



# MASCOT Search Results

## Protein View: RSSA\_HUMAN

40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4

**Database:** SwissProt  
**Score:** 95  
**Expect:** 6.6e-06  
**Monoisotopic mass (M<sub>r</sub>):** 32947  
**Calculated pI:** 4.79  
**Taxonomy:** Homo sapiens

Sequence similarity is available as [an NCBI BLAST search of RSSA\\_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:** 8

### Protein sequence coverage: 29%

Matched peptides shown in **bold red**.

```

1  MSGALDVLQM  KEEDVLKFLA  AGTHLGGTNL  DFQMEQYIYK  RKSDGIYIIN
51  LKRTWEKLLL  AARAIVAIEN  PADVSVISSR  NTGQRAVLKF  AAATGATPIA
101 GRFTPGTFTN  QIQAAFREPR  LLVVTDPDPRAD  HQPLTEASYV  NLPTIALCNT
151  DSPLRYVDIA  IPCNNKGAHS  VGLMWMLAR  EVLRMRGTIS  REHPWEVMPD
201  LYFYRDPEEI  EKEEQAAAEK  AVTKEEFQGE  WTAPAPEFTA  TQPEVADWSE
251  GVQVPSVPIQ  QFPTEDWSAQ  PATEDWSAAP  TAQATEWVGA  TTDWS
  
```

Unformatted sequence string: 295 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
58 - 63	656.4600	655.4527	655.4381	0.0147 0	<b>K.LLLAAR.A</b>
64 - 80	1741.0000	1739.9927	1739.9417	0.0510 0	<b>R.AIVAIENPADVSVISSR.N</b>
90 - 102	1203.6700	1202.6627	1202.6408	0.0220 0	<b>K.FAAATGATPIAGR.F</b>
103 - 117	1698.8500	1697.8427	1697.8526	-0.0098 0	<b>R.FTPGTFTNQIQAAFR.E</b>
103 - 120	2081.0500	2080.0427	2080.0490	-0.0063 1	<b>R.FTPGTFTNQIQAAFREPR.L</b>
121 - 128	912.5500	911.5427	911.5440	-0.0013 0	<b>R.LLVVTDPDPR.A</b>
156 - 166	1306.5700	1305.5627	1305.6387	-0.0760 0	<b>R.YVDIAIPCNNK.G</b>
167 - 180	1614.8200	1613.8127	1613.7959	0.0168 0	<b>K.GAHSVGLMWMLAR.E</b>

No match to: 621.9700, 650.0800, 842.5200, 1419.8000, 1816.9200