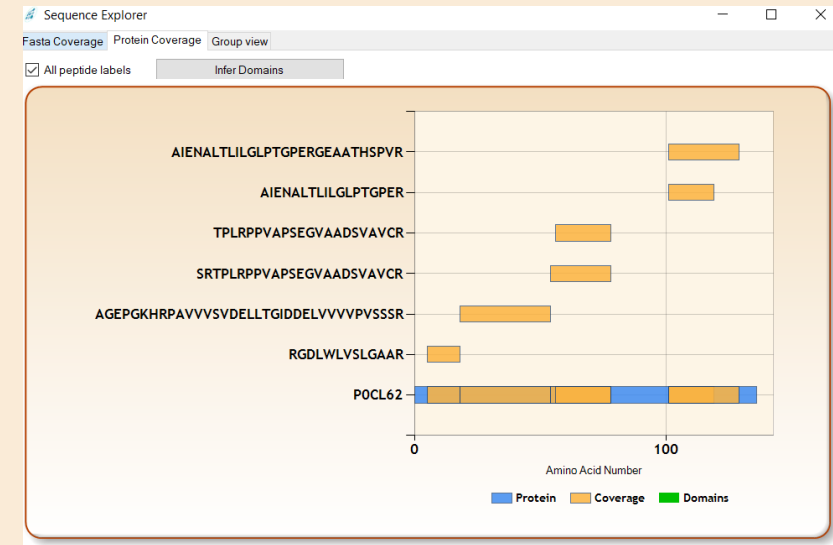


# MazF7 (Rv2063A) Possible toxin MazF7

Spec FDR: 0/0 = NaN% Pep FDR: 0/0 = NaN% Prot FDR: 0/0 = NaN% # Prot (Max Parsimony): 1635 Unique Prot: 1634 Unlabeled Decoys: 0/0

View mode:  Proteins  Proteins Max Pars  Peptides  Scans

Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description	
1	POCL62	958	Unique	136	6	14208.7	6	9	0.000572660478457528	0.7426	26.2139	Probable endoribonuclease MazF7 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mazF7 PE=1 SV=1

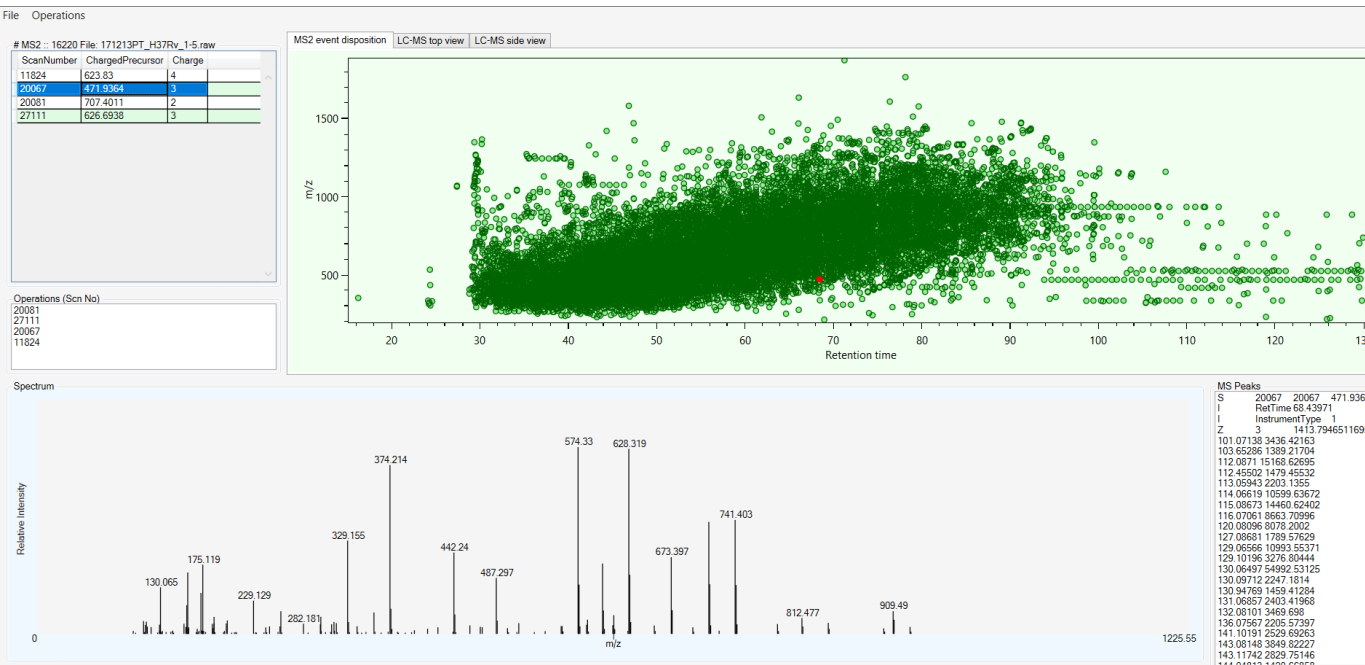


File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-5.sqt	13269	3	True	2250.169346	2249.170674	-2.07895	3.4005	10.5847061622308	0.5406	25	0.53012	R.TPLRPPVAPSEGVAADSVAVCR.G
171213_PT_H37Rv_1-5.sqt	23449	4	True	2884.563864	2883.568682	-2.83162	3.1984	8.36447210439857	0.5229	33	0.51318	R.AIENALTILGLPTGPERGEAATHSPVR.W
171213_PT_H37Rv_1-5.sqt	20081	2	True	1413.797537	1413.796109	1.01005	3.4682	7.93777477618463	0.4941	19	0.50783	R.RGDLWLVSLGAAR.A
171213_PT_H37Rv_1-5.sqt	27111	3	True	1878.06699	1878.06949	-1.33116	3.1224	7.56360667479839	0.4876	24	0.49616	R.AIENALTILGLPTGPER.G
171213_PT_H37Rv_1-5.sqt	20067	3	True	1413.793899	1413.796109	-1.56317	2.9076	6.08797544748883	0.4237	22	0.45541	R.RGDLWLVSLGAAR.A
171213_PT_H37Rv_1-5.sqt	26207	4	True	3726.988669	3726.007231	-5.87928	2.6753	5.17787121347217	0.4821	25	0.45319	R.AGEPGKHRPAVVVSVDELDTGIDDELVVVVPVSSSR.S
171213_PT_H37Rv_1-5.sqt	11824	4	True	2492.295193	2492.303813	-3.45866	3.1656	4.45675018086982	0.3782	39	0.41881	R.SRTPLRPPVAPSEGVAADSVAVCR.G
171213_PT_H37Rv_1-5.sqt	23502	3	True	2884.564427	2883.568682	-2.63645	1.9313	1.78379129957888	0.3476	18	0.39683	R.AIENALTILGLPTGPERGEAATHSPVR.W
171213_PT_H37Rv_1-5.sqt	27125	2	True	1878.061626	1878.06949	-4.1873	2.3446	4.21990778519745	0.3623	17	0.39378	R.AIENALTILGLPTGPER.G

>Mycobacterium tuberculosis H37Rv|Rv2063A|mazF7  
 LAEPR**RGDLWLVSLGAAR**AGEPGKHRPAVVVSVDELDTGIDDELVVVVPVSSSRSRTPLRPPVAPSEGVAADSVAVCRGVRVARARLVERLGALKPATMR**AIENALTILGLPTGPER**GEAATHSPVRWTGGRDP

In bold and red: Peptide spectra shown in next slides

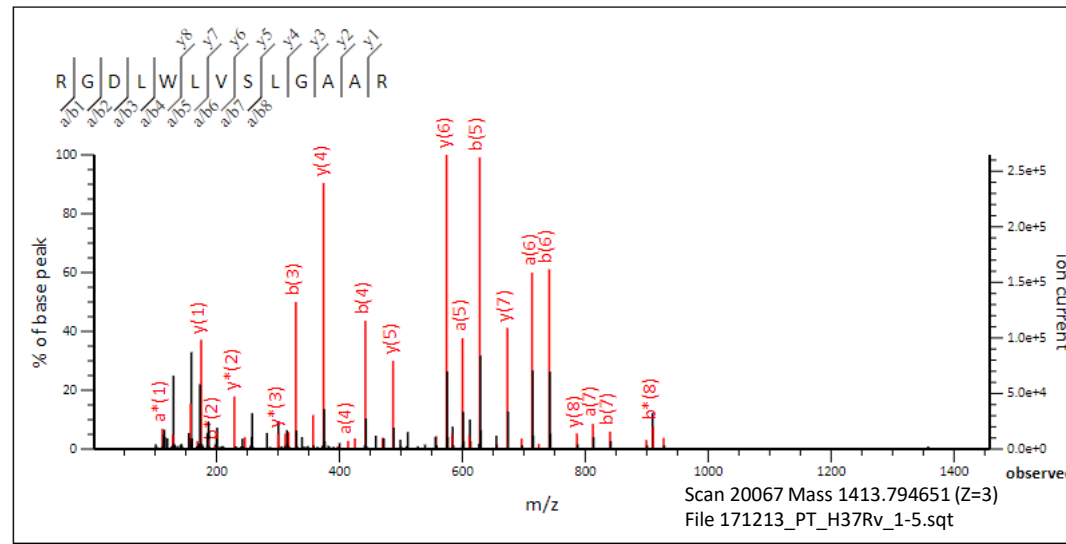
# MazF7 (Rv2063A) Possible toxin MazF7



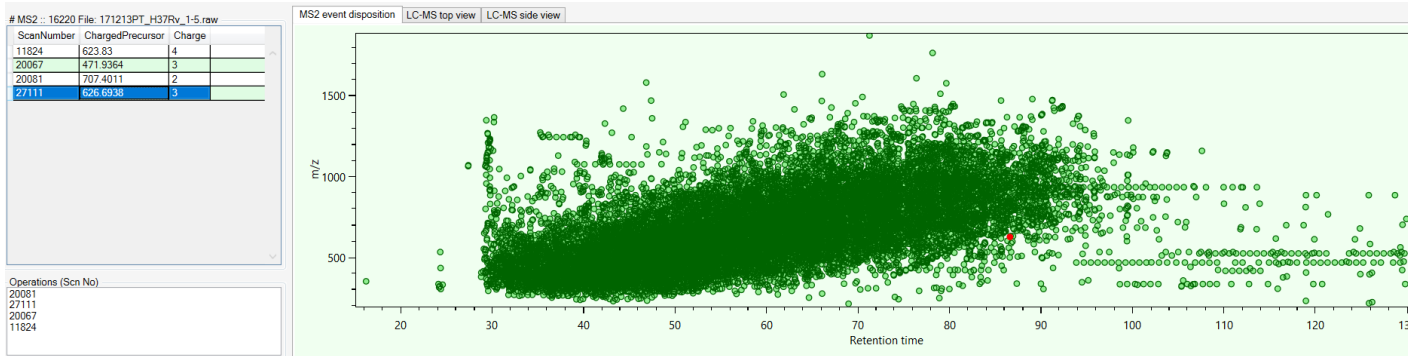
Peptide: RGDLWLVS LG AAR

MS/MS Fragmentation of **RGDLWLVS LG AAR**  
 Found in **WP\_003410654.1** in **NCBIprot**, MULTISPECIES: mRNA interferase MazF7 [Mycobacterium]

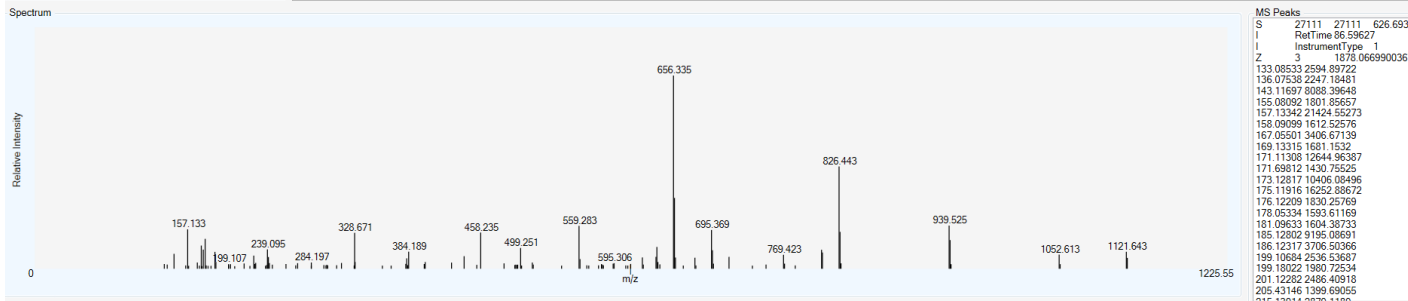
Match to Query 1: 1412.787375 from(1413.794651,1+) index(2)  
 Data file Scans MazF7.txt



# MazF7 (Rv2063A) Possible toxin MazF7

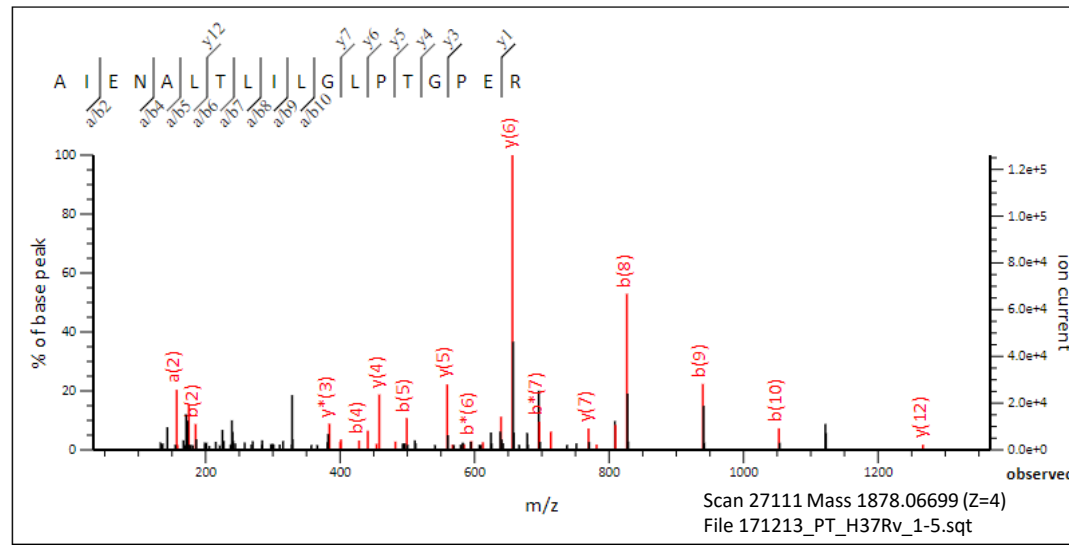


Peptide: AIENALTLILGLPTGPER



MS/MS Fragmentation of **AIENALTLILGLPTGPER**  
Found in **WP\_003410654.1** in **NCBIprot**, MULTISPECIES: mRNA interferase MazF7 [Mycobacterium]

Match to Query 3: 1877.059714 from(1878.066990,1+) index(4)  
Data file Scans MazF7.txt



# MbtL (Rv1344) Acyl carrier protein (ACP) MbtL

File Statistics Tools

Control Follow up Result Browser

Spec FDR: 0/0 = NaN% Pep FDR: 0/0 = NaN% Prot FDR: 0/0 = NaN% # Prot (Max Parsimony): 1642 Unique Prot: 1643 Unlabeled Decoys: 0/0

View mode:  Proteins  Proteins Max Pars  Peptides  Scans

Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1 P9WQF1	890	Unique	84	4	8945.5	4	5	0.000556871453134169	0.869	12.5988	Acyl carrier protein MbtL OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mbtL PE=1 SV=1

Sequence Explorer

Fasta Coverage Protein Coverage Group view

All peptide labels

**LGVALSEELLTCDTVGELEAAIAAK**  
**LVDDVGLDSVAFVGM(+15.994900)VAIEER**  
**LVDDVGLDSVAFVGMVAIEER**  
**TSSPSTVSTLLSILRDDLNIDLTR**  
**P9WQF1**

Amino Acid Number

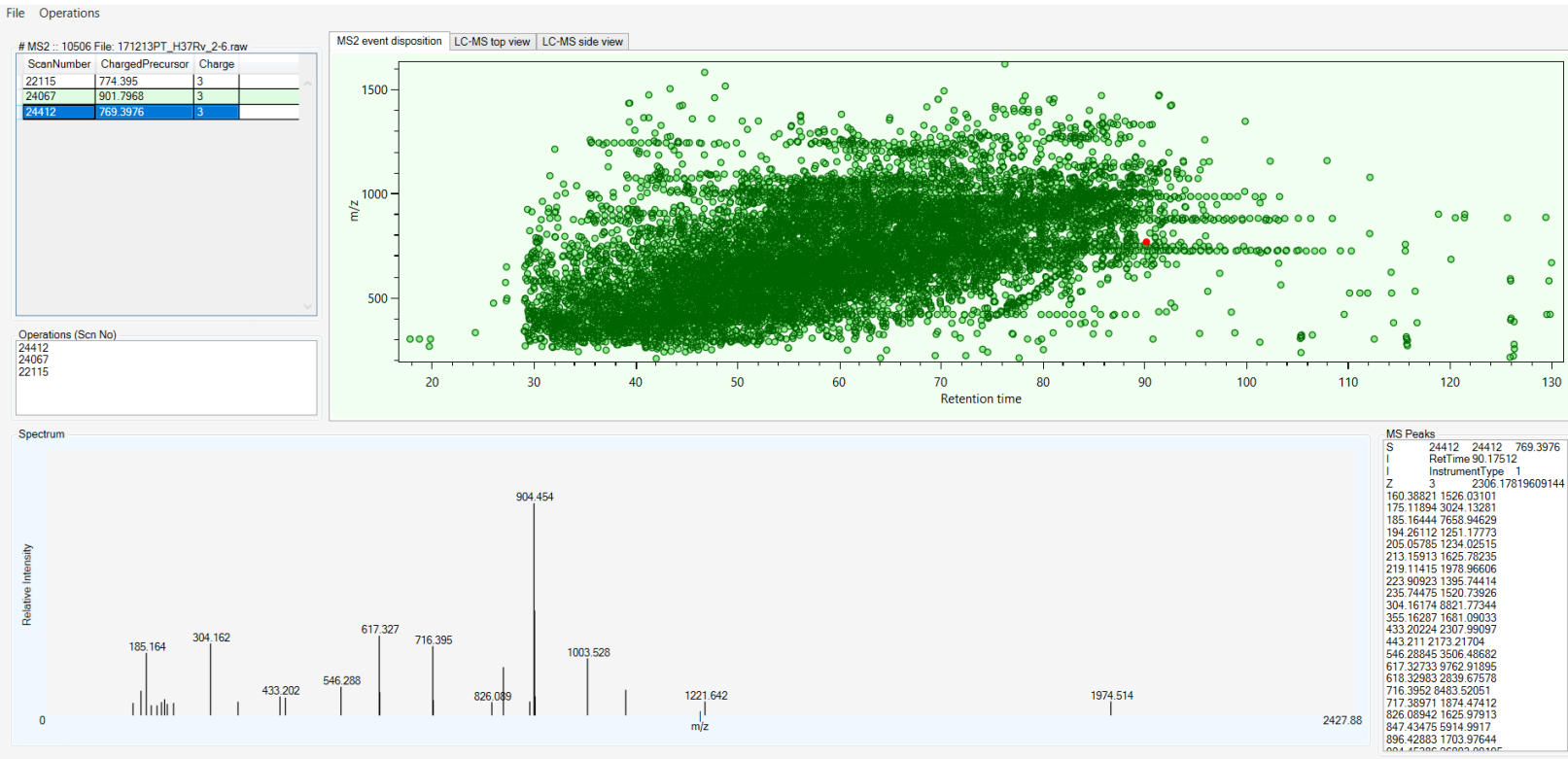
■ Protein ■ Coverage

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
1 171213_PT_H37Rv_2-6.sqt	24157	3	True	2719.449803	2718.451981	-2.03276	3.3616	6.40093767661368	0.4721	32	0.79142	M.TSSPSTVSTLLSILRDDLNIDLTR.V
2 171213_PT_H37Rv_2-6.sqt	24052	3	True	2703.379917	2702.380451	-1.43672	2.4312	4.66810998576197	0.5038	18	0.46976	R.LGVALSEELLTCDTVGELEAAIAAK.Y
3 171213_PT_H37Rv_2-6.sqt	24412	3	True	2306.182957	2305.174425	2.247	2.4455	6.57845153183954	0.4686	19	0.44444	R.LVDDVGLDSVAFVGMVAIEER.L
4 171213_PT_H37Rv_2-6.sqt	24067	3	True	2703.37723	2702.380451	-2.43066	2.4948	6.96644427533082	0.4436	22	0.42201	R.LGVALSEELLTCDTVGELEAAIAAK.Y
5 171213_PT_H37Rv_2-6.sqt	22115	3	True	2321.169416	2321.169325	0.0392	1.8657	2.46275384514687	0.3764	19	0.3838	R.LVDDVGLDSVAFVGM(+15.994900)VAIEER.L

>Mycobacterium tuberculosis H37Rv|Rv1344|mbtL  
 MWRYPLSTRALPNTPGVASFAMTSSPSTVSTLLSILRDDLNIDLTRVTPDAR**LVDDVGLDSVAFVGMVAIEER****LGVALSEELLTCDTVGELEAAIAAK**YRDE

In bold, red and green: Peptide spectra shown in next slides

# MbtL (Rv1344) Acyl carrier protein (ACP) MbtL



Peptide:

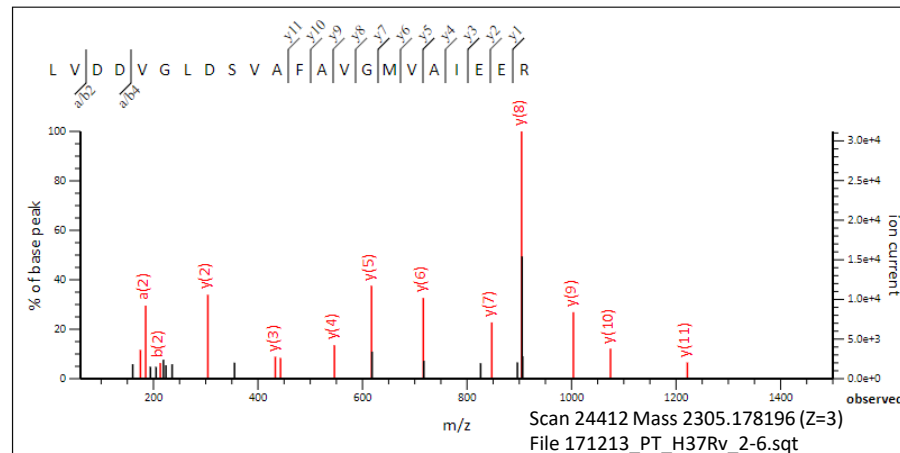
R.LVDDVGLDSVAFVAVGMVAIEER.L

Monoisotopic mass of neutral peptide Mr(calc): 2304.1672  
 Fixed modifications: Carboxymethyl (C) (apply to specified residues or termini only)  
 Ions Score: 94 Expect: 3.5e-05 ([help](#))

#	a	b	Seq.	y	y*	#
1	86.0964	114.0913	L			22
2	185.1648	213.1598	V	2192.0904	2175.0638	21
3	300.1918	328.1867	D	2093.0219	2075.9954	20
4	415.2187	443.2136	D	1977.9950	1960.9685	19
5	514.2871	542.2821	V	1862.9681	1845.9415	18
6	571.3086	599.3035	G	1763.8996	1746.8731	17
7	684.3927	712.3876	L	1706.8782	1689.8516	16
8	799.4196	827.4145	D	1593.7941	1576.7676	15
9	886.4516	914.4466	S	1478.7672	1461.7406	14
10	985.5201	1013.5150	V	1391.7351	1374.7086	13
11	1056.5572	1084.5521	A	1292.6667	1275.6402	12
12	1203.6256	1231.6205	F	1221.6296	1204.6031	11
13	1274.6627	1302.6576	A	1074.5612	1057.5347	10
14	1373.7311	1401.7260	V	1003.5241	986.4975	9
15	1430.7526	1458.7475	G	904.4557	887.4291	8
16	1561.7931	1589.7880	M	847.4342	830.4077	7
17	1660.8615	1688.8564	V	716.3937	699.3672	6
18	1731.8986	1759.8935	A	617.3253	600.2988	5
19	1844.9826	1872.9776	I	546.2882	529.2617	4
20	1974.0252	2002.0202	E	433.2041	416.1776	3
21	2103.0678	2131.0628	E	304.1615	287.1350	2
22			R	175.1190	158.0924	1

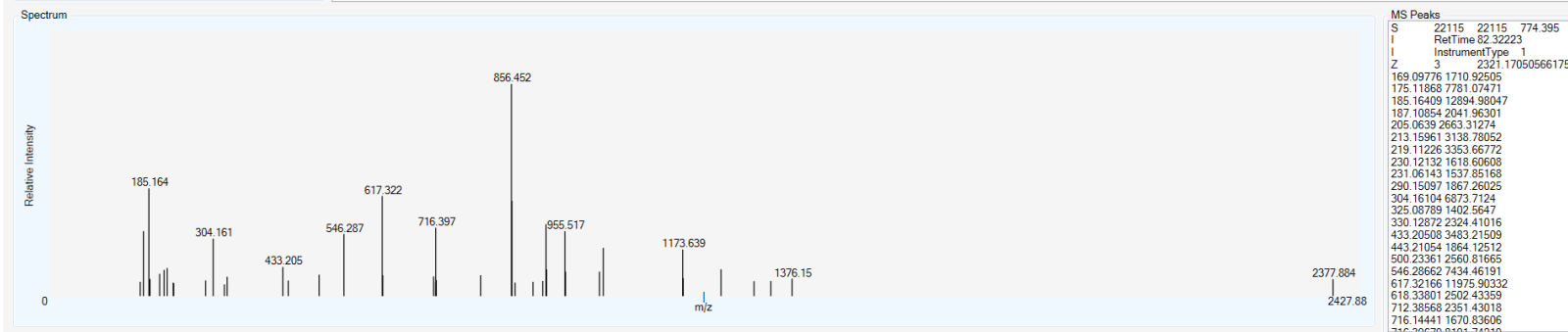
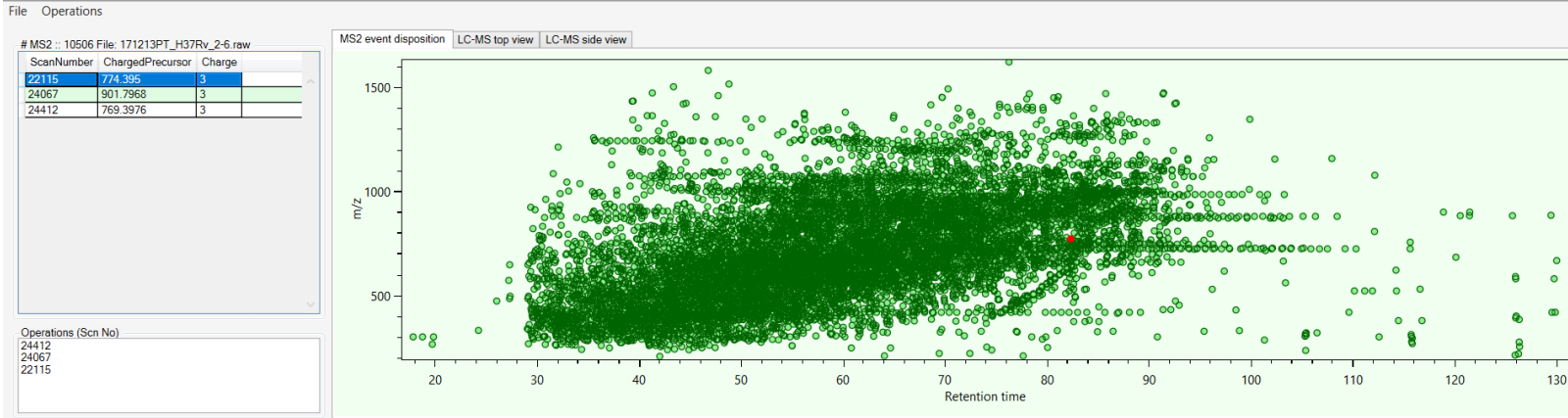
MS/MS Fragmentation of **LVDDVGLDSVAFVAVGMVAIEER**  
 Found in **Q73ZP6.1** in **NCBIprot**, RecName: Full=Acyl carrier protein MbtL; Short=ACP; AltName: Full=Mycobactin synthase protein L

Match to Query 1: 2304.170920 from(2305.178196,1+) index(2)  
 Data file Scans MbtL.txt



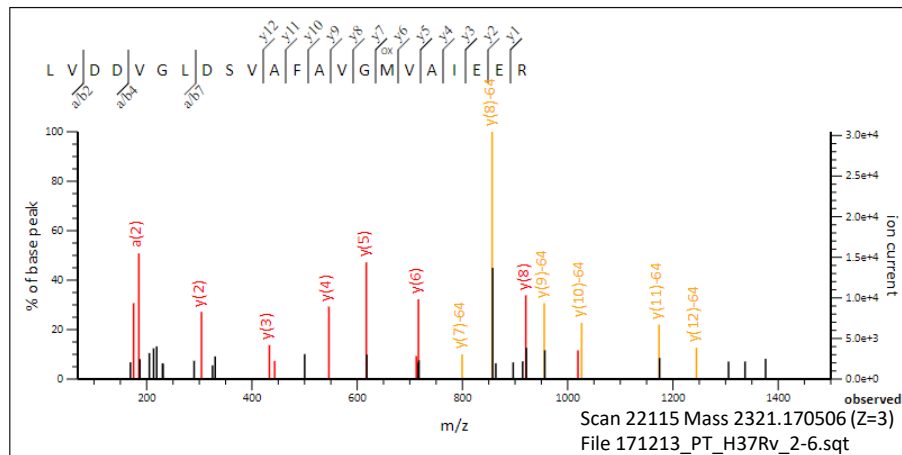
# MbtL (Rv1344) Acyl carrier protein (ACP) MbtL

## Utils :: Mass Spectra File Browser



MS/MS Fragmentation of **LVDDVGLDSVAFVGMVAIEER**  
 Found in **Q73ZP6.1** in **NCBIprot**, RecName= Full=Acyl carrier protein MbtL; Short=ACP; AltName= Full=Mycobactin synthase protein L

Match to Query 2: 2320.163230 from(2321.170506,1+) index(0)  
 Data file Scans MbtL.txt



## Peptide:

R.LVDDVGLDSVAFVGM(+15.994900)VAIEER.L

Monoisotopic mass of neutral peptide Mr(calc): 2320.1621  
 Fixed modifications: Carbonylmethyl (C) (apply to specified residues or termini only)  
 Variable modifications:  
 M16 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000  
 Ions Score: 77 Expect: 0.0019  
 Matches : 18/126 fragment ions using 29 most intense peaks ([help](#))

#	a	b	Seq.	y	y*	#
1	86.0964	114.0913	L			22
2	185.1648	213.1598	V	2144.0870	2127.0604	21
3	300.1918	328.1867	D	2045.0186	2027.9920	20
4	415.2187	443.2136	D	1929.9916	1912.9651	19
5	514.2871	542.2821	V	1814.9647	1797.9381	18
6	571.3086	599.3035	G	1715.8963	1698.8697	17
7	684.3927	712.3876	L	1658.8748	1641.8483	16
8	799.4196	827.4145	D	1545.7908	1528.7642	15
9	886.4516	914.4466	S	1430.7638	1413.7373	14
10	985.5201	1013.5150	V	1343.7318	1326.7052	13
11	1056.5572	1084.5521	A	1244.6634	1227.6368	12
12	1203.6256	1231.6205	F	1173.6263	1156.5997	11
13	1274.6627	1302.6576	A	1026.5578	1009.5313	10
14	1373.7311	1401.7260	V	955.5207	938.4942	9
15	1430.7526	1458.7475	G	856.4523	839.4258	8
16	1513.7897	1541.7846	M	799.4308	782.4043	7
17	1612.8581	1640.8530	V	716.3937	699.3672	6
18	1683.8952	1711.8901	A	617.3253	600.2988	5
19	1796.9793	1824.9742	I	546.2882	529.2617	4
20	1926.0219	1954.0168	E	433.2041	416.1776	3
21	2055.0645	2083.0594	E	304.1615	287.1350	2
22			R	175.1190	158.0924	1



# MbtL (Rv1344) Acyl carrier protein (ACP) MbtL

File Operations

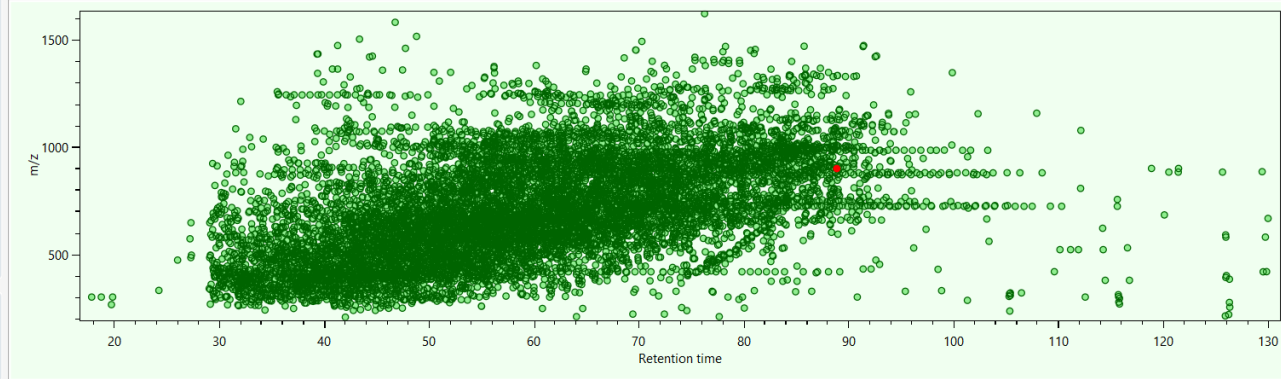
# MS2 : 10506 File: 171213PT\_H37Rv\_2-6.raw

ScanNumber	ChargedPrecursor	Charge
22115	774.395	3
24067	901.7968	3
24412	769.3976	3

Operations (Scn No)

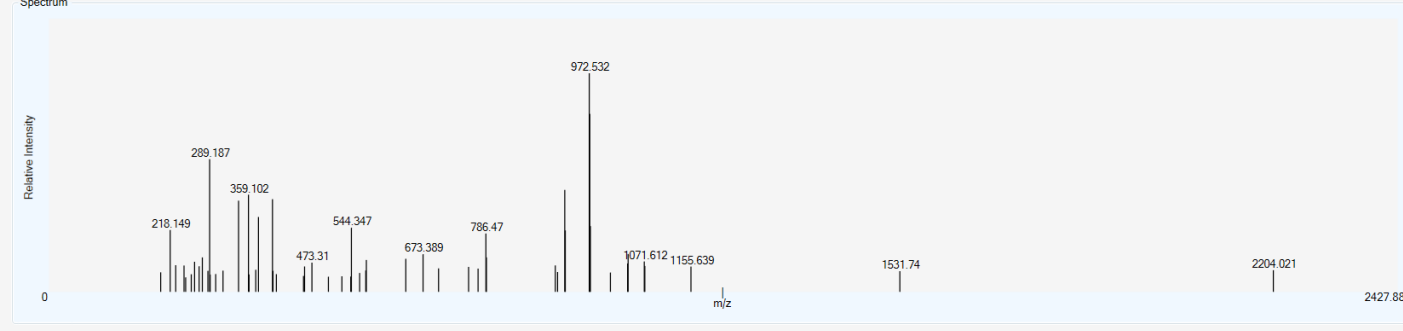
24412  
24067  
22115

MS2 event disposition LC-MS top view LC-MS side view



**Peptide:**  
R.LGVALSEEELLTCDTVGELEAAIAAK.Y

Spectrum



MS Peaks

S	24067	24067	901.7968
I		RetTime	88.86188
I		InstrumentType	1
Z	3		2703.3757065706
	201.12325	1966.03603	
	218.14899	6215.26758	
	228.13333	2678.50293	
	243.13339	2646.2417	
	246.08165	1459.82629	
	256.16498	1775.8772	
	262.08609	3023.99463	
	270.17966	2576.29028	
	276.06559	3466.73535	
	286.10434	2111.9126	
	289.1871	13337.43945	
	290.18945	1735.82202	
	300.15833	1790.54858	
	313.22321	2132.90112	
	341.21854	9160.98805	
	359.10199	9760.72559	
	360.10355	1752.99329	
	372.17712	2221.01221	
	377.11304	7521.22266	
	402.27271	9311.7666	
	403.27356	2114.43848	
	460.27356	3703.63663	

MS/MS Fragmentation of **LGVALSEELLTCDTVGELEAAIAAK**  
Found in **KBE54844.1** in **NCBIprot**, acyl carrier protein MbtL [Mycobacterium tuberculosis H2102]

Match to Query 2: 2702.368430 from(2703.375706,1+) index(1)  
Data file Scans MbtL.txt

