

Supplementary Information

Table S1

Summary of results for agonist-activated ΔI and ΔF responses at unlabeled and MTSR-labeled $\alpha 1$ -R19'C and $\alpha 3$ -R19'C GlyRs. Electrophysiological and fluorescence data are shown in normal and bold type, respectively.

Agonist	Construct	EC ₅₀ (μ M)	n _H	I _{max} (μ A)	ΔF_{max} (%)	ΔF half decay time / ΔI half decay time	n
glycine	$\alpha 3$ -WT unlabeled	74 ± 2	2.9 ± 0.2	5.4 ± 0.6	-	-	6
	$\alpha 3$ -WT labeled	71 ± 2	2.9 ± 0.2	5.6 ± 0.5	-	-	6
	$\alpha 3$-WT labeled ΔF	-	-	-	0	-	6
	$\alpha 3$ -19'C unlabeled	12700 ± 600a	1.4 ± 0.1a	1.7 ± 0.1a	-	-	7
	$\alpha 3$ -19'C labeled	1740 ± 270ab	1.2 ± 0.1a	3.1 ± 0.3a	-	5.1 ± 1.0	13
	$\alpha 3$-19'C labeled ΔF	1340 ± 210	1.1 ± 0.1	-	5.4 ± 0.5		13
	$\alpha 1$ -WT unlabeled	17.9 ± 1.5a	2.8 ± 0.1	4.8 ± 0.4	-	-	4
	$\alpha 1$ -WT labeled	17.1 ± 0.6a	2.8 ± 0.2	4.9 ± 0.7	-	-	4
	$\alpha 1$-WT labeled ΔF	-	-	-	0		4
	$\alpha 1$ -19'C unlabeled	4320 ± 220a	1.3 ± 0.1a	2.3 ± 0.4a	-	-	5
β -alanine	$\alpha 3$ -19'C labeled	2610 ± 940a	1.5 ± 0.3a	0.4 ± 0.05a	NA	4.7 ± 0.7	5
	$\alpha 3$-19'C labeled ΔF	22100 ± 2300c	1.1 ± 0.1	-	2.6 ± 0.5		5
taurine	$\alpha 3$ -19'C labeled	-	-	0.03 ± 0.01a	-	-	5
	$\alpha 3$-19'C labeled ΔF	5990 ± 780	1.3 ± 0.4	-	1.3 ± 0.2		5

a - significant difference to electrophysiological properties of glycine-activated unlabeled $\alpha 3$ -WT GlyRs (Student's t-test, $p < 0.05$)

b - significant difference to electrophysiological properties before labeling in the same mutant GlyR (Student's t-test, $p < 0.05$)

c - significant difference of fluorescence properties to electrophysiological properties after labeling in the same mutant GlyR (Student's t-test, $p < 0.05$)

$\alpha 1$ -WT data are reproduced from (36)

Table S2

Summary of results for glycine-activated ΔI and ΔF responses at chimeric and double mutant GlyRs incorporating MTSR labels at R19°C. Electrophysiological and fluorescence data are shown in normal and bold type, respectively.

Construct	EC_{50} (μM)	n_H	I_{max} (μA)	ΔF_{max} (%)	ΔF half decay time / ΔI half decay time	n
Chi1 unlabeled	2880 ± 390	3.2 ± 0.2	1.6 ± 0.5	-	-	5
Chi1 labeled	860 ± 490	1.1 ± 0.1	2.4 ± 0.5	-	3.2 ± 0.3b	5
Chi1 ΔF	1450 ± 310	1.3 ± 0.2	-	2.3 ± 0.2b		5
Chi2 unlabeled	2330 ± 520	2.7 ± 0.1	3.2 ± 0.4	-	-	5
Chi2 labeled	530 ± 160	1.1 ± 0.01	2.6 ± 0.4	-	4.2 ± 0.8b	6
Chi2 ΔF	970 ± 350	0.9 ± 0.3	-	4.8 ± 0.2b		6
Chi3 unlabeled	5710 ± 1020	1.3 ± 0.1	1.4 ± 0.1	-	-	5
Chi3 labeled	610 ± 30	1.8 ± 0.2	3.0 ± 0.2	-	1.0 ± 0.1a	6
Chi3 ΔF	1000 ± 190	1.3 ± 0.1	-	18.5 ± 3.3a		6
Chi4 unlabeled	5300 ± 220	1.7 ± 0.1	1.9 ± 0.04	-	-	4
Chi4 labeled	770 ± 80	1.2 ± 0.03	2.8 ± 0.3	-	5.7 ± 1.6b	5
Chi4 ΔF	640 ± 60	1.3 ± 0.05	-	4.4 ± 0.2b		5
Chi5 unlabeled	3840 ± 340	1.6 ± 0.1	3.2 ± 0.2	-	-	5
Chi5 labeled	500 ± 40	2.0 ± 0.3	2.5 ± 0.3	-	1.2 ± 0.2a	5
Chi5 ΔF	980 ± 210	1.3 ± 0.02	-	23.4 ± 3.7a		5
Chi6 unlabeled	5640 ± 250	1.8 ± 0.2	3.0 ± 0.5	-	-	5
Chi6 labeled	630 ± 240	2.1 ± 0.4	2.4 ± 0.4	-	0.7 ± 0.01a	5
Chi6 ΔF	1140 ± 190	1.0 ± 0.2	-	20.4 ± 3.2a		5
ChiA unlabeled	10800 ± 610	1.1 ± 0.1	1.1 ± 0.3	-	-	5
ChiA labeled	780 ± 140	2.0 ± 0.3	0.9 ± 0.1	-	3.5 ± 0.4b	7
ChiA ΔF	920 ± 240	0.8 ± 0.1	-	3.1 ± 0.5b		7
ChiB unlabeled	3650 ± 920	1.8 ± 0.2	2.4 ± 0.6	-	-	6
ChiB labeled	410 ± 60	1.5 ± 0.2	2.6 ± 0.3	-	1.0 ± 0.1a	7
ChiB ΔF	1150 ± 190	1.3 ± 0.2	-	21.9 ± 3.4a		7
$\alpha 3$ -R19°C,S346G unlabeled	6420 ± 370	1.5 ± 0.03	2.1 ± 0.2	-	-	5
$\alpha 3$ -R19°C,S346G labeled	710 ± 40	1.4 ± 0.05	2.8 ± 0.3	-	1.8 ± 0.5a	5
$\alpha 3$-R19°C,S346G ΔF	880 ± 210	1.3 ± 0.2	-	6.7 ± 0.5		5
$\alpha 3$ -R19°C,S346E unlabeled	8890 ± 280	1.8 ± 0.1	1.5 ± 0.1	-	-	5
$\alpha 3$ -R19°C,S346E labeled	800 ± 70	1.4 ± 0.1	2.4 ± 0.1	-	3.7 ± 1.1b	5
$\alpha 3$-R19°C,S346E ΔF	1230 ± 350	1.1 ± 0.1	-	2.2 ± 0.1		5

There was no significant difference among the EC_{50} , n_H or ΔI_{max} data using one way ANOVA followed by Dunnett's post hoc test. A statistical analysis of ΔF_{max} and $\Delta F/\Delta I$ half decay ratio data is presented in Fig. 3.

Table S3

Summary of results for agonist-activated ΔI and ΔF responses at MTS-TAMRA-labeled N203C mutant GlyRs. Electrophysiological and fluorescence data are shown in normal and bold type, respectively.

Construct	EC_{50} (μM)	n_H	I_{max} (μA)	ΔF_{max} (%)	n
$\alpha 3$ -N203C ΔI glycine	57 ± 8	2.5 ± 0.2	4.9 ± 0.2	-	5
$\alpha 3$-N203C ΔF glycine	732 ± 24	1.0 ± 0.1	-	4.0 ± 0.4	5
$\alpha 3$-N203C ΔF strychnine	-	-	-	5.5 ± 0.3	5
$\alpha 3$ -N203C-S346G ΔI glycine	43 ± 5	2.3 ± 0.2	4.7 ± 0.2	-	5
$\alpha 3$-N203C-S346G ΔF glycine	588 ± 35	1.2 ± 0.2	-	7.1 ± 0.5	5
$\alpha 3$-N203C-S346G ΔF strychnine	-	-	-	8.4 ± 0.2	5

Human_alpha1	ARSAPKPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVS	CNIFINSFGS	50
Rat_alpha3L	ARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVT	CNIFINSFGS	50
	***** . *****:*****:*****:*****:*****:	*****	
Human_alpha1	IAETTMDYRVNIFLQQWNDPRLAYNEYPPDSLDDPSMLDSIWKPDLFF	100	
Rat_alpha3L	IAETTMDYRVNIFLQRQWKNDPRLAYSEYPDDSLDDPSMLDSIWKPDLFF	100	
	*****:*****:***** . *****:*****:*****:*****	*****	
Human_alpha1	ANEKGAFHEITTDNKLLRISRNGNVLYSIRITLTACPMDLKNFPMDVQ	150	
Rat_alpha3L	ANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTTLSCPMDLKKNFPMDVQ	150	
	*****:*****:*****:*****:*****:*****:*****:*****	*****	
Human_alpha1	TCIMQLESFGYTMDNLIFEWFQEQQAVQVADGLTPQFILKEEKDLRYCTK	200	
Rat_alpha3L	TCIMQLESFGYTMDNLIFEWFQDEAPVQVAEGLTPQFLLKEEKDLRYCTK	200	
	*****:*****:*****:*****:*****:*****:*****:*****	*****	
Human_alpha1	HYNTGKFTCIEARFHLEHQMGYYLIQMYIPSLLIVILSWISFWINMDAAP	250	
Rat_alpha3L	HYNTGKFTCIEVRFHLEHQMGYYLIQMYIPSLLIVILSWVSFWINMDAAP	250	
	*****:*****:*****:*****:*****:*****:*****:*****	*****	
Human_alpha1	ARVLGLGITTVLTMTTQSSGS	RASLPKVSYVKAIDIWMAVCLLFVFSALLE	300
Rat_alpha3L	ARVALGITTVLTMTTQSSGS	RASLPKVSYVKAIDIWMAVCLLFVFSALLE	300
	*** . *****:*****:*****:*****:*****:*****:*****	*****	
Human_alpha1	YAAVNFSRQHKELLRFRRKRR-HHK-----	EDEAGEGRNF	336
Rat_alpha3L	YAAVNFSRQHKELLRFRRKRKNKTEFAALEKFYRF	SDTDDEVRESRLSF	350
	*****:*****:*****:*****:*****:*****:*****:*****	:**. *.*..*	
Human_alpha1	SAYGMGPACLQAKDGTSVKGANNSNTNPPPAPSKSPEEMRKLFIQRAKK	386	
Rat_alpha3L	TAYGMGP-CLQAKDGVVPKGPNHAVQVMP-----	KSADEMRKVFDRAKK	394
	:*****:*****:*****:*****:*****:*****:*****:*****	**. ;****;**;****	
Human_alpha1	IDKISRIGFPMAFLIFNMFYWIYKIVRREDVHNQ--	422	
Rat_alpha3L	IDTISRACFPFLAFLIFNIFYWVIIYKILRHEDIHHQQD	431	
	. ***:**:***:***:***:***:***:***:***	***	

Fig. S1. Amino acid sequence alignment of the coding region of the human $\alpha 1$ GlyR subunit (Uniprot accession number: P23415-2, isoform b) and the rat $\alpha 3\beta 2\gamma 2$ GlyR subunit (Uniprot accession number: P24524). The alignment was generated using ClustalW. The residues that were mutated in this study are shown in blue. In addition to S346, the residues shown in red are also predicted to be serine phosphorylation sites according to the NetPhos 2.0 Server. Orange vertical lines denote the locations of subunit join sites used in creating $\alpha 1-\alpha 3$ chimeras.

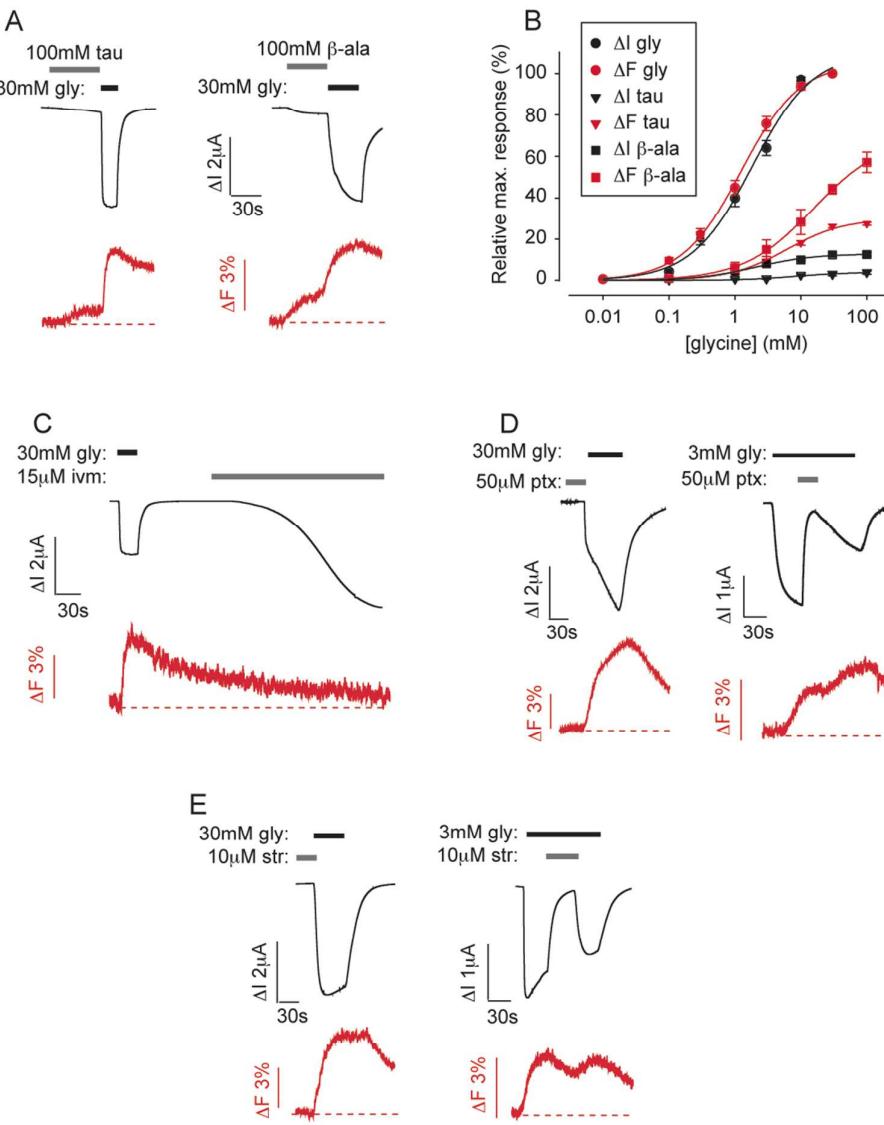


Fig. S2. Pharmacological characterization of MTSR-labeled $\alpha 3$ -R19'C GlyRs. A. Sample ΔI_{max} and ΔF_{max} recordings in response to consecutive applications of saturating taurine (tau) and glycine (gly, left panel) or saturating β -alanine (β -ala) and glycine (right panel). Gray bars indicate duration of applications of taurine and β -alanine. B. Averaged ΔI and ΔF dose-response relationships for glycine, taurine and β -alanine. All dose-response curves are normalised to those of glycine as measured in the same oocyte. Mean parameters of best fit to all dose-response curves are presented in Table S1. C. Sample ΔI_{max} and ΔF_{max} recordings in response to saturating applications of glycine (black bar) and ivermectin (ivm, gray bar). This recording is representative of 5 others in which no detectable ivermectin-induced ΔF was observed. D. Sample ΔI_{max} and ΔF_{max} recordings in response to the application of picrotoxin (ptx) alone (left) or co-application of EC₅₀ glycine with saturating picrotoxin (right). E. Sample ΔI_{max} and ΔF_{max} recordings in response to application of strychnine (str) alone (left) or co-application of EC₅₀ glycine with saturating strychnine (right). Averaged values for experiments in panels D and E are given in the main text.

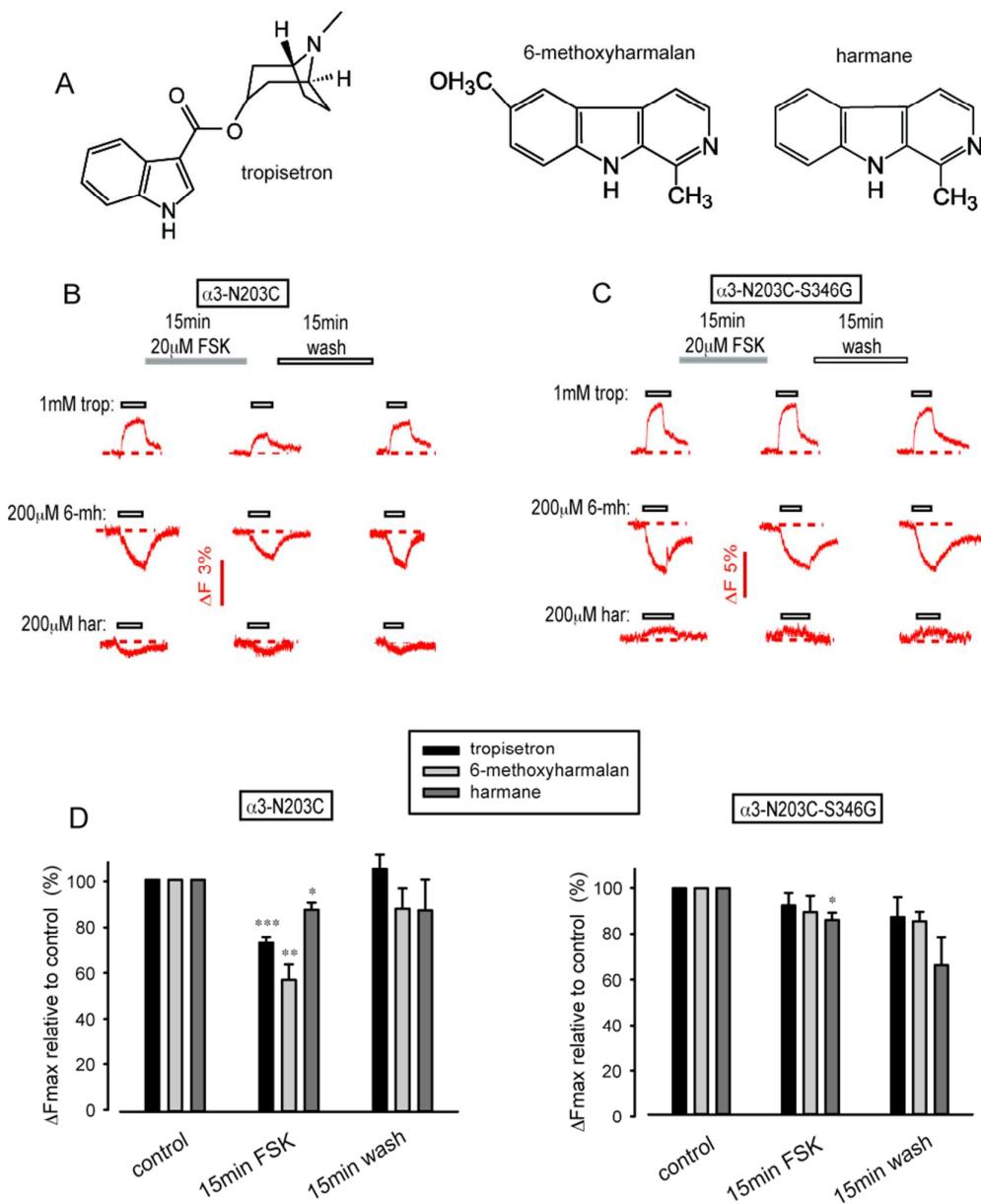


Fig. S3. Effects of phosphorylation on ΔF_{\max} responses induced by tropisetron, 6-methoxyharmalan and harmane in MTS-TAMRA-labeled $\alpha 3\text{-N}203\text{C}$ GlyRs. A. Structures of the three molecules. B. Examples of ΔF_{\max} responses induced by 1 mM tropisetron (trop), 200 μM 6-methoxyharmalan (6-mh) and 200 μM harmane (har) on MTS-TAMRA-labeled $\alpha 3\text{-N}203\text{C}$ GlyRs before and after a 15 min forskolin (FSK) treatment and a 15 min wash. C. Corresponding experiments on MTS-TAMRA-labeled $\alpha 3\text{-N}203\text{C-S}346\text{G}$ GlyRs. D. Averaged data for the experiments shown in B and C (all n = 6). * p < 0.05, ** p < 0.01, *** p < 0.001 relative to control using paired t-test.