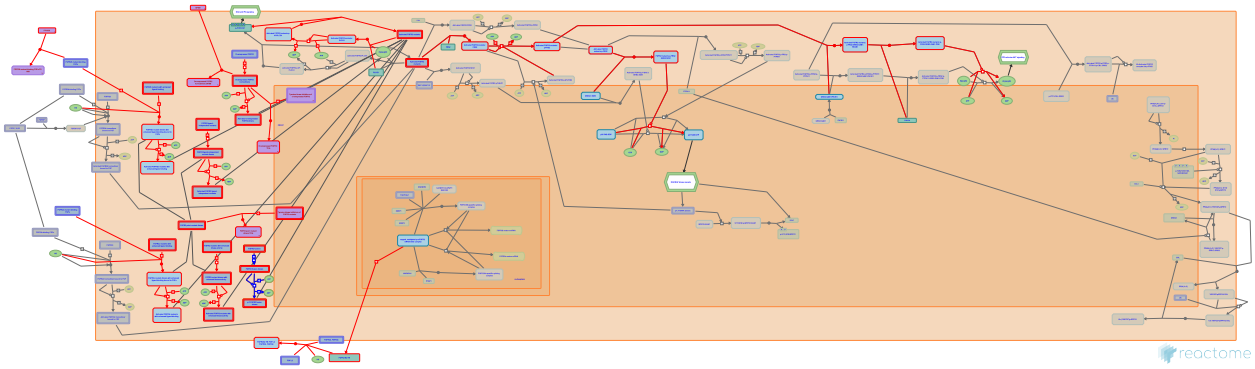
Signaling by FGFR2 fusions



Grose, RP., Rothfels, K.

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

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

28/04/2024

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. ↗

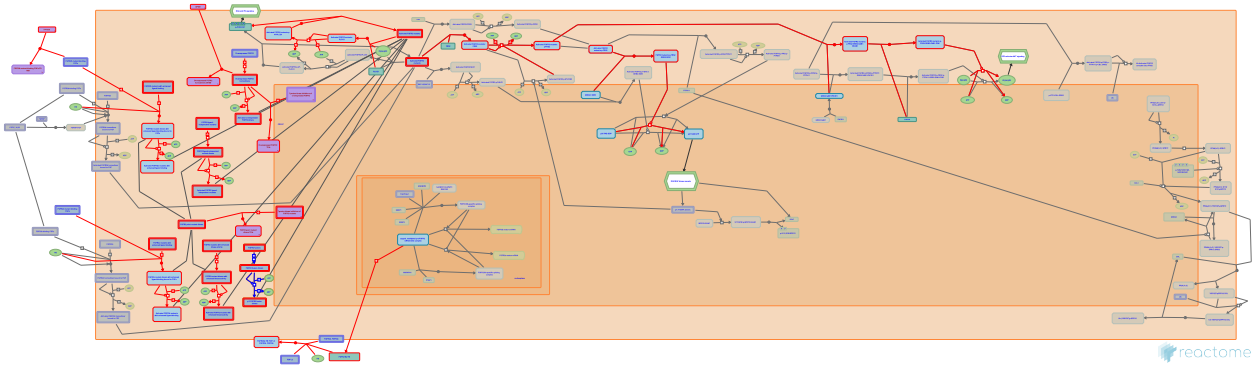
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Signaling by FGFR2 fusions ↗

Stable identifier: R-HSA-8853333

Diseases: cancer



FGFR2 fusions have been identified in cancers such as lung, breast, thyroid and cholangiocarcinoma (Wu et al, 2013; Seo et al, 2012; Arai et al, 2013). Of all the FGF receptors, FGFR2 shows the broadest range of 3' fusion partners, including BICC1, AHCYL1, CIT, CCDC6, CASP7, AFF3, OFD1 and CCAR2. Many of these fusion partners contain dimerization domains, suggesting that the resulting fusions may demonstrate constitutive ligand-independent activation (Wu et al, 2013; Arai et al, 2013; Seo et al, 2012; reviewed in Parker et al, 2014).

Literature references

Kang, JH., Seo, JS., Park, IK., Rhee, H., Kim, JI., Kim, JO. et al. (2012). The transcriptional landscape and mutational profile of lung adenocarcinoma. *Genome Res., 22*, 2109-19. ↗

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. ↗

Hosoda, F., Totoki, Y., Furuta, K., Kosuge, T., Okusaka, T., Shibata, T. et al. (2014). Fibroblast growth factor receptor 2 tyrosine kinase fusions define a unique molecular subtype of cholangiocarcinoma. *Hepatology, 59*, 1427-34. ↗

Parker, BC., Zhang, W., Annala, M., Engels, M. (2014). Emergence of FGFR family gene fusions as therapeutic targets in a wide spectrum of solid tumours. *J. Pathol., 232*, 4-15. ↗

Editions

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

FGFR2 fusions dimerize ↗

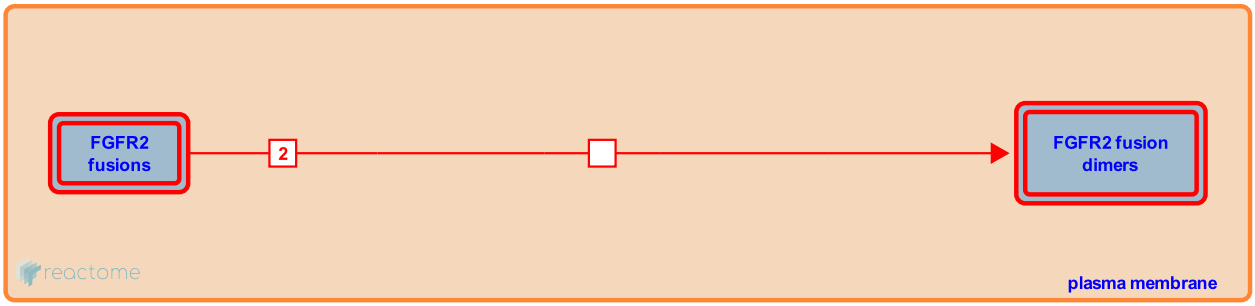
Location: Signaling by FGFR2 fusions

Stable identifier: R-HSA-8853319

Type: transition

Compartments: plasma membrane

Diseases: cancer



FGFR2 fusions have been identified in a number of cancers, including breast, thyroid, lung and cholangiocarcinoma (Wu et al, 2013; Seo et al, 2012; Arai et al, 2013; reviewed in Parker et al, 2014). Many of the 3' fusion partners contain dimerization domains, suggesting the fusion proteins may dimerize contstitutively independent of ligand binding, although this has not been explicitly demonstrated in all cases (Wu et al, 2013; reviewed in Parker et al, 2014).

Followed by: FGFR2 fusions autophosphorylate

Literature references

Kang, JH., Seo, JS., Park, IK., Rhee, H., Kim, JI., Kim, JO. et al. (2012). The transcriptional landscape and mutational profile of lung adenocarcinoma. *Genome Res., 22*, 2109-19. ↗

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. ↗

Hosoda, F., Totoki, Y., Furuta, K., Kosuge, T., Okusaka, T., Shibata, T. et al. (2014). Fibroblast growth factor receptor 2 tyrosine kinase fusions define a unique molecular subtype of cholangiocarcinoma. *Hepatology, 59*, 1427-34. ↗

Parker, BC., Zhang, W., Annala, M., Engels, M. (2014). Emergence of FGFR family gene fusions as therapeutic targets in a wide spectrum of solid tumours. *J. Pathol., 232*, 4-15. ↗

Editions

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

FGFR2 fusions autophosphorylate ↗

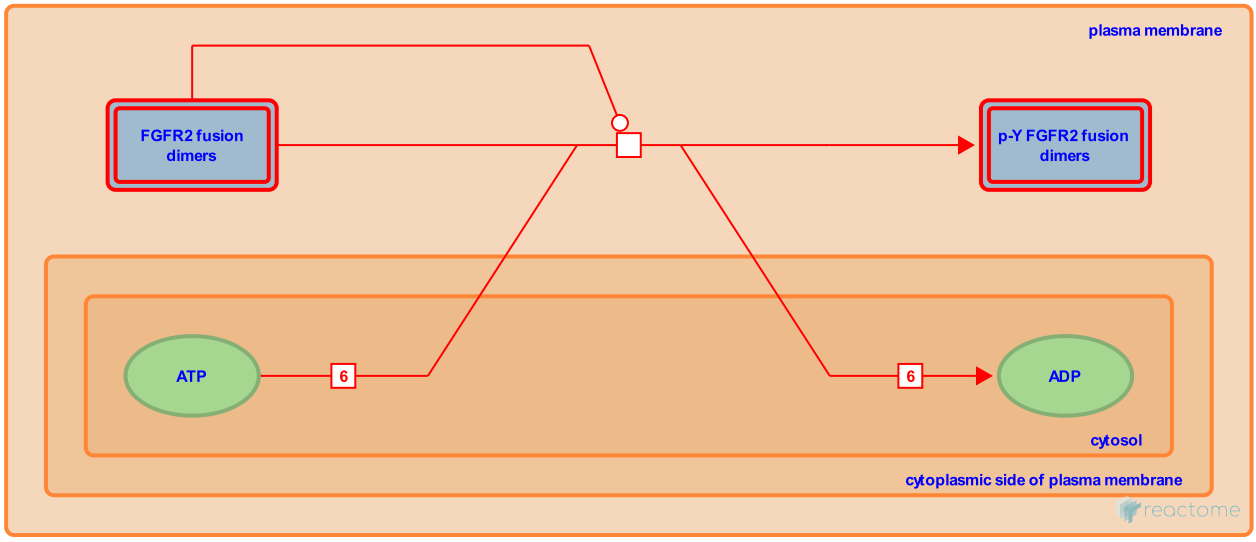
Location: Signaling by FGFR2 fusions

Stable identifier: R-HSA-8853313

Type: transition

Compartments: plasma membrane

Diseases: cancer



FGFR2 fusions in cholangiocarcinoma and cancers of the breast, lung and thyroid have been shown to promote anchorage independent growth, cellular proliferation and tumorigenesis. In some cases, such as for FGFR2-AHCYL1 and FGFR2-BICC1 fusions in cholangiocarcinoma, these activities have been shown to depend on the FGFR2 kinase domain, suggesting that the fusions undergo autophosphorylation after oligomerization, as is the case for WT FGFR2. FGFR2 fusions, where tested, also show sensitivity to kinase inhibitors such as PD173074 and pazopanib (Arai et al, 2013; Wu et al, 2013; Seo et al, 2012; reviewed in Parker et al, 2014).

Preceded by: FGFR2 fusions dimerize

Literature references

Kang, JH., Seo, JS., Park, IK., Rhee, H., Kim, JI., Kim, JO. et al. (2012). The transcriptional landscape and mutational profile of lung adenocarcinoma. *Genome Res., 22*, 2109-19. ↗

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. ↗

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Editions

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

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