

MATRIX SCIENCE MASCOT Search Results

Protein View: VIME_HUMAN

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

Database: SwissProt
 Score: 161
 Expect: 1.6e-12
 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: 15

Protein sequence coverage: 35%

Matched peptides shown in **bold red**.

1 MSTRSVSSSS YRRMFGGPGT ASRPSSRSY VTTSTRTYSL GSALRPSTSR
 51 SLYASSPGGV YATRSSAVRL **RSSVPGVRL** QDSVDFSLAD AINTEFKNTR
 101 **TNEKVELQEL** **NDRFANYIDK** **VRFLEQQNKI** **LLAELEQLKG** QGKSR**LGDLY**
 151 **EEEMRELRRQ** **VDQLTNDKAR** **VEVERDNLA** **DIMRLREKLQ** EEMLRQEEAE
 201 NTLQSFRQDV DNASLARLDL ER**KVESLQEE** **IAFLKKLHEE** EIQLQAQIQ
 251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSK**FADLSE**
 301 **AANRNNDALR** QAK**QESTEYR** **RQVQSLTCEV** DALKGTNESL ERQMREMEEN
 351 FAVEAANYQD TIGRL**QDEIQ** **NMKEEMARHL** REYQDLLNVK **MALDIEIATY**
 401 **RKLLEGEESR** **ISLPLPNFSS** **LNLRETNLDS** LPLVDTHSKR TLLIKTVETR
 451 **DGQVINETSQ** **HHDDLE**

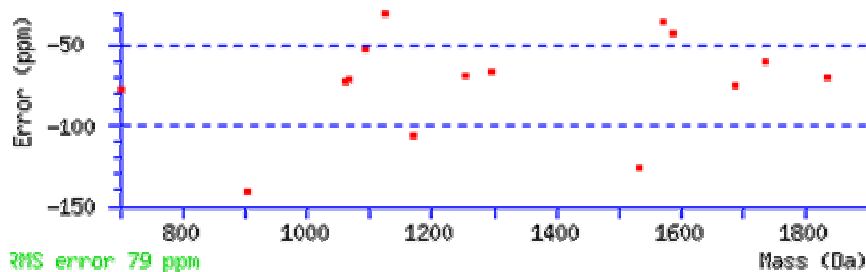
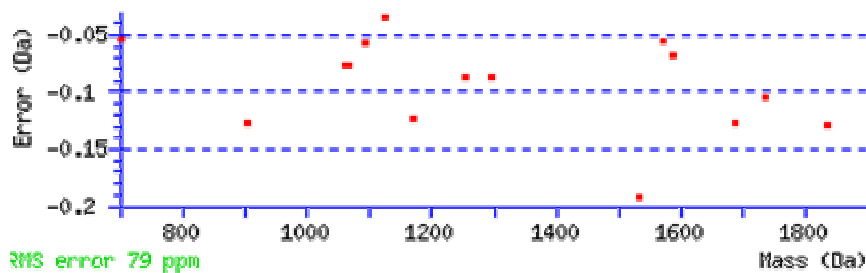
Unformatted sequence string: **466 residues** (for pasting into other applications).

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
72 - 78	701.3400	700.3327	700.3868	-0.0541 0	R.SSVPGVR.L
101 - 113	1587.7300	1586.7227	1586.7900	-0.0673 1	R.TNEKVELQELNDR.F
114 - 122	1125.5700	1124.5627	1124.5978	-0.0351 1	R.FANYIDKVR.F
123 - 129	906.3400	905.3327	905.4607	-0.1279 0	R.FLEQQNK.I
130 - 139	1169.5900	1168.5827	1168.7067	-0.1240 0	K.ILLAELEQLK.G
146 - 155	1254.4800	1253.4727	1253.5598	-0.0870 0	R.LGDLYEEEMR.E
160 - 168	1060.4500	1059.4427	1059.5197	-0.0769 0	R.QVDQLTNDK.A
171 - 184	1688.7000	1687.6927	1687.8199	-0.1272 1	R.VEVERDNLAEDIMR.L

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Peptide
224 - 236	1533.6600	1532.6527	1532.8450	-0.1922 1	K.VESLQEEIAFLKK.L
295 - 304	1093.4700	1092.4627	1092.5200	-0.0572 0	K.FADLSEAANR.N
314 - 321	1068.4300	1067.4227	1067.4996	-0.0768 1	K.QESTEYRR.Q
365 - 378	1734.7100	1733.7027	1733.8076	-0.1049 1	R.LQDEIQNMKEEMAR.H
391 - 401	1295.5800	1294.5727	1294.6591	-0.0864 0	K.MALDIEIATYR.K
411 - 424	1570.8400	1569.8327	1569.8878	-0.0551 0	R.ISLPLPNFSSLNLR.E
451 - 466	1836.6700	1835.6627	1835.7922	-0.1295 0	R.DGQVINETSQHDDLE.-

No match to: 804.3000, 994.3400



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]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Lymphoma;