

Signaling by EGFR in Cancer

Signaling by EGFRvIII in Cancer

Signaling by Ligand-Responsive EGFR Variants in Cancer

Signaling by Overexpressed Wild-Type EGFR in Cancer

D'Eustachio, P., Gillespie, M.E., Greulich, H., Haw, R., Jassal, B., Matthews, L., Orlic-Milacic, M., Savas, S., Wu, G.

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/about/licenses).

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](https://reactome.org/textbook).

17/05/2024

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 4 pathways ([see Table of Contents](#))

Signaling by EGFR in Cancer ↗

Stable identifier: R-HSA-1643713

Diseases: cancer



The pathway "Signaling by EGFR in Cancer" shows signaling by constitutively active EGFR cancer variants in the context of "Signaling by EGFR", allowing users to compare cancer events with the wild-type EGFR events. Red lines emphasize cancer related events and physical entities, while wild-type entities and events are shaded. Please refer to "Signaling by Ligand-Responsive EGFR Variants in Cancer", "Signaling by EGFRvIII in Cancer" and "Signaling by Overexpressed Wild-Type EGFR in Cancer" for detailed pathway summations.

Editions

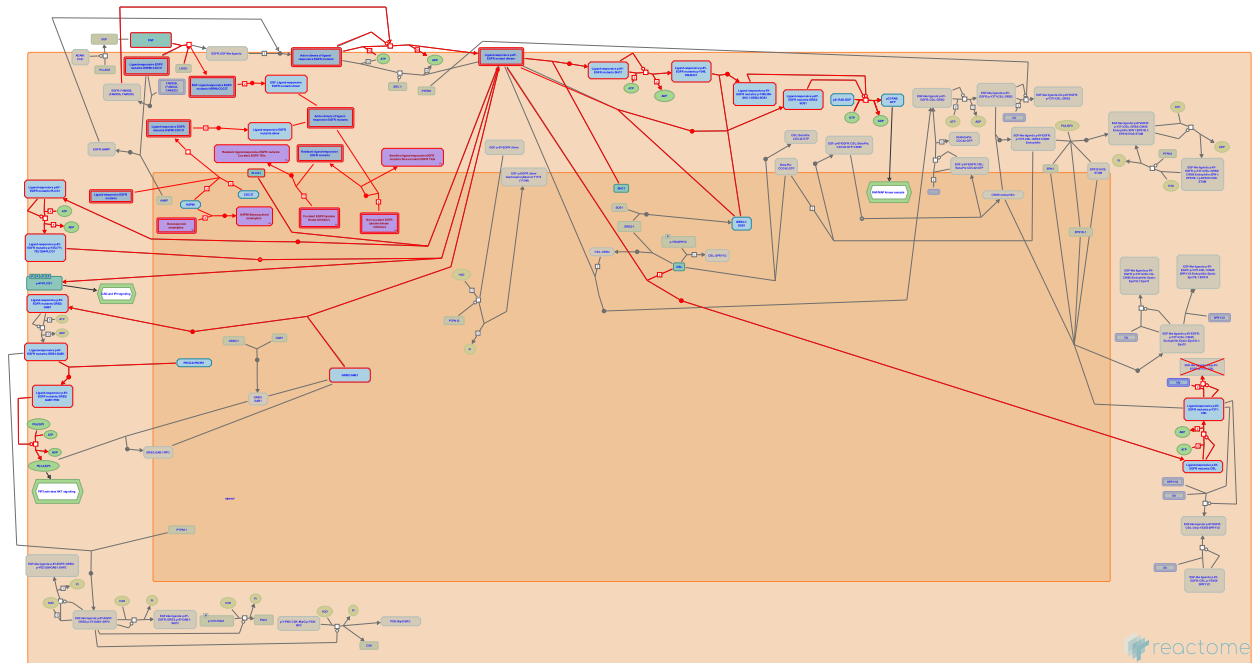
2011-11-04	Authored	Orlic-Milacic, M.
2011-11-07	Edited	Jassal, B., Gillespie, ME., Wu, G., D'Eustachio, P., Matthews, L., Haw, R.
2011-11-15	Reviewed	Greulich, H., Savas, S.

Signaling by Ligand-Responsive EGFR Variants in Cancer ↗

Location: [Signaling by EGFR in Cancer](#)

Stable identifier: R-HSA-5637815

Diseases: cancer



Ligand-responsive EGFR cancer variants harbor mutations in the kinase domain or point mutations in the extracellular domain. These altered EGFR proteins are able to signal in the absence of ligands, but their ligand binding ability is preserved and downstream signaling is potentiated when ligand is available (Greulich et al. 2005, Lee et al. 2006).

Literature references

Onofrio, R., Yoshimoto, K., Huang, JHY., Liao, LM., Xu, Q., Thomas, RK. et al. (2006). Epidermal growth factor receptor activation in glioblastoma through novel missense mutations in the extracellular domain. *PLoS Med*, 3, e485. ↗

Feng, WL., Hahn, WC., Chen, TH., Meyerson, M., Frank, DA., Sellers, WR. et al. (2005). Oncogenic transformation by inhibitor-sensitive and -resistant EGFR mutants. *PLoS Med*, 2, e313. ↗

Editions

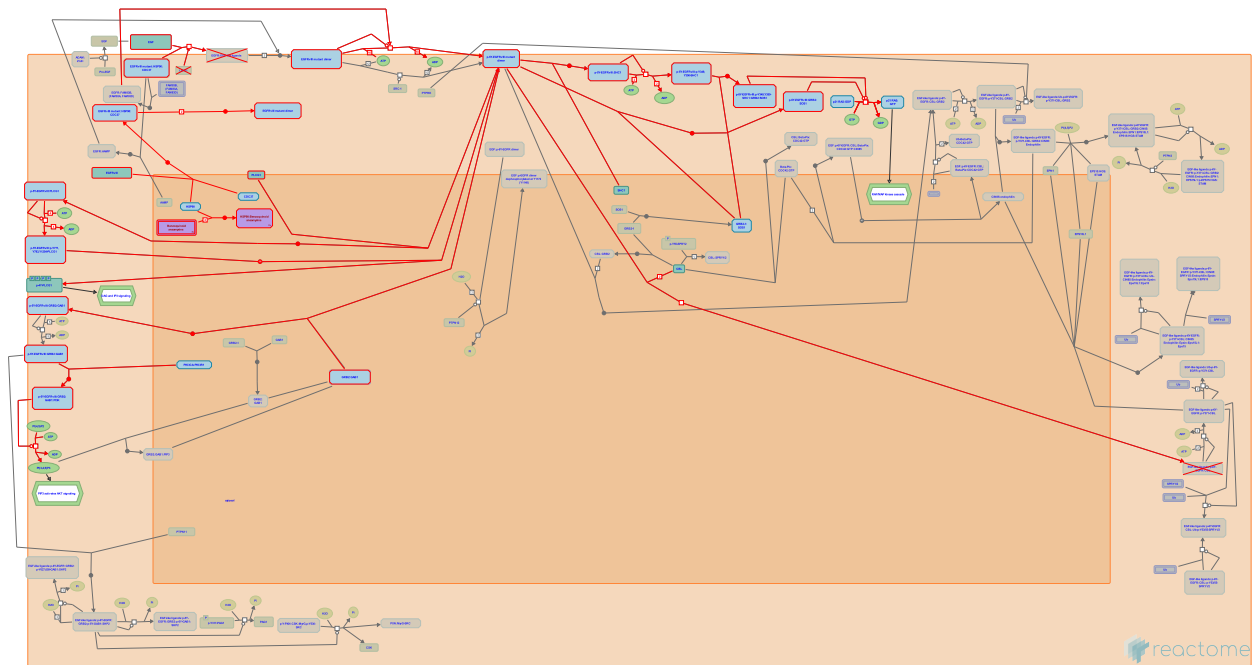
2011-11-04	Authored	Orlic-Milacic, M.
2011-11-07	Edited	Jassal, B., Gillespie, ME., Wu, G., D'Eustachio, P., Matthews, L., Haw, R.
2011-11-15	Reviewed	Greulich, H., Savas, S.

Signaling by EGFRvIII in Cancer ↗

Location: [Signaling by EGFR in Cancer](#)

Stable identifier: R-HSA-5637812

Diseases: cancer



EGFRvIII (EGFR V30_R297delinsG) is the most prevalent EGFR variant in glioblastoma, but it is also found in other cancer types. In-frame deletion of the ligand binding domain in EGFRvIII is frequently accompanied with genomic amplification, resulting in over-expression of EGFRvIII. EGFRvIII dimerizes and autophosphorylates spontaneously and is therefore constitutively active (Fernandes et al. 2001)

Literature references

Cohen, S., Fernandes, H., Bishayee, S. (2001). Glycosylation-induced conformational modification positively regulates receptor-receptor association: a study with an aberrant epidermal growth factor receptor (EGFRvIII/DeltaE-GFR) expressed in cancer cells. *J Biol Chem*, 276, 5375-83. ↗

Editions

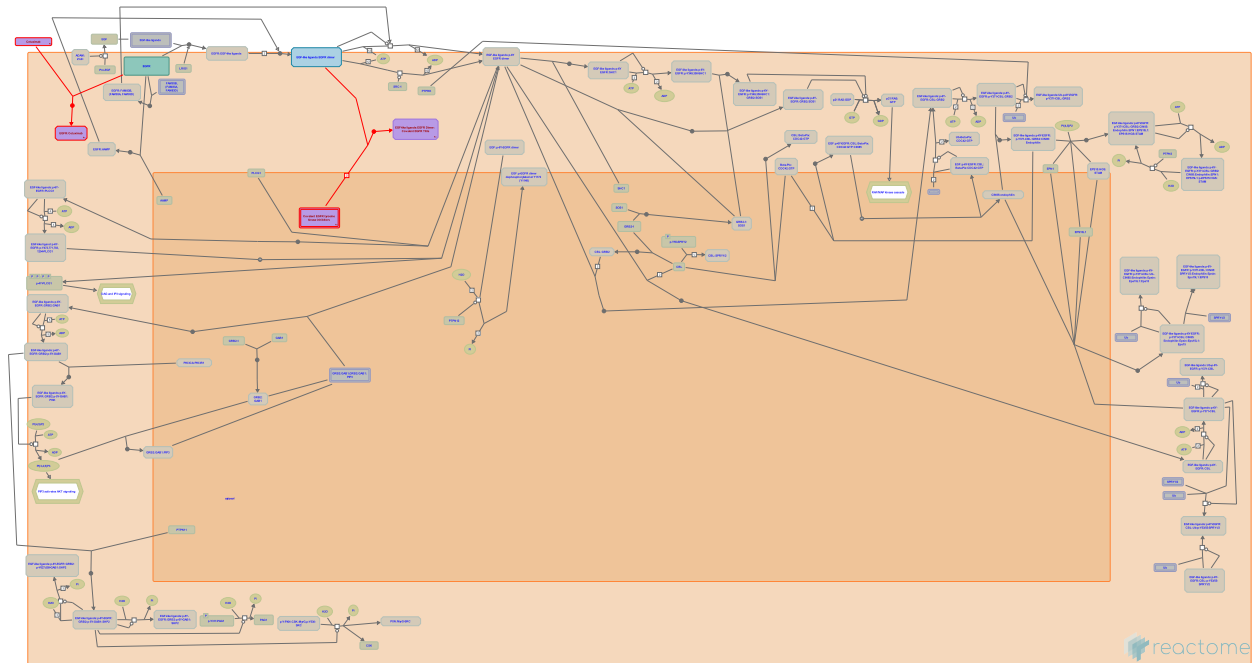
2011-11-04	Authored	Orlic-Milacic, M.
2011-11-07	Edited	Jassal, B., Gillespie, ME., Wu, G., D'Eustachio, P., Matthews, L., Haw, R.
2011-11-15	Reviewed	Greulich, H., Savas, S.

Signaling by Overexpressed Wild-Type EGFR in Cancer ↗

Location: [Signaling by EGFR in Cancer](#)

Stable identifier: R-HSA-5638302

Diseases: cancer



Signaling by EGFR is frequently activated in cancer through genomic amplification of the EGFR locus, resulting in over-expression of the wild-type protein (Wong et al. 1987).

Literature references

Vogelstein, B., Bigner, SH., Bigner, DD., Kinzler, KW., Hamilton, SR., Wong, AJ. (1987). Increased expression of the epidermal growth factor receptor gene in malignant gliomas is invariably associated with gene amplification. *Proc. Natl. Acad. Sci. U.S.A.*, 84, 6899-903. ↗

Editions

2011-11-04	Authored	Orlic-Milacic, M.
2011-11-07	Edited	Jassal, B., Gillespie, ME., Wu, G., D'Eustachio, P., Matthews, L., Haw, R.
2011-11-15	Reviewed	Greulich, H., Savas, S.

Table of Contents

Introduction	1
❖ Signaling by EGFR in Cancer	2
❖ Signaling by Ligand-Responsive EGFR Variants in Cancer	3
❖ Signaling by EGFRvIII in Cancer	4
❖ Signaling by Overexpressed Wild-Type EGFR in Cancer	5
Table of Contents	6