



MASCOT Search Results

Protein View: TPM2_HUMAN

Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1

Database: SwissProt
Score: 105
Expect: 6.4e-07
Monoisotopic mass (M_r): 32945
Calculated pI: 4.66
Taxonomy: Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of TPM2_HUMAN against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Mass values searched: 11
Mass values matched: 10

Protein sequence coverage: 22%

Matched peptides shown in **bold red**.

1 MDAIKKKMQM LK**LDKENAID** RAEQAEADKK QAEDRCKQLE EEQQALQKKL
 51 KGTEDVEVEKY SESVKEAQEK LEQAEKKATD AEADVASLNR **RIQLVEEELD**
 101 **RAQERLATAL** QKLEEAEEKAA DESERGMK**VI** **ENRAMKDEEK** MELQEMQLKE
 151 AK**HIAEDSDR** K**YEEVARKLV** **ILEGELERSE** ERAEVAESKC GDLEELKIV
 201 TNNLKSLEAQ ADKYSTKEDK YEEEIKLLEE **KLKEAETRAE** **FAERSVAKLE**
 251 KTIDDLEDEV YAQKMKYKAI SEELDNLND ITSL

Unformatted sequence string: **284 residues** (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
 Show ☒ matched peptides only ☐ predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Peptide
13 - 21	1073.4800	1072.4727	1072.5513	-0.0785 1	K.LDKENAIDR.A
91 - 101	1399.6200	1398.6127	1398.7467	-0.1339 1	R.RIQLVEEELDR.A
92 - 101	1243.6000	1242.5927	1242.6456	-0.0528 0	R.IQLVEEELDR.A
129 - 133	630.3200	629.3127	629.3497	-0.0369 0	K.VIENR.A
153 - 160	942.3400	941.3327	941.4203	-0.0875 0	K.HIAEDSDR.K
162 - 168	894.4100	893.4027	893.4606	-0.0579 1	K.YEEVARK.L
168 - 178	1298.6800	1297.6727	1297.7605	-0.0878 1	R.KLVILEGELER.S
169 - 178	1170.5800	1169.5727	1169.6656	-0.0928 0	K.LVILEGELER.S
232 - 238	846.4100	845.4027	845.4606	-0.0579 1	K.LKEAETR.A
239 - 244	722.2800	721.2727	721.3395	-0.0668 0	R.AEFAER.S

No match to: 916.4000