

# MATRIX SCIENCE MASCOT Search Results

## Protein View: GRP78\_HUMAN

78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2

Database: SwissProt  
Score: 121  
Expect: 1.6e-08  
Monoisotopic mass (M<sub>r</sub>): 72402  
Calculated pI: 5.07  
Taxonomy: Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of GRP78\\_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: 13  
Mass values matched: 11

### Protein sequence coverage: 20%

Matched peptides shown in **bold red**.

```

1  MKLSLVAAML LLLSAARAE EDKKEDVGTV VGIDLGTTYS CVGVFKNGRV
51  EIIANDQGNR ITPSYVAFTP EGERLIGDAA KNQLTSNPEN TVFDAKRLIG
101 R.TWNDPSVQQ DIKFLPFKVV EKKTKPYIQV DIGGGQTKTF APEEISAMVL
151 TKMKETAEEY LGKKVTHAVV TVPAYFNDAQ RQATKDAGTI AGLNVMRIIN
201 EPTAAAIAYG LDKREGEKNI LVFDLGGGTF DVSLLTIDNG VFEVVATNGD
251 THLGGEDFDQ RVMEHFIKLY KKKTKGDVRK DNRAVQKLRR EVEKAKRALS
301 SQHQARIEIE SFYEGEDFSE TLTRAKFEEL NMDLFRSTMK PVQKVLEDSD
351 LK.KSDIDEIV LVGGSTRIPK IQQLVKEFFN GKEPSRGINP DEAVAYGAAV
401 QAGVLSGDQD TGDLVLLDVC PLTLGIETVG GVMTKLIPRN TVVPTKKSQI
451 FSTASDNQPT VTIKVYEGER PLTKDNHLLG TFDLTGIPPA PRGVPQIEVT
501 FEIDVNGILR VTAEDKGTGN KNKITITNDQ NRLTPEEIER MVNDAEKFAE
551 EDKKLKERID TRNELESYAY SLKNQIGDKE KLGKGLSSED KETMEKAVEE
601 KIEWLESHQD ADIEDFKAKK KELEEIVQPI ISKLYGSAGP PPTGEEDTAE
651 KDEL

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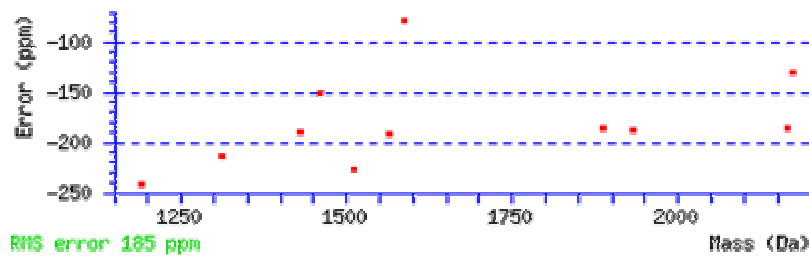
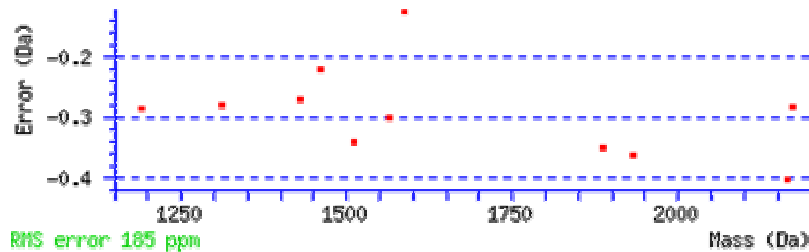
Unformatted sequence string: **654 residues** (for pasting into other applications).

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
61 - 74	1566.4800	1565.4727	1565.7726	-0.2998 0	<b>R.ITPSYVAFTPEGER.L</b>
102 - 113	1430.4200	1429.4127	1429.6838	-0.2710 0	<b>R.TWNDPSVQQDIK.F</b>
165 - 181	1887.6200	1886.6127	1886.9639	-0.3512 0	<b>K.VTHAVVTPPAYFNDAQ.R.Q</b>
307 - 324	2164.5900	2163.5827	2163.9848	-0.4021 0	<b>R.IEIESFYEGEDFSETLTR.A</b>
325 - 336	1512.4100	1511.4027	1511.7442	-0.3415 1	<b>R.AKFEELNMDLFR.S</b>
327 - 336	1313.3400	1312.3327	1312.6122	-0.2794 0	<b>K.FEELNMDLFR.S</b>
353 - 367	1588.7300	1587.7227	1587.8468	-0.1241 1	<b>K.KSDIDEIVLVGGSTR.I</b>

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
354 - 367	1460.5400	1459.5327	1459.7518	-0.2191 0	K.SDIDEIVLVGGSTR.I
465 - 474	1191.3500	1190.3427	1190.6295	-0.2868 0	K.VYEGERPLTK.D
475 - 492	1933.6500	1932.6427	1933.0058	-0.3630 0	K.DNHLLGTFDLTGIPPAPR.G
634 - 654	2175.7100	2174.7027	2174.9855	-0.2828 1	K.LYGSAGPPPTGEEDTAEKDEL.-

No match to: 1693.4900, 1976.6700



ID GRP78\_HUMAN Reviewed; 654 AA.  
AC P11021; B0QZ61; Q2EF78; Q9NPF1; Q9UK02;  
DT 01-JUL-1989, integrated into UniProtKB/Swiss-Prot.  
DT 11-JUL-2001, sequence version 2.  
DT 22-NOV-2017, entry version 208.  
DE RecName: Full=78 kDa glucose-regulated protein {ECO:0000303|PubMed:2840249};  
DE Short=GRP-78 {ECO:0000303|PubMed:2840249};  
DE AltName: Full=Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78 {ECO:0000303|PubMed:2840249};  
DE AltName: Full=Heat shock 70 kDa protein 5;  
DE AltName: Full=Immunoglobulin heavy chain-binding protein {ECO:0000250|UniProtKB:P20029};  
DE Short=BiP {ECO:0000250|UniProtKB:P20029};  
DE Flags: Precursor;  
GN Name=HSPA5 {ECO:0000312|HGNC:HGNC:5238};  
GN Synonyms=GRP78 {ECO:0000303|PubMed:2840249};  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX PubMed=2840249; DOI=10.1089/dna.1988.7.275;  
RA Ting J., Lee A.S.;  
RT "Human gene encoding the 78,000-dalton glucose-regulated protein and  
RT its pseudogene: structure, conservation, and regulation."  
RL DNA 7:275-286(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Cervix carcinoma;  
RA Chao C.C.K.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Fibroblast;  
RA Hansen J.J., Nielsen M.N., Jorgensen M.M., Gregersen N., Bolund L.;  
RT "Grp78 is involved in the quality control of the LDL-receptor."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [MRNA].