

Example Mascot search result from a sample analyzed by MALDI-TOF/TOF

For additional questions or assistance with the interpretation of your results, please contact a PMF staff member:

[http://www.pmf.colostate.edu/contact\\_us.html](http://www.pmf.colostate.edu/contact_us.html)

# MASCOT SCIENCE Mascot Search Results

## Mascot Protein Summary Report

User : jprenni  
Email : jprenni@colostate.edu  
Search title :  
MS data file : DATA.TXT  
Database : NCBIInr 20081107 (7294643 sequences; 2525198067 residues)  
Taxonomy : Viruses (522248 sequences)  
Timestamp : 3 Dec 2008 at 23:52:38 GMT  
Warning : A Peptide summary report will usually give a much clearer  
Top Score : 640 for gi|55669630, Chain A, Structure Of The Dengue Vir

Version and size of database used in the search.

\*\*Note, the actual # of sequences searched after the taxonomy filter (in this case "viruses")c

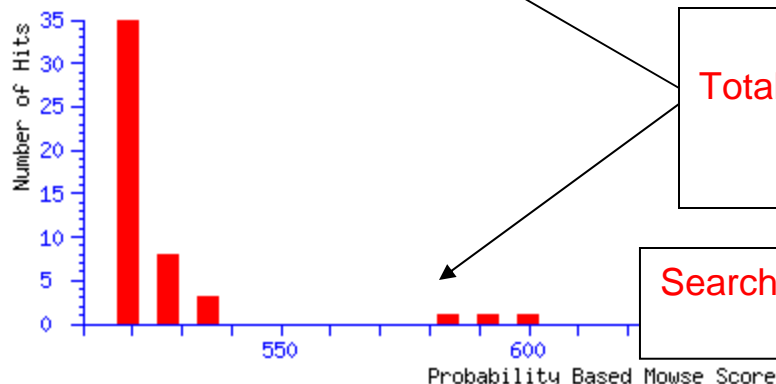
### Probability Based Mowse Score

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Protein scores greater than 70 are significant ( $p < 0.05$ ).

Protein scores are derived from ion scores as a non-probabilistic basis for ranking protein hits.

Top scoring protein (should be only 1 major protein if this is a gel band/spot or a purified protein)



Score Histogram and identity threshold  
Total protein score must be > 70 to be "statistically significant" based on the Mascot scoring algorithm using a threshold of  $p < 0.5$

Search contains both MS and MS/MS data. Threshold for individual peptide identifications (ion scores) from MS/MS spectra is 41

### Protein Summary Report

Format As	Protein Summary (deprecated) ▾		<a href="#">Help</a>
Significance threshold $p <$	0.05	Max. number of hits	5
Standard scoring <input checked="" type="radio"/>	MudPIT scoring <input type="radio"/>	Ions score or expect cut-off	41
Show pop-ups <input checked="" type="radio"/>	Suppress pop-ups <input type="radio"/>	Sort unassigned	Decreasing Score ▾
		Show sub-sets	0
		Require bold red	<input checked="" type="checkbox"/>

## Mascot Protein Summary Report

Accession	Mass	Score	Description
1. <a href="#">gi 55669630</a>	33362	640	Chain A, Structure Of The Dengue Virus 2'o Methyltransferase In Complex With S-Ad
2. <a href="#">gi 29726395</a>	34605	602	Chain A, Dengue Methyltransferase
3. <a href="#">gi 159024820</a>	103955	589	Nonstructu:
4. <a href="#">ai 118505369</a>	70986	581	nonstructu: lyprotei:

Top protein hits (In this case there are redundant entries for the same protein)

List of all the peptides identified by peptide mass  
Peptides that are also identified by their MS/MS fragmentation are indicated with an ion score (from the previous slide, this score needs to be > 41 to be significant in this search)

1. [gi|55669630](#) Mass: 33362 Score: 640 Expect: 5.2e-059 Queries matched: 22

Chain A, Structure Of The Dengue Virus 2'o Methyltransferase In Complex With S-Adenosyl Homocysteine And Ri

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
858.4339	857.4266	857.5083	-0.0817	14 - 21	1	---	---	K.SRLNALGK.S
875.4256	874.4183	874.4331	-0.0148	76 - 83	0	---	---	K.VVDLGCGR.G
903.4385	902.4312	902.4458	-0.0146	30 - 37	0	---	---	K.SGIQEVDR.T
914.4104	913.4032	913.4545	-0.0514	22 - 28	0	---	---	K.SEFQIYK.K
1005.5130	1004.5057	1004.5556	-0.0499	61 - 67	1	27	---	K.LRWFVER.N
1031.4844	1030.4771	1030.5407	-0.0636	29 - 37	1	---	---	K.KSGIQEVDR.T
1042.5541	1041.5468	1041.5495	-0.0027	22 - 29	1	25	---	K.SEFQIYK.S
1108.4494	1107.4422	1107.5057	-0.0636	47 - 56	0	---	---	R.GETDHHAVSR.G
1181.5493	1180.5421	1180.6209	-0.0788	237 - 245	1	---	---	R.MLINRFTMR.H
1247.5405	1246.5332	1246.5441	-0.0109	84 - 94	0	---	---	R.GGWSYYCGGLK.N
1264.5901	1263.5828	1263.6068	-0.0240	46 - 56	1	---	---	K.RGETDHHAVSR.G
1316.6804	1315.6731	1315.7096	-0.0364	30 - 41	1	---	---	K.SGIQEVDR.TLAK.E
1389.7415	1388.7342	1388.7374	-0.0031	181 - 192	0	---	---	K.VLNPYMPSVIEK.M
1405.7299	1404.7226	1404.7323	-0.0096	181 - 192	0	---	---	K.VLNPYMPSVIEK.M + Oxidation (M)
1480.6659	1479.6586	1479.6842	-0.0256	249 - 262	0	116	---	K.ATYEPDVDLGSCTR.N
1608.7326	1607.7253	1607.7791	-0.0538	248 - 262	1	---	---	K.KATYEPDVDLGSCTR.N
2118.0116	2117.0043	2117.1013	-0.0969	181 - 198	1	---	---	K.VLNPYMPSVIEKMEALQR.K
2197.0176	2196.0103	2196.0422	-0.0319	105 - 124	0	148	---	K.GGPGHEEPIPMSTYGWNLVR.L
2212.9927	2211.9854	2212.0371	-0.0517	105 - 124	0	---	---	K.GGPGHEEPIPMSTYGWNLVR.L + Oxidation (M)
2783.2181	2782.2108	2782.2803	-0.0695	212 - 236	0	141	---	R.NSTHEMYWVSNASGNIVSSVNMISR.M

Protein View will be included for top protein hit

## *{MATRIX}* *{SCIENCE}* Mascot Search Results

### Protein View

Match to: gi|55669630 Score: 640 Expect: 5.2e-059

Chain A, Structure Of The Dengue Virus 2'o Methyltransferase In Complex With S-Adenosyl Homocystein

Found in search of DATA.TXT

Nominal mass ( $M_r$ ): 33362; Calculated pI value: 9.00

NCBI BLAST search of [gi|55669630](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Dengue virus 2](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next

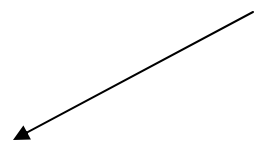
Sequence Coverage: 63%

Matched peptides shown in **Bold Red**

```

1 GSNIGETLGE KWSRLNALG KSEFQIYKKS GIQEVDRTLA KEGIKRGETD
51 HHAVSRGSAK LRWFVERNLV TPEGKVVDLG CGRGWSYYC GGLKNVREVK
101 GLTKGGPGHE EPIPMSTYGW NLVRLQSGVD VFFIPPERCD TLLCDIGESS
151 PNPTVEAGRT LRVLNLVENW LSNNTQFCVK VLNPYMPSVI EKMEALQRKH
201 GGALVRNPLS RNSTHEMYWV SNASGNIVSS VNMISRLIN RFTMRHKKAT
251 YEPDVDLGSG TRNIGIESET PNLDIIGKRI EKIKQEHETS WHYDQ
    
```

Sequence coverage map of identified protein. Red amino acids correspond to those that were matched to experimental data



Protein View will be included for top protein hit

List of peptides identifies (those with matching MS/MS data have an ion score those that are identified only by mass have "no match")

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss Sequence
14 - 21	858.4339	857.4266	857.5083	-0.0817	1 K.SRLNALGK.S (No match)
22 - 28	914.4104	913.4032	913.4545	-0.0514	0 K.SEFQIYK.K (No match)
22 - 29	1042.5541	1041.5468	1041.5495	-0.0027	1 K.SEFQIYKK.S (Ions score 25)
29 - 37	1031.4844	1030.4771	1030.5407	-0.0636	1 K.KSGIQEVDR.T (No match)
30 - 37	903.4385	902.4312	902.4458	-0.0146	0 K.SGIQEVDR.T (No match)
30 - 41	1316.6804	1315.6731	1315.7096	-0.0364	1 K.SGIQEVDRTLAK.E (No match)
46 - 56	1264.5901	1263.5828	1263.6068	-0.0240	1 K.RGETDHHAIVSR.G (No match)
47 - 56	1108.4494	1107.4422	1107.5057	-0.0636	0 R.GETDHHAIVSR.G (No match)
61 - 67	1005.5130	1004.5057	1004.5556	-0.0499	1 K.LRWFVER.N (Ions score 27)
76 - 83	875.4256	874.4183	874.4331	-0.0148	0 K.VVDLGCGR.G (No match)
84 - 94	1247.5405	1246.5332	1246.5441	-0.0109	0 R.GGWSYICGGLK.N (No match)
105 - 124	2197.0176	2196.0103	2196.0422	-0.0319	0 K.GGPGHEEIPMSTYGNLVR.L (Ions score 148)
105 - 124	2212.9927	2211.9854	2212.0371	-0.0517	0 K.GGPGHEEIPMSTYGNLVR.L Oxidation (M) (No match)
125 - 159	3875.7802	3874.7730	3874.8506	-0.0776	1 R.LQSGVDVFFIPPERCDTLLCDIGESSPNPTVEAGR.T (No match)
181 - 192	1389.7415	1388.7342	1388.7374	-0.0031	0 K.VLNPMPSVIEK.M (No match)
181 - 192	1405.7299	1404.7226	1404.7323	-0.0096	0 K.VLNPMPSVIEK.M Oxidation (M) (No match)
181 - 198	2118.0116	2117.0043	2117.1013	-0.0969	1 K.VLNPMPSVIEKMEALQR.K (No match)
212 - 236	2783.2181	2782.2108	2782.2803	-0.0695	0 R.NSTHEMYWVSNASGNIVSSVMISR.M (Ions score 141)
212 - 236	2799.2100	2798.2027	2798.2752	-0.0725	0 R.NSTHEMYWVSNASGNIVSSVMISR.M Oxidation (M) (No ma
237 - 245	1181.5493	1180.5421	1180.6209	-0.0788	1 R.MLINRFTMR.H (No match)
248 - 262	1608.7326	1607.7253	1607.7791	-0.0538	1 K.KATYEPDVDLGSCTR.N (No match)
249 - 262	1480.6659	1479.6586	1479.6842	-0.0256	0 K.ATYEPDVDLGSCTR.N (Ions score 116)

### General Rules:

If protein identification is only based on matching peptide masses you must match *at least 5 peptide masses* for a confident identification. Any additional matches to MS/MS spectrum (those with an ion score) add confidence to the identification.

If your identification is based only on MS/MS matches, you need to match *at least 2 unique peptides* for a confident identification