



UniProtKB

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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

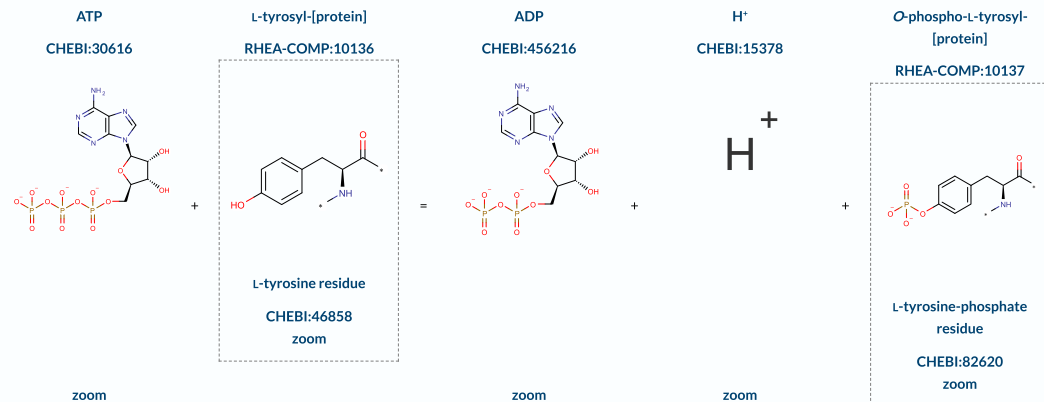
Annotation scoreⁱ

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](#)

Activity regulation

Present in an inactive conformation in the absence of bound ligand. Binding of VEGFA, VEGFC or VEGFD leads to dimerization and activation by autophosphorylation on tyrosine residues. Inhibited by the small molecule PTK inhibitor SU5614 ((3Z)-5-Chloro-3-[(3,5-dimethyl-1H-pyrrol-2-yl)methylene]-1,3-dihydro-2H-indol-2-one). May be regulated by hydrogen sulfide (H₂S) levels via a H₂S-sensitive intracellular disulfide bond. [4 Publications](#)

Features

Showing features for binding siteⁱ, active siteⁱ, siteⁱ.

TYPE	ID	POSITION(S)	DESCRIPTION
-- Select --			
▶ Binding site	840-848		ATP (UniProtKB ChEBI) Curated BLAST Add
▶ Disulfide site	840		ATP (UniProtKB ChEBI) Curated

UniProt

UniProtKB

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1

100200300400500600700800900

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

GO annotationsⁱ

Slimming set:

generic

all annotations

all molecular function

all biological process

Cell color indicative of number of GO terms

ASPECT

TERM

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

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

SignalLink

Expand table

Expand table

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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 [↗](#)

Reactome

R-HSA-194306 [↗](#)

Neurophilin interactions with VEGF and VEGFR

R-HSA-195399 [↗](#)

VEGF binds to VEGFR leading to receptor dimerization

R-HSA-216083 [↗](#)

Integrin cell surface interactions

R-HSA-4420097 [↗](#)

VEGFA-VEGFR2 Pathway

R-HSA-5218921 [↗](#)

VEGFR2 mediated cell proliferationR-HSA-9673768 [↗](#)

SIGNOR

P35968 [↗](#)

SignalLink

P35968 [↗](#)

ENZYME

Search... [↗](#)

Names & Taxonomyⁱ

Protein namesⁱ

Recommended name

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

EC number

EC:2.7.10.1 [\(UniProtKB | ENZYME \[↗\]\(#\) | Rhea \[↗\]\(#\)\)](#) [↗](#) [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 [↗](#) [Imported](#)

Synonyms

FLK1, VEGFR2

Organism names

Organismⁱ

Homo sapiens (Human)

Taxonomic identifierⁱ

9606 [NCBI \[↗\]\(#\)](#)

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

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Q40723
Q14178

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Proteomesⁱ

Identifier
UP000005640

Componentⁱ
Chromosome 4

Organism-specific databases

HGNC
HGNC:6307 [KDR](#)

MIM
191306 [gene](#)
602089 [phenotype](#)

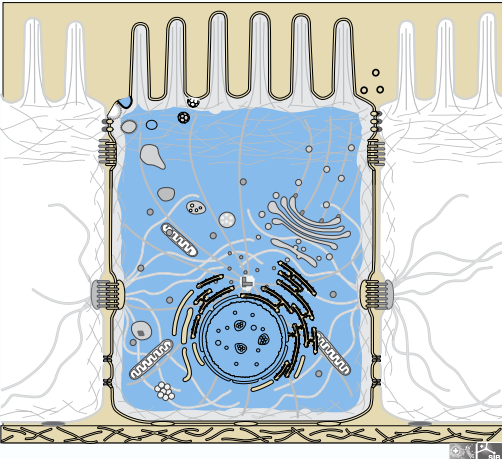
VEuPathDB
HostDB:ENSG00000128052 [↗](#)

neXtProt
NX_P35968 [↗](#)

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.



TYPE	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

Expand table

Keywordsⁱ

Cellular component

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

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Topological domain | 786-1356 | Cytoplasmic | Sequence Analysis

BLAST | Add

Expand table

Keywords¹

Cellular component

#Cell junction

#Cell membrane

#Cytoplasm

#Cytoplasmic vesicle

#Endoplasmic reticulum

More keywords

Disease & Variants¹

Involvement in disease¹

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

300

400

500

600

700

800

900

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

Expand table

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

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TYPE

ID

POSITION(S)

DESCRIPTION

-- Select --

► Mutagenesis726Strongly reduced autophosphorylation and activation of MAP kinases.1 Publication

► Mutagenesis731Strongly reduced autophosphorylation and activation of MAP kinases.1 Publication

► Mutagenesis801Abolishes stimulation of nitric oxide synthesis.1 Publication

► Mutagenesis868Loss of enzyme activity.1 Publication

► Mutagenesis951Abolishes reorganization of the actin cytoskeleton and cell migration in response to VEGFA.1 Publication

► Mutagenesis996Strongly reduced autophosphorylation. Reduces phosphorylation of PLCG1.1 Publication

► Mutagenesis1045Significantly higher kinase activity.1 Publication

► Mutagenesis1054Strongly reduced autophosphorylation. Abolishes phosphorylation of downstream signaling proteins; when associated with F-1059.1 Publication

► Mutagenesis1059Strongly 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

100200300400500600700800900

G

A

V

L

I

S

T

C

M

D

N

E

Q

R

K

H

F

Y

W

P

d

Variant ID(S)

Position(s)

Change

Description

Clinical Significance

Provenance

► CA356921577rs11870530332Q>H

► CA356921592rs13890006212Q>K

► CA356921585rs15605268872Q>P

► VAR_0420532Q>R

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

Variant of uncertain significance (UniProt)

UniProt

► CA356921569rs11773252773S>T

ClinGenTOPMed

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

[HGNC:6307](#)

3 Publications

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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

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, MYO6, 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 PUL3 (via thioredoxin fold region); the interaction leads to increased KDR/VEGFR2 abundance through

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Interacts (tyrosine phosphorylated) with CCDC88A/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

VEGR3_HUMAN

PTN6_HUMAN

ITGA2_HUMAN

NCK1_HUMAN

VEGFA_HUMAN

VEGFA_HUMAN

SRC_HUMAN

PGRB_HUMAN

LEG1_HUMAN

MET_HUMAN

PDCD6_HUMAN

GREM1_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	GREM1 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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STRING

9606.ENSPO0000263923

Chemistry

BindingDB

P35968

Structure



SOURCE	IDENTIFIER	METHOD	RESOLUTION	CHAIN	POSITIONS	LINKS
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 strand¹, turn¹, helix¹.



TYPE	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

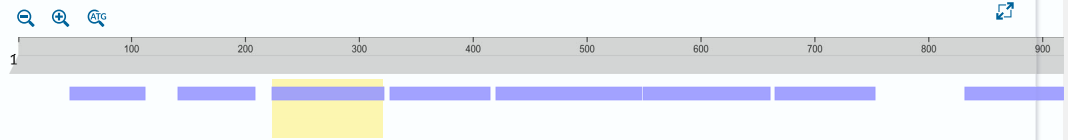
Similar Proteins

P35968 [↗](#)

Family & Domains

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: YDVLVSPSHGIELSVGEKLVLNCTARTELVNGIDFNWEYPPSSKHQHKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNST			
▶ 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 	BLAST  Add

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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Expression

Interaction

Structure

Family & Domains

Sequence & Isoforms

Similar Proteins

UniProtKB

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Search

IPK013/83 Ig-like fold

Entry 309 Feature viewer

Publications

External links

History

More InterPro links

PRINTS

PR01834 VEGFRECEPTR2

PROSITE

View protein in PROSITE

PS50835 IG_LIKE 5 hits

PS00107 PROTEIN_KINASE_ATP 1 hit

PS50011 PROTEIN_KINASE_DOM 1 hit

PS00109 PROTEIN_KINASE_TYR 1 hit

PS00240 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 & Isoforms

BLAST 3 isoforms Align 3 isoforms

Sequence status

Complete

This entry describes 3 isoforms produced by Alternative splicing.

Sequence processing

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

Checksum

59E7C44B05CFEBB3

MQSKVLLAVA

LWLCVETRAA

SVGLPSVSLD

LPRLSIQKDI

LTIKANTTLQ

ITCRGRDLD

WLWPNNSGGS

EQRVEVTECS

DGLFCKTLTI

PKVIGNDTGA

YKCFYRETDL

ASVIYVYVQD

YRSPFIASVS

DQHGVIYITE

NKNKTIVIPC

LGSISLNIVS

LCARYPEKRF

VPDGNRIISWD

SKKGFTIPSY

MISYAGMFC

EAKINDESQY

SIMYIVVVG

YRIYDVLLSP

SHGIELSVGE

KLVNCTART

ELNVGIDFNW

EYPSSKHQHK

KLVNRDLTQ

SGSEMCKFLS

TLTIDGVTRS

DQGLYTCAAS

SGLMTKKNST

FVRVHEKPFV

AFGSGMESLV

EATVGERVRI

PAKYLGVPPI

EIKWYKNGIP

LESNHTIKAG

HVLTIMEVSE

RDTGNYTVIL

TNPISKEKQS

HVSLVVVYP

PQIGEKSLIS

PVDSYQYGTI

QTLTCTVYAI

PPPHIHIWY

QLEEECANEP

SQAVSVTNPY

PCEEWRSVDE

FQGGNKIEVN

KNQFALIEGK

NKTVSTLVIQ

AANVSALYKC

EAVNKVGRGE

RVISFHVTRG

PEITLQPDQ

PTEQESVSLW

CTADRSTFEN

LTWYKLGQFP

LPIHVGELPT

PVCKNLDLTW

KLNATMFSNS

TNDILIMELK

NASLQDQGDY

VCLAQDRKTK

KRHCVVRQLT

VLERVAPTIT

GNLENQTISI

GSEIEVSCTA

SGNPPPPQIM

FKDNETLVED

SGIVLKDGNR

NLTIRVRKE

DEGLYTCQAC

SVLGCAKVEA

FFIIEGAQEK

TNLEIILVIG

TAVIAMFFWL

LLVILIRTVK

RANGGELKFG

YLSIVMDPDE

LPLDEHCERL

PYDASKWEFF

RDRILKLGKPL

GRGAFQVIE

ADAFGIDKTA

TCRTVAVKML

KEGATHSEHR

ALMSELKILI

HIGHHLNVVN

LLGACTKPGG

PLMVIVEFCK

FGNLSTYLR

KRNEFPVKY

KGARFRQKGD

YVGAIPVDLK

RRLDSITSSQ

SSASSGFVEE

KSLSDVEEEE

APEDLYKDFL

TLEHLICYSF

QVAKGMEFLA

SRKCIHRDLA

ARNILLSEKN

VVKICDFGLA

RDIYKDPDYV

RKGDARLPLK

WMAPETIFDR

VYTIQSDVWS

FGVLLWEIFS

LGASPPYGVK

IDEEFCRLRK

EGTRMRAPDY

TTPEMYQTML

DCWHGPEQSR

PTFSELVEHL

GNNLQANAQQ

DGKDYLVLPI

SETLSMEEDS

GLSLPTSPVS

CMEEEVCDP

KFHYDNTAGI

SQYLQNSKRR

SRPVSVKTFE

DIPLEEPEVK

VIPDDNQDTS

GMVLASEELK

TLEDRTKLSP

SFGGMVPSKS

RESVASEGSN

QTSYGYSQYH

SDDTDTTVYS

SEEAELKLI

EIGVQTGSTA

QILQPDSGTT

LSSPPV

P35968-2

Name

2

Synonyms

Differences from canonical

663-678: 663-678: ERVAPTITGNLENQTT → GRETILDHCAEAVGMP

1 Publication

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

1/1

Regeneron Pharmaceuticals, Inc. Exhibit 2036 Page 13
Celltrion, Inc. v. Regeneron Pharmaceuticals, Inc. IPR2023-00462



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

Entry	Feature viewer	Publications	External links	History
ADAFGLK1A	1030	1030	1030	1030
SRKCIHROCA	1030	1030	1030	1030
GLSLPTSPUS	1200	1200	1200	1200

P35968-2

Name
2
Synonyms
sVegfr-2

See also
sequence in UniParc or sequence clusters in UniRef
Differences from canonical
663-678: 663-678: ERVAPTITGNLEQTT → GRETILDHCAEAVGMP
679-1356: 679-1356: Missing

Show sequence

P35968-3

Name
3
Synonyms
VEGFR2-712

See also
sequence in UniParc or sequence clusters in UniRef
Differences from canonical
712-712: 712-712: G → E
713-1356: 713-1356: Missing

Show sequence

Features

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

TYPE	ID	POSITION(S)	DESCRIPTION
Sequence conflict		2	in Ref. 4; AAC16450
Alternative sequence	VSP_041988	663-678	in isoform 2
Alternative sequence	VSP_041989	679-1356	in isoform 2
Alternative sequence	VSP_041990	712	in isoform 3
Alternative sequence	VSP_041991	713-1356	in isoform 3
Sequence conflict		772	in Ref. 7; AAA59459/CAA43837
Sequence conflict		787	in Ref. 7; AAA59459/CAA43837
Sequence conflict		835	in Ref. 7; AAA59459/CAA43837
Compositional bias		1292-1315	Polar residues

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	
LD4947 [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]
MANE-Select
ENST00000263923.5 [ENSP00000263923.4] [NM_002253.4] [NP_002244.1]
GeneID
3791 [UCSC
uc003has.4 [human] [P35968-1]
KEGG
hsa:3791

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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