

MATRIX SCIENCE MASCOT Search Results

Protein View: VIME_HUMAN

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

Database: SwissProt
Score: 91
Expect: 1.5e-05
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: 13
Mass values matched: 9

Protein sequence coverage: 27%

Matched peptides shown in **bold red**.

1 MSTRSVSSSS YRRMFGGPGT ASRPSSSRSY VTTSTR**TYSL** **GSALRPSTSR**
51 **SLYASSPGGV** **YATR**SSAVRL RSSVPGVRL QDSVDFSLAD AINTEFKNTR
101 TNEKVELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLKG QGKSRLGDLY
151 EEEMRELRRQ VDQLTNDKAR **VEVERDNLA****E** **DIMRLREKLQ** **EEMLQREEAE**
201 **NTLQSF****R**QDV DNASLARLDL ERK**VESLQEE** **IAFLKK**LHEE EIQLQAQIQ
251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSKFADLSE
301 AANRNNDALR QAK**QEST****EYR** **RQVQSLTCEV** DALKGTNESL ERQMR**EMEEN**
351 **FAVEAANYQD** **TIGRLQDEIQ** **NMKEEMAR**HL REYQDLLNVK **MALDIEIATY**
401 **RKLLEGEESR** 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 |
|-------------|-----------|-----------|-----------|----------|--------------------------|
| 37 - 50 | 1495.9200 | 1494.9127 | 1494.7790 | 0.1337 0 | R.TYSLGSALRPSTSR.S |
| 51 - 64 | 1428.7800 | 1427.7727 | 1427.7045 | 0.0682 0 | R.SLYASSPGGVYATR.S |
| 171 - 184 | 1688.9400 | 1687.9327 | 1687.8199 | 0.1128 1 | R.VEVERDNLAEDIMR.L |
| 189 - 207 | 2351.1300 | 2350.1227 | 2350.1223 | 0.0005 1 | K.LQEEMLQREEAENTLQSF.R.Q |
| 224 - 236 | 1533.9300 | 1532.9227 | 1532.8450 | 0.0778 1 | K.VESLQEEIAFLKK.L |
| 314 - 321 | 1068.6400 | 1067.6327 | 1067.4996 | 0.1332 1 | K.QESTEYRR.Q |
| 346 - 364 | 2187.0900 | 2186.0827 | 2185.9586 | 0.1242 0 | R.EMEENFAVEAANYQDTIGR.L |
| 365 - 378 | 1734.9700 | 1733.9627 | 1733.8076 | 0.1551 1 | R.LQDEIQNMKEEMAR.H |
| 391 - 401 | 1295.6800 | 1294.6727 | 1294.6591 | 0.0136 0 | K.MALDIEIATYR.K |

No match to: 606.2100, 644.3900, 672.0600, 935.8300