

Dynamics of Membrane-Bound G12V-KRAS from Simulations and Single-Molecule FRET in Native Nanodiscs

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In Materials and Methods, the last sentence under the sub-heading MD Simulation should read:

The trajectory was analyzed primarily based on the distance between $C\alpha$ atoms of residues 132 and 183 (ζ) and the angle between a vector from residue 5 to residue 9 $C\alpha$ atoms and the membrane normal (Θ) (see Supporting Materials and Methods for details).

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