



MASCOT Search Results

Protein View: ACTB_HUMAN

Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1

Database: SwissProt
Score: 97
Expect: 4.1e-06
Monoisotopic mass (M_r): 42052
Calculated pI: 5.29
Taxonomy: Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of ACTB 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: 21%

Matched peptides shown in **bold red**.

1 MDDDIAALVV DNGSGMCK**AG FAGDDAPRAV** FPSIVGRPRH QGVMVGMGQK
 51 **DSYVGDEAQS KRGILTLKYP** IEHGIVTNWD DMEKIWHHTF YNELRVAPEE
 101 HPVLLTEAPL NPKANREKMT QIMFETFNTF AMYVAIQAVL SLYASGRRTG
 151 IVMDSGDGVHTVPIYEGYA LPHAILRLDL AGRDLTDYLM **KILTERGYSF**
 201 **TTTAEREIVR** DIKEKLCYVA LDFAQEMATA ASSSSLEK**SY ELPDGQVITI**
 251 **GNERFRCPEA** LFQPSFLGME SCGIHETTFN SIMK**CDVDIR KDLYANTVLS**
 301 GGTMYPGIA DRMQKEITAL APSTMKIKII APPERKYSVW IGGSILASLS
 351 TFQQMWISK**Q EYDESGPSIV HRKCF**

Unformatted sequence string: **375 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
19 - 28	976.2600	975.2527	975.4410	-0.1883 0	K.AGFAGDDAPR.A
51 - 61	1198.4400	1197.4327	1197.5150	-0.0822 0	K.DSYVGDEAQS.K
62 - 68	800.3800	799.3727	799.5280	-0.1552 1	K.RGILTLK.Y
192 - 196	631.3500	630.3427	630.3701	-0.0273 0	K.ILTER.G
197 - 206	1132.3100	1131.3027	1131.5197	-0.2169 0	R.GYSFTTTAER.E
239 - 254	1790.5300	1789.5227	1789.8846	-0.3619 0	K.SYELPDGQVITIGNER.F
285 - 291	905.4400	904.4327	904.4436	-0.0109 1	K.CDVDIRK.D
360 - 372	1516.4300	1515.4227	1515.6954	-0.2727 0	K.QEYDESGPSIVHR.K

No match to: 1185.7900, 1953.5600