Supporting Information

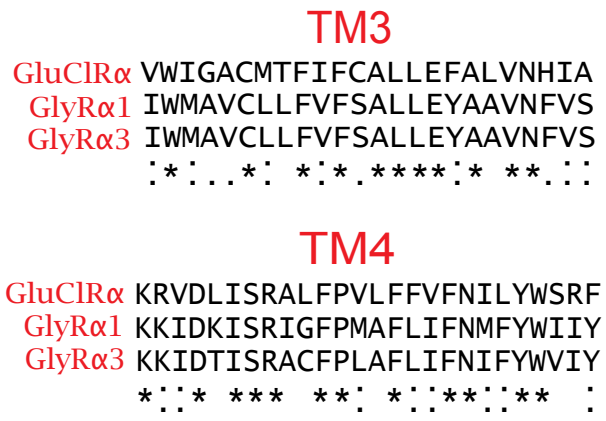

Figure S1. Amino acid sequence alignment of the TM3 and TM4 domains of the human α1 GlyR, the human α3 GlyR and the *C. elegans* α GluClR that were used to generate the structural models of α1 GlyR and α3 GlyR from the *C. elegans* α GluClR crystal structure (PDB code: 3RIF).

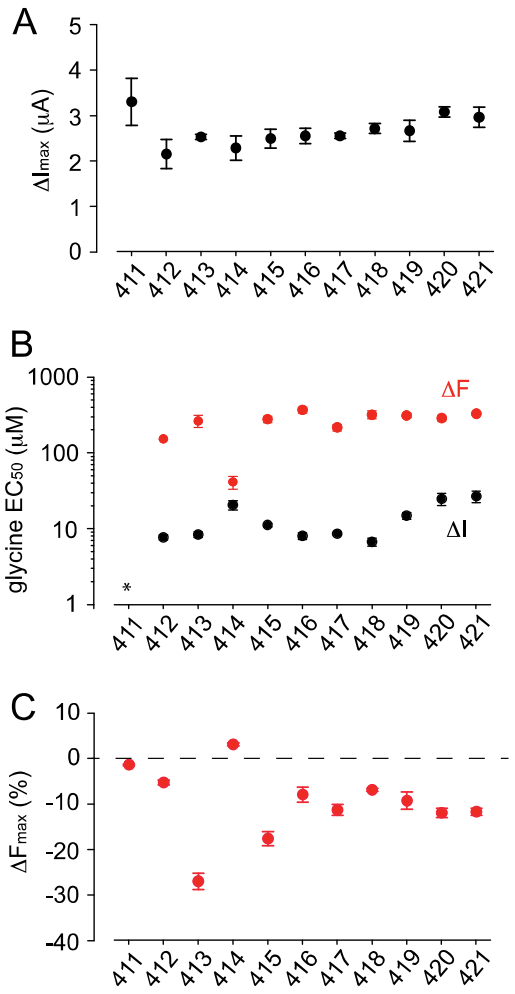

Figure S2. Functional comparison of MTS-TAMRA-labeled α1 GlyRs. A. Mean ΔI_{max} values for all labeled α1 GlyRs investigated here reveals no significant variation using ANOVA and post-hoc tests as described in the text. B. Mean ΔI EC_{50} and ΔF EC_{50} values (shown in black and red, respectively) differed by around an order of magnitude at all labeled sites except for R414C. C. Mean ΔF_{max} values were negative at all labeled sites except for R414C.