

ID VGR2_HUMAN Reviewed; 1356 AA.
AC P35968; 060723; Q14178;
DT 01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2009, 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-Vermazan 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 B., 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=1026417; DOI=10.1074/jbc.M312729200;
RA Holmqvist 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 C., Li Y., Hu Y., Tan Z., Stokes M., Sullivan L.,
RA Mitchell J., Wetzel R., Macneill 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=19136612; DOI=10.1096/fj.08-123810;
RA Mellberg S., Dimberg A., Bahram F., Hayashi M., Rennel E., Ameur 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.bmc.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:18529847; DOI=10.1021/jm8001185;
 RA Peifer C., Selig R., Kinkel K., Ott D., Totzke F., Schaechtele C.,
 RA Heidenreich R., Decken M., Schollmeyer D., Laufen S.;
 RT "Design, synthesis, and biological evaluation of novel 3-aryl-4-(1H-
 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 Sjoebom 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 Parnigiani 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;
 RP VAL-462; HIS-472; ARG-482; ARG-539; MET-689; ASN-814 AND THR-1065.
 RX PubMed:1734846; DOI=10.1038/nature05510;
 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'Meara 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., Small A., Torts C., Varian J., Webb T.,
 RA West S., Widada 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.,
 RT 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:FLI4; NbExp=1; IntAct=EBI-1005487, EBI-1005467;
 CC O14786:NRP1; NbExp=1; IntAct=EBI-1005487, EBI-1187100;
 CC P29358: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>
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 CC -----
 DR EMBL; AF035121; AAB88005.1; -; mRNA.
 DR EMBL; AF063658; AAC16450.1; -; mRNA.
 DR EMBL; L04947; A0459459.1; -; mRNA.
 DR EMBL; X61656; CA443837.1; -; mRNA.
 DR EMBL; X89776; CA61916.1; -; Genomic_DNA.
 DR IPI; IPI00021396; -;
 DR PIR; JCI402; JCI402.
 DR RefSeq; NP_002244.1; NM_002253.2.
 DR UniGene; Hs.479756; -;
 DR PDB; 1VR2; X-ray; 2.40 A; A=806-1171.
 DR PDB; 1Y6A; X-ray; 2.10 A; A=806-1171.
 DR PDB; 1Y6B; X-ray; 2.10 A; A=806-1171.
 DR PDB; 1YWN; X-ray; 1.71 A; A=806-1171.
 DR PDB; 20H4; X-ray; 2.05 A; A=806-1171.
 DR PDB; 2P2H; X-ray; 1.95 A; A=815-1171.
 DR PDB; 2P2I; X-ray; 2.40 A; A/B=815-1171.
 DR PDB; 2Q05; X-ray; 2.95 A; A=815-1171.
 DR PDB; 2Q06; X-ray; 2.10 A; A/B=815-1171.
 DR PDB; 2RL5; X-ray; 2.65 A; A=815-1171.
 DR PDB; 2X1W; X-ray; 2.70 A; L/M/N/O=120-326.
 DR PDB; 2X1X; X-ray; 3.10 A; R=120-326.
 DR PDB; 3B8Q; X-ray; 2.75 A; A/B=815-1171.
 DR PDB; 3B8R; X-ray; 2.70 A; A/B=815-1171.
 DR PDB; 3B8Z; X-ray; 1.75 A; A=815-1171.
 DR PDB; 3C7Q; X-ray; 2.10 A; A=806-1171.
 DR PDB; 3CJF; X-ray; 2.15 A; A=806-1168.
 DR PDB; 3CJG; X-ray; 2.25 A; A=806-1168.
 DR PDB; 3CP9; X-ray; 2.50 A; A/B=815-1171.
 DR PDB; 3CPB; X-ray; 2.70 A; A/B=815-1171.
 DR PDB; 3CPC; X-ray; 2.40 A; A/B=815-1171.
 DR PDB; 3OTW; X-ray; 2.90 A; A/B=815-1171.
 DR PDB; 3EFL; X-ray; 2.20 A; A/B=815-1171.
 DR PDB; 3EMH; X-ray; 1.60 A; A=815-1171.
 DR PDB; 3KVQ; X-ray; 2.70 A; A=657-764.
 DR PDBsum; 1VR2; -;
 DR PDBsum; 1Y6A; -;
 DR PDBsum; 1Y6B; -;
 DR PDBsum; 1YWN; -;

DR PDBsum; 20H4; --
DR PDBsum; 2P2H; --
DR PDBsum; 2P2I; --
DR PDBsum; 2Q05; --
DR PDBsum; 2Q06; --
DR PDBsum; 2R15; --
DR PDBsum; 2X1W; --
DR PDBsum; 2X1X; --
DR PDBsum; 3B8Q; --
DR PDBsum; 3B8R; --
DR PDBsum; 3BE2; --
DR PDBsum; 3C7Q; --
DR PDBsum; 3C7F; --
DR PDBsum; 3CJG; --
DR PDBsum; 3CP9; --
DR PDBsum; 3CPB; --
DR PDBsum; 3CPC; --
DR PDBsum; 3D1W; --
DR PDBsum; 3EFL; --
DR PDBsum; 3EWH; --
DR PDBsum; 3KVO; --
DR ProteinModelPortal; P35968; --
DR SMR; P35968; 35-113, 122-461, 560-756, 815-1171.
DR DIP; DIP-486N; --
DR DIP; DIP-5741N; --
DR IntAct; P35968; 7.
DR MINT; MINT-127732; --
DR STRING; P35968; --
DR PhosphoSite; P35968; --
DR PRIDE; P35968; --
DR Ensembl; ENS100000263923; 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 PharmGKB; 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; sip_sip1_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; DB000390; Sorafenib.
DR DrugBank; DB01268; Sunitinib.
DR NextBio; 14887; --
DR ArrayExpress; P35968; --
DR Bgee; P35968; --
DR CleanEx; HS_KDR; --
DR Genevestigator; P35968; --
DR GenMOnline; ENS00000128052; 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:0019838; 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:0058927; 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; IPR011009; 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; IGC2; 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; PS00249; 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
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.

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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;
FT 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
FT sample; somatic mutation).
FT /FTid=VAR_042055.
FT VARIANT     275 275 R -> L (in a colorectal cancer sample;
FT 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 HCI susceptibility; expression
FT of FLT1 in hemangioma endothelial cells
FT is markedly reduced and KDR activity is
FT increased compared to controls; low FLT1
FT expression in hemangioma cells is caused
FT by reduced activity of a pathway
FT involving ITGB1, ANTXR1, KDR and
FT NFATC2IP; the mutation predicts to result
FT in loss-of-function and disruption of the
FT normal association of these molecules;
FT 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;
FT 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 HCI; 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; AAA59459/CAA43837).
FT CONFLICT     787 787 R -> G (in Ref. 3; AAA59459/CAA43837).
FT CONFLICT     835 835 K -> N (in Ref. 3; AAA59459/CAA43837).
FT CONFLICT    1347 1347 S -> T (in Ref. 3; AAA59459/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
SQ SEQUENCE 1356 AA; 151527 Mw; 59E7C44B05CFEB83 CRC64;
MQSKVLLAAV LMLCVETRAA SVGLPSVSLD LPLRSIQKDI LTIKANITLQ ITCRGQRDLQ
WLPNNQSGS EQRVETEC S DGLFCKLTII PKVIGNDTGA YKCFYRETDL ASVIVYVQD
YRSPFIASVS DQHGVMVITE NKNKTVVTPC LGSISLNVLS LCARYPEKRF VPDGNRISWD
SKKGFTIPSY MISYAGMVFC EAKINDESQY SIMYIVVVVG YRIYDVVLSL SHGIELSVGE
KLVLNCTART ELNVGIDFNW EYPSSKHQHK KLVNRDLKTQ SGSEMCKFLS TLTIDGVTSS
DQGLVYTCAS SGLMTKKNST FVRVHEKPFV AFGSGMESLV EATVGERVRI PAKYLVGPPP
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PQTGEKSLIS PVDSYQVGTI QTLTCTVVAI PPPHHIHWYV QLEEECANEP SQAVSVTPNY
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VLERVAPITIT GNLENQTTISI GESIEVSCVA SGNPPQIMW FKDNELTLED SGIVLKDGNR
NLTIIRVRKE DGLYTCQAC SVLGCAKVEA FFIIEGAQEK TNLIIILVIG TAVIAMFPHL
LVLIIILRTVK RANGELTAGI VLSIVMDPDE LPLDEHCERL PYDASKWEP RDRLKLGKPL
GRGAFQVQIE ADAFGIDKTA TCRTVAVKML KEGATHSEHR ALMSKILTI HIGHHLNVVN
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DCMHEPESQR PTFSELVEHL GNLLQANAAQ DGKDYVILPI SETLSMEEDS GLSLPTSPVS
CHEEEELVDP KPHYNTAGI SQVLQSKRRK SRPVSVTFIE DIPLEEKPEK VIPDQNDYDS
GMWLASEELK TLEDRTKLSP SFGGMVPSKS RESVASSEGSN QTSGVQSGYH SDDTDTTVYS
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