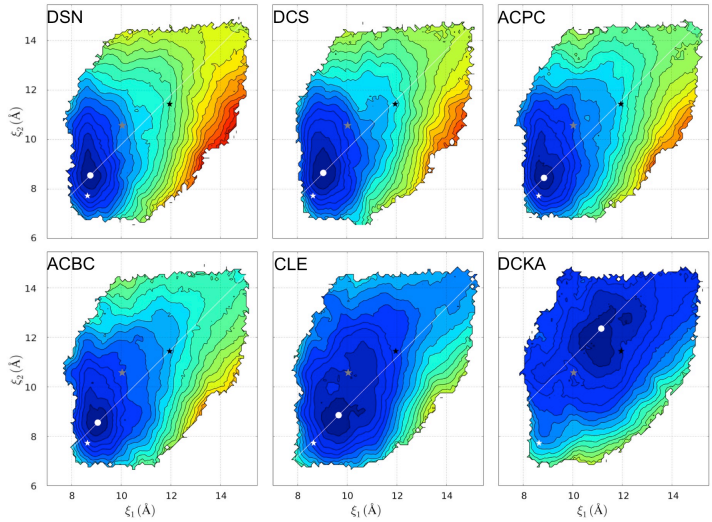

Figure S1, related to Figure 3. Free energy surfaces of the GluN1 LBD bound with six non-Gly ligands. The free energy minima are highlighted by a white dot for each indicated ligand. Also shown are (ξ_{1c}, ξ_{2c}) values calculated on the crystal structures of the LBD bound with three ligands: Gly (white star; PDB 1PB7), CLE (gray star; PDB 1Y1M), and DCKA (black star; PDB 1PBQ). The ξ_1' coordinate with ξ_2' fixed at ($\xi_{1m} - \xi_{2m}$)/2 is shown by a white line.

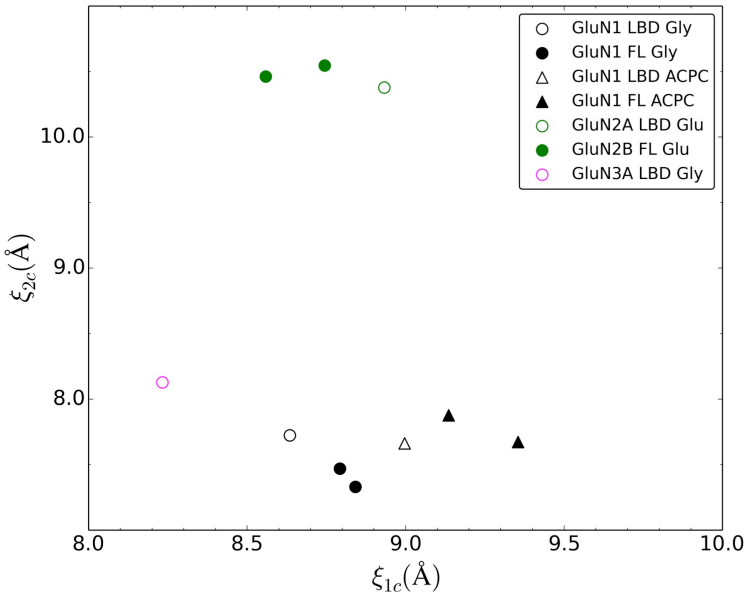

Figure S2, related to Figure 5. Values of (ξ_{1c}, ξ_{2c}) in crystal structures of isolated GluN1-3 LBDs or full-length (FL) NMDA receptors bound with Gly, ACPC, and glutamate (Glu).

Table S1

Ligand	PDB entry	(ξ_{1m}, ξ_{2m}) (Å)	(ξ_{1c}, ξ_{2c}) (Å)	d (Å)	ΔW_c (kcal/mol)
Gly	1PB7	(8.65, 8.45)	(8.64, 7.72)	0.73	1.96
DSN	1PB8	(8.75, 8.55)	(8.72, 7.74)	0.81	1.90
DCS	1PB9	(9.05, 8.65)	(8.79, 7.70)	0.99	2.61
ACPC	1Y20	(8.85, 8.45)	(9.00, 7.66)	0.80	2.03
ACBC	1Y1Z	(9.05, 8.55)	(9.10, 7.75)	0.80	2.28
CLE	1Y1M	(9.65, 8.85)	(10.00, 10.57)	1.76	1.97
DCKA	1PBQ	(11.15, 12.35)	(12.00, 11.44)	1.22	1.93

Table S1, related to Figures 2B & S1. Comparison of computed free-energy minimum positions and the counterparts in the crystal structures of the GluN1 LBD bound with seven ligands.

d: distance between (ξ_{1m}, ξ_{2m}) and (ξ_{1c}, ξ_{2c}).

ΔW_c: increase in free energy from (ξ_{1m}, ξ_{2m}) to (ξ_{1c}, ξ_{2c}).