



Function

Names & Taxonomy

Subcellular Location

Disease & Variants

PTM/Processing

Expression

Interaction

Structure

Family & Domains

Sequence & Isoforms

Similar Proteins

UniProtKB

Advanced | List

Search

P17948 · VGFR1_HUMAN

Proteinⁱ

Vascular endothelial growth factor receptor 1

Geneⁱ

FLT1

Statusⁱ

UniProtKB reviewed (Swiss-Prot)

Organismⁱ

Homo sapiens (Human)

Amino acids

1338

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, VEGFB and PGF, and plays an essential role in the development of embryonic vasculature, the regulation of angiogenesis, cell survival, cell migration, macrophage function, chemotaxis, and cancer cell invasion. Acts as a positive regulator of postnatal retinal hyaloid vessel regression (Ref.11). May play an essential role as a negative regulator of embryonic angiogenesis by inhibiting excessive proliferation of endothelial cells. Can promote endothelial cell proliferation, survival and angiogenesis in adulthood. Its function in promoting cell proliferation seems to be cell-type specific. Promotes PGF-mediated proliferation of endothelial cells, proliferation of some types of cancer cells, but does not promote proliferation of normal fibroblasts (in vitro). Has very high affinity for VEGFA and relatively low protein kinase activity; may function as a negative regulator of VEGFA signaling by limiting the amount of free VEGFA and preventing its binding to KDR. Modulates KDR signaling by forming heterodimers with KDR. Ligand binding leads to the activation of several signaling cascades. Activation of PLCG leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate and the activation of protein kinase C. Mediates phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase, leading to activation of phosphatidylinositol kinase and the downstream signaling pathway. Mediates activation of MAPK1/ERK2, MAPK3/ERK1 and the MAP kinase signaling pathway, as well as of the AKT1 signaling pathway. Phosphorylates SRC and YES1, and may also phosphorylate CBL. Promotes phosphorylation of AKT1 at 'Ser-473'. Promotes phosphorylation of PTK2/FAK1 (PubMed:16685275).

19 Publications

Isoform 1

Phosphorylates PLCG. 1 Publication

Isoform 2

May function as decoy receptor for VEGFA. 1 Publication

Isoform 3

May function as decoy receptor for VEGFA. 1 Publication

Isoform 4

May function as decoy receptor for VEGFA. 1 Publication

Isoform 7

Has a truncated kinase domain; it increases phosphorylation of SRC at 'Tyr-418' by unknown means and promotes tumor cell invasion. 1 Publication

Catalytic activity

ATP + L-tyrosyl-[protein] = ADP + H⁺ + O-phospho-L-tyrosyl-[protein]

PROSITE-ProRule Annotation

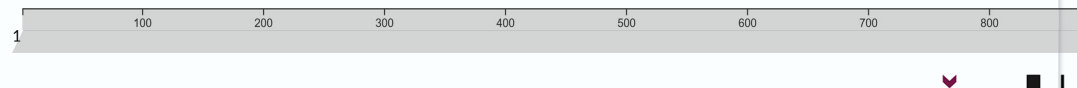
5 Publications

EC:2.7.10.1 ([UniProtKB](#) | [ENZYME](#) | [Rhea](#))Source: [Rhea 10596](#)[View Rhea reaction](#)

Activity regulation

Present in an inactive conformation in the absence of bound ligand. Binding of VEGFA, VEGFB or PGF leads to dimerization and activation by autophosphorylation on tyrosine residues.

Features

Showing features for siteⁱ, binding siteⁱ, active siteⁱ.

TYPE

ID POSITION(S)

DESCRIPTION

-- Select --

UniProt

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TYPE

-- Select --

ID

POSITION(S)

DESCRIPTION

► Site

767-768

Cleavage; by PSEN1

Curated

► Binding site

833-841

ATP (UniProtKB | ChEBI)

PROSITE-ProRule Annotation

BLAST

Add

► Binding site

861

ATP (UniProtKB | ChEBI)

PROSITE-ProRule Annotation

► Active site

1022

Proton acceptor

PROSITE-ProRule Annotation

Expand table

GO annotationsⁱ

Slimming set:

generic

all annotations

all molecular function

all biological process

all molecular function

all biological process

Cell color indicative of number of GO terms

ASPECT

TERM

Cellular Component

actin cytoskeleton

Source:HPA

Cellular Component

endosome

Source:UniProtKB-SubCell

Cellular Component

extracellular space

Source:ProtInc

1 Publication

Cellular Component

focal adhesion

Source:UniProtKB

1 Publication

Cellular Component

plasma membrane

Source:UniProtKB

1 Publication

Cellular Component

receptor complex

Source:MGI

1 Publication

Molecular Function

ATP binding

Source:UniProtKB-KW

Molecular Function

growth factor binding

Source:UniProtKB

5 Publications

Molecular Function

placental growth factor receptor activity

Source:UniProtKB

1 Publication

Molecular Function

transmembrane receptor protein tyrosine kinase activity

Source:GO_Central

1 Publication

Molecular Function

vascular endothelial growth factor receptor activity

Source:UniProtKB

3 Publications

Expand table

Complete GO annotation on QuickGO

↗

Keywordsⁱ

Molecular function

#Developmental protein

#Kinase

#Receptor

#Transferase

#Tyrosine-protein kinase

Biological process

#Angiogenesis

#Chemotaxis

#Differentiation

Ligand

#ATP-binding

#Nucleotide-binding

Enzyme and pathway databases

BRENDA

2.7.10.1

↗

 2681

PathwayCommons

P17948

↗

Reactome

R-HSA-194306

↗

 Neurophilin interactions with VEGF and VEGFR

R-HSA-195399

↗

 VEGF binds to VEGFR leading to receptor dimerization

SIGNOR

P17948

↗

SignaLink

P17948

↗

ENZYME

Search...

↗

https://www.uniprot.org/uniprotkb/P17948/entry#function

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R-HSA-194306

Neurophilin interactions with VEGF and VEGFR

R-HSA-195399

VEGF binds to VEGFR leading to receptor dimerization

Search...

Names & Taxonomyⁱ

Protein namesⁱ

Recommended name

Vascular endothelial growth factor receptor 1

EC number

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

Short names

VEGFR-1

Alternative names

Fms-like tyrosine kinase 1 (FLT-1)
Tyrosine-protein kinase FRT
Tyrosine-protein kinase receptor FLT (FLT)
Vascular permeability factor receptor

Gene namesⁱ

Name

FLT1

Synonyms

FLT, FRT, VEGFR1

Organism names

Organismⁱ

Homo sapiens (Human)

Taxonomic identifierⁱ

9606 NCBI [E](#)

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

P17948

Secondary accessions

A3E342
A3E344
A8KA71
B0LPF1
B2BF46
[More accessions](#)

Proteomesⁱ

Identifier

UP000005640

Componentⁱ

Chromosome 13

Organism-specific databases

HGNC

HGNC:3763 [E](#) FLT1

MIM

165070 [E](#) gene

VEuPathDB

HostDB:ENSG00000102755 [E](#)

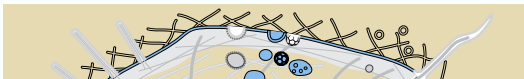
neXtProt

NX_P17948 [E](#)

Subcellular Locationⁱ

UniProt Annotation

GO Annotation



Isoform 1

Cell membrane

Single-pass type I membrane protein

Endosome

https://www.uniprot.org/uniprotkb/P17948/entry#names_and_taxonomy

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VEuPathDB

HGNC:3763 FLT1

HostDB:ENSG00000102755

MIM

165070 gene

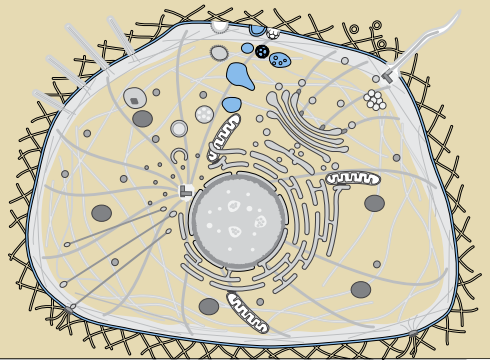
neXtProt

NX_P17948

Subcellular Locationⁱ

UniProt Annotation

GO Annotation



Isoform 1

Cell membrane ; Single-pass type I membrane protein

Endosome

Note: Autophosphorylation promotes ubiquitination and endocytosis.

Isoform 2

Secreted

1 Publication

Isoform 3

Secreted

Isoform 4

Secreted

Isoform 5

Cytoplasm

Curated

Isoform 6

Cytoplasm

Curated

Isoform 7

Cytoplasm

Curated

Features

Showing features for topological domainⁱ, transmembraneⁱ.

1

100

200

300

400

500

600

700

800

900

TYPE	ID	POSITION(S)	DESCRIPTION
Topological domain	27-758	Extracellular	Sequence Analysis BLAST Add
Transmembrane	759-780	Helical	Sequence Analysis BLAST Add
Topological domain	781-1338	Cytoplasmic	Sequence Analysis BLAST Add

Expand table

Keywordsⁱ

Cellular component

#Cell membrane

#Cytoplasm

#Endosome

#Membrane

#Secreted

Disease & Variantsⁱ

Involvement in diseaseⁱ

No disease ID

Feedback

Help

https://www.uniprot.org/uniprotkb/P17948/entry#subcellular_location

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#Cytoplasm

#Lysosome

#Membrane

#Secreted

Entry

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History

Disease & Variantsⁱ

Involvement in diseaseⁱ

No disease ID

Note

Can contribute to cancer cell survival, proliferation, migration, and invasion, and tumor angiogenesis and metastasis. May contribute to cancer pathogenesis by promoting inflammatory responses and recruitment of tumor-infiltrating macrophages

No disease ID

Note

Abnormally high expression of soluble isoforms (isoform 2, isoform 3 or isoform 4) may be a cause of preeclampsia

Features

Showing features for mutagenesisⁱ.

1

100

200

300

400

500

600

700

800

900

1,000

TYPE

ID POSITION(S)

DESCRIPTION

-- Select --

▶ Mutagenesis

767

Abolishes proteolytic cleavage by PSEN1.

1 Publication

▶ Mutagenesis

861

Abolishes enzyme activity. Abolishes interaction with PLCG.

1 Publication

▶ Mutagenesis

914

Reduces phosphorylation at other tyrosine residues.

1 Publication

▶ Mutagenesis

1050

Strongly increases kinase activity. Increases activity in promoting proliferation of endothelial cells.

1 Publication

▶ Mutagenesis

1169

Loss of phosphorylation site. Abolishes interaction with PLCG.

1 Publication

▶ Mutagenesis

1213

Loss of phosphorylation site. Abolishes interaction with PIK3R1.

1 Publication

▶ Mutagenesis

1242

Loss of phosphorylation site.

1 Publication

▶ Mutagenesis

1327

Loss of phosphorylation site.

1 Publication

▶ Mutagenesis

1333

Loss of phosphorylation site. Abolishes interaction with CBL.

2 Publications

Expand table

Variants

1

100

200

300

400

500

600

700

800

900

1,000

Filter Consequence

Likely disease

Predicted consequence

Likely benign

Uncertain

Filter Provenance

UniProt reviewed

ClinVar reviewed

Large scale studies

VARIANT ID(S)

POSITION(S)

CHANGE

DESCRIPTION

CLINICAL SIGNIFICANCE

PROVENANCE

▶ CA6930939

rs779796008

2

V>I

ClinGen
ExAC
TOPMed
gnomAD

https://www.uniprot.org/uniprotkb/P17948/entry#disease_variants

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13 Publications

External links

History

Establishes interaction with CBL. 2 Publications

Expand table

Filter Consequence

Likely disease

Predicted consequence

Likely benign

Uncertain

Filter Provenance

UniProt reviewed

ClinVar reviewed

Large scale studies

1

1002003004005006007008009001,000

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

CA6930939
rs779796008

2

V>I

ClinGen
ExAC
TOPMed
gnomAD

CA247658270
rs1047423171

3

S>G

ClinGen
TOPMed
gnomAD

CA247658269
rs930219341

4

Y>H

ClinGen
TOPMed

CA387694730
rs1182975792

4

Y>S

ClinGen
gnomAD

ClinGen
ClinVar

Expand table

Organism-specific databases

DisGeNET

2321

MIM

165070

gene

MalaCards

FLT1

OpenTargets

ENSG00000102755

Orphanet

275555

Preeclampsia

PharmGKB

PA28180

Chemistry

ChEMBL

CHEMBL1868

DrugBank

DB06626

Axitinib

DB05932

Denibulin

DB10770

Foreskin fibroblast (neonatal)

DB12010

Fostamatinib

DB06101

IMC-1C11

More DrugBank links

DrugCentral

P17948

GuidetoPHARMACOLOGY

1812

Genetic variation databases

BioMuta

FLT1

DMDM

143811474

ClinGen

HGNC:3763

GenCC

HGNC:3763

PTM/Processing

UniProt

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GlyGen

Entry 48

Feature viewer

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iPTMnet

P17948

Expressionⁱ

Tissue specificityⁱ

Detected in normal lung, but also in placenta, liver, kidney, heart and brain tissues. Specifically expressed in most of the vascular endothelial cells, and also expressed in peripheral blood monocytes. Isoform 2 is strongly expressed in placenta. Isoform 3 is expressed in corneal epithelial cells (at protein level). Isoform 3 is expressed in vascular smooth muscle cells (VSMC). [2 Publications](#)

Inductionⁱ

Up-regulated in coculture of VSMC/endothelial cell (EC) or by direct exposure to VEGF of VSMC monoculture. Up-regulated from the second trimester of pregnancy to the term and in the placenta of women with preeclampsia (PE). Up-regulated in monocytes exposed to bacterial lipopolysaccharide (LPS). [2 Publications](#)

Gene expression databases

Bgee

ENSG00000102755 [↗](#) Expressed in pericardium and 200 other tissues

Genevisible

P17948 [↗](#) HS

ExpressionAtlas

P17948 [↗](#) baseline and differential

Organism-specific databases

HPA

ENSG00000102755 [↗](#) Tissue enriched (placenta)

Interactionⁱ

Subunitⁱ

Interacts with VEGFA, VEGFB and PGF. Monomer in the absence of bound VEGFA, VEGFB or PGF. Homodimer in the presence of bound VEGFA, VEGFB and PGF. Can also form a heterodimer with KDR. Interacts (when tyrosine phosphorylated) with CBL, CRK, GRB2, NCK1, PIK3R1, PLCG, PSEN1 and PTPN11. Probably interacts also with PTPRB. Interacts with RACK1. Identified in a complex with CBL and CD2AP. [16 Publications](#)

Binary interactionsⁱ

P17948 has binary interactions with 7 proteins

Filter

Subcellular location

Select...

Diseases

Select...

Clear

VEGFR1_HUMAN

PTPRJ_HUMAN

PLGF_HUMAN

CRKL_HUMAN

P85A_HUMAN

CBL_HUMAN

VEGFA_HUMAN

VEGFA_HUMAN

VEGFR1_HUMAN

PTPRJ_HUMAN

PLGF_HUMAN

CRKL_HUMAN

P85A_HUMAN

CBL_HUMAN

VEGFA_HUMAN

VEGFA_HUMAN

TYPE

-- Select --

ENTRY 1

-- Select --

ENTRY 2

NUMBER OF EXPERIMENTS

INTACT

BINARY	P17948	CBL P22681	2	EBI-1026718, EBI-518228 ↗
BINARY	P17948	CRKL P46109	9	EBI-1026718, EBI-910 ↗
BINARY	P17948	PGF P49763	2	EBI-1026718, EBI-1037633 ↗
BINARY	P17948	PIK3R1 P27986	3	EBI-1026718, EBI-79464 ↗
BINARY	P17948	PTPRJ Q12913	2	EBI-1026718, EBI-2264500 ↗
BINARY	P17948	VEGFA P15692	4	EBI-1026718, EBI-1026643 ↗
BINARY	P17948	VEGFA P15692-4	3	EBI-1026718, EBI-1026691 ↗
BINARY	P17948-2	HSPG2 PRO_0000391621 P98160	2	EBI-6530464, EBI-6896259 ↗
BINARY	P17948-2	HSPG2 PRO_0000391622 P98160	2	EBI-6530464, EBI-6896607 ↗

Expand table

Protein-protein interaction databases

BioGRID

108609 [↗](#) 67 interactors

DIP

DIP-643N [↗](#)

IntAct

P17948 [↗](#) 177 interactors

MINT

P17948 [↗](#)

STRING

9606.ENSPP00000282397 [↗](#)

Chemistry

BindingDB

P17948 [↗](#)

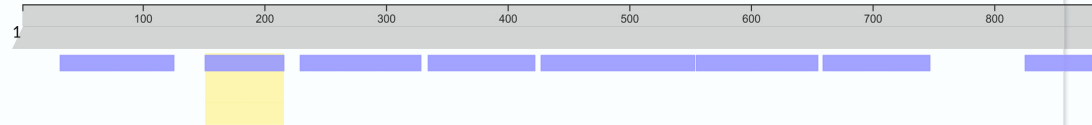
Structureⁱ

The structure viewer has not automatically been loaded on this device.

https://www.uniprot.org/uniprotkb/P17948/entry#expression

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DESCRIPTION

▼

► Domain	32-123	Ig-like C2-type 1	BLAST  Add
▼ Domain	151-214	Ig-like C2-type 2	BLAST  Add
Sequence: GRELVPCRVTSFNITVTLKKFPLDLPDGKRIIWDsrKGFIISNATYKEIGLLTCEATVNGH			
► Domain	230-327	Ig-like C2-type 3	BLAST  Add
► Domain	335-421	Ig-like C2-type 4	BLAST  Add
► Domain	428-553	Ig-like C2-type 5	BLAST  Add
► Domain	556-654	Ig-like C2-type 6	BLAST  Add
► Domain	661-747	Ig-like C2-type 7	BLAST  Add
► Domain	827-1158	Protein kinase  PROSITE-ProRule Annotation	BLAST  Add

[Collapse table](#)

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

2 Publications

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

PROSITE-ProRule Annotation

TRNSGFT [↗](#)

KOG0200  Eukaryota

SMART

UniProt

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Keywords

Domain

#Immunoglobulin domain

#Repeat

#Signal

#Transmembrane

#Transmembrane helix

Phylogenomic databases

GeneTree

ENSGT00940000158713

PhylomeDB

P17948

HOGENOM

CLU_000288_49_4_1

TreeFam

TF325768

InParanoid

P17948

eggNOG

KOG0200 Eukaryota

OMA

TRNSGFT

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

PRINTS

PR01833 VEGFRECEPTR1

PROSITE

View protein in PROSITE

PS50835 IG_LIKE 6 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

Pfam

View protein in Pfam

PF07679 I-set 2 hits

PF00047 ig 1 hit

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

SM00406 IGv 2 hits

SM00219 TyrKc 1 hit

SUPFAM

SSF48726 Immunoglobulin 7 hits

SSF56112 Protein kinase-like (PK-like) 1 hit

MobiDB

Search...

ProtoNet

Search...

Sequence & Isoformsⁱ

BLAST 8 isoforms

Align 8 isoforms

Sequence statusⁱ

Complete

Sequence processingⁱ

The displayed sequence is further processed into a mature form.

This entry describes 8 isoformsⁱ produced by **Alternative splicing**. Additional isoforms seem to exist.

P17948-1

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.

UniProt

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PR01833 [VEGFRCEPTR1](#)

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View protein in PROSITE

PS50835 [IG_LIKE](#) 6 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

SM00219 [TyrKc](#) 1 hit

SUPFAM

SSF48726 [Immunoglobulin](#) 7 hits

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

MobiDB

Search... [Search...](#)

ProtoNet

Search... [Search...](#)

Sequence & Isoformsⁱ

BLAST 8 isoforms

Align 8 isoforms

Sequence statusⁱ

Complete

Sequence processingⁱ

The displayed sequence is further processed into a mature form.

This entry describes 8 isoformsⁱ produced by **Alternative splicing**. Additional isoforms seem to exist.

P17948-1

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

Flt1

See also

sequence in **UniParc** or sequence clusters in **UniRef**

Tools

Download

Add

Highlight

Copy sequence

Length

1,338

Mass (Da)

150,769

Last updated

2007-04-03 v2

Checksumⁱ

FF3381EEFAF0787C

MVSYWDGTGL

10

LCALLSCLLL

20

TGSSSGSKLK

30

DPELSLKGTL

40

HIMQAGQTLH

50

LQCRGEAAHK

60

WSLPEMVSKE

70

SERLSITKSA

80

CGRNGKQFCS

90

TLTLNTAQAN

100

HTGFYSCKYL

110

AVPTSKKKET

120

ESAIYIFISD

130

TGRPFVEMYS

140

EIPEIIHMT

150

GRELVIPCRV

160

TSPNITVTLK

170

KFPLDTLIPD

180

GKRIWDSRK

190

GFIISNATYK

200

EIGLLTCEAT

210

VNGHLYKTN

220

LTHRQTNTII

230

DVQISTPRPV

240

KLLRGHTLVL

250

NCTATPLNT

260

RVQMTWSYDP

270

EKNKRASVRR

280

RIDQSNSHAN

290

IFYSVLTIDK

300

MQNKDKGLYT

310

CRVRSGPSFK

320

SVNTSVHIYD

330

KAFITVKHRK

340

QQVLETVAGK

350

RSYRLSMKVK

360

AFPSPEVWVL

370

KDGLPATEKS

380

ARYLTRGYSL

390

IIKDVTEEDA

400

GNYTLLSLIK

410

QSNVFKNLTA

420

TLIVNVKPOI

430

YEKAVSSFPD

440

PALYPLGSRQ

450

ILTCTAYGIP

460

QPTIKWFHP

470

CNNHSEAR

480

DFCSNNEESF

490

ILDADSNMGN

500

RIESITQMA

510

IIEGKNKMAS

520

TLVADSRIIS

530

GIYICIASNK

540

VGTVGRNISF

550

YITDVPNGFH

560

VNLEKMPTEG

570

EDLKLSTVNI

580

KFLYRDGTWI

590

LLRVTNNRMT

600

HYSISKQKMA

610

ITKEHSITLN

620

LTIMNVSQD

630

SGTYACRARN

640

VYTGEELQK

650

KEITIRDQEA

660

PYLLRNLSDH

670

TVAISSSTTL

680

DCHANGVPEP

690

QITWFKNNHK

700

IQQEPGIILG

710

PGSSTLFIER

720

VTEDEGVYH

730

CKATNQKGSV

740

ESSAYLTVOG

750

TSKSNLELI

760

TLTCTCVAAT

770

LFWLLTLFI

780

RKMKRSSSEI

790

KTDYLSIIMD

800

PDEVPLDEQC

810

ERLPYDASKW

820

EFARERLKL

830

KSLGRGAFGK

840

VVQASAFGIK

850

KSPTCRTVAV

860

KMLKEGATAS

870

EYKALMTELK

880

ILTHIGHHLN

890

VVNLGACTK

900

QGGPLMVIVE

910

YCKYGNLSNY

920

LKSKRDLFFL

930

NKDAALHMEP

940

KKEKMEPGLE

950

QGGKPRLDVS

960

TSSSFASSG

970

FQEDKSLSDV

980

EEEESDGFY

990

KEPITMEDLI

1000

SYSFQVARGM

1010

EFLSSRKCIH

1020

RDLAARNILL

1030

SENNVVKICD

1040

FGLARDIYKN

1050

PDYVRKGDTR

1060

LPLKWMAPES

1070

IFDKIYSTKS

1080

DVWSYGVLLW

1090

EIFSLGGSPY

1100

PGVQMDDFC

1110

SRLREGMRMR

1120

APEYSTPEIY

1130

QIMLDCWHRD

1140

PKERPRFAEL

1150

VEKLGDLQLA

1160

NVQQDGKDYI

1170

PINAILTGNS

1180

GFTYSTPAFS

1190

EDFFKESISA

1200

PKFNSGSSDD

1210

VRYVNAFKFM

1220

SLERIKTFEE

1230

LLPNATSMFD

1240

DYQGDSSTLL

1250

ASPMLKRFTV

1260

TDSKPKASLK

1270

IDLRVTSKSK

1280

ESGLSDVSVP

1290

SFCHSSCGHV

1300

SEKRRFTYD

1310

HAELERKIAC

1320

CSPPPDYNSV

1330

VLYSTPTPI

P17948-2

Name

2

Synonyms

Differences from canonical

657-687: 657-687: DQEA PYLLRNLS DHTVAISSSTTL DCHANGV →

GEHCNKA VFSRISKFKSTRNDCTQSNVKH

3 Publications

https://www.uniprot.org/uniprotkb/P17948/entry#sequences

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Synonyms

i21

Show sequence

See also

sequence in UniParc or sequence clusters in UniRef

Differences from canonical

1-995: 1-995: Missing 1 Publication

P17948-8

Name

8

See also

sequence in UniParc or sequence clusters in UniRef

Show sequence

Differences from canonical

1-7: 1-7: MVSYWDT → MNSDLLV 1 Publication

8-984: 8-984: Missing 1 Publication

Computationally mapped potential isoform sequences¹

There are 3 potential isoforms mapped to this entry

BLAST | Align | Add | View all

Entry	Entry name	Gene name	Length
☐ H9N1E7	H9N1E7_HUMAN	FLT1	433
☐ H9N1E8	H9N1E8_HUMAN	FLT1	85
☐ A0A1W2PNW4	A0A1W2PNW4_HUMAN	FLT1	665

Features

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

1

100200300400500600700800900

TYPE

-- Select --

ID

POSITION(S)

DESCRIPTION

▶ Alternative sequence	VSP_047759	1-7	in isoform 8 1 Publication	BLAST Add
▶ Alternative sequence	VSP_041985	1-782	in isoform 5 1 Publication	BLAST Add
▶ Alternative sequence	VSP_041984	1-875	in isoform 6 1 Publication	BLAST Add
▶ Alternative sequence	VSP_041983	1-995	in isoform 7 1 Publication	BLAST Add
▶ Alternative sequence	VSP_047760	8-984	in isoform 8 1 Publication	BLAST Add
▶ Sequence conflict		490	in Ref. 3; AAC16449 Curated	
▶ Alternative sequence	VSP_041929	518-541	in isoform 4 1 Publication	BLAST Add
▶ Alternative sequence	VSP_041930	542-1338	in isoform 4 1 Publication	BLAST Add

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Keywords¹

Coding sequence diversity

#Alternative splicing

Technical term

#3D-structure

#Direct protein sequencing

#Reference proteome

Sequence databases

CCDS

CCDS53860.1 [P17948-3]

CCDS53861.1 [P17948-4]

CCDS73556.1 [P17948-2]

CCDS9330.1 [P17948-1]

RefSeq

NP_001153392.1 [P17948-2]

NP_001153502.1 [P17948-3]

NP_001153503.1 [P17948-4]

NP_002010.2 [P17948-1]

PIR

A49636 A49636

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Alternative sequence

Alternative sequence

VSP_041983

VSP_0417760

VSP_041929

VSP_041930

1-995

8-984

490

518-541

542-1338

In isoform 7

In isoform 8

In Ref. 3; AAC16449

In isoform 4

In isoform 4

1 Publication

1 Publication

Curated

1 Publication

1 Publication

BLAST

BLAST

BLAST

BLAST

BLAST

Add

Add

Add

Add

Expand table

Keywordsⁱ

Coding sequence diversity

#Alternative splicing

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#3D-structure

#Direct protein sequencing

#Reference proteome

Sequence databases

CCDS

CCDS53860.1

CCDS53861.1

CCDS73556.1

CCDS9330.1

PIR

A49636

S09982

RefSeq

NP_001153392.1

NP_001153502.1

NP_001153503.1

NP_002010.2

Genome annotation databases

Ensembl

ENST00000282397.9

ENST00000539099.1

ENST00000541932.5

ENST00000543394.2

ENST00000615840.4

GenelD

2321

KEGG

hsa:2321

MANE-Select

uc001usb.4

UCSC

uc001usb.4

Similar Proteinsⁱ

100% identity

90% identity

50% identity

P17948-1, P17948-5, P17948-6, and P17948-7

UniRef100_P17948

Protein name	Organism	Length
receptor protein-tyrosine kinase	Homo sapiens (Human)	1338
Vascular endothelial growth factor receptor 1	Homo sapiens (Human)	433
Vascular endothelial growth factor receptor 1	Homo sapiens (Human)	85
FLT1 isoform 4	Pan troglodytes (Chimpanzee)	433
Protein kinase domain-containing protein	Pan paniscus (Pygmy chimpanzee) (Bonobo)	433
Vascular endothelial growth factor receptor 1	Pan troglodytes (Chimpanzee)	85
FLT1 isoform 3	Pan troglodytes (Chimpanzee)	85

Show all (7) UniProtKB entries

P17948-8

UniRef100_A0A2I3TIG8

Protein name	Organism	Length
Fms related receptor tyrosine kinase 1	Pan troglodytes (Chimpanzee)	361

Show all (1) UniProtKB entries

P17948-2, P17948-3, and P17948-4

No similar proteins at 100% identity for these isoforms.

View all

https://www.uniprot.org/uniprotkb/P17948/entry#similar_proteins

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