

Example Mascot search result from a sample analyzed by LC-MS/MS using the Thermo Scientific LTQ Ion trap mass spectrometer

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** Mascot Search Results

### Mascot Peptide Summary Report

**User** : Location and name of raw data file  
**Email** :  
**Search title** : standard protein search software test 8  
**MS data file** : C:\Program Files\Matrix Science\Mascot Daemon\data\trap-mgf\1x\_A  
**Database** : IPI\_human human\_20090518 (80128 sequences; 32865318 residues)  
**Timestamp** : 21 May 2009 at 19:24:38 GMT  
**Protein hits** : [IPI00022463](#) Tax\_Id=9606 Gene\_Symbol=TF Serotransferrin  
[IPI00465436](#) Tax\_Id=9606 Gene\_Symbol=CAT Catalase  
[IPI00217493](#) Tax\_Id=9606 Gene\_Symbol=MB Myoglobin  
[IPI00021808](#) Tax\_Id=9606 Gene\_Symbol=HARS Histidyl-tRNA synthetase, cytoplasmic  
[IPI00025499](#) Tax\_Id=9606 Gene\_Symbol=MAPT Isoform Tau-F of Microtubule-associated protein tau  
[IPI00000874](#) Tax\_Id=9606 Gene\_Symbol=PRDX1 Peroxiredoxin-1  
[IPI00032179](#) Tax\_Id=9606 Gene\_Symbol=SERPINC1 Antithrombin-III  
[IPI00215983](#) Tax\_Id=9606 Gene\_Symbol=CA1 Carbonic anhydrase 1  
[IPI000413587](#) Tax\_Id=9606 Gene\_Symbol=BID Isoform 1 of BH3-interacting domain death agonist  
 606 Gene\_Symbol=CYCS Cytochrome c  
 606 Gene\_Symbol=UBE2C Ubiquitin-conjugating enzyme E2 C  
 606 Gene\_Symbol=PPIA Peptidyl-prolyl cis-trans isomerase A  
[IPI00032291](#) Tax\_Id=9606 Gene\_Symbol=C5 Complement C5  
[IPI00027487](#) Tax\_Id=9606 Gene\_Symbol=CKM Creatine kinase M-type  
[IPI00220327](#) Tax\_Id=9606 Gene\_Symbol=KRT1 Keratin, type II cytoskeletal 1  
[IPI00216298](#) Tax\_Id=9606 Gene\_Symbol=TXN Thioredoxin  
[IPI00218733](#) Tax\_Id=9606 Gene\_Symbol=SOD1 Superoxide dismutase [Cu-Zn]  
[IPI00009865](#) Tax\_Id=9606 Gene\_Symbol=KRT10 Keratin, type I cytoskeletal 10  
[IPI00657682](#) Tax\_Id=9606 Gene\_Symbol=GSTA1 Glutathione S-transferase A1  
[IPI00001671](#) Tax\_Id=9606 Gene\_Symbol=TNF Tumor necrosis factor  
[IPI00022434](#) Tax\_Id=9606 Gene\_Symbol=ALB Putative uncharacterized protein ALB  
[IPI00219684](#) Tax\_Id=9606 Gene\_Symbol=FABP3 Fatty acid-binding protein, heart  
[IPI00298860](#) Tax\_Id=9606 Gene\_Symbol=LTF Growth-inhibiting protein 12  
[IPI00032957](#) Tax\_Id=9606 Gene\_Symbol=UBE2I SUMO-conjugating enzyme UBC9  
[IPI00218414](#) Tax\_Id=9606 Gene\_Symbol=CA2 Carbonic anhydrase 2  
[IPI00011229](#) Tax\_Id=9606 Gene\_Symbol=CTSD Cathepsin D  
[IPI00219757](#) Tax\_Id=9606 Gene\_Symbol=GSTP1 Glutathione S-transferase P  
[IPI00329801](#) Tax\_Id=9606 Gene\_Symbol=ANXA5 Annexin A5  
[IPI00021346](#) Tax\_Id=9606 Gene\_Symbol=UBE2E1 Ubiquitin-conjugating enzyme E2 E1  
[IPI00028064](#) Tax\_Id=9606 Gene\_Symbol=CTSG Cathepsin G  
[IPI000022420](#) Tax\_Id=9606 Gene\_Symbol=RRP4 Retinol-binding protein 4

Version and size of database used in the search

List of proteins identified and their accession #s

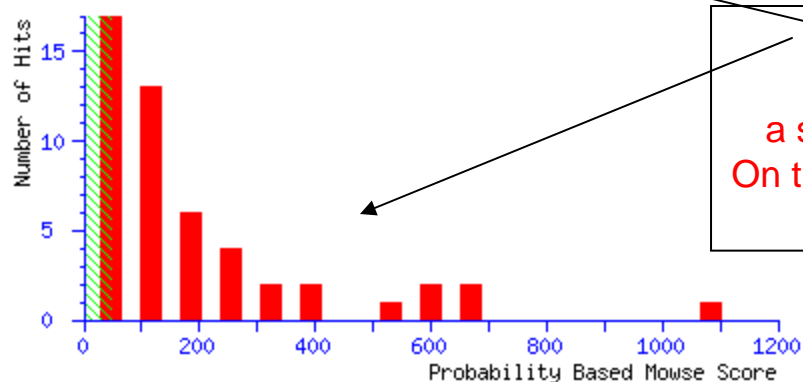
## Mascot Peptide Summary Report

### Probability Based Mowse Score

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

Individual ions scores  $> 46$  indicate identity or extensive homology ( $p < 0.05$ ).

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



**Score Histogram and identity threshold**  
Individual peptide identifications must have a score  $> 46$  to be "statistically significant" based on the Mascot scoring algorithm using a threshold of  $p < 0.5$

For simplicity, the report will be set to show only peptides with an ion score greater than the significance threshold (this value will NOT always be 46 and is largely dependent on the size of the data file and the size of the database searched).

### Peptide Summary Report

Format As	Peptide Summary		<a href="#">Help</a>
Significance threshold $p <$	0.05	Max. number of hits	AUTO
Standard scoring	<input type="radio"/> MudPIT scoring <input checked="" type="radio"/>	Ions score or expect cut-off	46
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"/>

Next is a list of each identified protein and information about all of the peptides identified

## Mascot Peptide Summary Report

1. [IPI00022463](#) Mass: 79331 Score: 1085  
 Tax\_Id=9606 Gene\_Symbol=TF Serotransferrin  
 Check to include this hit in error tolerant search

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> <a href="#">1557</a>	490.1410	978.2672	978.0569	0.2103	0	(59)	0.0029	1	K.DGAGDVAFVK.H
<input checked="" type="checkbox"/> <a href="#">1558</a>	490.2070	978.3992	978.0569	0.3423	0	70	0.00027	1	K.DGAGDVAFVK.H
<input checked="" type="checkbox"/> <a href="#">1559</a>	490.2430	978.4712	978.0569	0.4143	0	(62)	0.0016	1	K.DGAGDVAFVK.H
<input checked="" type="checkbox"/> <a href="#">2483</a>	598.7270	1195.4392	1195.3056	0.1337	0	(51)	0.01	1	K.DSGFQMNQLR.G
<input checked="" type="checkbox"/> <a href="#">2484</a>	598.7510	1195.4872	1195.3056	0.1817	0	(48)	0.023	1	K.DSGFQMNQLR.G
<input checked="" type="checkbox"/> <a href="#">2486</a>	598.8660	1195.7172	1195.3056	0.4117	0	52	0.011	1	K.DSGFQMNQLR.G
<input checked="" type="checkbox"/> <a href="#">2681</a>	625.6430	1249.2712	1249.3264	-0.0552	0	79	1.8e-005	1	K.SASDLTWDNLK.G
<input checked="" type="checkbox"/> <a href="#">2685</a>	625.8280	1249.6412	1249.3264	0.3148	0	(75)	4.3e-005	1	K.SASDLTWDNLK.G
<input checked="" type="checkbox"/> <a href="#">2687</a>	626.0300	1250.0452	1249.3264	0.7188	0	(73)	7.9e-005	1	K.SASDLTWDNLK.G
<input checked="" type="checkbox"/> <a href="#">2735</a>	637.1310	1272.2472	1273.3942	-1.1470	0	(48)	0.03	1	K.HSTIFENLANK.A
<input checked="" type="checkbox"/> <a href="#">2736</a>	637.8660	1273.7172	1273.3942	0.3230	0	50	0.016	1	K.HSTIFENLANK.A
<input checked="" type="checkbox"/> <a href="#">2747</a>	638.8270	1275.6392	1276.3966	-0.7573	0	51	0.013	1	K.EFQLFSSPHGK.D
<input checked="" type="checkbox"/> <a href="#">2767</a>	642.6600	1283.3052	1283.3444	-0.0392	0	(50)	0.014	1	K.EGYGYTGAFR.C
<input checked="" type="checkbox"/> <a href="#">2768</a>	642.8210	1283.6272	1283.3444	0.2828	0	(46)	0.038	1	K.EGYGYTGAFR.C
<input checked="" type="checkbox"/> <a href="#">2769</a>	643.0000	1283.9852	1283.3444	0.6408	0	66	0.00039	1	K.EGYGYTGAFR.C
<input checked="" type="checkbox"/> <a href="#">2849</a>	659.8300	1317.6452	1317.4270	0.2182	0	(59)	0.0028	1	R.WCAVSEHEATK.C
<input checked="" type="checkbox"/> <a href="#">2850</a>	659.8740	1317.7332	1317.4270	0.3062	0	67	0.00037	1	R.WCAVSEHEATK.C
<input checked="" type="checkbox"/> <a href="#">3141</a>	708.8100	1415.6052	1415.6116	-0.0064	0	66	0.00042	1	K.SVIPSDGSPVACVK.K
<input checked="" type="checkbox"/> <a href="#">3142</a>	708.8450	1415.6752	1415.6116	0.0636	0	(60)	0.0015	1	K.SVIPSDGSPVACVK.K
<input checked="" type="checkbox"/> <a href="#">3143</a>	708.8670	1415.7192	1415.6116	0.1076	0	(62)	0.00088	1	K.SVIPSDGSPVACVK.K
<input checked="" type="checkbox"/> <a href="#">1707</a>	508.2320	1521.6738	1521.6937	-0.0198	1	50	0.019	1	R.LKCDEWSVNSVGK.I
<input checked="" type="checkbox"/> <a href="#">3398</a>	766.7900	1531.5652	1531.7100	-0.1448	0	(102)	1.1e-007	1	K.CSTSSLLEACTFR.R

Mass error between experimental and theoretical peptide mass

Ion score in ( ) indicates lower scoring redundant matches for the same peptide

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

Protein View will be included for top 1-3 proteins (depending on the complexity of the sample)

### Protein View

Match to: IPI00022463 Score: 1085

Tax\_Id=9606 Gene\_Symbol=TF Serotransferrin

Found in search of C:\Program Files\Matrix Science\Mascot Daemon\data\trap-mgf\1x\_A\_msn.mgf

Nominal mass ( $M_r$ ): 79331; Calculated pI value: 6.81

NCBI BLAST search of [IPI00022463](#) against nr

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

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

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

Sequence Coverage: 32%

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

Matched peptides shown in **Bold Red**

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1  MRLAVGALLV CAVLGLCLAV PDKTVRWCAV SEHEATKCQS FRDHMKSVIP
51 SDGPSVACVK KASYLDCIRA IAANEADAVT LDAGLVYDAY LAPNNLKPVV
101 AEFYGSKEDP QTFYYAVAVV KKDSGFQMNQ LRGKKSCHTG LGRSAGWNIP
151 IGLLYCDLPE PRKPLEKAVA NFFSGSCAPC ADGTDFFQLC QLCPGCGCST
201 LNQYFGYSGA FKCLKDGAGD VAFVKHSTIF ENLANKARDR QYELLCLDNT
251 RKPVDEYKDC HLAQVPSHTV VARSMGGKED LIWELLNQAQ EHFGKDKSKE
301 FQLFSSPHGK DLLFKDSAAG FLKVPPRMDA KMYLGYEYVT AIRNLREGTC
351 PEAPTDECKP VKWCALSHHE RLKCDEWSVN SVGKIECVSA ETTEDCIAKI
401 MNGEADAMSL DGGFVYIAGK CGLVPVLAEN YNKSDNCEDT PEAGYFAVAV
451 VKKSASDLTW DNLKGGKKSCH TAVGRTAGWN IPMGLLYNKI NHCRFDEFFS
501 EGCAPGSKKD SSLCKLCMGS GLNLCEPNNK EGYYGYTGAF RCLVEKGDVA
551 FVKHQTVQPQN TGGKNPDPWA KNLNEKDYEL LCLDGTRKPV EEYANCHLAR
601 APNHAVVTRK DKEACVHKIL RQQQHLFGSN VTDCSGNFCL FRSETKDLLF
651 RDDTVCLAKL HDRNTYEKYL GEEYVKAAGN LRKCSTSSLL EACTFRRP
    
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General Rule:

You need to identify at least 2 unique peptides (repeat detection of the same peptide doesn't count!) to confidently identify a protein.