

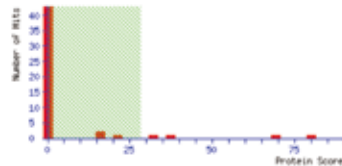
MASCOT Search Results

User :
 Email :
 Search title :
 MS data file :
 Database : NUSInr 20141019 (51471198 sequences: 18460256539 residues)
 Taxonomy : Saccharomyces Cerevisiae (baker's yeast) (50168 sequences)
 Timestamp :
 Protein hits :

- [x|16321879](#) Rtc3p [Saccharomyces cerevisiae S288c]
- [x|1322920148](#) Chain A, Crystal Structure Of Oxidized Form From Saccharomyces Cerevisiae
- [x|2131127](#) RPS21A [Saccharomyces cerevisiae]
- [x|6320275](#) Fmp16p [Saccharomyces cerevisiae S288c]
- [x|323308207](#) Mrp17p [Saccharomyces cerevisiae Fosters0]
- [x|323349895](#) Ccr4p [Saccharomyces cerevisiae Lalvin QA23]
- [x|16321935](#) Chs7p [Saccharomyces cerevisiae S288c]

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 > 28 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 Ions score or expect cut-off 0 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. [x|16321879](#) Mass: 12002 Score: 80 Matches: 2(2) Sequences: 2(2) eMPAI: 0.62
 Rtc3p [Saccharomyces cerevisiae S288c]

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"/> 104	495.2290	988.4434	988.4825	-0.0391	0	67	9.8e-06	1	U	R.GAEGELGAASK.A
<input checked="" type="checkbox"/> 110	511.2291	1020.4437	1020.4876	-0.0439	0	32	0.028	1	U	K.AGVENEFGK.G

Proteins matching the same set of peptides:

[x|130749784](#) Mass: 14164 Score: 80 Matches: 2(2) Sequences: 2(2)
 Chain A, Solution Nmr Structure Of Protein Yhr057w From Saccharomyces Cerevisiae, Northeast Structural Genomics Consortium Target Ytyst425

2. [x|1322920148](#) Mass: 12264 Score: 67 Matches: 6(2) Sequences: 3(2) eMPAI: 0.61
 Chain A, Crystal Structure Of Oxidized Form From Saccharomyces Cerevisiae

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"/> 85	351.6791	701.3437	701.3708	-0.0271	0	9	0.8	1	U	K.GAIASNV.-
<input checked="" type="checkbox"/> 97	466.7307	931.4468	931.4871	-0.0403	0	38	0.012	1	U	K.WIAPWIEK.F
<input checked="" type="checkbox"/> 99	470.2680	938.5214	938.5549	-0.0335	0	44	0.0028	1	U	R.VYGANPAAIK.Q
<input checked="" type="checkbox"/> 100	474.7274	947.4403	947.4820	-0.0416	0	(7)	14	1	U	K.WIAPWIEK.F + Oxidation (M)
<input checked="" type="checkbox"/> 101	474.7291	947.4436	947.4820	-0.0384	0	(24)	0.27	1	U	K.WIAPWIEK.F + Oxidation (M)
<input checked="" type="checkbox"/> 102	482.7255	963.4364	963.4769	-0.0405	0	(17)	1.1	1	U	K.WIAPWIEK.F + 2 Oxidation (M)

Proteins matching the same set of peptides:

[x|1323714537](#) Mass: 11238 Score: 67 Matches: 6(2) Sequences: 3(2)
 Chain A, Crystal Structure Of Mxr1 From Saccharomyces Cerevisiae In Complex With Trx2
[x|1349578415](#) Mass: 11341 Score: 67 Matches: 6(2) Sequences: 3(2)
 K7, Trx2p [Saccharomyces cerevisiae Kyokai no. 7]
[x|1383875712](#) Mass: 12248 Score: 67 Matches: 6(2) Sequences: 3(2)
 Chain B, Crystal Structure Of Peroxiredoxin Ahp1 From Saccharomyces Cerevisiae In Complex With Thioredoxin Trx2
[x|1398366149](#) Mass: 11311 Score: 67 Matches: 6(2) Sequences: 3(2)
 thioredoxin TRX2 [Saccharomyces cerevisiae S288c]

3. [x|2131127](#) Mass: 8882 Score: 38 Matches: 1(1) Sequences: 1(1) eMPAI: 0.38
 RPS21A [Saccharomyces cerevisiae]

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"/> 103	486.2563	970.5020	970.5447	-0.0427	0	38	0.012	1	U	R.LAQMGLLK.N

Proteins matching the same set of peptides:

[x|16322325](#) Mass: 9811 Score: 38 Matches: 1(1) Sequences: 1(1)
 ribosomal 40S subunit protein S21B [Saccharomyces cerevisiae S288c]
[x|1256272110](#) Mass: 9910 Score: 38 Matches: 1(1) Sequences: 1(1)
 Rps21bp [Saccharomyces cerevisiae JAY291]
[x|1398365233](#) Mass: 9797 Score: 38 Matches: 1(1) Sequences: 1(1)

Fig. S3. Mascot search results. Peptides derived from a tryptic digestion of a protein band of interest were separated and analyzed by nanoLC-ESI-Q-TOF mass spectrometry (MS/MS). The collected data were analyzed by database search using the MASCOT program.