH) (EC 1.1.1.42) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	0.62	P56063
IOZHT4	pgk HP_1345	Phosphoglycerate kinase (EC 2.7.2.3)	0.67	P56154
IOZJ77	rpmE HP_0551	50S ribosomal protein L31	2.14	P66185

<b>Cytochrome c oxidase related proteins</b>				
IOZEA8	HP_0144	Cytochrome c oxidase, heme b and copper-binding subunit, membrane-bound (FixN)	0.66	O24955
IOZEA9	HP_0145	Cytochrome c oxidase, monoheme subunit, membrane-bound (FixO)	0.65	O24956
<b>Flagellar related proteins</b>				
IOZB47	HP_0584	Flagellar switch protein (FlIN)	2.30	O25306
IOZEU3	HP_0353	Flagellar export protein (FlIH)	1.63	O25120
IOZH55	fliI HP_1420	Flagellum-specific ATP synthase (EC 7.1.2.2)	1.61	O07025
IOZE88	HP_0907	Basal-body rod modification protein FlgD	2.02	O25565
IOZD59	HP_1119	Flagellar hook-associated protein 1 (HAP1) (FlgK)	1.83	O25744
<b>Infection related proteins</b>				
IOZBK7	HP_0289	Toxin-like outer membrane protein	0.59	O25063
IOZBT4	HP_0286	Cell division protein (FtsH)	2.74	O25060
IOZDE4	coaX coaA	Type III pantothenate kinase (EC 2.7.1.33) (PanK-III) (Pantothenic acid kinase)	0.45	O25533
	HP_0862			
IOZH94	HP_0520	Cag pathogenicity island protein (Cag1)	0.38	O25257
IOZIG1	HP_0371	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	2.01	O25135
IOZJ86	HP_0543	Cag pathogenicity island protein (Cag22)	0.52	O25276
IOZFR9	HP_0924	Probable tautomerase HP_0924 (EC 5.3.2.-)	1.56	O25581
IOZHH0	hpaA	Neuraminylactose-binding hemagglutinin (Flagellar sheath adhesin) (N-acetylneuraminylactose-binding fibrillar hemagglutinin receptor-binding subunit) (NLBH)	1.73	P55969
	HP_0797			
IOZBG0	HP_0638	Outer membrane protein (OpiA)	0.42	O25355
IOZG47	HP_0807	Iron(III) dicitrate transport protein (FecA)	0.53	O25487
IOZGF7	psel HP_0178	Pseudaminic acid synthase (EC 2.5.1.97) (Pseudaminic acid biosynthesis protein I)	0.37	O24980

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**Table S2 The list of target proteins and corresponding peptides of daphnetin-treated *H. pylori*. Fifteen target proteins were identified with peptide sequences and product ions quantified by label-free PRM analysis.**

Protein Accession	Gene Name	Peptide Sequence	Precursor Charge	Product Ions	Adjusted p.value	Fold change
IOZBG0	HP17_05385	DAQNALNAVK	2	y7,y6,y5,y4,y3	0.011	0.20
		GLSIFYK	2	b3,y5,y4,y3,y2	0.011	0.11
IOZBK7	HP17_05155	DNATNLLLELASYTQQTSR	2	b2,y12,y11,y10,y9,y8	0.018	0.35
		FVGENTLLYR	2	b2,y9,y8,y7,y6,y1	0.010	0.36
		DYDFVVR	2	b2,y5,y4,y3,y2,y1	0.013	0.29
IOZBQ4	purA HP17_04970	NISSAVVSVK	2	b2,b3,y10,y9,y8,y3	0.011	0.32
		AHVILPYHAK	3	b2,b3,b4,y5,y4,y3	0.010	0.33
IOZE29	HP17_02863	SIFPIQDEHNR	3	b2,y7,y6,y5,y4,y3	0.035	0.60
		YDILNEEQQNISR	3	b3,y7,y6,y5,y4,y2	0.037	0.54
IOZFT3	dnaK HP17_00905	EAGTIAGLNVLRL	2	y10,y8,y7,y6,y4,y1	0.035	2.04
		NHADSLAHQTQK	3	b2,b3,b5,y5,y4,y3	0.041	2.78
		FGIVYQNYFGDPDR	3	b3,y10,y9,y8,y3,y1	0.011	0.33
IOZG47	HP17_08711	FVVNAFEPK	3	b2,y7,y6,y5,y4,y2	0.010	0.30
		SQGVELELYYTPIR	3	b2,b3,y10,y9,y8,y7	0.014	0.44
IOZHH0	HP17_07264	SLFLQLSSFLELRL	2	b3,y8,y7,y6,y1	0.037	0.33
		SEDIHSFGIDVSK	3	b2,b3,y9,y8,y7,y2	0.020	0.34
IOZIK8	HP17_06437	FTLSEIQSK	2	b2,b3,b6,y8,y7,y4	0.029	0.41
		AIVNLISLAPDEK	2	b2,y8,y7,y5,y4,y2	0.016	0.22
IOZJ86	HP17_05920	EINDGQDPQK	2	b2,y8,y7,y6,y4,y3	0.024	0.24
		YFQNIDEVTNK	2	y8,y7,y6,y4,y3,y2	0.030	0.36
IOZGF7	HP17_08384	ASTPLEWHAELFELAR	3	y9,y8,y7,y6,y5,y1	0.026	0.34
		SLFVIK	2	b2,b3,y5,y4,y3,y2	0.018	0.28
		TTLSSAAISAVLSLK	3	b6,y7,y6,y5,y4,y3	0.025	0.23
IOZE21	tuf HP17_02823	QVGVPHIVVFLNK	3	y7,y6,y5,y4,y3,y2	0.041	0.63
		FEGEIVVLSK	2	b2,y8,y5,y4,y3,y2	0.020	0.41