To directly test this model, we altered the tension of the GluN1 and GluN2A M3–S2 linkers through residue insertions (to decrease tension) or deletions (to increase tension). Based on single-channel analyses, we find that these manipulations specifically affect pore opening (as opposed to ligand binding) and that they alter gating more dramatically in GluN2A than in GluN1. All-atom molecular dynamics simulations on a modeled GluN1/GluN2A receptor showed that this subunit-specific difference may arise, in part, from the disparate extensions and orientations of the GluN1 vs GluN2A M3–S2 linkers. Our functional data also suggests that the GluN1 M3–S2 linker gates primarily through tension, using rate equilibrium free energy relationship (REFER) analysis and length-tension analysis, we find that for the GluN1 M3–S2 linker, tension arises primarily during the C1–O1 transition (assuming a linear kinetic scheme) with a spring constant of ~7.2 pN/nm, agreeing well with other biological springs. In contrast, our functional data suggests that mechanisms other than tension mainly mediate the role of the GluN2A M3–S2 linker in gating. Alternative mechanisms may include twisting and changes in electrostatic interactions.

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Unique Conformational Distributions for NMDA Receptor Glycine and Glutamate Ligand-Binding Domains
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Ionotropic glutamate receptors (iGluRs) mediate communication at most excitatory synapses in the brain. iGluRs are organized into three major families—the AMPA, kainate, and NMDA receptors. NMDA receptors are obligate heteromeric assemblies of glycine- and glutamate-binding subunits. Unexpectedly, crystal structures of the glycine-binding GluN1 and GluN3A ligand binding domains (LBDs) in their apo states reveal open and closed cleft conformations, respectively. Computed conformational free energy landscapes also exhibit minima at both open and closed cleft conformations for apo GluN1 and GluN3A LBDs. The minimum at the closed cleft conformation is preserved for the glycine-bound LBDs. In contrast, the free energy landscapes for the NMDA and AMPA receptor glutamate-binding subunits GluN2A and GluA2 show a shift in the minimum upon glutamate binding. Principal component analysis reveals a spectrum of conformational transitions that differ for the GluN1, GluN3A, GluN2A, and GluA2 LBDs. This variation highlights the structural complexity of signaling by iGluRs.

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Gating of GluA2 Receptors is Mediated by a Pivot in the M3 Helix
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Closure of the ligand-binding domain (LBD) of glutamate receptor channels opens their gate by a mechanism that is not fully clear. We find that glycine substitutions of pore facing residues in the conserved SYTANLAFF region in the transmembrane M3 helix of GluA2 improve gating, notably, replacing alanine 621 with glycine, two turns of the helix below the gate, resulted in a non-desensitizing channel with significant agonist-independent basal activity and ~36-fold increase in glutamate potency without changes in expression or binding. On GluA2(A621G), the partial agonist kainate acted as a full agonist and the antagonist CNQX acted as a partial agonist. In contrast, a glycine mutation above the channel gate, reduced activity and glutamate potency. Therefore, closure of the LBD opens the channel by pulling apart the M3 helix around a pivot at small flexible amino acids in the pore facing region below the gate, in a mechanism similar to potassium channel gating.

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Structural Mechanisms underlying AMPA Receptor Oligomerization
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Ionotropic glutamate receptors (iGluRs) are ligand-gated ion channels that play critical roles in excitatory neurotransmission. A functional iGluR is composed of four subunits, each containing an amino-terminal domain (ATD), a ligand-binding domain (LBD), a transmembrane domain (TMD) composed of three transmembrane helices (M1, M3 and M4) and a re-entrant loop (M2), as well as an intracellular carboxyl-terminal domain (CTD). Formation of the tetrameric complex, which is a prerequisite for the receptor’s surface expression and function, involves a dimeric intermediate. Nevertheless, the biophysical mechanisms underlying iGluR oligomerization remain largely unknown. We studied the relative energetic contributions of the different structural domains to the oligomerization of iGluRs using blue native PAGE and fluorescent size-exclusion chromatography (FSEC). We find that deletion of the M4 transmembrane helix renders AMPA receptors incapable of tetramerization and traps them in a dimeric form, suggesting that the crucial dimer-to-tetramer transition is driven by molecular interactions within the TMD. Further highlighting the importance of interactions within the TMD, the antagonist CNQX acted as a partial agonist. In contrast, the GluA1 subunit, which lacks ATD and LBD, still form tetramers. On the other hand, the GluA1 ATD is essential for the stability of homo-dimer intermediates, although its absence does not prevent tetramerization. Interestingly, the prokaryotic glutamate receptor GlrR0, which lacks both the ATD and the M4 helix, forms both dimers and functional tetramers. In contrast, GluA1 subunits lacking the ATD and the M4 helix (and thus topologically similar to GlrR0) do not oligomerize, forming monomers only. Our results indicate that the mechanisms for tetrameric assembly differ significantly between GluA1 and GlrR0 in terms of the energetic contributions of each structural domain. Such differences may have important implications in the evolution of iGluRs and their roles in fast excitatory neurotransmission.