Computational Modeling of Mg^{2+} Binding in the Active Site of Protein Farnesyltransferase

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Figure S1

Comparison of FPP^{3-} orientation found in WT2 MD simulation and from previous FTase/FPP^{3-} (without Mg^{2+}) MD simulation.

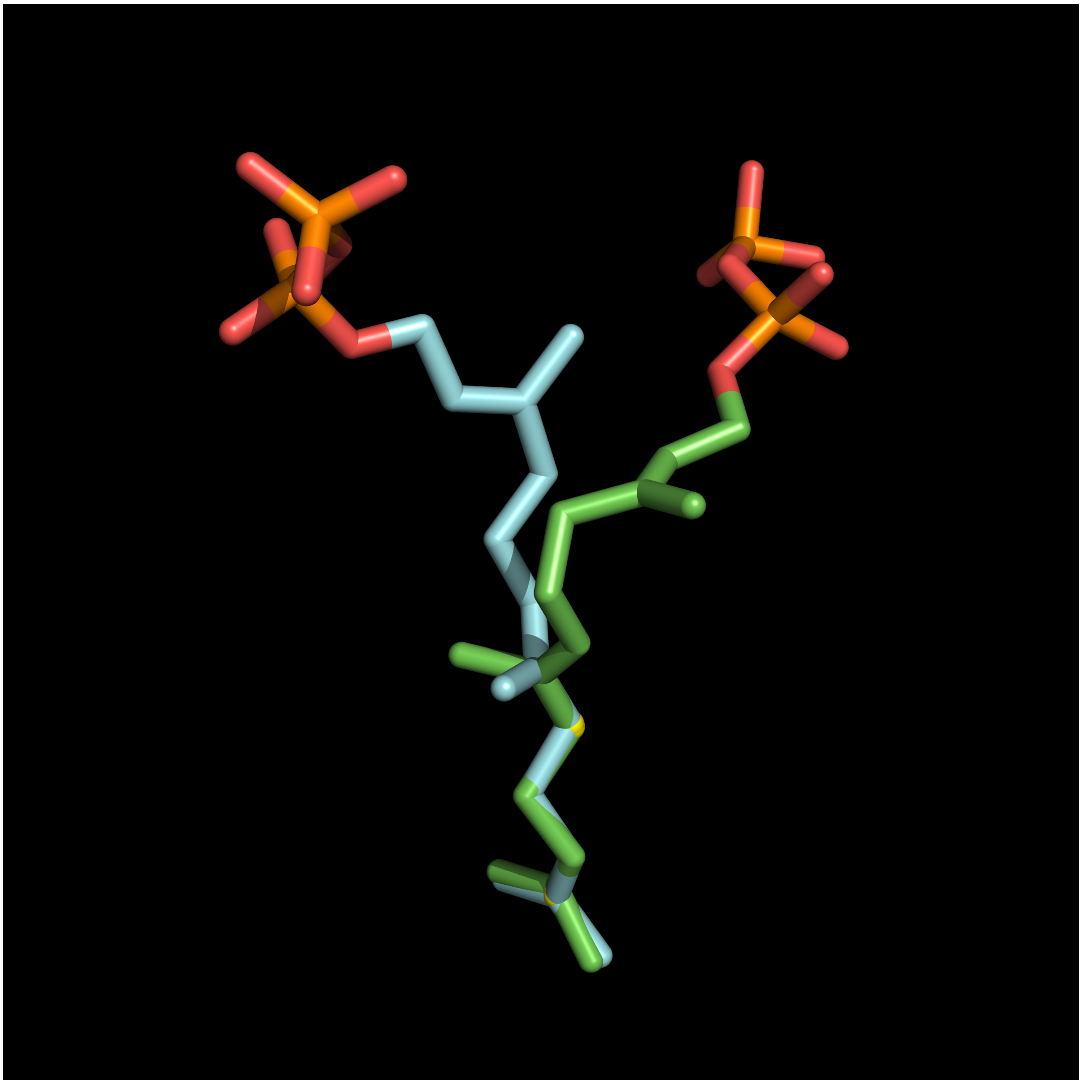

Figure S2

Distribution map of d_{RC} from WT2 MD simulations, in support to an intermediate state existing at ~5Å.