

MATRIX SCIENCE MASCOT Search Results

Protein View: VIME_HUMAN

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

Database: SwissProt
 Score: 180
 Expect: 2e-14
 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: 20
 Mass values matched: 17

Protein sequence coverage: 43%

Matched peptides shown in **bold red**.

1 MSTRSVSSSS YRR**MFGGPGT ASRPSSRSY** VTTSTR**TYSL GSALRPSTSR**
 51 **SLYASSPGGV YATR**SSAVRL RSSVPGVRL QDSVDFSLAD AINTEFKNTR
 101 **TNEKVELQEL NDR**FANYIDK VRFLEQQNKI LLAELEQLKG QGKSR**LGDL**
 151 **EEEMRELRRQ VDQLTNDKAR VEVERDNLA**E DIMRLREKLQ **EEMLQREEAE**
 201 **NTLQSFRQDV** DNASLARLDL ER**KVESLQEE** **IAFLKKLHEE** EIQELQAQIQ
 251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AK**NLQEAEEW YKSKFADLSE**
 301 **AANRNNDALR QAKQESTEYR RQVQSLTCEV** DALKGTNESL ERQMREMEEN
 351 FAVEAANYQD TIGRL**QDEIQ NMKEEMARHL** REYQDLLNVK **MALDIEIATY**
 401 **RKLLEGEESR ISLPLPNFSS LNLRETNLDS** LPLVDTHSKR TLLIKTVETR
 451 **DGQVINETSQ HHDDLE**

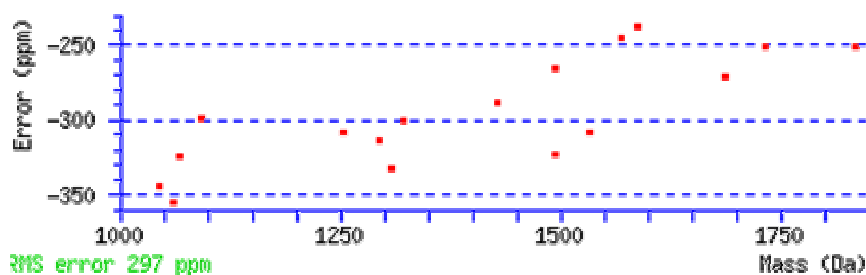
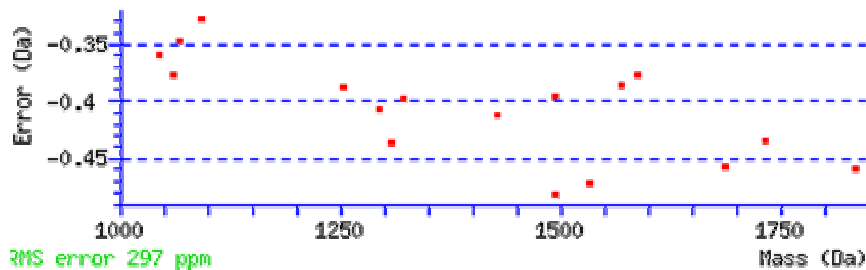
Unformatted sequence string: **466 residues** (for pasting into other applications).

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
14 - 28	1494.2300	1493.2227	1493.7045	-0.4818 0	R.MFGGPGTASRPSSSR.S
37 - 50	1495.3900	1494.3827	1494.7790	-0.3963 0	R.TYSLGSALRPSTSR.S
51 - 64	1428.3000	1427.2927	1427.7045	-0.4118 0	R.SLYASSPGGVYATR.S
101 - 113	1587.4200	1586.4127	1586.7900	-0.3773 1	R.TNEKVELQELNDR.F
146 - 155	1254.1800	1253.1727	1253.5598	-0.3870 0	R.LGDLYEEEMR.E
160 - 168	1060.1500	1059.1427	1059.5197	-0.3769 0	R.QVDQLTNDK.A
171 - 184	1688.3700	1687.3627	1687.8199	-0.4572 1	R.VEVERDNLAEDIMR.L
189 - 196	1046.1700	1045.1627	1045.5226	-0.3599 0	K.LQEEMLQR.E

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Peptide
197 - 207	1323.2200	1322.2127	1322.6102	-0.3975 0	R.EEAENTLQSFR.Q
224 - 236	1533.3800	1532.3727	1532.8450	-0.4722 1	K.VESLQEEIAFLKK.L
283 - 292	1309.1700	1308.1627	1308.5986	-0.4359 0	K.NLQEAEEWYK.S
295 - 304	1093.2000	1092.1927	1092.5200	-0.3272 0	K.FADLSEAANR.N
314 - 321	1068.1600	1067.1527	1067.4996	-0.3468 1	K.QESTEYRR.Q
365 - 378	1734.3800	1733.3727	1733.8076	-0.4349 1	R.LQDEIQNMKEEMAR.H
391 - 401	1295.2600	1294.2527	1294.6591	-0.4064 0	K.MALDIEIATYR.K
411 - 424	1570.5100	1569.5027	1569.8878	-0.3851 0	R.ISLPLPNFSSLNLR.E
451 - 466	1836.3400	1835.3327	1835.7922	-0.4595 0	R.DGQVINETSQHDDLE.-

No match to: 980.1300, 2186.4500, 2350.5700



ID VIME_HUMAN Reviewed; 466 AA.
AC P08670; B0YJC2; D3DRU4; Q15867; Q15868; Q15869; Q548L2; Q6LER9;
AC Q8N850; Q96ML2; Q9NTM3;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 4.
DT 20-DEC-2017, entry version 227.
DE RecName: Full=Vimentin;
GN Name=VIM;
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=3467175; DOI=10.1128/MCB.6.11.3614;
RA Ferrari S., Battini R., Kaczmarek L., Rittling S., Calabretta B.,
RA de Riel J.K., Philiponis V., Wei J.-F., Baserga R.;
RT "Coding sequence and growth regulation of the human vimentin gene.";
RL Mol. Cell. Biol. 6:3614-3620(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX PubMed=2251132; DOI=10.1093/nar/18.22.6692;
RA Honore B., Madsen P., Basse B., Andersen A., Walbum E., Celis J.E.,
RA Leffers H.;
RT "Nucleotide sequence of cDNA covering the complete coding part of the
RT human vimentin gene.";
RL Nucleic Acids Res. 18:6692-6692(1990).
RN [3]