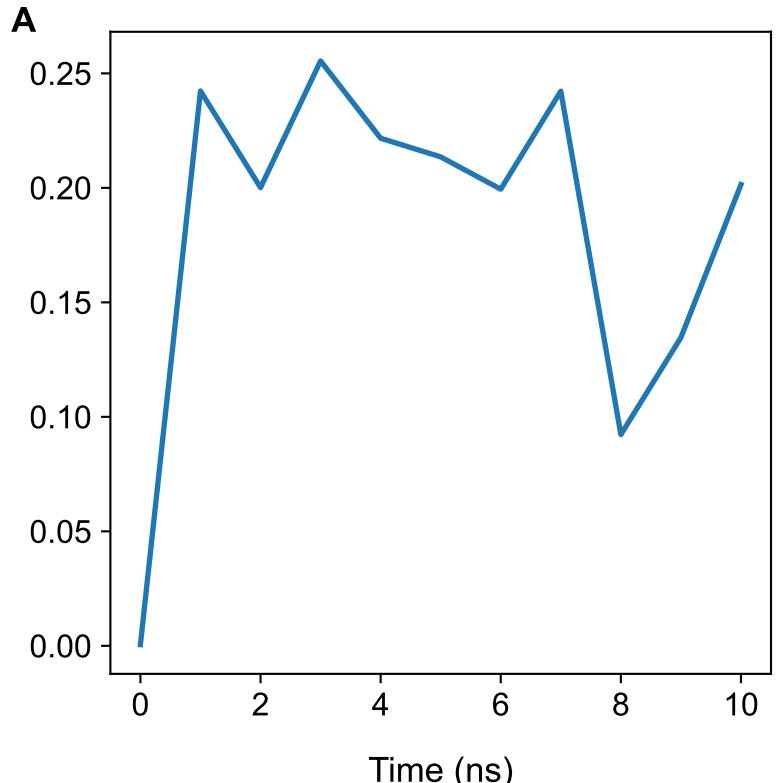
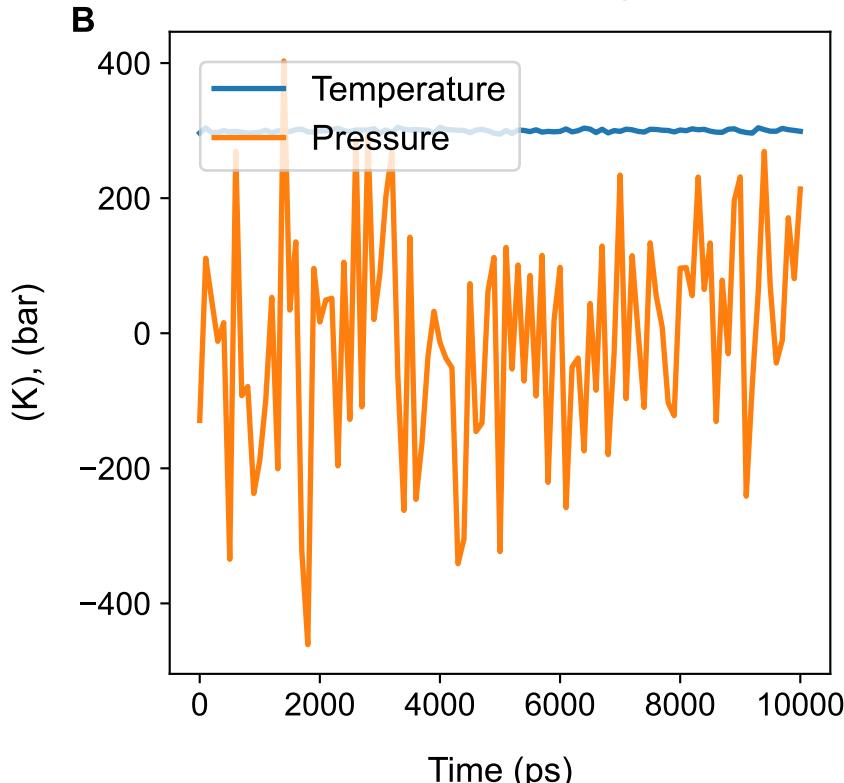


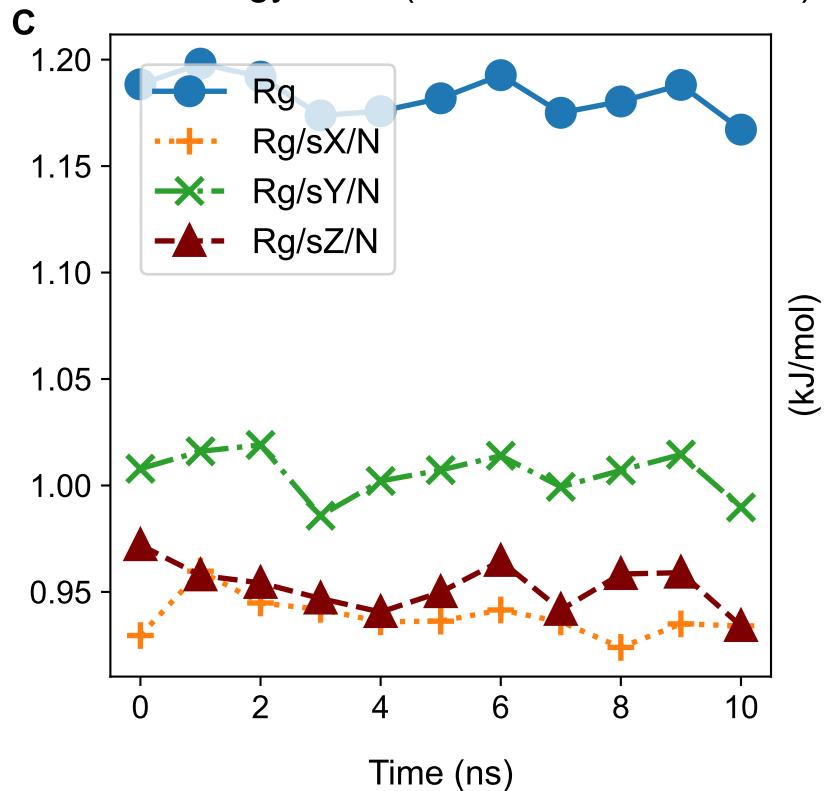
RMSD C-alpha after Isq fit to Protein



GROMACS Energies



Radius of gyration (total and around axes)



GROMACS Energies

