

ARHGEF2 (rho/rac guanine nucleotide exchange factor (GEF) 2)

Identity

Other names **DKFZp547L106**
DKFZp547P1516
GEF
GEF-H1
GEFH1
KIAA0651
LFP40
P40

Hugo [ARHGEF2](#)

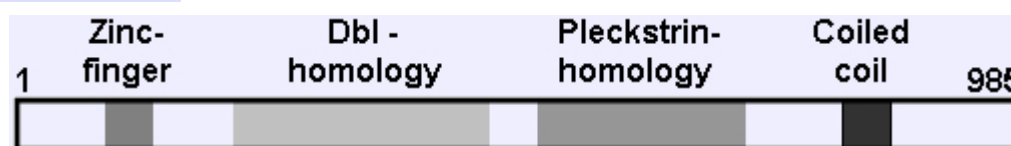
Location 1q22

DNA/RNA

Note Cloning of human ARHGEF2/GEF-H1 from HELA cells. Cloning and characterization of murine (Lfc) and canine (cGEF-H1) rho/rac guanine nucleotide exchange factors homologues to ARHGEF2/GEF-H1.

Transcription 4093 bp mRNA; 2877 bp open reading frame

Protein



A schematic representing the domain structure of full length ARHGEF2/GEF-H1

Description The gene encodes a guanine nucleotide exchange factor for Rho GTPase; 985 amino acids; NH2- Protein kinase C conserved region 1 (zinc finger motif), Dbl-homologous domain (DH domain), pleckstrin homology (PH) domain - coiled coil c-terminus domain -COOH.

Expression Wide (cochlea, bone marrow, lymph, blood, lung, ovary, cranial nerve, lymph node, colon, spleen, kidney, muscle, eye, bone, cervix, nerve, adrenal gland, heart, skin, thyroid, uterus, testis, pancreas, brain, mouth, stomach, thymus, pharynx, prostate, vascular, mammary gland, placenta).

Localisation Microtubules

Function ARHGEF2/GEF-H1 belongs to a Dbl family of Rho activators and exhibits Rho-specific GDP/GTP exchange activity for RhoA but not for Rac1 or Cdc42. ARHGEF2/GEF-H1 activity is downregulated by interaction of its C-terminus with microtubules. Therefore, ARHGEF2/GEF-H1 links changes in microtubule integrity to Rho-dependent regulation of the actin cytoskeleton. Activated [RhoA](#) transduces various signals into downstream signaling cascades, such as cytoskeleton reorganization, cellular invasion, and cell proliferation, all of which contribute to cancer progression. Like other RhoGEF Dbl members, ARHGEF2/GEF-H1 possesses the Dbl-homology (DH) domain responsible for its GEF activity the pleckstrin-homology (PH) domain, adjacent and C-terminal to the DH domain. In addition, ARHGEF2/GEF-H1 also contains a cysteine-rich zinc finger-like motif at its amino terminus and a proline-rich coiled coil domain at its carboxy terminus. The N- and C-terminal motifs mediate microtubule localization of ARHGEF2/GEF-H1. Point mutated (cys53 to arg) in a zinc finger-like motif, as well as N- and C-terminally truncated ARHGEF2/GEF-H1 proteins

are losing ability to bind microtubules. These truncated forms have no effect on microtubule stability, and displaying even higher GEF activity than microtubule-bound forms. The coiled coil domain at C-terminus may interact with SH3 domain-containing proteins and has a potential binding site for 14-3-3 proteins. The ser885 within the 14-3-3-binding site is a phosphorylation site for p21-activated kinase 1 (PAK1), an effector of RAC and CDC42 GTPases. The phosphorylation of ARHGEF2/GEFH1 by PAK may coordinate Rac/Cdc42- and Rho-dependent signaling pathways.

Homology The high level of homology has been shown for three known rho/rac guanine nucleotide exchange factors originated from human, mouse and dog.

Implicated in

Entity [gastrointestinal mesenchymal malignancies](#)

Disease Microarray analysis identified ARHGEF2/GEF-H1 as one of response markers for a treatment of gastrointestinal stromal tumors, implicating its role in the development of gastrointestinal mesenchymal malignancies.

Oncogenesis A cell line transformed by ARHGEF2/GEF-H1 transfection can induce tumor development after injection into nude mice. The increased ARHGEF2/GEF-H1 expression was found contributing to the tumor progression phenotype associated with the [p53](#) mutation.

External links

Nomenclature

Hugo [ARHGEF2](#)

GDB [ARHGEF2](#)

Entrez_Gene [ARHGEF2_9181](#) rho/rac guanine nucleotide exchange factor (GEF) 2

Cards

Atlas [ARHGEF2ID43150ch1q22](#)

GeneCards [ARHGEF2](#)

Ensembl [ARHGEF2](#)

GenAtlas [ARHGEF2](#)

GeneLynx [ARHGEF2](#)

eGenome [ARHGEF2](#)

euGene [9181](#)

Genomic and cartography

GoldenPath [ARHGEF2 - 1q22](#) [chr1:154183270-154214575 - 1q21-q22](#) (hg18-Mar_2006)

Ensembl [ARHGEF2 - 1q21-q22 \[CytoView\]](#)

NCBI [Mapview](#)

OMIM [Disease map \[OMIM\]](#)

HomoloGene [ARHGEF2](#)

Gene and transcription

Genbank [AB014551](#) [ENTREZ]

Genbank [AF486838](#) [ENTREZ]

Genbank [AL512715](#) [ENTREZ]

Genbank [AL832538](#) [ENTREZ]

Genbank [AM393305](#) [ENTREZ]

RefSeq [NM_004723](#) [SRS] [NM_004723](#) [ENTREZ]

RefSeq [AC_000044](#) [SRS] [AC_000044](#) [ENTREZ]

RefSeq [NC_000001](#) [SRS] [NC_000001](#) [ENTREZ]

RefSeq	NT_004487 [SRS] NT_004487 [ENTREZ]
RefSeq	NW_925683 [SRS] NW_925683 [ENTREZ]
AceView	ARHGEF2 AceView - NCBI
Unigene	Hs.655209 [SRS] Hs.655209 [NCBI] HS655209 [spliceNest]
Fast-db	17384
Protein : pattern, domain, 3D structure	
SwissProt	Q5VY92 [SRS] Q5VY92 [EXPASY] Q5VY92 [INTERPRO]
Prosite	PS50010 DH_2 [SRS] PS50010 DH_2 [Expasy]
Prosite	PS50003 PH_DOMAIN [SRS] PS50003 PH_DOMAIN [Expasy]
Prosite	PS00479 ZF_DAG_PE_1 [SRS] PS00479 ZF_DAG_PE_1 [Expasy]
Prosite	PS50081 ZF_DAG_PE_2 [SRS] PS50081 ZF_DAG_PE_2 [Expasy]
Interpro	IPR002219 DAG_PE_bd [SRS] IPR002219 DAG_PE_bd [EBI]
Interpro	IPR001849 PH [SRS] IPR001849 PH [EBI]
Interpro	IPR011993 PH_type [SRS] IPR011993 PH_type [EBI]
Interpro	IPR000219 RhoGEF [SRS] IPR000219 RhoGEF [EBI]
CluSTr	Q5VY92
Pfam	PF00130 C1_1 [SRS] PF00130 C1_1 [Sanger] pfam00130 [NCBI-CDD]
Pfam	PF00169 PH [SRS] PF00169 PH [Sanger] pfam00169 [NCBI-CDD]
Pfam	PF00621 RhoGEF [SRS] PF00621 RhoGEF [Sanger] pfam00621 [NCBI-CDD]
Smart	SM00109 C1 [EMBL]
Smart	SM00233 PH [EMBL]
Smart	SM00325 RhoGEF [EMBL]
Blocks	Q5VY92
HPRD	10458
Protein Interaction databases	
DIP	Q5VY92
IntAct	Q5VY92
Polymorphism : SNP, mutations, diseases	
OMIM	607560 [map]
GENECLINICS	607560
SNP	ARHGEF2 [dbSNP-NCBI]
SNP	NM_004723 [SNP-NCI]
SNP	ARHGEF2 [GeneSNPs - Utah] ARHGEF2 [HGBASE - SRS]
HAPMAP	ARHGEF2 [HAPMAP]
COSMIC	ARHGEF2 [Somatic mutation (COSMIC-CGP-Sanger)]
HGMD	ARHGEF2
General knowledge	
Family Browser	ARHGEF2 [UCSC Family Browser]
SOURCE	NM_004723
SMD	Hs.655209
SAGE	Hs.655209
GO	cell morphogenesis [Amigo] cell morphogenesis
GO	cell morphogenesis [Amigo] cell morphogenesis

[GO](#) [Rho guanyl-nucleotide exchange factor activity](#) [Amigo] [Rho guanyl-nucleotide exchange factor activity](#)
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[GO](#) [microtubule](#) [Amigo] [microtubule](#)
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[GO](#) [regulation of cell proliferation](#) [Amigo] [regulation of cell proliferation](#)
[GO](#) [metal ion binding](#) [Amigo] [metal ion binding](#)
[GO](#) [Rac GTPase binding](#) [Amigo] [Rac GTPase binding](#)
[GO](#) [Rac GTPase binding](#) [Amigo] [Rac GTPase binding](#)
[PubGene](#) [ARHGEF2](#)

Other databases

Probes

[Probe](#) [ARHGEF2 Related clones \(RZPD - Berlin\)](#)

PubMed

[PubMed](#) [24 Pubmed reference\(s\) in LocusLink](#)

Bibliography

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The Dbl-related protein, Lfc, localizes to microtubules and mediates the activation of Rac signaling pathways in cells.

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Medline [16778209](#)

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