

Supporting Information

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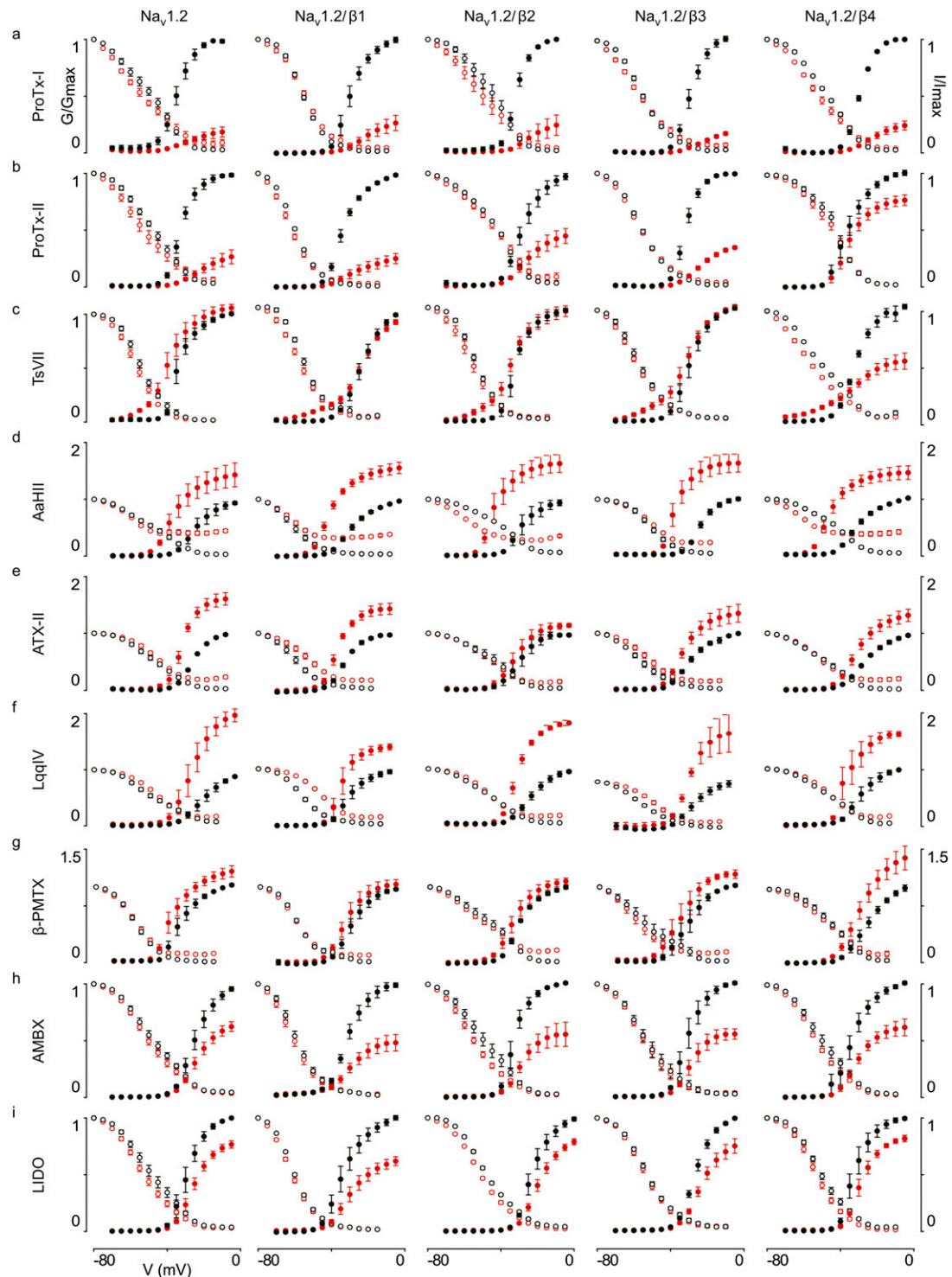


Fig. S1. Influence of β -subunits on the ligand susceptibility of the voltage-gated sodium channel $\text{Na}_v1.2$. Effect of 100 nM ProTx-I (A), 100 nM ProTx-II (B), 500 nM TsVII (C), 100 nM AaHII (D), 500 nM ATX-II (E), 100 nM LqIV (F), 10 μM β -PMTX (G), 10 mM lidocaine (LIDO) (H), and 500 μM ambroxol (AMBX) (I) (all saturating concentrations) on $\text{Na}_v1.2$ without and in the presence of β -subunits. Normalized conductance–voltage relationships (G/G_{max} ; black filled circle/red filled circle) and steady-state inactivation relationships (I/I_{max} ; black open circle/red open circle) are shown before (black) and after (red) toxin or drug application. Channel-expressing oocytes were depolarized in 5-mV steps from a holding potential of -90 mV. $n = 3$ –5; error bars represent S.E.M.

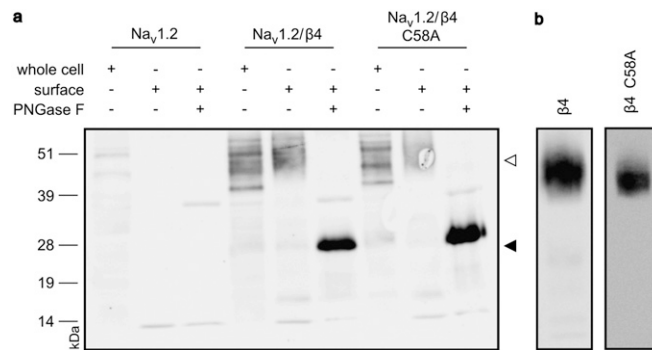


Fig. S5. $\beta 4$ and the C58A mutant are glycosylated and traffic to the membrane. (A) Western blot analysis and biotinylation experiments demonstrate the presence of $\beta 4$ and the C58A mutant on the oocyte membrane surface, albeit in a glycosylated form (open arrowhead). Removing $\beta 4$ glycosylation using Peptide-*N*-Glycosidase F (PNGase F) incubation reveals the correct predicted molecular mass of 28 kDa (filled arrowhead). This figure shows data related to that shown in Fig. 4 but over a more extensive range of protein masses. (B) Without $\text{Na}_v1.2$, $\beta 4$ (1) and the C58A mutant still traffic to the oocyte membrane in a glycosylated form. A ladder in kilodaltons (kDa) is shown on the left.

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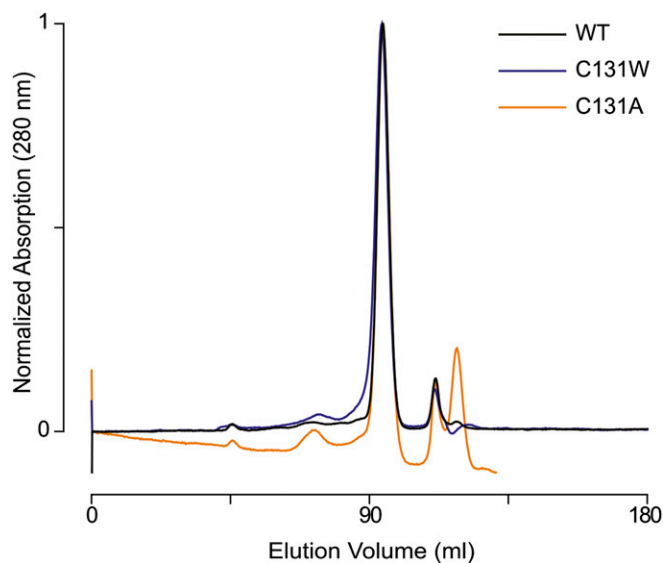


Fig. S6. Gel-filtration chromatograms of $\beta 4$, C131W, and C131A. All three chromatograms display a predominant peak corresponding to monomeric protein. Normalized absorption was recorded at 280 nm.

Table S1. Influence of ligands on the gating properties of $\text{Na}_v1.2$ and $\text{Na}_v1.2/\beta x$

Ligand	Parameter	$\text{Na}_v1.2$, mV		$\text{Na}_v1.2/\beta 1$, mV		$\text{Na}_v1.2/\beta 2$, mV		$\text{Na}_v1.2/\beta 3$, mV		$\text{Na}_v1.2/\beta 4$, mV	
		Before	After	Before	After	Before	After	Before	After	Before	After
ProTx-I	Activation ($V_{1/2}$)	-34.2 ± 1.4	$-28.0 \pm 1.1^*$	-29.8 ± 1.5	$-20.9 \pm 0.2^*$	-31.8 ± 0.9	$-22.5 \pm 1.8^*$	-29.1 ± 1.4	$-21.3 \pm 0.9^*$	-29.3 ± 0.2	$-22.8 \pm 0.6^*$
	Inactivation ($V_{1/2}$)	-50.2 ± 1.7	-56.6 ± 1.4	-55.5 ± 0.6	-55.8 ± 1.0	-45.2 ± 2.6	-53.1 ± 4.3	-55.7 ± 0.7	-61.7 ± 0.7	-47.9 ± 0.3	$-54.1 \pm 0.9^*$
ProTx-II	Activation ($V_{1/2}$)	-32.3 ± 0.9	$-22.5 \pm 0.2^*$	-33.6 ± 0.9	$-24.8 \pm 3.0^*$	-27.7 ± 2.1	-24.6 ± 2.1	-31.7 ± 1.0	$-24.0 \pm 0.9^*$	-31.1 ± 3.3	-34.6 ± 3.4
	Inactivation ($V_{1/2}$)	-49.2 ± 1.3	-55.2 ± 2.5	-60.0 ± 0.3	-63.5 ± 1.0	-43.0 ± 0.3	-46.3 ± 1.3	-56.1 ± 0.5	-57.8 ± 0.2	-43.2 ± 0.9	-44.7 ± 1.5
TsVII	Activation ($V_{1/2}$)	-33.5 ± 1.5	$-38.6 \pm 2.1^*$	-23.0 ± 1.8	-23.4 ± 1.2	-32.0 ± 0.9	-35.0 ± 0.9	-29.6 ± 1.9	-31.1 ± 2.4	-31.0 ± 1.0	-33.0 ± 1.7
	Inactivation ($V_{1/2}$)	-54.3 ± 1.0	-56.9 ± 1.0	-55.4 ± 0.4	-58.1 ± 0.8	-53.7 ± 0.7	-56.8 ± 1.8	-57.6 ± 1.2	-59.8 ± 1.1	-51.8 ± 0.6	$-59.4 \pm 1.5^*$
LqqIV	Activation ($V_{1/2}$)	-18.5 ± 0.7	$-24.4 \pm 1.4^*$	-28.2 ± 1.7	-31.8 ± 1.8	-24.5 ± 1.5	$-32.4 \pm 0.8^*$	-28.4 ± 1.7	-32.3 ± 1.8	-30.0 ± 2.3	-37.2 ± 3.0
	Inactivation ($V_{1/2}$)	-50.5 ± 1.5	-48.0 ± 0.8	-56.8 ± 0.6	$-48.1 \pm 0.3^*$	-47.7 ± 0.5	-48.9 ± 0.6	-56.9 ± 1.0	$-50.9 \pm 1.0^*$	-47.3 ± 0.5	-48.0 ± 0.6
AMBX	Activation ($V_{1/2}$)	-24.4 ± 1.9	-23.3 ± 1.8	-30.5 ± 1.7	-29.2 ± 1.7	-32.8 ± 1.5	-29.5 ± 0.6	-30.4 ± 2.1	-28.4 ± 1.3	-34.1 ± 2.7	-31.2 ± 1.7
	Inactivation ($V_{1/2}$)	-49.1 ± 2.0	-51.5 ± 1.5	-60.0 ± 1.2	-61.9 ± 1.4	-50.7 ± 2.6	-57.4 ± 1.4	-54.3 ± 1.9	-55.4 ± 1.3	-50.7 ± 2.0	-54.2 ± 0.8

Results are the average of three to five oocyte recordings and errors are SEM. The table presents data related to Fig. 1 in the main text.

*A statistically significant difference before and after toxin addition to $\text{Na}_v1.2$ without or in the presence of a particular β -subunit (Student *t* test with $P < 0.005$).

Table S2. Disease mutations mapped onto the $\beta 4$ structure

	Mutation (ref.)	Disease phenotype	Residue	Location	Solvent-accessible surface area, \AA^2 [†]
$\beta 1$	R85H (1)	Atrial fibrillation	K96	End of β_5	61.9
	E87Q (2)	Cardiac conduction defect	D98	β_5 - β_6 loop	21.4
	I106P (3)	Dravet syndrome	I116	β_7 , within hydrophobic core	0.7
	C121W (4)	GEFS+	C131	β_8 , affects conserved cysteine bond	0.9
	R125L (5)	GEFS+	N135	End of β_8 , lines pocket next to ^{58}Cys .	14.3
	R125C (6)	Dravet syndrome	N135	End of β_8 , lines pocket next to ^{58}Cys	14.3
	V138I (7)	Idiopathic epilepsy	—	Insertion in β_9 - β_{10} loop	—
$\beta 3$	V54G (8)	Idiopathic ventricular fibrillation	—	Insertion in β_2 - β_3 loop	—
	Q89L (9)	Colorectal cancer*	D98	β_5 - β_6 loop, surface accessible	21.4
	V110I (10)	Brugada syndrome	L121	β_7 - β_{10} loop, within hydrophobic core	0

Although several $\beta 2$ and $\beta 4$ mutations have been implicated in atrial fibrillation and LQTS in humans, the amino acid substitutions involved occur outside of the crystal structure reported in this work and are not represented in this table. GEFS+: generalized epilepsy plus febrile seizures plus.

*Mutation found in a screen of colorectal cancer sample. The pathogenicity of the mutation has not been established, but the same position is also affected in a $\beta 1$ mutation.

[†]Accessible surface area is for the side chain of the WT residue only.

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4. Wallace RH, et al. (1998) Febrile seizures and generalized epilepsy associated with a mutation in the Na⁺-channel beta1 subunit gene SCN1B. *Nat Genet* 19(4):366–370.
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