



# MASCOT Search Results

## Protein View: TPM4\_HUMAN

**Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3**

**Database:** SwissProt  
**Score:** 89  
**Expect:** 2.5e-05  
**Monoisotopic mass (M<sub>r</sub>):** 28619  
**Calculated pI:** 4.67  
**Taxonomy:** Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of TPM4\\_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:** 10  
**Mass values matched:** 8

### Protein sequence coverage: 22%

Matched peptides shown in **bold red**.

1 MAGLNSLEAV KR**KIQALQQQ ADEAEDRA**QG LQRELDGERE RREKAEGDVA  
 51 ALNRR**IQLVE EELDRA**QERL ATALQKLEEA EKAADESERG MKVIENRAMK  
 101 DEEKMEIQEM QLKEAK**HIAE EADRYEEVA RKLVILEGEL ERAEERA**EVs  
 151 ELKCGDLLEE LKNVTNNLKS LEAASEKYSE KEDKYEEEEK LLSDKLKEAE  
 201 TR**AEFAER**TV AKLEKTIDDL EEKLAQAKEE NVGLHQTLDDQ TLNELNCI

Unformatted sequence string: 248 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 - 27	1742.8000	1741.7927	1741.8595	-0.0667 1	R.KIQALQQQADEAEDR.A
56 - 65	1243.6300	1242.6227	1242.6456	-0.0228 0	R.IQLVEEELDR.A
117 - 124	940.4500	939.4427	939.4410	0.0017 0	K.HIAEEADR.K
117 - 125	1068.6200	1067.6127	1067.5359	0.0768 1	K.HIAEEADRK.Y
126 - 132	894.4500	893.4427	893.4606	-0.0179 1	K.YEEVARK.L
132 - 142	1298.7200	1297.7127	1297.7605	-0.0478 1	R.KLVILEGELER.A
133 - 142	1170.5900	1169.5827	1169.6656	-0.0828 0	K.LVILEGELER.A
203 - 208	722.3800	721.3727	721.3395	0.0332 0	R.AEFAER.T

No match to: 634.2000, 804.3300