Formation of tri-heterotetramers of GluN1 (GRIN1), GluN2A (GRIN2A) and GluN2D (GRIN2D)

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08/08/2021

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

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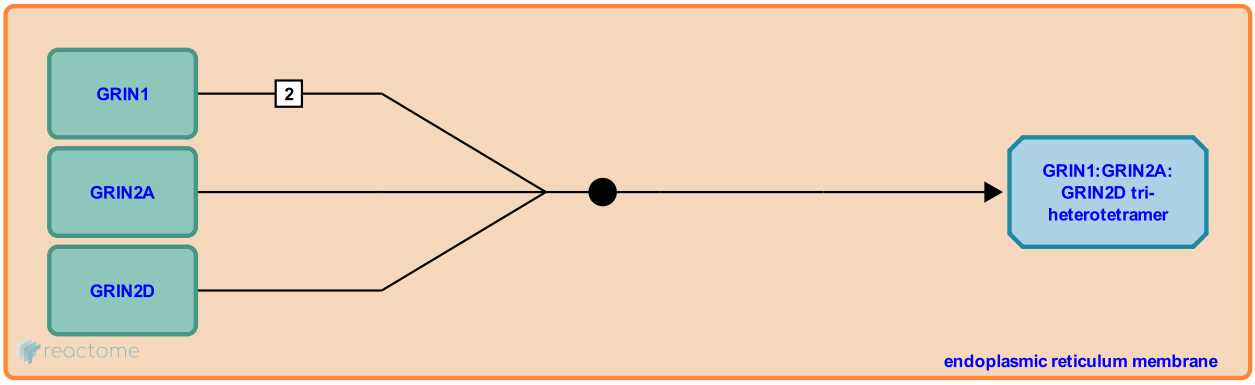
Formation of tri-heterotetramers of GluN1 (GRIN1), GluN2A (GRIN2A) and GluN2D (GRIN2D) ↗

Stable identifier: R-HSA-9610195

Type: binding

Compartments: endoplasmic reticulum membrane

Inferred from: Formation of tri-heterotetramers of GluN1 (Grin1), GluN2A (Grin2a) and GluN2D (Grin2d) (Rattus norvegicus)



GluN1 (GRIN1) is assumed to form a tri-heterotetramer with GluN2A (GRIN2A) and GluN2D (GRIN2D). The tetramer includes two molecules of GluN1, one molecule of GluN2A and one molecule of GluN2D (Dunah et al. 1998). The tetrameric structure of the GluN1:GluN2A:GluN2D (GRIN1:GRIN2A:GRIN2D) tri-heterotetramer is assumed to follow from the cryo-EM structure of the triheteromeric Xenopus GluN1:GluN2A:GluN2B NMDA receptor (Lu et al. 2017).

Editions

2019-01-05	Authored	Orlic-Milacic, M.
2019-02-11	Reviewed	Traynelis, SF., Bhattacharya, S., Camp, C.
2019-02-19	Edited	Orlic-Milacic, M.