

Autocatalytic phosphorylation of FGFR3 fusions

Grose, RP., Rothfels, K.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

11/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. [↗](#)

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)

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. [↗](#)

Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

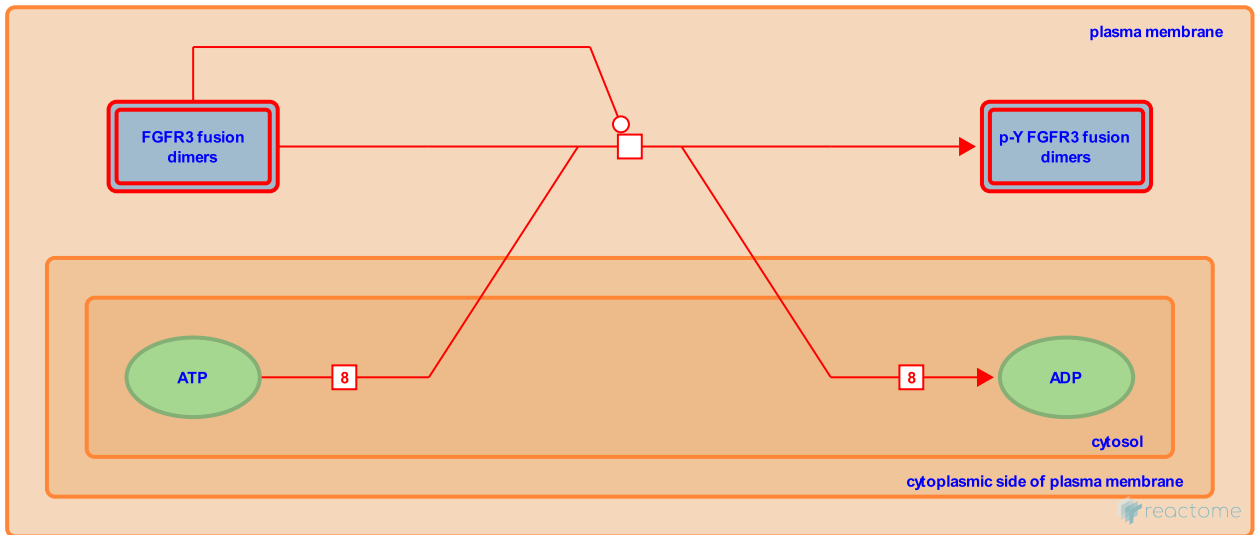
Autocatalytic phosphorylation of FGFR3 fusions ↗

Stable identifier: R-HSA-8853309

Type: transition

Compartments: plasma membrane

Diseases: cancer



FGFR3 fusions promote cellular proliferation and tumorigenesis that can be inhibited by tyrosine kinase inhibitors, suggesting that signaling is dependent on autophosphorylation of tyrosine residues in the intracellular region as is the case for WT FGFR3 (Singh et al, 2012; Parker et al, 2013; Williams et al, 2013; Wu et al, 2013; Yuan et al, 2014). FGFR3 fusions are reported to activate the ERK , STAT and AKT pathways, but not the PLC gamma pathway as the fusions generally lack the tyrosine residue required for PLC gamma recruitment (Parker et al, 2013; Williams et al, 2013; Wu et al, 2013; reviewed in Parker et al, 2014; Carter et al, 2015).

Literature references

Parker, BC., Sun, Y., Granberg, KJ., Zhang, W., Liu, CG., Ji, P. et al. (2013). The tumorigenic FGFR3-TACC3 gene fusion escapes miR-99a regulation in glioblastoma. *J. Clin. Invest.*, 123, 855-65. ↗

Knowles, MA., Williams, SV., Hurst, CD. (2013). Oncogenic FGFR3 gene fusions in bladder cancer. *Hum. Mol. Genet.*, 22, 795-803. ↗

Grose, RP., Carter, EP., Fearon, AE. (2015). Careless talk costs lives: fibroblast growth factor receptor signalling and the consequences of pathway malfunction. *Trends Cell Biol.*, 25, 221-33. ↗

Kalyana-Sundaram, S., Chinnaiyan, AM., Wang, R., Tomlins, SA., Ateeq, B., Cao, X. et al. (2013). Identification of targetable FGFR gene fusions in diverse cancers. *Cancer Discov*, 3, 636-47. ↗

Zeng, MS., Yuan, L., Liu, ZH., Lin, ZR., Zhong, Q., Xu, LH. (2014). Recurrent FGFR3-TACC3 fusion gene in nasopharyngeal carcinoma. *Cancer Biol. Ther.*, 15, 1613-21. ↗

Editions

2016-01-09	Authored, Edited	Rothfels, K.
2016-01-25	Reviewed	Grose, RP.