



APPENDIX P

ชำนักรหัสสมุด

Orthologous proteins in database matched with the peptide sequences generated from tryptic digestion of proteins in spot no. 1 to 33 (**Figure 62 A, B, C, D**) of *L. borgpetersenii* serogroup Tarassovi serovar *tarassovi* separated by 2DE at non-linear pH 3-5.6, 5.3-6.5, 6.2-7.5, non-linear pH 7-11 (**Table 12 and 13, Chapter V**).

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
3h2#1	NP_712836.1	60 kDa chaperonin (<i>L. interrogans</i> serovar Lai str. 56601)	5.79	5.29	67,500	57,970.4		236.37	37.73				24 (22 2 0 0 0)
		-.KTISCVAVK.-				1,006.22	2	3.42	0.30	603.0	1	15/16	
		-.NVTAGANPM*SLKR.-				1,375.58	2	3.012	0.25	513.3	1	17/24	
		-.DIEYNETAR.-				1,111.15	2	3.112	0.25	929.0	1	15/16	
		-.LLEGVVK.-				772.91	1	2.102	0.07	580.6	1	10/12	
		-.VTVDKENTTIEGK.-				1,547.73	2	4.21	0.31	2,050.4	1	20/26	
		-.LENTTLQM*LGR.-				1,292.49	2	3.75	0.11	1,219.3	1	17/20	
		-.LAGGVAVIHVGAATEVEM*KEK.-				2,126.46	3	3.57	0.34	700.0	1	30/80	
		-.LAGGVAVIHVGAATEVEM*KEK.-				2,126.46	3	3.94	0.46	1,059.9	1	35/80	
		-.LAGGVAVIHVGAATEVEM*K.-				1,869.18	2	5.11	0.44	1,302.3	1	26/36	
		-.LAGGVAVIHVGAATEVEM*K.-				1,869.18	2	5.28	0.44	1,326.9	1	26/36	
		-.LAGGVAVIHVGAATEVEM*K.-				1,869.18	3	5.33	0.36	1,056.8	1	35/72	
		-.ISSM*KDLIHILEK.-				1,543.85	3	4.04	0.26	1,072.2	1	24/48	
		-.DLIHILEK.-				981.17	2	2.73	0.00	850.3	11	12/14	
		-.SIETTLDVVEGM*QFDR.-				1,857.03	2	5.41	0.12	1,722.6	1	23/30	
		-.SIETTLDVVEGM*QFDR.-				1,857.03	3	6.19	0.03	2,550.0	1	34/60	
		-.AAVEEGIVPGGGLTLLK.-				1,624.90	2	4.13	0.19	1,075.9	1	24/32	
		-.AAVEEGIVPGGGLTLLK.-				1,624.90	3	2.74	0.25	647.6	31	27/64	
		-.DIANVASISANNNTIGNLIADAM*DK.-				2,677.88	2	5.32	0.56	1,280.2	1	27/50	
		-.DIANVASISANNNTIGNLIADAM*DKVVGK.-				2,962.24	3	4.16	0.31	529.4	1	32/112	
		-.SMLEDIAILTGGQVISEDLGM*K.-				2,337.69	3	5.56	0.47	1,988.5	1	39/84	

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
		-.SMLEDIAILTGGQVISEDLGM*K.-					2,337.69	2	6.73	0.48	3,390.0	1	30/42
		-.SMLEDIAILTGGQVISEDLGM*K.-					2,337.69	2	6.72	0.48	3,219.6	1	29/42
		-.TNDVAGDGTATTILAQSIINEGLK.-					2,504.73	2	6.25	0.42	1,603.2	1	25/48
		-.TNDVAGDGTATTILAQSIINEGLK.-					2,504.73	3	7.35	0.33	3,940.9	1	43/96
3h15#1	NP_712599	Possible hook-associated protein, flagellin family (<i>L. interrogans</i> serovar Lai str. 56601)	4.9	7.04	40,000	31,489.8			168.358	46.10			17 (16 1 0 0 0)
		-.FNSESM*GKDIEK.-					1,401.52	2	3.84	0.30	516.6	8	15/22
		-.DITDM*AEQM*TSFTR.-					1,565.66	2	4.38	0.37	1,554.0	1	18/24
		-.QRADLGAYYNR.-					1,327.43	2	3.24	0.23	472.5	2	16/20
		-.IRDTDM*AEQM*TSFTR.-					1,835.01	3	3.19	0.08	479.6	30	24/56
		-.IRDTDM*AEQM*TSFTR.-					1,835.01	3	3.20	0.07	352.0	21	23/56
		-.GLM*NAYENIQAAESR.-					1,683.82	3	4.82	0.32	2,135.5	1	30/56
		-.TQILGLR.-					800.97	2	2.62	0.03	763.8	22	11/12
		-.TQILGLR.-					800.97	1	2.07	0.10	324.6	1	10/12
		-.M*IINHNSAIFAHR.-					1,653.93	3	5.09	0.35	2,049.4	1	33/52
		-.PQTVLQLLK.-					1,040.28	2	2.74	0.18	789.9	1	14/16
		-.PQTVLQLLK.-					1,040.28	2	2.90	0.19	806.0	1	14/16
		-.RAEM*NTEDGM*SLIQTTEGYLQETHEIVQR.-					3,413.69	3	7.08	0.48	821.1	1	42/112
		-.AEM*NTEDGM*SLIQTTEGYLQETHEIVQR.-					3,257.51	3	7.17	0.51	1,295.9	1	36/108
		-.YQILTQAATAM*LAQANM*KPQTVLQLLK.-					3,021.58	3	6.37	0.50	2,583.3	1	44/104
		-.YQILTQAATAM*LAQANMKPQTVLQLLK.-					3,005.58	3	3.06	0.23	410.2	16	25/104
		-.YQILTQAATAMLAQANM*KPQTVLQLLK.-					3,005.58	3	3.24	0.05	634.8	1	29/104
		-.IRDTDM*AEQM*TSFTR.-					1,835.01	3	2.79	0.05	417.7	22	24/56

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
3h18#1	YP_001839	flagellin protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.1	6.54	38.7	31,306.3		100.30	21.35				10 (10 0 0 0 0)
		-.M*IINHNLAAINSHR.-					1,620.86	2	4.49	0.34	881.4	1	21/26
		-.M*IINHNLAAINSHR.-					1,620.86	3	4.34	0.26	3,201.9	1	36/52
		-.M*IINHNLAAINSHR.-					1,620.86	2	4.92	0.35	1,708.0	1	22/26
		-.ANLGAYFNR.-					1,026.13	2	2.89	0.28	1,025.4	1	14/16
		-.M*ALLQGDFAR.-					1,138.32	2	3.12	0.28	990.9	1	15/18
		-.PQSVLQLLR.-					1,054.26	2	3.18	0.13	597.1	3	13/16
		-.NQILVQSGTAM*LAQANVRPQSVLQLLR.-					2,966.45	3	6.05	0.51	968.8	1	35/104
		-.NQILVQSGTAMLAQANVRPQSVLQLLR.-					2,950.45	3	5.54	0.31	1,361.0	1	35/104
		-.NQILVQSGTAM*LAQANVRPQSVLQLLR.-					2,966.45	3	4.84	0.40	931.6	1	33/104
		-.NQILVQSGTAM*LAQANVRPQSVLQLLR.-					2,966.45	3	5.33	0.35	1,122.2	1	34/104
3h21	YP_001839	flagellin protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	4.35	6.54	35	31,306.3		56.32	18.15				6 (4 2 0 0 0)
#1		-.M*IINHNLAAINSHR.-					1,620.86	3	3.14	0.11	1,486.5	1	27/52
		-.VLAIQSSNGIYSAEDR.-					1,723.86	2	5.24	0.24	2,355.3	1	23/30
		-.NQILVQSGTAM*LAQANVRPQSVLQLLR.-					2,966.45	3	5.59	0.39	930.1	1	32/104
		-.NTEDGM*SLIQTTEGYLQETNDIIQR.-					2,887.08	2	3.46	0.32	597.5	2	17/48
		-.NTEDGM*SLIQTTEGYLQETNDIIQR.-					2,887.08	3	6.00	0.06	1,797.5	1	35/96
		-.NTEDGM*SLIQTTEGYLQETNDIIQR.-					2,887.08	2	3.55	0.27	830.8	1	19/48
#3	YP_000888	transketolase alpha subunit protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	4.35	8.27	35	31,841.4		50.29	21.35				5 (5 0 0 0 0)
		-.NFANELRK.-					992.11	2	2.35	0.02	580.9	138	12/14
		-.NGIQIDGFTK.-					1,093.21	2	3.09	0.22	900.0	1	16/18

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/		
			Gel	Theoret.	Gel	Theoret.							MH+	
#4	AAS21765	-.LDNLIAFM*DK.-					1,196.39	2	4.15	0.26	1,093.8	3	16/18	
		-.M*VTAANSNGHPGGPLGLADIYAVLYK.-					2,532.90	3	5.93	0.48	2,022.9	1	50/96	
		-.GSPTIILFKTVLGGK.-					1,474.81	2	2.79	0.28	745.5	1	16/26	
		LipL32 (<i>L. borgpetersenii</i>)	7.88		28,943.0				50.20	15.49				5 (5 0 0 0 0)
		-.QAIAAEESLK.-					1,060.18	2	2.00	0.01	141.0	50	9/18	
		-.SSFVLESESTVPGTNETVK.-					1,883.04	2	3.00	0.39	574.7	1	23/34	
		-.TFLPYGVSINYYGYVKGQAPDGLVDGK.-					3,134.48	3	3.87	0.41	684.7	1	40/112	
		-.TFLPYGVSINYYGYVKGQAPDGLVDGK.-					3,134.48	3	4.08	0.50	930.1	1	42/112	
#5	YP_002802	hypothetical protein LIC12886 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.19		26,976.5				30.20				3 (3 0 0 0 0)	
		-.GLKSEESEIR.-					1,148.24	2	2.12	0.20	493.6	5	12/18	
		-.GLKSEESEIR.-					1,148.24	2	2.71	0.21	897.7	1	15/18	
		-.LGGSLATSGSVSR.-					1,192.30	2	4.15	0.27	1,223.2	1	20/24	
5h6#1	NP_712957	ATP synthase F1, beta chain (<i>L. interrogans</i> serovar Lai str. 56601)	5.79	5.56	58,000	50,626.5			140.35	26.12			14 (14 0 0 0 0)	
		-.TVLCYGQM*NEPPGAR.-					1,709.89	2	5.04	0.10	808.5	1	19/28	
		-.TVLCYGQM*NEPPGAR.-					1,709.89	3	4.04	0.21	1,430.8	1	30/56	
		-.TVLCYGQM*NEPPGAR.-					1,709.89	2	4.91	0.13	673.0	1	18/28	
		-.TVLCYGQM*NEPPGAR.-					1,709.89	3	3.70	0.17	1,558.6	1	31/56	
		-.TIDEGPAITVK.-					1,144.30	2	2.94	0.05	749.1	1	17/20	
		-.TEVFETGIK.-					1,024.15	2	2.29	0.21	729.3	2	14/16	
		-.M*PSAVGYQPTLSTEM*GALQER.-					2,299.56	3	4.59	0.08	2,714.7	1	37/80	

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.M*PSAVGYQPTLSTEM*GALQER.-					2,299.56	3	4.51	0.05	2,697.5	1	37/80
		-.M*PSAVGYQPTLSTEM*GALQER.-					2,299.56	2	5.49	0.10	1,291.3	1	27/40
		-.M*PSAVGYQPTLSTEM*GALQER.-					2,299.56	2	4.87	0.07	1,375.6	1	28/40
		-.VALSALTM*AEHFR.-					1462.7	2	3.19	0.10	1,137.7	1	17/24
		-.EVISGNYDHLPEQAFYM*VGSIDDAIEK.-					3,058.32	3	6.07	0.38	1,935.4	1	38/104
		-.YKDLQDIIAILGM*DESEDDKVLVAR.-					2,980.38	3	7.05	0.05	1,278.9	1	41/100
		-.DLQDIIAILGM*DESEDDKVLVAR.-					2,689.03	3	4.85	0.09	1,282.6	1	38/92
#2	YP_002712	acetyl-CoA acetyltransferase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		6		47,281.0			110.30	25.40			11 (11 0 0 0 0)
		-.GVHPNNM*GIGQAVATK.-					1,610.82	2	4.49	0.42	897.4	1	22/30
		-.EGLVENPTR.-					1,015.10	2	2.50	0.18	929.1	1	15/16
		-.GVHPNNM*GIGQAVATK.-					1,610.82	2	3.79	0.43	583.5	1	18/30
		-.TPFAQIAK.-					876.03	2	2.20	0.06	631.9	9	12/14
		-.SDGAAGVIVTTVEK.-					1,347.49	2	3.98	0.26	1,439.1	1	21/26
		-.IVAEDILAK.-					972.16	2	2.66	0.14	650.9	1	15/16
		-.LKPSQIDGVVVGEGFSNAPNSAR.-					2,343.58	3	6.02	0.52	1,499.2	1	35/88
		-.LIANAIM*DLKEDSSANK.-					1,850.08	3	2.76	0.09	276.6	2	24/64
		-.LIANAIM*DLK.-					1,118.37	2	3.61	0.18	741.2	1	15/18
		-.LIANAIM*DLK.-					1,118.37	2	3.48	0.21	766.6	1	15/18
		-.AM*LM*FDNPGM*KFEFEK.-					1,984.31	3	4.16	0.38	507.4	1	26/60
#4	YP_001899	enolase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		6.06		47,045.2			40.28	11.11			4 (4 0 0 0 0)
		-.YVLGAENNK.-					1,008.11	2	2.12	0.01	691.4	5	12/16
		-.SGETEDVTISHIAVATNAGQIK.-					2,242.43	3	5.65	0.22	3,381.0	1	40/84

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.SGETEDVTISHIAVATNAGQIK.-					2,242.43	3	5.42	0.18	2,949.3	1	39/84
		-.EFSSAELVDYYANLVSK.-					1,936.11	2	5.35	0.47	1,612.5	1	23/32
5h15#1	YP_002791	elongation factor Tu (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.7	5.74	51.7	43,574.8			312.35	34.91			32 (28 4 0 0 0)
		-.VEQGVLK.-					772.91	1	1.63	0.00	553.2	3	10/12
		-.AVAYDQIDNAPEEK.-					1,563.64	2	4.40	0.36	2,409.5	1	22/26
		-.AEM*IEM*VEM*DVR.-					1,501.73	2	2.98	0.25	889.6	2	15/22
		-.LM*EALDTFVNPVK.-					1,491.73	2	4.42	0.37	1,850.1	1	20/24
		-.VNDEVEIIGIRPTTK.-					1,684.91	3	2.96	0.14	688.3	1	27/56
		-.ADM*LAADERAEM*IEM*VEM*DVR.-					2,490.79	3	6.40	0.35	2,046.4	1	41/80
		-.ADM*LAADERAEM*IEM*VEM*DVR.-					2,490.79	3	6.91	0.37	1,753.6	1	37/80
		-.LM*EALDTFVNPVK.-					1,491.73	2	4.26	0.34	1,810.7	1	20/24
		-.SKPHLNVGTIGHVDHGK.-					1,797.01	3	4.02	0.00	500.4	1	29/64
		-.TTLTAAITTLAK.-					1,306.53	2	4.24	0.24	1,781.7	1	21/24
		-.NM*ITGAAQM*DAAILVVSATDGPM*PQTK.-					2,781.17	2	4.24	0.28	1,604.1	1	25/52
		-.NM*ITGAAQMDAAILVVSATDGPM*PQTK.-					2,765.17	3	6.00	0.12	2,268.1	1	38/104
		-.NMITGAAQM*DAAILVVSATDGPM*PQTK.-					2,765.17	3	5.26	0.25	1,484.8	3	32/104
		-.QVGVPYVIVFINK.-					1,476.78	2	4.05	0.31	785.8	1	21/24
		-.QVGVPYVIVFINK.-					1,476.78	3	2.80	0.12	762.8	2	19/48
		-.SKPHLNVGTIGHVDHGK.-					1,797.01	3	4.34	0.06	642.5	1	30/64
		-.SKPHLNVGTIGHVDHGK.-					1,797.01	3	4.03	0.06	498.1	1	26/64
		-.TTLTAAITTLAK.-					1,306.53	2	3.11	0.30	1,315.2	1	21/24

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.TTLTAAITTLAK.-					1,306.53	2	3.53	0.29	1,460.4	1	20/24
		-.LM*EALDTFVNPVK.-					1,491.73	2	3.61	0.30	1,616.3	1	19/24
		-.NM*ITGAAQM*DAAILVVSATDGPM*PQTK.-					2,781.17	3	4.79	0.24	1,440.8	1	33/104
		-.NM*ITGAAQM*DAAILVVSATDGPM*PQTK.-					2,781.17	3	3.15	0.20	455.8	113	25/104
		-.QVGVPYVIVFINK.-					1,476.78	2	3.28	0.25	413.6	2	17/24
		-.QVGVPYVIVFINK.-					1,476.78	2	3.42	0.20	444.6	2	17/24
		-.SKPHLNVGTIGHVDHGK.-					1,797.01	3	2.76	0.10	582.1	1	28/64
		-.SKPHLNVGTIGHVDHGK.-					1,797.01	3	3.37	0.03	502.7	2	26/64
		-.TTLTAAITTLAK.-					1,306.53	2	3.52	0.21	1,527.8	1	20/24
		-.TTLTAAITTLAK.-					1,306.53	2	4.19	0.32	2,086.3	1	21/24
		-.NM*ITGAAQM*DAAILVVSATDGPM*PQTK.-					2,781.17	3	3.44	0.14	840.1	7	28/104
		-.NM*ITGAAQM*DAAILVVSATDGPM*PQTK.-					2,781.17	3	3.93	0.18	1,161.5	1	29/104
		-.SKPHLNVGTIGHVDHGK.-					1,797.01	3	2.68	0.01	373.9	10	24/64
		-.TTLTAAITTLAK.-					1,306.53	2	4.06	0.34	1,797.6	1	19/24
#1	YP_000467	hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.49		36,149.2			80.38	23.64			8 (8 0 0 0 0)
		-.TKTQPDFQK.-					1,093.21	2	2.98	0.26	561.7	1	11/16
		-.AFGNYNIK.-					927.03	2	2.77	0.08	500.6	4	13/14
		-.KKDILNSI.-					931.11	2	2.33	0.04	352.4	7	11/14
		-.SLLDGGLITQEEFDTK.-					1,766.92	2	6.19	0.44	1,990.2	1	24/30
		-.LKSLLDGLITQEEFDTK.-					2,008.25	3	4.72	0.22	2,028.3	1	34/68
		-.LSDFISEVVLK.-					1,250.46	2	4.28	0.29	1,646.9	1	18/20
		-.YGLEVVDFIQSINFQNDPNFQK.-					2,879.12	3	7.78	0.54	2,603.3	1	38/92

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/		
			Gel	Theoret.	Gel	Theoret.							MH+	
#2	YP_002791	-.YGLEVVDFFIQSINFQNDPNFQK.-					2,879.12	2	3.91	0.26	1,266.5	1	23/46	
		elongation factor Tu (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.74		43,574.8			68.29	22.19				7 (6 1 0 0 0)
		-.AVAYDQIDNAPEEK.-					1,563.64	2	4.35	0.28	1,651.7	1	21/26	
		-.VNDEVEIIGIRPTTK.-					1,684.91	3	2.75	0.12	575.3	1	24/56	
		-.ADM*LAADERAEM*IEM*VEM*DVR.-					2,490.79	3	5.74	0.43	1,091.2	1	31/80	
		-.LM*EALDTFVNPVK.-					1,491.73	2	4.06	0.31	1,584.2	1	19/24	
		-.LM*EALDTFVNPVK.-					1,491.73	2	4.08	0.36	1,787.9	1	20/24	
		-.TTLTAAITTLAK.-					1,306.53	2	4.56	0.43	1,906.0	1	21/24	
-.QVGVPYVIVFINK.-					1,476.78	2	3.42	0.21	616.7	1	19/24			
5h22#1	YP_000467	hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.78	5.49	42.4	36,149.2			88.3826	26.06				9 (8 1 0 0 0)
		-.TKTQPDFQK.-					1,093.21	2	2.81	0.20	642.6	1	12/16	
		-.TKTQPDFQK.-					1,093.21	2	2.91	0.25	698.8	1	12/16	
		-.AFGNYNK.-					927.03	2	2.35	0.07	510.5	7	13/14	
		-.VLTDKFEIETMGNM*YQQK.-					2,192.49	2	2.33	0.08	321.2	19	17/34	
		-.SLLDGGGLITQEEFDTK.-					1,766.92	2	6.84	0.40	1,980.2	1	24/30	
		-.LSDFISEVVLK.-					1,250.46	2	3.02	0.27	677.1	51	12/20	
		-.YGLEVVDFFIQSINFQNDPNFQK.-					2,879.12	3	6.39	0.34	2,214.7	1	33/92	
		-.YGLEVVDFFIQSINFQNDPNFQK.-					2,879.12	3	7.65	0.49	2,678.9	1	39/92	
		-.YGLEVVDFFIQSINFQNDPNFQK.-					2,879.12	2	5.41	0.47	1,292.0	1	23/46	

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/	%	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.		MH+	XC				coverage/ ΔCn
5h27#3	YP_000467	hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) -.YGLEVVDFFIQSINFDQNDPNFQK.- -.YGLEVVDFFIQSINFDQNDPNFQK.-	5.4	5.49	35,000	36,149.2		20.3395	7.27			2 (2 0 0 0 0)	
							2,879.12	3	6.79	0.48	1,992.0	1	35/92
							2,879.12	2	4.60	0.33	1,537.4	1	23/46
#5	AAQ98019	Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae) -.M*SAIM*PDQIAK.- -.ISFTTYKPGEVK.-		5.79		23,502.6		20.17	10.8				2 (2 0 0 0 0)
							1,237.47	2	3.58	0.23	860.0	2	15/20
							1,370.57	3	2.67	0.20	227.3	41	17/44
5h29#1	NP_714428	probable Methylthioadenosine phosphorylase (<i>L. interrogans</i> serovar Lai str. 56601) -.YSIITAPEKR.- -.QLGVVEIVAFSSVGSRLR.- -.EEIKPLDFVLP SQIIDR.- -.EEIKPLDFVLP SQIIDR.- -.VLFPEYF.- -.EGEESVTVEM*VIANLTK.- -.EGEESVTVEM*VIANLTK.- -.LLELIHVLGNGDDLSLK.- -.LLELIHVLGNGDDLSLK.- -.LLELIHVLGNGDDLSLK.-	6.2	6.67	36,800	32,031.8		100.28	29.97				10 (10 0 0 0 0)
							1,178.36	2	2.91	0.21	1,211.1	1	17/18
							1,792.02	2	5.60	0.46	2,197.7	1	25/32
							2,013.32	3	3.54	0.13	1,432.7	3	32/64
							2,013.32	2	4.01	0.40	1,088.9	1	22/32
							915.06	2	2.22	0.05	420.9	1	10/12
							1,866.08	2	3.75	0.37	1,099.6	1	20/32
							1,866.08	3	4.97	0.33	1,182.7	2	30/64
							1,937.22	2	5.72	0.41	701.7	1	20/34
							1,937.22	3	3.96	0.26	947.9	1	31/68
							1,937.22	2	5.37	0.34	1,115.0	1	23/34
#2	NP_713559	flagellar filament outer layer protein A (<i>L. interrogans</i> serovar Lai str. 56601) -.IYGVEFFPGVSK.- -.SRPDTSGETVYLFFDELRL.- -.SRPDTSGETVYLFFDELRL.-		8.25		36,063.8		50.32	8.92				5 (5 0 0 0 0)
							1,196.37	2	3.24	0.27	1,220.2	1	18/20
							2,133.30	3	4.54	0.26	1,824.2	1	30/68
							2,133.30	2	6.51	0.47	2,148.6	1	27/34

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.SRPDTSGETVYLFFDELRL-					2,133.30	3	2.85	0.15	414.3	17	24/68
		-.SRPDTSGETVYLFFDELRL-					2,133.30	2	3.14	0.37	727.2	1	19/34
5h34#1	NP_710593	Electron transfer flavoprotein beta-subunit (<i>L. interrogans</i> serovar Lai str. 56601)	5.78	5.58	35,100	27,084.9			110.279	37.55			11 (11 0 0 0 0)
		-.TAYAM*GADR.-					972.05	2	2.45	0.27	788.5	1	14/16
		-.QVPDTETSIKVGDK.-					1,517.66	2	2.12	0.26	713.7	1	18/26
		-.ATKEVEGGTQTVETSTPVALTAQK.-					2,447.68	3	4.64	0.35	748.9	1	33/92
		-.EVEGGTQTVETSTPVALTAQK.-					2,147.32	2	4.30	0.44	1,424.6	1	24/40
		-.HGGEVIAVSLGPDR.-					1,407.55	2	4.75	0.41	2,177.5	1	21/26
		-.HGGEVIAVSLGPDR.-					1,407.55	2	4.94	0.47	2,367.8	1	21/26
		-.IEIVGLEPPPPR.-					1,317.55	2	3.24	0.34	1,155.6	1	19/22
		-.IEIVGLEPPPPR.-					1,317.55	2	2.35	0.34	1,113.0	1	19/22
		-.WIISPYDEFAIEEGIR.-					1,939.15	2	5.58	0.44	1,836.4	1	25/30
		-.WIISPYDEFAIEEGIR.-					1,939.15	3	4.61	0.27	1,819.1	1	28/60
		-.HGGEVIAVSLGPDRVVEALR.-					2,075.35	3	2.68	0.26	356.4	2	25/76
#2	AAQ98019	Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae)	5.79		23,502.6				88.25	39.91			9 (8 1 0 0 0)
		-.LDDDDDGDDTYKEER.-					1,801.71	3	3.82	0.19	816.6	2	29/56
		-.LDDDDDGDDTYKEER.-					1,801.71	2	4.13	0.29	1,282.9	1	21/28
		-.LDDDDDGDDTYKEER.-					1,801.71	2	4.22	0.02	1,773.9	1	23/28
		-.PGQAPDGLVDGNKK.-					1,396.53	3	3.89	0.28	1,558.8	1	28/52
		-.M*SAIM*PDQIAK.-					1,237.47	2	3.53	0.21	868.2	2	15/20
		-.SFDDLKNIDTK.-					1,296.40	2	3.17	0.05	884.4	3	17/20

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.ISFTTYKPGEVK.-					1,370.57	2	3.35	0.22	1,049.5	1	16/22
		-.M*ISPTGEIGEPGDGLVSDAFK.-					2,252.44	2	4.81	0.19	1,595.5	1	30/42
		-.M*ISPTGEIGEPGDGLVSDAFK.-					2,252.44	3	4.53	0.41	1,154.2	1	33/84
#3	YP_001942	succinate dehydrogenase iron-sulfur subunit (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		6.22		26,650.6			60.27	27.57			6 (6 0 0 0 0)
		-.NASAM*LFVSAK.-					1,155.35	2	2.51	0.09	723.9	53	15/20
		-.VDADVSM DAATCIGCGACVASCK.-					2,419.62	3	5.38	0.34	2,174.6	1	41/88
		-.ITHLGLLPQGK.-					1,177.42	2	3.72	0.22	1,446.7	1	18/20
		-.DISPNM*SFLEM*LDVVNEELITK.-					2,570.91	2	4.38	0.44	714.1	1	22/42
		-.DISPNM*SFLEM*LDVVNEELITK.-					2,570.91	3	5.51	0.35	1,452.6	1	34/84
		-.DISPNM*SFLEM*LDVVNEELITK.-					2,570.91	3	4.909	0.33	1,640.3	1	36/84
#4	NP_711213	enoyl-CoA hydratase (<i>L. interrogans</i> serovar Lai str. 56601)		6.14		30,573.8			60.23	19.27			6 (6 0 0 0 0)
		-.VAIVADM*GSINR.-					1,262.46	2	4.50	0.42	1,434.0	1	18/22
		-.GINAVYDSPKPSIAAVQK.-					1,859.11	2	4.71	0.38	1,230.0	1	21/34
		-.HCIGGGLDLISACDIR.-					1,757.95	3	4.48	0.14	1,111.4	23	26/60
		-.FFDLILK.-					896.10	2	2.36	0.00	703.1	1	12/12
		-.FFDLILK.-					896.10	1	1.92	0.00	821.3	12	10/12
		-.FFDLILK.-					896.10	2	2.67	0.00	774.5	1	12/12
#5	AAS21765	LipL32 (<i>L. borgpetersenii</i>)		7.88		28,943.0			54.26	34.96			6 (5 0 0 1 0)
		-.LNDDDDGDDTYKEER.-					1,800.73	2	4.05	0.35	1403.5	3	21/28
		-.SSFVLESTVPGTNETVK.-					1,883.04	2	2.14	0.17	375.3	1	19/34
		-.SSFVLESTVPGTNETVK.-					1,883.04	2	3.03	0.31	482.6	1	21/34
		-.TFLPYGSVINYYGYVKPGQAPDGLVDGDK.-					3,134.48	3	4.34	0.53	633.8	1	39/112

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.TFLPYGSVINYYGYVK.-					1,885.15	2	4.36	0.40	1,421.4	1	25/30
		-.GSFVASVGLLFPFGIPGVSPLIHSNPEELQK.-					3,188.66	3	4.04	0.39	415.6	1	33/120
#19		hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)		5.49		36,149.2			20.35	7.27			2 (2 0 0 0 0)
		-.YGLEVVDFFIQSINFDQNDPNFQK.-					2,879.12	3	4.92	0.36	988.1	2	27/92
		-.YGLEVVDFFIQSINFDQNDPNFQK.-					2,879.12	3	7.16	0.51	2,123.3	1	35/92
#20		NifU-like protein (<i>L. interrogans</i> serovar Lai str. 56601)		5.65		29,044.5			20.32	7.98			2 (2 0 0 0 0)
		-.LAGANVEGADFTDAIYDIGTR.-					2,170.32	2	6.45	0.52	2,767.6	1	28/40
		-.LAGANVEGADFTDAIYDIGTR.-					2,170.32	2	5.91	0.55	2,703.4	1	28/40
5h36#1	NP_710593	Electron transfer flavoprotein beta-subunit (<i>L. interrogans</i> serovar Lai str. 56601)	6.31	5.58	33,500	27,084.9			110.27	35.97			11 (11 0 0 0 0)
		-.TAYAM*GADR.-					972.05	2	2.40	0.26	770.5	2	14/16
		-.SAADLGSPASK.-					1,004.07	2	2.96	0.21	1,160.8	1	18/20
		-.EVEGGTQTVETSTPVALTAQK.-					2,147.32	2	4.65	0.47	1,487.2	1	24/40
		-.EVEGGTQTVETSTPVALTAQK.-					2,147.32	3	5.51	0.31	815.6	1	32/80
		-.M*KIIVLVK.-					960.30	2	2.52	0.19	1,056.7	5	13/14
		-.M*KIIVLVK.-					960.30	2	2.61	0.13	1,410.7	3	14/14
		-.HGGEVIAVSLGPDR.-					1,407.55	2	4.45	0.45	2,410.2	1	21/26
		-.IEIVGLEPPPPR.-					1,317.55	2	2.80	0.09	878.3	1	19/22
		-.IEIVGLEPPPPR.-					1,317.55	2	2.87	0.03	831.1	1	19/22
		-.WIISPYDEFAIEEGIR.-					1,939.15	2	4.97	0.45	2,096.5	1	25/30
		-.WIISPYDEFAIEEGIR.-					1,939.15	2	5.21	0.44	1,737.0	1	24/30

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.						
#2	NP_711213	enoyl-CoA hydratase (<i>L. interrogans</i> serovar Lai str. 56601) -.VAIVADM*GSINR.- -.GINAVYDSPKPSIAAVQK.- -.FFDLILK.- -.FFDLILK.- -.FFDLILK.-		6.14		30,573.8		50.24	13.45			5 (5 0 0 0 0)
						1,262.46	2	4.46	0.38	1,385.0	1	18/22
						1,859.11	2	4.97	0.42	1,519.7	1	23/34
						896.10	2	2.55	0.00	690.1	1	12/12
						896.10	2	2.78	0.00	700.6	1	12/12
						896.10	1	1.83	0.00	756.2	12	10/12
#3	AAQ98019	Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae) -.M*SAIM*PDQIAK.- -.ISFTTYKPGEVK.- -.ISFTTYKPGEVK.- -.M*ISPTGEIGEPGDGLVSDAFK.-		5.79		23,502.6		40.23	21.13			4 (4 0 0 0 0)
						1,237.47	2	3.57	0.22	828.7	2	15/20
						1,370.57	2	2.26	0.13	922.3	1	15/22
						1,370.57	2	2.44	0.09	492.1	1	15/22
						2,252.44	2	4.64	0.50	901.3	1	24/42
5h37#2	AAQ98019	Lip L32 outer membrane protein (<i>L. interrogans</i> serovar Icterohaemorrhagiae) -.LDDDDDGDDTYKEER.- -.LDDDDDGDDTYKEER.- -.M*SAIM*PDQIAK.- -.ISFTTYKPGEVK.- -.M*ISPTGEIGEPGDGLVSDAFK.-	6.04	5.79	34,100	23,502.6		50.25	28.17			5 (5 0 0 0 0)
						1,801.71	3	3.68	0.21	680.2	4	28/56
						1,801.71	2	4.56	0.01	1,463.9	1	20/28
						1,237.47	2	3.61	0.24	833.5	2	15/20
						1,370.57	2	3.14	0.27	1,019.2	1	16/22
						2,252.44	2	5.12	0.49	1,368.5	1	28/42
#3	AAS21765	LipL32 (<i>L. borgpetersenii</i>) -.LNDDDDGDDTYKEER.- -.TFLPYGSVINYYGYVKPGQAPDGLVDGKNK.- -.TFLPYGSVINYYGYVKPGQAPDGLVDGKNK.-		7.88		28,943.0		36.24	28.2			4 (3 0 1 0 0)
						1,800.73	2	4.31	0.05	1,448.0	2	20/28
						3,134.48	3	3.80	0.40	460.4	1	36/112
						3,134.48	3	3.58	0.45	540.5	1	38/112

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/	%	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.		MH+	XC				coverage/ ΔCn
		-.GSFVASVGLLFPFGIPGVSPLIHSNPEELQK.-					3,188.66	3	4.85	0.42	889.6	1	37/120
5h40#1	YP_001188	peroxiredoxin (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.7	5.81	28,500	21,517.7							11 (10 1 0 0 0)
		-.NIDEAIR.-					830.90	1	2.15	0.03	275.2	30	9/12
		-.AEAVLGKEIK.-					1,058.25	2	2.82	0.16	1,384.9	1	16/18
		-.AEAVLGKEIK.-					1,058.25	2	2.78	0.04	1,068.0	6	14/18
		-.QATINDLPVGR.-					1,184.32	2	2.66	0.27	686.6	1	18/20
		-.M*PQVTS LAPDFK.-					1,350.56	2	3.45	0.29	2,197.5	1	20/22
		-.YPLIADLTK.-					1,034.23	2	2.53	0.05	1,063.8	13	15/16
		-.YPLIADLTK.-					1,034.23	1	1.79	0.02	591.0	1	12/16
		-.YPLIADLTK.-					1,034.23	1	2.83	0.18	606.9	1	12/16
		-.QATINDLPVGR.-					1,184.32	2	2.66	0.36	647.5	1	17/20
		-.YPLIADLTK.-					1,034.23	2	2.17	0.04	1,155.3	13	15/16
		-.QATINDLPVGR.-					1,184.32	2	2.53	0.33	324.8	3	13/20
5h44	YP_002046	single-stranded DNA binding protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.6	5.22	22,000	16,408.9							2 (2 0 0 0 0)
		-.SINGTSLVNFSLANGR.-					1,650.82	2	3.95	0.31	1,280.3	1	21/30
		-.IVVENFQLLGSK.-					1,347.59	2	3.73	0.35	1,510.1	1	20/22
5h53#1	YP_002544	hypothetical protein LIC12621 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.8	5.94	15,800	14,523.4							14 (13 1 0 0 0)
		-.GNITITGGQKK.-					1,117.28	2	2.99	0.25	1,028.9	1	16/20
		-.GNITITGGQK.-					989.10	2	3.09	0.20	936.0	1	15/18
		-.FEGEIK.-					722.80	1	1.75	0.00	509.7	8	8/10

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		-.FEGEIK.-					722.80	1	1.84	0.00	495.3	10	8/10
		-.IVEESFGGTR.-					1,095.18	2	2.93	0.24	960.9	1	17/18
		-.IDGKFEGEIK.-					1,136.28	2	2.10	0.10	833.4	3	14/18
		-.IDGKFEGEIK.-					1,136.28	2	2.11	0.07	786.1	1	15/18
		-.EVTVSGTM*IGNIK.-					1,365.57	2	5.02	0.29	1,424.7	1	20/24
		-.TDDTLYIGETGK.-					1,313.39	2	4.16	0.35	2,433.3	1	20/22
		-.FYIAGSLR.-					927.08	2	2.51	0.15	888.8	1	13/14
		-.FYIAGSLR.-					927.08	1	1.76	0.14	263.7	1	11/14
		-.FYIAGSLR.-					927.08	1	1.71	0.15	161.6	18	9/14
		-.ENNNSVIGPGSIFEGK.-					1,662.78	2	4.05	0.40	690.4	1	19/30
		-.FYIAGSLR.-					927.08	2	2.25	0.13	720.7	1	12/14
81.7_8	YP_000304.1	hypothetical protein LIC10314 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) K.SSEEISPNSNVTFYGEK.I R.TFEIVDGK.A	8.0	8.77	81.7	63,680.3			20.24	4.49			2 (2 0 0 0 0)
							1,888.96	2	4.72	0.30	1,059.6	1	22/32
							909.01	2	2.68	0.15	608.2	3	12/14
71.4_7.5	YP_003272.1	sulfite reductase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) R.PYSAEVGIVGQQAGGK.Y R.PYSAEVGIVGQQAGGK.Y R.SFPEVLNGIQK.V K.TNAYAIEVWLGDK.Q	7.5	6.22	71.4	62,468.4			30.23	6.95			4 (4 0 0 0 0)
							1,561.72	2	3.87	0.12	2,251.6	1	26/30
							1,561.72	2	3.37	0.04	1,954.0	1	25/30
							1,232.41	2	2.64	0.13	446.0	3	14/20
							1,367.48	2	4.50	0.45	1,989.8	1	19/22

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
	NP_713600.1	DNA-directed RNA polymerase beta subunit (<i>L. interrogans</i> serovar Lai str. 56601)	7.5	5.50	71.4	137,751.3		20.18	2.04				2 (2 0 0 0 0)
		R.QGEPSTIENATTELTR.L					1,747.84	2	3.56	0.28	1,163.8	1	21/30
		K.TFDLGEVGR.Y					994.08	2	3.51	0.16	956.5	1	15/16
68_8.1	YP_002499.1	cytoplasmic membrane protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.1	9.40	68.0	59,861.0		56.22	12.38				6 (5 0 1 0 0)
		R.IEALEASHR.I					1,026.12	2	2.68	0.07	1397.5	1	15/16
		K.ISDDTIKGGIEK.V					1,276.41	2	3.77	0.21	1685.8	1	20/22
		K.SDTNFLKNDK.Y					1,269.34	2	3.01	0.20	640.5	3	16/20
		K.NALDTHVQDQLR.L					1,410.51	2	3.97	0.25	1645.5	1	18/22
		R.ALESNYNLQNL.R.Y					1,435.56	2	4.43	0.23	2341.0	1	18/22
		R.ATISQDLLK.N					989.15	2	2.75	0.01	918.5	4	14/16
49_8.45	AAS21839.1	OmpL1 (<i>L. borgpetersenii</i>)	8.5	7.23	49.0	29,777.6		30.22	12.98				3 (3 0 0 0 0)
		R.TTGGIINAR.S					903.01	2	2.99	0.00	923.6	2	15/16
		K.DGLDAATYYGPVR.S					1,398.50	2	4.32	0.36	2,124.6	1	20/24
		R.ATGIAPNFLIGTQAR.V					1,530.75	2	4.09	0.26	870.1	1	20/28
46.4_7.3	AAS21807.1	LipL41 (<i>L. borgpetersenii</i>)	7.3	5.55	46.4	34,113.8		40.30	18.65				6 (6 0 0 0 0)
		K.EVNTGNPVS KPTGVR.M					1,684.83	2	2.01	0.07	212.9	21	14/30
		K.EVNTGNPVS KPTGVR.M					1,684.83	2	2.17	0.02	302.3	22	14/30
		R.NVGLAVEPPK.S					1,152.36	2	3.44	0.27	1,098.8	1	16/20
		K.ANLATYYFSVGD FEK.S					1,725.87	2	5.60	0.30	2,296.8	1	23/28
		K.ANLATYYFSVGD FEK.S					1,725.87	2	6.01	0.31	2,325.7	1	23/28

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
		R.ADILNEATLSLTGITK.S					1,660.89	2	5.12	0.44	1,816.6	1	22/30
5	BAE48275.1	lipoprotein LipL41 (<i>L. interrogans</i> serovar Icterohaemorrhagiae)	7.3	8.59	46.4	38,937.6			20.20	6.48			2 (2 0 0 0 0)
		K.VFVKDEDEEVK.E					1,337.45	2	3.55	0.16	1,432.9	3	17/20
		K.VAGFAASM*ATGK.D					1,127.29	2	3.04	0.39	1,280.5	1	17/22
42_7.4	YP_002016.1	cysteine synthase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.4	8.76	42.0	33,249.1			66.30	27.83			11 (10 0 1 0 0)
		R.IALSM*IEDAEKTGK.L					1,522.74	2	4.28	0.35	1,050.4	1	21/26
		R.IALSM*IEDAEK.T					1,236.41	2	3.95	0.22	1,351.7	1	17/20
		R.IALSM*IEDAEK.T					1,236.41	2	3.91	0.20	1,581.4	1	18/20
		K.VFAVEPEASPVISGGK.P					1,587.79	2	4.69	0.27	1,005.6	1	24/30
		R.IM*AAYGAEFELTPR.E					1,585.80	2	5.50	0.43	2,352.9	1	22/26
		R.IMAAYGAEFELTPR.E					1,585.80	2	3.01	0.46	1,009.6	4	17/26
		R.IM*AAYGAEFELTPR.E					1,585.80	2	5.8995	0.4307	2,430.1	1	22/26
		K.EEGLFIGVSSGAALAAVAK.K					1,791.03	2	6.0319	0.4512	2,690.8	1	30/36
		K.EEGLFIGVSSGAALAAVAK.K					1,791.03	2	6.0692	0.4760	2,930.1	1	30/36
		K.DSIIVEPTSGNTGIGLALVAVK.G					2,226.55	3	5.0851	0.3125	1,609.6	1	38/88
		R.IM*AAYGAEFELTPR.E					1,585.80	2	3.1212	0.3489	1,060.9	1	18/26
2	YP_003074.1	hypothetical protein LIC13166 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.4	8.76	42.0	36,213.1			50.27	22.22			7 (7 0 0 0 0)
		K.YGKDSPEYK.H					1,087.16	2	2.39	0.09	715.6	1	12/16
		K.AINHLDEIKNPDLR.E					1,648.84	2	4.37	0.26	1,032.7	1	19/26
		K.GYDKNFQELHQLSK.A					1,707.86	3	3.43	0.21	1,160.7	4	24/52
		K.GYDKNFQELHQLSK.A					1,707.86	3	3.45	0.10	1,181.0	3	26/52

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
		K.YLASCYAFEENM*IKK.N					1,884.13	2	4.32	0.42	817.7	1	21/28
		K.YLASCYAFEENM*IKK.N					1,884.13	2	5.02	0.35	918.2	1	22/28
		K.HIVNLVnkDEVISVRP					1,833.12	2	5.38	0.28	1,923.9	1	22/30
5	YP_002729.1	serine protease MucD precursor (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.4	8.89	42.0	41,115.9			20.18	8.76			3 (3 0 0 0 0)
		K.INSPEEVVSTVK.K					1,302.45	2	3.03	0.15	694.2	4	16/22
		K.INSPEEVVSTVK.K					1,302.45	2	2.53	0.08	609.3	8	15/22
		R.MIASQSGGSVGIGFAIPINEAK.A					2,164.46	2	2.87	0.15	313.0	9	14/42
42.2_7.8	YP_003074.1	hypothetical protein LIC13166 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.8	8.76	42.2	36,213.1			30.23	9.48			4 (4 0 0 0 0)
		K.AINHLDEIK.N					1,053.19	2	2.95	0.16	915.2	2	14/16
		K.AINHLDEIKNPDLR.E					1,648.84	2	4.40	0.26	1,024.8	1	19/26
		K.AINHLDEIKNPDLR.E					1,648.84	2	4.67	0.27	913.7	1	18/26
		K.AIQEQEALWKNPDFK.G					1,818.02	2	3.69	0.17	1,338.4	1	21/28
41.6_7.3	YP_003074.1	hypothetical protein LIC13166 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.3	8.76	41.6	36,213.1			100.30	31.7			18 (18 0 0 0 0)
		K.AINHLDEIKNPDLR.E					1,648.84	3	3.80	0.14	801.1	4	28/52
		K.AINHLDEIKNPDLR.E					1,648.84	2	4.61	0.26	1,037.0	1	19/26
		K.NFQELHQLSK.A					1,244.38	2	3.93	0.10	859.8	3	15/18
		K.NFQELHQLSK.A					1,244.38	2	4.01	0.07	847.0	5	15/18
		K.GYDKNFQELHQLSK.A					1,707.86	2	3.67	0.16	832.9	1	16/26
		K.GYDKNFQELHQLSK.A					1,707.86	3	4.50	0.17	2,134.3	1	28/52
		K.YLASCYAFEENM*IKK.N					1,884.13	2	5.08	0.38	763.3	1	20/28

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
		K.HIVNLVnkDEVISVRP					1,833.12	2	5.16	0.25	2,365.2	1	22/30
		K.HIVNLVnkDEVISVRP					1,833.12	3	5.17	0.34	2,440.6	1	33/60
		K.IDELLKgelVPEDDDKnlTEEQK.R					2,671.89	3	4.98	0.28	1,714.2	1	36/88
		K.IDELLKgelVPEDDDKnlTEEQK.R					2,671.89	3	5.01	0.20	1,677.8	1	37/88
		K.YLASCYAFENM*IK.K					1,755.96	2	5.87	0.35	2,924.2	1	23/26
		K.AIQEQEALWKNPDFK.G					1,818.02	2	4.23	0.18	1,193.5	1	20/28
		K.AIQEQEALWKNPDFK.G					1,818.02	3	3.09	0.38	489.2	1	27/56
		K.AIQEQEALWKNPDFK.G					1,818.02	2	4.28	0.24	1,191.9	1	20/28
		K.YLASCYAFENMIK.K					1,739.96	2	5.92	0.41	2,795.3	1	22/26
		K.YLASCYAFENMIK.K					1,739.96	2	5.50	0.44	2,619.0	1	22/26
		K.HIVNLVnkDEVISVRP.-					1,833.12	3	3.11	0.31	291.3	151	22/60
35.5_8.3	YP_002016.1	cysteine synthase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) R.IALSM*IEDAEK.T	8.3	8.76	35.5	33,249.1			34.2	15.53			5 (4 0 0 1 0)
		R.IM*AAYGAEFELTPR.E					1,236.42	2	2.84	0.20	1,349.8	1	17/20
		R.IMAAYGAEFELTPR.E					1,585.81	2	5.15	0.42	2,425.8	1	23/26
		R.IMAAYGAEFELTPR.E					1,585.81	2	2.6671	0.0743	900.0	16	16/26
		K.DSIIVEPTSGNTGIGLALVAVK.G					2,226.56	3	3.8333	0.1936	759.4	3	29/88
		K.DSIIVEPTSGNTGIGLALVAVK.G					2,226.56	3	3.7132	0.1061	1,223.9	1	32/88
2	YP_003074.1	hypothetical protein LIC13166 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) K.YLASCYAFENM*IKK.N	8.3	8.76	35.5	36,213.1			30.26	10.13			4 (4 0 0 0 0)
		K.HIVNLVnkDEVISVRP.-					1,884.13	2	3.01	0.28	504.4	1	17/28
		K.HIVNLVnkDEVISVRP.-					1,833.12	3	2.95	0.06	436.0	13	24/60
		K.HIVNLVnkDEVISVRP					1,833.12	2	4.55	0.36	1,803.3	1	20/30

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
		K.HIVNLVnkDEVISVRP					1,833.12	2	5.16	0.27	1,925.6	1	21/30
4	AAS21839.1	OmpL1 (<i>L. borgpetersenii</i>)	8.3	7.23	35.5	29,776.6		20.21	9.12				3 (3 0 0 0 0)
		K.PAGEGNYVGVGTR.R					1,277.36	2	3.40	0.35	1,121.0	1	17/24
		K.PAGEGNYVGVGTR.R					1,277.36	2	3.48	0.31	1,088.3	1	16/24
		K.DGLDAATYYGPVR.S					1,398.50	2	4.16	0.45	2,038.1	1	19/24
5	AAZ73230.1	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejrøe)	8.3	5.66	35.5	27,493.1		20.18	9.16				3 (3 0 0 0 0)
		R.ISFTTYKPGEVK.G					1,370.57	2	2.46	0.04	692.4	11	14/22
		K.SFDDLKNIDTK.K					1,296.40	2	3.66	0.19	814.3	2	17/20
		R.ISFTTYKPGEVK.G					1,370.57	2	2.86	0.12	1,005.8	38	16/22
	A40660	A40660 outer membrane protein OmpL1 - <i>L. alstoni</i>	8.3	8.88	35.5	33,530.0		10.30	5.63				1 (1 0 0 0 0)
		K.GAM*VGGNLM*VGYESDFGK.Y					1,865.07	2	5.97	0.47	2,074.8	1	26/34
32.5_8.3	YP_000829.1	uridylyate kinase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.3	8.38	32.5	27005.8		20.29	12.1				3 (3 0 0 0 0)
		R.YSQISFM*ESINR.R					1,491.65	2	4.13	0.31	1,329.5	1	18/22
		K.LSGEALAGEGEGFIDTNK.A					1,808.92	2	5.87	0.51	2,676.9	1	26/34
		K.LSGEALAGEGEGFIDTNK.A					1,808.92	2	5.63	0.45	2,362.6	1	25/34
30.3_8.5	YP_003456.1	3-oxoacyl-(acyl-carrier protein) reductase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.5	8.42	30.3	26,063.9		20.23	9.84				3 (3 0 0 0 0)
		K.AVALEM*ASR.K					964.12	2	2.6253	0.0268	668.9	3	12/16
		K.AGANLVIADLNEESSK.A					1,631.76	2	4.1728	0.1814	1,689.7	1	22/30
		K.AGANLVIADLNEESSK.A					1,631.76	2	4.5398	0.2428	1,583.7	3	21/30

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)			Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.	MH+						
29_7.15	YP_000656.1	hypothetical protein LIC10672 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.2	9.13	29.0	26,923.1		68.25	33.19			11 (10 1 0 0 0)	
		K.IKEVELASEKK.R					1,274.48	2	3.71	0.27	1,183.5	1	17/20
		K.IKEVELASEK.K					1,146.31	2	2.86	0.10	595.6	5	15/18
		K.LERFDKIENTK.V					1,393.57	2	3.04	0.07	782.0	3	17/20
		K.LERFDKIENTK.V					1,393.57	2	3.12	0.03	914.3	15	15/20
		R.SDVFSEQSSYTK.S					1,435.47	2	4.95	0.44	1,830.8	1	20/24
		K.GQADLSRSDVFSEQSSYTK.S					2,163.24	3	5.07	0.23	2,379.5	1	34/76
		R.IQYEFAFENKR.L					1,445.60	2	3.19	0.15	905.9	1	16/20
		R.IQYEFAFENKR.L					1,445.60	2	3.67	0.21	968.5	1	16/20
		K.VQTIVTEDIPFTFDEGYESNLLK.Y					2,659.92	2	3.62	0.20	370.3	1	19/44
		K.VQTIVTEDIPFTFDEGYESNLLK.Y					2,659.92	3	4.42	0.30	976.7	1	30/88
		K.VQTIVTEDIPFTFDEGYESNLLK.Y					2,659.92	3	4.73	0.28	1,077.6	1	32/88
28.15_8_9	YP_003074.1	hypothetical protein LIC13166 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.9	8.76	28.2	36,213.1		10.22	5.23			1 (1 0 0 0 0)	
		K.HIVNLVnkDEVISVRP					1,833.12	3	4.41	0.37	2,190.4	1	34/60
7	YP_003345.1	glutathione peroxidase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.9	9.03	28.2	19,077.6		4.42	6.06			1 (1 0 0 0 0)	
		K.ASGFFGNSIK.W					1,028.14	2	2.83	0.23	566.6	9	14/18
22.9_8_5	YP_002737.1	hypothetical protein LIC12821 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.5	9.09	22.9	15,852.2		20.32	22.6			4 (4 0 0 0 0)	
		K.NSSEVTNSTIGENSYFSGK.F					2,022.07	2	6.44	0.52	2,177.5	1	28/36
		K.NSSEVTNSTIGENSYFSGK.F					2,022.07	2	6.25	0.53	2,690.7	1	29/36
		K.SLQAEQLYIGVTGK.V					1,507.71	2	4.35	0.32	1,992.5	1	20/26

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		Charge	Score/ XC	% coverage/ ΔCn	Sp	RSp	Peptides (Hits)/	
			Gel	Theoret.	Gel	Theoret.							MH+
		K.SLQAEQLYIGVTGK.V					1,507.71	2	4.54	0.37	2,201.3	1	20/26
	YP_000656.1	hypothetical protein LIC10672 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) R.IDIM*IALYK.D	8.5	9.13	22.9	26,923.1		20.22	13.97				2 (2 0 0 0 0)
		K.VQTIVTEDIPFTFDEGYESNLLK.Y					1,096.36	2	3.22	0.23	1,081.7	1	14/16
		K.VQTIVTEDIPFTFDEGYESNLLK.Y					2,659.92	3	4.34	0.26	961.3	1	32/88
3	AAZ73230.1	outer membrane lipoprotein LipL32 (<i>L. interrogans</i> serovar Sejroe) K.SFDDLKNIDTK.K	8.5	5.66	22.9	27,494.1		20.19	9.16				2 (2 0 0 0 0)
		R.ISFTTYKPGEVK.G					1,296.40	2	3.05	0.16	645.1	8	16/20
		R.ISFTTYKPGEVK.G					1,370.57	2	2.70	0.11	902.2	16	16/22
16.3_8.5	YP_002737.1	hypothetical protein LIC12821 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) K.NSSEVTNSTIGENSYFSGK.F	8.5	9.09	16.3	15,852.2		30.36	32.88				3 (3 0 0 0 0)
		K.SLQAEQLYIGVTGK.V					2,022.07	2	7.13	0.46	2,406.9	1	28/36
		K.SLQAEQLYIGVTGK.V					1,507.71	2	4.41	0.33	2,173.8	1	21/26
		R.TPELIIQNGVILEGR.C					1,652.91	2	5.92	0.37	2,661.3	1	23/28

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