

ID VGFRI_HUMAN Reviewed; 1338 AA.
AC P17948; A8KA71; O60722; P16057; Q12954;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 03-APR-2007, sequence version 2.
DT 11-JAN-2011, entry version 140.
DE RecName: Full=Vascular endothelial growth factor receptor 1;
DE Short=VEGFR-1;
DE EC=2.7.10.1;
DE AltName: Full=Fms-like tyrosine kinase 1;
DE Short=FLT-1;
DE AltName: Full=Tyrosine-protein kinase FRT;
DE AltName: Full=Tyrosine-protein kinase receptor FLT;
DE AltName: Full=Vascular permeability factor receptor;
DE Flags: Precursor;
GN Name=FLT1; Synonyms=FLT, FRT;
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]
RC NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM FLT1).
RP TISSUE=Placenta;
RX MEDLINE=9021591; PubMed=2158038;
RA Shibuya M., Yamaguchi S., Yamane A., Ikeda T., Tojo A., Matsushime H.,
RA Sato M.;
RT "Nucleotide sequence and expression of a novel human receptor-type
RT tyrosine kinase gene (flt) closely related to the fms family.";
RL Oncogene 5:519-524(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM FLT1).
RC TISSUE=Umbilical vein;
RA Yu Y., Whitney R.G., Sato J.D.;
RT "Coding region for human VEGF receptor FLT1 (VEGFR-1).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SFLT1), AND PROTEIN SEQUENCE OF
RP N-TERMINUS.
RC TISSUE=Umbilical vein;
RX MEDLINE=94068470; PubMed=8248162; DOI=10.1073/pnas.90.22.10705;
RA Kendall R.L., Thomas K.A.;
RT "Inhibition of vascular endothelial cell growth factor activity by an
RT endogenously encoded soluble receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10705-10709(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SFLT1).
RC TISSUE=Trachea;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Oshima H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunaga H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,
RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,
RA Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
RA Hannenhalli S., Turner R., Yooseph S., Lu F., Nusskern D.R.,
RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
RA Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,
RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
RA Venter J.C.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SFLT1).
RC TISSUE=Ovary;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
RN [7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1018-1058 (ISOFORM FLT1).
RX MEDLINE=87307638; PubMed=3040650;
RA Matsushime H., Yoshida M.C., Sasaki M., Shibuya M.;
RT "A possible new member of tyrosine kinase family, human frt sequence,
RT is highly conserved in vertebrates and located on human chromosome
RT 13.";
RL Jpn. J. Cancer Res. 78:655-661(1987).
RN [8]
RP PARTIAL PROTEIN SEQUENCE, PHOSPHORYLATION AT TYR-1213; TYR-1242;
RP TYR-1327 AND TYR-1333, AND MUTAGENESIS OF TYR-914; TYR-1213; TYR-1242;
RP TYR-1327 AND TYR-1333;
RX MEDLINE=98389777; PubMed=9722576; DOI=10.1074/jbc.273.36.23410;
RA Ito N., Wernstedt C., Engstrom U., Claesson-Welsh L.;
RT "Identification of vascular endothelial growth factor receptor-1
RT tyrosine phosphorylation sites and binding of SH2 domain-containing
RT molecules.";
RL J. Biol. Chem. 273:23410-23418(1998).
RN [9]
RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-1048 AND TYR-1053, 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).

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RN [10]
RP STRUCTURE BY NMR OF 129-229.
RX MEDLINE=20013066; PubMed=10543948; DOI=10.1006/jmbi.1999.3134;
RA Starovasnik M.A., Christinger H.W., Wiesmann C., Champe M.A.,
RA de Vos A.M., Skelton N.J.;
RT "Solution structure of the VEGF-binding domain of Flt-1: comparison of
RT its free and bound states.";
RL J. Mol. Biol. 293:531-544(1999).
RN [11]
RP VARIANTS [LARGE SCALE ANALYSIS] THR-60; LYS-144; GLN-281; ILE-422;
RP GLN-781; VAL-938; ALA-982 AND VAL-1061.
RX 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'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., 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).
CC -!- FUNCTION: Receptor for VEGF, VEGFB and PGF. 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. Isoform sFlt1 may have an inhibitory role
CC in angiogenesis.
CC -!- CATALYTIC ACTIVITY: ATP + a [protein]-L-tyrosine = ADP + a
CC [protein]-L-tyrosine phosphate.
CC -!- SUBUNIT: Interacts in vitro with various phosphotyrosine-binding
CC proteins, including PLC-gammas, PTPN11, GRB2, CRK and NCK1.
CC -!- SUBCELLULAR LOCATION: Isoform Flt1: Cell membrane; Single-pass
CC type I membrane protein.
CC -!- SUBCELLULAR LOCATION: Isoform sFlt1: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=Flt1;
CC IsoId=P17948-1; Sequence=Displayed;
CC Name=sFlt1;
CC IsoId=P17948-2; Sequence=VSP_002955, VSP_002956;
CC -!- TISSUE SPECIFICITY: Mostly in normal lung, but also in placenta,
CC liver, kidney, heart and brain tissues. Specifically expressed in
CC most of the vascular endothelial cells, and also expressed in
CC peripheral blood monocytes. It is not expressed in tumor cell
CC lines. Isoform sFlt1 is strongly expressed in placenta.
CC -!- SIMILARITY: Belongs to the protein kinase superfamily. Tyr protein
CC kinase family. CSF-1/PDGF receptor subfamily.
CC -!- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC -!- SIMILARITY: Contains 1 protein kinase domain.
CC -----
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CC -----
DR EMBL; X51602; CAA35946.1; -; mRNA.
DR EMBL; AF063657; AAC16449.2; -; mRNA.
DR EMBL; U01134; AAC50060.1; -; mRNA.
DR EMBL; AK292936; BAF85625.1; -; mRNA.
DR EMBL; CH471075; EAX08431.1; -; Genomic_DNA.
DR EMBL; BC039007; AAH39007.1; -; mRNA.
DR EMBL; D00133; BAA00000.1; -; Genomic_DNA.
DR IPI; IPI00018335; -.
DR IPI; IPI00216043; -.
DR PIR; A49636; A49636.
DR PIR; S09982; S09982.
DR RefSeq; NP_001153392.1; NM_001159920.1.
DR RefSeq; NP_002010.2; NM_002019.4.
DR UniGene; Hs.594454; -.
DR PDB; 1FLT; X-ray; 1.70 A; X/Y=132-226.
DR PDB; 1QSV; NMR; -; A=129-229.
DR PDB; 1QSZ; NMR; -; A=129-229.
DR PDB; 1QTV; X-ray; 2.70 A; T/U/X/Y=129-229.
DR PDB; 1RV6; X-ray; 2.45 A; X/Y=130-229.
DR PDB; 2XAC; X-ray; 2.71 A; C/X=129-226.
DR PDB; 3HNG; X-ray; 2.70 A; A=801-1158.
DR PDBsum; 1FLT; -.
DR PDBsum; 1QSV; -.
DR PDBsum; 1QSZ; -.
DR PDBsum; 1QTV; -.
DR PDBsum; 1RV6; -.
DR PDBsum; 2XAC; -.
DR PDBsum; 3HNG; -.
DR ProteinModelPortal; P17948; -.
DR SMR; P17948; 33-471, 527-749, 803-1165.
DR DIP; DIP-643N; -.
DR MINT; MINT-127610; -.
DR STRING; P17948; -.
DR PhosphoSite; P17948; -.
DR PRIDE; P17948; -.
DR Ensembl; ENST00000282397; ENSP00000282397; ENSG00000102755.
DR GeneID; 2321; -.
DR KEGG; hsa:2321; -.
DR UCSC; uc001usb.2; human.
DR UCSC; uc001usc.2; human.
DR CTD; 2321; -.
DR GeneCards; GC13M028874; -.
DR HGNC; HGNC:3763; FLT1.
DR HPA; HPA011740; -.
DR HPA; HPA014290; -.
DR MIM; 165070; gene.
DR HOGONOM; HBG402887; -.
DR HOVERGEN; HBG053432; -.
DR InParanoid; P17948; -.
DR OMA; KPQIYEK; -.
DR OrthoDB; EO09VDSHT; -.
DR PhylomeDB; P17948; -.
DR BRENDA; 2.7.10.1; 247.
DR Pathway_Interaction_DB; glypican_1pathway; Glypican 1 network.
DR Pathway_Interaction_DB; slp_slp3_pathway; SLP3 pathway.
DR Pathway_Interaction_DB; vegfr1_2_pathway; Signaling events mediated by VEGFR1 and VEGFR2.
DR Pathway_Interaction_DB; vegfr1_pathway; VEGFR1 specific signals.
DR Reactome; REACT_12529; Signaling by VEGF.
DR DrugBank; DB01268; Sunitinib.
DR NextBio; 9421; -.
DR ArrayExpress; P17948; -.
DR Bgee; P17948; -.
DR CleanEx; HS_FLT1; -.
DR Genevestigator; P17948; -.
DR GERMOnline; ENSG00000102755; Homo sapiens.
DR GO; GO:0005737; C:cytoplasm; IDA:HPA.
DR GO; GO:0005615; C:extracellular space; TAS:ProtInc.
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:UniProtKB.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor activity; IDA:BHF-UCL.
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DR GO; GO:0030154; P:cell differentiation; IEA:UniProtKB-KW.
 DR GO; GO:0007565; P:female pregnancy; TAS:ProtInc.
 DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IEA:InterPro.
 DR GO; GO:0030949; P:positive regulation of vascular endothelial growth factor receptor signaling pathway; IDA:BHF-UCL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR013783; Ig-like_fold.
 DR InterPro; IPR013898; Ig_I-set.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR003598; Ig_sub2.
 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; IPR020722; Tyr_kinase_VEGF1_rcpt.
 DR InterPro; IPR020635; Tyr_Pkinase_cat_dom.
 DR InterPro; IPR020685; Tyr_prot_kinase.
 DR InterPro; IPR000266; Tyr_prot_kinase_AS.
 DR InterPro; IPR001824; Tyr_prot_kinase_rcpt_3_CS.
 DR InterPro; IPR009135; Tyr_prot_kinase_VEGFR1_rcpt_N.
 DR InterPro; IPR009134; Tyr_prot_kinase_VEGFR1_rcpt_N.
 DR Gene3D; G3DSA:2.60.40.10; Ig-like_fold; 8.
 DR PANTHER; PTHR23256:SF225; Tyr_kinase_VEGF1_rcpt; 1.
 DR PANTHER; PTHR23256; Tyr_prot_kinase; 1.
 DR Pfam; PF07679; I-set; 4.
 DR Pfam; PF07714; Pkinase_Tyr; 1.
 DR PRINTS; PR01832; VEGFRECEPTOR.
 DR PRINTS; PR01833; VEGFRECEPTR1.
 DR SMART; SM00409; IG; 5.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00219; TyrKc; 1.
 DR SUPFAM; SSF56112; Kinase_like; 1.
 DR PROSITE; PS50835; IG_LIKE; 6.
 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; Alternative splicing; Angiogenesis; ATP-binding;
 KW Cell membrane; Complete proteome; Developmental protein;
 KW Differentiation; Direct protein sequencing; Disulfide bond;
 KW Glycoprotein; Immunoglobulin domain; Kinase; Membrane;
 KW Nucleotide-binding; Phosphoprotein; Polymorphism; Receptor; Repeat;
 KW Secreted; Signal; Transferase; Transmembrane; Transmembrane helix;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 26
 FT CHAIN 27 1338 Vascular endothelial growth factor
 FT receptor 1.
 FT /FTId=PRO_0000016768.
 FT TOPO_DOM 27 758 Extracellular (Potential).
 FT TRANSMEM 759 780 Helical; (Potential).
 FT TOPO_DOM 781 1338 Cytoplasmic (Potential).
 FT DOMAIN 32 123 Ig-like C2-type 1.
 FT DOMAIN 151 214 Ig-like C2-type 2.
 FT DOMAIN 230 327 Ig-like C2-type 3.
 FT DOMAIN 335 421 Ig-like C2-type 4.
 FT DOMAIN 428 553 Ig-like C2-type 5.
 FT DOMAIN 556 654 Ig-like C2-type 6.
 FT DOMAIN 661 747 Ig-like C2-type 7.
 FT DOMAIN 827 1158 Protein kinase.
 FT NP_BIND 833 841 ATP (By similarity).
 FT ACT_SITE 1022 1022 Proton acceptor (By similarity).
 FT BINDING 861 861 ATP (By similarity).
 FT MOD_RES 1048 1048 Phosphotyrosine.
 FT MOD_RES 1053 1053 Phosphotyrosine; by autocatalysis (By
 FT similarity).
 FT MOD_RES 1169 1169 Phosphotyrosine; by autocatalysis (By
 FT similarity).
 FT MOD_RES 1213 1213 Phosphotyrosine; by autocatalysis.
 FT MOD_RES 1242 1242 Phosphotyrosine; by autocatalysis.
 FT MOD_RES 1327 1327 Phosphotyrosine; by autocatalysis.
 FT MOD_RES 1333 1333 Phosphotyrosine; by autocatalysis.
 FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 164 164 N-linked (GlcNAc...) (Potential).
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 FT CARBOHYD 474 474 N-linked (GlcNAc...) (Potential).
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 FT CARBOHYD 620 620 N-linked (GlcNAc...) (Potential).
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 FT CARBOHYD 666 666 N-linked (GlcNAc...) (Potential).
 FT DISULFID 53 107 Potential.
 FT DISULFID 158 207 Potential.
 FT DISULFID 252 311 Potential.
 FT DISULFID 454 535 Potential.
 FT DISULFID 577 636 Potential.
 FT DISULFID 682 731 Potential.
 FT VAR_SEQ 657 687 DQAPYLRLNSDHTVAISSSTLDCHANGV -> GEHCNK
 FT KAVFSRISKFKSTRNDOCTTQSNVKH (in isoform
 FT sFlt1).
 FT /FTId=VSP_002955.
 FT VAR_SEQ 688 1338 Missing (in isoform sFlt1).
 FT /FTId=VSP_002956.
 FT VARIANT 60 60 K -> T (in dbSNP:rs56409818).
 FT /FTId=VAR_042045.
 FT VARIANT 128 128 I -> L (in dbSNP:rs35073261).
 FT /FTId=VAR_049719.
 FT VARIANT 144 144 E -> K (in dbSNP:rs55974987).
 FT /FTId=VAR_042046.
 FT VARIANT 281 281 R -> Q (in dbSNP:rs55687105).
 FT /FTId=VAR_042047.
 FT VARIANT 422 422 L -> I (in a lung adenocarcinoma sample;
 FT somatic mutation).
 FT /FTId=VAR_042048.
 FT VARIANT 781 781 R -> Q (in a glioma low grade
 FT oligodendroglioma sample; somatic
 FT mutation).
 FT /FTId=VAR_042049.
 FT VARIANT 938 938 M -> V (in dbSNP:rs35549791).
 FT /FTId=VAR_042050.
 FT VARIANT 982 982 E -> A (in dbSNP:rs35832528).
 FT /FTId=VAR_042051.
 FT VARIANT 1061 1061 L -> V (in a bladder transitional cell
 FT carcinoma sample; somatic mutation).
 FT /FTId=VAR_042052.
 FT MUTAGEN 914 914 Y->F: No loss of phosphorylation.
 FT MUTAGEN 1213 1213 Y->F: Loss of phosphorylation.
 FT MUTAGEN 1242 1242 Y->F: Loss of phosphorylation.
 FT MUTAGEN 1327 1327 Y->F: Loss of phosphorylation.
 FT MUTAGEN 1333 1333 Y->F: Loss of phosphorylation.
 FT CONFLICT 490 490 F -> S (in Ref. 2; AAC16449).
 FT CONFLICT 779 779 F -> L (in Ref. 1; CAA35946).
 FT STRAND 135 137
 FT STRAND 144 148
 FT STRAND 154 156
 FT STRAND 168 171
 FT TURN 172 174

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FT STRAND 175 177
FT STRAND 181 187
FT TURN 188 190
FT STRAND 191 196
FT HELIX 199 201
FT STRAND 203 211
FT STRAND 214 224
SQ SEQUENCE 1338 AA; 150769 MW; FF3381EEFAF0787C CRC64;
MVSVMVSVL LCALLSCLL TGSSSGSKLK DPELSLKGTO HIMQAGQTLH LQCRGEAAHK
WSLPVMVSK SERLSITKSA CGRNGKQFCS TLTNTAQAN HTGFYSCKYL AVPTSKKKET
ESAIYIFISD TGRPFVEMYS EIPEIHMTE GRELVPCRV TSPNITVTLK KFPLDTLIPD
GKRIIWSRK GFIIISNATYK EIGLLTCEAT VNGHLYKTNV LTHRQTNTII DVQISTPRPV
KLLRGHTLVL NCTATTPLNT RVQMTWSYPD EKNKRASVRR RIDQSNSHAN IFYSVLTIDK
MQNKDKGLYT CRVRSGPSFK SVNTSVHIYD KAFITVKHRK QQVLETVAGK RSYRLSMKVK
AFPSPEVVVL KDGLPATEKS ARYLTRGYSL IIKOVTEEDA GNYTILLSIK QSNVFNKLTA
TLIVNVKPII YEKAVSSFPD PALVPLGSRQ ILTCTAYGIP QTIKMFNHP CNHNSSEARC
DFCSNNEESF ILDADSNMGN RIESITQRMA IIEGKNKMAS TLVADSRIS GIYICIASNK
VGTVGRNISF YITDVPNGFH VNLEKMPTEG EDLKLSCVTN KFLYRDVTWJ LLRTVNNRTM
HYSISKQKMA ITKEHSITLN LTIMNVSLQD SGTVACRARN VYTGEIILQK KEITIRDQEA
PYLLRNLSDH TVAISSSTTL DCHANGVPEP QITWFKNNHK IQQEPGIILG PGSSTLFIER
VTEEDGCVYH KATNQKGSV ESSAYLTVQG TSDKSNLELI TLTCTCVAAT LFWLLTLFI
RKMRSSEI KTDYLSIIMD PDEVPLDEQC ERLPYDASKW EFARERKLKG KSLGRGAFGK
VQASAFGIK KSPTCRTVAV KMLKEGATAS EYKALMTELK ILTHIGHHLN VVNLGACTK
QGGPLMWIVE YCKYGNLSNY LKSKRDLLFFL NKDAALHMEP KKEKMEPGL EGGKPRLDSV
TSSESFASSG PQEDKSLSDV EEEEDSDGFY KEPITMEDLI SYSFQVARGM EFLSSRKKCIH
RDLAARNILL SEMNVKICD FGLARDIYKN PDYVRKGOTR LPLKWMAPES IFDKIYSTKS
DWNYSVLLW EIFSLGGSPV PGVQMDQDFC SRLREGMRMR APEYSTPEIV QIMLDCMHRD
PKERPFAEL VEKLGDLQQA NVQQQGDVVI PINAILTGNS GFTYSTPAFS EDFKESISA
PKFNSGSSDD VRYVNAFKFM SLERIKTFEE LLPNATSMFD DYQGDSTLL ASPMLKRFTW
TDSKPKASKL IDLRVTSKSK ESGLSDVSRP SFCHSSCGHV SEGKRRFTYD HAELEKRIAC
CSPPPDYNSV VLYSTPPI
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