

GABA_B receptors in GtoPdb v.2021.2

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Abstract

Functional GABA_B receptors (**nomenclature as agreed by the NC-IUPHAR Subcommittee on GABA_B receptors [11, 71]**) are formed from the heterodimerization of two similar 7TM subunits termed GABA_{B1} and GABA_{B2} [11, 70, 28, 71, 87]. GABA_B receptors are widespread in the CNS and regulate both pre- and postsynaptic activity. The GABA_{B1} subunit, when expressed alone, binds both antagonists and agonists, but the affinity of the latter is generally 10-100-fold less than for the native receptor. Co-expression of GABA_{B1} and GABA_{B2} subunits allows transport of GABA_{B1} to the cell surface and generates a functional receptor that can couple to signal transduction pathways such as high-voltage-activated Ca²⁺ channels (Ca_v2.1, Ca_v2.2), or inwardly rectifying potassium channels (Kir3) [12, 11, 5]. The GABA_{B1} subunit harbours the GABA (orthosteric)-binding site within an extracellular domain (ECD) venus flytrap module (VTM), whereas the GABA_{B2} subunit mediates G protein-coupled signalling [11, 70, 40, 39]. The cryo-electron microscopy structures of the human full-length GABAB1-GABAB2 heterodimer have been solved in the inactive apo state, two intermediate agonist-bound forms and an active state in which the heterodimer is bound to an agonist and a positive allosteric modulator [81]. The positive allosteric modulator binds to the transmembrane dimerization interface and stabilizes the active state. Recent evidence indicates that higher order assemblies of GABA_B receptor comprising dimers of heterodimers occur in recombinant expression systems and *in vivo* and that such complexes exhibit negative functional cooperativity between heterodimers [69, 22]. Adding further complexity, KCTD (potassium channel tetramerization proteins) 8, 12, 12b and 16 associate as tetramers with the carboxy terminus of the GABA_{B2} subunit to impart altered signalling kinetics and agonist potency to the receptor complex [86, 3, 79] and are reviewed by [72]. The molecular complexity of GABA_B receptors is further increased through association with trafficking and effector proteins [80] and reviewed by [68]. The predominant GABA_{B1a} and GABA_{B1b} isoforms, which are most prevalent in neonatal and adult brain tissue respectively, differ in their ECD sequences as a result of the use of alternative transcription initiation sites. GABA_{B1a}-containing heterodimers localise to distal axons and mediate inhibition of glutamate release in the CA3-CA1 terminals, and GABA release onto the layer 5 pyramidal neurons, whereas GABA_{B1b}-containing receptors occur within dendritic spines and mediate slow postsynaptic inhibition [74, 91]. Amyloid precursor protein (APP) and soluble APP (sAPP) bind to the N-terminal sushi domain of the GABA_{B1a} isoform to regulate axonal trafficking of GABA_B receptors and release of neurotransmitters [76].

Contents

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GABA_B receptors

<https://www.guidetopharmacology.org/GRAC/FamilyDisplayForward?familyId=26>

Introduction to GABA_B receptors

<https://www.guidetopharmacology.org/GRAC/FamilyIntroductionForward?familyId=26>

Receptors

Complexes

GABA_B receptor

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=242>

Receptors and Subunits

GABA_{B1}

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=240>

GABA_{B2}

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=241>

Accessory Proteins

KCTD8

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=1917>

KCTD12

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=1918>

kctd12b

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=1919>

KCTD16

<https://www.guidetopharmacology.org/GRAC/ObjectDisplayForward?objectId=1920>

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