



MASCOT Search Results

Protein View: ANXA5_HUMAN

Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2

Database: SwissProt
Score: 83
Expect: 9.9e-05
Monoisotopic mass (M_r): 35971
Calculated pI: 4.94
Taxonomy: Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of ANXA5 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: 7

Protein sequence coverage: 22%

Matched peptides shown in **bold red**.

```

1  MAQVLRGTVT DFPGFDERAD AETLRKAMKLGTDEESILT LLTSRSNAQR
51  QEISAAFKTL FGRDLLDDLK SELTGKFEKL IVALMKPSRL YDAYELKHAL
101 KGAGTNEKVL TEIIASRTPE ELRAIKQVYE EEYGSSLEDD VVGDTSGYYQ
151 RMLVVLLQAN RDPDAGIDEA QVEQDAQALF QAGELKWGTD EEKFITIFGT
201 RSVSHLRKVF DKYMTISGFQ IEETIDRETS GNLEQLLLAV VKSIRSIPAY
251 LAETLYYAMK GAGTDDHTLI RVMVSRSEID LFNIRKEFRK NFATSLYSMI
301 KGDTSGDYKK ALLLLCGEDD
  
```

Unformatted sequence string: **320 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
7 - 18	1340.3400	1339.3327	1339.6045	-0.2718 0	R.GTVTDFPGFDER.A
30 - 45	1704.4600	1703.4527	1703.8941	-0.4414 0	K.GLG TDEESILTLLTSR.S
194 - 201	954.2800	953.2727	953.5335	-0.2607 0	K.FITIFGTR.S
202 - 207	698.1600	697.1527	697.3871	-0.2344 0	R.SVSHLR.K
261 - 271	1155.4300	1154.4227	1154.5680	-0.1453 0	K.GAGTDDHTLIR.V
277 - 286	1234.5000	1233.4927	1233.6717	-0.1790 1	R.SEIDL F NIRK.E
302 - 309	842.1200	841.1127	841.3454	-0.2327 0	K.GDTSGDYK.K

No match to: 621.7900, 649.7700, 1339.2300