A Candidate Ion-Retaining State in the Inward-Facing Conformation of Sodium/Galactose Symporter: Clues from Atomistic Simulations

Full Supporting Material

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Binding sites

During the 125 ns of MD simulation, the galactose remained stable in its binding site. We report the distances of the substrate from some of the residues important in keeping it in place through hydrogen bonds (values in Å): Gal(O2)-E88(CD) 4.7 (±0.9); Gal(O4)-N260(CG) 4.6 (±0.7); Gal(O5)-Q428(CD) 4.0 (±0.5); Gal(O4)-Y87(O) 3.6 (±0.6). Also the Y263, considered the intracellular gate,[1] stably interacts with N64, another galactose hydrogen-bonding residue

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(N64(ND)-Y263(OH) 3.1 ($\pm$0.2)).

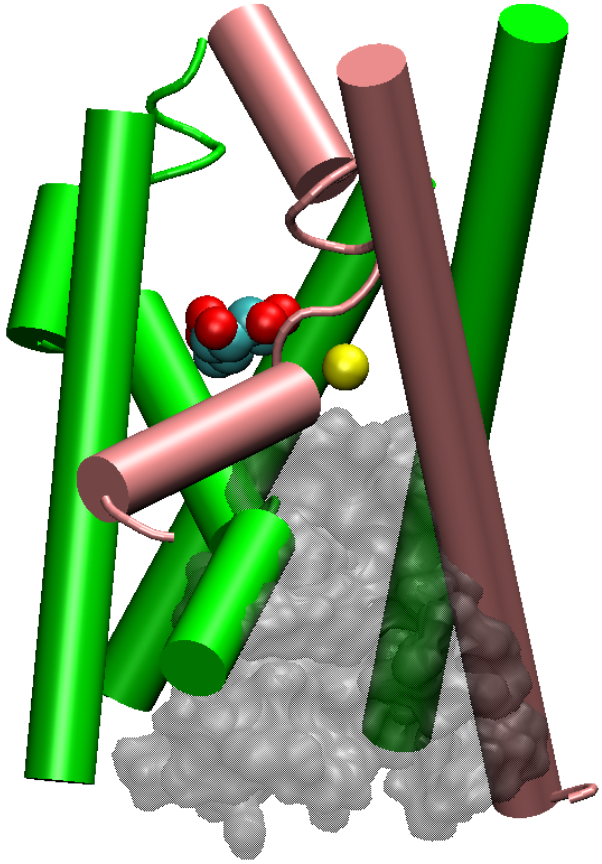

Figure 1: Part of the protein in cartoon, showing TM2 and TM9 helices forming sodium binding site, colored in pink. The ion is represented in yellow, while galactose in cyan and red. The hydrophilic cavity is shown in gray.

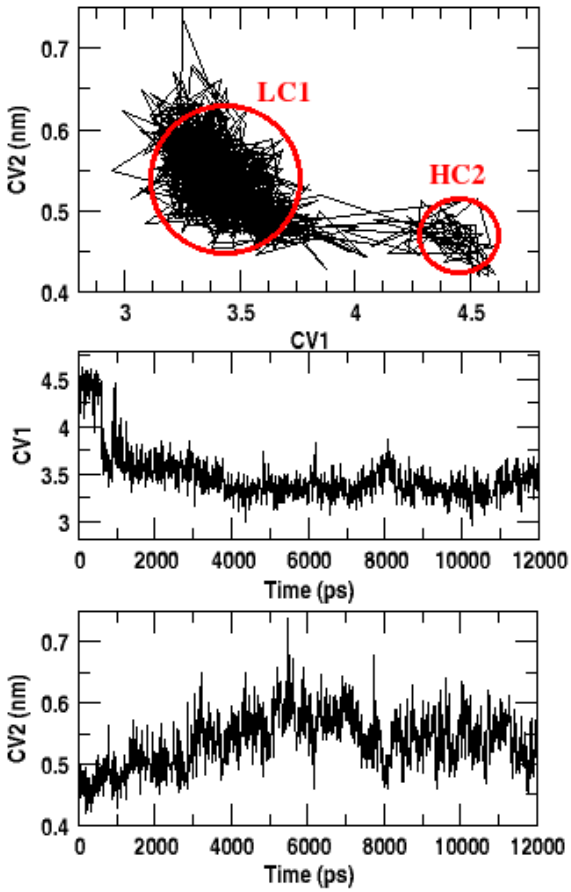

Figure 2: One of the 12 ns-long MD simulations started from HC2 site, reporting the values assumed by the two CVs (top), CV1 values as a function of time (center) and CV2 values as a function of time (bottom). After the first ns, sodium ion moves towards the LC1 site, remaining stably placed until the end of the run. On the top panel is visible that LC1 is a more populated state than HC2.

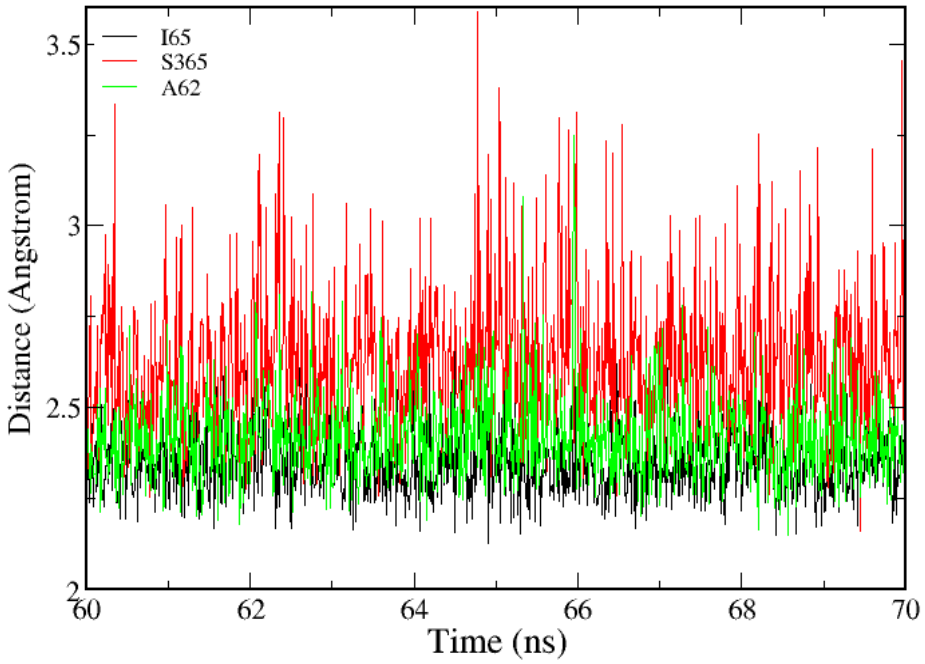

Figure 3: Distances (Å) between sodium ion and the oxygen of coordinating aminoacids (Oγ for serine, carbonyl oxygens for the other residues) in the last 10 ns of a 70 ns MD simulation.

References

(1) Faham, S.; Watanabe, A.; Besserer, G. M.; Cascio, D.; Specht, A.; Hirayama, B. A.; Wright, E. M.; Abramson, J. *Science* **2008**, *321*, 810–814.