

MATRIX SCIENCE MASCOT Search Results

Protein View: ACTB_HUMAN

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

Database: SwissProt
 Score: 160
 Expect: 2e-12
 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: 20
 Mass values matched: 15

Protein sequence coverage: 37%

Matched peptides shown in **bold red**.

1 MDDDIAALVV DNGSGMCK**AG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK**
 51 DSYVGDEAQS **KRGILTLKYP** IEHGIVTNWD DMEK**IWHHTF YNELRVAPEE**
 101 **HPVLLTEAPL NPK**ANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRRTG
 151 IVMDSGDGVT HTVPIYEGYA LPHAILR**LDL AGRDLTDYLM KILTERGYSF**
 201 **TTTAEREIVR** DIKEKLCYVA LDFEQEMATA ASSSSLEK**SY ELPDGQVITI**
 251 **GNERFRCPEA** LFQPSFLGME SCGIHETTFN SIMK**CDVDIR KDLYANTVLS**
 301 **GGTMYPGIA DR**MQKEITAL APSTMKIK**II APPERKYSVW** IGGSILASLS
 351 TFQQMWISKQ 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	976.4900	975.4827	975.4410	0.0417 0	K.AGFAGDDAPR.A
29 - 39	1198.7900	1197.7827	1197.6982	0.0845 0	R.AVFPSIVGRPR.H
40 - 50	1171.6300	1170.6227	1170.5638	0.0589 0	R.HQGVMVGMGQK.D
40 - 50	1187.5200	1186.5127	1186.5587	-0.0460 0	R.HQGVMVGMGQK.D + Oxidation (M)
62 - 68	800.5500	799.5427	799.5280	0.0148 1	K.RGILTLK.Y
85 - 95	1515.8000	1514.7927	1514.7419	0.0509 0	K.IWHHTFYNELR.V
96 - 113	1954.1100	1953.1027	1953.0571	0.0456 0	R.VAPEEHPVLLTEAPLNPK.A
178 - 183	644.3400	643.3327	643.3653	-0.0326 0	R.LDLAGR.D
192 - 196	631.4500	630.4427	630.3701	0.0727 0	K.ILTER.G
197 - 206	1132.5900	1131.5827	1131.5197	0.0631 0	R.GYSFTTTAER.E
239 - 254	1791.0200	1790.0127	1789.8846	0.1281 0	K.SYELPDGQVITIGNER.F
285 - 291	905.4500	904.4427	904.4436	-0.0009 1	K.CDVDIRK.D
292 - 312	2215.1600	2214.1527	2214.0627	0.0900 0	K.DLYANTVLSGGTTMYPGIADR.M
329 - 335	795.4900	794.4827	794.4650	0.0177 0	K.IIAPPER.K
329 - 336	923.6000	922.5927	922.5600	0.0328 1	K.IIAPPERK.Y

No match to: 621.8800, 622.1400, 796.6700, 842.5400, 945.5200