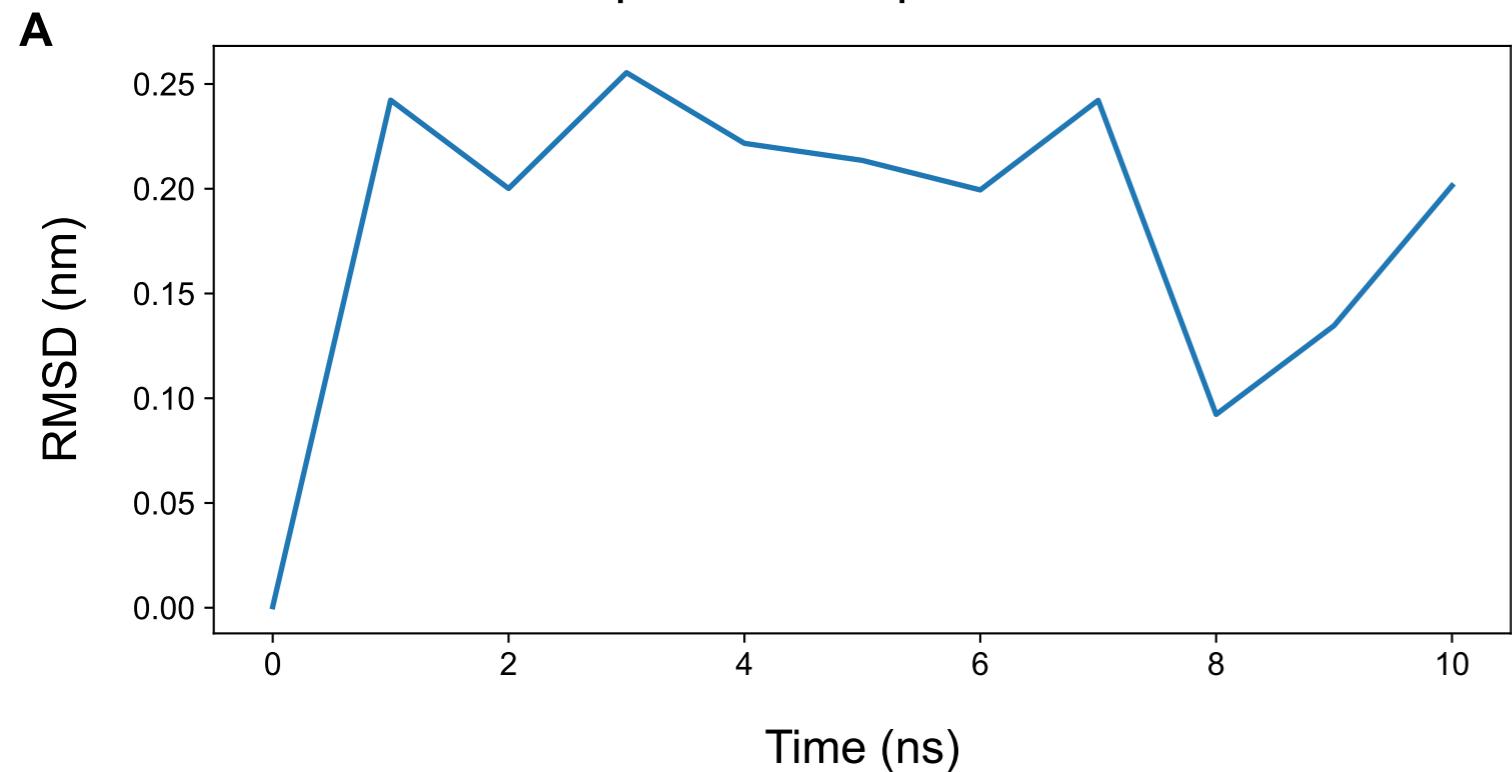
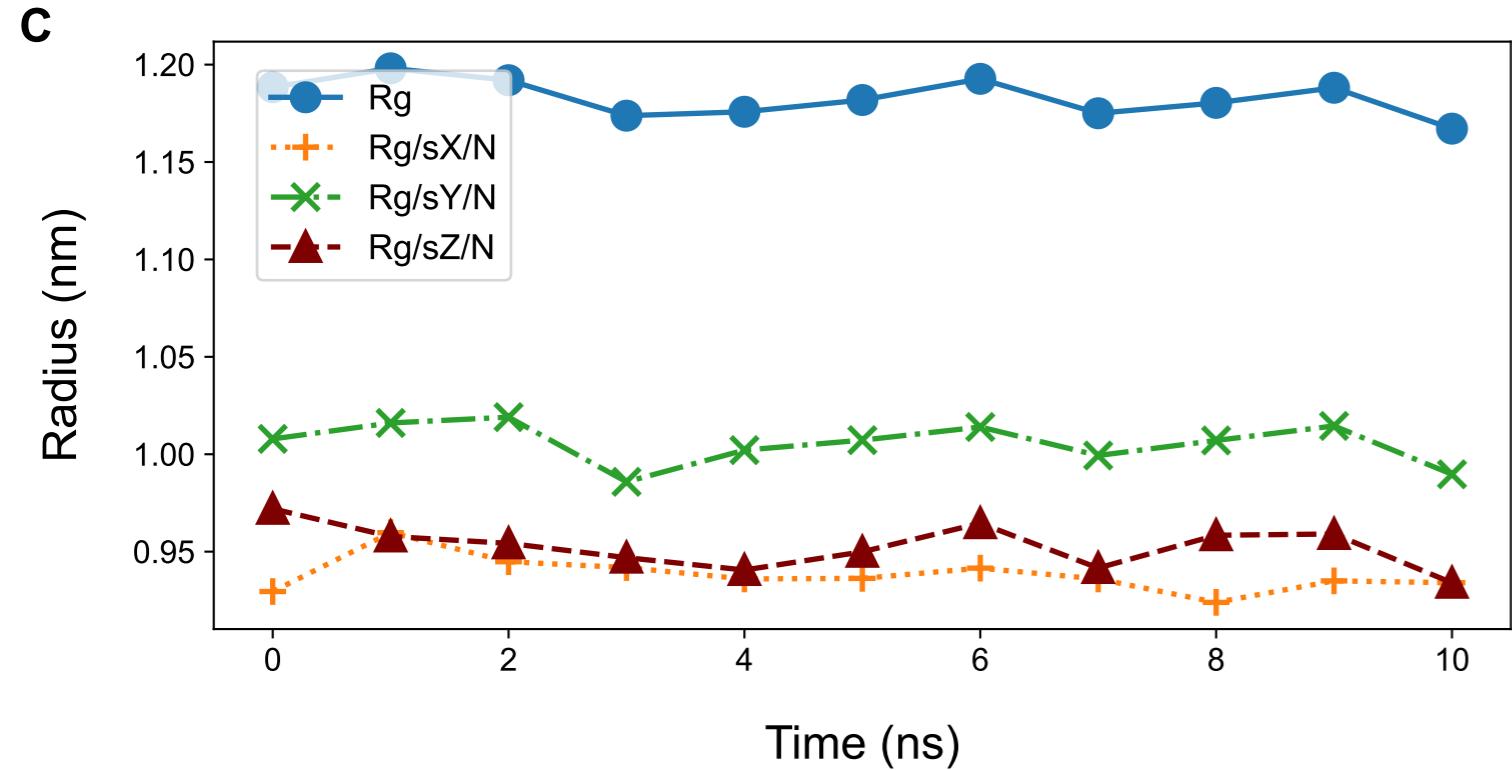


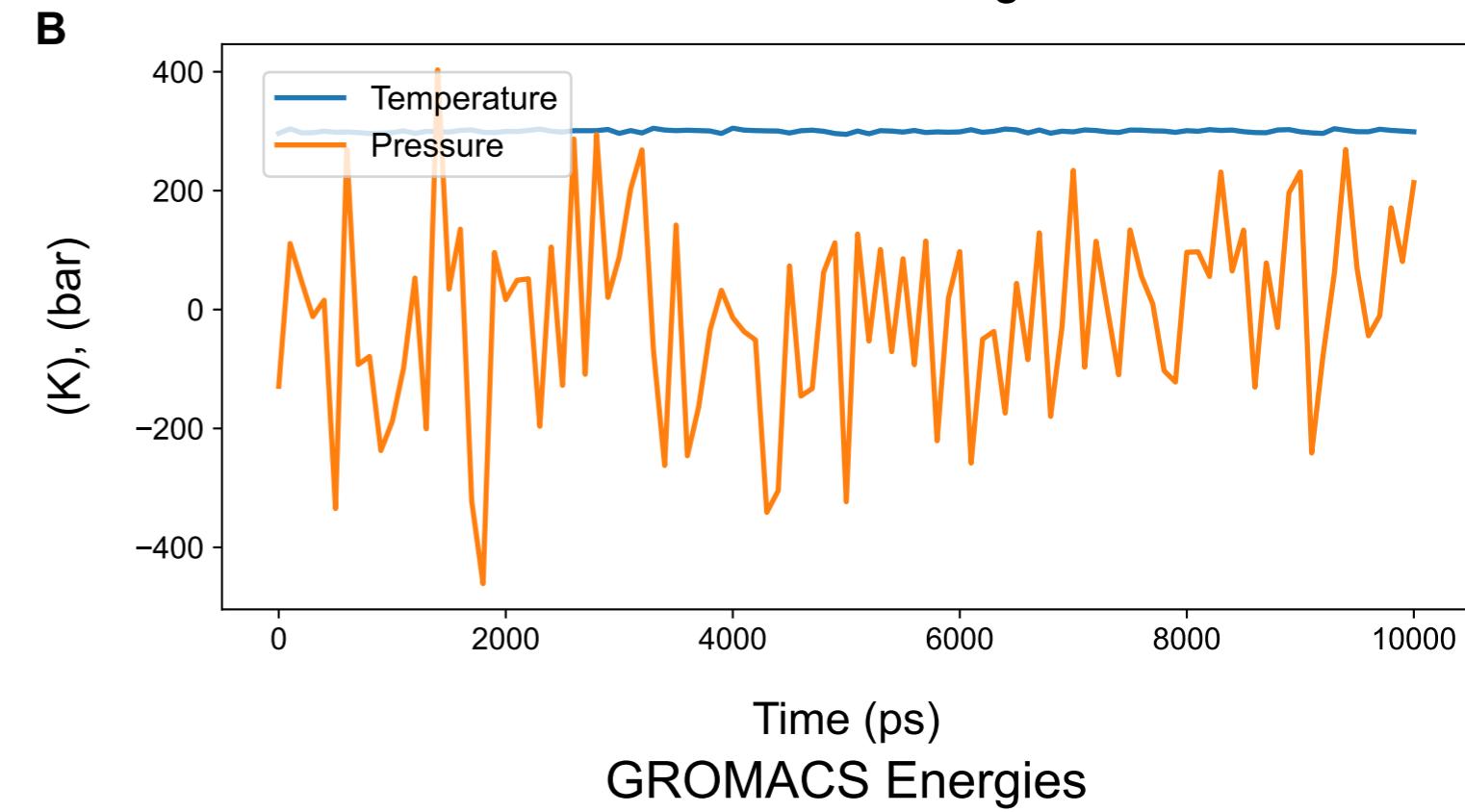
RMSD C-alpha after lsq fit to Protein



Radius of gyration (total and around axes)



GROMACS Energies



GROMACS Energies

