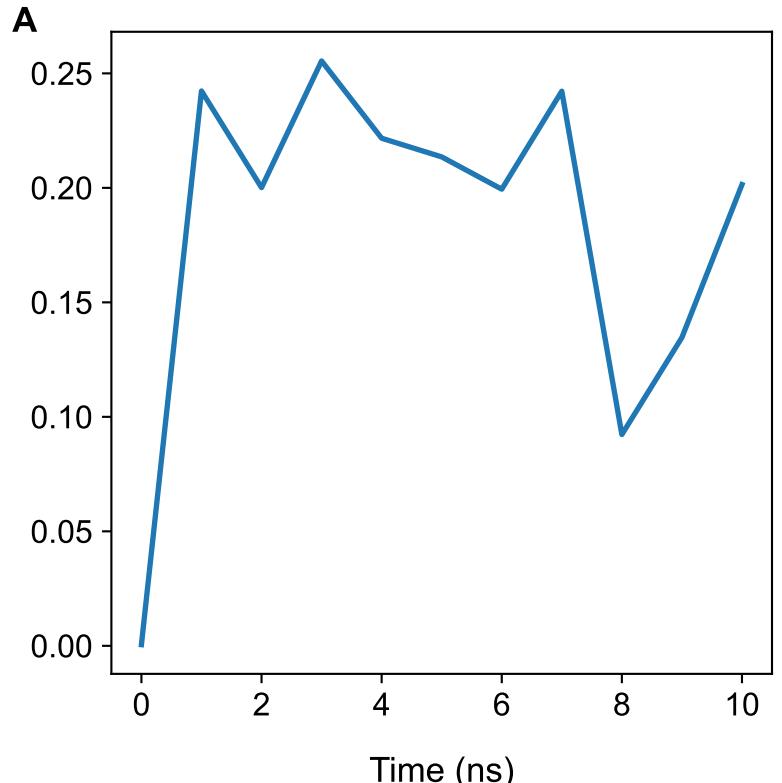
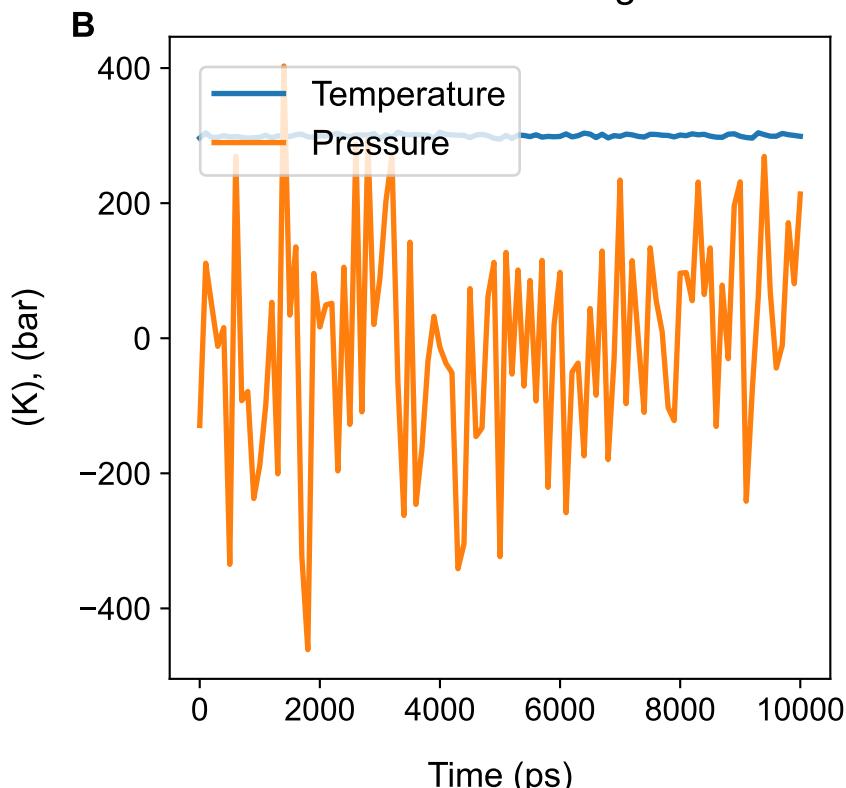


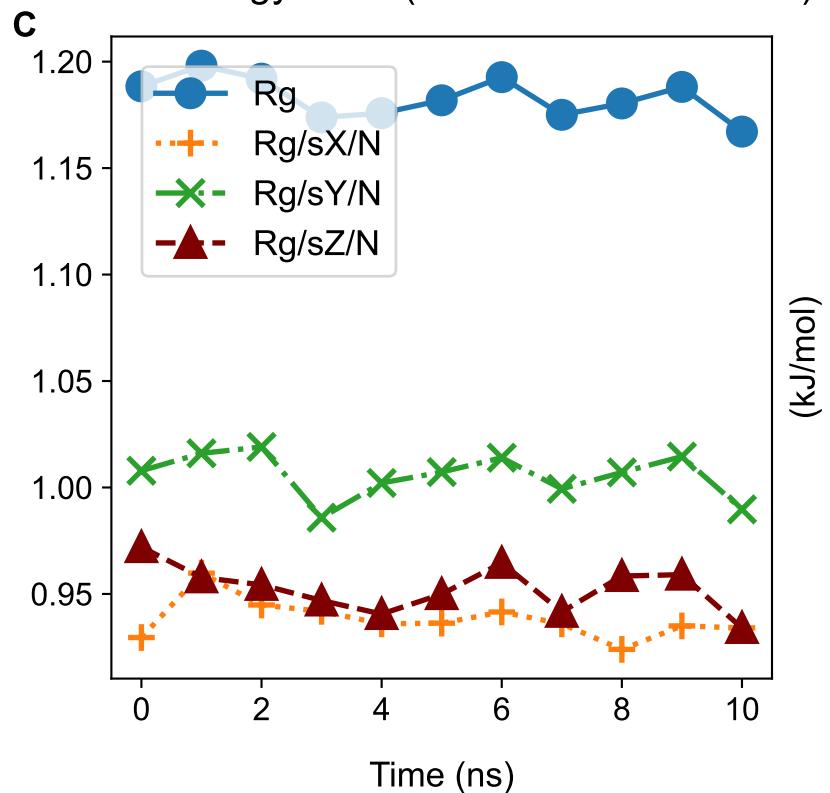
RMSD
C-alpha after lsq fit to Protein



GROMACS Energies



Radius of gyration (total and around axes)



GROMACS Energies

