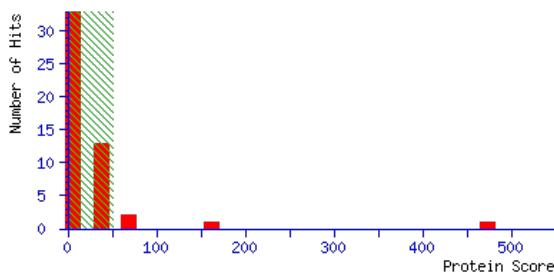


MATRIX SCIENCE Mascot Search Results

User : Genome
 Email : yejini1@hotmail.com
 Search title : Project: won, Spot Set: won¥130814, Label: 004, Spot Id: 289938, Peak List Id: 460376, MS Job Run Id: 23922
 MS data file : 4.txt
 Database : NCBI nr 20130816 (31601460 sequences: 10937649309 residues)
 Taxonomy : Proteobacteria (purple bacteria) (9866941 sequences)
 Timestamp : 21 Aug 2013 at 02:56:03 GMT
 Protein hits : [gi|17987064](#) DNA-directed RNA polymerase subunit alpha [Brucella melitensis bv. 1 str. 16M]
[gi|490993952](#) DNA-directed RNA polymerase subunit alpha [Bartonella doshiae]
[gi|494647237](#) DNA-directed RNA polymerase subunit alpha [Shingomonas sp. S17]
[gi|519020260](#) DNA-directed RNA polymerase subunit alpha [Methyloferula stellata]
[gi|85858173](#) DNA-directed RNA polymerase subunit alpha [Syntrophus aciditrophicus SB]
[gi|158520750](#) DNA-directed RNA polymerase subunit alpha [Desulfococcus oleovorans Hxd3]
[gi|209964064](#) DNA-directed RNA polymerase subunit alpha [Rhodospirillum centenum SW]
[gi|308272953](#) DNA-directed RNA polymerase subunit alpha [uncultured Desulfobacterium sp.]
[gi|490209505](#) hypothetical protein [Rhizobium freirei PRF 81]
[gi|518914335](#) Acr/RND family transmembrane transporter [Burkholderia bryophila]

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 > 51 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 [Help](#)

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

Preferred taxonomy

Error tolerant

1. [gi|17987064](#) Mass: 37460 Score: 473 Matches: 8(5) Sequences: 8(5)
 DNA-directed RNA polymerase subunit alpha [Brucella melitensis bv. 1 str. 16M]
 Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1		R.GFGLTLGNALR.R
<input checked="" type="checkbox"/> 29	2012.1104	2011.1031	2011.0626	0.0405	0	69	0.00097	1	U	R.AEDAPIGLIPVDSLSPVR.K
<input checked="" type="checkbox"/> 32	2048.1167	2047.1094	2047.0626	0.0468	0	40	0.81	1	U	R.IIQDQLSIFVNFEEPQK.E
<input checked="" type="checkbox"/> 37	2140.2141	2139.2068	2139.1575	0.0493	1	57	0.014	1	U	R.AEDAPIGLIPVDSLSPVRK.V
<input checked="" type="checkbox"/> 44	2282.2666	2281.2593	2281.1967	0.0626	1	54	0.03	1	U	K.NWQELIKPNKVDFITHGSR.T
<input checked="" type="checkbox"/> 49	2323.3120	2322.3047	2322.2332	0.0715	0	95	1.9e-06	1		R.GAAVTAVQIDGVLHEFSSIPGVR.E
<input checked="" type="checkbox"/> 63	3312.7571	3311.7498	3311.6157	0.1341	1	95	1.3e-06	1	U	R.EGQVLDYDKLTLNIETNGSVTGEDAVAYAAR.I
<input checked="" type="checkbox"/> 72	3803.0554	3802.0481	3801.8731	0.1750	0	22	15	1	U	K.EGPGVVTAGDIQTVDVEILNPEHVICTLDEGAIEIR.M

Proteins matching the same set of peptides:

- [gi|23502086](#) Mass: 37462 Score: 472 Matches: 8(5) Sequences: 8(5)
DNA-directed RNA polymerase subunit alpha [Brucella suis 1330]
- [gi|62290120](#) Mass: 37475 Score: 472 Matches: 8(5) Sequences: 8(5)
DNA-directed RNA polymerase subunit alpha [Brucella abortus bv. 1 str. 9-941]
- [gi|161619164](#) Mass: 37490 Score: 472 Matches: 8(5) Sequences: 8(5)
DNA-directed RNA polymerase subunit alpha [Brucella canis ATCC 23365]
- [gi|490826365](#) Mass: 37503 Score: 472 Matches: 8(5) Sequences: 8(5)
DNA-directed RNA polymerase subunit alpha [Brucella neotomae]
- [gi|496220120](#) Mass: 37449 Score: 472 Matches: 8(5) Sequences: 8(5)
DNA-directed RNA polymerase subunit alpha [Brucella sp. NVSL 07-0026]

2. [gi|490993952](#) Mass: 37704 Score: 176 Matches: 3(1) Sequences: 3(1)
 DNA-directed RNA polymerase subunit alpha [Bartonella doshiae]
 Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1		R.GFGLTLGNALR.R

32	1118.6533	1117.6460	1117.6244	0.0468	0	40	0.81	1	U	R. ILQDQLSLFVNFEEPK. E
49	2323.3120	2322.3047	2322.2332	0.0715	0	95	1.9e-06	1		R. GAAVTAVQIDGVLHEFSSIPGVR. E

Proteins matching the same set of peptides:

[gi|490997418](#) Mass: 37852 Score: 176 Matches: 3(1) Sequences: 3(1)
DNA-directed RNA polymerase subunit alpha [Bartonella taylorii]
[gi|494817160](#) Mass: 37812 Score: 176 Matches: 3(1) Sequences: 3(1)
DNA-directed RNA polymerase subunit alpha [Bartonella sp. DB5-6]

3. [gi|494647237](#) Mass: 38360 Score: 58 Matches: 2(0) Sequences: 2(0)
DNA-directed RNA polymerase subunit alpha [Sphingomonas sp. S17]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1	U	R. GFGLTLGNALR. R
63	3312.7571	3311.7498	3311.6045	0.1453	1	17	77	2	U	R. VGQDLDYDKLTLVETDGTVPEDAVAYAAR. I

4. [gi|519020260](#) Mass: 37544 Score: 53 Matches: 2(0) Sequences: 2(0)
DNA-directed RNA polymerase subunit alpha [Methyloferula stellata]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1	U	R. GFGLTLGNALR. R
37	2140.2141	2139.2068	2139.1575	0.0493	1	13	3.9e+02	3	U	R. GEDAPIGLIPIIDSLYSPVRK. V

5. [gi|85858173](#) Mass: 38746 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [Syntrophus aciditrophicus SB]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1	U	R. GFGLTLGNALR. R

Proteins matching the same set of peptides:

[gi|116749017](#) Mass: 38075 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [Syntrophobacter fumaroxidans MPOB]

6. [gi|158520750](#) Mass: 37525 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [Desulfococcus oleovorans Hxd3]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1	U	R. GFGLTLGNALR. R

Proteins matching the same set of peptides:

[gi|493464250](#) Mass: 43253 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [delta proteobacterium NaphS2]

7. [gi|209964064](#) Mass: 37216 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [Rhodospirillum centenum SW]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1	U	R. GFGLTLGNALR. R

Proteins matching the same set of peptides:

[gi|524158064](#) Mass: 37189 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [Proteobacteria bacterium CAG:495]

8. [gi|308272953](#) Mass: 38577 Score: 41 Matches: 1(0) Sequences: 1(0)
DNA-directed RNA polymerase subunit alpha [uncultured Desulfobacterium sp.]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
6	1118.6533	1117.6460	1117.6244	0.0216	0	41	1.2	1	U	R. GFGLTLGNALR. R

9. [gi|490209505](#) Score: 28 Matches: 1(0) Sequences: 1(0)
hypothetical protein [Rhizobium freirei PRF 81]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
29	2012.1104	2011.1031	2011.0374	0.0657	0	28	13	2	U	R. LLAADIGLDGHDILFASDR. L

10. [gi|518914335](#) Score: 26 Matches: 1(0) Sequences: 1(0)
Acr/RND family transmembrane transporter [Burkholderia bryophila]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
29	2012.1104	2011.1031	2011.0521	0.0510	0	26	23	3	U	R. AGGQAVLIGIVT ^{MQ} PGGDVIR. L + Oxidation (M)

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 54	2410.3936	2409.3863	2409.2270	0.1593	1	5	1.4e+03	1		RPAAE <u>M</u> AAGMRPHYPRGAALVR + 2 Oxidation (M)
<input checked="" type="checkbox"/> 1	804.3128	803.3055								
<input checked="" type="checkbox"/> 2	873.3818	872.3745								
<input checked="" type="checkbox"/> 3	943.6271	942.6199								
<input checked="" type="checkbox"/> 4	1117.6229	1116.6156								
<input checked="" type="checkbox"/> 5	1118.6533	1117.6460								
<input checked="" type="checkbox"/> 7	1141.6302	1140.6229								
<input checked="" type="checkbox"/> 8	1142.1316	1141.1243								
<input checked="" type="checkbox"/> 9	1187.6859	1186.6786								
<input checked="" type="checkbox"/> 10	1240.6930	1239.6857								
<input checked="" type="checkbox"/> 11	1258.6680	1257.6607								
<input checked="" type="checkbox"/> 12	1269.7186	1268.7113								
<input checked="" type="checkbox"/> 13	1273.7262	1272.7189								
<input checked="" type="checkbox"/> 14	1274.7562	1273.7489								
<input checked="" type="checkbox"/> 15	1322.7316	1321.7243								
<input checked="" type="checkbox"/> 16	1336.7371	1335.7298								
<input checked="" type="checkbox"/> 17	1504.8224	1503.8151								
<input checked="" type="checkbox"/> 18	1630.8575	1629.8502								
<input checked="" type="checkbox"/> 19	1696.9999	1695.9926								
<input checked="" type="checkbox"/> 20	1782.0148	1781.0075								
<input checked="" type="checkbox"/> 21	1782.5073	1781.5000								
<input checked="" type="checkbox"/> 22	1825.0920	1824.0847								
<input checked="" type="checkbox"/> 23	1841.0825	1840.0752								
<input checked="" type="checkbox"/> 24	1950.0771	1949.0698								
<input checked="" type="checkbox"/> 25	1968.0853	1967.0780								
<input checked="" type="checkbox"/> 26	1982.0938	1981.0865								
<input checked="" type="checkbox"/> 27	1995.0940	1994.0867								
<input checked="" type="checkbox"/> 28	2012.1104	2011.1031								
<input checked="" type="checkbox"/> 30	2026.1217	2025.1144								
<input checked="" type="checkbox"/> 31	2048.1167	2047.1094								
<input checked="" type="checkbox"/> 33	2050.4751	2049.4678								
<input checked="" type="checkbox"/> 34	2062.1331	2061.1258								
<input checked="" type="checkbox"/> 35	2097.1873	2096.1800								
<input checked="" type="checkbox"/> 36	2140.2141	2139.2068								
<input checked="" type="checkbox"/> 38	2142.6123	2141.6050								
<input checked="" type="checkbox"/> 39	2154.2263	2153.2190								
<input checked="" type="checkbox"/> 40	2178.1746	2177.1673								
<input checked="" type="checkbox"/> 41	2265.2046	2264.1973								
<input checked="" type="checkbox"/> 42	2266.1794	2265.1721								
<input checked="" type="checkbox"/> 43	2282.2666	2281.2593								
<input checked="" type="checkbox"/> 45	2296.2617	2295.2544								
<input checked="" type="checkbox"/> 46	2298.2634	2297.2561								
<input checked="" type="checkbox"/> 47	2314.2427	2313.2354								
<input checked="" type="checkbox"/> 48	2323.3120	2322.3047								
<input checked="" type="checkbox"/> 50	2335.2749	2334.2676								
<input checked="" type="checkbox"/> 51	2337.2759	2336.2686								
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<input checked="" type="checkbox"/> 55	2651.5513	2650.5440								
<input checked="" type="checkbox"/> 56	2652.4985	2651.4912								
<input checked="" type="checkbox"/> 57	2960.5544	2959.5471								
<input checked="" type="checkbox"/> 58	2976.6055	2975.5982								
<input checked="" type="checkbox"/> 59	3009.6338	3008.6265								
<input checked="" type="checkbox"/> 60	3295.6970	3294.6897								
<input checked="" type="checkbox"/> 61	3298.5991	3297.5918								
<input checked="" type="checkbox"/> 62	3312.7571	3311.7498								
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<input checked="" type="checkbox"/> 65	3563.0459	3562.0386								
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<input checked="" type="checkbox"/> 67	3566.9500	3565.9427								
<input checked="" type="checkbox"/> 68	3645.0437	3644.0364								
<input checked="" type="checkbox"/> 69	3662.0107	3661.0034								
<input checked="" type="checkbox"/> 70	3786.9326	3785.9253								
<input checked="" type="checkbox"/> 71	3803.0554	3802.0481								
<input checked="" type="checkbox"/> 73	3818.0581	3817.0508								
<input checked="" type="checkbox"/> 74	3931.0759	3930.0686								
<input checked="" type="checkbox"/> 75	3997.2671	3996.2598								

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted

Peptide Mass Tolerance : \pm 0.2 Da
Fragment Mass Tolerance: \pm 0.15 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 75

Mascot: <http://www.matrixscience.com/>