

Supporting Information

TM3

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GluCIR $\alpha$  VWIGACMTFIFCALLEFALVNHIA  
GlyR $\alpha$ 1 IWMAVCLLFVFSALLEYAAVNFVS  
GlyR $\alpha$ 3 IWMAVCLLFVFSALLEYAAVNFVS  
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TM4

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GluCIR $\alpha$  KRVDLISRALFPVLFFVFNILYWSRF  
GlyR $\alpha$ 1 KKIDKISRIGFPMAFLIFNMFYWIIY  
GlyR $\alpha$ 3 KKIDTISRACFPLAFLIFNIFYWVIY  
*:.:* *** *: *:.:*:*:*:*:
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Figure S1. Amino acid sequence alignment of the TM3 and TM4 domains of the human α 1 GlyR, the human α 3 GlyR and the *C. elegans* α GluCIR that were used to generate the structural models of α 1 GlyR and α 3 GlyR from the *C. elegans* α GluCIR crystal structure (PDB code: 3RIF).

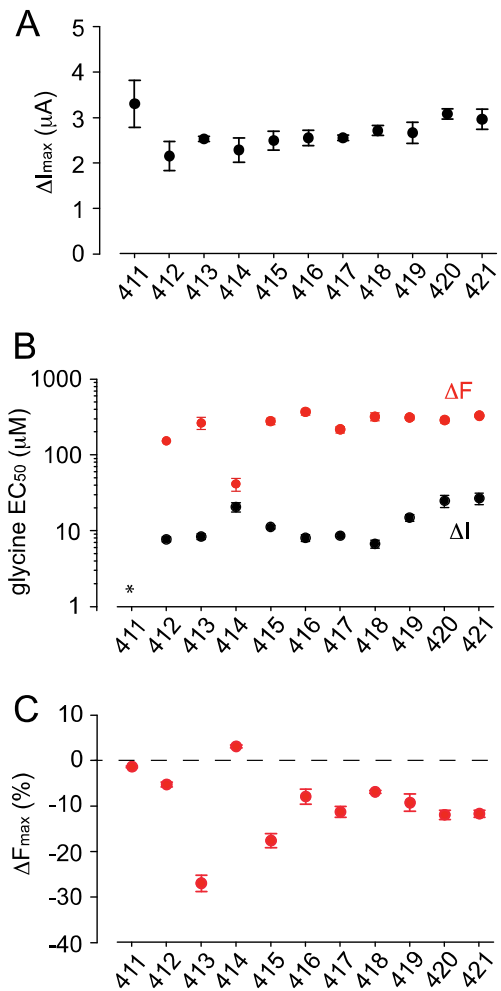


Figure S2. Functional comparison of MTS-TAMRA-labeled $\alpha 1$ GlyRs. A. Mean ΔI_{\max} values for all labeled $\alpha 1$ GlyRs investigated here reveals no significant variation using ANOVA and post-hoc tests as described in the text. B. Mean ΔI EC₅₀ and ΔF EC₅₀ values (shown in black and red, respectively) 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.