

- UniProt
- Function
- Names & Taxonomy
- Subcellular Location
- Disease & Variants
- PTM/Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequence & Isoforms
- Similar Proteins

P35968 · VGFR2_HUMAN

Proteinⁱ
Vascular endothelial growth factor receptor 2
Geneⁱ
KDR
Statusⁱ
UniProtKB reviewed (Swiss-Prot)
Organismⁱ
Homo sapiens (Human)

Amino acids
1356
Protein existenceⁱ
Evidence at protein level
Annotation scoreⁱ
5/5

Entry Feature viewer Publications External links History

BLAST Align Download Add Add a publication Entry feedback

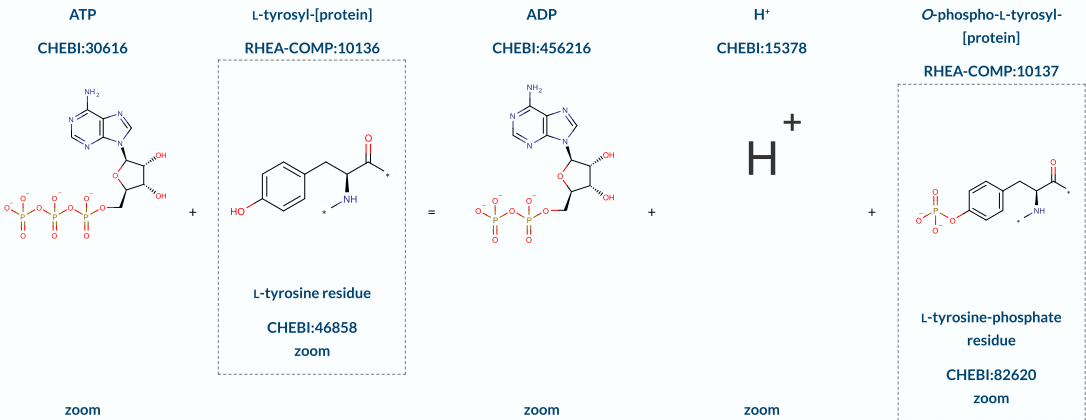
Functionⁱ

Tyrosine-protein kinase that acts as a cell-surface receptor for VEGFA, VEGFC and VEGFD. Plays an essential role in the regulation of angiogenesis, vascular development, vascular permeability, and embryonic hematopoiesis. Promotes proliferation, survival, migration and differentiation of endothelial cells. Promotes reorganization of the actin cytoskeleton. Isoforms lacking a transmembrane domain, such as isoform 2 and isoform 3, may function as decoy receptors for VEGFA, VEGFC and/or VEGFD. Isoform 2 plays an important role as negative regulator of VEGFA- and VEGFC-mediated lymphangiogenesis by limiting the amount of free VEGFA and/or VEGFC and preventing their binding to FLT4. Modulates FLT1 and FLT4 signaling by forming heterodimers. Binding of vascular growth factors to isoform 1 leads to the activation of several signaling cascades. Activation of PLCG1 leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate and the activation of protein kinase C. Mediates activation of MAPK1/ERK2, MAPK3/ERK1 and the MAP kinase signaling pathway, as well as of the AKT1 signaling pathway. Mediates phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase, reorganization of the actin cytoskeleton and activation of PTK2/FAK1. Required for VEGFA-mediated induction of NOS2 and NOS3, leading to the production of the signaling molecule nitric oxide (NO) by endothelial cells. Phosphorylates PLCG1. Promotes phosphorylation of FYN, NCK1, NOS3, PIK3R1, PTK2/FAK1 and SRC. [23 Publications](#)

Catalytic activity

ATP + L-tyrosyl-[protein] = ADP + H⁺ + O-phospho-L-tyrosyl-[protein] [PROSITE-ProRule Annotation](#) [2 Publications](#)
EC:2.7.10.1 ([UniProtKB](#) | [ENZYME](#) | [Rhea](#))
Source: [Rhea 10596](#)

Hide Rhea reaction



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History

1

100

200

300

400

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700

800

900

TYPE

-- Select --

ID

POSITION(S)

DESCRIPTION

▶ Binding site

840-848

ATP (UniProtKB | ChEBI) Curated

BLAST

Add

▶ Binding site

868

ATP (UniProtKB | ChEBI) Curated

▶ Active site

1028

Proton acceptor PROSITE-ProRule Annotation

▶ Site

1175

Interaction with SHB By Similarity

Expand table

GO annotationsⁱ

Slimming set:

generic

all annotations

all molecular function

all biological process

Cellular Component

anchoring junction Source:UniProtKB-SubCell

Cellular Component

cell junction Source:UniProtKB

Cellular Component

early endosome Source:BHF-UCL

Cellular Component

endoplasmic reticulum Source:UniProtKB 1 Publication

Cellular Component

endosome Source:UniProtKB 1 Publication

Cellular Component

external side of plasma membrane Source:Ensembl

Cellular Component

extracellular region Source:UniProtKB-SubCell

Expand table

Complete GO annotation on QuickGO ↗

Keywordsⁱ

Molecular function

#Developmental protein

#Kinase

#Receptor

#Transferase

#Tyrosine-protein kinase

Biological process

#Angiogenesis

#Differentiation

#Host-virus interaction

Ligand

#ATP-binding

#Nucleotide-binding

Enzyme and pathway databases

BRENDA

2.7.10.1 ↗ 2681

PathwayCommons

SIGNOR

P35968 ↗

Signalink

https://www.uniprot.org/uniprotkb/P35968/entry#function

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#Host-virus interaction

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Ligand

#ATP-binding

#Nucleotide-binding

Enzyme and pathway databases

BRENDA

2.7.10.1 [2681](#)

PathwayCommons

P35968 [2](#)

Reactome

R-HSA-194306 [2](#) Neuphilin interactions with VEGF and VEGFR

R-HSA-195399 [2](#) VEGF binds to VEGFR leading to receptor dimerization

R-HSA-216083 [2](#) Integrin cell surface interactions

R-HSA-4420097 [2](#) VEGFA-VEGFR2 Pathway

R-HSA-5218921 [2](#) VEGFR2 mediated cell proliferation

R-HSA-9673768 [2](#) Signaling by membrane-tethered fusions of PDGFRA or PDGFRB

SIGNOR

P35968 [2](#)

SignalLink

P35968 [2](#)

ENZYME

Search... [2](#)

Names & Taxonomyⁱ

Protein namesⁱ

Recommended name

Vascular endothelial growth factor receptor 2 [2](#) [Curated](#)

EC number

EC:2.7.10.1 ([UniProtKB](#) | [ENZYME](#) [2](#) | [Rhea](#) [2](#)) [2](#) [Publications](#)

Short names

VEGFR-2

Alternative names

Fetal liver kinase 1 (FLK-1)

Kinase insert domain receptor (KDR)

Protein-tyrosine kinase receptor flk-1

CD Antigen Name

CD309

Gene namesⁱ

Name

KDR [2](#) [Imported](#)

Synonyms

FLK1, VEGFR2

Organism names

Organismⁱ

Homo sapiens (Human)

Taxonomic identifierⁱ

9606 [NCBI](#) [2](#)

Taxonomic lineageⁱ

cellular organisms > [Eukaryota \(eucaryotes\)](#) > [Opisthokonta](#) > [Metazoa \(metazoans\)](#) > [Eumetazoa](#) > [Bilateria](#) > [Deuterostomia](#) > [Chordata \(chordates\)](#) > [Craniata](#) > [Vertebrata \(vertebrates\)](#) > [Gnathostomata \(jawed vertebrates\)](#) > [Teleostomi](#) > [Euteleostomi \(bony vertebrates\)](#) > [Sarcopterygii](#) > [Dipnotetrapodomorpha](#) > [Tetrapoda \(tetrapods\)](#) > [Amniota \(amniotes\)](#) > [Mammalia \(mammals\)](#) > [Theria](#) > [Eutheria \(placentals\)](#) > [Boreoeutheria](#) > [Euarchontoglires](#) > [Primates](#) > [Haplorrhini](#) > [Simiiformes](#) > [Catarrhini](#) > [Hominoidea \(apes\)](#) > [Hominidae \(great apes\)](#) > [Homininae](#) > [Homo](#)

Accessions

Primary accession

P35968

Secondary accessions

A2RRS0

B5A925

C5IFA0

O60723

Q14178

Proteomesⁱ

Identifier

Feedback

Help

https://www.uniprot.org/uniprotkb/P35968/entry#function

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Q14178

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External links

History

Proteomesⁱ

Identifier

UP000005640

Componentⁱ

Chromosome 4

Organism-specific databases

HGNC

HGNC:6307 [KDR](#)

MIM

191306 [gene](#)

602089 [phenotype](#)

VEuPathDB

HostDB:ENSG00000128052 [KDR](#)

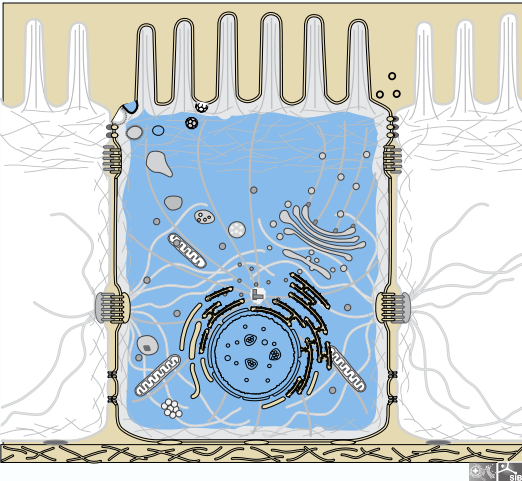
neXtProt

NX_P35968 [KDR](#)

Subcellular Locationⁱ

UniProt Annotation

GO Annotation



Cell junction

Endoplasmic reticulum

Cell membrane

Note: Localized with RAP1A at cell-cell junctions (By similarity). Colocalizes with ERN1 and XBP1 in the endoplasmic reticulum in endothelial cells in a vascular endothelial growth factor (VEGF)-dependent manner (PubMed:23529610).

Isoform 1

Cell membrane ; Single-pass type I membrane protein

Cytoplasm

Nucleus

Cytoplasmic vesicle

Early endosome

Note: Detected on caveolae-enriched lipid rafts at the cell surface. Is recycled from the plasma membrane to endosomes and back again. Phosphorylation triggered by VEGFA binding promotes internalization and subsequent degradation. VEGFA binding triggers internalization and translocation to the nucleus.

Isoform 2

Secreted

Isoform 3

Secreted

Features

Showing features for topological domainⁱ, transmembraneⁱ.

1

100

200

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TYPE

-- Select --

ID

POSITION(S)

DESCRIPTION

▶ Topological domain

20-764

Extracellular

Sequence Analysis

BLAST

Add

▶ Transmembrane

765-785

Helical

Sequence Analysis

BLAST

Add

▶ Topological domain

786-1356

Cytoplasmic

Sequence Analysis

BLAST

Add

Keywordsⁱ

Cellular component

Expand table

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Cytoplasmic

Sequence Analysis

BLAST

Add

Keywordsⁱ

Cellular component

#Cell junction

#Cell membrane

#Cytoplasm

#Cytoplasmic vesicle

#Endoplasmic reticulum

More keywords

Disease & Variantsⁱ

Involvement in diseaseⁱ

Hemangioma, capillary infantile (HCI)

3 Publications

Note

Disease susceptibility is associated with variants affecting the gene represented in this entry

Description

A condition characterized by dull red, firm, dome-shaped hemangiomas, sharply demarcated from surrounding skin, usually presenting at birth or occurring within the first two or three months of life. They result from highly proliferative, localized growth of capillary endothelium and generally undergo regression and involution without scarring.

See also

MIM:602089

Natural variants in HCI

VARIANT ID	POSITION(S)	CHANGE	DESCRIPTION
VAR_042057	482	C>R	in HCI; associated with disease 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
VAR_063147	1147	P>S	in HCI; somatic mutation; dbSNP:rs121917766

No disease ID

Note

Plays a major role in tumor angiogenesis. In case of HIV-1 infection, the interaction with extracellular viral Tat protein seems to enhance angiogenesis in Kaposi's sarcoma lesions

Features

Showing features for mutagenesis¹.

1

100

200

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700

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TYPE

ID

POSITION(S)

DESCRIPTION

-- Select --

Mutagenesis

726

Strongly reduced autophosphorylation and activation of MAP kinases.

1 Publication

Mutagenesis

731

Strongly reduced autophosphorylation and activation of MAP kinases.

1 Publication

Mutagenesis

801

Abolishes stimulation of nitric oxide synthesis.

1 Publication

Mutagenesis

868

Loss of enzyme activity.

1 Publication

Mutagenesis

951

Abolishes reorganization of the actin cytoskeleton and cell migration in response to VEGFA.

1 Publication

Mutagenesis

996

Strongly reduced autophosphorylation. Reduces phosphorylation of PLCG1.

1 Publication

Mutagenesis

1045

Significantly higher kinase activity.

1 Publication

Mutagenesis

1054

Strongly reduced autophosphorylation. Abolishes phosphorylation of downstream signaling proteins; when associated with F-1059.

1 Publication

Mutagenesis

1059

Strongly reduced autophosphorylation. Abolishes phosphorylation of downstream signaling proteins; when

1 Publication

https://www.uniprot.org/uniprotkb/P35968/entry#disease_variants

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TYPE

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DESCRIPTION

-- Select --

▶ Mutagenesis

726

Strongly reduced autophosphorylation and activation of MAP kinases. 1 Publication

▶ Mutagenesis

731

Strongly reduced autophosphorylation and activation of MAP kinases. 1 Publication

▶ Mutagenesis

801

Abolishes stimulation of nitric oxide synthesis. 1 Publication

▶ Mutagenesis

868

Loss of enzyme activity. 1 Publication

▶ Mutagenesis

951

Abolishes reorganization of the actin cytoskeleton and cell migration in response to VEGFA. 1 Publication

▶ Mutagenesis

996

Strongly reduced autophosphorylation. Reduces phosphorylation of PLCG1. 1 Publication

▶ Mutagenesis

1045

Significantly higher kinase activity. 1 Publication

▶ Mutagenesis

1054

Strongly reduced autophosphorylation. Abolishes phosphorylation of downstream signaling proteins; when associated with F-1059. 1 Publication

▶ Mutagenesis

1059

Strongly reduced autophosphorylation. Abolishes phosphorylation of downstream signaling proteins; when

Expand table

Variants

Filter Consequence

Likely disease

Predicted consequence

Likely benign

Uncertain

Filter Provenance

UniProt reviewed

ClinVar reviewed

Large scale studies

1

100

200

300

400

500

600

700

800

900

G

A

V

L

I

S

T

C

M

D

N

E

Q

R

K

H

F

Y

N

P

d

.

VARIANT ID(S)

POSITION(S)

CHANGE

DESCRIPTION

CLINICAL SIGNIFICANCE

PROVENANCE

▶ CA356921577

rs1187053033

2

Q>H

ClinGen

gnomAD

▶ CA356921592

rs1389000621

2

Q>K

ClinGen

gnomAD

▶ CA356921585

rs1560526887

2

Q>P

ClinGen

Ensembl

▶ VAR_042053

2

Q>R

a lung adenocarcinoma sample; somatic mutation (UniProt) 1 Publication

Variant of uncertain significance (UniProt)

UniProt

▶ CA356921569

rs1177325277

3

S>T

ClinGen

TOPMed

CA356921521

ClinGen

Expand table

Organism-specific databases

DisGeNET

3791

MIM

191306 gene

602089 phenotype

MalaCards

KDR

OpenTargets

ENSG00000128052

Orphanet

464293 NON RARE IN EUROPE: Infantile capillary hemangioma

3303 Tetralogy of Fallot

PharmGKB

PA30086

Chemistry

UniProt

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Organism-specific databases

DisGeNET

3791

MIM

191306

gene

602089

phenotype

MalaCards

KDR

OpenTargets

ENSG00000128052

Orphanet

464293

NON RARE IN EUROPE: Infantile capillary hemangioma

3303

Tetralogy of Fallot

PharmGKB

PA30086

Chemistry

ChEMBL

CHEMBL279

DrugBank

DB04727

1-{4-[4-Amino-6-(4-methoxyphenyl)furo[2,3-d]pyrimidin-5-yl]phenyl}-3-[2-fluoro-5-(trifluoromethyl)phenyl]urea

DB07514

3-(2-aminoquinazolin-6-yl)-1-(3,3-dimethylindolin-6-yl)-4-methylpyridin-2(1H)-one

DB07528

3-(2-aminoquinazolin-6-yl)-4-methyl-1-[3-(trifluoromethyl)phenyl]pyridin-2(1H)-one

DB06938

4-[[2-[[4-chloro-3-(trifluoromethyl)phenyl]amino]-3H-benzimidazol-5-yl]oxy]-N-methyl-pyridine-2-carboxamide

DB07326

6-chloro-N-pyrimidin-5-yl-3-[[3-(trifluoromethyl)phenyl]amino]-1,2-benzisoxazole-7-carboxamide

More DrugBank links

DrugCentral

P35968

GuidetoPHARMACOLOGY

1813

Genetic variation databases

BioMuta

KDR

DMDM

9087218

ClinGen

HGNC:6307

GenCC

HGNC:6307

PTM/Processing

Features

Showing features for signalⁱ, chainⁱ, glycosylationⁱ, disulfide bondⁱ, modified residueⁱ, modified residue (large scale)ⁱ.

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TYPE

-- Select --

ID

POSITION(S)

SOURCE

-- Select --

DESCRIPTION

► Signal

1-19

UniProt

Sequence Analysis

BLAST

Add

► Chain

PRO_0000016771 20-1356

UniProt

Vascular endothelial growth factor receptor 2

BLAST

Add

► Glycosylation

46

UniProt

N-linked (GlcNAc...) asparagine

Sequence Analysis

► Disulfide bond

53-103

UniProt

PROSITE-ProRule Annotation

BLAST

Add

► Glycosylation

66

UniProt

N-linked (GlcNAc...) asparagine

Sequence Analysis

Expand table

Post-translational modificationⁱ

N-glycosylated.

3 Publications

Ubiquitinated. Tyrosine phosphorylation of the receptor promotes its poly-ubiquitination, leading to its degradation via the proteasome or lysosomal proteases.

3 Publications

Feedback

Help

https://www.uniprot.org/uniprotkb/P35968/entry#disease_variants

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N-linked (GlcNAc...) asparagine

Sequence Analysis

Expand table

Post-translational modificationⁱ

N-glycosylated.

3 Publications

Ubiquitinated. Tyrosine phosphorylation of the receptor promotes its poly-ubiquitination, leading to its degradation via the proteasome or lysosomal proteases.

3 Publications

Autophosphorylated on tyrosine residues upon ligand binding. Autophosphorylation occurs in trans, i.e. one subunit of the dimeric receptor phosphorylates tyrosine residues on the other subunit. Phosphorylation at Tyr-951 is important for interaction with SH2D2A/TSAD and VEGFA-mediated reorganization of the actin cytoskeleton. Phosphorylation at Tyr-1175 is important for interaction with PLCG1 and SHB. Phosphorylation at Tyr-1214 is important for interaction with NCK1 and FYN. Dephosphorylated by PTPRB. Dephosphorylated by PTPRJ at Tyr-951, Tyr-996, Tyr-1054, Tyr-1059, Tyr-1175 and Tyr-1214.

9 Publications

The inhibitory disulfide bond between Cys-1024 and Cys-1045 may serve as a specific molecular switch for H₂S-induced modification that regulates KDR/VEGFR2 function.

Keywordsⁱ

PTM

#Disulfide bond

#Glycoprotein

#Phosphoprotein

#Ubl conjugation

Proteomic databases

EPD

P35968

MassIVE

P35968

MaxQB

P35968

PaxDb

P35968

PeptideAtlas

P35968

ProteomicsDB

55169 [P35968-1]

55170 [P35968-2]

55171 [P35968-3]

jPOST

P35968

PTM databases

CarbonylDB

P35968

GlyGen

P35968 20 sites, 1 Thr glycan (1 site)

PhosphoSitePlus

P35968

iPTMnet

P35968

Expressionⁱ

Tissue specificityⁱ

Detected in cornea (at protein level). Widely expressed.

1 Publication

Gene expression databases

Bgee

ENSG00000128052 Expressed in germinal epithelium of ovary and 188 other tissues

Genevisible

P35968 HS

Organism-specific databases

HPA

ENSG00000128052 Low tissue specificity

Interactionⁱ

Subunitⁱ

Homodimer in the presence of bound dimeric VEGFA, VEGFC or VEGFD ligands; monomeric in the absence of bound ligands. Can also form heterodimers with FLT1/VEGFR1 and KDR/VEGFR2. Interacts (tyrosine phosphorylated) with LFYN, NCK1, PLCG1. Interacts (tyrosine-phosphorylated active form preferentially) with DAB2IP (via C2 domain and active form preferentially); the interaction occurs at the late phase of VEGFA response and inhibits KDR/VEGFR2 activity. Interacts with SHB/SH2D2A/TSAD, GRB2, MYOF, CBL and PDCD6. Interacts (via C-terminus domain) with ERN1 (via kinase domain); the interaction is facilitated in a XBP1 isoform 1- and vascular endothelial growth factor (VEGF)-dependent manner in endothelial cells (PubMed:23529610). Interacts (via juxtamembrane region) with chaperone PDCL3 (via thioredoxin fold region); the interaction leads to increased KDR/VEGFR2 abundance through inhibition of its ubiquitination and degradation (PubMed:23792958, PubMed:26059764).

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interacts (via juxtamembrane region) with chaperone PDLCL3 (via thioredoxin fold region); the interaction leads to increased KDR/VEGFR2 abundance through

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Interacts (tyrosine phosphorylated) with CDC88A/GIV (via SH2-like region); binding requires autophosphorylation of the KDR/VEGFR2 C-terminal region (PubMed:25187647).

Interacts with isoform 2 of BSG (PubMed:25825981). 26 Publications

(Microbial infection) Interacts with HIV-1 Tat. 1 Publication

Binary interactionsⁱ

P35968 has binary interactions with 18 proteins

Filter

Subcellular location Select...

Diseases Select...

Clear

VEGFR2_HUMAN

VEGFA_CANLF

PTPRJ_HUMAN

PGBM_HUMAN

VEGFC_HUMAN

VEGFR3_HUMAN

PTN6_HUMAN

ITGA2_HUMAN

NCK1_HUMAN

VEGFA_HUMAN

SRC_HUMAN

PGFRB_HUMAN

LEG1_HUMAN

MET_HUMAN

PDGFRB_HUMAN

GRM1_HUMAN

NRP1_HUMAN

IMA3_HUMAN

TYPE

-- Select --

ENTRY 1

-- Select --

ENTRY 2

NUMBER OF EXPERIMENTS

INTACT

BINARY	P35968	FLT4 P35916	5	EBI-1005487, EBI-1005467
BINARY	P35968	GRM1 O60565	4	EBI-1005487, EBI-944395
BINARY	P35968	HSPG2 P98160	5	EBI-1005487, EBI-947664
BINARY	P35968	HSPG2 PRO_0000391621 P98160	2	EBI-1005487, EBI-6896259
BINARY	P35968	HSPG2 PRO_0000391622 P98160	2	EBI-1005487, EBI-6896607
BINARY	P35968	ITGA2 P17301	2	EBI-1005487, EBI-702960
BINARY	P35968	KDR P35968	4	EBI-1005487, EBI-1005487
BINARY	P35968	KPNA4 O00629	4	EBI-1005487, EBI-396343
BINARY	P35968	LGALS1 P09382	3	EBI-1005487, EBI-1048875
BINARY	P35968	MET P08581	3	EBI-1005487, EBI-1039152

Expand table

Protein-protein interaction databases

BioGRID

109992 77 interactors

CORUM

P35968

DIP

DIP-486N

IntAct

P35968 224 interactors

MINT

P35968

STRING

9606.ENSP00000263923

Chemistry

BindingDB

P35968

Structureⁱ

https://www.uniprot.org/uniprotkb/P35968/entry#interaction

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DIP

Entry86N

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History

STRING

9606.ENSP00000263923

Chemistry

BindingDB

P35968

Structure



SOURCE

-- Select --

IDENTIFIER

METHOD

-- Select --

RESOLUTION

CHAIN

POSITIONS

LINKS

PDB	1VR2	X-ray	2.40 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	1Y6A	X-ray	2.10 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	1Y6B	X-ray	2.10 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	1YWN	X-ray	1.71 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	2M59	NMR		A/B	759-795	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	2MET	NMR		A/B/C	759-795	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	2MEU	NMR		A/B	759-795	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	2OH4	X-ray	2.05 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	2P2H	X-ray	1.95 Å	A	815-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download
PDB	2P2I	X-ray	2.40 Å	A/B	815-1171	PDBe · RCSB-PDB · PDBj · PDBsum	Download

Features

Showing features for beta strand¹, turn¹, helix¹.

1

100

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TYPE

-- Select --

ID

POSITION(S)

DESCRIPTION

▶ Beta strand	134-138	Combined Sources	BLAST Add
▶ Beta strand	145-148	Combined Sources	BLAST Add
▶ Beta strand	152-154	Combined Sources	BLAST Add
▶ Beta strand	159-164	Combined Sources	BLAST Add
▶ Turn	165-167	Combined Sources	BLAST Add
▶ Beta strand	168-170	Combined Sources	BLAST Add
▶ Beta strand	174-176	Combined Sources	BLAST Add
▶ Beta strand	178-180	Combined Sources	BLAST Add

3D structure databases

Expand table

Function

Names & Taxonomy

Subcellular Location

Disease & Variants

PTM/Processing

Expression

Interaction

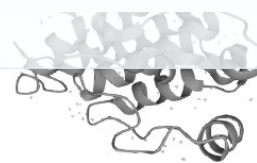
Structure

Family & Domains

Sequence & Isoforms

Similar Proteins

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[Publications](#)
[External links](#)
[History](#)



SOURCE	IDENTIFIER	METHOD	RESOLUTION	CHAIN	POSITIONS	LINKS
-- Select --		-- Select --				
PDB	1VR2	X-ray	2.40 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	1Y6A	X-ray	2.10 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	1Y6B	X-ray	2.10 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	1YWN	X-ray	1.71 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	2M59	NMR		A/B	759-795	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	2MET	NMR		A/B/C	759-795	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	2MEU	NMR		A/B	759-795	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	2OH4	X-ray	2.05 Å	A	806-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	2P2H	X-ray	1.95 Å	A	815-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗
PDB	2P2I	X-ray	2.40 Å	A/B	815-1171	PDBe · RCSB-PDB · PDBj · PDBSum 🔗

Features

Showing features for beta strandⁱ, turnⁱ, helixⁱ

TYPE	ID	POSITION(S)	DESCRIPTION
-- Select --			
▶ Beta strand	134-138	Combined Sources	BLAST 📦 Add
▶ Beta strand	145-148	Combined Sources	BLAST 📦 Add
▶ Beta strand	152-154	Combined Sources	BLAST 📦 Add
▶ Beta strand	159-164	Combined Sources	BLAST 📦 Add
▶ Turn	165-167	Combined Sources	BLAST 📦 Add
▶ Beta strand	168-170	Combined Sources	BLAST 📦 Add
▶ Beta strand	174-176	Combined Sources	BLAST 📦 Add
▶ Beta strand	178-180	Combined Sources	BLAST 📦 Add

Expand table

3D structure databases

AlphaFoldDB

[P35968](#)

BMRB

[P35968](#)

SMR

[P35968](#)

ModBase

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PDBe-KB

Search...

Miscellaneous

EvolutionaryTrace

[P35968](#)

Family & Domainsⁱ

Features

Showing features for domainⁱ, regionⁱ, compositional biasⁱ

Features

Showing features for domainⁱ, regionⁱ, compositional biasⁱ.

TYPE	ID	POSITION(S)	DESCRIPTION
Domain			
▶ Domain	46-110	Ig-like C2-type 1	BLAST 🔗 Add
▶ Domain	141-207	Ig-like C2-type 2	BLAST 🔗 Add
▼ Domain	224-320	Ig-like C2-type 3	BLAST 🔗 Add
Sequence: YDVVLSPSHGIELSVGEKLVLNCTARTELVNGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNST			
▶ Domain	328-414	Ig-like C2-type 4	BLAST 🔗 Add
▶ Domain	421-548	Ig-like C2-type 5	BLAST 🔗 Add
▶ Domain	551-660	Ig-like C2-type 6	BLAST 🔗 Add
▶ Domain	667-753	Ig-like C2-type 7	BLAST 🔗 Add
▶ Domain	834-1162	Protein kinase PROSITE-ProRule Annotation	BLAST 🔗 Add

[Collapse table](#)Domainⁱ

The second and third Ig-like C2-type (immunoglobulin-like) domains are sufficient for VEGFC binding.  1 Publication

Sequence similaritiesⁱ

Belongs to the **protein kinase superfamily**. **Tyr protein kinase family**. **CSF-1/PDGF receptor subfamily**. PROSITE-ProRule Annotation

Keywordsⁱ

```
Domain
#Immunoglobulin domain
#Repeat
#Signal
#Transmembrane
#Transmembrane helix
```

Phylogenomic databases

GeneTree
ENSGT00940000156710 [↗](#)

HOGENOM
CLU_000288_49_4_1

InParanoid
P35968 [↗](#)

OMA
RIFWDSK 

PhylomeDB
P35968 

TreeFam
TF325768 

eggNOG
KOG0200  Eukaryota

Family and domain databases

Gene3D
2.60.40.10 7 hits

InterPro
View protein in InterPro [↗](#)
IPR007110 [↗](#) Ig-like_dom
IPR036179 [↗](#) Ig-like_dom_sf
IPR013783 [↗](#) Ig-like_fold
IPR013098 [↗](#) Ig_I-set
[More InterPro links](#)

Pfam
[View protein in Pfam](#)
PF07679 [I-set](#) 2 hits
PF07714 [PK_Tyr_Ser-Thr](#) 1 hit
PF17988 [VEGFR-2_TMD](#) 1 hit

SMART
[View protein in SMART](#)
SM00409 [IG](#) 7 hits
SM00408 [IGc2](#) 5 hits

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IPK013/83 IG-like fold

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[More InterPro links](#)

PRINTS

PRO1834 [VEGFRECEPTR2](#)

PROSITE

[View protein in PROSITE](#)

P550835 [IG_LIKE](#) 5 hits

P500107 [PROTEIN_KINASE_ATP](#) 1 hit

P550011 [PROTEIN_KINASE_DOM](#) 1 hit

P500109 [PROTEIN_KINASE_TYR](#) 1 hit

P500240 [RECEPTOR_TYR_KIN_III](#) 1 hit

[View protein in SMART](#)

SM00409 [IG](#) 7 hits

SM00408 [IGc2](#) 5 hits

SM00219 [TyrKc](#) 1 hit

SUPFAM

SSF48726 [Immunoglobulin](#) 6 hits

SSF56112 [Protein kinase-like \(PK-like\)](#) 1 hit

MobiDB

[Search...](#)

ProtoNet

[Search...](#)

Sequence & Isoformsⁱ

[BLAST 3 isoforms](#) [Align 3 isoforms](#)

Sequence statusⁱ

Complete

This entry describes 3 isoformsⁱ produced by **Alternative splicing**.

Sequence processingⁱ

The displayed sequence is further processed into a mature form.

P35968-1

This isoform has been chosen as the **canonical** sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

Name

1

Synonyms

mbVegfr-2

See also

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

Tools

[Download](#) [Add](#) [Highlight](#) [Copy sequence](#)

Length

1,356

Mass (Da)

151,527

Last updated

2000-12-01 v2

Checksumⁱ

59E7C44B05CFEBB3

MQSKVLLAFA¹⁰ LWLCVETRAA²⁰ SVGLPSVSLD³⁰ LPRLSIQKDI⁴⁰ LTIKANTTLQ⁵⁰ ITCRGQRDL⁶⁰ WLWPNQSGS⁷⁰ EQRVEVECS⁸⁰ DGLFCKTLTI⁹⁰ PKVIGNDTGA¹⁰⁰

YKCFYRETDL¹¹⁰ ASVIYVVVD¹²⁰ YRSPFIASVS¹³⁰ DQHGVMVITE¹⁴⁰ NKNKTVVIPC¹⁵⁰ LGSISNLNVS¹⁶⁰ LCARYPEKRF¹⁷⁰ VPDGNRIWD¹⁸⁰ SKKGFTIPSY¹⁹⁰ MISYAGMVFC²⁰⁰

EAKINDESQY²¹⁰ SIMYIVVVVG²²⁰ YRIYDVVLSP²³⁰ SHGIELSVGE²⁴⁰ KLVNCTART²⁵⁰ ELNVGIDFNW²⁶⁰ EYPSSKHQHK²⁷⁰ KLVNRDLKTQ²⁸⁰ SGSEMKFSL²⁹⁰ TLTIDGVTRS³⁰⁰

DQGLYTCAAS³¹⁰ SGLMTKKNST³²⁰ FVRVHEKPFV³³⁰ AFGSGMESLV³⁴⁰ EATVGERVRI³⁵⁰ PAKYLGYPPI³⁶⁰ EIKWYKNGIP³⁷⁰ LESNHTIKAG³⁸⁰ HVLTIMEVSE³⁹⁰ RDTGNYTVIL⁴⁰⁰

TNPISKEKQS⁴¹⁰ HVSLSLVVVP⁴²⁰ PQIGEKSLIS⁴³⁰ PVDVSYQYGT⁴⁴⁰ QTLTCTVYAI⁴⁵⁰ PPPHHIHWY⁴⁶⁰ QLEEECANEP⁴⁷⁰ SQAVSVTNPY⁴⁸⁰ PCEEWRSDVD⁴⁹⁰ FQGGNKIEVN⁵⁰⁰

KNQFALTEGK⁵¹⁰ NKTVSTLVIQ⁵²⁰ AANVSALYKC⁵³⁰ EAVNKVGRGE⁵⁴⁰ RVISFHVTRG⁵⁵⁰ PEITLQPDQ⁵⁶⁰ PTEQESVSLW⁵⁷⁰ CTADRSTFEN⁵⁸⁰ LTWYKLGQPQ⁵⁹⁰ LPIHVGELPT⁶⁰⁰

PVCKNLDTLW⁶¹⁰ KLNATMFSNS⁶²⁰ TNDILIMELK⁶³⁰ NASLQDQGDY⁶⁴⁰ VCLAQDRKTK⁶⁵⁰ KRHCVRQLT⁶⁶⁰ VLERVAPTIT⁶⁷⁰ GNLENQTTSI⁶⁸⁰ GESIEVSCTA⁶⁹⁰ SGNPPPIIMW⁷⁰⁰

FKDNETLVED⁷¹⁰ SGIVLKDGNR⁷²⁰ NLTIIRVRKE⁷³⁰ DEGLYTCQAC⁷⁴⁰ SVLGCAKVEA⁷⁵⁰ FFIIEGAQEK⁷⁶⁰ TNLEIILVIG⁷⁷⁰ TAVIAMFFWL⁷⁸⁰ LLVIILRTVK⁷⁹⁰ RANGGELKTG⁸⁰⁰

YLSIVMDPDE⁸¹⁰ LPLDEHCERL⁸²⁰ PYDASKWEFP⁸³⁰ RDRLKLGKPL⁸⁴⁰ GRGAFGVIE⁸⁵⁰ ADAFGIDKTA⁸⁶⁰ TCRTVAVKML⁸⁷⁰ KEGATHSEHR⁸⁸⁰ ALMSELKILI⁸⁹⁰ HIGHHLNVVN⁹⁰⁰

LLGACTKPGG⁹¹⁰ PLMVIVEFCK⁹²⁰ FGNLSTYLRS⁹³⁰ KRNEFVPYKT⁹⁴⁰ KGARFRQGD⁹⁵⁰ YVGAIPVDLK⁹⁶⁰ RRLDSITSSQ⁹⁷⁰ SSASSGFVEE⁹⁸⁰ KSLSDVEEEE⁹⁹⁰ APEDLYKDFL¹⁰⁰⁰

TLEHLCYCSF¹⁰¹⁰ QVAKGMEFLA¹⁰²⁰ SRKCIHRDLA¹⁰³⁰ ARNILLSEKN¹⁰⁴⁰ VVKICDFGLA¹⁰⁵⁰ RDIYKDPD¹⁰⁶⁰ RKGDARLPLK¹⁰⁷⁰ WMAPETIFDR¹⁰⁸⁰ VYTIQSDVWS¹⁰⁹⁰ FGVLLEWIFS¹¹⁰⁰

LGASPPYGVK¹¹¹⁰ IDEEFCRRRK¹¹²⁰ EGTRMRAPDY¹¹³⁰ TTPEMYQTML¹¹⁴⁰ DCWHGEPQSR¹¹⁵⁰ PTFSELVEHL¹¹⁶⁰ GNLLQANAQQ¹¹⁷⁰ DGKDYIVLPI¹¹⁸⁰ SETLSMEEDS¹¹⁹⁰ GLSLPTSPVS¹²⁰⁰

CMEEEVCDP¹²¹⁰ KFHYDNTAGI¹²²⁰ SQYLQNSKRK¹²³⁰ SRPVSVKTFE¹²⁴⁰ DIPLEEPEVK¹²⁵⁰ VIPDDNQDTS¹²⁶⁰ GMVLASEELK¹²⁷⁰ TLEDRTKLSP¹²⁸⁰ SFGGMVPSKS¹²⁹⁰ RESVASEGSN¹³⁰⁰

QTSYGYSGYH¹³¹⁰ SDDTDTTVYS¹³²⁰ SEEAELLKLI¹³³⁰ EIGVQTGSTA¹³⁴⁰ QILQPDSTGT¹³⁵⁰ LSSPPV

P35968-2

Name

2

Synonyms

Differences from canonical

663-678: 663-678: ERVAPTITGNLENQTT → GRETILDHCAEAVGMP

1 Publication

Feedback

Help

https://www.uniprot.org/uniprotkb/P35968/entry#structure

Exhibit 2084

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External links

History

SRKCIHRDLA

ARNILLSEKN

VVKICDFGLA

RDIYKDPDVV

RKGDARLPCK

WMAPEITFDK

VYTIQSDVWS

FGVLWEIIFS

LGASPYPGVK

IDEEFCRRLK

EGTRMRAPDY

TTPEMYQIML

DCMHGEPQSR

PTFSELVEHL

GNLLQANAQQ

DGKDYIVLPI

SETLSMEEDS

GLSLPTSPVS

CMEEEVCDP

KFHYDNTAGI

SQVYQNSRRK

SRPVSVKTFE

DIPLEEPEVK

VIPDDNQDTS

GMVLASEELK

TLEDRTKLSP

SFGGMVPSKS

RESVASSEGN

QTSQVQSYGH

SDDTDITVYS

SEEAELLRLI

EIGVQTGSTA

QILQPDSTGT

LSSPPV

P35968-2

Name

2

Synonyms

sVegfr-2

Show sequence

See also

sequence in UniParc or sequence clusters in UniRef

Differences from canonical

663-678: 663-678: ERVAPTITGNLENQTT → GRETILDHCAEAVGMP

1 Publication

679-1356: 679-1356: Missing

1 Publication

P35968-3

Name

3

Synonyms

VEGFR2-712

Show sequence

See also

sequence in UniParc or sequence clusters in UniRef

Differences from canonical

712-712: 712-712: G → E

1 Publication

713-1356: 713-1356: Missing

1 Publication

Features

Showing features for sequence conflict¹, alternative sequence¹, compositional bias¹.

1

100

200

300

400

500

600

700

800

900

1,000

1,100

1,200

1,300

1,356

TYPE

-- Select --

ID

POSITION(S)

DESCRIPTION

▶ Sequence conflict

2

in Ref. 4: AAC16450

Curated

▶ Alternative sequence

VSP_041988

663-678

in isoform 2

1 Publication

BLAST

Add

▶ Alternative sequence

VSP_041989

679-1356

in isoform 2

1 Publication

BLAST

Add

▶ Alternative sequence

VSP_041990

712

in isoform 3

1 Publication

BLAST

Add

▶ Alternative sequence

VSP_041991

713-1356

in isoform 3

1 Publication

BLAST

Add

▶ Sequence conflict

772

in Ref. 7: AAA59459/CAA43837

Curated

▶ Sequence conflict

787

in Ref. 7: AAA59459/CAA43837

Curated

▶ Sequence conflict

835

in Ref. 7: AAA59459/CAA43837

Curated

▶ Compositional bias

1292-1315

Polar residues

Automatic Annotation

BLAST

Add

Keywords¹

Coding sequence diversity

#Alternative splicing

Technical term

#3D-structure

#Reference proteome

Sequence databases

CCDS

CCDS3497.1

↗

 [P35968-1]

RefSeq

NP_002244.1

↗

 NM_002253.2

↗

 [P35968-1]

PIR

JC1402

↗

 JC1402

SEQUENCE

PROTEIN

MOLECULE TYPE

STATUS

EU826563 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

ACF47599.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

FJ899739 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

ACR78514.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

AF035121 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

AAB88005.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

AF063658 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

AAC16450.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

BC131822 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

AAI31823.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

L04947 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

AAA59459.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

X61656 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

CAA43837.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

mRNA

X89776 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

CAA61916.1 (EMBL

↗

 | GenBank

↗

 | DDBJ

↗

)

Genomic DNA

Genome annotation databases

Ensembl

ENST00000263923.5

↗

 ENSP00000263923.4

↗

 ENSG00000128052.10

↗

 [P35968-1]

GeneID

3791

↗

KEGG

hsa:3791

↗

MANE-Select

ENST00000263923.5

↗

 ENSP00000263923.4

↗

 NM_002253.4

↗

 NP_002244.1

↗

UCSC

uc003has.4

↗

 human [P35968-1]

Similar Proteins¹

100% identity

90% identity

50% identity

P35968-1, P35968-2, and P35968-3

No similar proteins at 100% identity for these isoforms.

View all

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