



APPENDIX N

ชำนักรหัสสมุด

Orthologous proteins in database matched with the peptide sequences generated from tryptic digestion of proteins in spot no. 1 to 11 (**Figure 32**) of *L. interrogans* serogroup Pomona serovar Pomona separated by 2DE at linear pH 3-10, 18 cm (**Table 10, Section 2.2, and Chapter V**).

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.							
1	24753762	DNA polymerase III, beta subunit (<i>L. interrogans</i>)	5.30	4.89	35,144.1	41,425.9			82.14	19.84	41,424.9		10 (9 0 0 0 1)
		K.ISGM*DADEIK.T					1,095.21	2	2.90	0.32	1,139.0	1	15/18
		K.TSYAIAHEDQR.F					1,291.35	2	2.62	0.35	606.2	1	14/20
		R.QVLTAEEPSR.Q					1,201.31	2	2.36	0.22	523.6	1	14/20
		K.FSTSISK.E					769.87	1	1.83	0.07	539.2	2	9/12
		K.ISGMDADEIK.T					1,079.21	2	2.12	0.05	1,154.5	1	16/18
		K.DSIIVPAK.A					843.00	1	1.96	0.05	525.7	50	10/14
		K.DSIIVPAK.A					843.00	1	1.91	0.16	539.7	19	10/14
		K.VNTSEFLK.A					938.06	2	2.13	0.06	251.7	25	12/14
		K.EEFQVSLR.Q					1,008.11	2	2.13	0.16	567.5	119	12/14
		K.LIFVGTDGR.R					978.13	2	2.17	0.27	644.6	2	13/16
2	45656381	hypothetical protein LIC10483 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.70	5.40	31,069.9	36,149.2			70.20	19.09	36,148.2		9 (8 0 0 1 0)
		K.FDHDGVDK.L					932.96	2	2.25	0.10	617.0	5	12/14
		K.FDHDGVDK.L					932.96	2	2.56	0.12	952.5	1	13/14
		K.TKTQPDFQK.Y					1,093.22	2	2.54	0.14	578.3	36	11/16
		R.AFGNYNIK.V					927.04	2	2.36	0.06	392.4	28	12/14
		K.TGNIPVLEK.L					971.13	2	2.61	0.29	815.7	3	13/16
		K.SFVNTVVGTHQK.F					1,317.48	2	3.68	0.29	1,146.7	1	18/22
		R.AFGNYNIK.V					927.04	2	2.86	0.00	492.4	6	12/14
		K.DILNSI-					674.77	1	1.67	0.00	218.7	56	7/10
		R.LSDFISEVVLK.N					1,250.47	2	4.03	0.32	1,411.9	1	18/20

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.							
3	45657753	flagellin protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) K.FQNNEVAK.N	5.30	6.66	28,498.4	31,306.3			100.25	23.49	31,305.3		21 (17 1 2 1 0)
		K.NM*ETLSSGM*R.I					950.03	2	2.51	0.09	722.4	16	14/14
		K.NM*ETLSSGM*R.I					1,158.29	2	2.21	0.31	355.5	91	10/18
		K.FQNNEVAK.N					950.03	2	2.37	0.09	585.5	51	13/14
		K.NM*ETLSSGMR.I					1,142.29	2	2.90	0.09	806.1	11	15/18
		K.NMETLSSGMR.I					1,142.29	2	2.62	0.15	875.9	9	15/18
		K.NMETLSSGM*R.I					1,142.29	2	2.45	0.18	772.0	20	15/18
		R.DTDM*AEETVAFTK.N					1,474.57	2	4.33	0.28	2,471.9	1	20/24
		K.NMETLSSGM*R.I					1,142.29	2	2.90	0.03	663.8	25	14/18
		K.NMETLSSGMR.I					1,142.29	2	2.49	0.14	595.4	61	14/18
		K.NMETLSSGM*R.I					1,142.29	2	3.28	0.13	842.1	3	15/18
		K.NMETLSSGMR.I					1,142.29	2	2.83	0.21	836.5	4	16/18
		R.DTDM*AEETVAFTK.N					1,474.57	2	4.34	0.28	2,210.3	1	20/24
		K.NMETLSSGMR.I					1,126.29	2	3.38	0.16	1,076.3	4	15/18
		K.NMETLSSGMR.I					1,126.29	2	3.29	0.13	760.6	6	15/18
		R.VLAIQSSNGIYSAEDR.Q					1,723.87	2	4.52	0.24	2,335.8	1	23/30
		R.DTDMAEETVAFTK.N					1,458.57	2	5.07	0.45	2,336.0	1	20/24
		R.DTDMAEETVAFTK.N					1,458.57	2	4.89	0.44	2,397.0	1	20/24
		R.ANLGAYFNR.L					1,026.13	2	2.84	0.17	962.1	1	14/16
		K.MALLQGDFAR.G					1,122.32	2	3.12	0.18	916.1	6	15/18
		K.MALLQGDFAR.G					1,122.32	2	3.22	0.13	837.6	3	15/18

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/	% Coverage/	MW	RSp	Peptides (Hits)/						
			Gel	Theoret.	Gel	Theoret.			X_{corr}	ΔCn			Sp	Ions					
4	45656681	flagellar filament sheath protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	7.15	7.91	27,952.7	34,889.4			40.17	9.52	34,888.4		5 (5 0 0 0 0)						
		K.AYLDANNQKK.V											1,165.28	2	2.10	0.10	846.0	38	13/18
		K.AYLDANNQK.K											1,037.11	1	1.90	0.15	432.3	14	11/16
		K.AYLDANNQK.K											1,037.11	2	2.14	0.04	778.7	4	12/16
		K.AM*SVWVCGR.G											1,082.25	2	2.70	0.33	788.7	3	12/16
K.IYGVFEPGVSK.A	1,196.38	2	3.36	0.22	994.4	2	17/20												
5	45657711	hypothetical protein LIC11848 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	8.20	8.54	26,827.2	32,022.1			80.20	25.72	32,021.1		14 (12 2 0 0 0)						
		K.NNM*VLEDK.I											979.09	2	2.92	0.11	893.6	14	13/14
		K.HLDQFDR.L											930.99	2	2.78	0.09	751.2	1	12/12
		K.IISEVM*DR.G											979.13	2	2.09	0.00	431.0	1	13/14
		K.NNMVLEDK.I											963.09	2	3.05	0.13	1,071.8	14	13/14
		K.NNMVLEDK.I											963.09	1	2.45	0.03	334.3	99	10/14
		K.ANNDLECTPAINQEDPANN CIR.V											2,417.48	3	3.86	0.02	1,314.8	2	31/80
		K.NNMVLEDK.I											963.09	1	2.32	0.07	294.9	22	10/14
		K.ANNDLECTPAINQEDPANN CIR.V											2,417.48	2	3.92	0.17	750.3	2	18/40
		K.HLDQFDR.L											930.99	2	2.30	0.03	900.6	3	11/12
		K.HLDQFDR.L											930.99	2	2.05	0.03	434.4	23	9/12
		K.IISEVMDR.G											963.13	2	2.59	0.00	468.2	1	13/14
		K.YILAGVENTK.T											1,108.27	2	3.19	0.17	1,151.5	2	17/18
		K.SQPSSAQLGQSILETER.K											1,831.96	2	3.48	0.26	460.8	1	20/32
		K.SQPSSAQLGQSILETER.K											1,831.96	2	4.07	0.42	1,104.5	1	24/32

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions								
			Gel	Theoret.	Gel	Theoret.															
6	24215117	Possible hook-associated protein, flagellin family (<i>L. interrogans</i> serovar Lai str. 56601)	7.40		25,168.2	31551.6			20.20	4.60	31,550.6		3 (3 0 0 0 0)								
		R.AGDDAIGFAM*SEK.M												1,328.43	2	4.03	0.00	1,274.3	1	19/24	
		R.AGDDAIGFAMSEK.M												1,312.43	2	4.08	0.00	1,373.8	1	20/24	
			R.AGDDAIGFAMSEK.M						1,312.43	2	3.86	0.00	1,281.1	1	20/24						
	45657405	flagellin protein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)							16.20		31,550.6		3 (0 3 0 0 0)								
		R.AGDDALGFAM*SEK.M												1,328.43	2	4.03	0.27	1,274.3	1	19/24	
		R.AGDDALGFAMSEK.M												1,312.43	2	4.08	0.30	1,373.8	1	20/24	
			R.AGDDALGFAMSEK.M						1,312.43	2	3.86	0.31	1,281.1	1	20/24						
	45657856	succinate dehydrogenase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)							10.15	4.50	26,649.5		4 (4 0 0 0 0)								
														K.DGDTVYVEPWR.A	1,337.42	2	3.01	0.24	922.8	14	15/20
														K.DGDTVYVEPWR.A	1,337.42	2	3.01	0.19	928.5	12	15/20
														K.DGDTVYVEPWR.A	1,337.42	2	2.03	0.14	465.2	151	10/20
														K.DGDTVYVEPWR.A	1,337.42	2	2.23	0.06	604.9	91	12/20
	45657244	hypothetical protein LIC11366 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)							10.15	10.15	32,667.9		2 (2 0 0 0 0)								
														R.GFTNTYDPGVASK.T	1,357.45	2	2.68	0.17	600.6	22	13/24
R.GFTNTYDPGVASK.T														1,357.45	2	2.90	0.26	498.7	10	14/24	
7	45656264	electron transport flavoprotein beta subunit (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.10	5.47	24,666.9	27068.9			70.29	30.04	27,067.8		49 (49 0 0 0 0)								
		R.TAYAM*GADR.A												972.06	2	2.33	0.16	795.6	1	14/16	
		K.SAADLGSPASK.I												1,004.08	2	3.05	0.30	956.0	2	16/20	
		R.TAYAM*GADR.A												972.06	2	2.58	0.29	979.6	1	14/16	

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.							
7 (cont.)	45656264	electron transport flavoprotein beta subunit (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	6.10	5.47	24,666.9	27068.9			70.29	30.04	27,067.8		49 (49 0 0 0 0)
		R.TAYAM*GADR.A					972.06	2	2.33	0.16	795.6	1	14/16
		K.SAADLGSPASK.I					1,004.08	2	3.05	0.30	956.0	2	16/20
		R.TAYAM*GADR.A					972.06	2	2.58	0.29	979.6	1	14/16
		K.SAADLGSPASK.I					1,004.08	1	2.16	0.22	339.9	7	10/20
		R.TAYAMGADR.A					956.06	2	2.64	0.32	1,135.6	1	15/16
		R.TAYAM*GADR.A					972.06	2	2.24	0.16	728.0	1	13/16
		R.TAYAMGADR.A					956.06	1	2.29	0.27	212.9	17	11/16
		K.SINETGIK.W					861.96	1	1.61	0.01	266.0	68	8/14
		R.TAYAMGADR.A					956.06	1	2.56	0.29	179.0	8	10/16
		R.TAYAM*GADR.A					972.06	2	2.39	0.17	942.3	1	14/16
		R.TAYAMGADR.A					956.06	1	2.14	0.12	170.7	4	10/16
		R.TAYAMGADR.A					956.06	2	2.47	0.16	1,218.0	1	15/16
		K.SAADLGSPASK.I					1,004.08	2	2.87	0.21	1,101.4	2	17/20
		K.AENADVIIGGR.Q					1,115.22	2	3.30	0.29	1,347.9	2	17/20
		K.AENADVIIGGR.Q					1,115.22	2	3.31	0.08	1,503.1	3	18/20
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	5.76	0.52	1,197.5	1	22/40
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	3	4.91	0.35	844.4	2	30/80
		K.AENADVIIGGR.Q					1,115.22	1	2.70	0.03	467.8	42	13/20
		K.AENADVIIGGR.Q					1,115.22	2	3.80	0.15	2,074.2	3	18/20
		K.SAADLGSPASK.I					1,004.08	2	2.23	0.13	735.1	6	14/20
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	5.54	0.46	1,522.3	1	23/40

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.							
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	3	4.42	0.25	1,148.8	1	32/80
		K.AENADVIIGGR.Q					1,115.22	2	3.86	0.15	2,145.0	3	18/20
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	4.57	0.52	1,300.0	1	23/40
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	4.77	0.46	1,525.7	1	24/40
		K.AENADVIIGGR.Q					1,115.22	2	3.59	0.25	1,730.6	8	17/20
		R.TAYAMGADR.A					956.06	2	2.22	0.30	956.5	1	13/16
		R.TAYAMGADR.A					956.06	2	2.19	0.27	977.0	1	14/16
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	4.15	0.46	784.9	1	19/40
		K.SAADLGSPASK.I					1,004.08	2	2.47	0.27	863.0	1	15/20
		K.SAADLGSPASK.I					1,004.08	2	2.23	0.21	623.2	54	12/20
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	3.12	0.30	634.3	1	17/40
		K.AENADVIIGGR.Q					1,115.22	2	3.16	0.16	1,051.1	5	17/20
		K.AENADVIIGGR.Q					1,115.22	2	3.49	0.15	2,094.1	2	18/20
		K.WIISPYDEFAIEEGIR.L					1,939.16	2	4.74	0.42	1,620.5	1	23/30
		K.WIISPYDEFAIEEGIR.L					1,939.16	2	4.52	0.32	1,445.6	1	23/30
		R.TAYAMGADR.A					956.06	2	2.54	0.08	1,047.7	1	14/16
		K.SAADLGSPASK.I					1,004.08	2	2.99	0.33	775.8	12	15/20
		K.EVEGGTQTVETSTPVALTAQK.G					2,147.33	2	3.15	0.48	813.3	1	21/40
		K.AENADVIIGGR.Q					1,115.22	2	2.63	0.23	1,050.2	47	15/20
		K.AENADVIIGGR.Q					1,115.22	2	3.39	0.16	1,247.0	9	16/20
		K.SAADLGSPASK.I					1,004.08	2	2.42	0.15	693.9	12	13/20
		K.SAADLGSPASK.I					1,004.08	2	2.20	0.18	495.0	45	12/20

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Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/	% Coverage/	MW	RSp	Peptides (Hits)/
			Gel	Theoret.	Gel	Theoret.			X_{corr}	ΔCn			Sp
		K.SAADLGSPASK.I					1,004.08	2	2.37	0.25	859.1	6	15/20
		K.SAADLGSPASK.I					1,004.08	2	2.43	0.13	629.8	124	13/20
		K.AENADVIIGGR.Q					1,115.22	2	3.21	0.18	1,081.7	3	18/20
		K.AENADVIIGGR.Q					1,115.22	2	2.27	0.07	1,270.8	5	15/20
		K.SAADLGSPASK.I					1,004.08	2	2.36	0.23	600.1	29	13/20
8	45657522	transaldolase (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)	5.50	4.95	22,162.2	23,491.1			28.16	13.08	23,490.1		5 (4 1 0 0 0)
		K.TVVELTKR.N					946.13	2	2.60	0.08	679.8	4	11/14
		R.EIYDNYGYDTR.I					1,409.44	2	3.13	0.36	1,369.8	1	17/20
		R.EIYDNYGYDTR.I					1,409.44	2	2.58	0.31	596.9	1	16/20
		K.VPLIPEGLK.T					966.20	2	2.31	0.13	349.2	33	11/16
		K.VPLIPEGLK.T					966.20	2	2.03	0.16	258.7	193	10/16
	45657748	putative lipoprotein (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130)				44,714.5			20.26		44,713.5		2 (2 0 0 0 0)
		R.TIYNAAATGTYK.V					1,304.43	2	3.62	0.41	801.4	1	17/22
		K.TQVDTENVEGSPLIK.I					1,630.78	2	5.20	0.41	2,479.6	1	22/28
9	24215996	elongation factor Ts (<i>L. interrogans</i> serovar Lai str. 56601)	6.30	5.61	22,086.3	22,172.5			48.19	18.10	22,171.4		9 (6 2 1 0 0)
		K.KALEENNADIEK.A					1,374.48	2	3.87	0.11	1,205.9	1	16/22
		K.ALEENNADIEK.A					1,246.31	2	3.73	0.16	1,211.4	1	16/20
		K.NEDFEALGK.E					1,023.08	2	2.53	0.10	479.0	18	12/16
		K.NEDFEALGK.E					1,023.08	1	1.88	0.09	356.8	1	12/16
		K.FGENITIAR.F					1,021.15	2	2.87	0.13	812.0	51	13/16
		K.FGENITIAR.F					1,021.15	2	2.01	0.08	597.8	59	13/16
		R.FQVGGL.-					620.72	1	1.69	0.06	578.4	5	8/10

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.							
		R.FQVGGL-					620.72	1	2.13	0.08	560.5	4	8/10
10	45657102	peroxiredoxin (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) K.KEGGIGEIK.Y	6.50	5.74	21,359.1	21517.7			80.20	37.80	21,516.7		14 (11 1 2 0 0)
		K.HGEVCPANWDEGKK.T					931.07	2	2.52	0.05	717.1	12	13/16
		R.NIDEAIR.L					1,627.73	3	3.47	0.11	991.3	1	24/52
		K.HGEVCPANWDEGK.K					830.91	2	2.18	0.00	423.8	16	11/12
		K.EGGIGEIK.Y					1,499.56	3	2.54	0.01	848.0	52	21/48
		K.HGEVCPANWDEGK.K					802.90	1	1.65	0.08	187.7	17	10/14
		K.HGEVCPANWDEGK.K					1,499.56	2	3.91	0.41	1,384.6	1	17/24
		R.QATINDLPVGR.N					1,499.56	2	3.78	0.30	1,304.7	1	17/24
		K.DYFAAVN.-					1,184.33	2	3.28	0.33	723.1	2	17/20
		R.QATINDLPVGR.N					799.85	1	1.62	0.08	196.3	78	8/12
		R.DYNVLTEGGVALR.G					1,184.33	2	2.27	0.20	398.3	4	14/20
		R.DYNVLTEGGVALR.G					1,407.55	2	3.94	0.17	1,101.5	3	17/24
		R.GTFIIDPAGVIR.Q					1,407.55	2	3.45	0.22	1,324.4	2	18/24
		R.GTFIIDPAGVIR.Q					1,259.48	2	2.42	0.34	844.3	1	15/22
		R.GTFIIDPAGVIR.Q					1,259.48	2	2.54	0.15	722.2	9	14/22
11	45658458	hypothetical protein LIC12621 (<i>L. interrogans</i> serovar Copenhageni str. Fiocruz L1-130) K.GNITITGGQKK.D	6.60	5.86	16,207.9	14,523.4			56.22	36.80	14,522.4		17 (14 0 2 1 0)
		K.GNITITGGQK.K					1,117.28	2	2.71	0.14	951.2	1	15/20
		K.GNITITGGQK.K					989.11	2	2.49	0.18	928.4	6	14/18
		K.KIVEESFGGTR.T					989.11	1	2.32	0.20	399.3	4	11/18
		K.KIVEESFGGTR.T					1,223.36	2	2.21	0.11	290.6	51	14/20

Continued

Circle number	Accession no.	Orthologous proteins (s)/ Sequence (s)	PI (pH units)		Mol. mass (Da)		MH+	Charge	Score/ X_{corr}	% Coverage/ ΔCn	MW Sp	RSp	Peptides (Hits)/ Ions
			Gel	Theoret.	Gel	Theoret.							
		K.IVEESFGGTR.T					1,095.19	2	3.10	0.16	815.3	1	17/18
		K.IVEESFGGTR.T					1,095.19	1	1.78	0.06	329.9	195	11/18
		K.GNITITGGQK.K					989.11	2	2.46	0.20	548.0	43	12/18
		K.GNITITGGQK.K					989.11	2	2.62	0.19	709.8	5	13/18
		K.TDDTLYIGETGK.V					1,313.39	2	3.48	0.21	1,625.1	1	18/22
		K.TDDTLYIGETGK.V					1,313.39	2	4.30	0.31	2,107.0	1	19/22
		K.TDDTLYIGETGK.V					1,313.39	1	2.48	0.32	788.6	1	15/22
		K.IVEESFGGTR.T					1,095.19	2	2.87	0.15	1,032.4	1	15/18
		K.TDDTLYIGETGK.V					1,313.39	2	4.22	0.33	1,564.2	1	18/22
		K.IVEESFGGTR.T					1,095.19	2	2.39	0.29	204.2	78	11/18
		R.ENNSVIGPGSIFEGK.F					1,662.78	2	2.05	0.18	204.5	87	13/30
		R.ENNSVIGPGSIFEGK.F					1,662.78	2	3.96	0.30	616.4	1	17/30
		K.TDDTLYIGETGK.V					1,313.39	2	2.53	0.13	938.3	1	13/22

MH+, protonated molecular mass; X_{corr} , cross correlation; ΔCn , delta correlation.