Supplementary Figure 2. A superimposition of the structures of the ligand-binding pockets of GluRδ2 in complex with D-serine (green), NR1 in complex with D-serine (magenta; PDB entry 1PB8) and NR1 in complex with glycine (grey; 1PB7). Amino-acid residues within 5 Å of ligands are shown. Residue numbering is according to GluRδ2. Water molecules are shown as spheres. No water molecule within hydrogen-bonding distance of D-serine is seen in the binding cleft of GluRδ2, which is in marked contrast to X-ray data for other iGluRs. In the NR1-S1S2 structure with bound D-serine or glycine, two water molecules are found in the ligand-binding pocket. One of these is sterically occluded in GluRδ2 due to the presence of a tyrosine (Tyr543), which is a glutamine in NR1 (Gln536). The other water molecule is sterically occluded due to limited space in the proximity of Ala523 and Asp742, thereby giving rise to a hydrogen-bonding network in GluRδ2, which is different from the one observed in the NR1-S1S2 structure with bound D-serine.