



APPENDIX O

สำนักหอสมุด

Orthologous proteins in database matched with the peptide sequences generated from tryptic digestion of proteins in circles no. 1 to 22 of *L. borgpetersenii* serogroup Tarassovi serovar Tarassovi separated by 2DE at non-linear pH 3-10 (**Figure 45A**); Immunome of MAb LPF1; circle no 3-20 (**Figure 45B**); Immunome of LPF2, circle no. 1 to 22 (**Figure 45C**), (**Table 11, Chapter V**).

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
1	YP_002075	UDP-glucose 4-epimerase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5	8.46	48,900.33	38942.9			30.13	7.27	3 (3 0 0 0)
		-.SLLITGGTGSFGK.-					1238.42	2	2.69	0.00	20/24
		-.SLLITGGTGSFGK.-					1238.42	2	2.50	0.00	18/24
		-.GSVIPLFIEQVK.-					1330.60	2	2.41	0.02	14/22
	YP_003221	ABC transporter, ATP-binding protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.93			34872.9			20.14	10.68	2 (2 0 0 0)
		-.VGIAQALLGNPR.-					1209.42	2	2.36	0.15	16/22
		-.IGYLPETPPLYPELSVQDYLK.-					2436.78	2	2.81	0.30	18/40
2	YP_000509	GrpE (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	4.8	4.68	39756.66	24232.6			60.24	16.04	6 (6 0 0 0)
		-.ERAEFQNFK.-					1169.27	2	2.97	0.12	14/16
		-.RSAQEFVSIR.-					1193.34	2	3.88	0.12	17/18
		-.SAQEFVSIR.-					1037.15	2	2.69	0.20	14/16
		-.SLVSGFLNPIDNLER.-					1674.88	2	4.73	0.40	21/28
		-.SLVSGFLNPIDNLER.-					1674.88	2	3.75	0.25	16/28
		-.SLVSGFLNPIDNLER.-					1674.88	2	4.27	0.30	19/28
	YP_001839	flagellin protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.54			31306.3			30.24	12.81	3 (3 0 0 0)
		-.NM*ETLSSGM*R.-					1158.29	2	2.75	0.22	13/18
		-.VLAIQSSNGIYSAEDR.-					1723.87	2	4.73	0.31	25/30
		-.M*ALLQGFAR.-					1138.32	2	2.55	0.13	15/18
3	NP_712836	60 kDa chaperonin (<i>L. interrogans</i> serovar Lai str. 56601)	5.3	5.29	36645.6	57970.4			64.33	11.54	7 (4 3 0 0)
		-.VTVDKENTTHIEGK.-					1547.73	2	4.32	0.30	20/26
		-.LENTTLQM*LGR.-					1292.49	2	4.05	0.26	17/20
		-.LENTTLQMLGR.-					1276.49	2	3.34	0.32	17/20
		-.SIETTLDVVEGM*QFDR.-					1857.03	2	4.51	0.10	22/30

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
		-SMLEDIAILTTGGQVISEDLMG*K.-					2337.70	3	4.01	0.19	35/84
		-SMLEDIAILTTGGQVISEDLMG*K.-					2337.70	2	6.25	0.13	30/42
		-SMLEDIAILTTGGQVISEDLMG*K.-					2337.70	2	6.24	0.09	29/42
AAZ73230		outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe)		5.74		27494.0			30.21	16.73	3 (3 0 0 0)
		-M*SAIM*PDQIAK.-					1237.47	2	3.40	0.25	15/20
		-M*SAIM*PDQIAK.-					1237.47	2	3.57	0.24	15/20
		-GSFVASVGLLFPFGIPGVSPLIHSNPEELQK.-					3188.67	3	4.25	0.36	34/120
4	YP_000467	hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.4	5.49	350000	36149.2			20.34	7.27	2 (2 0 0 0)
		-YGLEVVDFFIQSINFDQNDPNFQK.-					2879.13	3	6.79	0.49	35/92
		-YGLEVVDFFIQSINFDQNDPNFQK.-					2879.13	2	4.60	0.34	23/46
AAQ98019		Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae)		5.79		23502.6			20.18	10.80	2 (2 0 0 0)
		-M*SAIM*PDQIAK.-					1237.47	2	3.58	0.23	15/20
		-ISFTTYKPGEVK.-					1370.58	3	2.68	0.20	17/44
5	NP_714855	spermidine synthase (<i>L. interrogans</i> serovar Lai str. 56601)	5.9	5.89	36645.6	32088.9			70.21	18.51	7 (7 0 0 0)
		-RPFYETM*ANCLK.-					1546.77	2	3.17	0.25	17/22
		-RPFYETM*ANCLK.-					1546.77	2	3.60	0.28	17/22
		-IDVFESVGFR.-					1226.36	2	3.54	0.35	18/20
		-IDVFESVGFR.-					1226.36	2	4.21	0.32	18/20
		-GVIDVCYEFPEIANAM*K.-					2136.40	2	3.87	0.50	24/34
		-ELFNFIPEIFK.-					1397.64	2	3.71	0.19	17/20
		-ELFNFIPEIFK.-					1397.64	2	2.93	0.08	17/20
AAZ73230		outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe)		5.74		27494.1			60.19	39.84	6 (6 0 0 0)
		-M*SAIM*PDQIAK.-					1237.47	2	3.85	0.29	16/20
		-PGQAPDGLVDGNK.-					1268.36	2	3.29	0.38	19/24
		-PGQAPDGLVDGNK.-					1268.36	2	3.59	0.39	18/24

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions	
			Gel	Theoret.	Gel	Theoret.						
5 (cont.)		-ISFTTYKPGEVK.-					1370.58	2	3.18	0.25	15/22	
		-M*SAIM*PDQIAK.-					1237.47	2	2.17	0.16	13/20	
		-AAYLYVWIPAVIAEM*GVR.-					2131.53	3	3.44	0.30	28/68	
	YP_002699	hydroxymethylglutaryl-CoA lyase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.69		32331.7			20.27	5.70	2 (2 0 0 0 0)	
		-GYVSTVIDCPYEGK.-					1588.73	2	3.18	0.32	21/26	
		-GAAGNLATDDLVFLEK.-					1797.99	2	5.31	0.24	23/32	
6	AAZ73230	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe)	6.1	5.74	36645.6	27494.1			100.28	17.13	10 (10 0 0 0 0)	
			-M*SAIM*PDQIAK.-					1237.47	2	3.48	0.27	17/20
			-PGQAPDGLVDGNK.-					1268.36	2	3.75	0.41	18/24
			-SFDDLKNIDTK.-					1296.41	2	3.46	0.21	17/20
			-SFDDLKNIDTK.-					1296.41	2	3.72	0.21	17/20
			-M*SAIM*PDQIAK.-					1237.47	2	2.82	0.12	15/20
			-M*SAIM*PDQIAK.-					1237.47	2	2.99	0.21	15/20
			-ISFTTYKPGEVK.-					1370.58	2	2.91	0.24	16/22
			-M*ISPTGEIGEPGDGLVSDAFK.-					2252.44	2	5.59	0.50	26/42
			-GSFVASVGLLFPFGIPGVSPLIHSNPEELQK.-					3188.67	3	3.42	0.36	32/120
			-GSFVASVGLLFPFGIPGVSPLIHSNPEELQK.-					3188.67	3	3.62	0.36	37/120
AAV88032		outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Javanica)		5.37		25121.4			40.26	12.78	4 (4 0 0 0 0)	
		-TFLPYGSVINYYGYVKPQAPDGLVDGNK.-					3134.49	3	4.30	0.53	39/112	
		-TFLPYGSVINYYGYVK.-					1885.15	2	5.28	0.49	23/30	
		-TFLPYGSVINYYGYVK.-					1885.15	3	3.85	0.26	28/60	
		-TFLPYGSVINYYGYVK.-					1885.15	3	3.96	0.30	29/60	
7	NP_710593	Electron transfer flavoprotein beta-subunit (<i>L. interrogans</i> serovar Lai str. 56601)	6.3	5.58	36645.6	27084.9			110.28	37.55	11 (11 0 0 0 0)	
			-TAYAM*GADR.-					972.06	2	2.46	0.28	14/16
			-QVPDTETSIKVGDK.-					1517.66	2	2.13	0.26	18/26

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
7 (cont.)		-ATKEVEGGTQTVETSTPVALTAQK.-					2447.68	3	4.64	0.35	33/92
		-EVEGGTQTVETSTPVALTAQK.-					2147.33	2	4.31	0.44	24/40
		-HGGEVIAVSLGPDR.-					1407.56	2	4.75	0.42	21/26
		-HGGEVIAVSLGPDR.-					1407.56	2	4.95	0.48	21/26
		-IEIVGLEPPPPR.-					1317.56	2	3.25	0.34	19/22
		-IEIVGLEPPPPR.-					1317.56	2	2.35	0.34	19/22
		-WIISPYDEFAIEEGIR.-					1939.16	2	5.59	0.44	25/30
		-WIISPYDEFAIEEGIR.-					1939.16	3	4.61	0.28	28/60
		-HGGEVIAVSLGPDRVVEALR.-					2075.36	3	2.69	0.26	25/76
AAQ98019		Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae)		5.79		23502.6			88.25	39.91	9 (8 1 0 0 0)
		-LDDDDDGDDTYKEER.-					1801.72	3	3.82	0.19	29/56
		-LDDDDDGDDTYKEER.-					1801.72	2	4.14	0.29	21/28
		-LDDDDDGDDTYKEER.-					1801.72	2	4.23	0.02	23/28
		-PGQAPDGLVDGNKK.-					1396.53	3	3.90	0.29	28/52
		-M*SAIM*PDQIAK.-					1237.47	2	3.53	0.21	15/20
		-SFDDLKNIDTK.-					1296.41	2	3.17	0.06	17/20
		-ISFTTYKPGEVK.-					1370.58	2	3.35	0.23	16/22
		-M*ISPTGEIGEPGDGLVSDAFK.-					2252.44	2	4.82	0.19	30/42
		-M*ISPTGEIGEPGDGLVSDAFK.-					2252.44	3	4.54	0.42	33/84
YP_001942		succinate dehydrogenase iron-sulfur subunit (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		6.22	35100	26650.6			60.28	25.57	6 (6 0 0 0 0)
		-NASAM*LFVSAK.-					1155.35	2	2.52	0.09	15/20
		-VDADVSM DAATCIGCGACVASCK.-					2419.62	3	5.39	0.34	41/88
		-ITHLGLLPQ GK.-					1177.42	2	3.73	0.23	18/20
		-DISPNM*SFLEM*LDVVNEELITK.-					2570.92	2	4.39	0.44	22/42
		-DISPNM*SFLEM*LDVVNEELITK.-					2570.92	3	5.52	0.36	34/84
		-DISPNM*SFLEM*LDVVNEELITK.-					2570.92	3	4.91	0.33	36/84

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
7 (cont.)	NP_711213	enoyl-CoA hydratase (<i>L. interrogans</i> serovar Lai str. 56601)		6.14		30573.8			60.24	19.27	6 (6 0 0 0)
		-VAIVADM*GSINR.-					1262.46	2	4.50	0.42	18/22
		-GINAVYDSPKPSIAAVQK.-					1859.12	2	4.72	0.38	21/34
		-HCIGGGLDLISACDIR.-					1757.96	3	4.49	0.14	26/60
		-FFDLILK.-					896.11	2	2.37	0.00	12/12
		-FFDLILK.-					896.11	1	1.92	0.00	10/12
		-FFDLILK.-					896.11	2	2.67	0.00	12/12
AAS21765	LipL32 (<i>L. borgpetersenii</i>)			7.88		28943.0			54.27	34.96	6 (5 0 0 1 0)
		-LNDDDDGDDTYKEER.-					1800.73	2	4.06	0.36	21/28
		-SSFVLESTVPGTNETVK.-					1883.05	2	2.14	0.17	19/34
		-SSFVLESTVPGTNETVK.-					1883.05	2	3.03	0.31	21/34
		-TFLPYGSVINYYGYVKPGQAPDGLVDGNK.-					3134.49	3	4.35	0.53	39/112
		-TFLPYGSVINYYGYVK.-					1885.15	2	4.36	0.41	25/30
		-GSFVASVGLLFPPIGPGVSPLIHSNPEELQK.-					3188.67	3	4.04	0.39	33/120
YP_000467	hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fioc 130)										2 (2 0 0 0)
		-YGLEVVDFFIQSINFQNDPNFQK.-					2879.13	3	4.92	0.37	27/92
		-YGLEVVDFFIQSINFQNDPNFQK.-					2879.13	3	7.17	0.51	35/92
NP_711200	NifU-like protein (<i>L. interrogans</i> serovar Lai str. 56601)			5.65		29044.5			20.36	7.98	2 (2 0 0 0)
		-LAGANVEGADFTDAIYDIGTR.-					2170.32	2	6.46	0.53	28/40
		-LAGANVEGADFTDAIYDIGTR.-					2170.32	2	5.92	0.56	28/40
NP_713559	flagellar filament outer layer protein A (<i>L. interrogans</i> serovar Lai str. 56601)			8.25		36063.8			20.28	5.54	2 (2 0 0 0)
		-SRPDTSGETVYLFFDELK.-					2133.30	3	4.12	0.26	29/68
		-SRPDTSGETVYLFFDELK.-					2133.30	2	5.67	0.50	25/34
AAZ73230	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe)		6.3	5.74	36645.6	27494.1			40.16	17.13	4 (4 0 0 0)
		-PGQAPDGLVDGNK.-					1268.36	2	2.35	0.35	13/24
		-ISFTTYKPGEVK.-					1370.58	2	2.69	0.12	15/22

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/	% coverage/	Peptides(Hits)/
			Gel	Theoret.	Gel	Theoret.			X _{corr}	ΔCn	Ions
7 (cont.)		-AYYLYVWIPAVIAEM*GVR.-					2131.53	2	2.15	0.16	23/34
		-AYYLYVWIPAVIAEM*GVR.-					2131.53	2	3.12	0.31	20/34
AAV88032		outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Javanica)		5.37		25121.4			30.26	12.78	3 (3 0 0 0)
		-TFLPYGSVINYYGYVKPGQAPDGLVDGNK.-					3134.49	3	3.89	0.41	37/112
		-TFLPYGSVINYYGYVK.-					1885.15	2	4.20	0.46	23/30
		-TFLPYGSVINYYGYVK.-					1885.15	2	5.24	0.42	25/30
YP_002699		hydroxymethylglutaryl-CoA lyase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.69		32331.7			20.25	11.42	2 (2 0 0 0)
		-GAAGNLATDDL VYFLEK.-					1797.99	2	4.64	0.24	20/32
		-GAAGNLATDDL VYFLEK.-					1797.99	2	4.92	0.24	22/32
YP_001500		2-dehydro-3-deoxyphosphooctonate aldolase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		6.96		31949.5			12.26	11.42	2 (1 0 0 1)
		-GTSFGYGNLIFDGR.-					1504.63	2	3.50	0.20	21/26
		-IGGDEPFFLISGPCVMENR.-					2139.41	2	2.58	0.10	14/36
8	NP_710593	electron transport flavoprotein beta subunit (<i>L. interrogans</i> serovar Lai str. 56601)	5.7	5.58	34841.83	27084.9			110.27	35.97	11 (11 0 0 0)
		-TAYAM*GADR.-					972.06	2	2.20	0.33	14/16
		-ATKEVEGGTQTVETSTPVALTAQK.-					2447.68	3	4.65	0.40	38/92
		-ATKEVEGGTQTVETSTPVALTAQK.-					2447.68	3	5.04	0.44	36/92
		-EVEGGTQTVETSTPVALTAQK.-					2147.33	2	4.28	0.40	24/40
		-EVEGGTQTVETSTPVALTAQK.-					2147.33	3	5.30	0.40	36/80
		-HGGEVIAVSLGPDR.-					1407.56	2	4.30	0.35	22/26
		-HGGEVIAVSLGPDR.-					1407.56	2	4.75	0.36	21/26
		-IEIVGLEPPPPR.-					1317.56	2	2.43	0.16	16/22
		-WIISPYDEFAIEEGIR.-					1939.16	2	5.36	0.45	24/30
		-WIISPYDEFAIEEGIR.-					1939.16	3	4.31	0.31	30/60
		-WIISPYDEFAIEEGIR.-					1939.16	3	4.46	0.36	32/60

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
8 (cont.)	AAQ98019	Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae)		5.79		23502.6			50.26	21.13	5 (5 0 0 0 0)
		-LDDDDDGDDTYKEER.-				1801.72	3	3.69	0.21	28/56	
		-LDDDDDGDDTYKEER.-				1801.72	2	4.56	0.01	20/28	
		-M*SAIM*PDQIAK.-				1237.47	2	3.61	0.25	15/20	
		-ISFTTYKPGEVK.-				1370.58	2	3.14	0.27	16/22	
		-M*ISPTGEIGEPGDGLVSDAFK.-				2252.44	2	5.12	0.50	28/42	
AAZ73230	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe)		5.7	5.74	34841.83	27494.1		50.19	37.05	5 (5 0 0 0 0)	
		-QAIAAEESLKK.-				1188.36	2	2.83	0.13	13/20	
		-M*SAIM*PDQIAK.-				1237.47	2	3.77	0.21	15/20	
		-M*ISPTGEIGEPGDGLVSDAFK.-				2252.44	3	3.13	0.14	28/84	
		-GSFVASVGLLFPPIPGVSPLIHSNPEELQK.-				3188.67	3	3.10	0.28	35/120	
		-AYLYVWIPAVIAEM*GVR.-				2131.53	2	3.20	0.35	23/34	
AAV88032	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Javanica)		5.7	5.37	34841.83	25121.4		30.19	22.47	3 (3 0 0 0 0)	
		-M*ISPTGEIGEPGDGLVSDAFK.-				2266.47	2	2.56	0.08	17/42	
		-TFLPYGSVINYYGYVKPGQAPDGLVDGNK.-				3134.49	3	3.24	0.40	36/112	
		-TFLPYGSVINYYGYVK.-				1885.15	2	3.81	0.40	22/30	
9	AAQ98019	Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae)	6.04	5.79	34100	23502.6		50.26	28.17	5 (5 0 0 0 0)	
		-LDDDDDGDDTYKEER.-				1801.72	3	3.69	0.21	28/56	
		-LDDDDDGDDTYKEER.-				1801.72	2	4.56	0.01	20/28	
		-M*SAIM*PDQIAK.-				1237.47	2	3.61	0.25	15/20	
		-ISFTTYKPGEVK.-				1370.58	2	3.14	0.27	16/22	
		-M*ISPTGEIGEPGDGLVSDAFK.-				2252.44	2	5.12	0.50	28/42	
AAS21765	LipL32 (<i>L. borgpetersenii</i>)		7.88		28943.0		36.24	28.20	4 (3 0 1 0 0)		
		-LNDDDDGDDTYKEER.-				1800.73	2	4.31	0.06	20/28	
		-TFLPYGSVINYYGYVKPGQAPDGLVDGNK.-				3134.49	3	3.81	0.40	36/112	
		-TFLPYGSVINYYGYVKPGQAPDGLVDGNK.-				3134.49	3	3.58	0.45	38/112	

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
9 (con)		-GSFVASVGLLPPPGIPGVSPLIHSNPEELQK.-					3188.67	3	4.86	0.43	37/120
10	YP_001491	flagellin protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.3	6.86	34841.83	31551.6	1328.43	2	4.23	0.31	3 (3 0 0 0)
		-AGDDALGFAM*SEK.-					1799.02	2	5.10	0.37	19/24
		-LVQLEVDQLIEEVDR.-					2822.15	2	5.12	0.42	23/28
		-NVM*DGVSFIQVTEGTLEQVNNILQR.-						3	5.12	0.42	37/96
	YP_003032	hypothetical protein LIC13123 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		6.39		33140.0			30.19	7.22	3 (3 0 0 0)
		-SLENHPYLK.-					1101.24	2	2.73	0.19	13/16
		-ETVNFLVSTLEK.-					1380.57	2	3.59	0.32	19/22
		-ETVNFLVSTLEK.-					1380.57	2	3.81	0.36	19/22
11	NP_713477	elongation factor Ts (<i>L. interrogans</i> serovar Lai str. 56601)	5.5	5.72	31396.13	22172.5			40.20	20.10	4 (4 0 0 0)
		-ALEENNADIEK.-					1246.31	2	3.30	0.17	16/20
		-FGENITAR.-					1021.15	2	3.03	0.14	15/16
		-FQVGGL.-					620.72	1	1.77	0.04	8/10
		-YVSEVCLVNQAFFK.-					1704.94	2	3.91	0.40	23/26
12	YP_002791	elongation factor Tu (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.7	5.74	32098.26	43574.8			40.31	9.98	4 (4 0 0 0)
		-AVAYDQIDNAPEEK.-					1563.65	2	4.13	0.30	22/26
		-LM*EALDTFVPNPK.-					1491.73	2	4.14	0.41	20/24
		-LM*EALDTFVPNPK.-					1491.73	2	3.85	0.35	20/24
		-TTLTAAITTLAK.-					1306.53	2	4.53	0.29	21/24
13	YP_000684	3-oxoacyl-(acyl-carrier-protein) reductase oxidoreductase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6	8.33	32834.47	27699.7			20.19	4.63	2 (2 0 0 0)
		-LDFLVNNAAGVVK.-					1303.53	2	3.44	0.10	18/22
		-LDFLVNNAAGVVK.-					1303.53	2	3.89	0.23	20/22
14	YP_001517	tRNA (guanine-N1)-methyltransferase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6	5.8	31743.09	25594.9			30.18	11.69	3 (3 0 0 0)
		-IQSYFSEGLQK.-					1428.57	2	3.44	0.34	18/22

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/	% coverage/	Peptides(Hits)/
			Gel	Theoret.	Gel	Theoret.			X _{corr}	ΔCn	Ions
14 (cont.)		-VDDTIYGGGPGM*LLR.-					1580.79	2	3.62	0.36	20/28
		-VDDTIYGGGPGM*LLR.-					1580.79	2	3.52	0.23	19/28
15	YP_003658	ParA (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.2	6.19	32834.47	27500.7			20.21	14.40	2 (2 0 0 0)
		-IFETSISDGVAVGESHLAK.-					1961.16	3	2.69	0.19	21/72
		-FSVDGIVGLQQTITSIK.-					1807.08	2	4.25	0.36	24/32
	YP_000224	ABC transporter ATP-binding protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.99		24946.7			20.21	4.89	2 (2 0 0 0)
		-NLM*ALILELQK.-				1302.61	2	4.22	0.24	16/20	
		-NLM*ALILELQK.-				1302.61	2	3.90	0.22	16/20	
16	YP_003658	ParA (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.1	6.19	32098.26	27500.7			40.19	19.6	4 (4 0 0 0)
		-TTTSLNLSM*GLAR.-					1381.58	2	3.02	0.24	18/24
		-TTTSLNLSM*GLAR.-					1381.58	2	3.55	0.23	16/24
		-IFETSISDGVAVGESHLAK.-					1961.16	3	3.23	0.25	25/72
		-FSVDGIVGLQQTITSIK.-					1807.08	2	3.85	0.32	24/32
	YP_000224	ABC transporter ATP-binding protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.99		24946.7			30.22	4.89	3 (3 0 0 0)
		-NLM*ALILELQK.-				1302.61	2	4.41	0.23	16/20	
		-NLM*ALILELQK.-				1302.61	2	3.42	0.23	16/20	
		-NLM*ALILELQK.-				1302.61	2	3.73	0.20	14/20	
17	NP_712836	60 kDa chaperonin (<i>L. interrogans</i> serovar Lai str. 56601)	5.7	5.29	29471.76	57970.4			30.24	7.51	3 (3 0 0 0)
		-SIETTLDVVEGM*QFDR.-					1857.03	2	4.82	0.11	23/30
		-TNDVAGDGTTTATILAQSIINEGLK.-					2504.73	2	4.66	0.35	28/48
		-TNDVAGDGTTTATILAQSIINEGLK.-					2504.73	2	4.35	0.30	25/48
NP_713477	elongation factor Ts (<i>L. interrogans</i> serovar Lai str. 56601)		5.72		22172.5			30.21	12.56	3 (3 0 0 0)	
		-ALEENNADIEK.-				1246.31	2	3.56	0.20	17/20	
		-ALEENNADIEK.-				1246.31	2	3.37	0.24	17/20	
		-YVSEVCLVNQAFFK.-				1704.94	2	4.23	0.39	23/26	

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
	AAZ73230	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe) -GSFVASVGLLFPPGIPGVSPLIHSNPEELQK.- -AYYLYVWIPAVIAEM*GVR.-		5.29		27494.1	3188.67 2131.53	3 2	20.19 3.90 2.99	19.52 0.26 0.30	2 (2 0 0 0) 32/120 21/34
18	YP_001188	peroxiredoxin (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -NIDEAIR.- -NIDEAIR.- -M*PQVTSLAPDFK.- -M*PQVTSLAPDFK.- -QATINDLPVGR.- -QATINDLPVGR.- -YPLIADLTK.-	5.7	5.81	27262.07	21517.7	830.91 830.91 1350.57 1350.57 1184.33 1184.33 1034.23	1 1 2 2 2 2 1	68.19 1.91 2.10 3.88 3.69 2.25 2.17 1.75	20.21 0.00 0.00 0.28 0.26 0.11 0.10 0.05	7 (6 1 0 0) 9/12 9/12 20/22 19/22 11/20 13/20 12/16
	AAZ73230	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe) -M*SAIM*PDQIAK.- -M*SAIM*PDQIAK.- -GSFVASVGLLFPPGIPGVSPLIHSNPEELQK.- -GSFVASVGLLFPPGIPGVSPLIHSNPEELQK.- -AYYLYVWIPAVIAEM*GVR.-		5.29		27494.1	1237.47 1237.47 3188.67 3188.67 2131.53	2 2 3 3 2	50.19 3.43 3.70 3.84 3.63 2.41	23.90 0.14 0.25 0.32 0.27 0.20	5 (5 0 0 0) 15/20 16/20 32/120 31/120 16/34
	YP_002791	elongation factor Tu (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -AVAYDQIDNAPEEK.- -TTLTAAITTLAK.-		5.74		43574.8	1563.65 1306.53	2 2	20.20 3.91 4.08	6.73 0.27 0.32	2 (2 0 0 0) 21/26 21/24
19	YP_002381	hypothetical protein LIC12452 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -LSDLPAPVEVK.- -LSDLPAPVEVK.- -SSLDTLAIIAYK.-	6	5.11	27262.07	20849.0	1168.37 1168.37 1295.51	2 2 2	30.16 2.78 2.92 3.20	12.30 0.23 0.21 0.27	3 (3 0 0 0) 16/20 17/20 18/22

Continued

Spot no.	Accession no.	Orthologous proteins (s)/peptides	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% coverage/ ΔCn	Peptides(Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.					
19	YP_000728	transcription antitermination protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -IPTM*DVAEM*K.- -FLIQLPSVSTFVGSK.-		6.64		20455.6			20.17	14.36	2 (2 0 0 0)
(cont.)							1167.38	2	2.64	0.28	13/18
							1711.00	2	3.44	0.21	23/30
20	YP_000744	hypothetical protein LIC10764 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -LESVIDVLVSK.-	6.3	8.87	25375.96	18365.1			10.17	6.75	1 (1 0 0 0)
							1202.42	2	3.48	0.33	18/20
21	YP_002260	hypothetical protein LIC12326 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -VIM*DILDSLQK.-	4.5	4.42	21368.66	14273.9			20.17	8.94	2 (2 0 0 0)
							1291.54	2	3.38	0.17	16/20
22		No matched SLDLDLSIAEVK	4.5		20496.57						

MH+, protonated molecular mass; X_{corr} , cross correlation; ΔCn , delta correlation, X_{corr} ; Cross correlation, factor that indicates how well the spectra matched the peptide sequence, $X_{corr} > 1.8$ for 1+ ion, (> 1.3 , less stringent criteria), $X_{corr} > 2.5$ for 2+ ion, (> 2.0 , less stringent criteria), $X_{corr} > 3.5$ for 3+ ion, (> 3.0 , less stringent criteria), ΔCn ; Delta Correlation, indicates degree of confidence of assignment relative to next best peptide match. A higher number is better, greater than 0.08 is normal cutoff