

ID VGFR2_HUMAN Reviewed; 1356 AA.
AC P35968; 060723; Q14178;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 11-JAN-2011, entry version 127.
DE RecName: Full=Vascular endothelial growth factor receptor 2;
DE Short=VEGFR-2;
DE EC=2.7.10.1;
DE AltName: Full=Fetal liver kinase 1;
DE Short=FLK-1;
DE AltName: Full=Kinase insert domain receptor;
DE AltName: Full=Protein-tyrosine kinase receptor flk-1;
DE AltName: CD_antigen=CD309;
DE Flags: Precursor;
GN Name=KDR; Synonyms=FLK1;
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 [MRNA].
RA Yin L.Y., Wu Y., Patterson C.;
RT "Full length human KDR/flk-1 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Umbilical vein;
RA Yu Y., Whitney R.G., Sato J.D.;
RT "Coding region for human VEGF receptor KDR (VEGFR-2).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 3-1356, AND VARIANT GLU-848.
RC TISSUE=Umbilical vein;
RX MEDLINE=92019839; PubMed=1656371;
RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,
RA Shows T.B.;
RT "Identification of a new endothelial cell growth factor receptor
RT tyrosine kinase.";
RL Oncogene 6:1677-1683(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-22.
RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT receptor for vascular endothelial growth factor.";
RL J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION.
RX MEDLINE=93038639; PubMed=1417831; DOI=10.1016/0006-291X(92)90483-2;
RA Terman B.I., Doughen-Vermazen M., Carrion M.E., Dimitrov D.,
RA Armellino D.C., Gospodarowicz D., Boehlen P.;
RT "Identification of the KDR tyrosine kinase as a receptor for vascular
RT endothelial cell growth factor.";
RL Biochem. Biophys. Res. Commun. 187:1579-1586(1992).
RN [6]
RP INTERACTION WITH HIV-1 TAT.
RX PubMed=10590123; DOI=10.1128/JVI.74.1.344-353.2000;
RA Mitola S., Soldi R., Zanon I., Barra L., Gutierrez M.I., Berkhout B.,
RA Giacca M., Bussolino F.;
RT "Identification of specific molecular structures of human
RT immunodeficiency virus type 1 Tat relevant for its biological effects
RT on vascular endothelial cells.";
RL J. Virol. 74:344-353(2000).
RN [7]
RP INTERACTION WITH SHB.
RX PubMed=15026417; DOI=10.1074/jbc.M312729200;
RA Holmquist K., Cross M.J., Rolny C., Haegerkvist R., Rahimi N.,
RA Matsumoto T., Claesson-Welsh L., Welsh M.;
RT "The adaptor protein shb binds to tyrosine 1175 in vascular
RT endothelial growth factor (VEGF) receptor-2 and regulates VEGF-
RT dependent cellular migration.";
RL J. Biol. Chem. 279:22267-22275(2004).
RN [8]
RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-1054 AND TYR-1059, AND
RP MASS SPECTROMETRY.
RC TISSUE=Lung carcinoma;
RX PubMed=18083107; DOI=10.1016/j.cell.2007.11.025;
RA Rikova K., Guo A., Zeng Q., Possemato A., Yu J., Haack H., Nardone J.,
RA Lee K., Reeves G., Li Y., Hu Y., Tan Z., Stokes M., Sullivan L.,
RA Mitchell J., Wetzel R., Macneil J., Ren J.M., Yuan J.,
RA Bakalarski C.E., Villen J., Kornhauser J.M., Smith B., Li D., Zhou X.,
RA Gygi S.P., Gu T.-L., Polakiewicz R.D., Rush J., Comb M.J.;
RT "Global survey of phosphotyrosine signaling identifies oncogenic
RT kinases in lung cancer.";
RL Cell 131:1190-1203(2007).
RN [9]
RP PHOSPHORYLATION AT TYR-951; TYR-1175 AND TYR-1214, AND
RP DEPHOSPHORYLATION BY PTPRB.
RX PubMed=19105612; DOI=10.1096/fj.08-123810;
RA Mellberg S., Dimberg A., Bahram F., Hayashi M., Rennel E., Ameer A.,
RA Westholm J.O., Larsson E., Lindahl P., Cross M.J., Claesson-Welsh L.;
RT "Transcriptional profiling reveals a critical role for tyrosine
RT phosphatase VE-PTP in regulation of VEGFR2 activity and endothelial
RT cell morphogenesis.";
RL FASEB J. 23:1490-1502(2009).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 806-1171, FUNCTION,
RP PHOSPHORYLATION AT TYR-1059, AND MASS SPECTROMETRY.
RX PubMed=10368301; DOI=10.1016/S0969-2126(99)80042-2;
RA McTigue M.A., Wickersham J.A., Pinko C., Showalter R.E., Parast C.V.,
RA Tempczyk-Russell A., Gehring M.R., Mroczkowski B., Kan C.-C.,
RA Villafranca J.E., Appelt K.;
RT "Crystal structure of the kinase domain of human vascular endothelial
RT growth factor receptor 2: a key enzyme in angiogenesis.";
RL Structure 7:319-330(1999).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.71 ANGSTROMS) OF 806-1171 IN COMPLEX WITH
RP SYNTHETIC INHIBITOR.
RX PubMed=15837294; DOI=10.1016/j.bmcl.2005.03.034;
RA Miyazaki Y., Matsunaga S., Tang J., Maeda Y., Nakano M.,
RA Philippe R.J., Shibahara M., Liu W., Sato H., Wang L., Nolte R.T.;
RT "Novel 4-amino-furo[2,3-d]pyrimidines as Tie-2 and VEGFR2 dual
RT inhibitors.";
RL Bioorg. Med. Chem. Lett. 15:2203-2207(2005).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 815-1171 IN COMPLEX WITH
RP SYNTHETIC INHIBITOR.
RX PubMed=17253678; DOI=10.1021/jm0611071;
RA Hodous B.L., Geuns-Meyer S.D., Hughes P.E., Albrecht B.K., Bellon S.,
RA Bready J., Caenepeel S., Cee V.J., Chaffee S.C., Coxon A., Emery M.,
RA Fretland J., Gallant P., Gu Y., Hoffman D., Johnson R.E., Kendall R.,
RA Kim J.L., Long A.M., Morrison M., Olivieri P.R., Patel V.F.,
RA Polverino A., Rose P., Tempest P., Wang L., Whittington D.A., Zhao H.;
RT "Evolution of a highly selective and potent 2-(pyridin-2-yl)-1,3,5-
RT triazine Tie-2 kinase inhibitor.";
RL J. Med. Chem. 50:611-626(2007).
RN [13]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 806-1171 IN COMPLEX WITH
RP SYNTHETIC INHIBITOR, AND FUNCTION.
RX PubMed=18529047; DOI=10.1021/jm8001185;
RA Peifer C., Selig R., Kinkel K., Ott D., Totzke F., Schaechtele C.,
RA Heidenreich R., Roeken M., Schollmeyer D., Laufer S.;
RT "Design, synthesis, and biological evaluation of novel 3-aryl-4-(1H-
RT indole-3-yl)-1,5-dihydro-2H-pyrrole-2-ones as vascular endothelial
RT growth factor receptor (VEGF-R) inhibitors.";
RL J. Med. Chem. 51:3814-3824(2008).
RN [14]
RP VARIANT HCI SER-1147.
RX PubMed=11807987; DOI=10.1002/gcc.10028;
RA Walter J.W., North P.E., Waner M., Mizeracki A., Blei F.,
RA Walker J.W.T., Reinisch J.F., Marchuk D.A.;
RT "Somatic mutation of vascular endothelial growth factor receptors in
RT juvenile hemangioma.";
RL Genes Chromosomes Cancer 33:295-303(2002).
RN [15]
RP VARIANTS [LARGE SCALE ANALYSIS] LEU-275 AND ARG-873.
RX PubMed=16959974; DOI=10.1126/science.1133427;
RA Sjöebloom T., Jones S., Wood L.D., Parsons D.W., Lin J., Barber T.D.,
RA Mandelker D., Leary R.J., Ptak J., Silliman N., Szabo S.,
RA Buckhaults P., Farrell C., Meeh P., Markowitz S.D., Willis J.,
RA Dawson D., Willson J.K.V., Gazdar A.F., Hartigan J., Wu L., Liu C.,
RA Parmigiani G., Park B.H., Bachman K.E., Papadopoulos N.,
RA Vogelstein B., Kinzler K.W., Velculescu V.E.;
RT "The consensus coding sequences of human breast and colorectal
RT cancers.";
RL Science 314:268-274(2006).
RN [16]
RP VARIANTS [LARGE SCALE ANALYSIS] ARG-2; MET-136; GLY-248; ILE-297;
RX VAL-462; HIS-472; ARG-482; ARG-539; MET-689; ASN-814 AND THR-1065.
RP PubMed=17344846; DOI=10.1038/nature05610;
RA Greenman C., Stephens P., Smith R., Dalgleish G.L., Hunter C.,
RA Bignell G., Davies H., Teague J., Butler A., Stevens C., Edkins S.,
RA O'Heara S., Vastrik I., Schmidt E.E., Avis T., Barthorpe S.,
RA Bhamra G., Buck G., Choudhury B., Clements J., Cole J., Dicks E.,
RA Forbes S., Gray K., Halliday K., Harrison R., Hills K., Hinton J.,
RA Jenkinson A., Jones D., Menzies A., Mironenko T., Perry J., Raine K.,
RA Richardson D., Shepherd R., Small A., Tofts C., Varian J., Webb T.,
RA West S., Widaa S., Yates A., Cahill D.P., Louis D.N., Goldstraw P.,
RA Nicholson A.G., Brasseur F., Looijenga L., Weber B.L., Chiew Y.-E.,
RA DeFazio A., Greaves M.F., Green A.R., Campbell P., Birney E.,
RA Easton D.F., Chenevix-Trench G., Tan M.-H., Khoo S.K., Teh B.T.,
RA Yuen S.T., Leung S.Y., Wooster R., Futreal P.A., Stratton M.R.;
RT "Patterns of somatic mutation in human cancer genomes.";
RL Nature 446:153-158(2007).
RN [17]
RP VARIANT HCI SUSCEPTIBILITY ARG-482.
RX PubMed=18931684; DOI=10.1038/nm.1877;
RA Jinnin M., Medici D., Park L., Limaye N., Liu Y., Boscolo E.,
RA Bischoff J., Vikkula M., Boye E., Olsen B.R.;
RT "Suppressed NFAT-dependent VEGFR1 expression and constitutive VEGFR2
RT signaling in infantile hemangioma.";
RL Nat. Med. 14:1236-1246(2008).
CC -I- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
CC kinase activity. The VEGF-kinase ligand/receptor signaling system
CC plays a key role in vascular development and regulation of
CC vascular permeability. In case of HIV-1 infection, the interaction
CC with extracellular viral Tat protein seems to enhance angiogenesis
CC in Kaposi's sarcoma lesions.
CC -I- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a
CC [protein]-L-tyrosine phosphate.
CC -I- SUBUNIT: Interacts with MYOF (By similarity). Interacts with SHB;
CC upon VEGF activation. Interacts with HIV-1 Tat.
CC -I- INTERACTION:
CC P35916:FLT4; NbExp=1; IntAct=EBI-1005487, EBI-1005467;
CC O14786:NRP1; NbExp=1; IntAct=EBI-1005487, EBI-1187100;
CC P29350:PTPN6; NbExp=1; IntAct=EBI-1005487, EBI-78260;
CC P12931:SRC; NbExp=2; IntAct=EBI-1005487, EBI-621482;
CC -I- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane
CC protein.
CC -I- PTM: Dephosphorylated by PTPRB.
CC -I- DISEASE: Defects in KDR are associated with susceptibility to
CC hemangioma capillary infantile (HCI) [MIM:602089]. HCI are benign,
CC highly proliferative lesions involving aberrant localized growth
CC of capillary endothelium. They are the most common tumor of
CC infancy, occurring in up to 10% of all births. Hemangiomas tend to
CC appear shortly after birth and show rapid neonatal growth for up
CC to 12 months characterized by endothelial hypercellularity and
CC increased numbers of mast cells. This phase is followed by slow
CC involution at a rate of about 10% per year and replacement by
CC fibrofatty stroma.
CC -I- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC kinase family. CSF-1/PDGF receptor subfamily.
CC -I- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -I- SIMILARITY: Contains 1 protein kinase domain.
CC -----
CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution (CC BY 4.0) License
CC -----
DR EMBL: AF035121; AAB88005.1; -; mRNA.
DR EMBL: AF063658; AAC16450.1; -; mRNA.
DR EMBL: L04947; AAA59459.1; -; mRNA.
DR EMBL: X61656; CAA43837.1; -; mRNA.
DR EMBL: X89776; CAA61916.1; -; Genomic_DNA.
DR IPI: IPI00021396; -.
DR PIR: JC1402; JC1402.
DR RefSeq: NP_002244.1; NM_002253.2.
DR UniGene: Hs.479756; -.
DR PDB: 1VR2; X-ray; 2.40 Å; A=806-1171.
DR PDB: 1Y6A; X-ray; 2.10 Å; A=806-1171.
DR PDB: 1Y6B; X-ray; 2.10 Å; A=806-1171.
DR PDB: 1YWN; X-ray; 1.71 Å; A=806-1171.
DR PDB: 2OH4; X-ray; 2.05 Å; A=806-1171.
DR PDB: 2P2H; X-ray; 1.95 Å; A=815-1171.
DR PDB: 2P2I; X-ray; 2.40 Å; A/B=815-1171.
DR PDB: 2QU5; X-ray; 2.95 Å; A=815-1171.
DR PDB: 2QU6; X-ray; 2.10 Å; A/B=815-1171.
DR PDB: 2RL5; X-ray; 2.65 Å; A=815-1171.
DR PDB: 2XJW; X-ray; 2.70 Å; L/J/M/O=120-326.
DR PDB: 2XIX; X-ray; 3.10 Å; R=120-326.
DR PDB: 3B8Q; X-ray; 2.75 Å; A/B=815-1171.
DR PDB: 3B8R; X-ray; 2.70 Å; A/B=815-1171.
DR PDB: 3BE2; X-ray; 1.75 Å; A=815-1171.
DR PDB: 3C7Q; X-ray; 2.10 Å; A=806-1171.
DR PDB: 3CJF; X-ray; 2.15 Å; A=806-1168.
DR PDB: 3CJG; X-ray; 2.25 Å; A=806-1168.
DR PDB: 3CP9; X-ray; 2.50 Å; A/B=815-1171.
DR PDB: 3CPB; X-ray; 2.70 Å; A/B=815-1171.
DR PDB: 3CPC; X-ray; 2.40 Å; A/B=815-1171.
DR PDB: 3D7W; X-ray; 2.90 Å; A/B=815-1171.
DR PDB: 3EFL; X-ray; 2.20 Å; A/B=815-1171.
DR PDB: 3ENH; X-ray; 1.60 Å; A=815-1171.
DR PDB: 3KVQ; X-ray; 2.70 Å; A=657-764.
DR PDBsum: 1VR2; -.
DR PDBsum: 1Y6A; -.
DR PDBsum: 1Y6B; -.
DR PDBsum: 1YWN; -.

DR PDBsum; 2OH4; -.
DR PDBsum; 2P2H; -.
DR PDBsum; 2P2I; -.
DR PDBsum; 2QU5; -.
DR PDBsum; 2QU6; -.
DR PDBsum; 2RL5; -.
DR PDBsum; 2KIM; -.
DR PDBsum; 2XIX; -.
DR PDBsum; 3B8Q; -.
DR PDBsum; 3B8R; -.
DR PDBsum; 3BE2; -.
DR PDBsum; 3C7Q; -.
DR PDBsum; 3CJF; -.
DR PDBsum; 3CJG; -.
DR PDBsum; 3CP9; -.
DR PDBsum; 3CPB; -.
DR PDBsum; 3CPG; -.
DR PDBsum; 3DTW; -.
DR PDBsum; 3EFL; -.
DR PDBsum; 3EWH; -.
DR PDBsum; 3KVQ; -.
DR ProteinModelPortal; P35968; -.
DR SMR; P35968; 35-113, 122-461, 560-756, 815-1171.
DR DIP; DIP-486N; -.
DR DIP; DIP-574IN; -.
DR IntAct; P35968; 7.
DR MINT; MINT-127732; -.
DR STRING; P35968; -.
DR PhosphoSite; P35968; -.
DR PRIDE; P35968; -.
DR Ensembl; ENSM00000263923; ENSP00000263923; ENSG00000128052.
DR GeneID; 3791; -.
DR KEGG; hsa:3791; -.
DR UCSC; uc003has.1; human.
DR CTD; 3791; -.
DR GeneCards; GC04M055944; -.
DR H-InvDB; HIX0031357; -.
DR HGNC; HGNC:6307; KDR.
DR HPA; CAB004028; -.
DR MIM; 191306; gene.
DR MIM; 602089; phenotype.
DR Orphanet; 91415; Familial capillary hemangioma.
DR PharmKB; PA30086; -.
DR HOVERGEN; HBG053432; -.
DR InParanoid; P35968; -.
DR OMA; QDVRSPF; -.
DR OrthoDB; EOG954S2G; -.
DR PhylomeDB; P35968; -.
DR BRENDA; 2.7.10.1; 247.
DR Pathway_Interaction_DB; avb3_integrin_pathway; Integrins in angiogenesis.
DR Pathway_Interaction_DB; slp_slp1_pathway; S1P1 pathway.
DR Pathway_Interaction_DB; vegfr1_2_pathway; Signaling events mediated by VEGFR1 and VEGFR2.
DR Reactome; REACT_12529; Signaling by VEGF.
DR DrugBank; DB00398; Sorafenib.
DR DrugBank; DB01268; Sunitinib.
DR NextBio; 14887; -.
DR ArrayExpress; P35968; -.
DR Bgee; P35968; -.
DR CleanEx; HS_KDR; -.
DR Genevestigator; P35968; -.
DR GermOnline; ENSG00000128052; Homo sapiens.
DR GO; GO:0005887; C:integral to plasma membrane; TAS:ProtInc.
DR GO; GO:0005524; F:ATP binding; IEA:UniProtKB-KW.
DR GO; GO:0019038; F:growth factor binding; IPI:BHF-UCL.
DR GO; GO:0051879; F:hsp90 protein binding; TAS:BHF-UCL.
DR GO; GO:0005178; F:integrin binding; IPI:BHF-UCL.
DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase activity; TAS:BHF-UCL.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor activity; IDA:BHF-UCL.
DR GO; GO:0001525; P:angiogenesis; TAS:BHF-UCL.
DR GO; GO:0044419; P:interspecies interaction between organisms; IEA:UniProtKB-KW.
DR GO; GO:0010595; P:positive regulation of endothelial cell migration; IMP:BHF-UCL.
DR GO; GO:0001938; P:positive regulation of endothelial cell proliferation; IMP:BHF-UCL.
DR GO; GO:0051894; P:positive regulation of focal adhesion assembly; IDA:BHF-UCL.
DR GO; GO:0005027; P:positive regulation of positive chemotaxis; IDA:BHF-UCL.
DR GO; GO:0006468; P:protein phosphorylation; IEA:InterPro.
DR GO; GO:0008360; P:regulation of cell shape; IDA:BHF-UCL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR013783; Ig-like_fold.
DR InterPro; IPR013098; Ig_I-set.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR003598; Ig_sub2.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR013099; Kinase-like_dom.
DR InterPro; IPR000719; Prot_kinase_cat_dom.
DR InterPro; IPR017441; Protein_kinase_ATP_BS.
DR InterPro; IPR001245; Ser-Thr/Tyr-Pkinase.
DR InterPro; IPR020635; Tyr_Pkinase_cat_dom.
DR InterPro; IPR020685; Tyr_prot_kinase.
DR InterPro; IPR008266; Tyr_prot_kinase_AS.
DR InterPro; IPR001824; Tyr_prot_kinase_rcpt_3_CS.
DR InterPro; IPR009136; Tyr_prot_kinase_VEGFR2_rcpt.
DR InterPro; IPR009134; Tyr_prot_kinase_VEGFR_rcpt_N.
DR Gene3D; G3DSA:2.60.40.10; Ig-like_fold; 8.
DR PANTHER; PTHR23256; Tyr_prot_kinase; 1.
DR PANTHER; PTHR23256:SF298; Tyr_prot_kinase_VEGFR2_rcpt; 1.
DR Pfam; PF07679; I-set; 2.
DR Pfam; PF07714; Pkinase_Tyr; 1.
DR Pfam; PF07686; V-set; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR PRINTS; PR01834; VEGFRECEPTR2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IG2; 2.
DR SMART; SM00219; TyrKc; 1.
DR SUPFAM; SSF56112; Kinase_like; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
PE 1: Evidence at protein level;
KW 3D-structure; Angiogenesis; ATP-binding; Complete proteome;
KW Developmental protein; Differentiation; Glycoprotein;
KW Host-virus interaction; Immunoglobulin domain; Kinase; Membrane;
KW Nucleotide-binding; Phosphoprotein; Polymorphism; Receptor; Repeat;
KW Signal; Transferase; Transmembrane; Transmembrane helix;
KW Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1356 Vascular endothelial growth factor
FT receptor 2.
FT /FTId=PRO_0000016771.
FT TOPO_DOM 20 764 Extracellular (Potential).
FT TRANSMEM 765 789 Helical; (Potential).
FT TOPO_DOM 790 1356 Cytoplasmic (Potential).
FT DOMAIN 46 110 Ig-like C2-type 1.
FT DOMAIN 141 207 Ig-like C2-type 2.
FT DOMAIN 224 320 Ig-like C2-type 3.
FT DOMAIN 328 414 Ig-like C2-type 4.
FT DOMAIN 421 548 Ig-like C2-type 5.
FT DOMAIN 551 660 Ig-like C2-type 6.
FT DOMAIN 667 753 Ig-like C2-type 7.

FT	DOMAIN	834	1162	Protein kinase.
FT	NP_BIND	840	848	ATP (By similarity).
FT	ACT_SITE	1028	1028	Proton acceptor (By similarity).
FT	BINDING	868	868	ATP (By similarity).
FT	SITE	1175	1175	Interaction with SHB (By similarity).
FT	MOD_RES	951	951	Phosphotyrosine.
FT	MOD_RES	1054	1054	Phosphotyrosine.
FT	MOD_RES	1059	1059	Phosphotyrosine; by autocatalysis.
FT	MOD_RES	1175	1175	Phosphotyrosine.
FT	MOD_RES	1214	1214	Phosphotyrosine.
FT	CARBOHYD	46	46	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	66	66	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	96	96	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	143	143	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	158	158	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	245	245	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	318	318	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	374	374	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	395	395	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	511	511	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	523	523	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	580	580	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	613	613	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	619	619	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	631	631	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	675	675	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	704	704	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	721	721	N-linked (GlcNAc...) (Potential).
FT	VARIANT	2	2	Q -> R (in a lung adenocarcinoma sample; somatic mutation).
FT				/FTId=VAR_042053.
FT	VARIANT	136	136	V -> M (in dbSNP:rs35636987).
FT				/FTId=VAR_042054.
FT	VARIANT	248	248	A -> G (in a renal clear cell carcinoma sample; somatic mutation).
FT				/FTId=VAR_042055.
FT	VARIANT	275	275	R -> L (in a colorectal cancer sample; somatic mutation).
FT				/FTId=VAR_036126.
FT	VARIANT	297	297	V -> I (in dbSNP:rs2305948).
FT				/FTId=VAR_022071.
FT	VARIANT	462	462	L -> V (in dbSNP:rs56286620).
FT				/FTId=VAR_042056.
FT	VARIANT	472	472	Q -> H (in dbSNP:rs1870377).
FT				/FTId=VAR_020353.
FT	VARIANT	482	482	C -> R (in HCl susceptibility; expression of FLT1 in hemangioma endothelial cells is markedly reduced and KDR activity is increased compared to controls; low FLT1 expression in hemangioma cells is caused by reduced activity of a pathway involving ITGB1, ANTXR1, KDR and NFATC2IP; the mutation predicts to result in loss-of-function and disruption of the normal association of these molecules; dbSNP:rs34231037).
FT				/FTId=VAR_042057.
FT	VARIANT	539	539	G -> R (in dbSNP:rs55716939).
FT				/FTId=VAR_042058.
FT	VARIANT	689	689	T -> M (in dbSNP:rs34038364).
FT				/FTId=VAR_042059.
FT	VARIANT	814	814	D -> N (in dbSNP:rs35603373).
FT				/FTId=VAR_042060.
FT	VARIANT	848	848	V -> E (in dbSNP:rs1139776).
FT				/FTId=VAR_046679.
FT	VARIANT	873	873	G -> R (in a colorectal cancer sample; somatic mutation).
FT				/FTId=VAR_036127.
FT	VARIANT	952	952	V -> I (in dbSNP:rs13129474).
FT				/FTId=VAR_046680.
FT	VARIANT	1065	1065	A -> T (in dbSNP:rs56302315).
FT				/FTId=VAR_042061.
FT	VARIANT	1147	1147	P -> S (in HCl; somatic mutation).
FT				/FTId=VAR_063147.
FT	CONFLICT	2	2	Q -> E (in Ref. 2; AAC16450).
FT	CONFLICT	772	772	A -> T (in Ref. 3; AAAS9459/CAA43837).
FT	CONFLICT	787	787	R -> G (in Ref. 3; AAAS9459/CAA43837).
FT	CONFLICT	835	835	K -> N (in Ref. 3; AAAS9459/CAA43837).
FT	CONFLICT	1347	1347	S -> T (in Ref. 3; AAAS9459/CAA43837).
FT	HELIX	824	827	
FT	HELIX	831	833	
FT	STRAND	834	841	
FT	STRAND	844	855	
FT	STRAND	858	860	
FT	STRAND	862	870	
FT	HELIX	876	892	
FT	STRAND	901	905	
FT	STRAND	907	910	
FT	STRAND	913	917	
FT	HELIX	924	929	
FT	TURN	930	933	
FT	HELIX	1002	1021	
FT	HELIX	1031	1033	
FT	STRAND	1034	1036	
FT	STRAND	1042	1044	
FT	HELIX	1068	1071	
FT	HELIX	1074	1077	
FT	HELIX	1084	1099	
FT	HELIX	1115	1120	
FT	HELIX	1133	1142	
FT	HELIX	1147	1149	
FT	HELIX	1153	1167	
SEQUENCE	1356 AA; 151527 MW; 59E7C44B05CFEBB3 CRC64;			
SQ	MQSKVLLAVA LHLVCETRAA SVGLPSVSLD LPRLSIQKDI LTIKANNTLQ ITCRGQRDL D			
	WLWPNQSGS EQRVEVTECS DGLFCKTLTI PKVIGNDTGA YKCFYRETDL ASVIVYVQD			
	YRSPFIASVS DQHGVMVYTE NKNKTIVIPC LGSISNLNVS LCARYPEKRF VPDGNRISWD			
	SKKGFITPSY MTSYAGMVF C EAKINDESQY SIMYIVVVG YRIYDVVLS P SHGIELSVGE			
	KLVNLCTART ELNVGIDFNW EYPSSKHQHK KLVNRLDKTQ SGSEMKFELS TLIDGVTRTS			
	DQGLYTCAAS SGLMTKKNST FVRVHEKPFV AFGSGMESLV EATVGERVRI PAKYLGYPVP			
	EIKWYKNGIP LESNHTIKAG HVLTIMEVSE RDTGNITYVIL TNPISEKQKS HVVSLVYVVP			
	PQGGKSLIS PDQSVYQGTI QTLTCTVVAI PPPHHIHWY QLEECANEP SQAVSVTNPY			
	PCEARSVED PQGNGIEVN KMQFALIEGK NKTVSTLVIG AANVSALYKC EAVNKVGRSE			
	RVISFHVTRG PEITLQPDQM PTEQESVSLW CTADRTFFEN LTWYKLGPO LPINHGELPT			
	PVCKNLDTLW KLNATMFNS TNDILIMELK NASLDQDQGY VCLAQDRKTK KRHCVRQLT			
	VLVERAPTIT GNLENGTTSI GESIEVSCTA SGNPPQIMW FKDNETLVED SGIVLKDGNR			
	NLTIIRVRKE DEGLYTCQAC SVLGCAKVEA FFIEGAQEK TNLIEIILVG TAVIAMFFWL			
	LLVIILRTVK RANGELKTG YLSIVMDPDE LPLDEHCERL PYDASKWEFP RDRLLKLGKPL			
	GRGAFQVIE ADAFGIDKTA TCRTVAVKML KEGATHSEHR ALMSELKIL HIGHHLNVN			
	LLGACTKPGG PLMWIVEFCK FGNLSTYLRs KRNEFPVYKT KGARFRQGD YVGAIPVDLK			
	RRLDSTSSQ SSASSGFVEE KSLSDVEEE APEDLYKDFL TLEHLICYSF QVAKMEFLA			
	SRKCHRDLA ANKLSEKN YKICDFGLA RDYKDPDYV RKGDAFLPK WMAPETIFDR			
	VYTIQSDQWS FGVLLEWIFS LGASPPGVK IDEEFCRLK EGTMRAPDY TPEMYQTL			
	DCHMGPSQR PTFSSELVHL GNLLQANAQ DGKDYVLP I SETLSMEEDS GLSLTSPVS			
	CMEEEVCDP KFHYNDAITG SQYLQNSKRK SRPVSVKTFE DIPLLEEPEV VIPDDNQTS			
	GMVLASEELK TLEDRTKLSP SFGGMWPKS RESVASEGSN QTSGYQSGYH SDDTDTVYS			
	SEAEALLKLI EIGVQTGSTA QILQPDGTT LSSPPV			

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