

# Formation of tri-heterotetramers of GluN1 (GRIN1), GluN2A (GRIN2A) and GluN2B (GRIN2B)

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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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Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

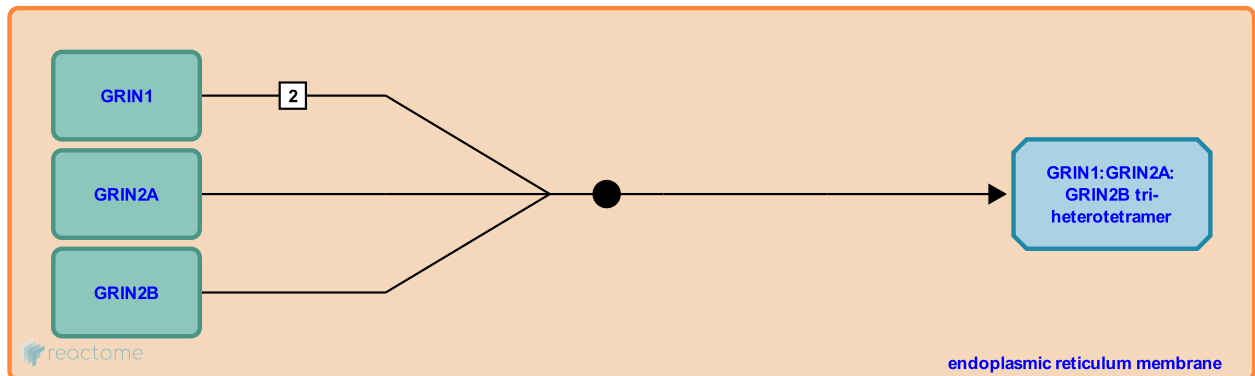
## Formation of tri-heterotetramers of GluN1 (GRIN1), GluN2A (GRIN2A) and GluN2B (GRIN2B) ↗

**Stable identifier:** R-HSA-9609746

**Type:** binding

**Compartments:** endoplasmic reticulum membrane

**Inferred from:** [Formation of tri-heterotetramers of GluN1 \(Grin1\), GluN2A \(Grin2a\) and GluN2B \(Grin2b\) \(Rattus norvegicus\)](#)



GluN1 (GRIN1) forms a tri-heterotetramer with GluN2A (GRIN2A) and GluN2B (GRIN2B). The tetramer includes two molecules of GluN1, one molecule of GluN2A and one molecule of GluN2B (Sheng et al. 1994). The tetrameric structure of the GluN1:GluN2A:GluN2B (GRIN1:GRIN2A:GRIN2B) triheteromeric NMDA receptor was demonstrated on the cryo-EM structure of the *Xenopus* orthologue (Lu et al. 2017). The majority of native NMDA receptors in adult forebrain are GluN1:GluN2A:GluN2B tri-heteromers, and their pharmacological properties are distinct from the properties of GluN1:GluN2A and GluN1:GluN2B di-heteromers (Hansen et al. 2014).

### Editions

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