

MATRIX SCIENCE MASCOT Search Results

Protein View: VIME_HUMAN

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

Database: SwissProt
 Score: 129
 Expect: 2.5e-09
 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: 14
 Mass values matched: 12

Protein sequence coverage: 30%

Matched peptides shown in **bold red**.

1 MSTRSVSSSS YRRMFGGPGT ASRPSSRSY VTTSTRTYSL GSALRPSTSR
 51 SLYASSPGGV YATRSSAVRL RSSVPGVRL QDSVDFSLAD AINTEFKNTR
 101 **TNEKVELQEL** NDRFANYIDK VR**FLEQQNKI** **LLAELEQLKG** QGKSRLGDLY
 151 EEEMRELRRQ **VDQLTNDK**AR VEVERDNLAE DIMRLREKLQ EEMLQREEAE
 201 NTLQSFRQDV DNASLARLDL ERK**VESLQEE** **IAFLKKLHEE** EIQLQAQIQ
 251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSKFADLSE
 301 AANR**NNDALR** QAK**QESTEYR** RQVQSLTCEV DALKGTNESL ERQMR**EMEEN**
 351 **FAVEAANYQD** **TIGRLQDEIQ** **NMKEEMAR**HL REYQDLLNVK **MALDIEIATY**
 401 **RKLLEGEESR** **ISLPLPNFSS** **LNLRETNLDS** LPLVDTHSKR TLLIKTVETR
 451 **DGQVINETSQ** **HHDDLE**

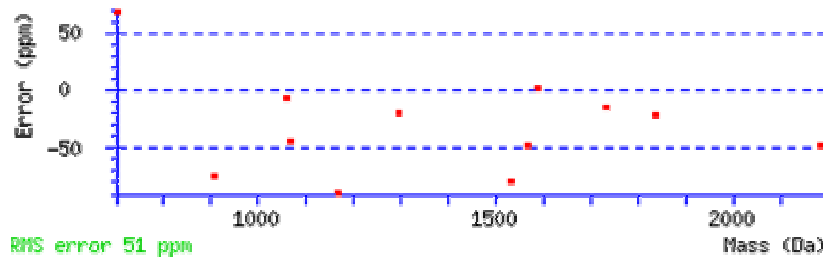
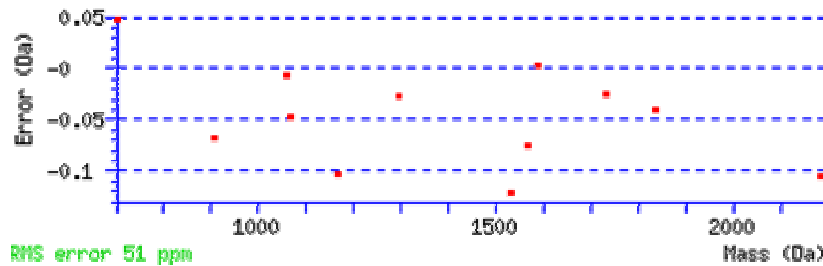
Unformatted sequence string: **466 residues** (for pasting into other applications).

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 |
|-------------|-----------|-----------|-----------|-----------|--------------------------------|
| 101 - 113 | 1587.8000 | 1586.7927 | 1586.7900 | 0.0027 1 | R.TNEKVELQELNDR.F |
| 123 - 129 | 906.4000 | 905.3927 | 905.4607 | -0.0679 0 | R.FLEQQNK.I |
| 130 - 139 | 1169.6100 | 1168.6027 | 1168.7067 | -0.1040 0 | K.ILLAELEQLK.G |
| 160 - 168 | 1060.5200 | 1059.5127 | 1059.5197 | -0.0069 0 | R.QVDQLTNDK.A |
| 224 - 236 | 1533.7300 | 1532.7227 | 1532.8450 | -0.1222 1 | K.VESLQEEIAFLKK.L |
| 305 - 310 | 702.4000 | 701.3927 | 701.3456 | 0.0471 0 | R.NNDALR.Q |
| 314 - 321 | 1068.4600 | 1067.4527 | 1067.4996 | -0.0468 1 | K.QESTEYRR.Q |
| 346 - 364 | 2186.8600 | 2185.8527 | 2185.9586 | -0.1058 0 | R.EMEENFAVEAANYQDTIGR.L |
| 365 - 378 | 1734.7900 | 1733.7827 | 1733.8076 | -0.0249 1 | R.LQDEIQNMKEEMAR.H |
| 391 - 401 | 1295.6400 | 1294.6327 | 1294.6591 | -0.0264 0 | K.MALDIEIATYR.K |
| 411 - 424 | 1570.8200 | 1569.8127 | 1569.8878 | -0.0751 0 | R.ISLPLPNFSSLNLR.E |

| Start - End | Observed | Mr(expt) | Mr(calc) | Delta M | Peptide |
|-------------|-----------|-----------|-----------|-----------|---------------------|
| 451 - 466 | 1836.7600 | 1835.7527 | 1835.7922 | -0.0395 0 | R.DGQVINETSQHDDLE.- |

No match to: 621.9500, 804.3200



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;
RX PubMed=14996095; DOI=10.1111/j.1365-2133.2004.05651.x;
RA Hartmann T.B., Thiel D., Dummer R., Schadendorf D., Eichmueller S.;
RT "SEREX identification of new tumour-associated antigens in cutaneous
RT T-cell lymphoma.";
RL Br. J. Dermatol. 150:252-258(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Testis;
RA Zimbelmann R.;
RL Submitted (JUN-2007) to the EMBL/GenBank/DDBJ databases.