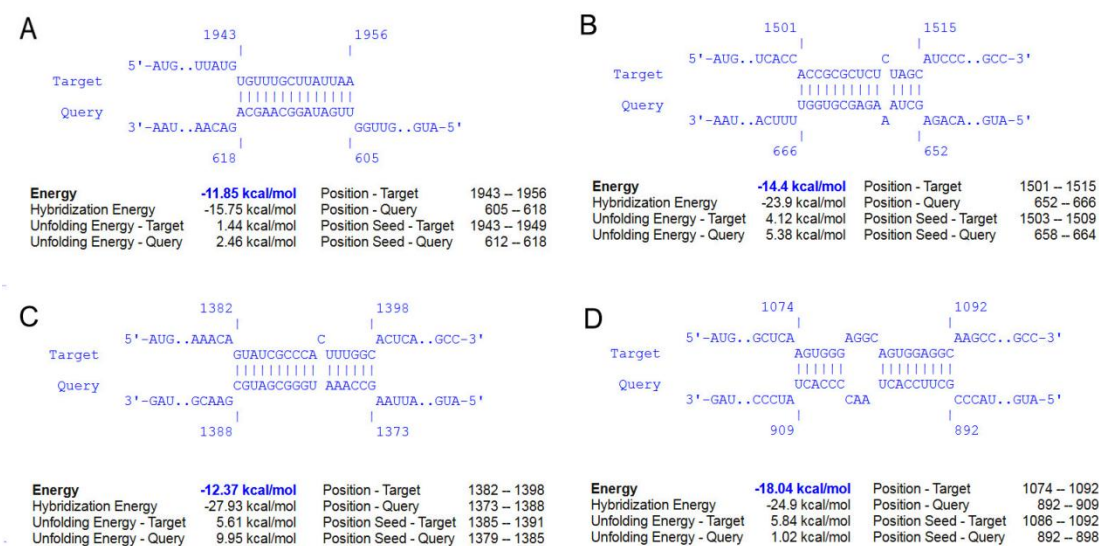


Supplementary Materials

Study on the Adhesive Effect of Deoxyshikonin on *Helicobacter pylori*

Pairwise RNA-RNA interaction predictions were performed using IntaRNA (Freiburg RNA Tools web server, <http://rna.informatik.uni-freiburg.de/>) with default parameters. Nucleotide sequences of *ureA*, *ureB*, *sabA*, and *babA* were retrieved from the NCBI Nucleotide database (*H. pylori* strain 26695). The analysis predicted potential transcript-level interactions between urease and adhesin mRNAs; however, these predictions are exploratory and computational in nature and require experimental validation (e.g., by RIP-seq or EMSA) before any mechanistic conclusions can be drawn.



Supplementary Figure 1 RNA interaction analysis of urease and adhesin genes. A: *UreA-sabA* interaction; B: *UreA-babA* interaction; C: *UreB-sabA* interaction; D: *UreB-babA* interaction.

Supplementary Table 1. Mass spectrometry identification parameters of the 11 candidate target proteins screened by DARTS.

No.	Gene	UniProt ID	Protein name	MW (kDa)	DMSO control			Deoxyshikonin)				
					Unused	Coverage (%)	Unique pep.	iBAQ	Unused	Coverage (%)	Unique pep.	iBAQ
1	<i>ureA</i>	P14916	Urease subunit alpha	26.5	16.42	26.05	9	3117.37	22.44	40.34	11	3924.58
2	<i>ureB</i>	P69996	Urease subunit beta	61.7	21.25	26.89	10	1277.66	15.52	18.63	9	1827.47
3	<i>groEL</i>	P42383	60 kDa chaperonin	58.3	52.33	46.70	27	4957.35	49.07	45.97	26	5699.05
4	<i>groESP0A</i>	R3	10 kDa chaperonin	13.0	6.70	30.51	4	4712.81	5.33	22.88	3	5059.86
5	<i>tuf</i>	P56003	Elongation factor Tu	43.6	17.66	27.32	10	1839.97	18.35	24.81	10	2887.41
6	<i>tsf</i>	P55975	Elongation factor Ts	39.7	2.18	3.10	1	705.20	5.76	10.70	3	921.67
7	<i>glnA</i>	P94845	Glutamine synthetase	54.5	3.88	6.65	3	120.04	4.86	6.65	3	189.94
8	<i>aspA</i>	P56149	Aspartate ammonia-lyase	52.0	2.73	6.84	3	204.23	4.62	11.11	4	291.59
9	<i>katA</i>	P77872	Catalase 3-	58.6	32.41	38.81	18	2980.64	31.77	33.47	15	4278.45
10	<i>aroQ</i>	Q48255	Dehydroquinate dehydratase	18.5	3.84	22.75	3	3734.78	6.79	25.15	4	5779.43
11	<i>amiE</i>	O25067	Amidase	37.7	12.31	24.48	7	1054.71	14.65	27.73	8	1383.66

Proteins were identified using ProteinPilot software (v5.0, AB SCIEX) with the Paragon algorithm against the H. pylori 26695 proteome database (UniProt, 1,799 sequences). The unused ProtScore reflects the amount of unique peptide evidence supporting each protein identification

(score ≥ 1.3 corresponds to $\geq 95\%$ confidence). MW, molecular weight.