Supporting Information

Elucidating biophysical basis of binding of inhibitors to SARS-CoV-2 main protease by using molecular dynamics simulations and free energy calculations

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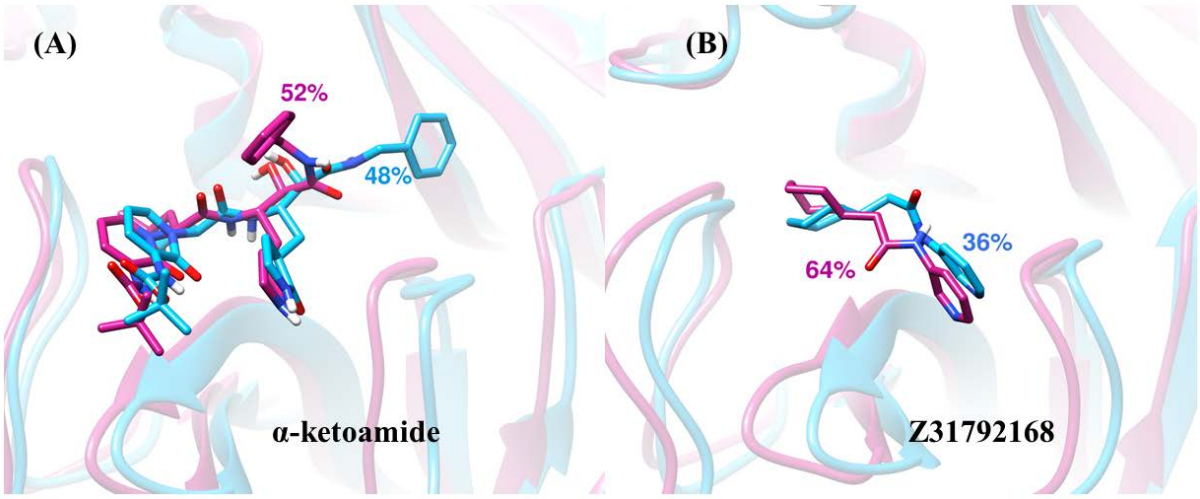

Figure S1: Orientation of the dominant conformation of inhibitors (A) α-ketoamide and (B) Z31792168 obtained from the K-means clustering analysis.

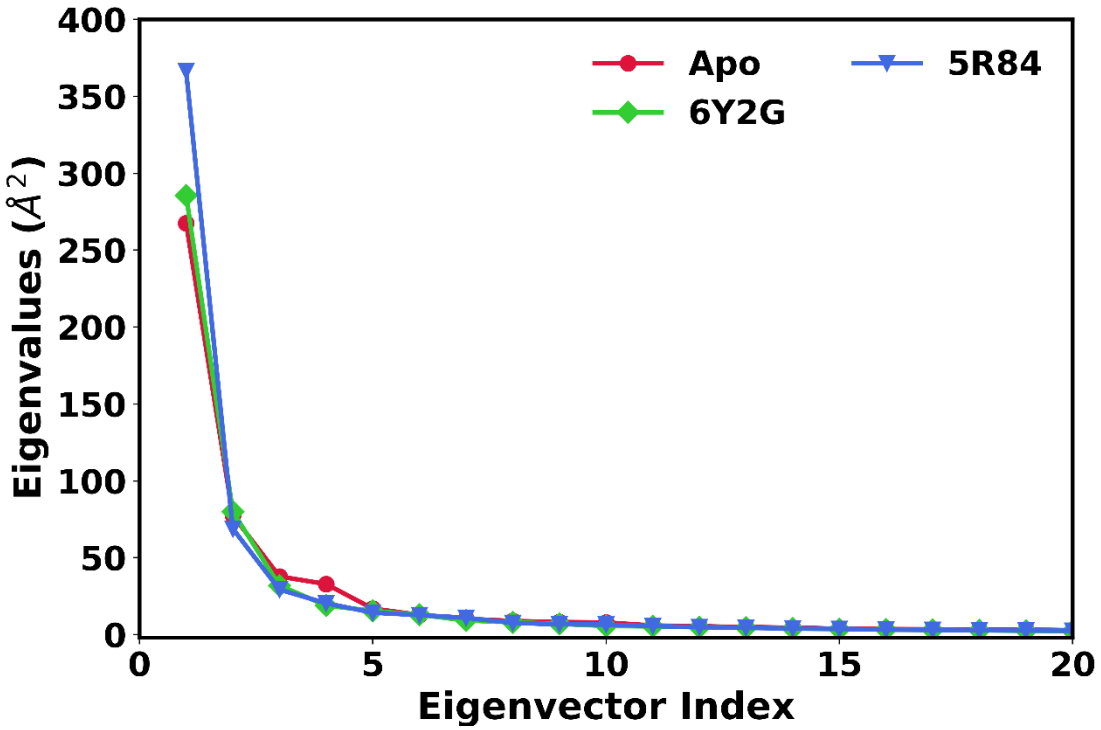

Figure S2: Comparison of the eigenvalues plotted against the corresponding eigenvector indices for apo (red), $3CL^{pro}$/α-ketoamide (green), and $3CL^{pro}$/Z31792168 (blue).

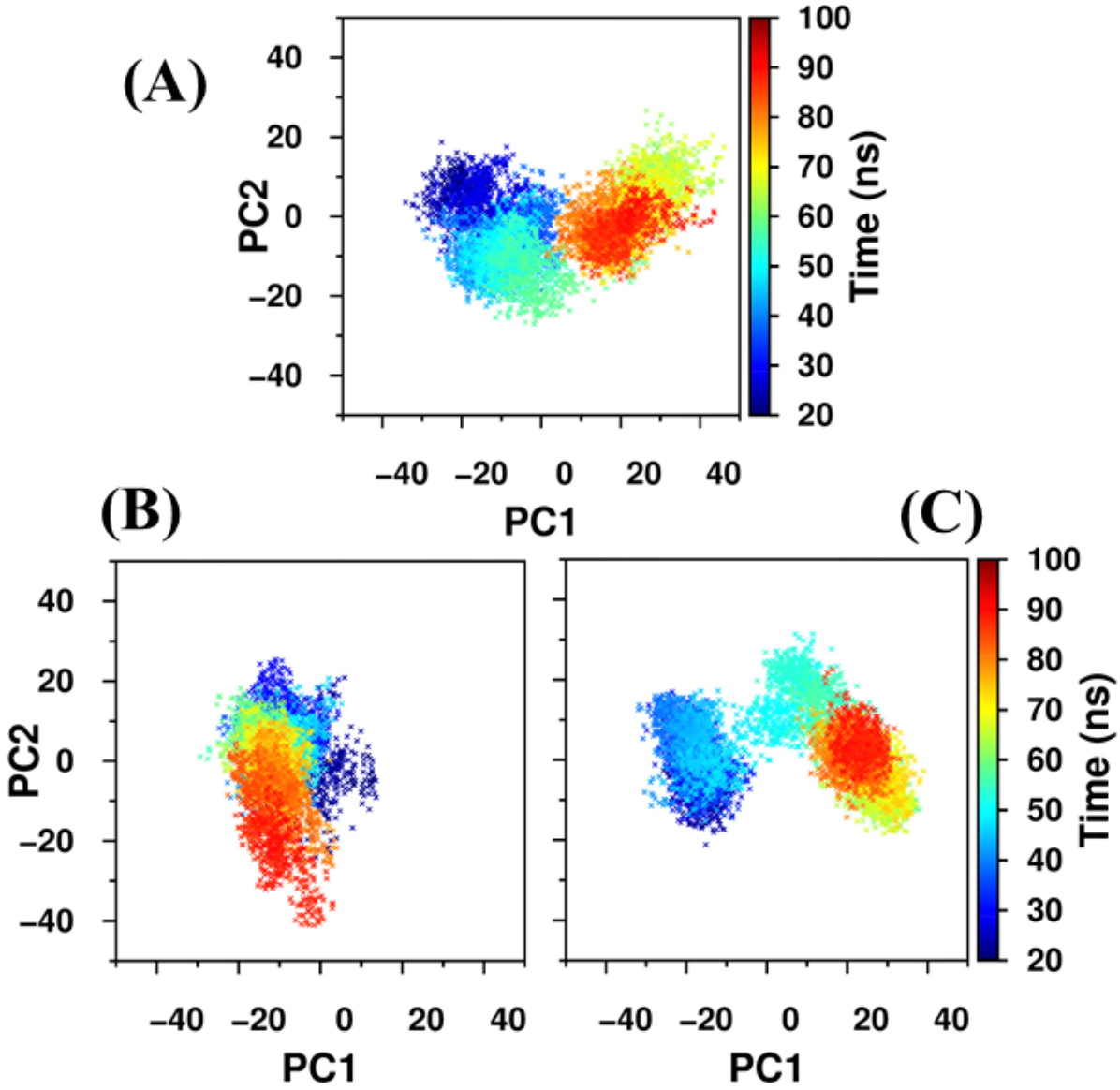

Figure S3: The maps of PC1 and PC2 during MD simulation of (A) apo, (B) $3CL^{pro}$/α-ketoamide, and (C) $3CL^{pro}$/Z31792168. Colour codes represent the simulation time.

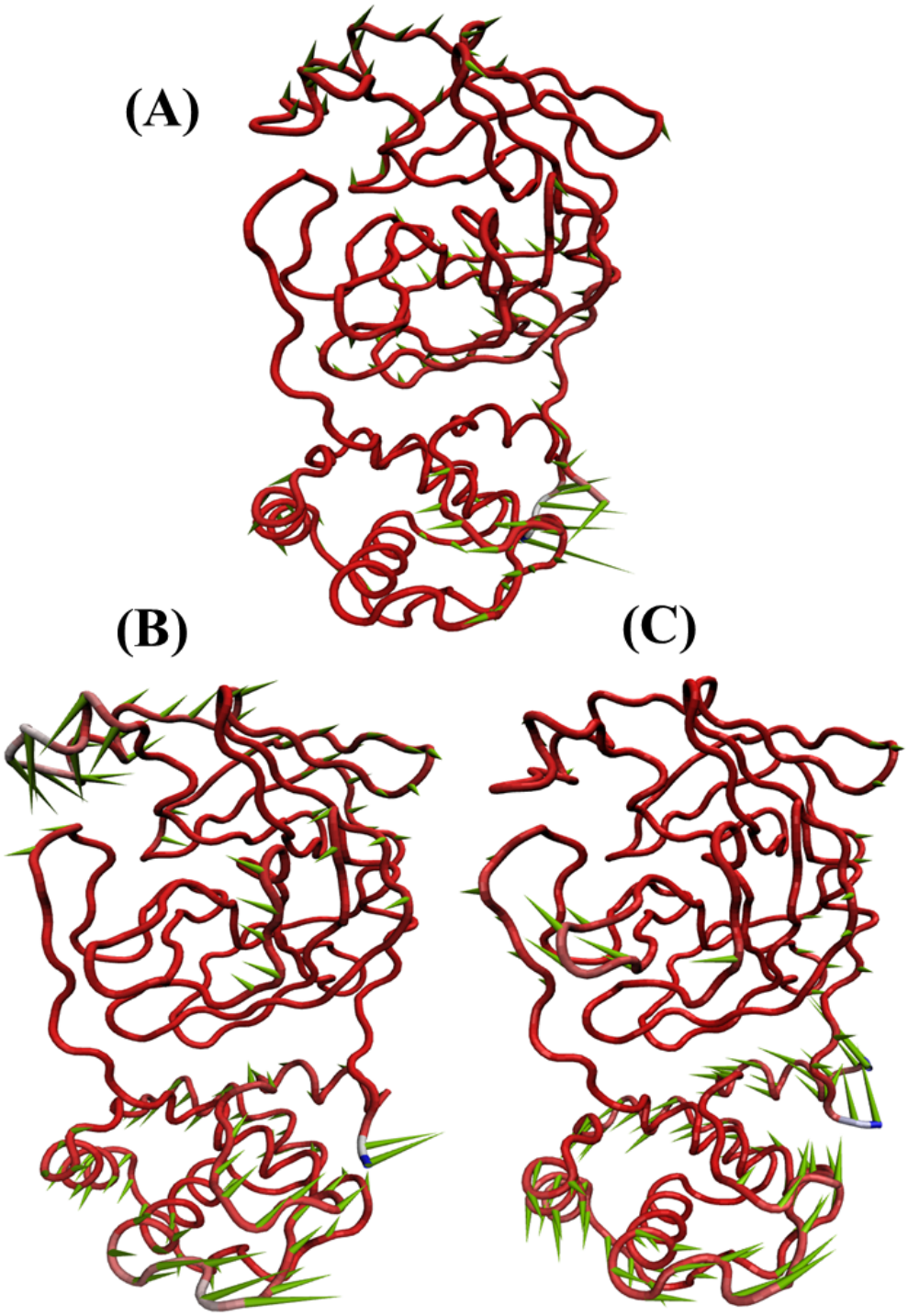

Figure S4: Porcupine plots showing prominent motions for (A) apo, (B) $3CL^{pro}$/α-ketoamide and (C) $3CL^{pro}$/Z31792168. Green represent eigenvector showing the direction of prominent movements. Length of the eigenvectors represents the magnitude of the movements.

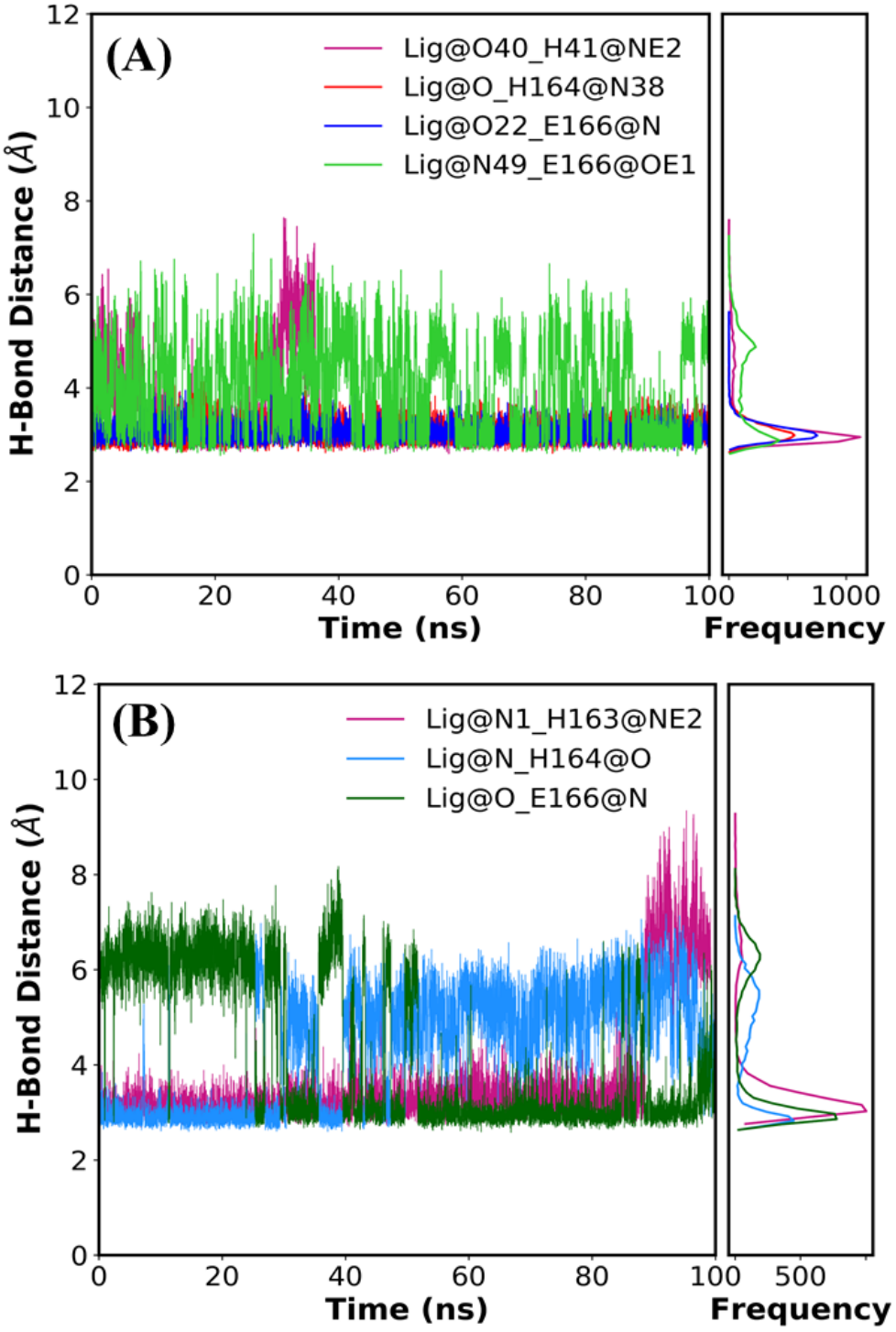

Figure S5: Time evolution of hydrogen bond distances and the probability distribution of (A) $3CL^{pro}$/α-ketoamide and (B) $3CL^{pro}$/Z31792168 complexes.

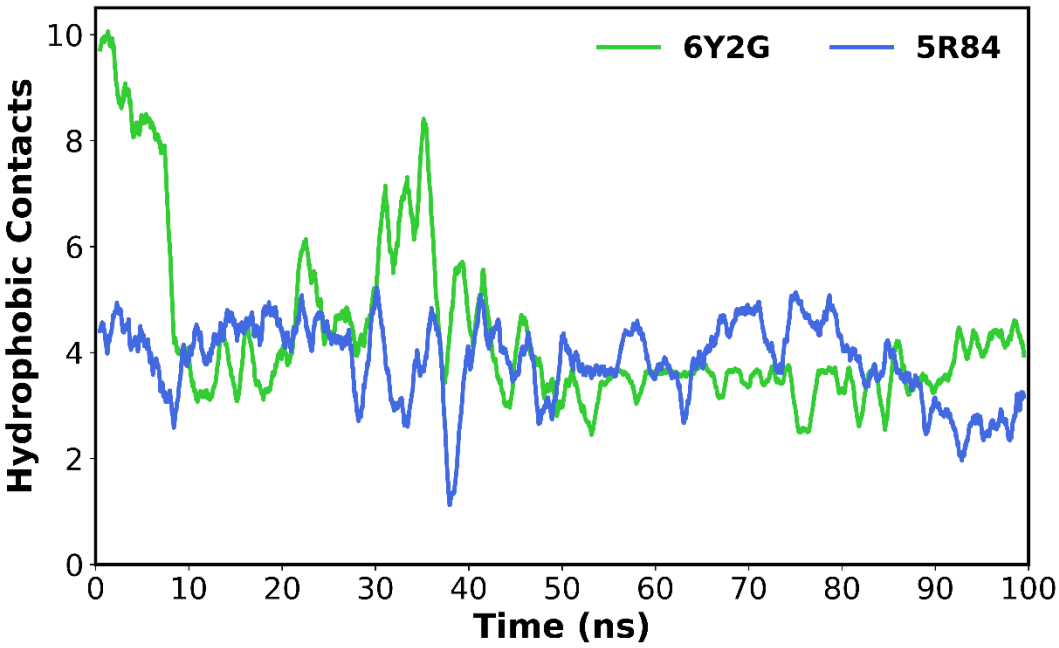

Figure S6: The time evolution of hydrophobic contacts for $3CL^{pro}$/α-ketoamide (green) and $3CL^{pro}$/Z31792168 (blue).