Supplementary Information

SARS-CoV-2 Variants and Bebtelovimab: Immune Escape Mechanisms Revealed by Computational Studies

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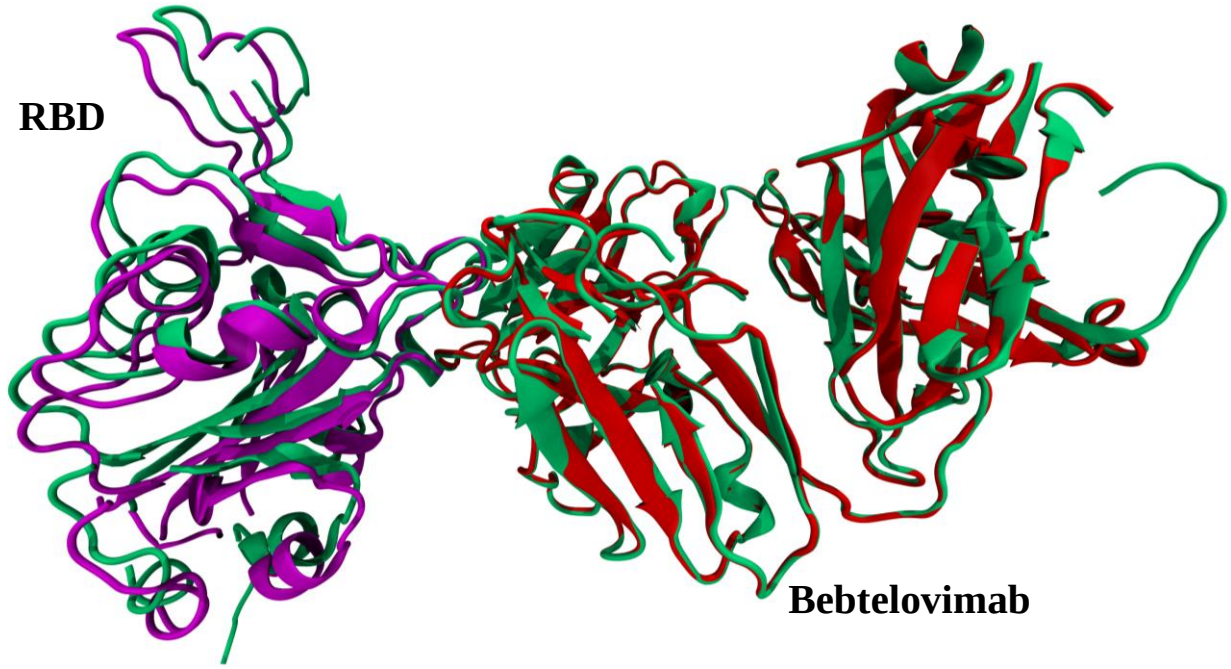

Figure S1: Crystal structure (Green) superimposed with Docked (Magenta/Red) structure of RBD (Wild type variant) attached with bebtelovimab.

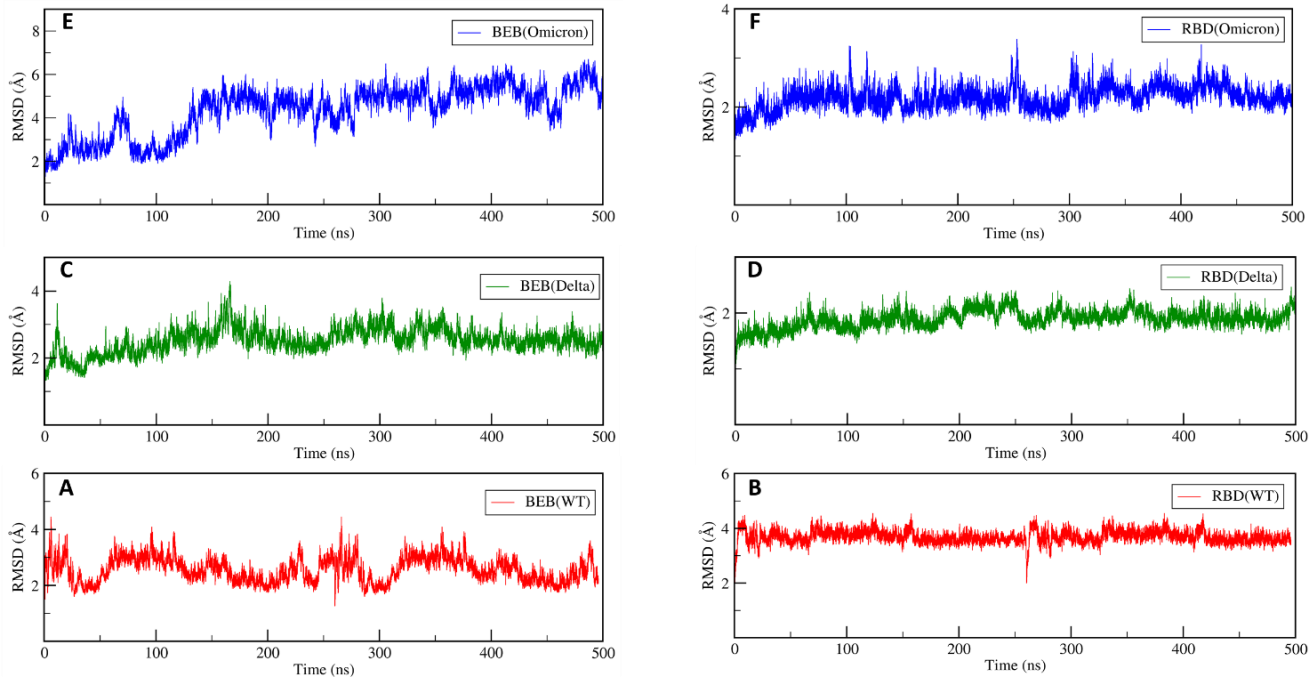

Figure S2: Root mean square deviation (RMSD) vs. time plot for (A,C,E) Bebtelovimab and (B,D,F) Receptor binding domain of wild type(Red) , Delta(Green) and Omicron(Blue) variants, respectively.

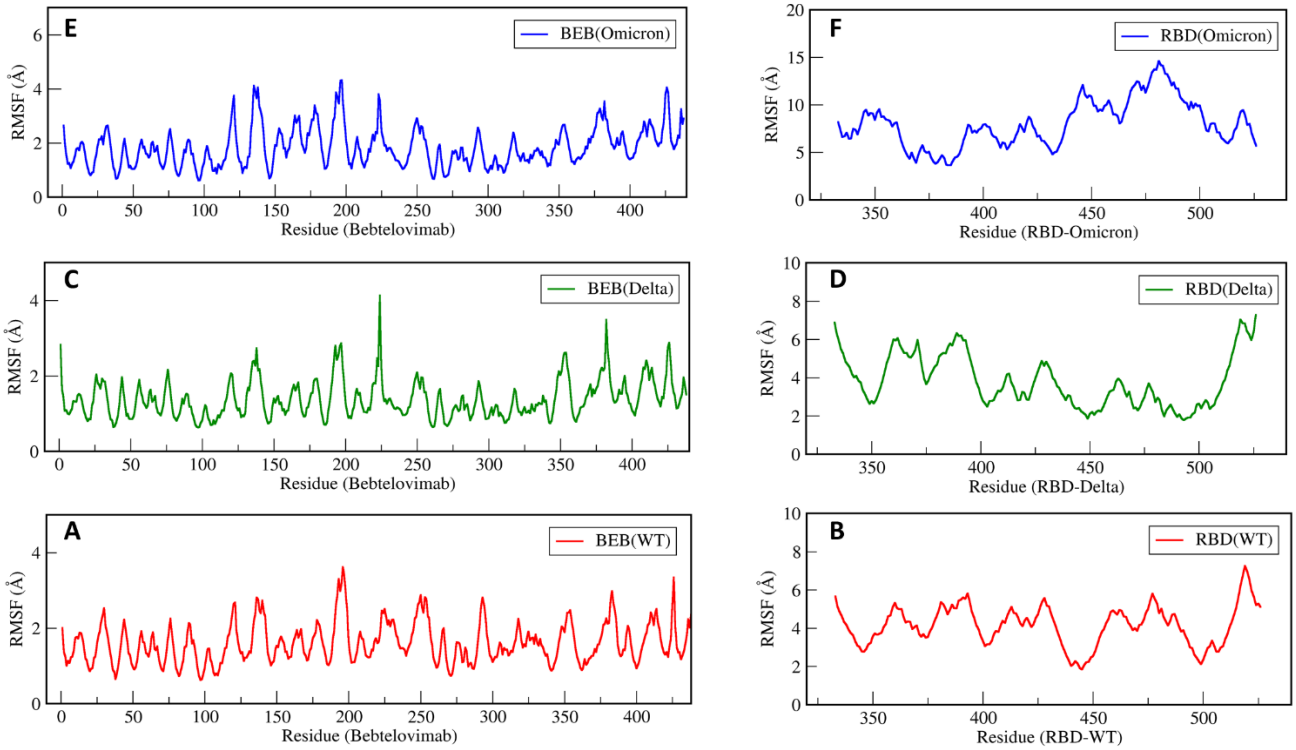

Figure S3: Root mean square fluctuation (RMSF) plot for (A,C,E) Bebtelovimab and (B,D,F) Receptor binding domain of wild type(Red) , Delta(Green) and Omicron(Blue) variants respectively.

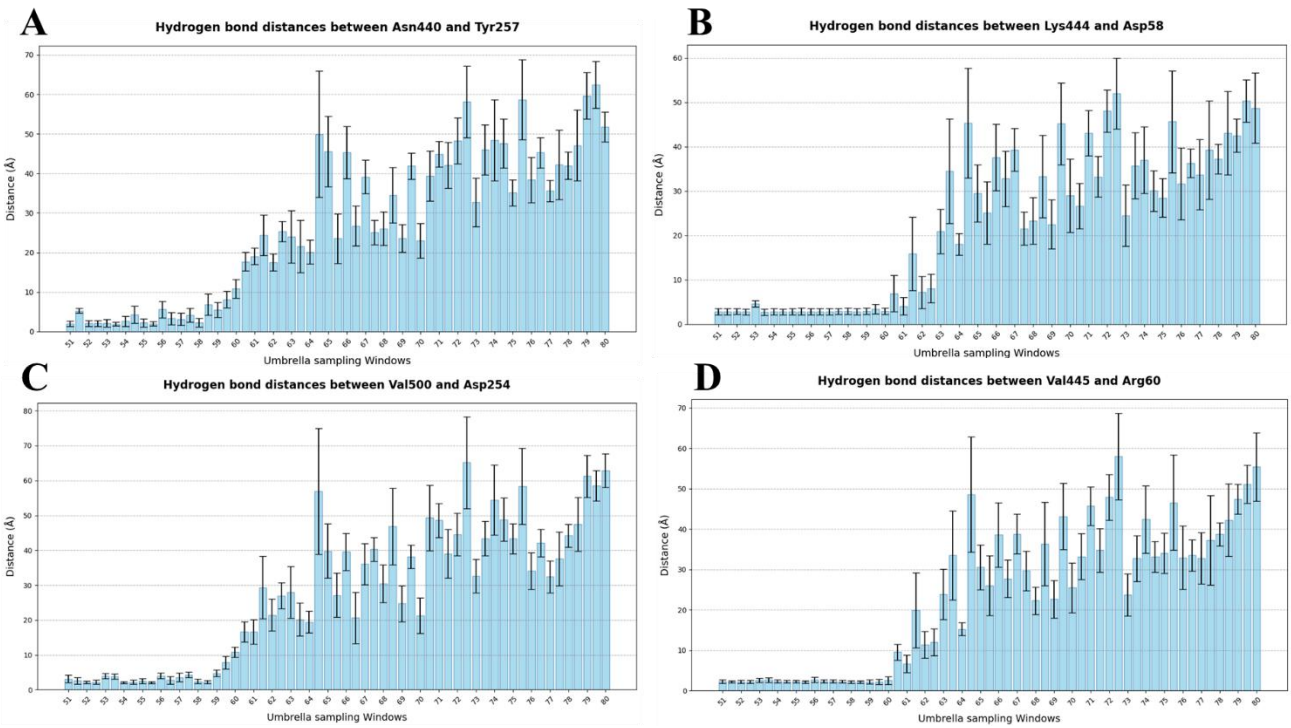

Figure S4: Hydrogen bond distances over the unbinding process (Pulling distance) for major interactions between RBD residues ASN440, LYS444, VAL500 and VAL45 with bebtelovimab residues TYR257 (A), ASP58 (B), ASP254 (C), and ARG60 (D) respectively.

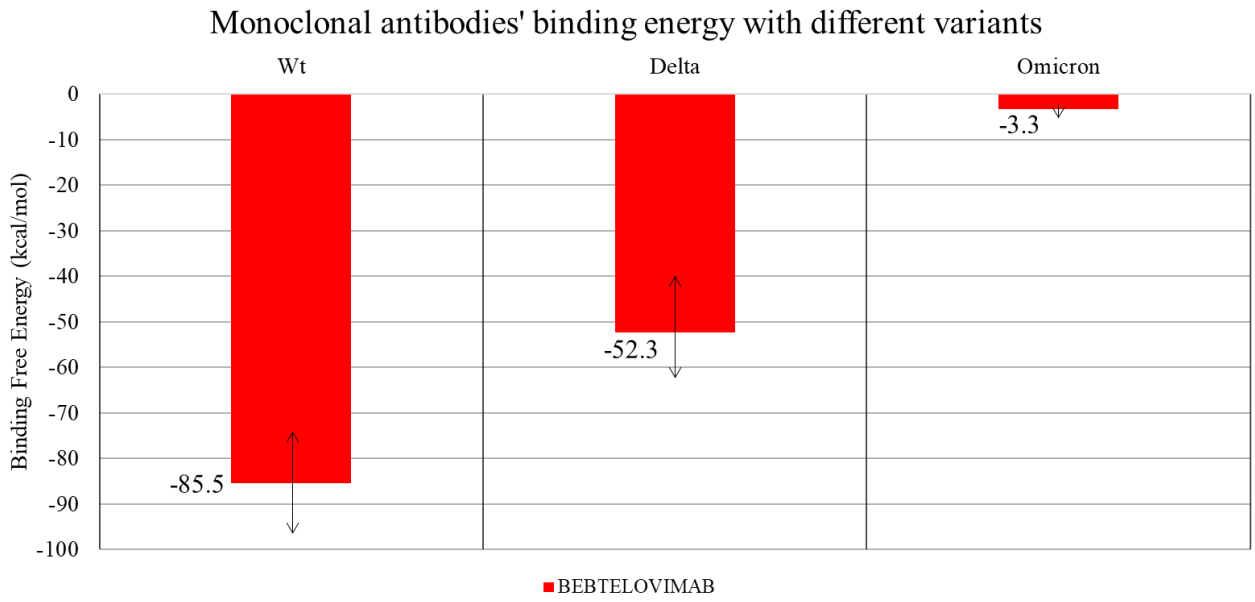

Figure S5: Total binding free energy (ΔG_{bind}) of Wild type, Delta, and Omicron variants with bebtelovimab

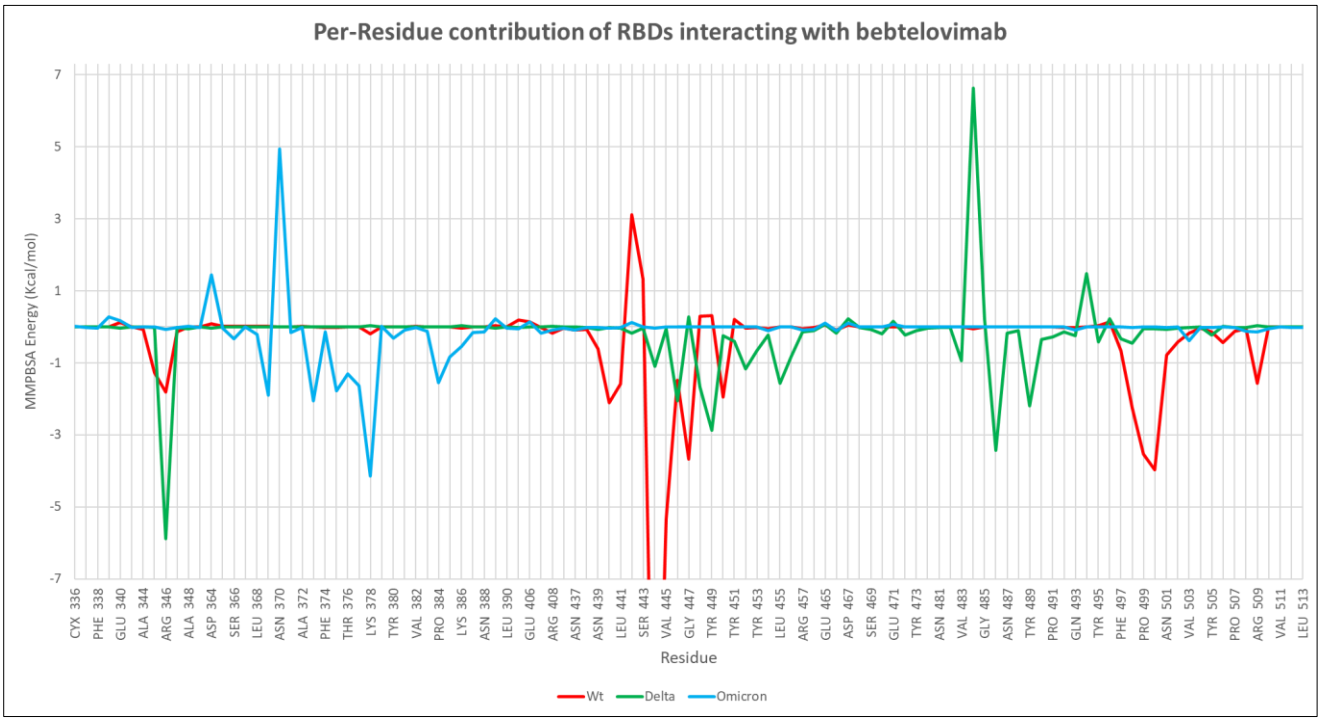

Figure S6: Per-residue contribution of RBD residues of wild type (Red), Delta (Green) and Omicron (Blue) to binding free energy with bebtelovimab (Monoclonal antibody).

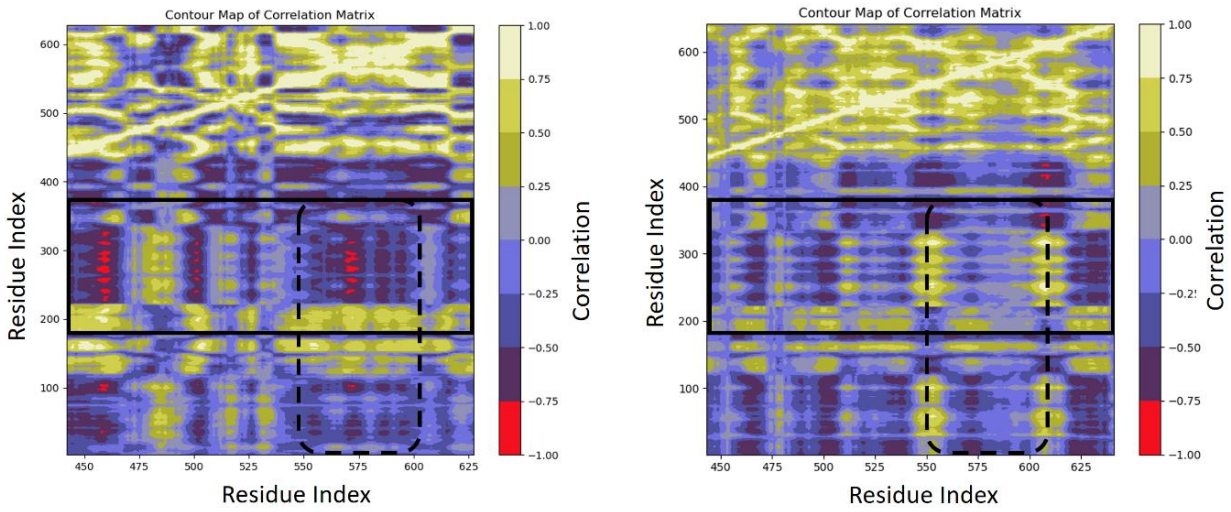

Figure S7: The dynamic cross-correlation maps for the Omicron (a) and wild-type (b) variants complexed with bebtelovimab. The Omicron variant exhibits significantly lower binding energy compared to the wild type and Delta variants. This reduction in binding energy can be partially explained by the dynamic cross-correlation matrix (DCCM) analysis, which reveals substantial anti-correlated motions between the RBD and bebtelovimab during the simulation. The higher number of mutations in the Omicron variant, particularly S477N, T478K, and E484A, contribute to these pronounced anti-correlated movements. These mutations likely induce conformational changes that disrupt the binding interface, resulting in decreased overall binding energy.