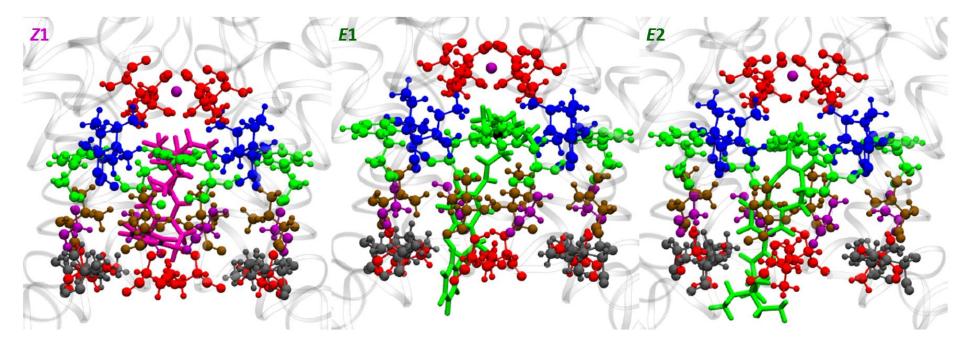
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Deciphering the Shape Selective Conformational Equilibrium of *E*- and *Z*-Locked Azobenzene-Tetraethyl Ammonium Ion in Regulating Photo-switchable K^+ -ion Channel Blocking

Rinsha Cholasseri^{*a*} and Susmita De^{*^{*b*}}

^{*a*}Theoretical and Computational Chemistry Laboratory, Department of Chemistry, National Institute of Technology Calicut, Kozhikode, Kerala, India - 673 601.

^bDepartment of Chemistry, University of Calicut, Calicut University P. O., Malappuram, Kerala, India - 673 635. E-mail: <u>susmita@uoc.ac.in</u>



The representative structures used for SAPT0 calculation are shown. The protein and LAB-TEA are represented as the ribbon and stick (*Z*: magenta and *E*: green), respectively, and the interacting residues THR-75 (red), ILE-100 (blue), PHE-103 (green), GLY-104 (purple), VAL-106 (ochre), THR-107 (red), and LEU-110 (grey) from the extracellular to intracellular region are shown as a ball and stick model.