

APPENDIX M

สำนักหอสมุด

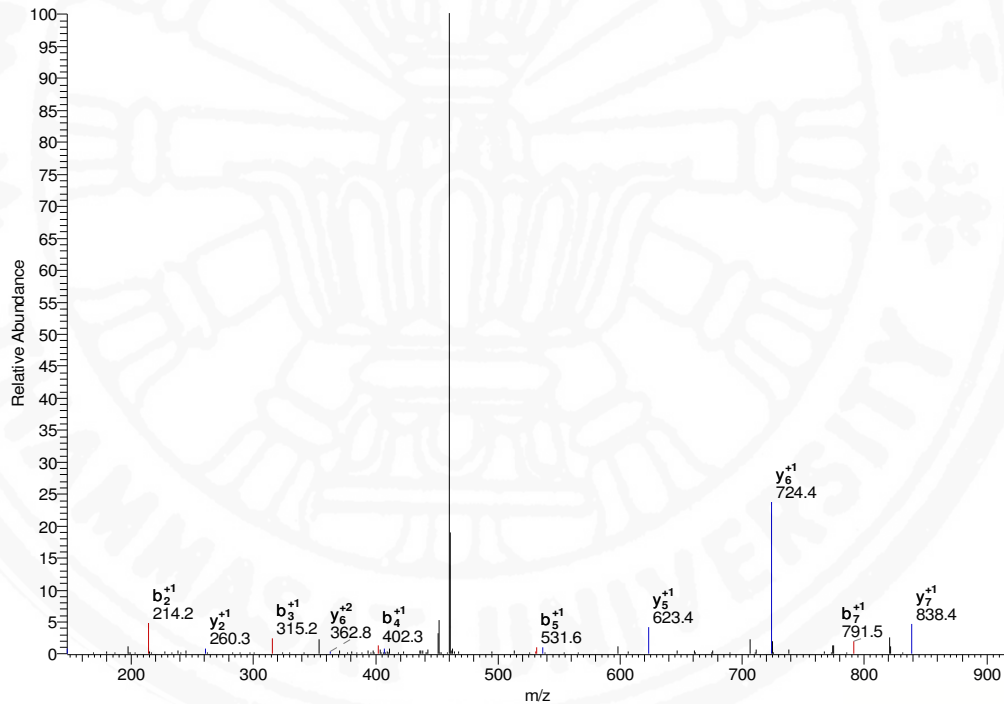
Orthologous proteins, peptide sequences and mass spectra obtained from LC/MS/MS analysis of proteins in spot numbers 1 to 11 of *L. interrogans* serogroup Pomona serovar Pomona separated by 2DE at linear pH 3-10 (Figure 32 and Table 10, Chapter V).

1. Spot no. 1, DNA polymerase III, beta subunit (*L. interrogans*)

Average MW 41425.9, PI 4.89

MKIK**VNTSEFLK**AIHAVEGVITREIKSILSNLKIEAEGKETFLSATDLEISIKTSVPADVTEQGNVSLPAKQLSS
FFKTIHFEDTNLSLEESDNSIVYITDASGKNKYK**ISGMDADEIKT**ISKIDSSQVSSFPSTLINDMIRK**TSYA**
IAHEDQRFIFNGLYMIPNGDK**LIFVGTDGR**RLCKIERTLPSPLOFK**DSIIVPAK**AIREISKMIATSEVGNIGLIDG
QIYVSANNIELLCKLIEGNFPNYEQVIPKNTK**FSTISKEEFQVSLRQVLTAAEESP**RQVRLTF SKNNLNLFAQTL
GASEASINKPIEYSGDEVTI AFKGEYLMDFRSIDDNEVKIEFSDANSPIIFKDPSPDPEFISVIMPVKL

#3229-3229 RT:13.61-13.61 NL: 2.82E3



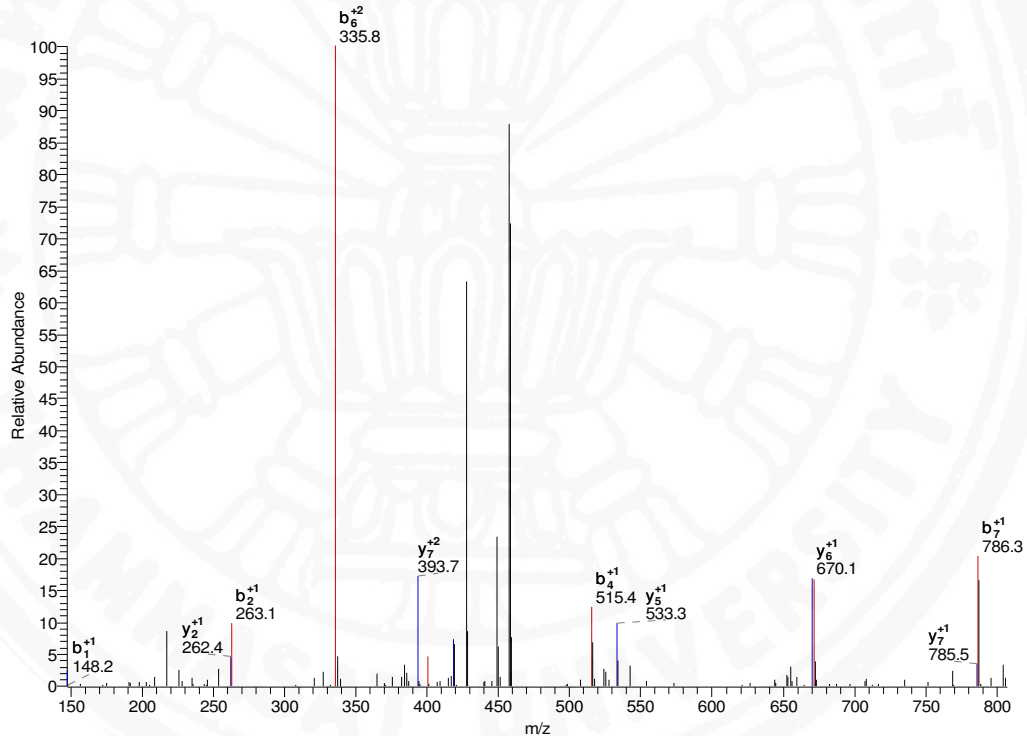
	AA	B Ions	Y Ions	
1	V	100.08	-	8
2	N	214.12	838.43	7
3	T	315.17	724.39	6
4	S	402.20	623.34	5
5	E	531.24	536.31	4
6	F	678.31	407.27	3
7	L	791.39	260.20	2
8	K	-	147.11	1

2. Spot no. 2, hypothetical protein LIC10483 (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 36149.2, PI 5.40

MALIDVIKYEQPGEIVWKFPRNDISYFGQLVVNESQEAVFFKEGKALDVFPGTHLTK**TGNIPVLEKLVNLPFGG**
 QTPFTAENVVYNKSVINMTWGTPAPIQIEDPKYHITLGVR**AFGNYNIKVIDSKSFVNTVVG**TQH**KFDHGDV**DKLLK
 PMVTR**LSDFISEVVLK**NGVPITQISQHLEASSAG**TKTQPDFQK**YGLEVVDFFIQSINFDQNDPNFQKIQKVL
 DKFEIETMGNMYQQKRLDIGEAAANNPSSAGEGMSAGMGLGMGMNMGMMANMMGQNGGAKPAGEDATARLAK
 LKSLLDGGLITQEEFDTKKK**DILNSI**

#2610-2610 RT:10.39-10.39 NL: 7.46E2



	AA	B Ions	Y Ions	
1	F	148.08	-	8
2	D	263.10	785.34	7
3	H	400.16	670.32	6
4	D	515.19	533.26	5
5	G	572.21	418.23	4
6	V	671.28	361.21	3
7	D	786.31	262.14	2
8	K	-	147.11	1

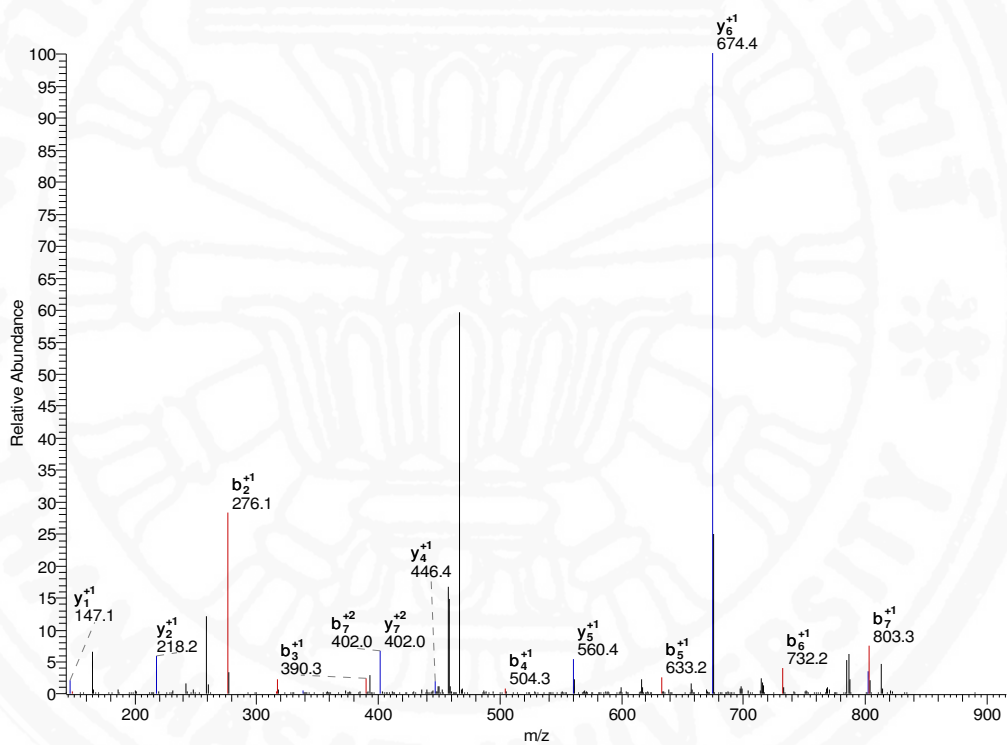
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3. Spot no. 3, flagellin protein (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 31306.3, PI 666

MIINHNLAAINSHRVLK**FQ**NEVAK**NMETLSSGMR**INRAGDDASGLAVSEKMR**TQVKGLRQAERN**TEDGMSLIQTT
EGYLQ**ETNDI**IQRIR**VLAIQSSNGIYSAEDR**QMIQVEVSQLVDEIDRIASQAEFN**KMALLQGDF**ARGSR**TSSMWFH**
IGPNQHQRERVYIATMTAKSLNLIKADGSLTLSTA**E**FANDAIGTLDDALMKINKQR**ANL**GAY**FNR**LEHASKGLMV
AYENIQASESRIR**DTDMAEETVAF**TKNQIILVQSGTAMLAQANVRPQSVLQLLR

#2721-2723 RT:10.49-10.50 NL: 5.95E5



	AA	B Ions	Y Ions	
1	F	148.08	-	8
2	Q	276.13	802.41	7
3	N	390.18	674.35	6
4	N	504.22	560.30	5
5	E	633.26	446.26	4
6	V	732.33	317.22	3
7	A	803.37	218.15	2
8	K	-	147.11	1

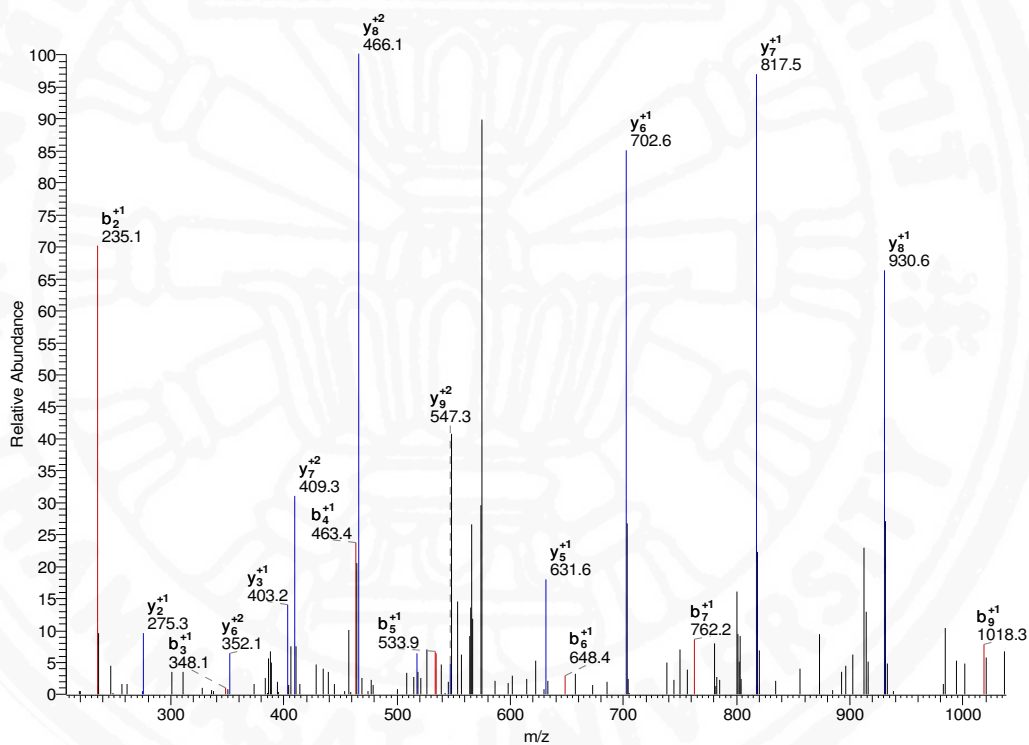
4. Spot no. 4-2, flagellar filament sheath protein (*L. interrogans* serovar

Copenhageni str. Fiocruz L1-130)

Average MW 34889.4, PI 7.91

MRRFMNSFKITAALTTILGGVILLGIVNGQNIKKGKRGIDTATGIDVSGLELRSITVESWDNPAPSAPYGWEVTTD
KDTQQPQGGQQQAYQATAQNAQALREVKLI SGKPGDIKNVDAGTAKVLGVKFQFTYPGENAVTIRPPRIPEYEILR
TK**AYLDANNQKKVSK**I**YGVEFP**GVSKAMSV**WVCGR**GNEYNLEGWIEDWKGDTHILQFGLDFIGWRPLTVYIPQGV
PQDVNSYPQVKTIIVFKQFKVRSRPDTSGETVYLFFDELRLVLSDFEVVHFDGASIDFDEDCRSKHKLDKMLKTKVE
KECGGGGAAGK _

#2663-2665 RT:10.57-10.58 NL: 1.26E2



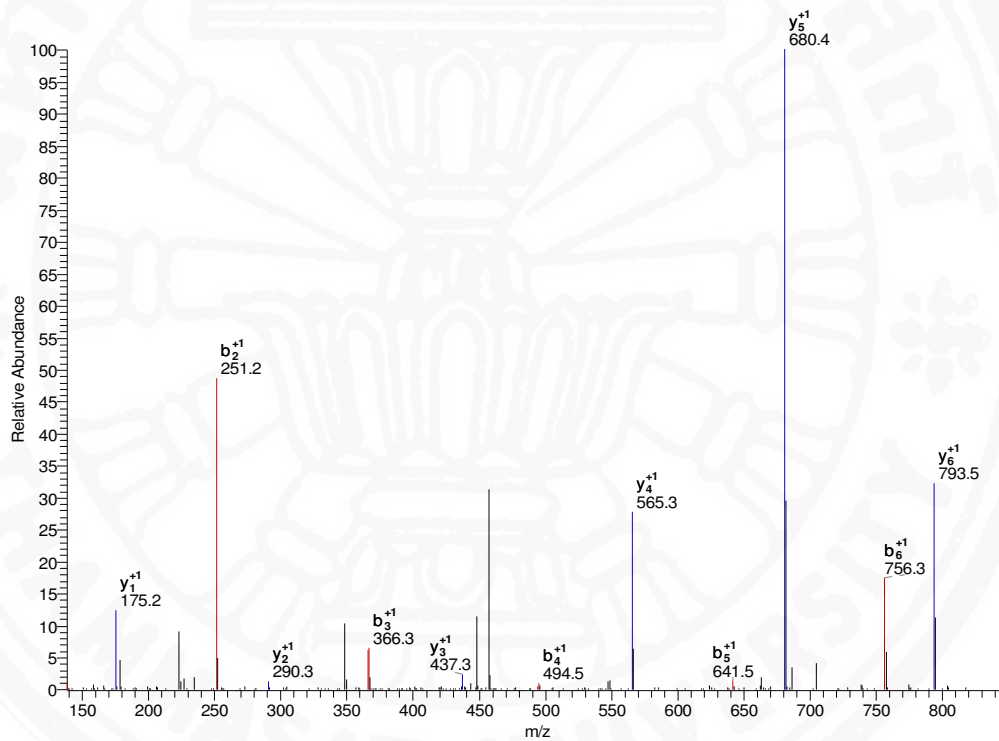
AA	B Ions	Y Ions	
1	A	72.04	10
2	Y	235.11	9
3	L	348.19	8
4	D	463.22	7
5	A	534.26	6
6	N	648.30	5
7	N	762.34	4
8	Q	890.40	3
9	K	1018.50	2
10	K	-	1

5. Spot no. 5, hypothetical protein LIC11848 (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 32022.1, PI 8.54

MKLQKLF~~LA~~VLI~~AI~~STAVFSQQNSGSDQK**SQPSSAQLGQSILE**TERKLDEKIFELNQRLRTRHTVLMKMKVRLVLPFR
TVLFRGK**ANDECTPAINQEDPANNCIR**VEVYDFIRDEERGLNKNVQGALAKYMEIYFEGQNSNDPEPRTEPPRNI
NKLKSKIYK**NNMVLEDKIISEVM**DRGPNTQPSHNDKVEVFFQKDNYPEYGRPETPAEKGVGK**YILAGVENTK**THPI
RNSFKKEFYIK**HLDQFDR**LFTKIFDYNDQLGNENYKENVDALKDSLRY _

#2664-2666 RT:11.66-11.67 NL: 5.33E3



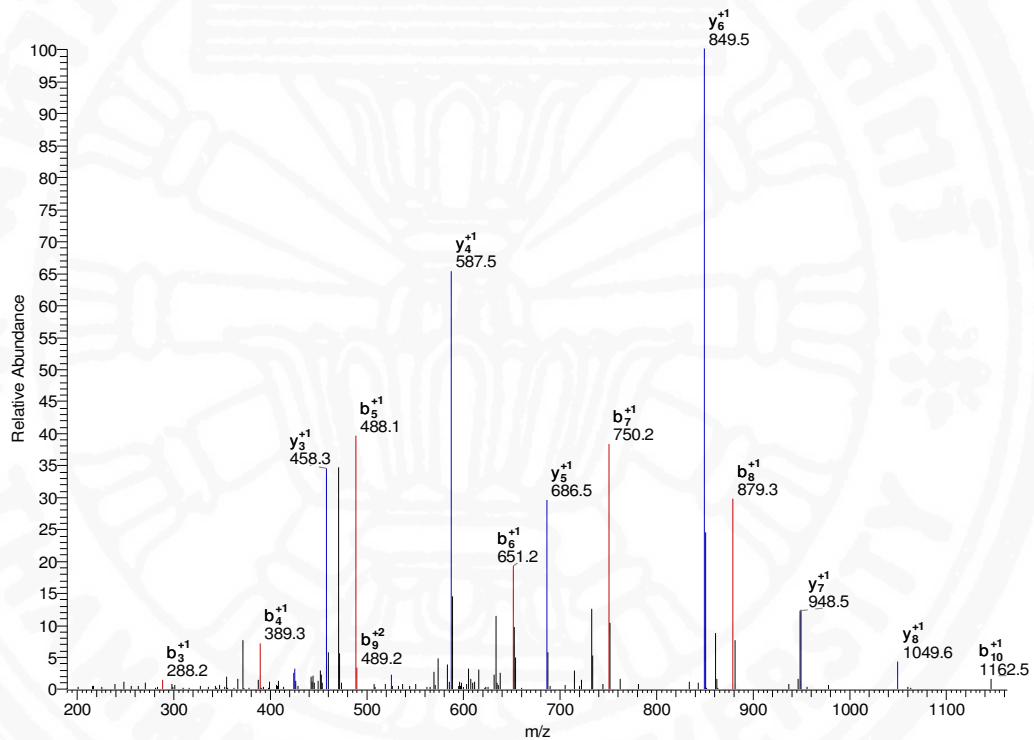
	AA	B Ions	Y Ions	
1	H	138.07	-	7
2	L	251.15	793.38	6
3	D	366.18	680.30	5
4	Q	494.24	565.27	4
5	F	641.30	437.21	3
6	D	756.33	290.15	2
7	R	-	175.12	1

6. Spot no. 6, succinate dehydrogenase (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 26650.6, PI 6.23

MDLKLKVVRRQKSGETKGIVDYNAKDISPNMSFLEMLDVVNEELITKGEDPIAFEHDCREGICGSCNLMINGQAHG
PHQGVTSQQLHMRSFK**DGDTVYVEPWR**AKAFPVLKDLVVDRAFDRIIQAGGFISVNTGGAPDANALPIPKVDADV
SMDAATCIGCGACVASCKNASAMLFVSAKITHLGLLPQKVEQKERVKKMINAMDQEGFGNCTNQYECEAVCPKSI
KRDFIRTLNRDYILS

#3601-3601 RT:14.55-14.55 NL: 9.55E2



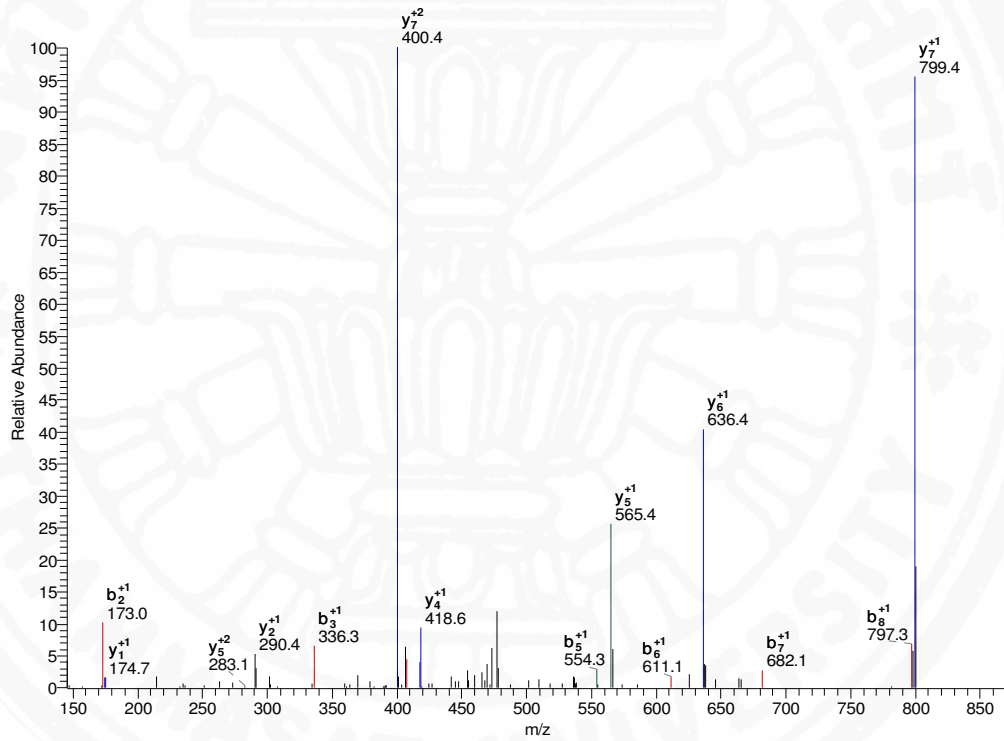
	AA	B Ions	Y Ions	
1	D	116.03	-	11
2	G	173.06	1221.59	10
3	D	288.08	1164.57	9
4	T	389.13	1049.54	8
5	V	488.20	948.49	7
6	Y	651.26	849.43	6
7	V	750.33	686.36	5
8	E	879.37	587.29	4
9	P	976.43	458.25	3
10	W	1162.51	361.20	2
11	R	-	175.12	1

7. Spot no. 7, electron transport flavoprotein beta subunit (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 27068.9, PI 5.47

MKIIIVLVKQVPDTETSIKVGDK**SINETGIKWII**SPYDEFAIEEGIRLREKHGGVEIVAVSLGPDRVVEALR**TAYAMG**
ADRAVHIKVDNYVPFDTNNTAELISNFAK**AENADVIIGGR**QSIDTDSSQVVIQVAELLGIPHIAFAINLEINGTAV
 KATK**EVEGGTQTVETSTPVALTAQK**GLNEPRYPYSLKGMTAKKKPVETK**SAADLGSPASK**IEIVGLEPPPPRIPGR
 KLEAADANAFAAQLVKALREEAKVI _

#2281-2283 RT:9.94-9.95 NL: 6.84E2



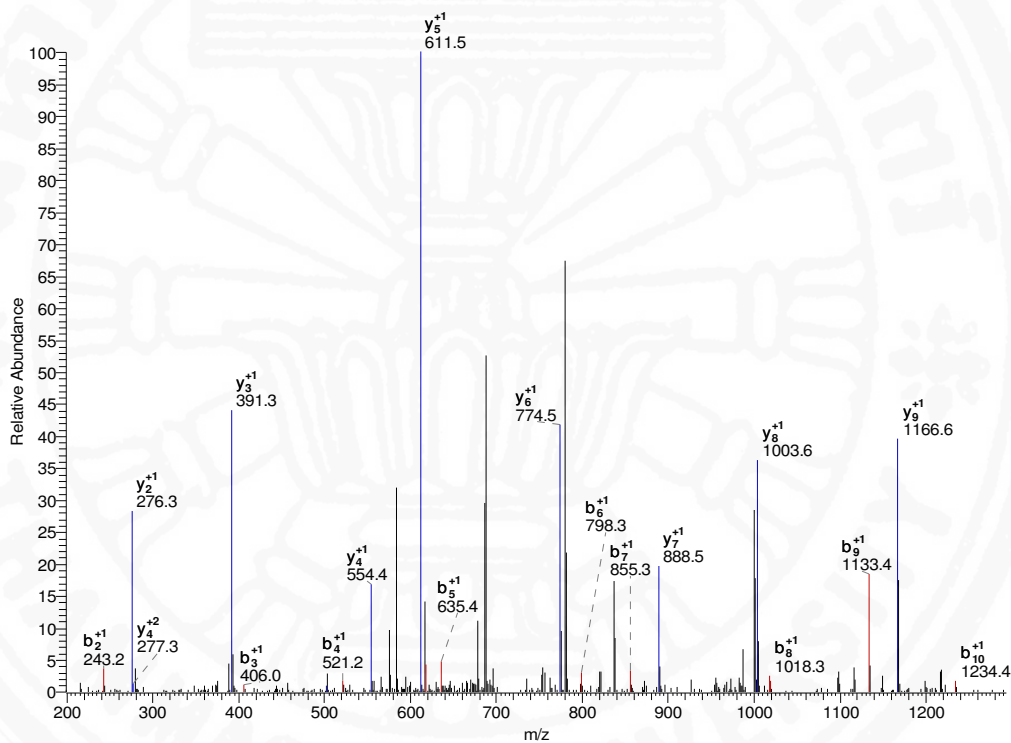
	AA	B Ions	Y Ions	
1	T	102.05	-	9
2	A	173.09	870.38	8
3	Y	336.16	799.34	7
4	A	407.19	636.28	6
5	M*	554.23	565.24	5
6	G	611.25	418.20	4
7	A	682.29	361.18	3
8	D	797.32	290.15	2
9	R	-	175.12	1

8. Spot no. 8, transaldolase (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 23491.1, PI 4.95

MELYLDTANVDEIKEIASYGLVDGVTNPSLIAKSGRSFKEVIKEICSIIVSGPVSAEVLSTKFDGMKEALELVEI
AENVVIK**VPLIPEGLKTVVELTKR**NIPTNVTLCFSAPQALLAAKAGATFISPFIGRVDDTSDGMELISEIRE**EIYD**
NYGYDTRILAAASIRGPIHLKESALRGADCATMPHSAFLQLFKHPLTDIGLEKFLKFLDSKLLK _

#3185-3187 RT:13.36-13.37 NL: 1.73E3



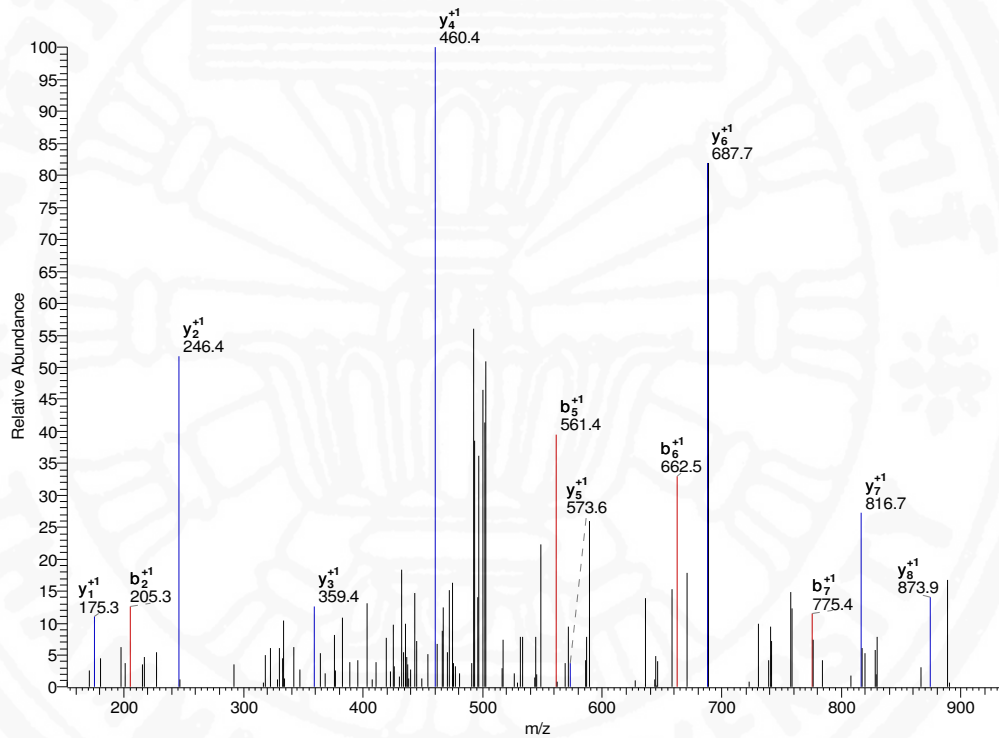
	AA	B Ions	Y Ions	
1	E	130.05	-	11
2	I	243.13	1279.56	10
3	Y	406.20	1166.47	9
4	D	521.22	1003.41	8
5	N	635.27	888.38	7
6	Y	798.33	774.34	6
7	G	855.35	611.28	5
8	Y	1018.42	554.26	4
9	D	1133.44	391.19	3
10	T	1234.49	276.17	2
11	R	-	175.12	1

9. Spot no. 9, elongation factor Ts (*L. interrogans* serovar Lai str. 56601)

Average MW 22172.5, PI 5.61

MAAVTTDLIRELRERTSAGMMDCK**KALEENNADIEK**AITWLREKGIAKAAKAGRETKEGRVVS⁺YIHGNGKIGVLV
ELNSE⁺TDFVSK**NEDFEALGKE**ICMQIAAMNPLYLNEESIPAADLEKEKTIMRSQLEAEGKKADQIEKILPGKIKKY
VSEVCLVNQAFKDDSKTIDDLVKEAIAK**FGENITLARFIRFQVGGL**

#3458-3458 FT:14.59-14.59 NL: 1.20E2



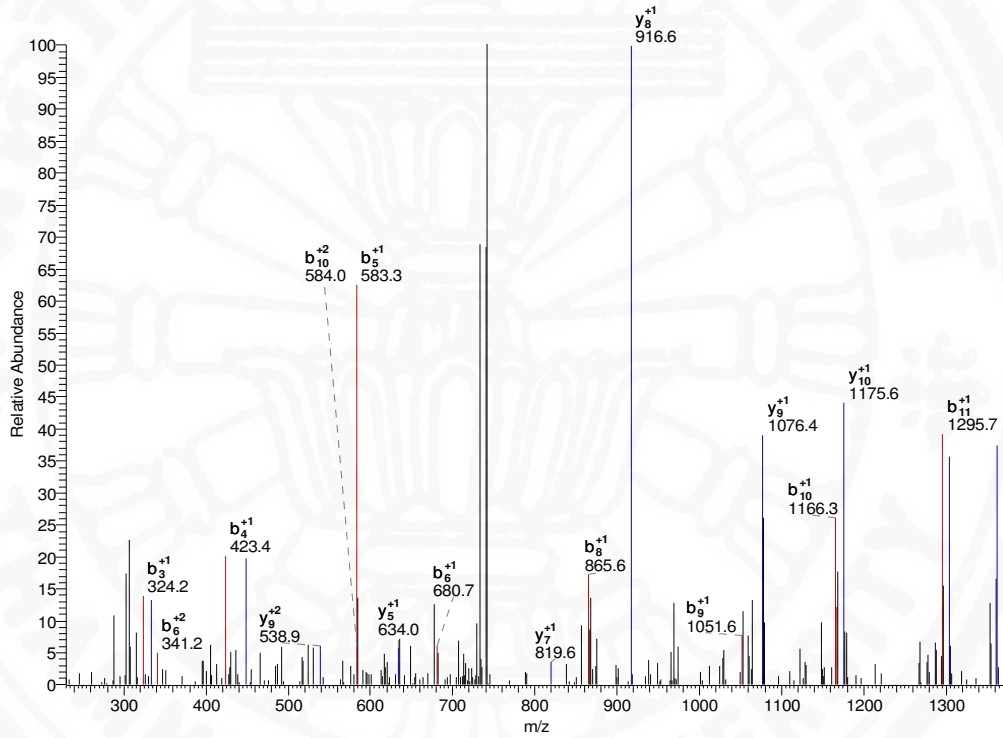
AA	B Ions	Y Ions	
1 F	148.08	-	9
2 G	205.10	873.48	8
3 E	334.14	816.46	7
4 N	448.18	687.41	6
5 I	561.27	573.37	5
6 T	662.31	460.29	4
7 I	775.40	359.24	3
8 A	846.44	246.16	2
9 R	-	175.12	1

10. Spot no. 10, peroxiredoxin (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 21517.7, PI 5.74

MPQVTS LAPDFKAEAVLGKEIKEIKLS DYK GKWV LFF YPLDFTFVCPTEIIEYDNKLAEFK KLGTEVLGVS VDSA
 FTHLAWKNTPK**KEGGIG EIK**YPLIADLTKSISR**DYNVLT EGGVALRGTFIIDPAGVIRQATINDLPVGRNIDEAIR**
 LIKAFQFVEK**HGEVCPANWDEGKK**TMKADPEKSK**DYFAAVN**

#2990-2990 RT:12.61-12.61 NL: 3.23E2



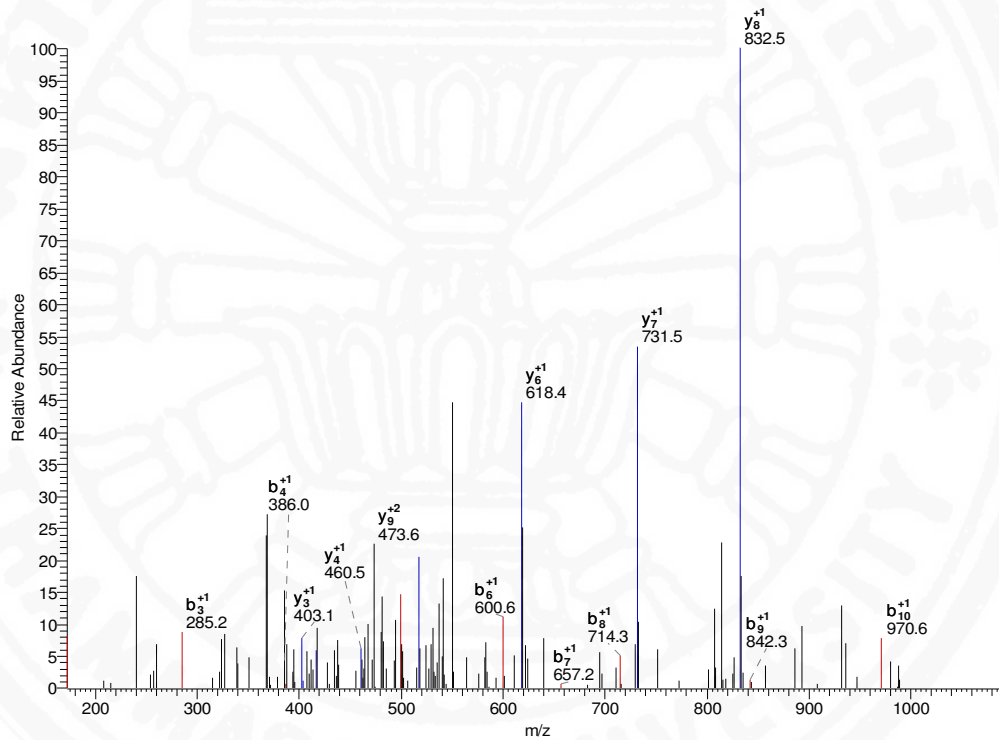
AA	B Ions	Y Ions	
1	H	138.07	-
2	G	195.09	1361.71
3	E	324.13	1304.69
4	V	423.20	1175.65
5	C	583.36	1076.58
6	P	680.42	916.42
7	A	751.45	819.36
8	N	865.50	748.33
9	W	1051.58	634.28
10	D	1166.60	448.20
11	E	1295.65	333.18
12	G	1352.67	204.13
13	K	-	147.11

11. Spot no. 11, hypothetical protein LIC12621 (*L. interrogans* serovar Copenhageni str. Fiocruz L1-130)

Average MW 14523.4, PI 5.86

MAIGRENNNSVIGPGSIFEGK FYIAGSLRIDGKFEGEIK **TDDTLYIGETGK** VRTNISAREVTVSGTMIGNIKAENE
VRLEETGRLLGDIIPALHLAKGVVAK **GNITITGGQKKDVKKIVEESFGGTR** TLDNGKDE

#2732-2734 RT:11.22-11.22 NL: 1.47E2



	AA	B Ions	Y Ions	
1	G	58.03	-	11
2	N	172.07	1059.62	10
3	I	285.16	945.57	9
4	T	386.20	832.49	8
5	I	499.29	731.44	7
6	T	600.34	618.36	6
7	G	657.36	517.31	5
8	G	714.38	460.29	4
9	Q	842.44	403.27	3
10	K	970.53	275.21	2
11	K	-	147.11	1