



MASCOT Search Results

Protein View: GSTP1_HUMAN

Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2

Database: SwissProt
Score: 75
Expect: 0.00069
Monoisotopic mass (M_r): 23569
Calculated pI: 5.43
Taxonomy: Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of GSTP1_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: 7

Protein sequence coverage: 47%

Matched peptides shown in **bold red**.

1 **MPPYTVVYFP VR**GRCAALRM LLADQGQSWK EEVTVVETWQ EGS**LKASCLY**
 51 **GQLPKFQDGD LTLYQSN**TIL RHLGRTLGLY GK**DQQE**AALV **DMVNDGVEDL**
 101 **RCKYISLIYT NYEAGKDDYV KALPGQLKPF ETLLSQNQGG K**TFIVGDQIS
 151 FADYNLLDLL LIHEVLAPGC LDAFPLLSAY VGR**LSARPKL** KAFLASPEYV
 201 NLPINGNGKQ

Unformatted sequence string: 210 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
2 - 12	1337.4000	1336.3927	1336.7180	-0.3252 0	M.PPYTVVYFPVR.G
46 - 55	1136.1900	1135.1827	1135.5696	-0.3868 0	K.ASCLYGQLPK.F
56 - 71	1883.5800	1882.5727	1882.9425	-0.3698 0	K.FQDGLTLTYQSN TILR.H
83 - 101	2116.5000	2115.4927	2115.9743	-0.4815 0	K.DQQE AALV DMVNDGVEDL .C
104 - 121	2154.5900	2153.5827	2154.0521	-0.4693 1	K.YISLIYTNYEAGKDDYV .A
122 - 141	2125.7400	2124.7327	2125.1531	-0.4204 0	K.ALPGQLKPFETLLSQNQGGK .T
184 - 189	671.1200	670.1127	670.4126	-0.2999 0	R.LSARPK.L

No match to: 621.6300, 648.3900, 649.9900, 670.6200, 673.2000, 681.8800, 702.2100, 717.0400, 729.5100, 842.0700, 843.2500, 874.7200, 1339.9400