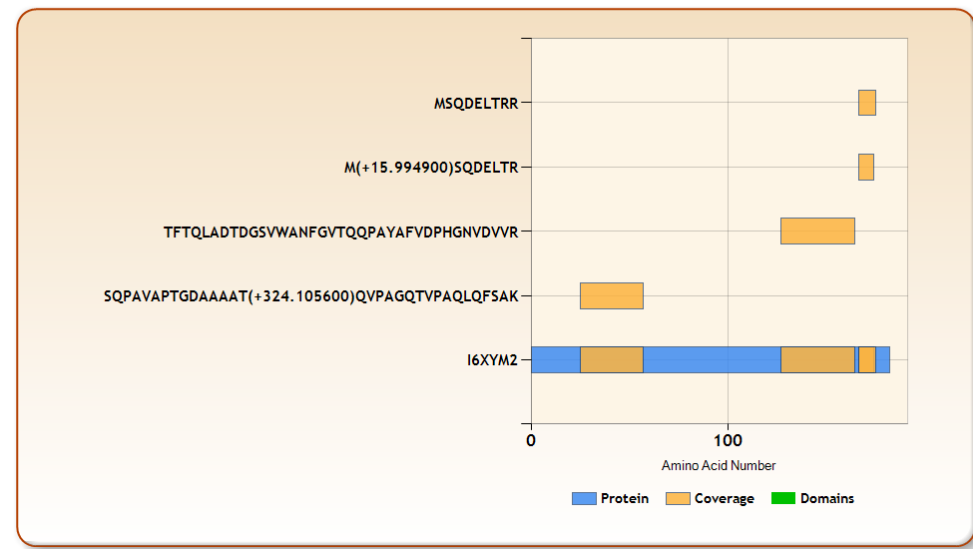


Probable conserved lipoprotein DsbF (Rv1677) Modification: Hex-Hex

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-5.sqt	23510	4	True	4023.931051	4022.930772	-0.76318	3.7776	12.5207833903699	0.5146	48	0.63195	K.TFTQLADTDGSVWVWVNGVVTQQPAYAFVDPHGNDVVR.G
171213_PT_H37Rv_1-5.sqt	23537	3	True	4025.932224	4022.930772	-2.13565	3.23	11.2660653870387	0.5172	34	0.61561	K.TFTQLADTDGSVWVWVNGVVTQQPAYAFVDPHGNDVVR.G
171213_PT_H37Rv_1-5.sqt	14987	3	True	3403.688206	3402.691054	-1.82097	3.433	9.45752050111863	0.4195	28	0.53295	K.SQPAVAPTGDAAAAT(+324.105600)QVPAGQTVPAQLQFSAK.T
171213_PT_H37Rv_1-5.sqt	5339	2	True	995.445299	995.446222	-0.92722	1.3154	0.179126665897435	0.274	7	0.37592	R.M(+15.994900)SQDELTR.R
171213_PT_H37Rv_1-5.sqt	6210	3	True	1135.551226	1135.552433	-1.06292	1.6862	0.603306476560156	0.1518	12	0.33335	R.MSQDELTRR.V

All peptide labels Infer Domains

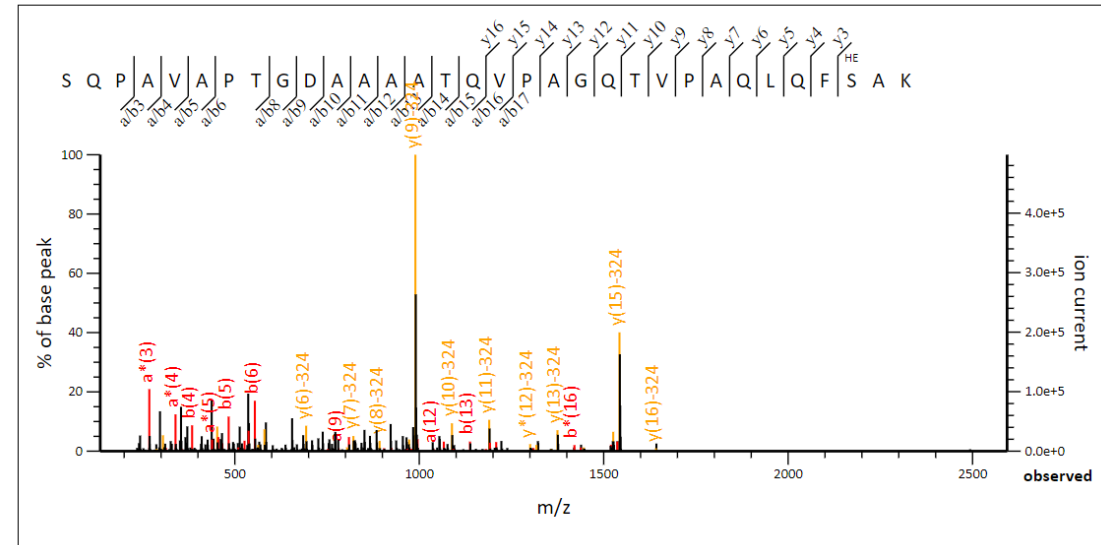


Peptide View

MS/MS Fragmentation of **SQPAVAPTGDAAAATQVPAGQTVPAQLQFSAK**
Found in **AFE16571.1** in **NCBIprot**, putative lipoprotein DSBF [Mycobacterium tuberculosis RGTB327]

Match to Query 4: 3401.680930 from(3402.688206,1+) index(1)
Data file Scans DsbF Hex-Hex Mascot.txt

171213_PT_H37Rv_1-5.sqt
Scan=14987 z=3



Protein family 1 (out of 1)

10 per page 1

Accession contains

Accession	Score	Mass	Matches	Sequences
AFE16571.1	75	19224	2 (2)	putative lipoprotein DSBF [Mycobacterium tuberculosis RGTB327]
1.1 AFE16571.1	75	19224	2 (2)	1 (1) putative lipoprotein DSBF [Mycobacterium tuberculosis RGTB327]

▶ 23 same sets of AFE16571.1

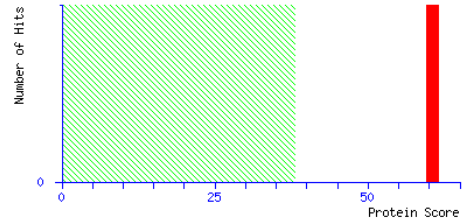
▶ 2 peptide matches (1 non-duplicate, 1 duplicate)

Auto-fit to window

Query	Dupes	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	Peptide
4	1	3402.6882	3401.6809	3401.6838	-0.85	0	48	9.2e-05	1	U	K.SQPAVAPTGDAAAATQVPAGQTVPAQLQFSAK.T + Hex(2) (ST)
3		3402.6834	3401.6762	3401.6838	-2.25	0	(47)	0.00012	1	U	K.SQPAVAPTGDAAAATQVPAGQTVPAQLQFSAK.T + Hex(2) (ST)

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As: Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits: AUTO

Standard scoring: MudPIT scoring Display non-significant matches Show sub-sets: 0

Show pop-ups: Suppress pop-ups Sort unassigned: Decreasing Score Require bold red

Preferred taxonomy: All entries

Select All Select None Search Selected Error tolerant

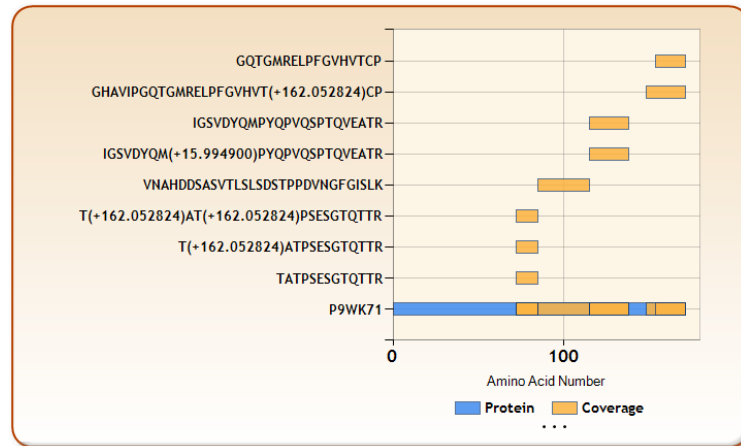
1. [CKZ21714.1](#) Mass: 12789 Score: 61 Matches: 3(3) Sequences: 1(1)
lipoprotein [Mycobacterium tuberculosis]
- Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 1	1336.6320	1335.6247	1335.6266	-1.44	0	(45)	0.017	1	U	R.TATPSESGTQTR.V
<input checked="" type="checkbox"/> 2	1498.6841	1497.6769	1497.6795	-1.75	0	61	0.00034	1	U	R.TATPSESGTQTR.V + Hex (ST)
<input checked="" type="checkbox"/> 3	1660.7371	1659.7298	1659.7323	-1.49	0	(48)	0.0048	1	U	R.TATPSESGTQTR.V + 2 Hex (ST)

[Sequence Explorer](#)

Fasta Coverage Protein Coverage Group view

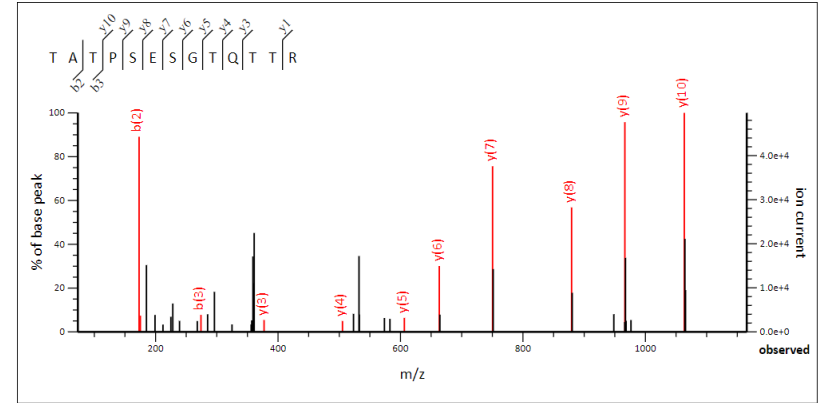
All peptide labels Infer Domains



Lipoprotein O (LppO, Rv2290) Modification: Hex

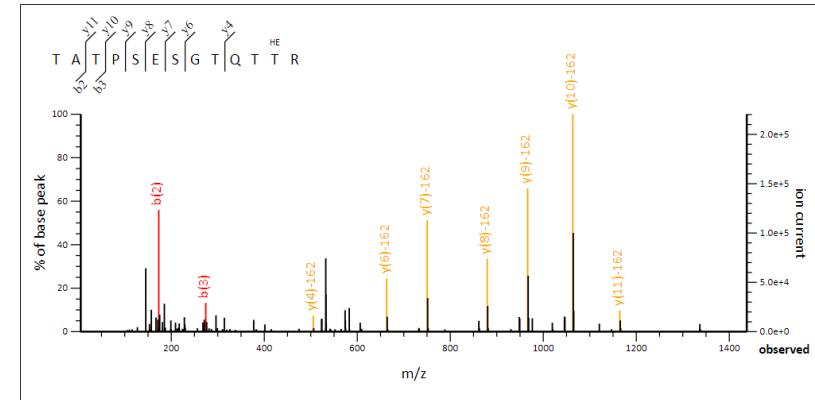
Match to Query 1: 1335.624730 from(1336.632006,1+) index(2)
Data file P9WK71 R1-5.txt

171213_PT_H37Rv_1-5.sqt
Scan=3796 z=2



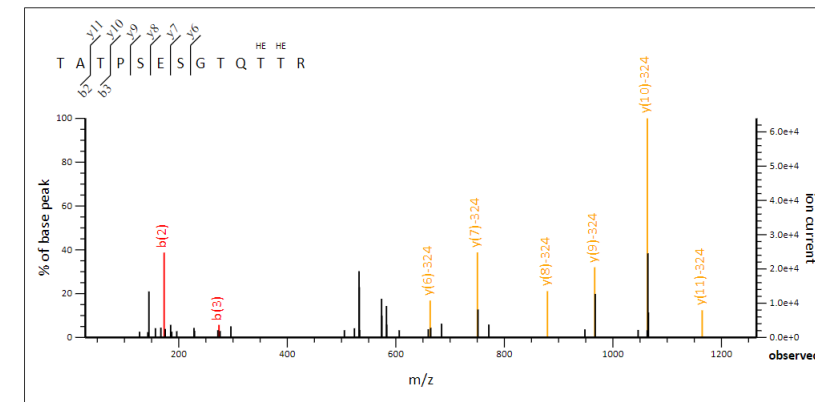
Match to Query 2: 1497.676854 from(1498.684130,1+) index(1)
Data file P9WK71 R1-5.txt

171213_PT_H37Rv_1-5.sqt
Scan=3473 z=2



Match to Query 3: 1659.729832 from(1660.737108,1+) index(0)
Data file P9WK71 R1-5.txt

171213_PT_H37Rv_1-5.sqt
Scan=3439 z=2



Periplasmic phosphate-binding lipoprotein PstS1 (Rv0934)

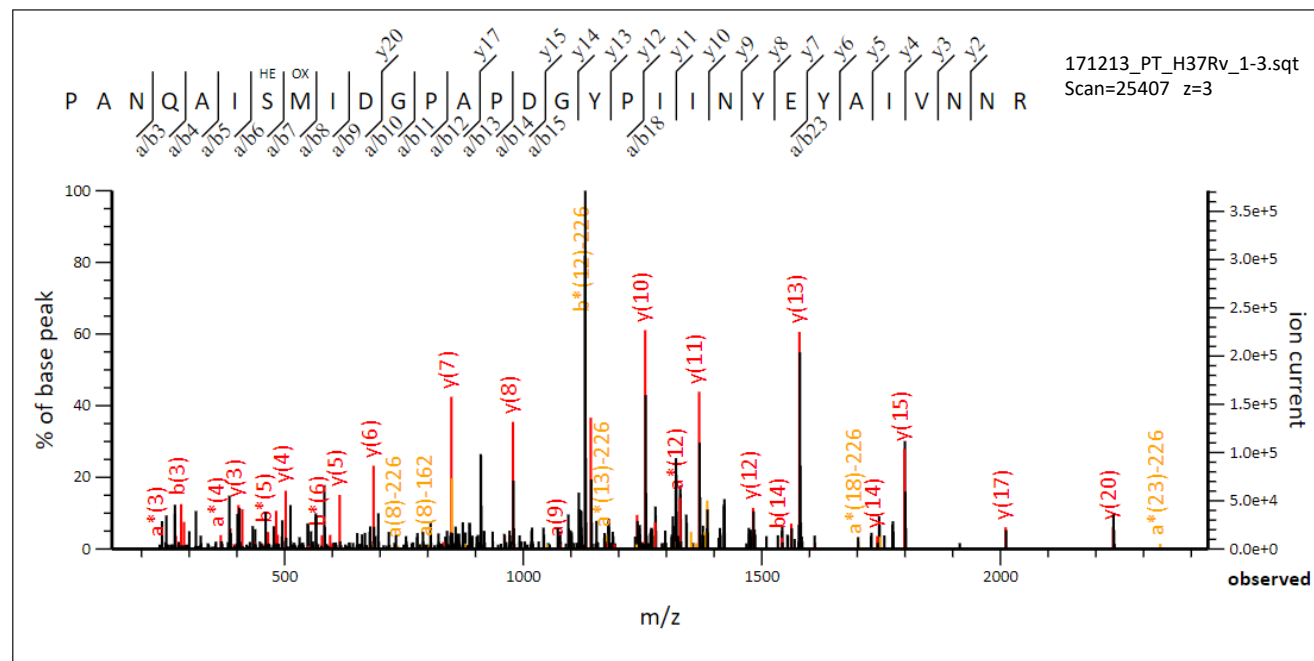
Modification: Hex

MS/MS Fragmentation of **PANQAISMIDGYPDGYPHIINYEYAIVNNR**

Found in **WP_014585113.1** in **NCBIprot**, phosphate ABC transporter substrate-binding protein PstS [Mycobacterium tuberculosis]

Match to Query 3: 3453.638816 from(3454.646092,1+) index(2)

Data file Scans pstS1 Hex Mascot.txt

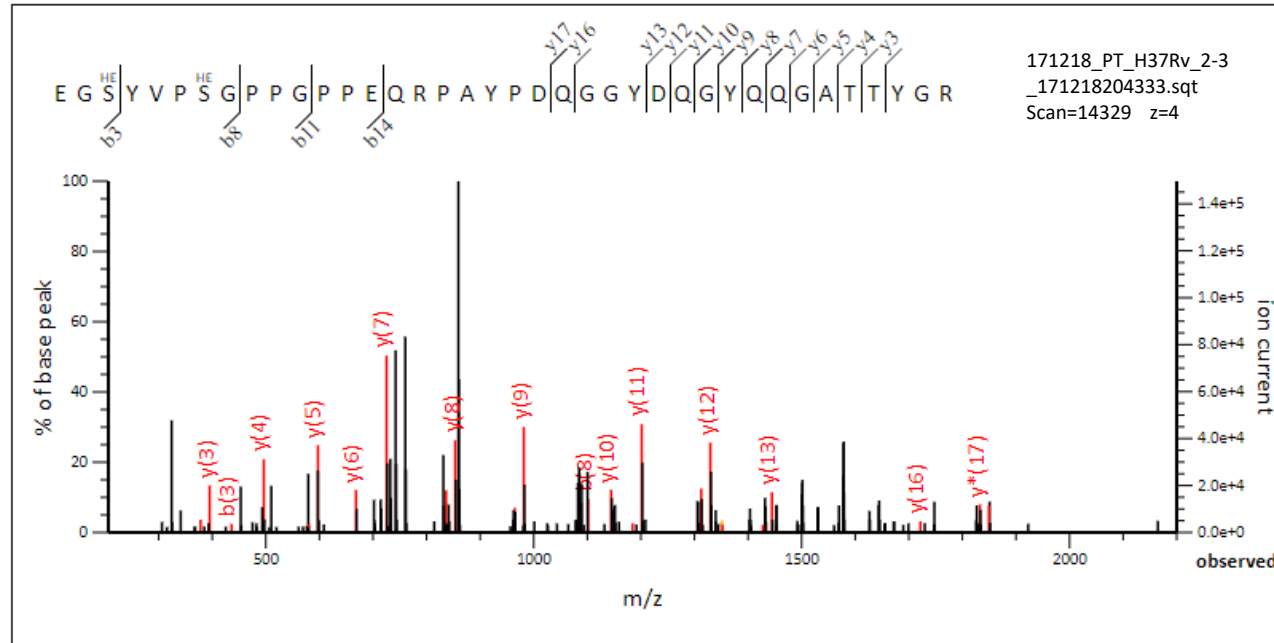


#	a	a*	b	b*	Seq.	y	y*	#
1	70.0651		98.0600		P			30
2	141.1022		169.0972		A	3357.5944	3340.5678	29
3	255.1452	238.1186	283.1401	266.1135	N	3286.5573	3269.5307	28
4	383.2037	366.1772	411.1987	394.1721	Q	3172.5143	3155.4878	27
5	454.2409	437.2143	482.2358	465.2092	A	3044.4557	3027.4292	26
6	567.3249	550.2984	595.3198	578.2933	I	2973.4186	2956.3921	25
7	816.4098	799.3832	844.4047	827.3781	S	2860.3346	2843.3080	24
8	963.4452	946.4186	991.4401	974.4135	M	2611.2497	2594.2232	23
9	1076.5292	1059.5027	1104.5242	1087.4976	I	2464.2143	2447.1878	22
10	1191.5562	1174.5296	1219.5511	1202.5245	D	2351.1303	2334.1037	21
11	1248.5776	1231.5511	1276.5726	1259.5460	G	2236.1033	2219.0768	20
12	1345.6304	1328.6039	1373.6253	1356.5988	P	2179.0818	2162.0553	19
13	1416.6675	1399.6410	1444.6624	1427.6359	A	2082.0291	2065.0025	18
14	1513.7203	1496.6937	1541.7152	1524.6887	P	2010.9920	1993.9654	17
15	1628.7472	1611.7207	1656.7421	1639.7156	D	1913.9392	1896.9127	16
16	1685.7687	1668.7421	1713.7636	1696.7371	G	1798.9123	1781.8857	15
17	1848.8320	1831.8055	1876.8269	1859.8004	Y	1741.8908	1724.8642	14
18	1945.8848	1928.8582	1973.8797	1956.8532	P	1578.8275	1561.8009	13
19	2058.9689	2041.9423	2086.9638	2069.9372	I	1481.7747	1464.7482	12
20	2172.0529	2155.0264	2200.0478	2183.0213	I	1368.6906	1351.6641	11
21	2286.0958	2269.0693	2314.0908	2297.0642	N	1255.6066	1238.5800	10
22	2449.1592	2432.1326	2477.1541	2460.1275	Y	1141.5636	1124.5371	9
23	2578.2018	2561.1752	2606.1967	2589.1701	E	978.5003	961.4738	8
24	2741.2651	2724.2385	2769.2600	2752.2335	Y	849.4577	832.4312	7
25	2812.3022	2795.2757	2840.2971	2823.2706	A	686.3944	669.3678	6
26	2925.3863	2908.3597	2953.3812	2936.3546	I	615.3573	598.3307	5
27	3024.4547	3007.4281	3052.4496	3035.4231	V	502.2732	485.2467	4
28	3138.4976	3121.4711	3166.4925	3149.4660	N	403.2048	386.1783	3
29	3252.5405	3235.5140	3280.5355	3263.5089	N	289.1619	272.1353	2
30					R	175.1190	158.0924	1

Conserved protein with FHA domain, FhaA (Rv0020c)
Modification: Hex

MS/MS Fragmentation of **EGSYVPSGPPGPEQRPAYPDQGGYDQGYQQGATTYGR**
Found in **WP_003912368.1** in **NCBIprot**, phosphopeptide-binding protein [Mycobacterium tuberculosis]

Match to Query 3: 4350.924996 from(4351.932272,1+) index(2)
Data file Scans FhaA Hex-Hex-Hex Mascot.txt



#	a	a*	b	b*	Seq.	y	y*	#
1	102.0550		130.0499		E			38
2	159.0764		187.0713		G	4222.8748	4205.8483	37
3	408.1613		436.1562		S	4165.8534	4148.8268	36
4	571.2246		599.2195		Y	3916.7685	3899.7420	35
5	670.2930		698.2879		V	3753.7052	3736.6786	34
6	767.3458		795.3407		P	3654.6368	3637.6102	33
7	1016.4306		1044.4255		S	3557.5840	3540.5575	32
8	1073.4521		1101.4470		G	3308.4992	3291.4726	31
9	1170.5049		1198.4998		P	3251.4777	3234.4512	30
10	1267.5576		1295.5525		P	3154.4249	3137.3984	29
11	1324.5791		1352.5740		G	3057.3722	3040.3456	28
12	1421.6318		1449.6268		P	3000.3507	2983.3242	27
13	1518.6846		1546.6795		P	2903.2979	2886.2714	26
14	1647.7272		1675.7221		E	2806.2452	2789.2186	25
15	1775.7858	1758.7592	1803.7807	1786.7541	Q	2677.2026	2660.1760	24
16	1931.8869	1914.8603	1959.8818	1942.8553	R	2549.1440	2532.1175	23
17	2028.9397	2011.9131	2056.9346	2039.9080	P	2393.0429	2376.0164	22
18	2099.9768	2082.9502	2127.9717	2110.9451	A	2295.9901	2278.9636	21
19	2263.0401	2246.0136	2291.0350	2274.0085	Y	2224.9530	2207.9265	20
20	2360.0929	2343.0663	2388.0878	2371.0612	P	2061.8897	2044.8631	19
21	2475.1198	2458.0933	2503.1147	2486.0882	D	1964.8369	1947.8104	18
22	2603.1784	2586.1518	2631.1733	2614.1468	Q	1849.8100	1832.7834	17
23	2660.1999	2643.1733	2688.1948	2671.1682	G	1721.7514	1704.7249	16
24	2717.2213	2700.1948	2745.2162	2728.1897	G	1664.7299	1647.7034	15
25	2880.2846	2863.2581	2908.2796	2891.2530	Y	1607.7085	1590.6819	14
26	2995.3116	2978.2850	3023.3065	3006.2800	D	1444.6452	1427.6186	13
27	3123.3702	3106.3436	3151.3651	3134.3385	Q	1329.6182	1312.5917	12
28	3180.3916	3163.3651	3208.3865	3191.3600	G	1201.5596	1184.5331	11
29	3343.4550	3326.4284	3371.4499	3354.4233	Y	1144.5382	1127.5116	10
30	3471.5135	3454.4870	3499.5085	3482.4819	Q	981.4748	964.4483	9
31	3599.5721	3582.5456	3627.5670	3610.5405	Q	853.4163	836.3897	8
32	3656.5936	3639.5670	3684.5885	3667.5619	G	725.3577	708.3311	7
33	3727.6307	3710.6041	3755.6256	3738.5991	A	668.3362	651.3097	6
34	3828.6784	3811.6518	3856.6733	3839.6467	T	597.2991	580.2726	5
35	3929.7261	3912.6995	3957.7210	3940.6944	T	496.2514	479.2249	4
36	4092.7894	4075.7628	4120.7843	4103.7577	Y	395.2037	378.1772	3
37	4149.8108	4132.7843	4177.8058	4160.7792	G	232.1404	215.1139	2
38					R	175.1190	158.0924	1

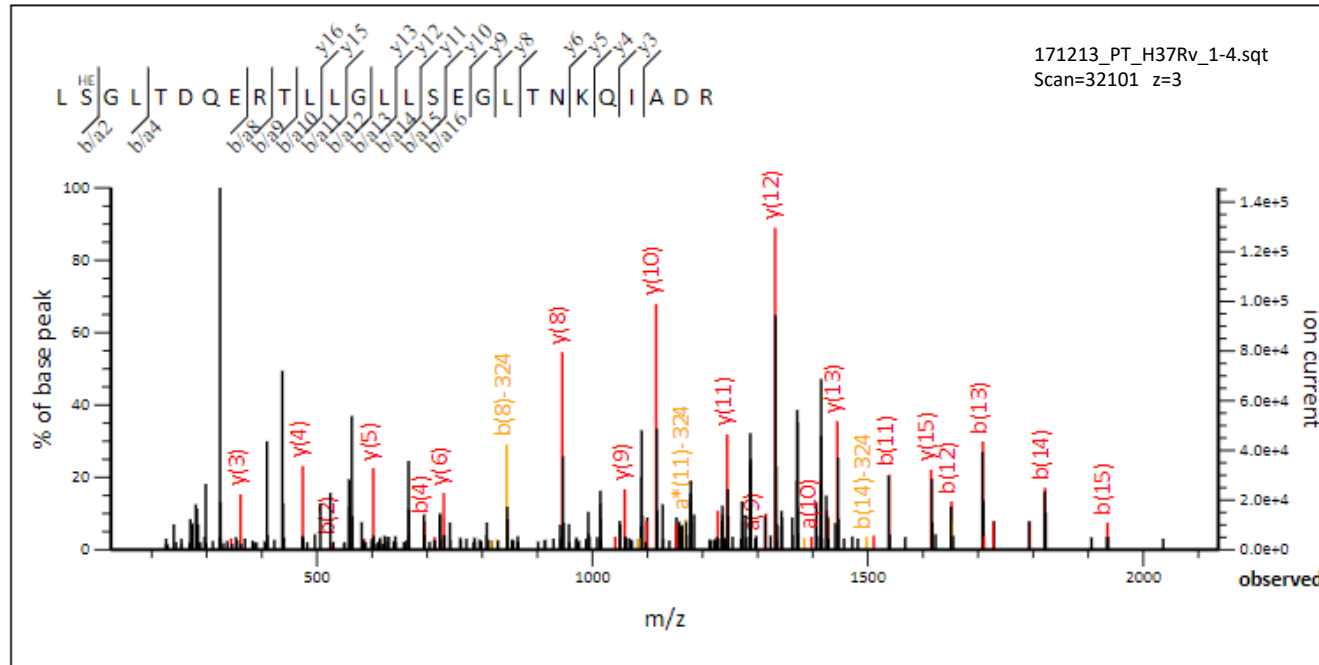
Two component transcriptional regulatory protein DevR (Rv3133c) Modification: Hex-Hex

MS/MS Fragmentation of **LSGLTDQERTLLGLLSEGLTNKQIADR**

Found in **AFE17937.1** in **NCBIprot**, two component transcriptional regulatory protein [Mycobacterium tuberculosis RGTB327]

Match to Query 3: 3264.691184 from(3265.698460,1+) index(1)

Data file Scans DevR Hex-Hex Mascot.txt



#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		L			27
2	497.2341		525.2290		S	3152.6169	3135.5903	26
3	554.2556		582.2505		G	2741.4792	2724.4527	25
4	667.3396		695.3345		L	2684.4577	2667.4312	24
5	768.3873		796.3822		T	2571.3737	2554.3471	23
6	883.4143		911.4092		D	2470.3260	2453.2994	22
7	1011.4728	994.4463	1039.4677	1022.4412	Q	2355.2990	2338.2725	21
8	1140.5154	1123.4889	1168.5103	1151.4838	E	2227.2405	2210.2139	20
9	1296.6165	1279.5900	1324.6114	1307.5849	R	2098.1979	2081.1713	19
10	1397.6642	1380.6377	1425.6591	1408.6326	T	1942.0968	1925.0702	18
11	1510.7483	1493.7217	1538.7432	1521.7166	L	1841.0491	1824.0225	17
12	1623.8323	1606.8058	1651.8273	1634.8007	L	1727.9650	1710.9385	16
13	1680.8538	1663.8273	1708.8487	1691.8222	G	1614.8810	1597.8544	15
14	1793.9379	1776.9113	1821.9328	1804.9062	L	1557.8595	1540.8329	14
15	1907.0219	1889.9954	1935.0168	1917.9903	L	1444.7754	1427.7489	13
16	1994.0540	1977.0274	2022.0489	2005.0223	S	1331.6914	1314.6648	12
17	2123.0966	2106.0700	2151.0915	2134.0649	E	1244.6593	1227.6328	11
18	2180.1180	2163.0915	2208.1129	2191.0864	G	1115.6167	1098.5902	10
19	2293.2021	2276.1755	2321.1970	2304.1704	L	1058.5953	1041.5687	9
20	2394.2498	2377.2232	2422.2447	2405.2181	T	945.5112	928.4847	8
21	2508.2927	2491.2661	2536.2876	2519.2611	N	844.4635	827.4370	7
22	2636.3876	2619.3611	2664.3826	2647.3560	K	730.4206	713.3941	6
23	2764.4462	2747.4197	2792.4411	2775.4146	Q	602.3257	585.2991	5
24	2877.5303	2860.5037	2905.5252	2888.4987	I	474.2671	457.2405	4
25	2948.5674	2931.5409	2976.5623	2959.5358	A	361.1830	344.1565	3
26	3063.5943	3046.5678	3091.5893	3074.5627	D	290.1459	273.1193	2
27					R	175.1190	158.0924	1

Probable chaperone protein DnaK (heat shock 70 kDa protein) (Rv0350) Modification: Hex

File Statistics Tools
Control Follow up Result Browser

Spec FDR: 37 / 31498 = 0.12% Pep FDR: 20 / 16716 = 0.12% Prot FDR: 15 / 1515 = 0.99% # Prot (Max Parsimony): 1494 Unique Prot: 1494 Unlabeled Decoys: 0 / 0

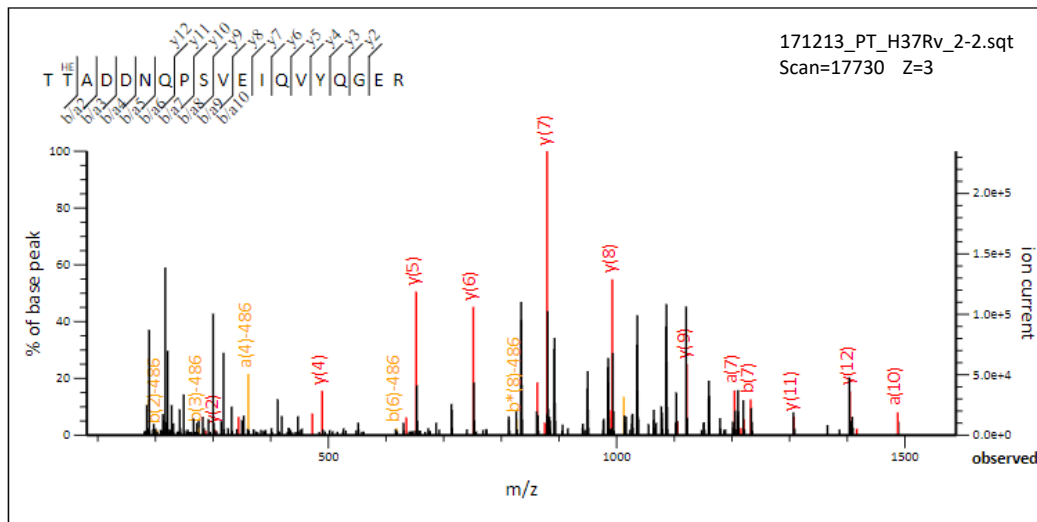
View mode: Proteins Proteins Max Pars Peptides Scans

Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description	
1	P9WMJ9	390	Unique	625	98	66772.3	98	488	0.00748752008761512	0.8992	1509.3163	Chaperone protein DnaK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dnaK PE=1 SV=1

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
60 171213_PT_H37Rv_2-2.sqt	25666	3	True	2461.292053	2461.297318	-2.13912	3.4778	13.9803852011545	0.5712	27	0.85316	N.LPYITVDADKNPLFLDEQLTRA
61 171213_PT_H37Rv_2-2.sqt	37067	3	True	2998.528172	2998.53275	-1.52675	2.8112	8.28608147045285	0.5301	29	0.85249	R.AVGIDLGTNSVSVLEGGDPVWVANSEGSRT
62 171213_PT_H37Rv_2-2.sqt	27075	4	True	3909.032858	3907.033505	-1.87949	4.6529	10.0519875608546	0.4877	46	0.85128	K.AKIELSSQSTINLPYITVDADKNPLFLDEQLTRA
63 171213_PT_H37Rv_2-2.sqt	26709	3	True	2999.540928	2998.53275	1.60958	3.6122	10.854054620534	0.5095	32	0.85102	R.AVGIDLGTNSVSVLEGGDPVWVANSEGSRT
64 171213_PT_H37Rv_2-2.sqt	26909	4	True	4271.256491	4269.247355	0.57032	4.1619	7.86226722367649	0.3927	44	0.85067	M.ARAVGIDLGTNSVSVLEGGDPVWVANSEGRTPPSIVAFARN
65 171213_PT_H37Rv_2-2.sqt	12707	4	True	3199.433737	3198.431867	-0.46258	5.0243	16.3500277083056	0.5868	43	0.85065	A.SQATGAHPGGEPGAHPGSAADDVDAEVDVDDGR E
66 171213_PT_H37Rv_2-2.sqt	17730	3	True	2636.184055	2635.174016	2.53738	3.0236	6.57845153183954	0.3888	21	0.84933	F.TT(+486.158400)ADDNQPSVQIQVYQGER.E

MS/MS Fragmentation of **TTADDNQPSVEIQVYQGER**
Found in **CND86259.1** in **NCBIprot**, Chaperone protein DnaK (Hsp 70) [Mycobacterium tuberculosis]

Match to Query 2: 2635.176779 from(2636.184055,1+) index(0)
Data file scans dnaK Hex-Hex-Hex Mascot.txt



#	a	a*	b	b*	Seq.	y	y*	#
1	74.0600		102.0550		T			19
2	661.2662		689.2611		T	2535.1104	2518.0839	18
3	732.3033		760.2982		A	1947.9043	1930.8777	17
4	847.3302		875.3252		D	1876.8672	1859.8406	16
5	962.3572		990.3521		D	1761.8402	1744.8137	15
6	1076.4001	1059.3736	1104.3950	1087.3685	N	1646.8133	1629.7867	14
7	1204.4587	1187.4321	1232.4536	1215.4271	Q	1532.7703	1515.7438	13
8	1301.5115	1284.4849	1329.5064	1312.4798	P	1404.7118	1387.6852	12
9	1388.5435	1371.5169	1416.5384	1399.5119	S	1307.6590	1290.6325	11
10	1487.6119	1470.5854	1515.6068	1498.5803	V	1220.6270	1203.6004	10
11	1616.6545	1599.6279	1644.6494	1627.6229	E	1121.5586	1104.5320	9
12	1729.7386	1712.7120	1757.7335	1740.7069	I	992.5160	975.4894	8
13	1857.7971	1840.7706	1885.7921	1868.7655	Q	879.4319	862.4054	7
14	1956.8656	1939.8390	1984.8605	1967.8339	V	751.3733	734.3468	6
15	2119.9289	2102.9023	2147.9238	2130.8972	Y	652.3049	635.2784	5
16	2247.9875	2230.9609	2275.9824	2258.9558	Q	489.2416	472.2150	4
17	2305.0089	2287.9824	2333.0038	2315.9773	G	361.1830	344.1565	3
18	2434.0515	2417.0250	2462.0464	2445.0199	E	304.1615	287.1350	2
19					R	175.1190	158.0924	1

Probable transmembrane carbonic anhydrase Rv3273 (Rv3273)

Modification: Hex-Hex-Hex

Filter :: Search Engine Processor (SEPro - for PSMs)

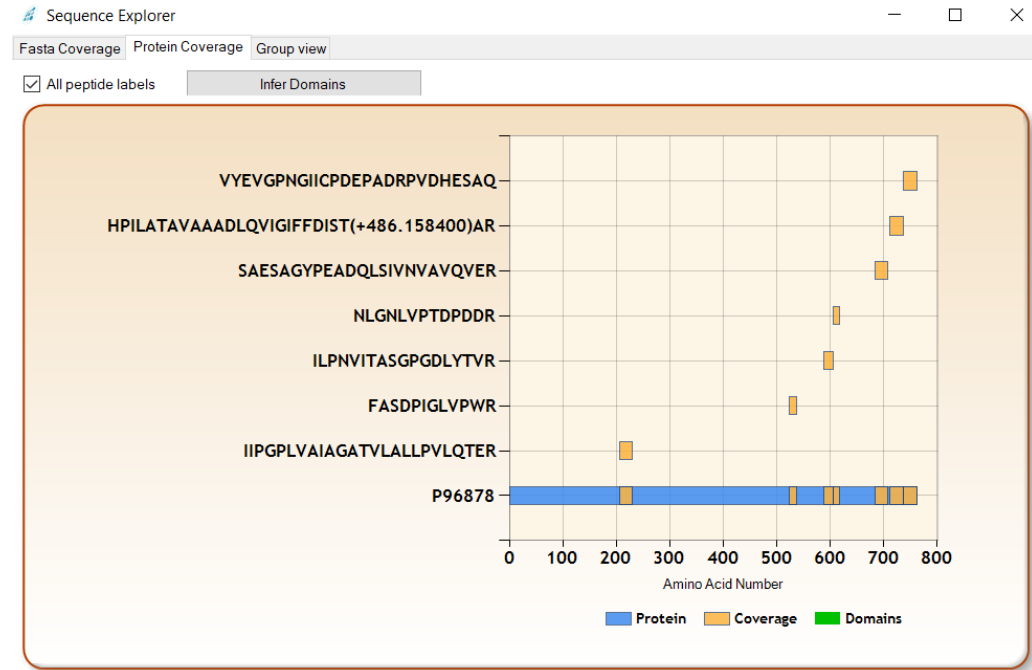
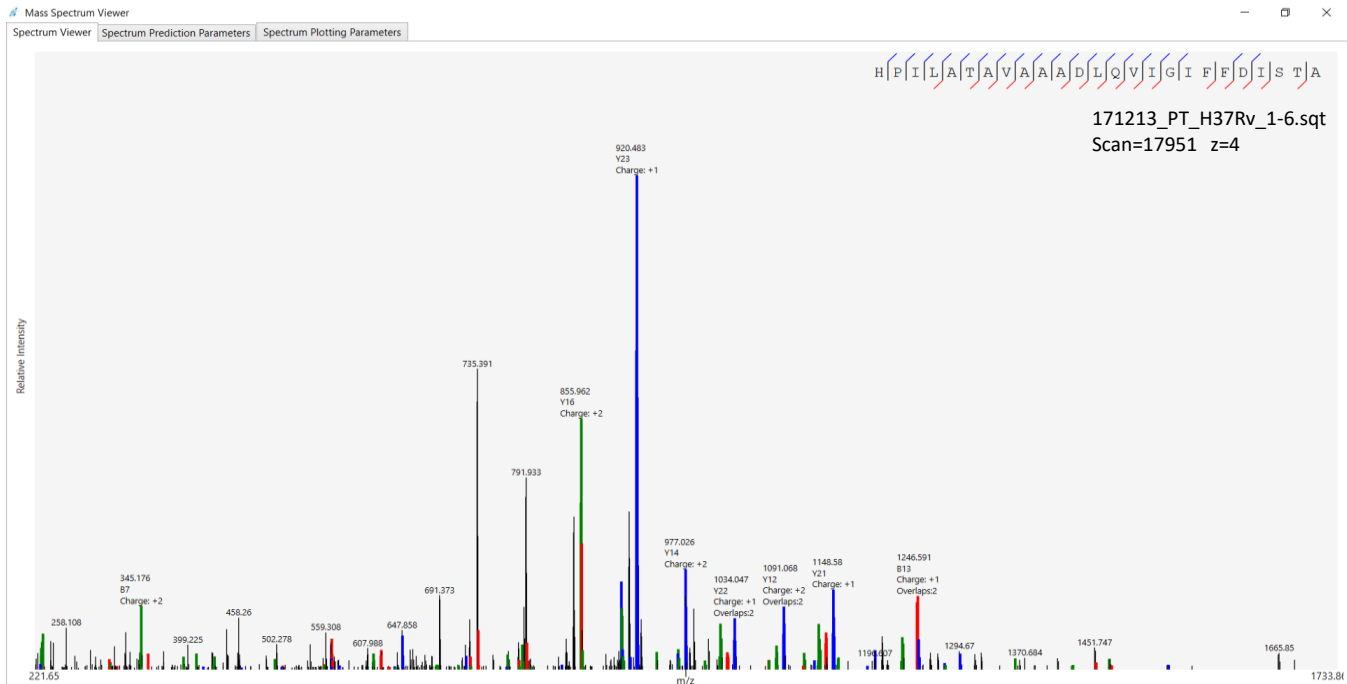
File Statistics Tools
Control Follow up Result Browser

Spec FDR: 49 / 36000 = 0.14% Pep FDR: 24 / 17635 = 0.14% Prot FDR: 15 / 1505 = 1% # Prot (Max Parsimony): 1487 Unique Prot: 1482 Unlabeled Decoys: 0 / 0

View mode: Proteins Proteins Max Pars Peptides Scans Rv3273

GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1 Unique	764	7	80497.1	7	11	0.000123414288781237	0.1728	30.9285	Probable transmembrane carbonic anhydrase (Carbonate dehydratase) (Carbonic dehydratase) OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3273 PE=1 SV=2

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-4.sqt	16134	3	True	2865.310154	2864.31556	-3.05586	3.2453	9.98036859687209	0.5101	27	0.8811	R.VYEVGPNIGICPDEADRPVDHESQA-
171213_PT_H37Rv_1-4.sqt	24164	3	True	2532.257916	2532.257638	0.10978	3.9406	16.5785450673992	0.5792	28	0.62509	R.SAESAGYPEADQLSIVNVAQVER.L
171213_PT_H37Rv_1-4.sqt	22480	2	True	1886.034742	1886.03819	-1.82617	2.9223	9.38827158046884	0.5969	22	0.60742	R.ILPNVITASGPGDLYTVR.N
171213_PT_H37Rv_1-4.sqt	24195	2	True	2534.260058	2532.257638	-1.68886	3.085	11.5444161320616	0.5075	20	0.53697	R.SAESAGYPEADQLSIVNVAQVER.L
171213_PT_H37Rv_1-4.sqt	16911	2	True	1425.693385	1425.696848	-2.42899	2.6798	7.55592909389935	0.4837	16	0.52171	R.NLGNLVPTDPDDR.S
171213_PT_H37Rv_1-1.sqt	44996	3	True	2526.548924	2525.542908	1.05519	1.7869	1.45243416362444	0.3143	19	0.41375	R.IIPGPLVAIAGATVLLALLPVLTQTER.I
171213_PT_H37Rv_1-6.sqt	17951	4	True	3196.626557	3196.651064	-7.66652	2.9672	1.22077992264232	0.2011	31	0.37945	R.HPILATAVAAADLQVIGIFFDIST(+486.158400)AR.V
171213_PT_H37Rv_1-5.sqt	19314	4	True	3196.630365	3196.651064	-6.47526	2.9064	-0.22314355131421	0.1369	30	0.37126	R.HPILATAVAAADLQVIGIFFDIST(+486.158400)AR.V
171213_PT_H37Rv_1-3.sqt	23086	4	True	3196.630882	3196.651064	-6.31352	2.7563	-0.139761942375159	0.0895	30	0.36972	R.HPILATAVAAADLQVIGIFFDIST(+486.158400)AR.V
171213_PT_H37Rv_1-2.sqt	23433	4	True	3196.629441	3196.651064	-6.76431	2.619	-1.03673688495002	0.0557	29	0.3633	R.HPILATAVAAADLQVIGIFFDIST(+486.158400)AR.V
171213_PT_H37Rv_1-4.sqt	25248	2	True	1358.722826	1357.726298	-5.02089	2.0197	3.04282388108784	0.3802	13	0.86206	H.FASDPIGLVPWR.S



Probable isocitrate dehydrogenase [NADP] Icd2 (Rv0066c)

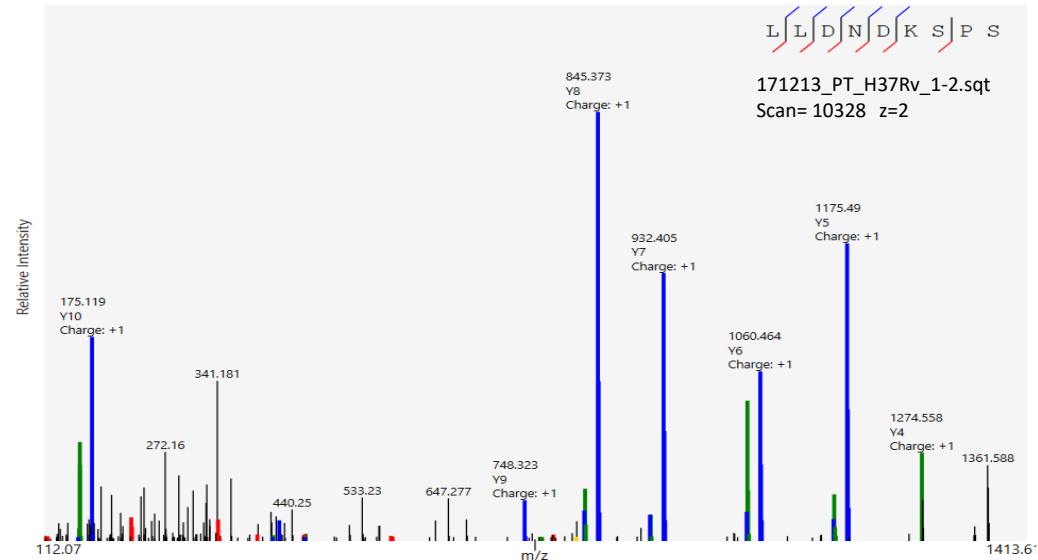
Modification: Hex-Hex-Hex

File	Statistics	Tools									
Control Follow up Result Browser											
Spec FDR: 49 / 36000 = 0.14% Pep FDR: 24 / 17635 = 0.14% Prot FDR: 15 / 1505 = 1% # Prot (Max Parsimony): 1487 Unique Prot: 1482 Unlabeled Decoys: 0 / 0											
View mode: <input checked="" type="radio"/> Proteins <input type="radio"/> Proteins Max Pars <input type="radio"/> Peptides <input type="radio"/> Scans <input type="radio"/> Icd2											
Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1_053611	2	Unique	745	70	82479.6	70	143	0.00164530297473188	0.8148	426.9556	isocitrate dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=icd2 PE=1 SV=1

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-1.sqt	9824	3	True	1640.739505	1640.742041	-1.54564	2.5435	6.3367757323964	0.4812	26	0.52035	R.KHPHSMGEWMSMASR.T
171213_PT_H37Rv_1-1.sqt	9850	4	True	1807.829272	1807.832643	-1.86467	2.8478	3.5648934743295	0.3102	26	0.40338	R.CHEHRPELAMVDSAR.G
171213_PT_H37Rv_1-1.sqt	9853	2	True	1640.741747	1640.742041	-0.17919	2.3621	11.45465656568463	0.6184	16	0.60275	R.KHPHSMGEWMSMASR.T
171213_PT_H37Rv_1-1.sqt	9877	4	True	1640.739068	1640.742041	-1.81199	1.8825	0.0747235461959364	0.2233	24	0.37579	R.KHPHSMGEWMSMASR.T
171213_PT_H37Rv_1-3.sqt	10270	2	True	1632.744163	1630.754078	-10.17612	1.6712	-1.30251275218084	0.0955	9	0.30473	K.LLDNDKSPS(+486.158400)R.K
171213_PT_H37Rv_1-2.sqt	10328	2	True	1632.745375	1630.754078	-9.4339	1.9178	0.619896718820353	0.1459	11	0.30923	K.LLDNDKSPS(+486.158400)R.K
171213_PT_H37Rv_1-2.sqt	10354	2	True	788.450629	788.451245	-0.78128	1.3248	-2.00821403239147	0.1581	9	0.3438	K.TLDAAGK.L
171213_PT_H37Rv_1-1.sqt	10652	2	True	789.452379	788.451245	-2.80701	1.6396	1.8578992717326	0.2814	9	0.38279	K.TLDAAGK.L
171213_PT_H37Rv_1-1.sqt	10681	2	True	788.450497	788.451245	-0.9487	1.4266	0.202116184122134	0.2568	9	0.35368	K.TLDAAGK.L
171213_PT_H37Rv_1-2.sqt	11345	4	True	1318.734525	1318.737866	-2.53349	2.2022	2.44992568089275	0.2692	26	0.41477	K.VSHPIVFGHAVR.I
171213_PT_H37Rv_1-1.sqt	11452	4	True	1318.734595	1318.737866	-2.40041	2.4445	3.11226608980994	0.3324	26	0.4476	K.VSHPIVFGHAVR.I
171213_PT_H37Rv_1-1.sqt	11463	3	True	1318.736951	1318.737866	-0.69385	2.637	6.05333995082607	0.4563	20	0.51641	K.VSHPIVFGHAVR.I
171213_PT_H37Rv_1-1.sqt	11557	2	True	1318.735295	1318.737866	-1.9496	2.2498	4.6831317274578	0.3506	11	0.4507	K.VSHPIVFGHAVR.I
171213_PT_H37Rv_1-1.sqt	12496	2	True	1107.542331	1107.542914	-0.52639	2.3404	8.73410619297981	0.5606	12	0.58235	K.AVNPSTFSR.I

Mass Spectrum Viewer

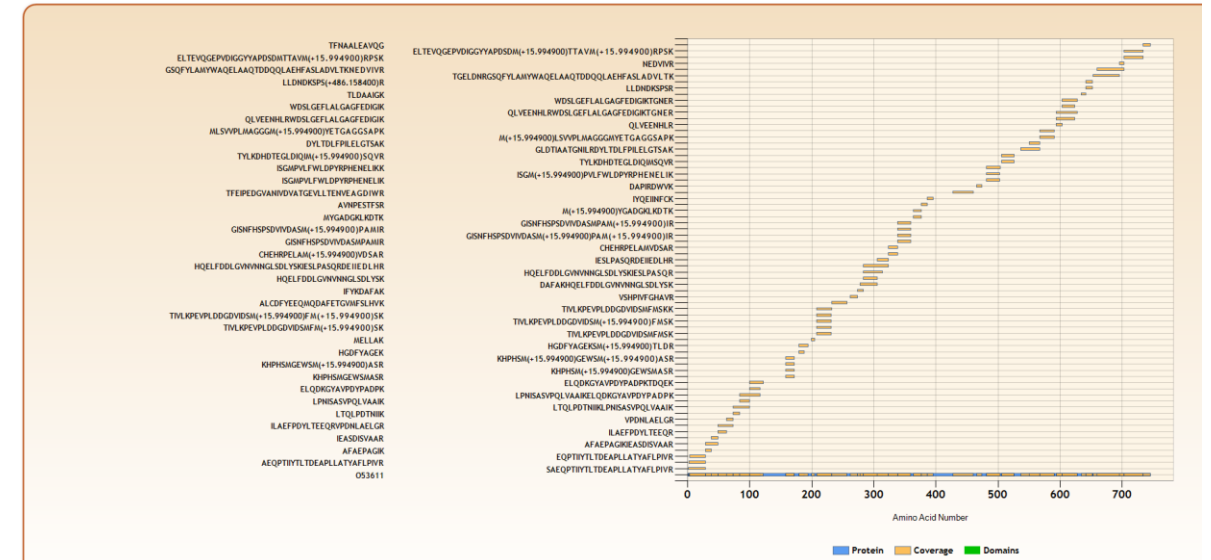
Spectrum Viewer Spectrum Prediction Parameters Spectrum Plotting Parameters



Sequence Explorer

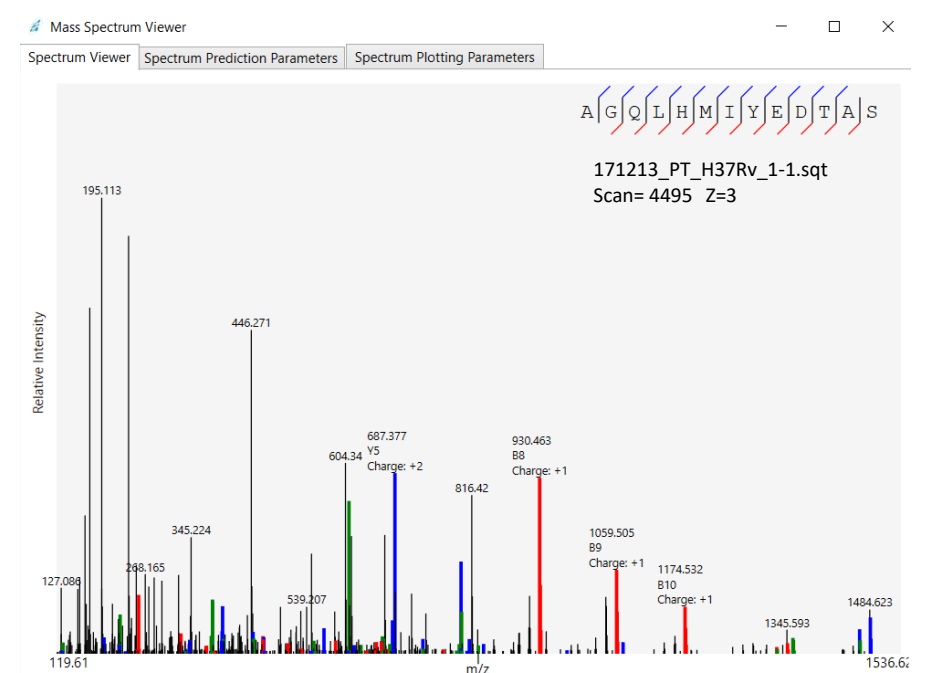
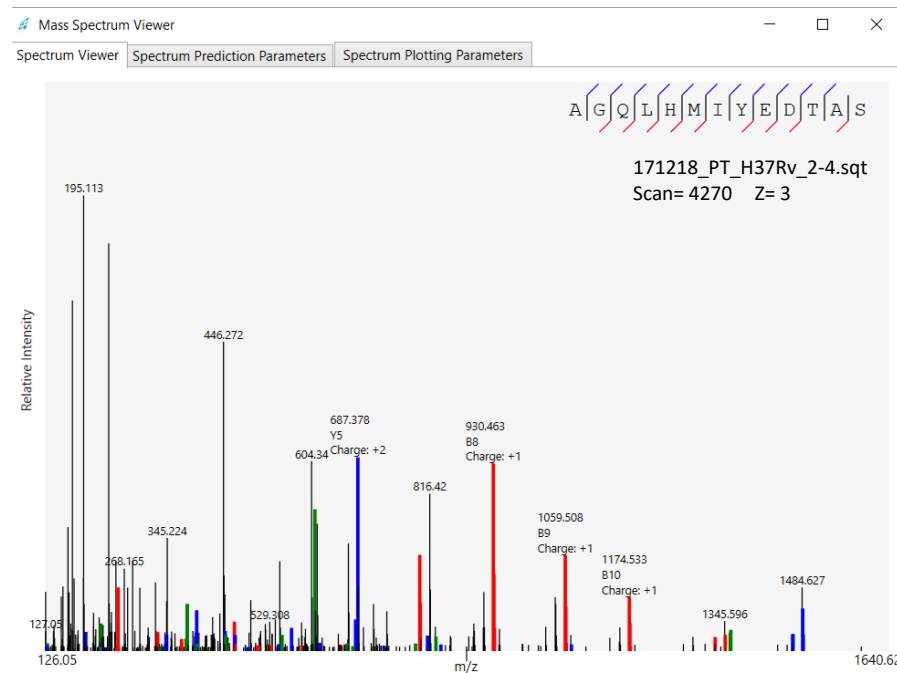
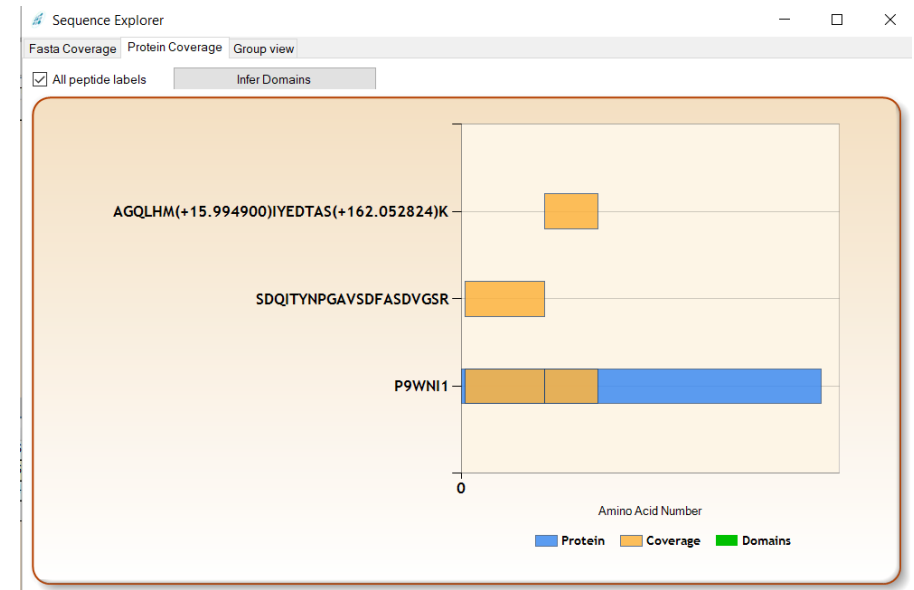
Fasta Coverage Protein Coverage Group view

All peptide labels Infer Domains



ESAT-6 like protein EsxC (Rv3890c) Modification: Hex

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_2-6.sqt	15515	2	True	2186.00048	2185.999632	0.1903	3.4083	11.9813303728523	0.5915	20	0.76328	M.SDQITYNPGAVSDFASDVGSRA
171213_PT_H37Rv_2-6.sqt	15526	3	True	2185.998203	2185.999632	-0.65371	2.705	6.48248754357779	0.5006	25	0.74421	M.SDQITYNPGAVSDFASDVGSRA
171218_PT_H37Rv_2-4.sqt	4270	3	True	1741.790379	1741.794893	-2.59159	2.2142	2.59160138845896	0.3148	15	0.33938	R.AGQLHM(+15.994900)IYEDTAS(+162.052824)K.T
171213_PT_H37Rv_2-1.sqt	4565	3	True	1741.789708	1741.794893	-2.97682	2.1344	2.57046453814965	0.2736	15	0.3278	R.AGQLHM(+15.994900)IYEDTAS(+162.052824)K.T



Probable adenosylhomocysteinase SahH (AhcY) (Rv3248c)

Modification: Hex

File Statistics Tools
Control Follow up Result Browser

Spec FDR: 37 / 31147 = 0.12% Pep FDR: 22 / 16603 = 0.13% Prot FDR: 15 / 1509 = 0.99% # Prot (Max Parsimony): 1488 Unique Prot: 1486 Unlabeled Decoys: 0 / 0

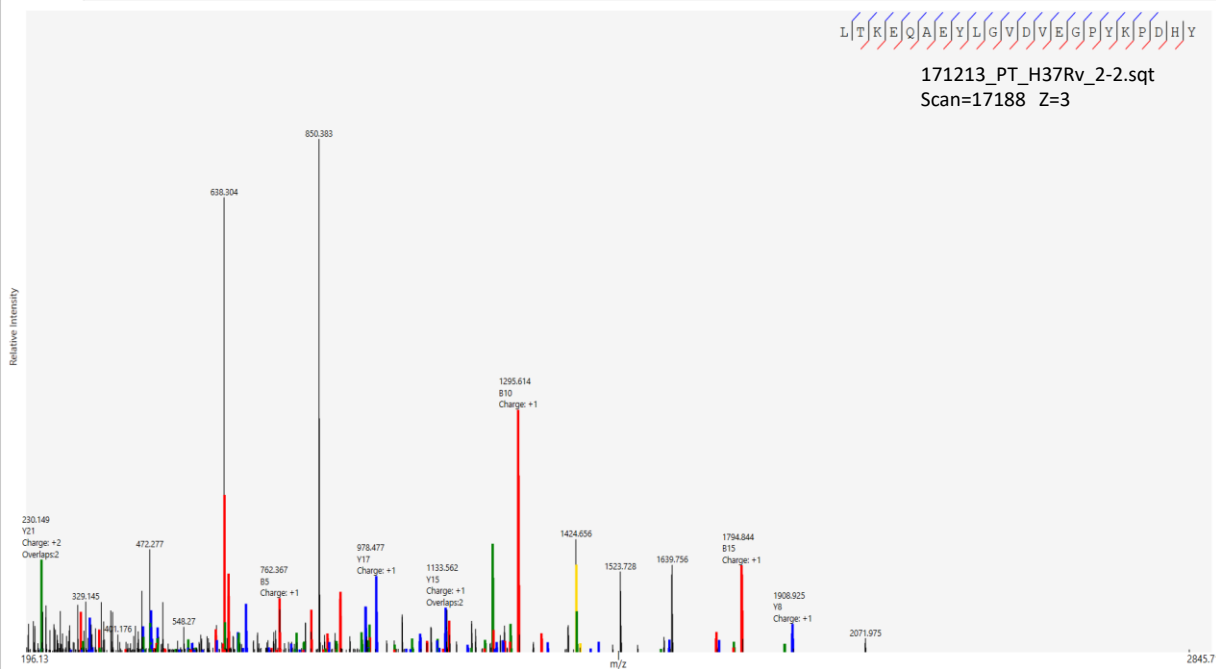
View mode: Proteins Proteins Max Pars Peptides Scans Ahc

pepctumCount	NSAF	Coverage	Protein Score	Description
17	0.00286976490106402	0.7576	429.7266	Adenosylhomocysteinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ahcY PE=1 SV=1

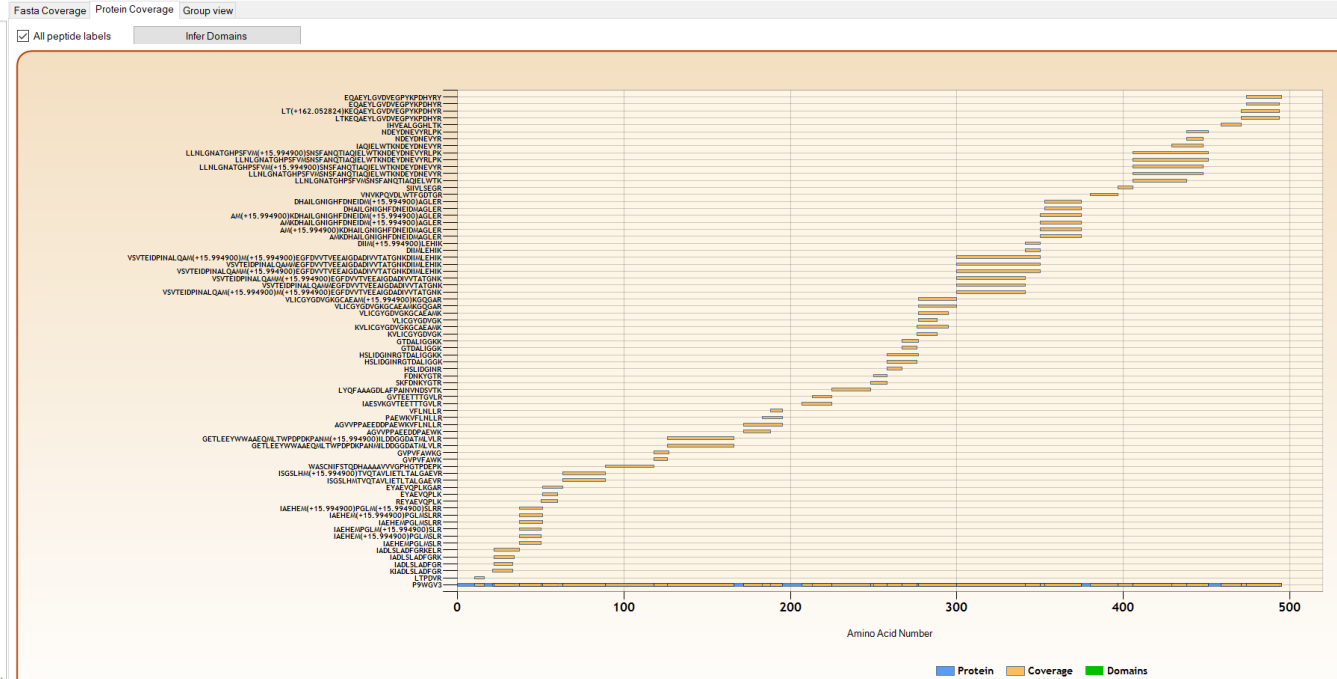
File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_2-2.sqt	19852	3	True	1703.942395	1703.943895	-0.88031	2.5693	2.23492644452023	0.2307	21	0.34125	K.IADLSLADFGRKELR I
171213_PT_H37Rv_2-2.sqt	15132	3	True	1890.016683	1890.017848	-0.6164	4.6398	13.7478519094905	0.5602	29	0.63567	K.IAESVKGVTTEITTVGLRL
171213_PT_H37Rv_2-2.sqt	15704	3	True	1890.019932	1890.017848	1.10263	3.9995	11.0682396437088	0.4863	30	0.55449	K.IAESVKGVTTEITTVGLRL
171213_PT_H37Rv_2-2.sqt	15158	2	True	1890.016343	1890.017848	-0.79629	3.8123	9.25533773790692	0.4951	24	0.53721	K.IAESVKGVTTEITTVGLRL
171213_PT_H37Rv_2-2.sqt	13411	3	True	1308.696873	1308.698031	-0.88485	2.7638	8.97132347150568	0.4936	23	0.52891	K.KVLCYGVGVGK G
171213_PT_H37Rv_2-2.sqt	17188	3	True	2870.396264	2869.389046	1.34755	2.1728	0.715392789507265	0.1657	24	0.33857	K.LT(+162_052824)KEQAEVLGVVDEGPKPDHYR.Y
171213_PT_H37Rv_2-2.sqt	17161	4	True	2870.398478	2869.389046	2.11887	2.8529	2.6200393237795	0.2192	34	0.34759	K.LT(+162_052824)KEQAEVLGVVDEGPKPDHYR.Y
171213_PT_H37Rv_2-2.sqt	14930	3	True	1654.771344	1654.770742	0.3638	3.1164	6.87819647674059	0.431	19	0.48468	K.NDEYDVEYRLPK.H

Mass Spectrum Viewer

Spectrum Viewer Spectrum Prediction Parameters Spectrum Plotting Parameters

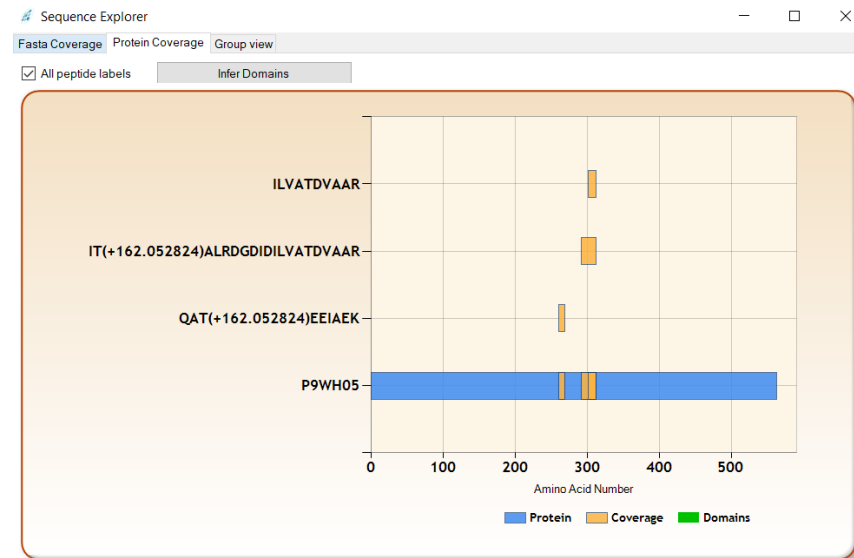


Sequence Explorer



Probable cold-shock DeaD-box protein A homolog DeaD (Rv1253) Modification: Hex

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_2-2.sqt	26209	3	True	2260.216892	2260.203083	6.10959	3.6222	9.04482593349861	0.4626	29	0.73782	T.IT(+162.052824)ALRDGDIDILVATDVAAR.G
171213_PT_H37Rv_2-1.sqt	27626	3	True	2261.225071	2260.203083	8.24243	3.1385	7.3697907385787	0.4117	23	0.71018	T.IT(+162.052824)ALRDGDIDILVATDVAAR.G
171213_PT_H37Rv_2-2.sqt	11311	2	True	1181.564388	1180.557955	2.60925	1.7886	0.805196684368568	0.2194	11	0.3386	K.QAT(+162.052824)EEIAEK.L
171213_PT_H37Rv_2-1.sqt	11837	2	True	1181.56621	1180.557955	4.15127	1.627	-1.18172719537862	0.0711	11	0.31228	K.QAT(+162.052824)EEIAEK.L
171213_PT_H37Rv_2-1.sqt	14580	2	True	1028.608446	1028.609871	-1.38537	2.0285	0.959720289801491	0.3592	12	0.68362	D.ILVATDVAAR.G

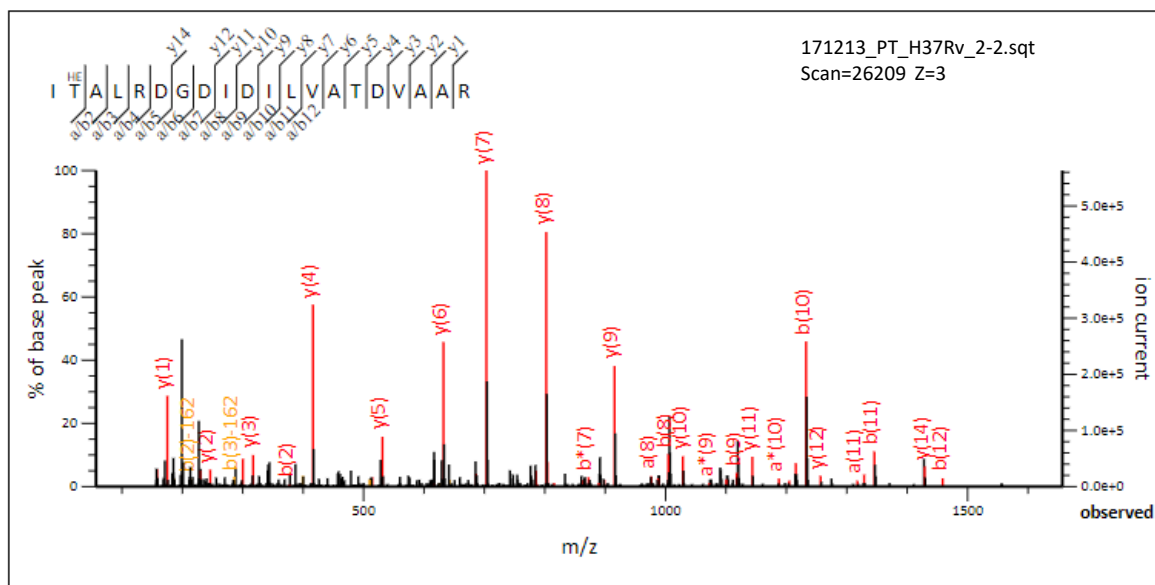


MS/MS Fragmentation of **ITALRDGDIDILVATDVAAR**

Found in **CNW03826.1** in **NCBIprot**, cold-shock DEAD-box protein A [Mycobacterium tuberculosis]

Match to Query 2: 2259.209616 from(2260.216892,1+) index(1)

Data file scans DeaD Hex Mascot.txt



#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		I			20
2	349.1969		377.1918		T	2147.1190	2130.0925	19
3	420.2340		448.2290		A	1884.0185	1866.9920	18
4	533.3181		561.3130		L	1812.9814	1795.9549	17
5	689.4192	672.3927	717.4141	700.3876	R	1699.8973	1682.8708	16
6	804.4462	787.4196	832.4411	815.4145	D	1543.7962	1526.7697	15
7	861.4676	844.4411	889.4625	872.4360	G	1428.7693	1411.7427	14
8	976.4946	959.4680	1004.4895	987.4629	D	1371.7478	1354.7213	13
9	1089.5786	1072.5521	1117.5735	1100.5470	I	1256.7209	1239.6943	12
10	1204.6056	1187.5790	1232.6005	1215.5739	D	1143.6368	1126.6103	11
11	1317.6896	1300.6631	1345.6846	1328.6580	I	1028.6099	1011.5833	10
12	1430.7737	1413.7472	1458.7686	1441.7421	L	915.5258	898.4993	9
13	1529.8421	1512.8156	1557.8370	1540.8105	V	802.4417	785.4152	8
14	1600.8792	1583.8527	1628.8741	1611.8476	A	703.3733	686.3468	7
15	1701.9269	1684.9004	1729.9218	1712.8953	T	632.3362	615.3097	6
16	1816.9539	1799.9273	1844.9488	1827.9222	D	531.2885	514.2620	5
17	1916.0223	1898.9957	1944.0172	1926.9906	V	416.2616	399.2350	4
18	1987.0594	1970.0328	2015.0543	1998.0277	A	317.1932	300.1666	3
19	2058.0965	2041.0699	2086.0914	2069.0649	A	246.1561	229.1295	2
20					R	175.1190	158.0924	1

Probable polyketide synthase Pks5 (Rv1527C) Modification: Hex-Hex-Hex

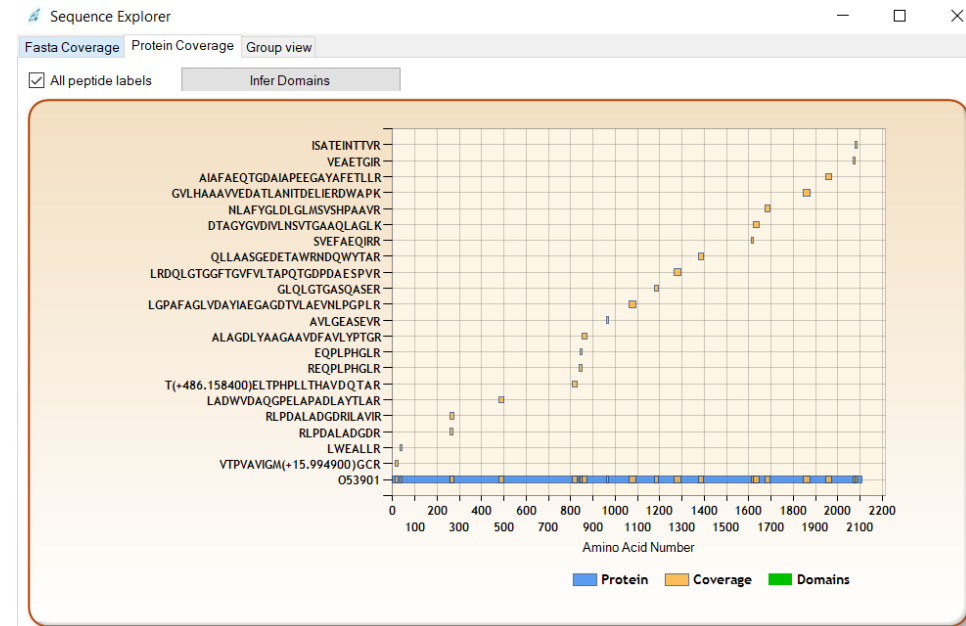
File Statistics Tools
Control Follow-up Result Browser

Spec FDR: 49 / 36000 = 0.14% Pep FDR: 24 / 17635 = 0.14% Prot FDR: 15 / 1505 = 1% # Prot (Max Parsimony): 1487 Unique Prot: 1482 Unlabeled Decoys: 0 / 0

View mode: Proteins Proteins Max Pars Peptides Scans pks5

Locus	Group	GroupType	Length	#UniquePeptides	Mo/Wt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1_053901	1399	Some	2108	14	223731.9	21	24	9.759032254152E-05	0.1565	69.2663	Mycoseroid acid synthase-like polyketide synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pks5 PE=1 SV=2

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-1.sqt	26484	3	True	3202.624851	3201.617483	1.2546	3.9814	14.927208086181	0.588	30	0.62926	R.LRDQLGTGGFTGVFVLTAPQTGDPDAESPVR.G
171213_PT_H37Rv_1-1.sqt	37697	3	True	3168.669773	3166.678292	-4.80296	4.4336	13.6585068091546	0.5782	34	0.60394	R.LGPAFAGLVDAIEAGAGDTVLAENVLPGPLR.S
171213_PT_H37Rv_1-1.sqt	35476	2	True	2334.233446	2333.234717	-1.97966	3.5114	13.2731862671389	0.5838	20	0.61053	R.DTAGYGDIVLNSVTGAAQLAGL.K
171213_PT_H37Rv_1-1.sqt	32620	3	True	2283.178318	2282.18156	-2.8872	4.4933	12.833432085521	0.5772	34	0.62047	R.ALAGDLYAAGAADFVLYPTGR.L
171213_PT_H37Rv_1-1.sqt	32797	4	True	3118.620749	3117.621506	-1.31693	5.4759	12.3136578562101	0.5409	38	0.60693	R.GVLHAAAVVEDATLANITDELIERDWAPKA
171213_PT_H37Rv_1-1.sqt	25327	3	False	1864.073914	1864.076307	-1.28375	3.8732	10.9140889638815	0.5816	30	0.62143	K.RLPDALADGDRILAVIR.G
171213_PT_H37Rv_1-1.sqt	37624	3	True	3167.68137	3166.678292	-0.08587	4.2994	10.8606002789305	0.5488	36	0.59866	R.LGPAFAGLVDAIEAGAGDTVLAENVLPGPLR.S
171213_PT_H37Rv_1-1.sqt	30620	2	True	2457.251024	2456.245616	0.83752	4.0152	8.61701352669845	0.4888	24	0.54504	R.LADWVDAQGPELAPADLAYTLAR.R
171213_PT_H37Rv_1-1.sqt	32293	3	True	2756.356175	2754.362103	-4.58141	3.1139	8.44023215028011	0.4666	26	0.50612	R.AIAFAEQTGDIAPEEGAYAFETLLR.H
171213_PT_H37Rv_1-1.sqt	12190	2	True	1374.693773	1374.697183	-2.48055	2.2444	6.63772814176908	0.4112	11	0.41716	R.GLQLGTGASQASER.A
171213_PT_H37Rv_1-1.sqt	33012	3	True	2486.22855	2486.214365	5.70543	3.1085	6.53619172254965	0.3578	20	0.86098	F.T(+486.158400)ELTPHLLTHAVDQTAR.S

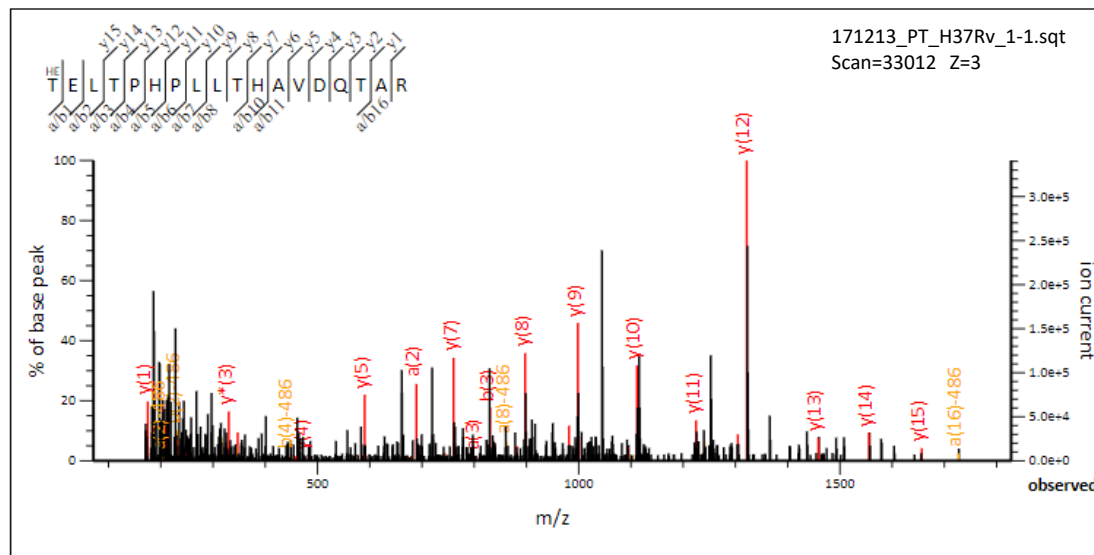


MS/MS Fragmentation of TELTPHLLTHAVDQTAR

Found in **WP_003901190.1** in **NCBIprot**, type I polyketide synthase [Mycobacterium tuberculosis]

Match to Query 1: 2485.221274 from(2486.228550,1+) index(1)

Data file scans pks5 Mascot.txt



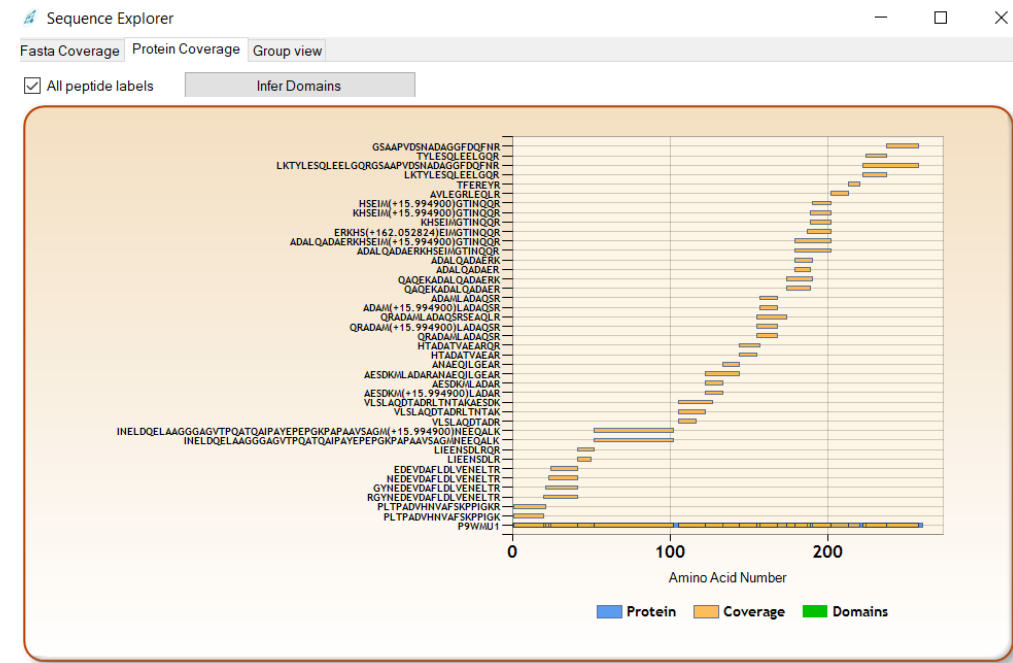
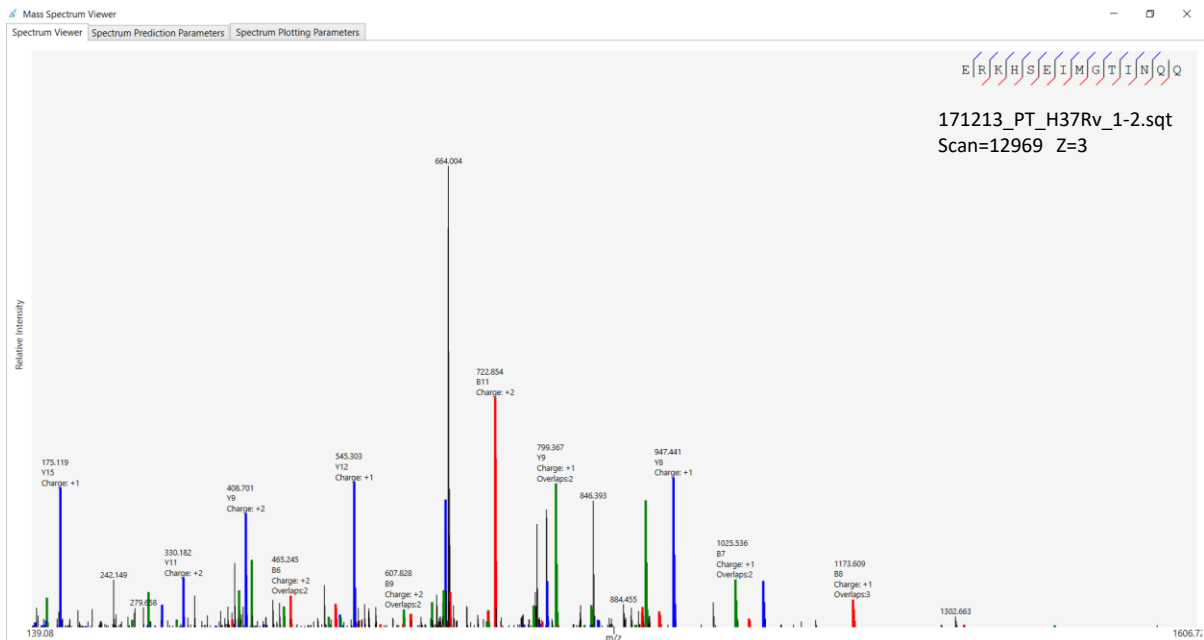
#	a	a*	b	b*	Seq.	y	y*	#
1	560.2185		588.2134		T			18
2	689.2611		717.2560		E	1899.0083	1881.9817	17
3	802.3452		830.3401		L	1769.9657	1752.9391	16
4	903.3928		931.3878		T	1656.8816	1639.8551	15
5	1000.4456		1028.4405		P	1555.8340	1538.8074	14
6	1137.5045		1165.4994		H	1458.7812	1441.7546	13
7	1234.5573		1262.5522		P	1321.7223	1304.6957	12
8	1347.6414		1375.6363		L	1224.6695	1207.6430	11
9	1460.7254		1488.7203		L	1111.5854	1094.5589	10
10	1561.7731		1589.7680		T	998.5014	981.4748	9
11	1698.8320		1726.8269		H	897.4537	880.4272	8
12	1769.8691		1797.8640		A	760.3948	743.3682	7
13	1868.9375		1896.9324		V	689.3577	672.3311	6
14	1983.9645		2011.9594		D	590.2893	573.2627	5
15	2112.0231	2094.9965	2140.0180	2122.9914	Q	475.2623	458.2358	4
16	2213.0707	2196.0442	2241.0656	2224.0391	T	347.2037	330.1772	3
17	2284.1078	2267.0813	2312.1028	2295.0762	A	246.1561	229.1295	2
18					R	175.1190	158.0924	1

Diviva family protein Wag31 (Rv2145c)

Modification: Hex

File	Statistics	Tools										
Control	Follow up	Result Browser										
Spec FDR: 44 / 36033 = 0.12% Pep FDR: 27 / 17879 = 0.15% Prot FDR: 14 / 1494 = 0.94% # Prot (Max Parsimony): 1474 Unique Prot: 1473 Unlabeled Decoys: 0 / 0												
View mode: <input checked="" type="radio"/> Proteins <input type="radio"/> Proteins Max Pars <input type="radio"/> Peptides <input type="radio"/> Scans <input type="text" value="wag31"/>												
Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description	
1	P9WMU1	11	Unique	260	40	28242.1	40	110	0.00362012636416144	0.9654	314.54	Cell wall synthesis protein Wag31 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=wag31 PE=1 SV=1

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-4.sqt	19526	4	True	4974.448874	4973.447298	-0.35662	3.4989	2.80676617404137	0.231	40	0.4147	R.INELDQELAAGGGAGVTPQATQAI PAYEPEPGKPAPA AVSAGM(+15.994900) NEEQALK A
171213_PT_H37Rv_1-3.sqt	14800	4	True	2145.198385	2144.197484	-1.14162	2.5633	2.88419089882108	0.3028	32	0.72722	M.PLTPADVHN VAFSKPPIGKR G
171213_PT_H37Rv_1-3.sqt	37701	3	True	2343.069554	2341.083027	-8.60965	2.1896	2.93181894781034	0.288	18	0.45205	R.GYNEVDVDFLDLVENELTR L
171213_PT_H37Rv_1-2.sqt	12969	3	True	1988.998219	1988.981814	8.24787	2.8999	3.00578260940749	0.2997	25	0.68917	A.ERKHS(+162.052824)EIMG TINGQR A
171213_PT_H37Rv_1-3.sqt	6115	2	True	1187.599723	1187.601491	-1.48872	2.4279	3.00983119793349	0.3261	13	0.41932	KADALQADAERK H



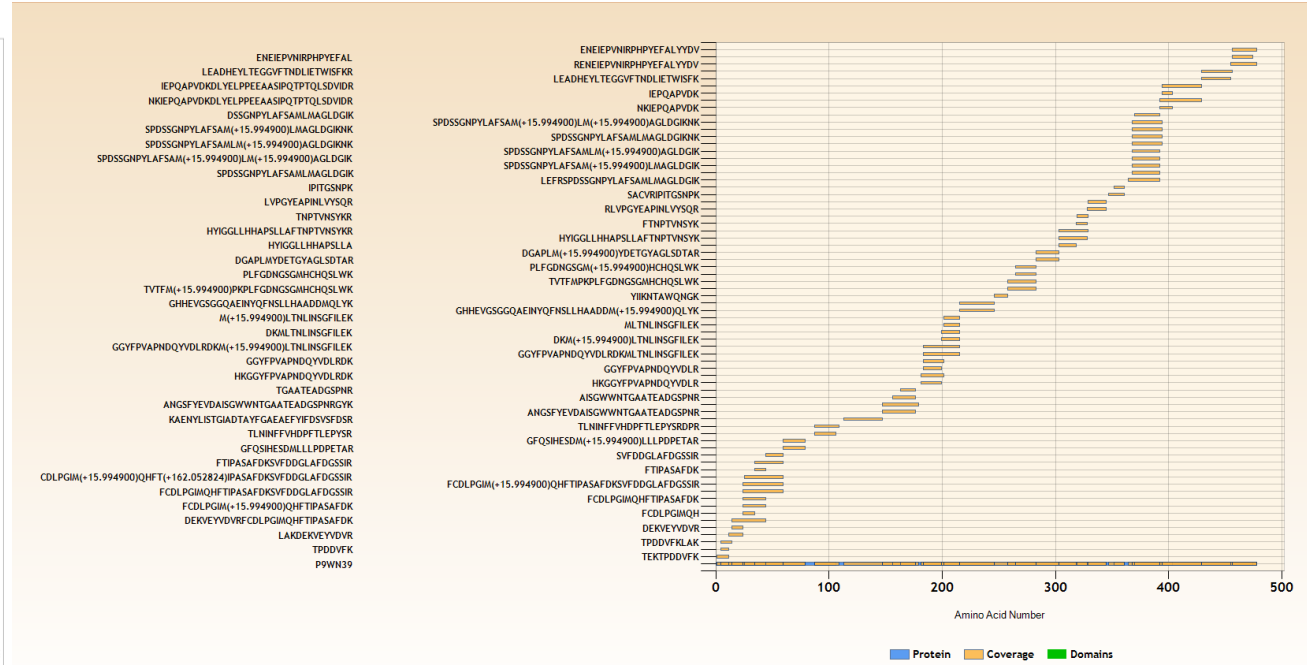
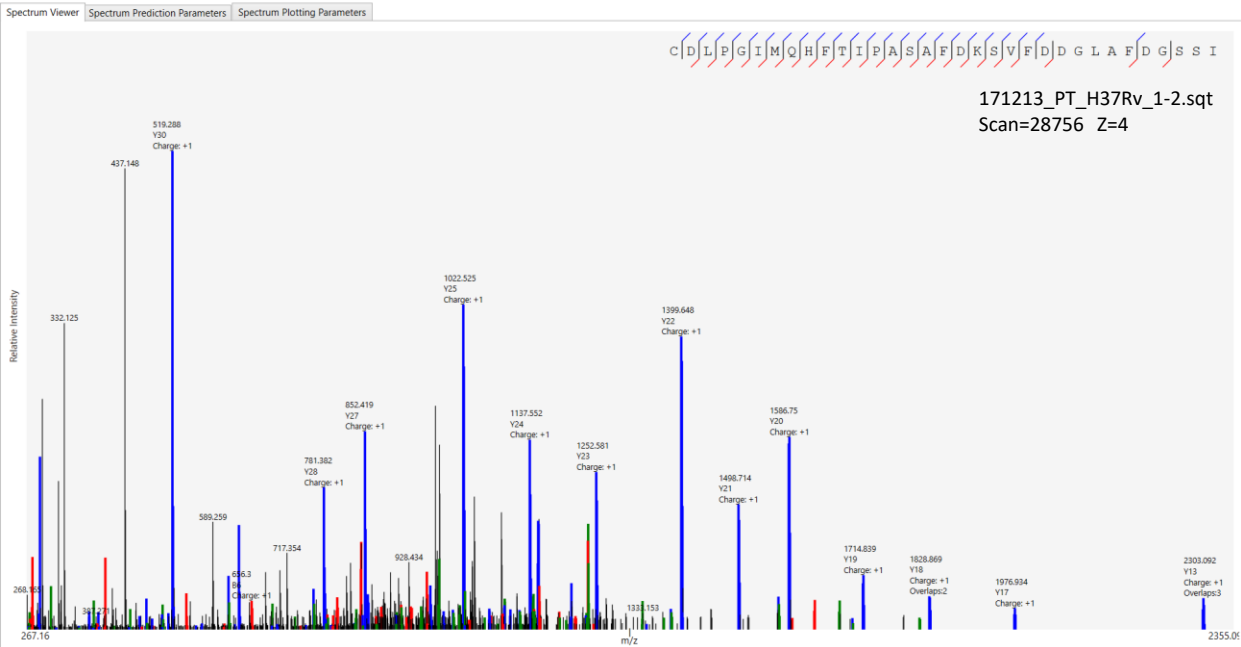
Glutamine synthetase GlnA1 (glutamine synthase) (Rv2220)

Modification: Hex

File	Statistics	Tools									
Control	Follow up	Result Browser									
Spec FDR: 44 / 36033 = 0.12% Pep FDR: 27 / 17879 = 0.15% Prot FDR: 14 / 1494 = 0.94% # Prot (Max Parsimony): 1474 Unique Prot: 1473 Unlabeled Decoys: 0 / 0											
View mode: <input checked="" type="radio"/> Proteins <input type="radio"/> Proteins Max Pars <input type="radio"/> Peptides <input type="radio"/> Scans <input type="text" value="glna1"/>											
Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1 P9WN39	387	Unique	478	71	53518.3	71	255	0.00456474663263414	0.9582	781.0605	Glutamine synthetase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=glnA1 PE=1 SV=1

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-2.sqt	11970	2	True	1170.578477	1170.578965	-0.41689	1.9344	5.24572491642887	0.4547	10	0.71804	A.FTNPTVNSYK.R
171213_PT_H37Rv_1-2.sqt	21954	2	True	2060.937108	2060.942058	-2.40182	3.2584	11.5610658402982	0.5561	21	0.78502	D.AISGWVNTGAATEADGSPNR.G
171213_PT_H37Rv_1-2.sqt	28756	4	True	3893.832907	3892.804416	6.45662	3.4408	7.39551562981713	0.394	32	0.69643	F.CDLPGIM(+15.994900)QHFT(+162.052824)IPASAFDKSVFDDGLAFDGGSSIR.G

Mass Spectrum Viewer

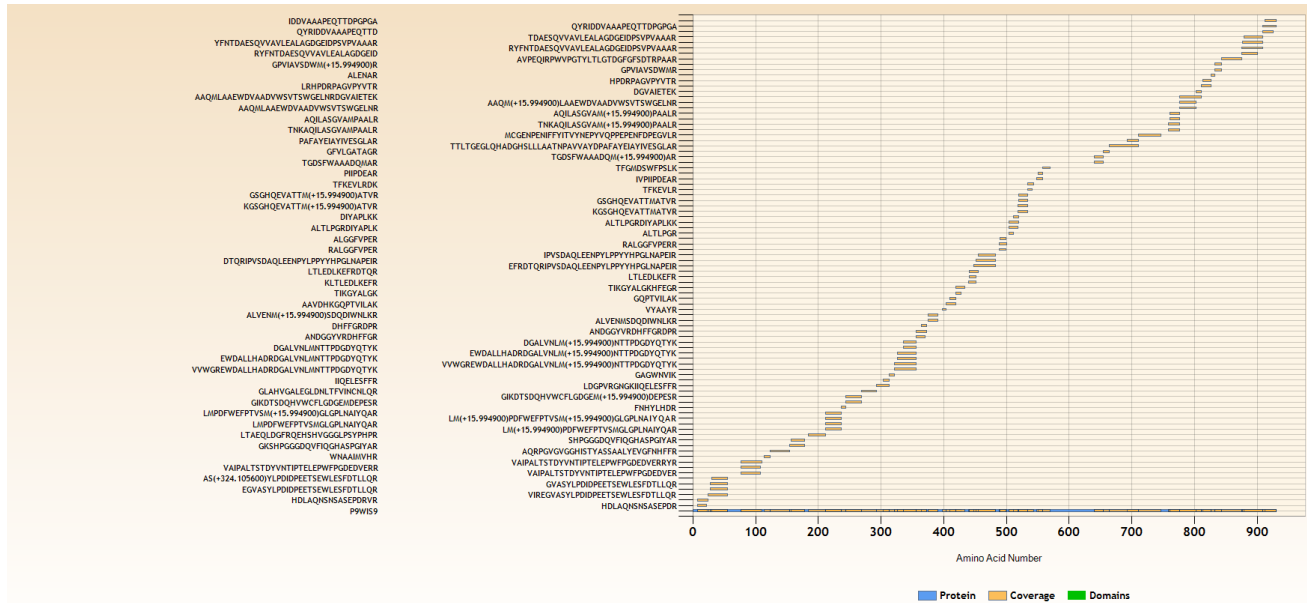
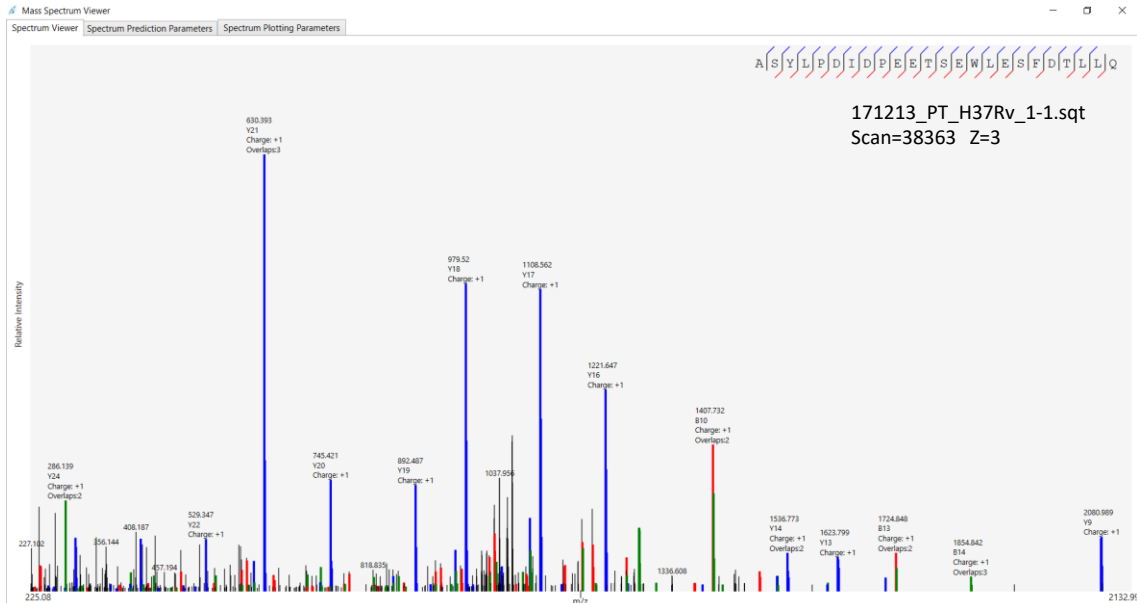


Pyruvate dehydrogenase E1 component AceE (Rv2241)

Modification: Hex-Hex

File	Statistics	Tools								
Control	Follow up	Result Browser								
Spec FDR: 47 / 35750 = 0.13% Pep FDR: 22 / 17513 = 0.13% Prot FDR: 14 / 1467 = 0.95% # Prot (Max Parsimony): 1454 Unique Prot: 1453 Unlabeled Decoys: 0 / 0										
View mode: <input checked="" type="radio"/> Proteins <input type="radio"/> Proteins Max Pars <input type="radio"/> Peptides <input type="radio"/> Scans <input type="text" value="aceE"/>										
Run	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
14	Unique	930	90	103357.7	90	214	0.00202507891638625	0.8151	676.7804	Pyruvate dehydrogenase E1 component OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=aceE PE=1 SV=2

#	File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
1	171213_PT_H37Rv_1-1.sqt	38117	2	True	3111.495409	3110.484069	2.5679	3.2319	13.2790171874497	0.6285	22	0.93698	E GVASYLPDIDPEETSEWESFDTLQR.C
2	171213_PT_H37Rv_1-1.sqt	37668	3	True	1869.974407	1869.974527	-0.06417	3.3911	11.8221717153379	0.5613	24	0.93157	D PAFAYEIAIYVESGLAR.M
3	171213_PT_H37Rv_1-1.sqt	16045	2	True	2172.018485	2172.020367	-0.86648	3.2571	9.61680598041793	0.4964	16	0.95554	R QYRIDDVAAAEQITDTPGPGA.-
4	171213_PT_H37Rv_1-1.sqt	38363	3	True	3278.464573	3278.499791	-10.74222	4.3373	9.40757254150589	0.4517	28	0.91656	V AS(+324.105600)YLPDIDPEETSEWESFDTLQR.C
5	171213_PT_H37Rv_1-1.sqt	19309	2	True	910.497789	910.499258	-1.6134	1.8293	4.78071475850302	0.461	10	0.93096	V.PIIPDEAR.T
6	171213_PT_H37Rv_1-1.sqt	36529	3	True	2951.49625	2950.500387	-2.53668	2.6998	7.42024895984882	0.4364	31	0.93501	N.TDAESQVVAVLEALAGDGEIDPVPVAAAR.Q
7	171213_PT_H37Rv_1-1.sqt	37136	2	True	2683.276659	2682.289332	-5.97143	3.2781	5.7603528261446	0.4105	15	0.93915	R.RYFNTDAESQVVAVLEALAGDGEID.P
8	171213_PT_H37Rv_1-1.sqt	38033	3	True	3111.466892	3110.484069	-6.59721	3.1188	7.59293428989291	0.4028	26	0.93788	E GVASYLPDIDPEETSEWESFDTLQR.C
9	171213_PT_H37Rv_1-1.sqt	16058	3	True	2172.017831	2172.020367	-1.16758	2.7533	6.4377516497364	0.4052	17	0.90881	R.QYRIDDVAAAEQITDTPGPGA.-



Fatty-acid-AMP ligase FadD28 (Rv2941)

Modification: Hex

File Statistics Tools
Control Follow up Result Browser

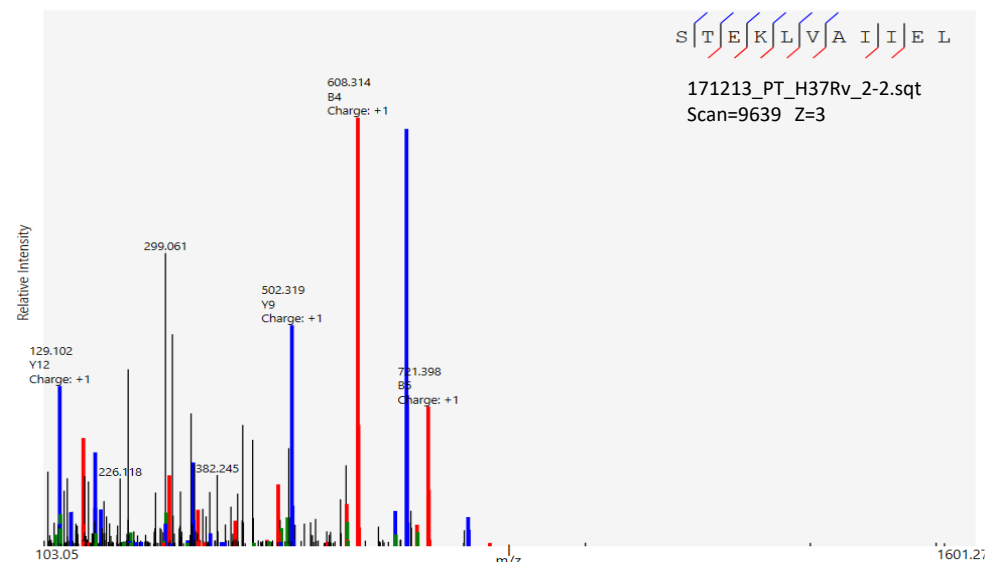
Spec FDR: 37 / 31147 = 0.12% Pep FDR: 22 / 16603 = 0.13% Prot FDR: 15 / 1509 = 0.99% # Prot (Max Parsimony): 1488 Unique Prot: 1486 Unlabeled Decoys: 0 / 0

View mode: Proteins Proteins Max Pars Peptides Scans

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_2-1.sqt	20235	3	False	1189.73013	1189.730321	-0.16054	2.4978	4.6428720531721	0.4145	21	0.4628	R.IKDLLVYGR.N
171213_PT_H37Rv_2-2.sqt	19340	3	False	1189.728983	1189.730321	-1.12463	2.0969	2.30659311439158	0.3255	19	0.39348	R.IKDLLVYGR.N
171213_PT_H37Rv_2-2.sqt	21678	4	True	4350.901999	4347.919349	-6.29754	2.6813	4.14774533894922	0.3125	44	0.37931	R.IVDSDTCIKCPDGTVEIWHGDNVANGYVQKPDSEER.T
171213_PT_H37Rv_2-1.sqt	24480	2	False	1838.883104	1838.887897	-2.60647	3.7584	15.9357740941644	0.603	16	0.66115	R.NHSPDIEATIQTETR.G
171213_PT_H37Rv_2-1.sqt	24445	3	False	1838.887955	1838.887897	0.03154	3.7266	11.8126801186563	0.5265	25	0.60756	R.NHSPDIEATIQTETR.G
171213_PT_H37Rv_2-2.sqt	23341	3	False	1838.884576	1838.887897	-1.80599	3.8194	10.274551233927	0.5151	28	0.58964	R.NHSPDIEATIQTETR.G
171213_PT_H37Rv_2-2.sqt	23414	2	False	1838.886214	1838.887897	-0.91523	2.5368	8.58440194110969	0.4653	13	0.52388	R.NHSPDIEATIQTETR.G
171213_PT_H37Rv_2-1.sqt	9782	3	True	1883.890221	1883.892935	-1.44064	2.9674	7.66918130029538	0.4167	23	0.47575	R.RGACVEQYRQDFAR.L
171213_PT_H37Rv_2-2.sqt	9325	4	True	1884.891501	1883.892935	-2.53008	2.9072	6.2450673059069	0.3678	28	0.44459	R.RGACVEQYRQDFAR.L
171213_PT_H37Rv_2-1.sqt	29686	4	True	4895.328268	4892.342497	-4.95963	7.0607	17.2575299341467	0.6037	56	0.66912	R.RPGESPPSIEVDLLDLPAPNGYTFKEDYFSTAYLQYTSGSTRT
171213_PT_H37Rv_2-2.sqt	28086	4	True	4895.3561	4892.342497	0.72579	4.9942	11.2739085644997	0.5075	53	0.57662	R.RPGESPPSIEVDLLDLPAPNGYTFKEDYFSTAYLQYTSGSTRT
171213_PT_H37Rv_2-1.sqt	30264	3	True	2956.487339	2955.490551	-2.21953	4.437	17.3254073565498	0.6214	26	0.68377	R.SDSVLSDSPPVAILTSSAVDDVQHVARR
171213_PT_H37Rv_2-2.sqt	9639	3	True	1505.877642	1505.867268	6.88901	1.6934	0.556869562267398	0.1352	15	0.28775	R.ST(+162.052824)EKLVAIIELK.K

Mass Spectrum Viewer

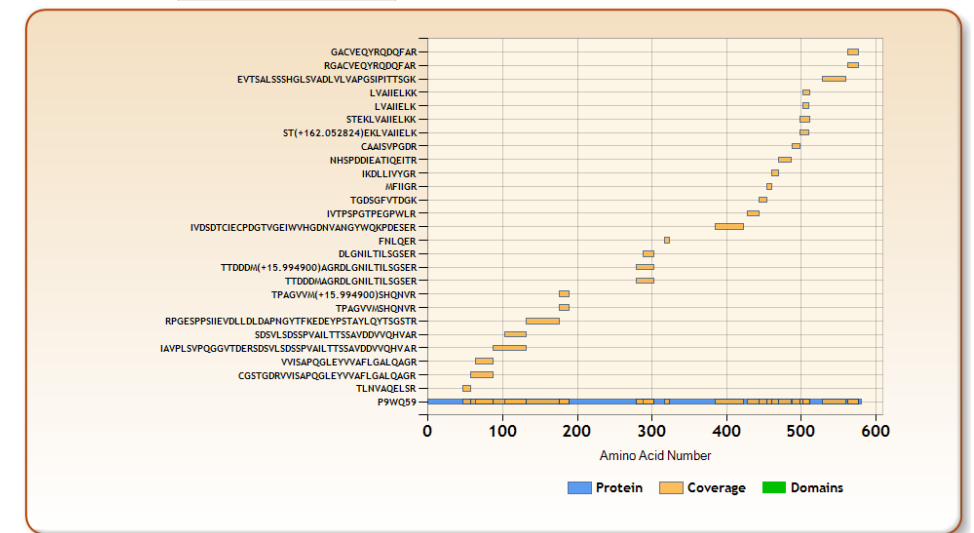
Spectrum Viewer Spectrum Prediction Parameters Spectrum Plotting Parameters



Sequence Explorer

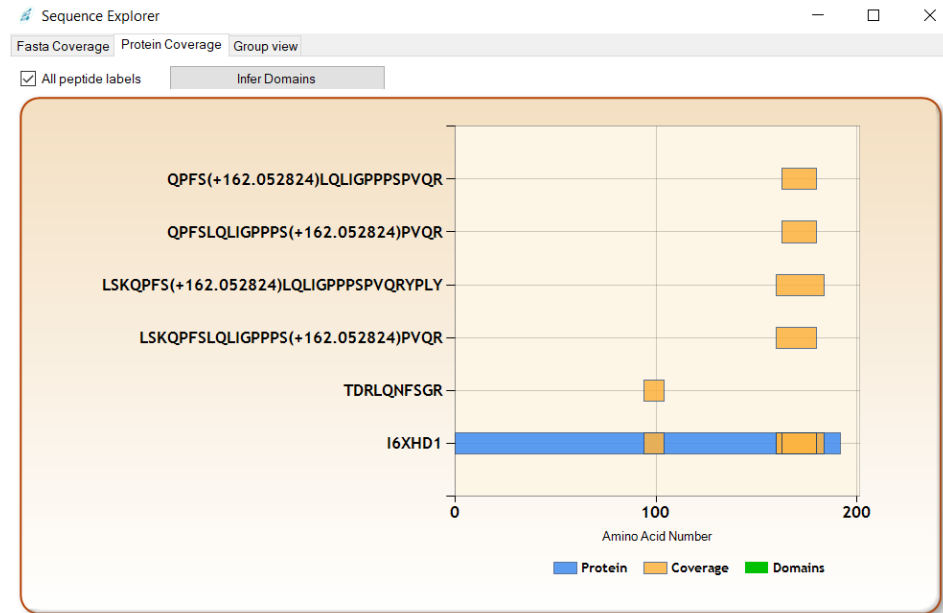
Fasta Coverage Protein Coverage Group view

All peptide labels Infer Domains



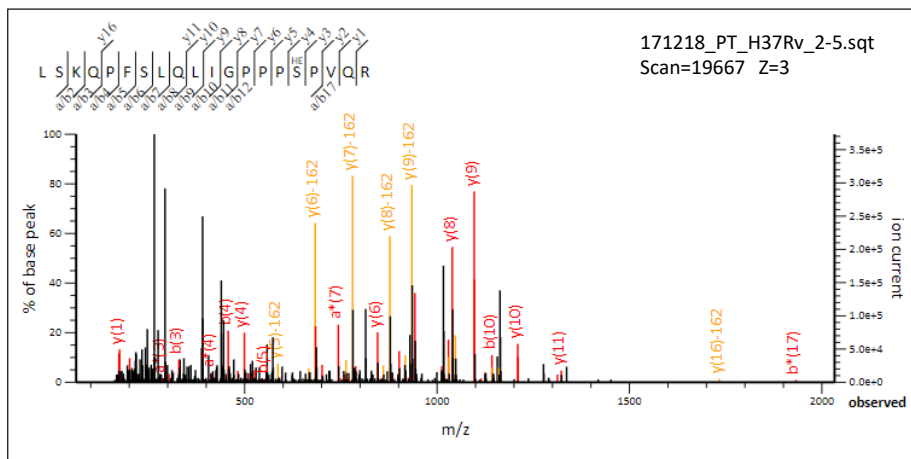
Unknown protein (Rv3491) Modification: Hex

File	Statistics	Tools										
Control	Follow up	Result Browser										
Spec FDR: 37 / 31147 = 0.12% Pep FDR: 22 / 16603 = 0.13% Prot FDR: 15 / 1509 = 0.99% # Prot (Max Parsimony): 1488 Unique Prot: 1486 Unlabeled Decoys: 0 / 0												
View mode: <input checked="" type="radio"/> Proteins <input type="radio"/> Proteins Max Pars <input type="radio"/> Peptides <input type="radio"/> Scans <input type="text" value="Rv3491"/>												
Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description	
1 I6XHD1	925	Unique	192	5	20331.8	5	6	0.000301984189206354	0.1771	16.8178	Uncharacterized protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3491 PE=1 SV=1	
File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
1 171218_PT_H37Rv_2-5.sqt	8463	3	True	1193.599548	1193.60216	-2.18834	3.0441	10.9822972139081	0.5206	19	0.56245	R.TDRLQNFSGR.A
2 171218_PT_H37Rv_2-5.sqt	8468	2	True	1193.601558	1193.60216	-0.50436	2.2999	4.79754207863555	0.4506	15	0.46533	R.TDRLQNFSGR.A
3 171218_PT_H37Rv_2-5.sqt	19667	3	True	2351.293435	2351.296924	-1.48386	2.2638	3.13040717688059	0.2353	23	0.35155	K.LSKQPFSLQLIGPPPS(+162.052824)PVQR.Y
4 171218_PT_H37Rv_2-5.sqt	21659	3	True	2023.083586	2023.085869	-1.12848	2.7994	6.93409925432174	0.394	17	0.37973	K.QPFS(+162.052824)LQLIGPPPSPVQR.Y
5 171218_PT_H37Rv_2-5.sqt	21683	2	True	2023.082922	2023.085869	-1.45669	2.9962	7.48757377423508	0.4112	17	0.45811	K.QPFS(+162.052824)LQLIGPPPSPVQR.Y



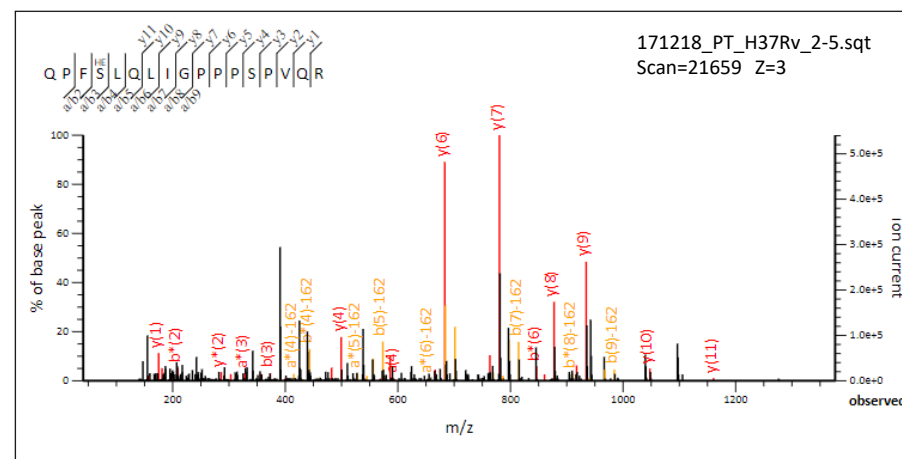
MS/MS Fragmentation of **LSKQPFSLQLIGPPPSVQR**
Found in **WP_015303914.1** in **NCBIprot**, hypothetical protein [Mycobacterium canettii]

Match to Query 3: 2350.286093 from(2351.293369,1+) index(1)
Data file Scans Rv3491 Hex Mascot.txt



MS/MS Fragmentation of **QPFSLQLIGPPPSVQR**
Found in **WP_015303914.1** in **NCBIprot**, hypothetical protein [Mycobacterium canettii]

Match to Query 2: 2022.076316 from(2023.083592,1+) index(2)
Data file Scans Rv3491 Hex Mascot.txt



Conserved protein (Rv1352) Modification: Hex-Hex

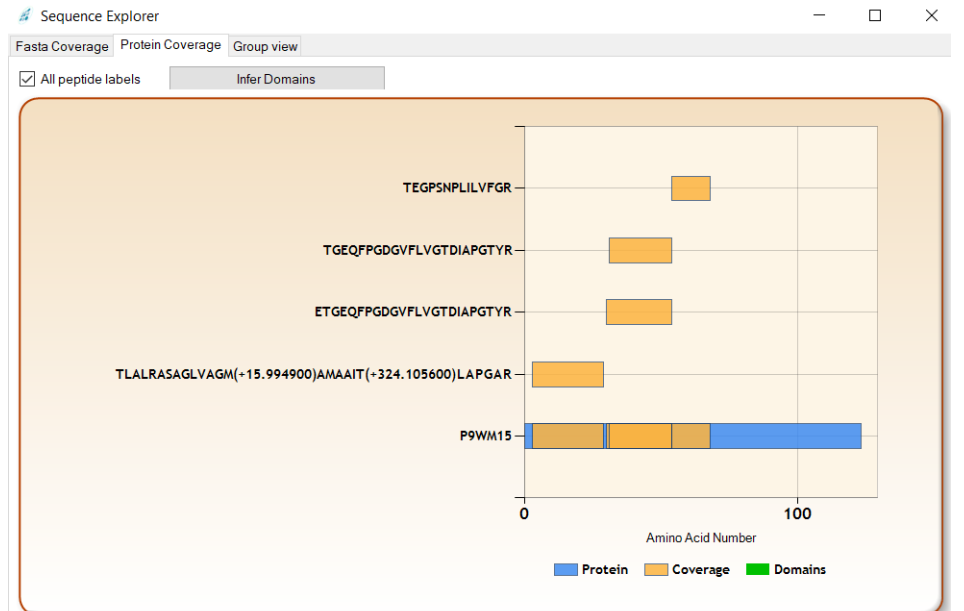
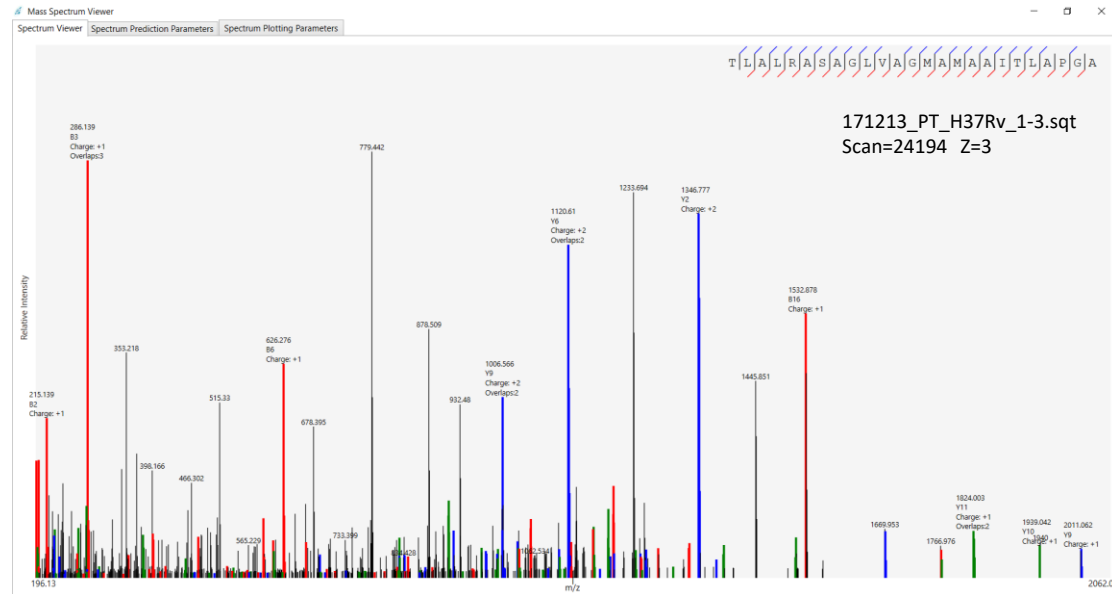
File Statistics Tools
Control Follow up Result Browser

Spec FDR: 47 / 35750 = 0.13% Pep FDR: 22 / 17513 = 0.13% Prot FDR: 14 / 1467 = 0.95% # Prot (Max Parsimony): 1454 Unique Prot: 1453 U

View mode: Proteins Proteins Max Pars Peptides Scans

Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1	P9WM15	1001	Unique	123	4	12823.4	4	0.000858592838951088	0.1138	36.1674	Uncharacterized protein Rv1352 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1352 PE=1 SV=1

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence	
1	171213_PT_H37Rv_1-5.sqt	24532	2	True	1499.817492	1499.821655	-2.77567	2.9231	10.0660064820339	0.5725	15	0.65036	R.TEGPSNPLILVFGR.V
2	171213_PT_H37Rv_1-6.sqt	22696	2	True	1499.817064	1499.821655	-3.06104	2.8106	8.9327086353779	0.5493	16	0.61982	R.TEGPSNPLILVFGR.V
3	171213_PT_H37Rv_1-6.sqt	22847	3	True	1499.818241	1499.821655	-2.27628	2.5044	8.44487252983661	0.4651	15	0.54015	R.TEGPSNPLILVFGR.V
4	171213_PT_H37Rv_1-6.sqt	20762	2	True	2527.214892	2526.21471	-1.25355	2.9491	10.4586134351987	0.566	20	0.96767	A.ETGEQFPDGGVFLVGTDIAPGTYR.T
5	171213_PT_H37Rv_1-5.sqt	22407	2	True	2526.220018	2526.21471	2.10116	3.0742	14.5473985668407	0.5598	16	0.96993	A.ETGEQFPDGGVFLVGTDIAPGTYR.T
6	171213_PT_H37Rv_1-6.sqt	20753	3	True	2526.209049	2526.21471	-2.24091	3.7423	10.4586134351987	0.5297	24	0.97328	A.ETGEQFPDGGVFLVGTDIAPGTYR.T
7	171213_PT_H37Rv_1-6.sqt	20773	3	True	2398.170567	2397.172117	-2.04322	4.0363	8.33904700603276	0.4986	28	0.94559	E.TGEQFPDGGVFLVGTDIAPGTYR.T
8	171213_PT_H37Rv_1-5.sqt	22306	3	True	2526.216903	2526.21471	0.8681	3.6539	9.9463950535474	0.5049	29	0.97466	A.ETGEQFPDGGVFLVGTDIAPGTYR.T
9	171213_PT_H37Rv_1-5.sqt	22369	2	True	2527.212206	2526.21471	-2.31639	2.5605	8.57376354290463	0.5368	16	0.9686	A.ETGEQFPDGGVFLVGTDIAPGTYR.T
10	171213_PT_H37Rv_1-6.sqt	20835	2	True	2398.171923	2397.172117	-1.47779	2.6253	8.40833878650415	0.4584	14	0.94638	E.TGEQFPDGGVFLVGTDIAPGTYR.T
11	171213_PT_H37Rv_1-6.sqt	21045	3	True	2526.206333	2526.21471	-3.31604	3.2405	8.23578073197805	0.4159	27	0.96993	A.ETGEQFPDGGVFLVGTDIAPGTYR.T
12	171213_PT_H37Rv_1-3.sqt	24194	3	True	2795.470616	2794.468831	-0.55983	2.0472	0.215671536475509	0.0643	19	0.31251	R.TLALRASAGLVAGM(+15.994900)AMAAIT(+324.105600)LAPGAR.A

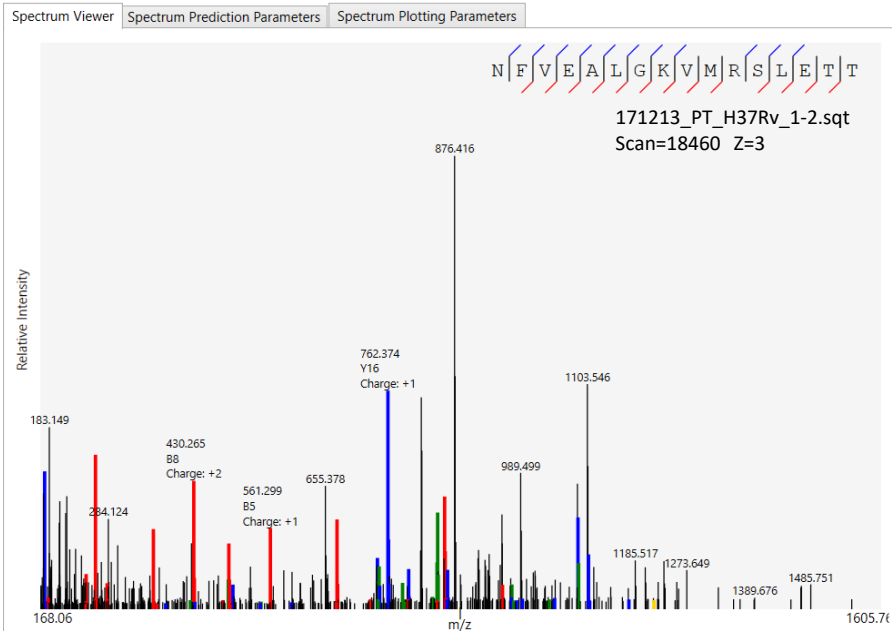


Probable carbamoyl-phosphate synthase large chain CarB (Rv1384) Modification: Hex-Hex-Hex

Locus	Group	GroupType	Length	#UniquePeptides	MolWt	SequenceCount	SpectrumCount	NSAF	Coverage	Protein Score	Description
1	P9WPK3	902	Unique	1115	10	11868.8	10	14	0.000107626517146687	32.3775	Carbamoyl-phosphate synthase large chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=carB PE=1 SV=1

File Name	Scan No	Z	Unique	MeasuredMH	TheoreticalMH	PPM	PrimaryScore	SecondaryScore	DeltaCN	PeaksMatched	BayesianScore	PeptideSequence
171213_PT_H37Rv_1-1.sqt	32499	3	True	3685.94199	3684.948319	-2.62592	4.8518	11.6778001081605	0.539	32	0.58967	R.LADAGVPIVGTPEAIDLAEDRGAFGDLLSAAGLPAPK.Y
171213_PT_H37Rv_1-1.sqt	27698	2	True	2002.94371	2002.950497	-3.38851	2.7751	6.66873837851164	0.4982	19	0.52184	R.AGFWTAPDDPGGIEEALTR.L
171213_PT_H37Rv_1-1.sqt	13664	3	True	1561.833225	1561.833282	-0.0365	2.6406	5.94077143279246	0.4122	22	0.4849	R.ATQLSPEHPVLVDR.F
171213_PT_H37Rv_1-1.sqt	36507	3	True	3132.708592	3130.699422	0.78846	2.6471	3.34670919637809	0.325	29	0.44915	R.GNKIDALLATLGGQTALNTAVALYESGVLEKY
171213_PT_H37Rv_1-1.sqt	36494	4	True	3132.710104	3130.699422	1.2711	2.6701	1.72036947314138	0.1999	35	0.40734	R.GNKIDALLATLGGQTALNTAVALYESGVLEKY
171213_PT_H37Rv_1-1.sqt	25169	3	True	2189.211704	2188.212466	-1.8783	2.4102	1.95899538860397	0.2309	20	0.38849	R.IAEEIGYVPLVRPSYVLGGR.G
171213_PT_H37Rv_1-1.sqt	36617	4	True	3130.704733	3130.699422	1.69642	2.3481	0.142716302201595	0.1241	37	0.38255	R.GNKIDALLATLGGQTALNTAVALYESGVLEKY
171213_PT_H37Rv_1-4.sqt	30194	4	True	3630.891175	3628.875167	2.56356	2.6021	0.944175935363691	0.1424	42	0.36121	R.IDGYEIRSAAVAGNICPITTVQGASAAVQIEAGIR.G
171213_PT_H37Rv_1-2.sqt	18460	3	True	2454.182163	2453.196258	-7.10827	2.0717	0.539568092631645	0.1547	22	0.34467	R.NFVEALGKVM(+15.994900)RSLETT(+486.158400)R.A
171213_PT_H37Rv_1-3.sqt	18252	3	True	2454.186375	2453.196258	-5.39201	1.7961	0.0954101848046582	0.022	21	0.34178	R.NFVEALGKVM(+15.994900)RSLETT(+486.158400)R.A

Mass Spectrum Viewer



Sequence Explorer

