Formation of di-heterotetramers of GluN1 (GRIN1) and GluN2B (GRIN2B)

Bhattacharya, S., Camp, C., Orlic-Milacic, M., Traynelis, SF.

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

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

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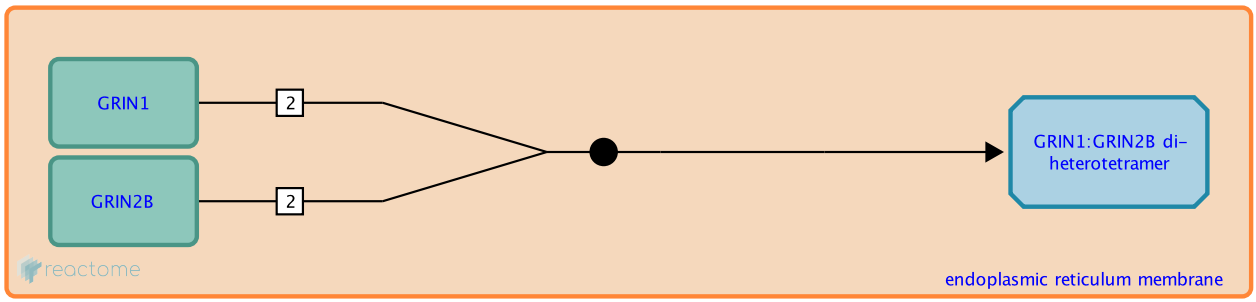
Stable identifier: R-HSA-9609744

Type: binding

Compartments: endoplasmic reticulum membrane

Inferred from: Formation of di-heterotetramers of GluN1 and GluN2b (Rattus norvegicus)



GluN2B (GRIN2B) forms a di-heterotetramer with GluN1 (GRIN1). The tetramer includes two molecules of GluN1 and two molecules of GluN2B. GluN2B expression starts during embryonic development and continues in adult brain (Monyer et al. 1992, Sheng et al. 1994). The tetrameric structure is deduced from the crystal structure of the rat GluN1:GluN2B (Grin1:Grin2b) NMDA receptor (Karakas and Furukawa 2014) and the Xenopus GluN1:GluN2B NMDA receptor (Lee et al. 2014).

Editions

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