reactome

Phosphorylated GPNMB recruits PTK6 and LRRK2 in the presence of LINC01139

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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

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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. ↗

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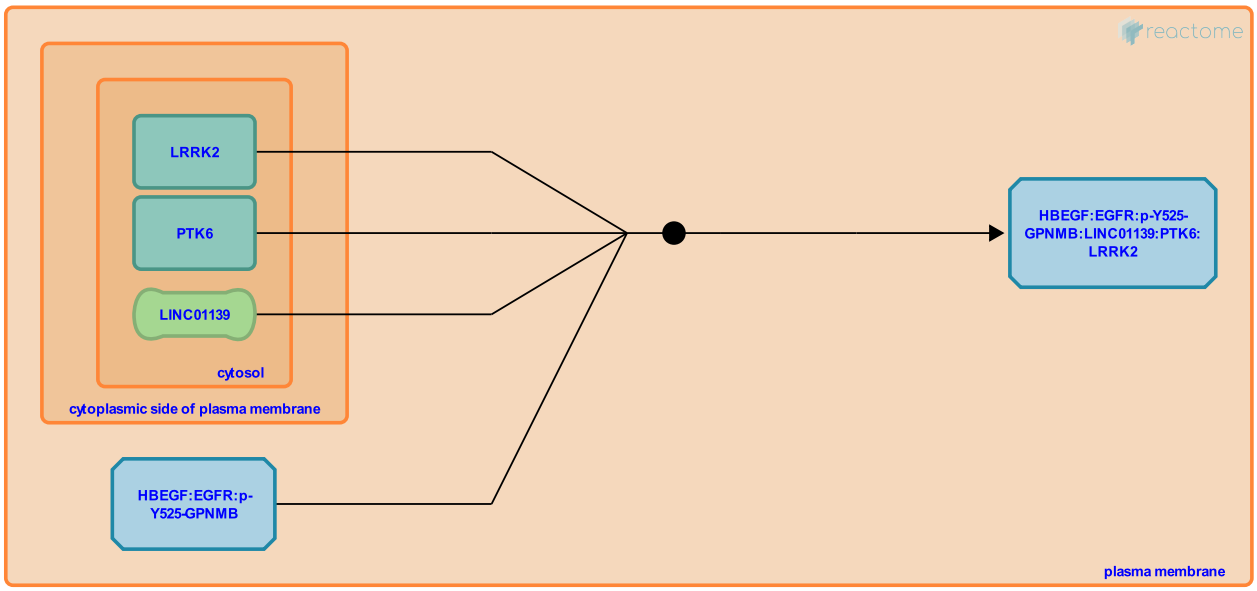
Stable identifier: R-HSA-8857565

Type: binding

Compartments: cytosol, plasma membrane



Phosphorylation of GPNBM at tyrosine residue Y525 upon heterodimerization with HBEGF-bound EGFR promotes, in the presence of long non-coding RNA LINC011139 (LINK-A), the recruitment of PTK6 (BRK). In addition to PTK6, LINC01139 simultaneously recruits serine/threonine kinase LRRK2 to phosphorylated GPNBM (Lin et al. 2016).

Literature references

Marks, JR., Yang, L., Zhou, Y., Ma, G., Wang, S., Xing, Z. et al. (2016). The LINK-A lncRNA activates normoxic HIF1α signalling in triple-negative breast cancer. *Nat. Cell Biol., 18*, 213-24. ↗

Editions

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