Supporting Information

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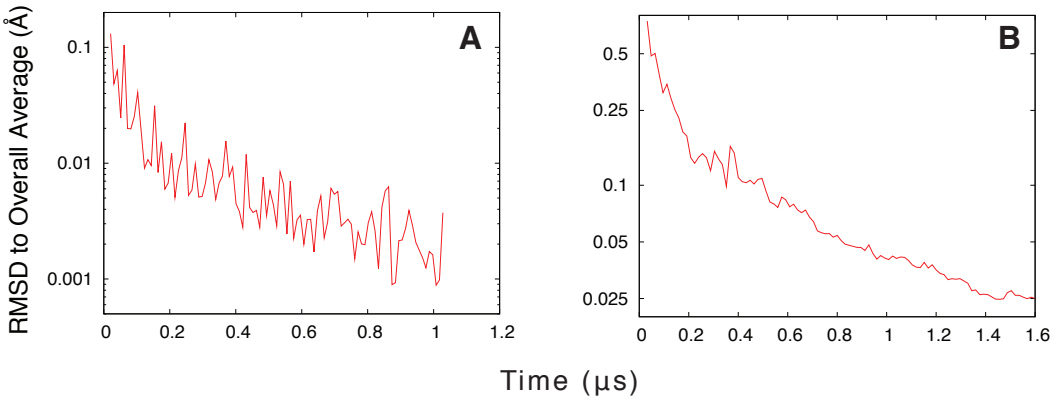

Figure SI1: The RMSD between successive running average structures for the dileucine simulation (panel A) and rhodopsin (panel B). This is the RMSD between the average structure for $t = 0$ to $t = i$ and the average structure for $t = 0$ to $t = i + 1$. All non-hydrogen atoms were used for the dileucine RMSD while only transmembrane α-carbons were used for the rhodopsin RMSD.

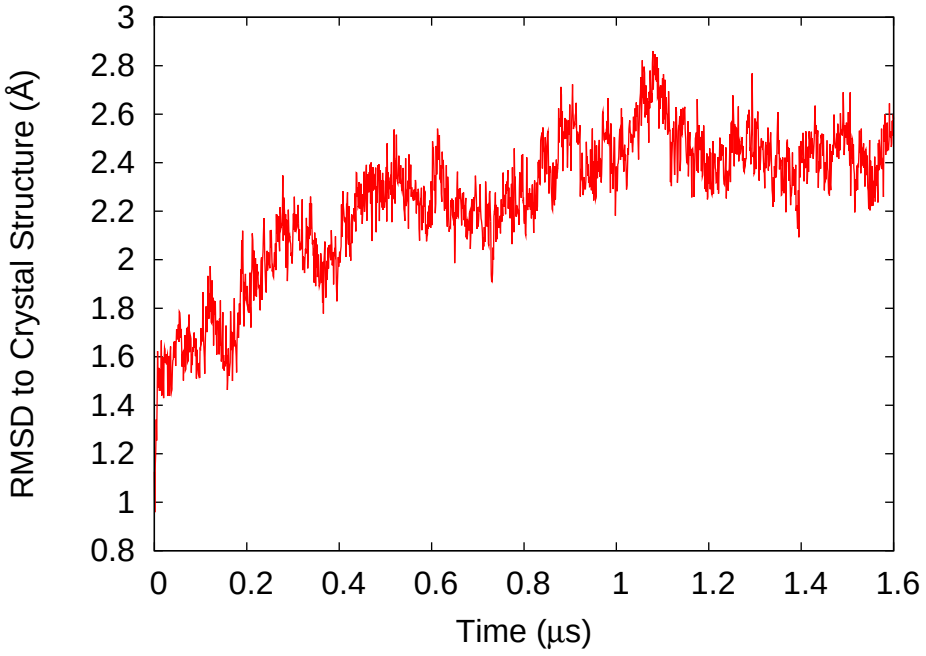

Figure SI2: The RMSD between each frame of the rhodopsin trajectory and the starting crystal structure using only transmembrane α-carbons.

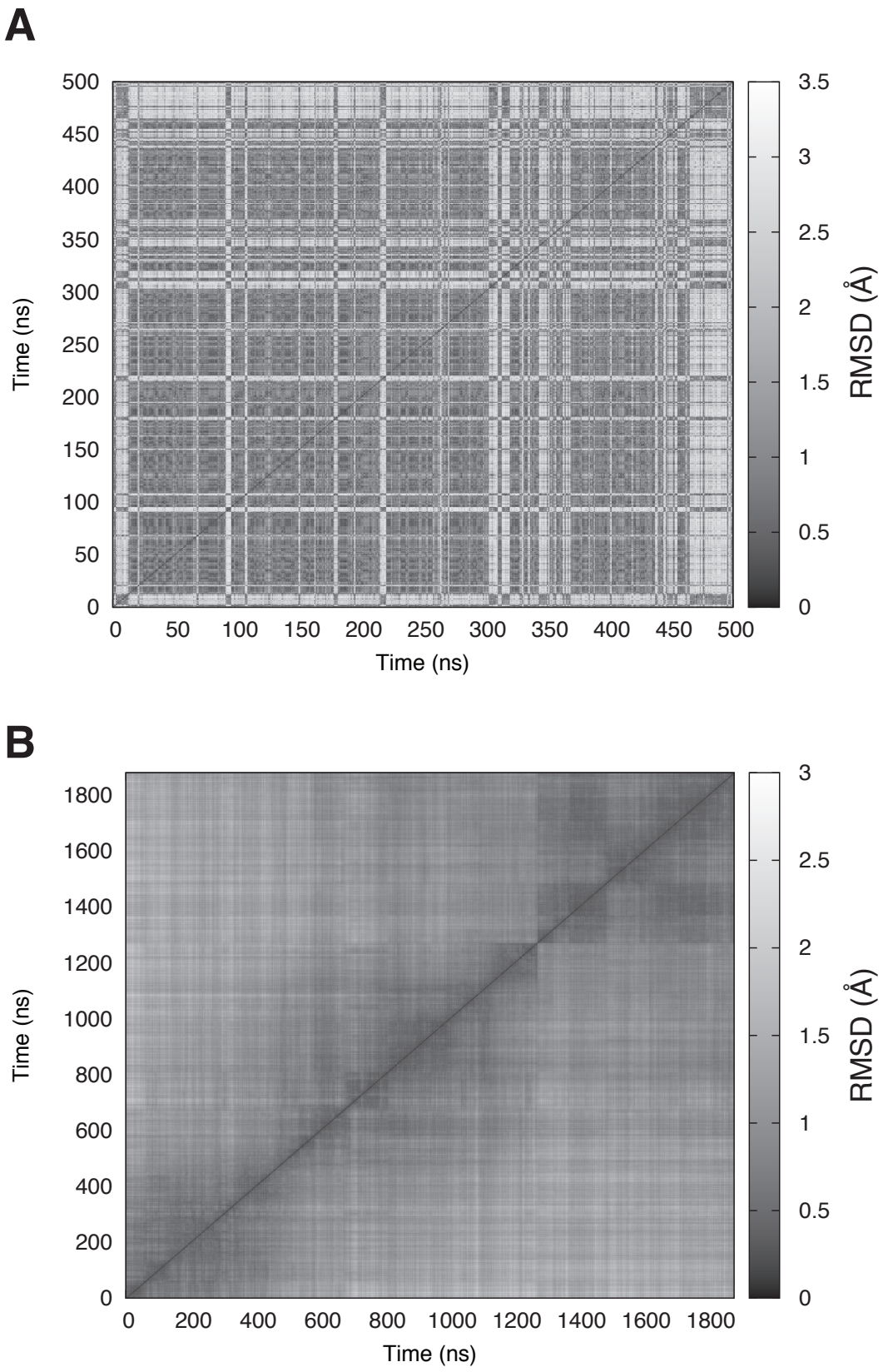

Figure SI3: All-to-all RMSD for the dileucine simulation (panel A) and CB2 (panel B). All non-hydrogen atoms are used for the dileucine RMSD and only transmembrane α-carbons are used for the CB2 RMSD.