

MATRIX SCIENCE MASCOT Search Results

Protein View: VIME_HUMAN

Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Database: SwissProt
Score: 116
Expect: 5.1e-08
Monoisotopic mass (M_r): 53676
Calculated pI: 5.06
Taxonomy: [Homo sapiens](#)

Sequence similarity is available as [an NCBI BLAST search of VIME_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: 17
Mass values matched: 13

Protein sequence coverage: 29%

Matched peptides shown in **bold red**.

```

1  MSTRSVSSSS YRRMFGGPGT ASRPSSRSY VTTSTRTYSL GSALRPSTSR
51  SLYASSPGGV YATRSSAVRL RSSVPGVRL QDSVDFSLAD AINTEFKNTR
101 TNEKVELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLKG QGKSRLGDLY
151 EEEMRELRRQ VDQLTNDKAR VEVERDNLAE DIMRLREKLQ EEMLQREEAE
201 NTLQSFRQDV DNASLARLDL ERKVESLQEE IAFLKKLHEE EIQLQAQIQ
251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSKFADLSE
301 AANRNNDALR QAKQESTEYR RQVQSLTCEV DALKGTNESL ERQMREMEEN
351 FAVEAANYQD TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY
401 RKLLEGESR ISLPLPNFSS LNLRETNLDS LPLVDTHSKR TLLIKTVETR
451 DGQVINETSQ HHDDLE

```

Unformatted sequence string: [466 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
51 - 64	1428.6300	1427.6227	1427.7045	-0.0818 0	R.SLYASSPGGVYATR.S
146 - 155	1254.5000	1253.4927	1253.5598	-0.0670 0	R.LGDLYEEEMR.E
171 - 184	1688.6900	1687.6827	1687.8199	-0.1372 1	R.VEVERDNLAEIMR.L
189 - 196	1046.4600	1045.4527	1045.5226	-0.0699 0	K.LQEEMLQR.E
224 - 236	1533.6300	1532.6227	1532.8450	-0.2222 1	K.VESLQEEIAFLKK.L
295 - 304	1093.4700	1092.4627	1092.5200	-0.0572 0	K.FADLSEAANR.N
305 - 310	702.3600	701.3527	701.3456	0.0071 0	R.NNDALR.Q
314 - 321	1068.4100	1067.4027	1067.4996	-0.0968 1	K.QESTEYRR.Q
365 - 378	1734.7100	1733.7027	1733.8076	-0.1049 1	R.LQDEIQNMKEEMAR.H
365 - 378	1750.6100	1749.6027	1749.8025	-0.1998 1	R.LQDEIQNMKEEMAR.H + Oxidation (M)
391 - 401	1295.5500	1294.5427	1294.6591	-0.1164 0	K.MALDIEIATYR.K
411 - 424	1570.7900	1569.7827	1569.8878	-0.1051 0	R.ISLPLPNFSSNLNR.E
425 - 440	1824.8200	1823.8127	1823.9377	-0.1250 1	R.ETNLDSLPLVDTHSKR.T

No match to: 621.9400, 804.3400, 974.4500, 1144.5200