

Supporting Information

N-terminal Mutations in SARS-CoV-2 NSP1 Alter the Structure and Dynamics of its C-terminal Disordered Region, Impacting mRNA Translation in Ribosomes: Insights from Molecular Dynamics Simulations

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Figures and tables

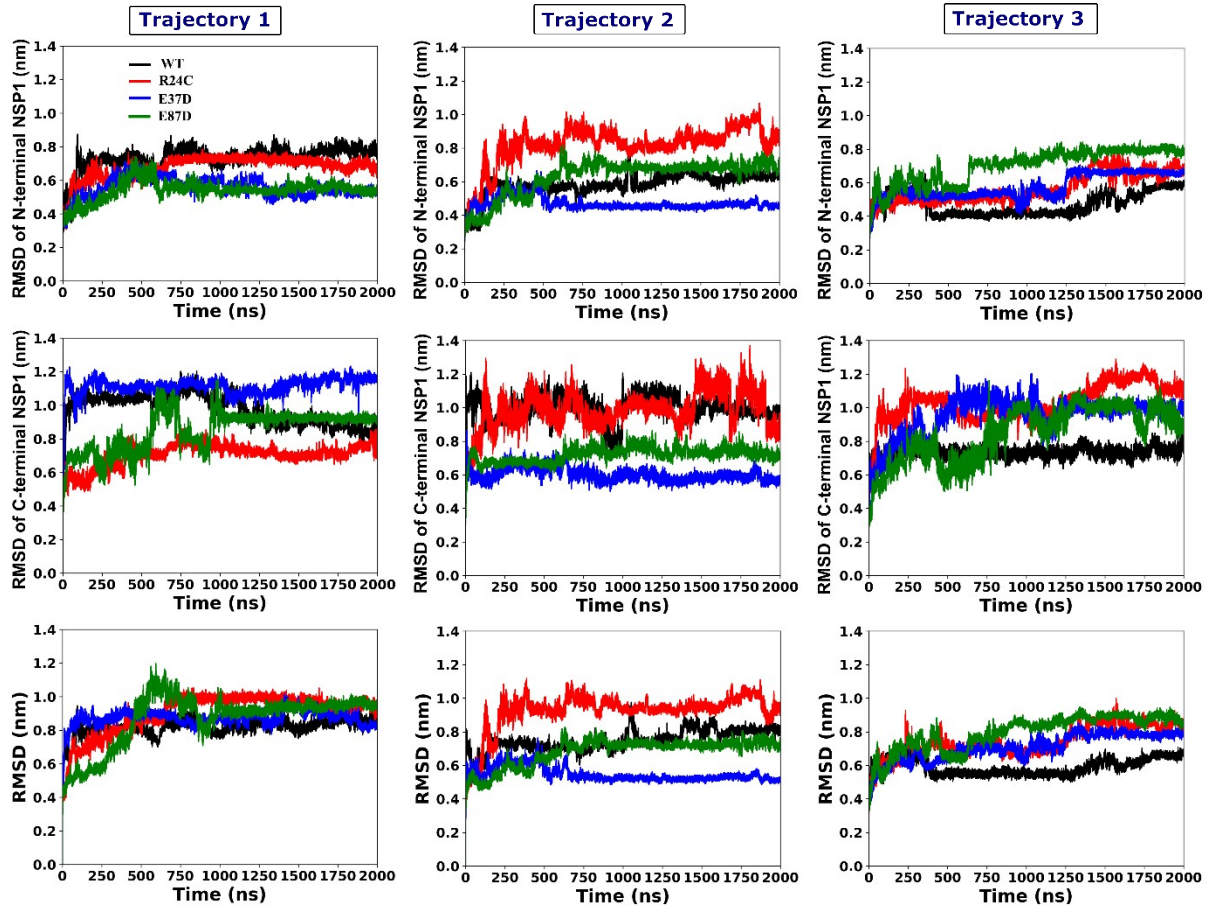


Figure S1: Root mean square deviation (RMSD) profiles of NSP1 wild type (WT) and the mutants R24C, E37D, and E87D across three independent molecular dynamics trajectories. RMSD values are reported separately for the N-terminal domain, C-terminal domain, and the full-length NSP1 protein.

Table S1: Incidence of the major global mutations in the N-terminal domain of NSP1 across continents¹. The data represent variant frequency (%).

	North America	South America	Europe	Asia	Oceania	Africa
E87D	0.3475	0.1021	2.0835	0.1243	0.0806	0.1441
R24C	0.3421	0.2229	0.2628	0.2001	0.1796	0.1723
E37D	0.0728	0.1344	0.1480	0	0.0147	0.0752

Reference

1. Ghaleh, S. S.; Rahimian, K.; Mahmanzar, M.; Mahdavi, B.; Tokhanbigli, S.; Sisakht, M. M.; Farhadi, A.; Bakhtiari, M. M.; Kuehu, D. L.; Deng, Y., SARS-CoV-2 Non-structural protein 1(NSP1) mutation virulence and natural selection: Evolutionary trends in the six continents. *Virus Res* **2023**, 323, 199016.