

# Active Flt3:Grb2 binds Gab2

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# Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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### Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18,* 142. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, *14*, e1005968. *オ*

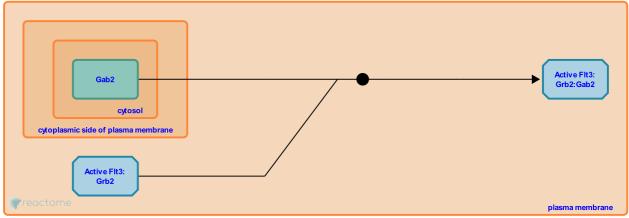
This document contains 1 reaction (see Table of Contents)

## Active Flt3:Grb2 binds Gab2 ↗

Stable identifier: R-MMU-9606623

Type: binding

Compartments: cytosol, plasma membrane



Feline McDonough Sarcoma-like tyrosine kinase (Flt3) is a member of the class III tyrosine kinase receptor family. Ligand binding induces conformational changes in the Flt3 receptor, which facilitates its dimerization and autophosphorylation. Once fully active, Flt3 receptors can associate with growth factor receptor-bound protein 2 (Grb2). Subsequently, Grb2-associated-binding protein 2 (Gab2) binds Grb2 (Zhang et al. 2000, Masson et al. 2009, Chonabayashi et al. 2013).

#### Literature references

- Masson, K., Sun, J., Khan, R., Liu, T., Rönnstrand, L. (2009). A role of Gab2 association in Flt3 ITD mediated Stat5 phosphorylation and cell survival. *Br. J. Haematol.*, *146*, 193-202.
- Zhang, S., Broxmeyer, HE. (2000). Flt3 ligand induces tyrosine phosphorylation of gab1 and gab2 and their association with shp-2, grb2, and PI3 kinase. *Biochem. Biophys. Res. Commun., 277*, 195-9.
- Ishikawa, T., Kawamata, S., Ohno, T., Chonabayashi, K., Hishizawa, M., Uchiyama, T. et al. (2013). Direct binding of Grb2 has an important role in the development of myeloproliferative disease induced by ETV6/FLT3. *Leukemia*, 27, 1433-6. *¬*

#### **Editions**

2019-01-14	Authored, Edited	Varusai, TM.
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