

Table S15: Protein Homologies of Bacterial Virulence Factors in Six Strains of *L. interrogans* Blasted in VFDB Software

Virulence function	Homologous bacterial virulence factor	Gene	Langkawi	782	898	1489	1548	1530
O	lipopolysaccharide biosynthesis protein [LPS] [<i>Bordetella pertussis</i> Tohama I]	<i>bplC</i>	9.00E-72	9.00E-72	8.00E-60	4.00E-58	2.00E-71	1.00E-59
O	lipopolysaccharide biosynthesis protein [LPS] [<i>Bordetella pertussis</i> Tohama I]	<i>bplF</i>	1.00E-94	1.00E-94	1.00E-94	1.00E-94	9.00E-95	1.00E-94
D	capsular polysaccharide synthesis enzyme Cap8D [<i>Staphylococcus aureus</i>]	<i>cap8D</i>	e-112	e-112	e-112	e-113	e-112	e-122
D	capsular polysaccharide synthesis enzyme Cap8E [<i>Staphylococcus aureus</i>]	<i>cap8E</i>	e-126	e-126	e-126	9.00E-69	8.00E-69	e-126
D	capsular polysaccharide synthesis enzyme Cap8F [<i>Staphylococcus aureus</i>]	<i>cap8F</i>	8.00E-92	4.00E-92	8.00E-92	*N/S	*N/S	6.00E-92
D	capsular polysaccharide synthesis enzyme Cap8G [<i>Staphylococcus aureus</i>]	<i>cap8G</i>	e-115	e-115	e-115	*N/S	*N/S	e-115
N	cytochrome c heme lyase subunit CcmF [<i>Legionella pneumophila</i>]	<i>ccmF</i>	3.00E-58	3.00E-58	2.00E-55	3.00E-58	9.00E-64	1.00E-63
O	Type III secretion system ATPase [TTSS] [<i>Chlamydia trachomatis</i>]	<i>cdsN</i>	1.00E-96	1.00E-96	1.00E-96	1.00E-96	1.00E-96	1.00E-96
O	chemotaxis protein CheA peritrichous flagella [<i>Yersinia enterocolitica</i>]	<i>cheA</i>	3.00E-84	3.00E-83	8.00E-84	2.00E-83	8.00E-84	2.00E-78
O	chemotaxis histidine kinase [<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>]	<i>cheA</i>	5.00E-93	6.00E-94	6.00E-94	6.00E-94	5.00E-93	5.00E-93
O	chemotaxis-specific methylesterase CheB [<i>Yersinia enterocolitica</i>]	<i>cheB</i>	1.00E-88	1.00E-88	1.00E-88	1.00E-88	1.00E-88	3.00E-93
O	chemotaxis-specific methylesterase [<i>Burkholderia pseudomallei</i>]	<i>cheB</i>	2.00E-81	3.00E-69	3.00E-69	3.00E-69	3.00E-69	3.00E-69
D	endopeptidase Clp ATP-binding chain C [<i>Listeria monocytogenes</i> EGD-e]	<i>clpC</i>	0.0	0.0	0.0	0.0	0.0	0.0
D	endopeptidase Clp ATP-binding chain C [<i>Listeria monocytogenes</i> EGD-e]	<i>clpC</i>	e-143	0.0	e-142	e-142	e-143	e-143
D	endopeptidase Clp ATP-binding chain C [<i>Listeria monocytogenes</i> EGD-e]	<i>clpC</i>	0.0	0.0	0.0	0.0	0.0	0.0
D	ATP-dependent Clp protease proteolytic subunit [<i>Listeria monocytogenes</i>]	<i>clpP</i>	4.00E-57	4.00E-57	4.00E-57	4.00E-57	4.00E-57	4.00E-57
N	collagenase [kappa-toxin] [<i>Clostridium perfringens</i> str. 13]	<i>colA</i>	2.00E-70	2.00E-70	2.00E-70	2.00E-70	7.00E-71	2.00E-70

N	glucose-1-phosphate cytidylyltransferase [O-antigen][Yersinia enterocolitica]	ddhA	7.00E-80	7.00E-80	7.00E-80	1.00E-67	1.00E-67	7.00E-80
N	CDP-glucose 4,6-dehydratase [O-antigen] [Yersinia enterocolitica]	ddhB	8.00E-92	8.00E-92	8.00E-92	4.00E-96	7.00E-96	8.00E-92
N	GDP-fucose synthetase [O-antigen] [Yersinia enterocolitica]	fcl	e-102	e-102	e-102	7.00E-97	7.00E-97	e-102
N	ferrous iron transporter B [FeoAB] [Legionella pneumophila]	feoB	2.00E-78	3.00E-78	2.00E-78	3.00E-78	4.00E-78	3.00E-78
O	flagellar synthesis regulator FleN [polar flagella][Legionella pneumophila]	fleN	3.00E-54	3.00E-54	2.00E-54	3.00E-54	3.00E-54	3.00E-54
O	transcriptional regulator FleQ [polar flagella] [Legionella pneumophila]	fleQ	2.00E-68	2.00E-68	2.00E-68	2.00E-68	2.00E-68	2.00E-68
O	sigma 54-dependent response regulator [Legionella pneumophila]	fleR/flrC	5.00E-83	3.00E-83	5.00E-83	5.00E-83	5.00E-83	5.00E-43
O	flagellar basal-body rod protein [Helicobacter pylori 26695]	flgG	1.00E-74	1.00E-74	1.00E-74	1.00E-74	1.00E-74	1.00E-74
O	flagellar P-ring protein precursor [Pseudomonas aeruginosa PAO1]	flgI	6.00E-55	8.00E-55	6.00E-55	6.00E-55	6.00E-55	6.00E-55
O	flagellar biosynthesis protein FlhA [Pseudomonas aeruginosa PAO1]	flhA	e-110	e-110	e-110	e-110	e-110	e-110
O	flagellar motor switch protein G [Helicobacter pylori]	fliG	3.00E-60	3.00E-60	3.00E-60	3.00E-60	3.00E-60	3.00E-60
O	flagellar motor switch protein FlhM [Helicobacter pylori]	fliM	3.00E-60	3.00E-60	3.00E-60	3.00E-60	3.00E-60	3.00E-60
O	UDP-glucose 4-epimerase [LOS] [Haemophilus influenzae]	galE	4.00E-58	1.00E-57	1.00E-57	1.00E-57	1.00E-57	1.00E-57
O	GDP-mannose 4,6-dehydratase [LPS] [Brucella melitensis]	gmd	e-122	e-122	e-122	e-122	e-122	e-122
O	general secretion pathway protein D [T2SS] [Shigella dysenteriae]	gspD	2.00E-54	2.00E-54	2.00E-54	2.00E-54	2.00E-54	2.00E-54
O	general secretion pathway protein E [T2SS] [Shigella dysenteriae]	gspE	e-120	e-120	e-120	e-120	e-120	e-120
O	beta-hemolysin [-hemolysin] [Staphylococcus aureus subsp. aureus]	hlyB	2.00E-62	2.00E-57	2.00E-62	2.00E-62	2.00E-57	2.00E-57
O	beta-hemolysin [-hemolysin] [Staphylococcus aureus subsp. aureus]	hlyB	3.00E-55	3.00E-55	3.00E-55	6.00E-52	3.00E-55	3.00E-55
O	hemolysin transport protein [Hemolysin] [Escherichia coli O157:H7]	hlyB	2.00E-56	2.00E-56	8.00E-56	2.00E-56	2.00E-56	2.00E-56
O	60K heat shock protein HtpB [Hsp60] [Legionella pneumophila]	htpB	1.00E-169	e-169	e-169	e-169	e-169	e-169
O	catalase [KatA] [Neisseria meningitidis MC58]	katA	e-157	e-157	e-157	e-157	e-157	e-157
O	2-dehydro-3-deoxyphosphooctonate aldolase [LPS] [Brucella melitensis]	kdsA	1.00E-71	1.00E-71	1.00E-71	1.00E-71	1.00E-71	1.00E-71
O	D-arabinose 5-phosphate isomerase [Capsule] [Campylobacter jejuni]	kpsF	5.00E-61	5.00E-61	5.00E-61	2.00E-61	1.00E-60	2.00E-61
O	UDP-N-acetylglucosamine acyltransferase [LOS] [Haemophilus influenzae]	lpxA	2.00E-53	2.00E-53	2.00E-53	2.00E-53	2.00E-53	2.00E-53
O	lipid-A-disaccharide synthase [LOS] [Haemophilus influenzae Rd KW20]	lpxB	1.00E-53	1.00E-53	2.00E-53	2.00E-53	1.00E-53	2.00E-53

O	UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase [LOS] [Haemophilus influenzae]	lpxC	9.00E-53	9.00E-53	9.00E-53	9.00E-53	9.00E-53	9.00E-53
N	Mg2+ transport protein [MgtBC] [Salmonella enterica]	mgtB	e-133	e-147	e-147	e-147	e-146	e-146
O	lipid transporter ATP-binding/permease [LOS] [Haemophilus influenzae Rd]	msbA	3.00E-88	2.00E-88	8.00E-88	3.00E-88	3.00E-88	3.00E-88
O	lipid transporter ATP-binding/permease [LOS] [Haemophilus influenzae Rd]	msbA	5.00E-84	4.00E-84	4.00E-84	4.00E-84	5.00E-84	4.00E-84
D	multiple transferable resistance system protein MtrD [Neisseria meningitidis MC58]	mtrD	2.00E-56	5.00E-54	2.00E-54	2.00E-56	2.00E-56	2.00E-69
D	multiple transferable resistance system protein MtrD [Neisseria meningitidis MC58]	mtrD	5.00E-56	2.00E-56	e-56	5.00E-54	5.00E-54	1.00E-91
D	multiple transferable resistance system protein MtrD [Neisseria meningitidis MC58]	mtrD	2.00E-69	1.00E-69	5.00E-92	2.00E-69	2.00E-69	5.00E-54
D	multiple transferable resistance system protein MtrD [Neisseria meningitidis MC58]	mtrD	9.00E-92	7.00E-92	5.00E-92	1.00E-91	1.00E-91	2.00E-56
D	N-acetyl neuramic acid synthetase NeuB [Streptococcus agalactiae]	neuB	5.00E-93	5.00E-93	5.00E-93	7.00E-53	7.00E-53	5.00E-93
D	N-acetyl neuramic acid synthetase NeuB [Streptococcus agalactiae 2603V/R]	neuB	N	N	N	*2E-91	*2E-91	N
D	UDP-N-acetylglucosamine-2-epimerase[Streptococcus agalactiae 2603V/R]	neuC	5.00E-65	6.00E-64	5.00E-65	*1E-79	*1E-79	5.00E-65
O	Perosamine synthetase [LPS] [Brucella melitensis]	per	8.00E-55	8.00E-55	1.00E-54	6.00E-156	4.00E-160	8.00E-55
O	UDP-N-acetylglucosamine 4,6-dehydratase[Helicobacter pylori 26695]	pseB	8.00E-66	8.00E-66	7.00E-66	*2E-97	*2E-97	8.00E-66
O	C4 aminotransferase [Campylobacter jejuni subsp. jejuni NCTC 11168]	pseC	N	N	N	*4E-65	*4E-65	N
O	N-acetylneuraminic acid synthetase[Campylobacter jejuni.]	psel	8.00E-52	6.00E-52	8.00E-52	*8E-65	*7E-65	8.00E-52
D	DNA repair protein RecN [RecN] [Neisseria meningitidis]	recN	7.00E-66	7.00E-66	7.00E-66	7.00E-66	7.00E-66	7.00E-66
R	probable GTP pyrophosphokinase RelA [Mycobacterium tuberculosis]	relA	e-149	e-149	e-149	e-149	e-149	e-149
O	ADP-L-glycero-D-mannoheptose-6-epimerase [Haemophilus influenzae]	rfaD	2.00E-57	4.00E-58	4.00E-58	4.00E-58	3.00E-57	1.00E-57
O	dTDP-glucose 46-dehydratase [LOS] [Haemophilus influenzae]	rffG	2.00E-97	2.00E-97	2.00E-97	2.00E-97	1.00E-97	2.00E-97
N	sphingomyelinase-c [SMase] [Listeria ivanovii]	smcL	1.00E-59	1.00E-59	2.00E-59	1.00E-59	1.00E-59	1.00E-59
N	sphingomyelinase-c [SMase] [Listeria ivanovii]	smcL	1.00E-69	1.00E-69	4.00E-69	1.00E-69	1.00E-69	1.00E-69

O	general secretion pathway protein F [<i>Pseudomonas aeruginosa</i>]	<i>xcpS</i>	2.00E-56	2.00E-56	2.00E-56	2.00E-56	2.00E-56	2.00E-56
O	phosphomannomutase [LOS] [<i>Haemophilus influenzae</i>]	<i>yhxB/manB</i>	1.00E-62	6.00E-63	6.00E-63	2.00E-62	6.00E-63	2.00E-65
O	beta-hemolysin [-hemolysin] [<i>Staphylococcus aureus</i>]	<i>hlyB</i>	2.00E-62	2.00E-57	2.00E-62	2.00E-62	2.00E-57	2.00E-57
O	beta-hemolysin [-hemolysin] [<i>Staphylococcus aureus</i> subsp. <i>aureus</i> COL]	<i>hlyB</i>	3.00E-55	3.00E-55	3.00E-55	6.00E-52	3.00E-55	3.00E-55
O	hemolysin transport protein [Hemolysin] [<i>Escherichia coli</i> O157:H7 str. EDL933]	<i>hlyB</i>	2.00E-56	2.00E-56	8.00E-56	2.00E-56	2.00E-56	2.00E-56
O	Hsp60, 60K heat shock protein HtpB [Hsp60] [<i>Legionella pneumophila</i>]	<i>htpB</i>	1.00E-169	e-169	e-169	e-169	e-169	e-169
O	catalase [KatA] [<i>Neisseria meningitidis</i> MC58]	<i>katA</i>	e-157	e-157	e-157	e-157	e-157	e-157
O	2-dehydro-3-deoxyphosphooctonate aldolase [LPS] [<i>Brucella melitensis</i>]	<i>kdsA</i>	1.00E-71	1.00E-71	1.00E-71	1.00E-71	1.00E-71	1.00E-71
O	D-arabinose 5-phosphate isomerase [<i>Campylobacter jejuni</i>]	<i>kpsF</i>	5.00E-61	5.00E-61	5.00E-61	2.00E-61	1.00E-60	2.00E-61
O	UDP-N-acetylglucosamine acyltransferase [<i>Haemophilus influenzae</i>]	<i>lpxA</i>	2.00E-53	2.00E-53	2.00E-53	2.00E-53	2.00E-53	2.00E-53
O	lipid-A-disaccharide synthase [LOS] [<i>Haemophilus influenzae</i>]	<i>lpxB</i>	1.00E-53	1.00E-53	2.00E-53	2.00E-53	1.00E-53	2.00E-53
O	UDP-3-O-N-acetylglucosamine deacetylase [<i>Haemophilus influenzae</i>]	<i>lpxC</i>	9.00E-53	9.00E-53	9.00E-53	9.00E-53	9.00E-53	9.00E-53
N	Mg2+ transport protein [MgtBC] [<i>Salmonella enterica</i>]	<i>mgtB</i>	e-133	e-147	e-147	e-147	e-146	e-146
O	lipid transporter ATP-binding/permease [LOS] [<i>Haemophilus influenzae</i>]	<i>msbA</i>	3.00E-88	2.00E-88	8.00E-88	3.00E-88	3.00E-88	3.00E-88
O	lipid transporter ATP-binding/permease [LOS] [<i>Haemophilus influenzae</i>]	<i>msbA</i>	5.00E-84	4.00E-84	4.00E-84	4.00E-84	5.00E-84	4.00E-84
D	multiple transferable resistance system protein MtrD [<i>Neisseria meningitidis</i>]	<i>mtrD</i>	2.00E-56	5.00E-54	2.00E-54	2.00E-56	2.00E-56	2.00E-69
D	multiple transferable resistance system protein MtrD [<i>Neisseria meningitidis</i>]	<i>mtrD</i>	5.00E-56	2.00E-56	e-56	5.00E-54	5.00E-54	1.00E-91
D	multiple transferable resistance system protein MtrD [<i>Neisseria meningitidis</i>]	<i>mtrD</i>	2.00E-69	1.00E-69	5.00E-92	2.00E-69	2.00E-69	5.00E-54
D	multiple transferable resistance system protein MtrD [<i>Neisseria meningitidis</i>]	<i>mtrD</i>	9.00E-92	7.00E-92	5.00E-92	1.00E-91	1.00E-91	2.00E-56
D	N-acetyl neuramic acid synthetase NeuB [Capsule][<i>Streptococcus agalactiae</i>]	<i>neuB</i>	5.00E-93	5.00E-93	5.00E-93	7.00E-53	7.00E-53	5.00E-93

D	N-acetyl neuramic acid synthetase NeuB [Capsule][<i>Streptococcus agalactiae</i>]	<i>neuB</i>	N	N	N	*2E-91	*2E-91	N
D	UDP-N-acetylglucosamine-2-epimerase NeuC [<i>Streptococcus agalactiae</i> 2603V/R]	<i>neuC</i>	5.00E-65	6.00E-64	5.00E-65	*1E-79	*1E-79	5.00E-65
O	Perosamine synthetase [LPS] [<i>Brucella melitensis</i>]	<i>per</i>	8.00E-55	8.00E-55	1.00E-54	6.00E-156	4.00E-160	8.00E-55
O	UDP-N-acetylglucosamine 4,6-dehydratase [<i>Helicobacter pylori</i>]	<i>pseB</i>	8.00E-66	8.00E-66	7.00E-66	*2E-97	*2E-97	8.00E-66
O	C4 aminotransferase [<i>Campylobacter jejuni</i>]	<i>pseC</i>	N	N	N	*4E-65	*4E-65	N
O	N-acetylneuraminic acid synthetase [<i>Campylobacter jejuni</i>]	<i>psel</i>	8.00E-52	6.00E-52	8.00E-52	*8E-65	*7E-65	8.00E-52
D	DNA repair protein RecN [RecN] [<i>Neisseria meningitidis</i>]	<i>recN</i>	7.00E-66	7.00E-66	7.00E-66	7.00E-66	7.00E-66	7.00E-66
R	probable GTP pyrophosphokinase [<i>Mycobacterium tuberculosis</i>]	<i>relA</i>	e-149	e-149	e-149	e-149	e-149	e-149
O	ADP-L-glycero-D-mannoheptose-6-epimerase [<i>Haemophilus influenzae</i>]	<i>rfaD</i>	2.00E-57	4.00E-58	4.00E-58	4.00E-58	3.00E-57	1.00E-57
O	dTDP-glucose 46-dehydratase [LOS] [<i>Haemophilus influenzae</i>]	<i>rffG</i>	2.00E-97	2.00E-97	2.00E-97	2.00E-97	1.00E-97	2.00E-97
N	sphingomyelinase-c [SMase] [<i>Listeria ivanovii</i>]	<i>smcL</i>	1.00E-59	1.00E-59	2.00E-59	1.00E-59	1.00E-59	1.00E-59
N	sphingomyelinase-c [SMase] [<i>Listeria ivanovii</i>]	<i>smcL</i>	1.00E-69	1.00E-69	4.00E-69	1.00E-69	1.00E-69	1.00E-69
O	general secretion pathway protein F [<i>Pseudomonas aeruginosa</i>]	<i>xcpS</i>	2.00E-56	2.00E-56	2.00E-56	2.00E-56	2.00E-56	2.00E-56
O	phosphomannomutase [LOS] [<i>Haemophilus influenzae</i>]	<i>yhxB/manB</i>	1.00E-62	6.00E-63	6.00E-63	2.00E-62	6.00E-63	2.00E-65

N, blast result \geq e-value 1e-52 or score of alignment \leq 200 (ie. not significant)

*Similarities found only between 1489 and 1548

Green (D) defensive virulence factors; red (O) offensive virulence factors; pink (R) regulatory; yellow (N) nonspecific.