



MASCOT Search Results

Protein View: ANXA5_HUMAN

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

Database: SwissProt
Score: 79
Expect: 0.00027
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: 11
Mass values matched: 7

Protein sequence coverage: 21%

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	1704.5100	1703.5027	1703.8941	-0.3914 0	K.GLGTDDEESILTLTSR.S
194 - 201	954.3200	953.3127	953.5335	-0.2207 0	K.FITIFGTR.S
202 - 207	698.2200	697.2127	697.3871	-0.1744 0	R.SVSHLR.K
261 - 271	1155.3000	1154.2927	1154.5680	-0.2753 0	K.GAGTDDHTLIR.V
277 - 285	1106.3200	1105.3127	1105.5768	-0.2640 0	R.SEIDLFNIR.K
302 - 309	842.2600	841.2527	841.3454	-0.0927 0	K.GDTSGDYK.K

No match to: 621.8100, 665.8600, 728.2000, 804.1400