Supplementary Table 1. **List of the Outer Membrane Proteins of *H. pylori* Identified by PA-SUB**

S. No.	Swiss-Prot ID	*Name of the Protein*
1	Q47952	Hemoglobin and hemoglobin-haptoglobin-binding
2	Q7VL53	Outer-membrane lipoprotein lolB
3	Q7VKZ9	LPS-assembly protein
4	Q7VKP4	Probable outer membrane protein
5	Q7VL30	Putative uncharacterized protein
6	Q7VL47	Lytic murein transglycosylase A
7	Q7VM93	28kDa outer membrane lipoprotein
8	Q7VMB2	Outer membrane protein P1
9	Q7VN89	VacJ lipoprotein
10	Q7VP25	Probable fimbrial outer membrane usher protein
11	Q93PM2	Integral outer membrane protein

Supplementary Table 2. **Classification of Uncharacterized Essential Proteins of *H. ducreyi* Using SVMProt Web Server**

S. No.	Swiss-Prot ID	Protein Family	P-Value (%)*
1	Q7VKG3	DNA repair	58.6
2	Q7VKH1	Transferases – Glycosyltransferases	99.0
3	Q7VKJ5	TC 3.A.1 ATP-binding cassette (ABC) family	58.6
4	Q7VKJ7	All lipid-binding proteins	85.4
5	Q7VKS4	Transmembrane	98.9
6	Q7VKS8	All DNA-binding	89.3
7	Q7VKU0	Transferases - Glycosyltransferases	71.3
8	Q7VL10	Hydrolases - Acting on Ester Bonds	97.5
9	Q7VL30	Zinc-binding	91.3
10	Q7VL31	All lipid-binding proteins	97.8
11	Q7VL60	All lipid-binding proteins	82.2
12	Q7VL61	Transmembrane	98.6
13	Q7VL78	Oxidoreductases - Acting on the CH-OH group of donors	96.1
14	Q7VLF5	Transmembrane	62.2
15	Q7VLH1	Oxidoreductases - Acting on the CH-OH group of donors	98.8
16	Q7VLL8	All DNA-binding	89.3
17	Q7VLQ1	All lipid-binding proteins	78.4
18	Q7VLQ3	Transmembrane	93.6
19	Q7VLR6	Manganese-binding	78.4
20	Q7VLS4	Transferases - Glycosyltransferases	98.1
21	Q7VLT8	Transmembrane	99.0
22	Q7VLV9	Transmembrane	94.2

(Table S2). Contd…..

S. No.	Swiss-Prot ID	Protein Family	P-Value (%)*
23	Q7VLZ4	Transmembrane	98.9
24	Q7VM63	All lipid-binding proteins	98.3
25	Q7VM79	Transmembrane	98.9
26	Q7VMD4	Metal-binding	58.6
27	Q7VME3	All DNA-binding	73.8
28	Q7VMH5	Transferases - Transferring Phosphorus-Containing Groups	90.3
29	Q7VMJ2	Zinc-binding	86.8
30	Q7VMT6	Transmembrane	98.9
31	Q7VMT8	Iron-binding	68.5
32	Q7VMZ7	Transferases - Transferring Phosphorus-Containing Groups	98.2
33	Q7VN01	All lipid-binding proteins	65.4
34	Q7VN17	Zinc-binding	62.2
35	Q7VN61	All DNA-binding	68.5
36	Q7VNB2	All lipid-binding proteins	68.5
37	Q7VNE9	Zinc-binding	98.8
38	Q7VNH8	Zinc-binding	80.4
39	Q7VNI1	Transmembrane	98.1
40	Q7VNI2	Transmembrane	98.2
41	Q7VNN9	Transferases - Glycosyltransferases	90.3
42	Q7VNS5	Zinc-binding	62.2
43	Q7VNV4	Transmembrane	94.7
44	Q7VNW4	TC 2.A. Electrochemical Potential-driven transporters - Porters (uniporters, symporters, antiporters)	98.4
45	Q7VP09	All DNA-binding	62.2
46	Q7VP52	Transmembrane	99.2
47	Q7VPC1	Hydrolases - Acting on Ester Bonds	58.6
48	Q7VPF3	Zinc-binding	98.8
49	Q7VPM0	All lipid-binding proteins	78.4
50	Q8GNB9	Transmembrane	91.3

* P-Value is the expected classification accuracy in terms of percentage.

Supplementary Table 3. Essential Proteins of *H. ducreyi* Involved in Several Pathogen Specific Metabolic Pathways

S. No.	Pathways Present Exclusively in *H. ducreyi*	Protein Name	Swiss Prot ID	Gene Name	Involvement in Other Metabolic Pathways
1	Photosynthesis	F0F1 ATP synthase subunit delta	Q7VPP3	atpH	Oxidative phosphorylation
		F0F1 ATP synthase subunit epsilon	Q7VPN9	atpC	Oxidative phosphorylation
		F0F1 ATP synthase subunit B	Q7VPP4	atpF	Oxidative phosphorylation
		F0F1 ATP synthase subunit A	Q7VPP6	atpB	Oxidative phosphorylation

(Table S3). Contd…..

S. No.	Pathways Present Exclusively in *H. ducreyi*	Protein Name	Swiss Prot ID	Gene Name	Involvement in Other Metabolic Pathways
2	Carbon fixation in photosynthetic organisms	fructose-bisphosphate aldolase	Q7VMV1	fbaA	Glycolysis/Gluconeogenesis, Pentose phosphate pathway, Fructose and mannose metabolism
3	D-Alanine metabolism	alanine racemase	Q7VNC9	alr	Alanine and aspartate metabolism
		D-alanine--D-alanine ligase	Q7VMY2	ddl	Peptidoglycan biosynthesis
4	Lipopolysaccharide biosynthesis	UDP-N-acetylglucosamine acyltransferase	Q7VM26	lpxA	
		UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	Q7VMY6	lpxC	
		UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Q7VM24	lpxD	
		UDP-2,3-diacylglucosamine hydrolase	Q7VKH0	lpxH	
		lipid-A-disaccharide synthase	Q7VMW5	lpxB	
		tetraacyldisaccharide 4'-kinase	Q7VP80	lpxK	
		3-deoxy-D-manno-octulosonic-acid transferase	Q7VNN6	waaA	
		lipid A biosynthesis lauroyl acyltransferase	Q7VM88	lpxL	
		lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase	Q9L7U9	lpxM	
		D,D-heptose 1,7-bisphosphate phosphatase	Q7VL21		
		phosphoheptose isomerase	Q7VN00	gmhA	
		ADP-heptose--lipooligosaccharide heptosyltransferase II	Q7VNA4	waaF	
5	Biosynthesis of siderophore group nonribosomal peptides	menaquinone-specific isochorismate synthase	Q7VND2	menF	Ubiquinone and menaquinone biosynthesis
6	Tetracycline biosynthesis	acetyl-CoA carboxylase carboxyltransferase subunit alpha	Q7VPL3	accA	Fatty acid biosynthesis, Pyruvate metabolism , Propanoate metabolism
7	Bacterial secretion system	preprotein translocase subunit SecD	Q7VKW0	secD	Protein export
		preprotein translocase subunit SecY	Q7VKF3	secY	Protein export
		preprotein translocase subunit SecA	Q7VKT3	secA, azi, div	Protein export
		preprotein translocase subunit SecB	Q7VN99	SecB	Protein export
		sec-independent protein secretion pathway component TatC	Q7VN65	tatC	Protein export

(Table S3). Contd…..

S. No.	Pathways Present Exclusively in *H. ducreyi*	Protein Name	Swiss Prot ID	Gene Name	Involvement in Other Metabolic Pathways
8	Phosphotransferase system (PTS)	phosphoenolpyruvate-protein phosphotransferase	Q7VP72	ptsI	
		glucose-specific PTS system component	Q7VP73	crr	Glycolysis / Gluconeogenesis, Starch and sucrose metabolism, Amino sugar and nucleotide sugar metabolism,
		mannose-specific phosphotransferase IIAB component	Q7VN23	manX	Fructose and mannose metabolism, Amino sugar and nucleotide sugar metabolism,
		PTS system, nitrogen regulatory IIA-like protein	Q9L7V4	ptsN	
		ascorbate-specific PTS system enzyme IIC/IIB	Q7U333	ulaA, sgaT	Ascorbate and aldarate metabolism,
9	Two-component system	two-component sensor protein	Q7VLH5	cpxA	
		transcriptional regulatory protein CpxR	Q7VLH6	cpxR	
		two-component response regulator	Q7VP30	arcA	
		citrate CoA-transferase subunit	Q7VLZ0	citF	Citrate cycle (TCA cycle)
		nitrate/nitrite response regulator protein	Q7VP06	narP	
		fumarate reductase subunit D	P59844	frdD	Citrate cycle (TCA cycle), Oxidative phosphorylation, Butanoate metabolism, Reductive carboxylate cycle (CO2 fixation)
		putative nitrogen regulatory protein P-II	Q7VPK6	glnB	
10	Bacterial chemotaxis	heme-binding protein A	Q7VP82	hbpA	ABC transporters,
11	Vibrio cholerae phathogenic cycle	adenylate cyclase	Q7VND7	cyaA	Purine metabolism