Molecular Dynamics Protocol

File Structure and Trajectory Processing

The initial trajectory structure is in .dcd and the topology file in .parm format, and we utilized the CPPTRAJ program for its conversion to .pdb format.

Sampling Rate

We employed the 'skip 1 last 15' skipping technique, which processes the trajectory from the first to the last frame by skipping every 15 frames. This method effectively reduces the trajectory's size, by frames like 1, 15, 30, 45, etc., all aligned with the initial frame. From the sampled MD trajectory, we generate distance maps that serve as the main geometric descriptors of the structure throughout the simulation.

Frame Generation Process

We utilized Namd software for dynamic calculations to generate .dcd trajectories that depict the temporal evolution of atomic conformations. Subsequently, CPPTRAJ was employed to align and calculate RMSD or RMSF, focusing on changes relative to the first frame.

System Labeling

The systems are labeled according to established literature.

Mutation Insertion

The crystallographic structure of the wild-type SARS-CoV-2 Spike protein was obtained from the Protein Data Bank (PDB ID: 6m0j). Residues 333-527, which correspond to the RBD of the Spike protein, were selected manually using the PyMOL graphics software (The PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC). We then comparatively modeled a total of 37 RBD mutants monitored by the WHO, with the wild-type structure being used as a template, using the SWISS-MODEL to model the mutated protein.