Supporting Material

Molecular basis for membrane interaction of β2e subunit of voltage-gated Ca^{2+} channels

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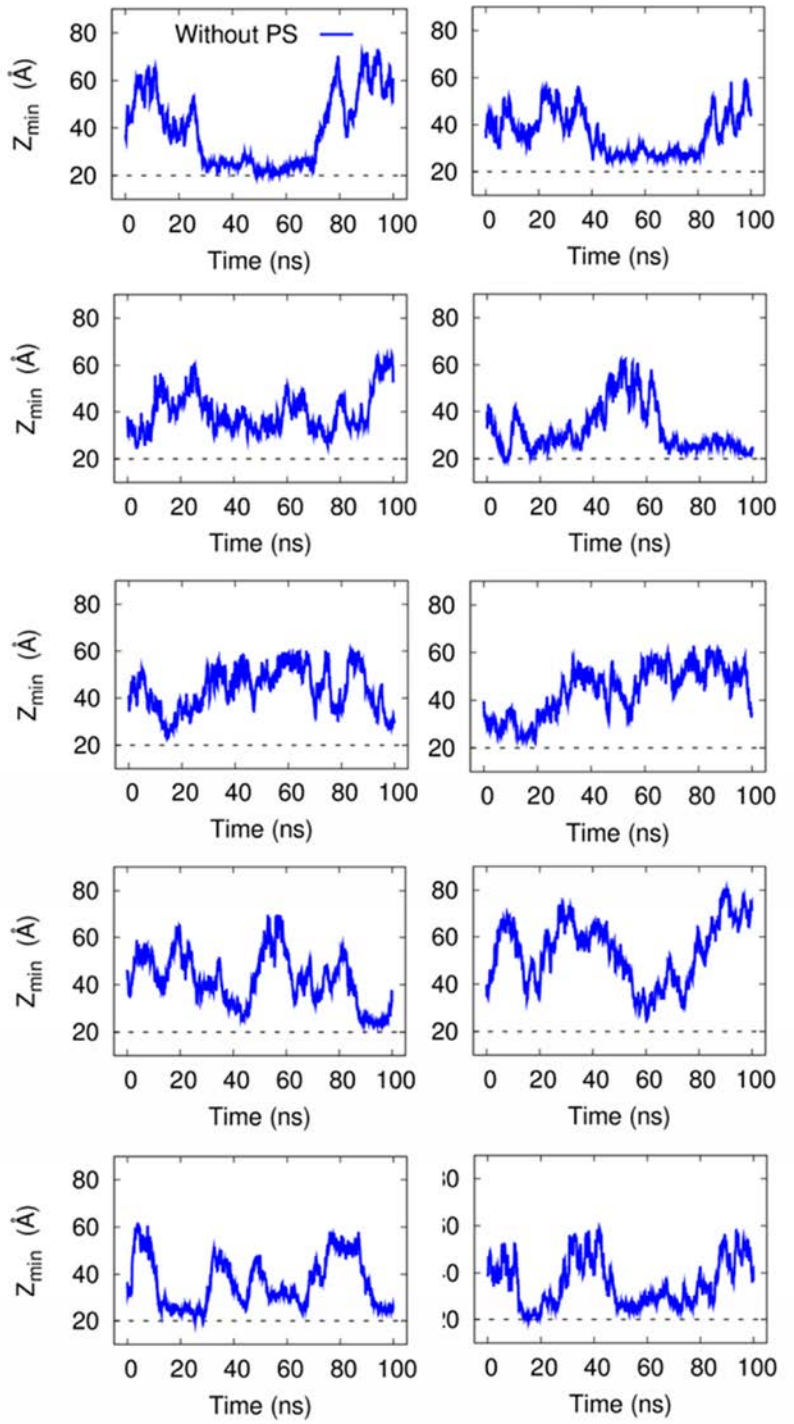
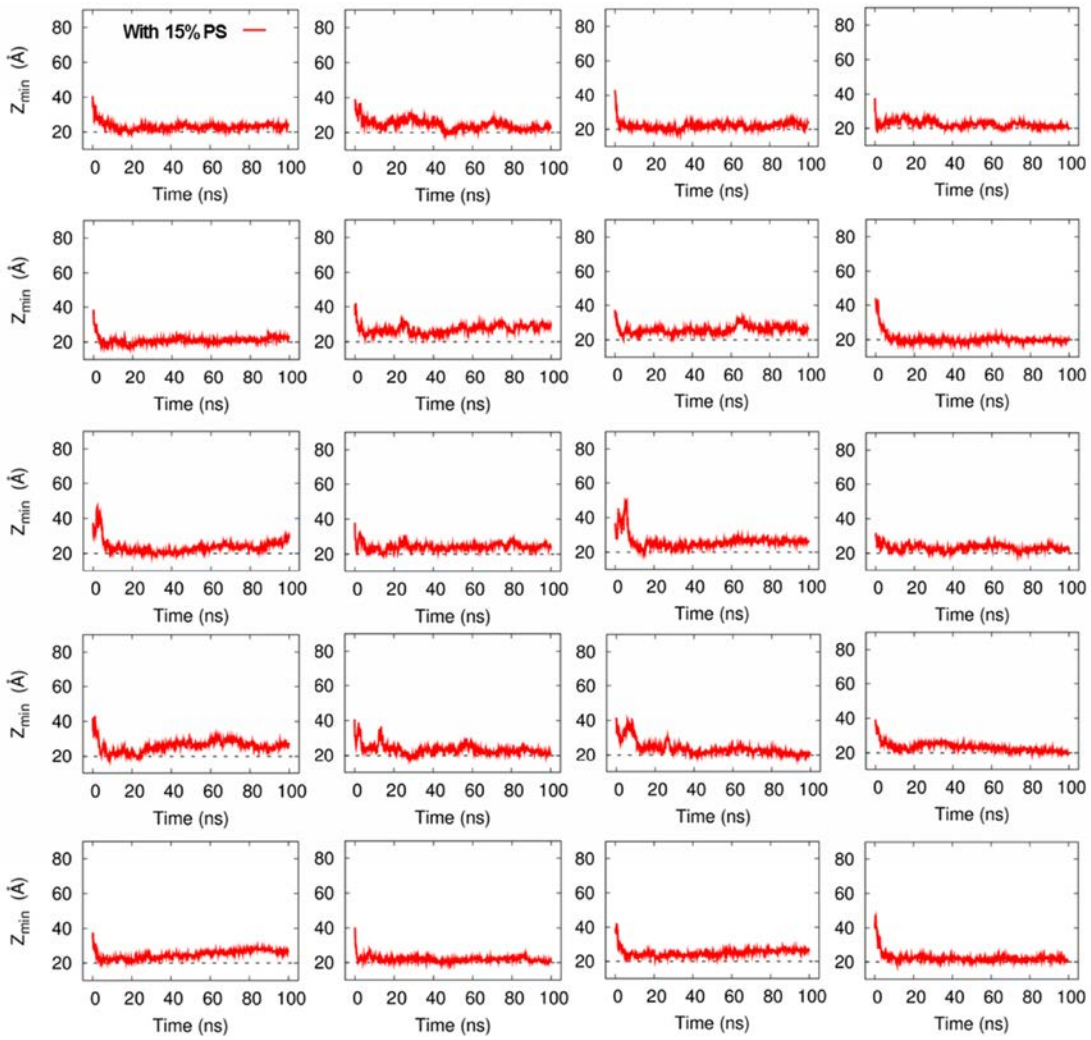
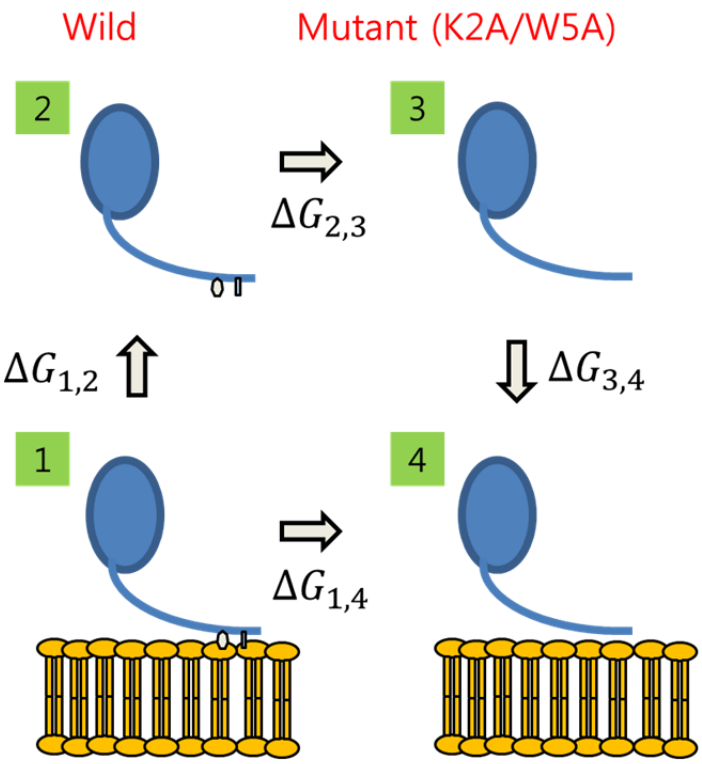

Without PS
Z_{min} (Å)
Time (ns)
80
60
40
20
0
20
40
60
80
100



Supplementary FIGURE 1 The time evolution of the minimum of the height coordinate Z_{min} from each of other a trajectories in ATMD (blue line) and CGMD (red line). The N-terminal fragment (1-23 amino acids) of b2e subunit comes down to touch and moves away from (approaches and binds to) the membrane with 0% (15%) PS in the membrane

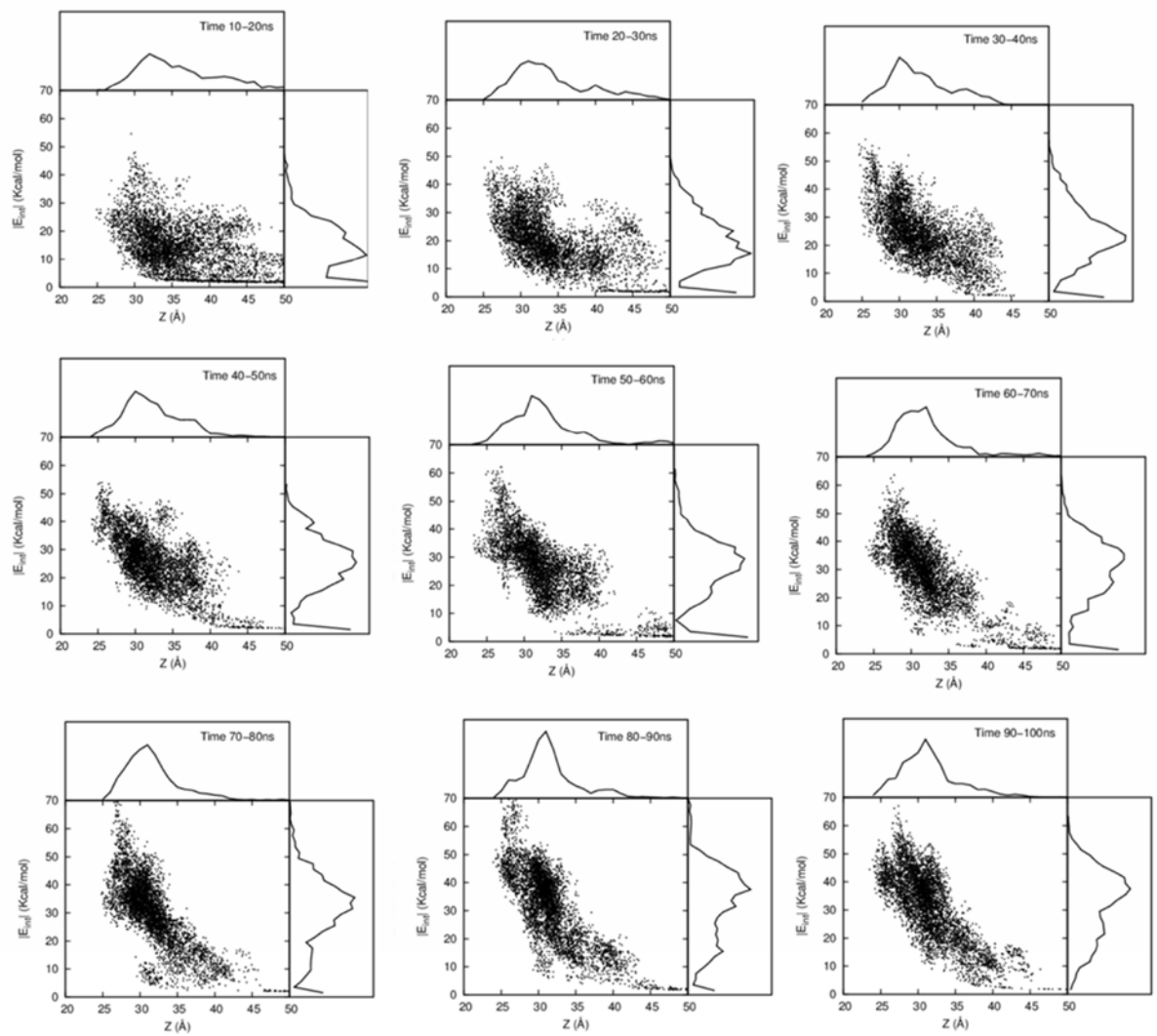


Thermodynamic cycle

$$\Delta G_{1,2} + \Delta G_{2,3} + \Delta G_{3,4} - \Delta G_{1,4} = 0$$

$$\Delta\Delta G = \Delta G_{3,4} - \Delta G_{2,1} = \Delta G_{1,4} - \Delta G_{2,3}$$

Supplementary FIGURE 2 Thermodynamic cycle in the process for a wild and a mutant protein binding to the membrane. The binding free energy could be evaluated by using the thermodynamic equality and the thermodynamic integration method. $\Delta G_{2,1}(\Delta G_{3,4})$ is the difference between the free energy of a wild (a mutant) protein which was bounded to the membrane lipid and that of a wild (a mutant) protein in the solution. $\Delta G_{2,3}(\Delta G_{1,4})$ is the difference between the free energy of a mutant protein in the solution (a bounded mutant to the membrane lipid) and that of a wild protein in the solution (a bounded wild protein to the membrane lipid). The thermodynamic equality $\Delta G_{1,2} + \Delta G_{2,3} + \Delta G_{3,4} - \Delta G_{1,4} = 0$ holds around a thermodynamic cycle, where $\Delta G_{1,2} = -\Delta G_{2,1}$. This gives the binding free energy of a mutant with respect to that of a wild protein, namely $\Delta\Delta G = \Delta G_{3,4} - \Delta G_{2,1} = \Delta G_{1,4} - \Delta G_{2,3}$.



Supplementary FIGURE 3 The correlation between the reaction coordinate Z and the magnitude of interaction energy $|E_{int}|$ based on 5,000 conformation of a β2e subunit (1-143) in 10 ns time window from 10 ns to 100 ns. The top (right) panel shows the distribution of the value of reaction coordinate Z (the interaction energy $|E_{int}|$). As the time advances, the region where these two distribution functions attain the maximum value moves from the region of high Z and low $|E_{int}|$ to the region of low Z and high $|E_{int}|$. At the short time scale the character of binding mode is the type II agglomerate binding and it changes to the type I stretched bind as the time advances. At the long time limit, the bind through the type I becomes dominant to give rise to the strong and stable binding.