

SUPPLEMENTAL DATA

Parallel homodimer structures of the extracellular domains of the voltage-gated sodium channel $\beta 4$ subunit explain its role in cell-cell adhesion

Hideaki Shimizu^{1,2,3}, Asako Tosaki³, Noboru Ohsawa^{1,2}, Yoshiko Ishizuka-Katsura^{1,2}, Shisako Shoji^{1,2}, Haruko Miyazaki^{3,4,5}, Fumitaka Oyama^{3,6}, Takaho Terada^{1,7}, Mikako Shirouzu^{1,2}, Shun-ichi Sekine^{1,2}, Nobuyuki Nukina^{3,4,5} and Shigeyuki Yokoyama^{1,7}

¹ RIKEN Systems and Structural Biology Center, Tsurumi, Yokohama 230-0045, Japan

² RIKEN Center for Life Science Technologies, Tsurumi, Yokohama 230-0045, Japan

³ Laboratory for Structural Neuropathology, RIKEN Brain Science Institute, Wako, Saitama 351-0198, Japan

⁴ Department of Neuroscience for Neurodegenerative Disorders, Juntendo University Graduate School of Medicine, Tokyo 113-8421, Japan

⁵ Laboratory of Structural Neuropathology, Doshisha University Graduate School of Brain Science, 1-3 Tatara Miyakodani, Kyotanabe-shi, Kyoto 610-0394, Japan

⁶ Department of Chemistry and Life Science, Kogakuin University, Hachioji, Tokyo 192-0015, Japan

⁷ RIKEN Structural Biology Laboratory, Tsurumi, Yokohama 230-0045, Japan

SUPPLEMENTAL FIGURE LEGENDS

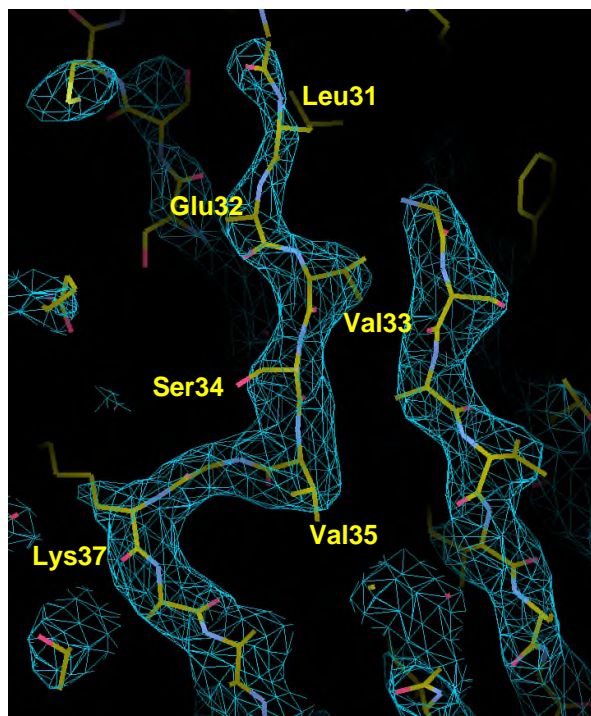
SUPPLEMENTAL FIGURE S1. Electron densities ($2Fo-Fc$ composite omit map contoured at 1.5σ) of the N-terminal segments of the mouse and human $\beta 4ex$ structures.

SUPPLEMENTAL FIGURE S2. Full-length blots and gels presented in the main figures.

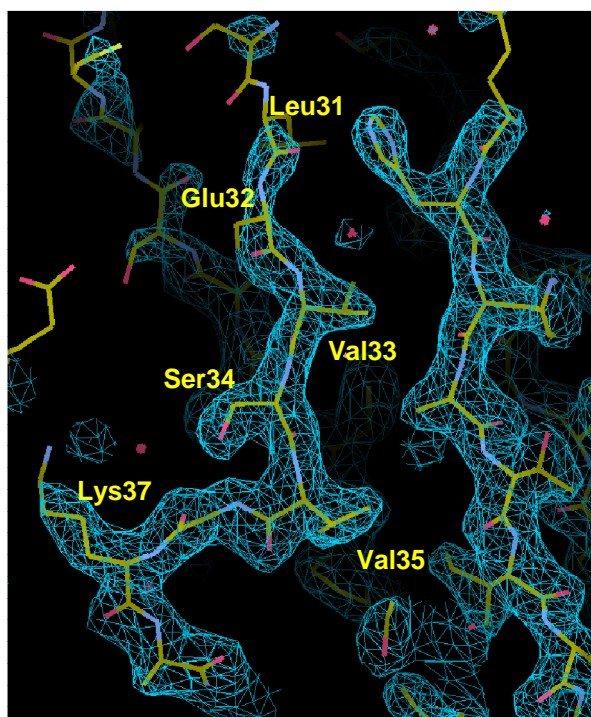
SUPPLEMENTAL TABLE LEGENDS

SUPPLEMENTAL TABLE S1. Data collection and refinement statistics.

Supplemental Figure S1



Mouse $\beta 4$ cubic form



Human $\beta 4$ hexagonal form

Supplemental Figure S2

Fig. 4

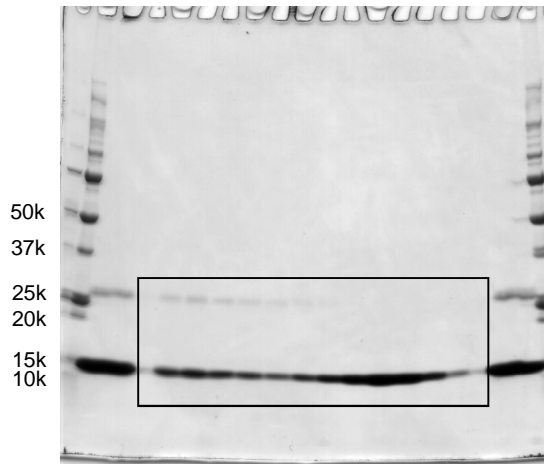


Fig. 5A

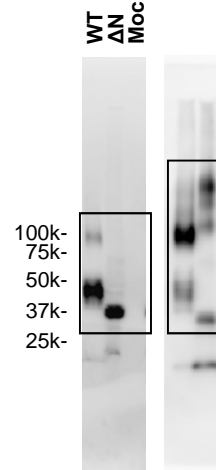


Fig. 5F

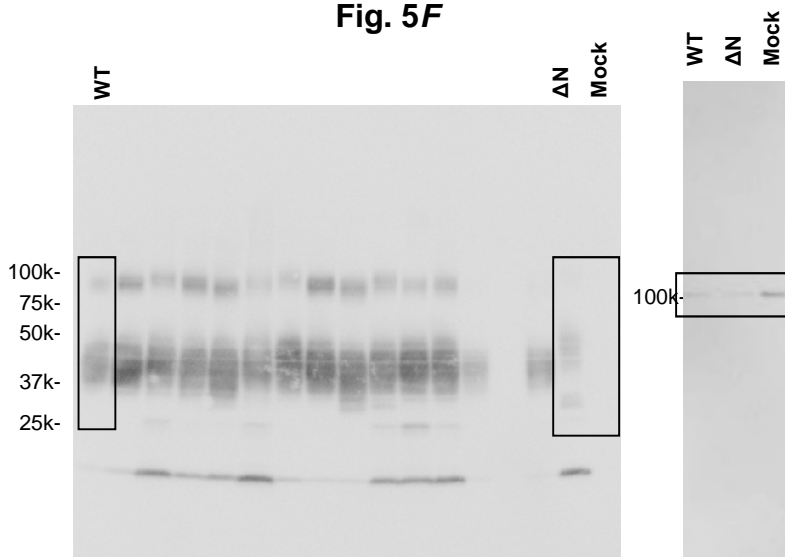


Fig. 6B

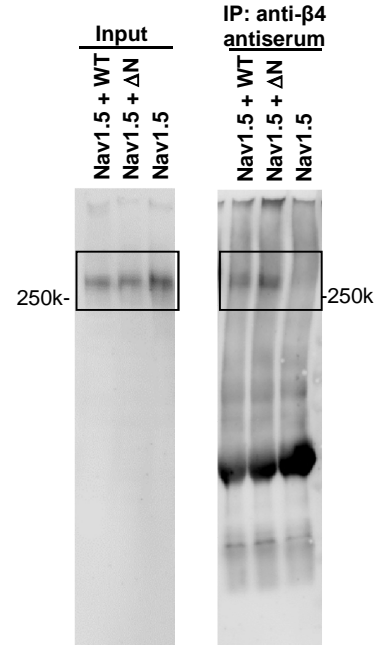


Fig. 6C



Supplemental Table S1

	Mouse β 4 cubic form	Human β 4 hexagonal form
Data collection		
Space group	<i>I</i> 23	<i>P</i> 32
Unit-cell parameters (\AA , $^\circ$)	131.5, 131.5, 131.5, 90, 90, 90	57.1, 57.1, 72.0, 90, 90, 120
Resolution (\AA)	100–2.9 (3.00–2.9)	100–2.1 (2.18–2.1)
R_{sym} (%)	8.6 (143.5)	7.3 (47.4)
$I/\sigma(I)$	31.4 (1.8)	32.5 (1.7)
Completeness (%)	99.6 (100)	97.4 (79.4)
Redundancy	7.9 (8.0)	6.4 (3.1)
CC _{1/2}	0.999 (0.545)	0.998 (0.846)
Refinement		
Resolution (\AA)	35.2–2.9 (3.08–2.9)	29.1–2.1 (2.17–2.1)
No. reflections	8526 (1267)	14834 (1045)
$R_{\text{work}}/R_{\text{free}}$ (%)	24.6/30.0 (34.6/39.2)	20.4/26.4 (24.5/34.9)
No. atoms		
Protein	1885	1765
Water	0	41
Ligand	6	95
B-factor (\AA^2)		
Protein	90.4	50.7
Water	-	53.6
Ligand	59.0	53.9
R.m.s. deviations		
Bond lengths (\AA)	0.005	0.007
Bond angles ($^\circ$)	0.978	0.964
Ramachandran plot		
Favored (%)	91.2	97.6
Outliers (%)	0.4	0

Values in parentheses are for the highest-resolution shell.