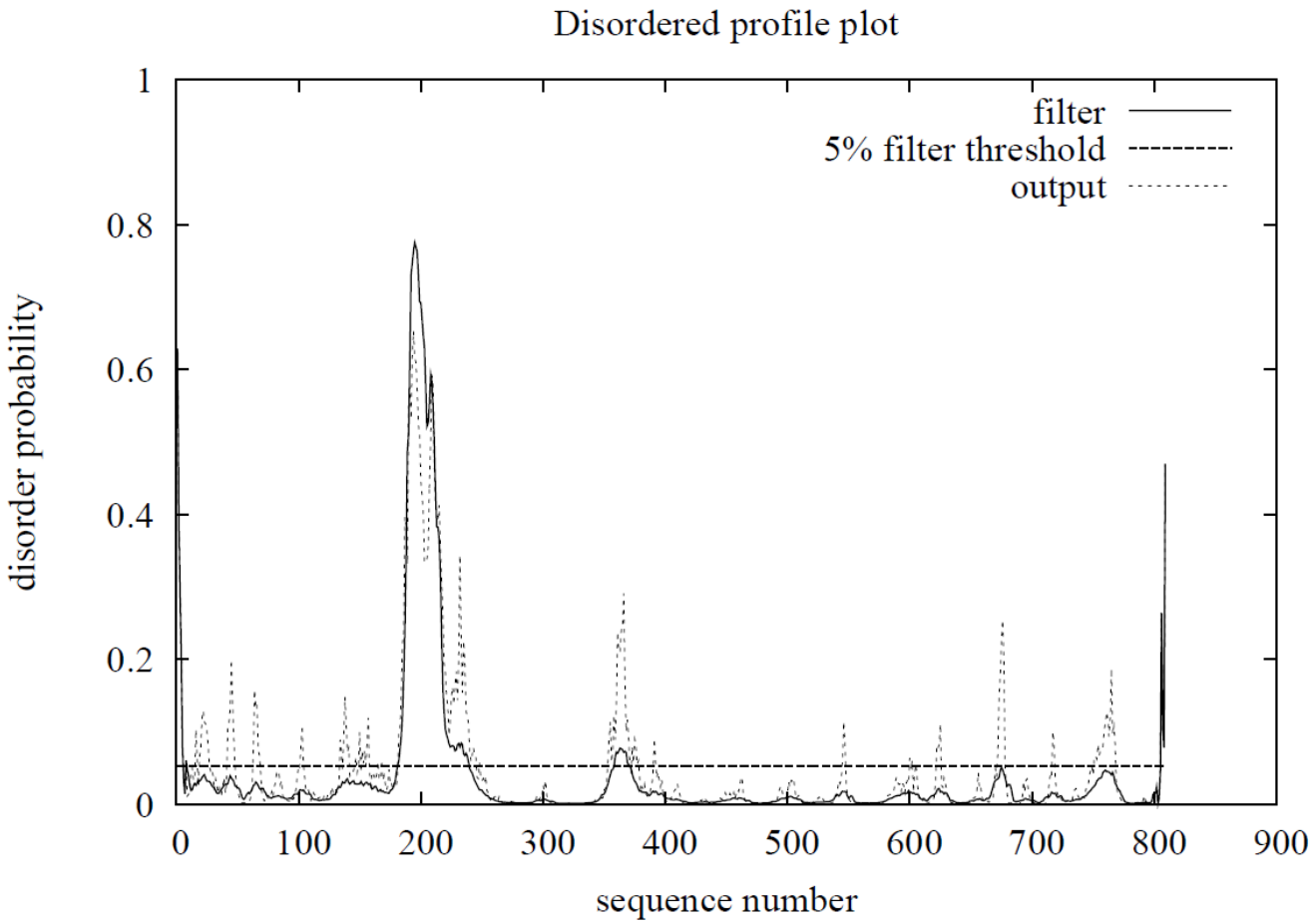

Figure S1. Disorder Prediction Analysis of the Primary Sequence of Gln4. The probability of disorder is shown on the y-axis and the residue number is shown on the x-axis. The linker connecting the N-terminal and C-terminal domains extends from residue 188 to 214. Disorder probability was calculated using DISOPRED2.

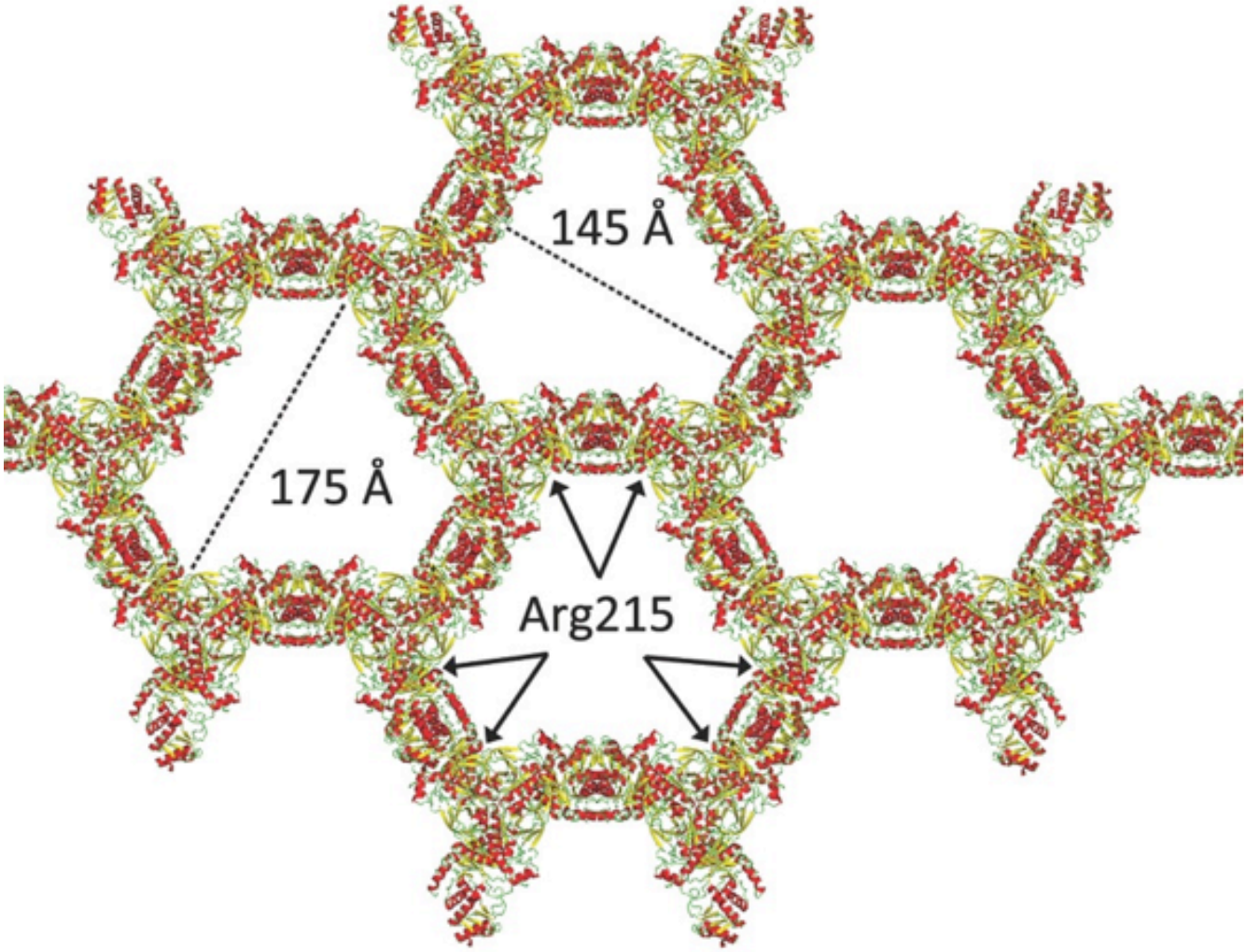

Figure S2. Crystallographic Packing Arrangement of Gln4. Shown oriented with the z-axis perpendicular to the page. Minimum and maximum diameters of solvent channels are labeled with dashed lines. Arg215 is labeled.

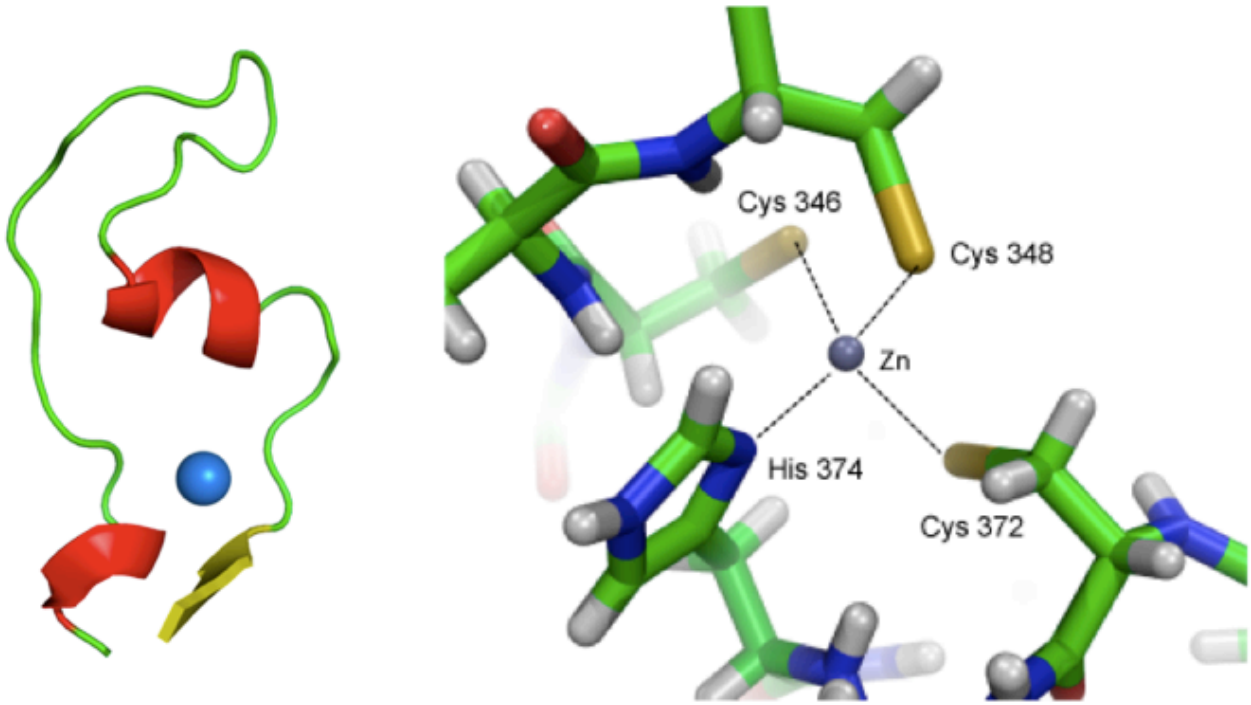

Figure S3. Zinc Finger Motif in Gln4. Left: Zinc ion shown as a blue sphere. Right: Zinc finger motif residues shown coordinating zinc ion.

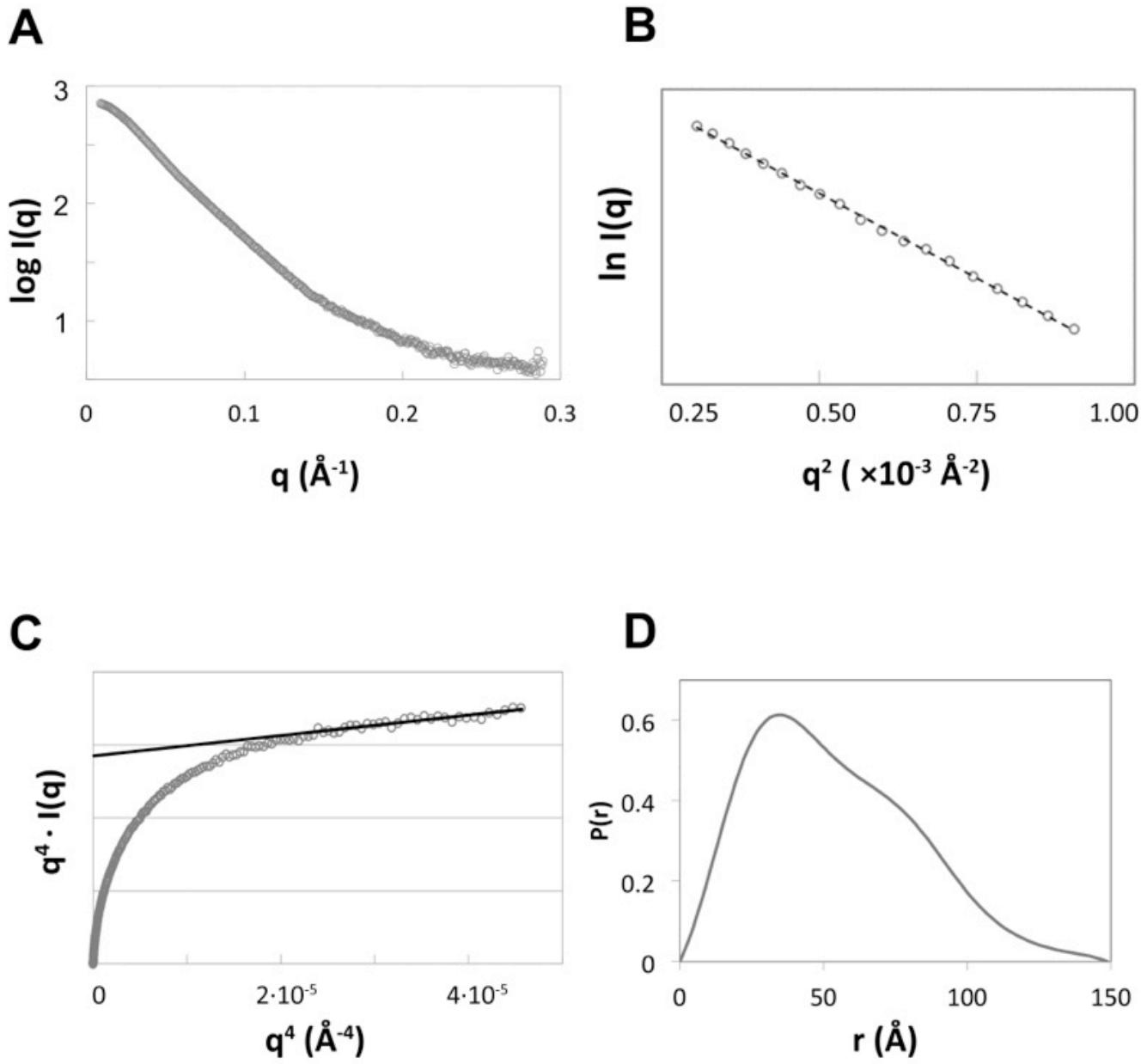

Figure S4. SAXS data of full-length Gln4. A. The log of the scattering intensity plotted as a function of momentum transfer (q). B. Guinier plot. The dashed line shows linearity in the Guinier region, indicating monodispersity of the particles in solution[21]. C. Porod-Debye plot with linear fit shown in Porod region. For a globular protein, the slope of this line will approach zero[22]. Flexible proteins will show positive slopes. D. Pair distribution function. The left-skewed distribution demonstrates an elongated particle shape.

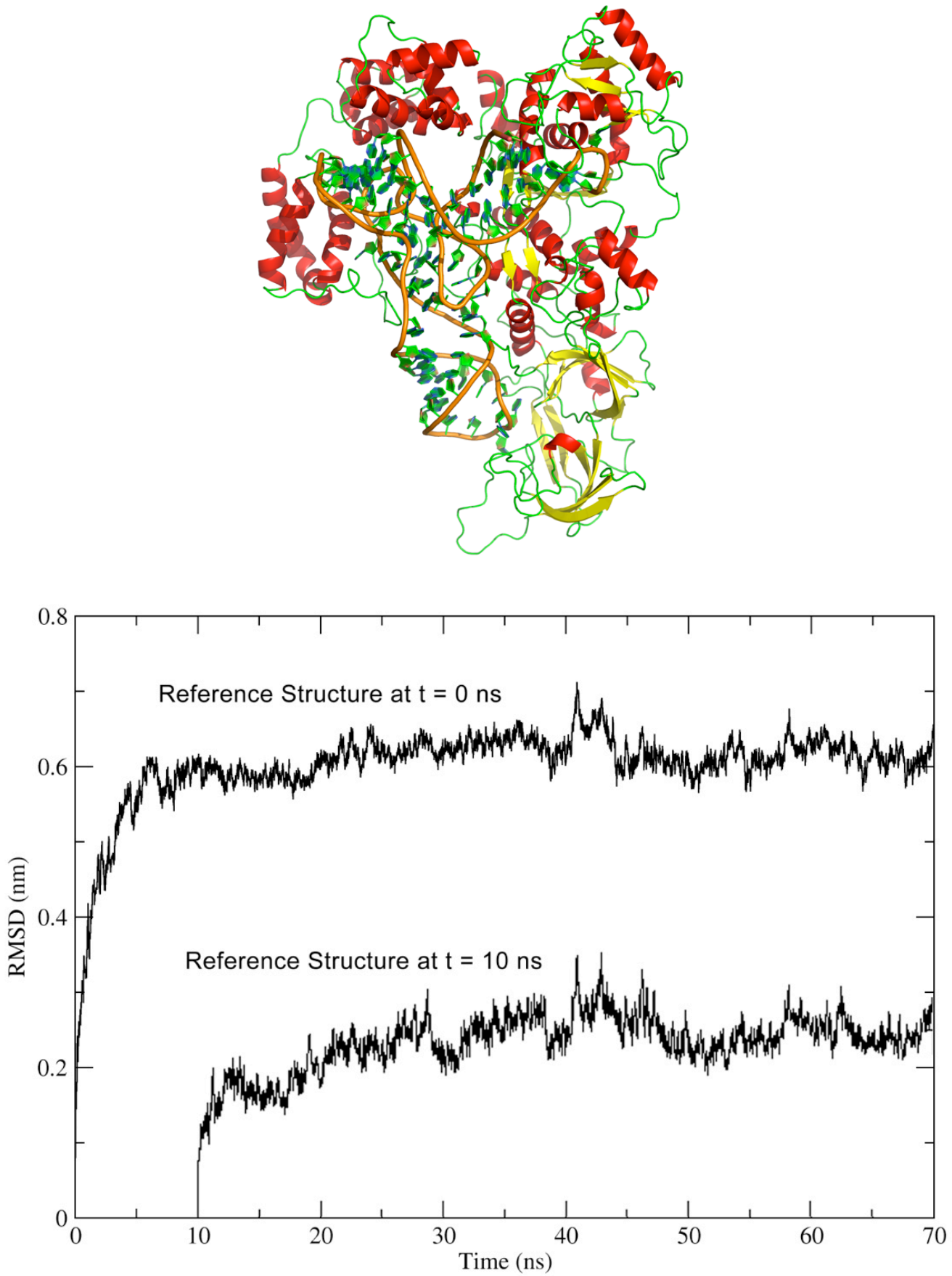

Figure S5. Molecular Dynamics Simulation of Gln4 bound to tRNA^{gln}. Top: Gln4 bound to tRNA^{gln} after 70 nanoseconds of molecular dynamics simulation colored according to secondary structure. Bottom: Plot of backbone RMSD of molecular dynamics trajectory as a function of time fit to structure at time t=0 ns and t=10 ns.