





**Supplementary information to:**

**Original article:**

**MUTATIONS IN THE SARS-COV-2 SPIKE PROTEIN MODULATE  
THE VIRUS AFFINITY TO THE HUMAN ACE2 RECEPTOR,  
AN *IN SILICO* ANALYSIS**

Joseph Thomas Ortega<sup>a</sup> , Flor Helene Pujol<sup>b</sup> , Beata Jastrzebska<sup>a\*</sup> ,  
Hector R. Rangel<sup>b\*</sup> 

<sup>a</sup> Department of Pharmacology, Cleveland Center for Membrane and Structural Biology,  
School of Medicine, Case Western Reserve University, Cleveland, OH, USA

<sup>b</sup> Laboratorio de Virología Molecular, Centro de Microbiología y Biología Celular, Instituto  
Venezolano de Investigaciones Científicas, Apdo 20632, Caracas 1020A, Venezuela

\* **Corresponding authors:** Hector R. Rangel, Ph.D., Laboratorio de Virología Molecular,  
Centro de Microbiología y Biología Celular, Instituto Venezolano de Investigaciones  
Científicas, Caracas, Venezuela; Phone: 58-412-7075300.

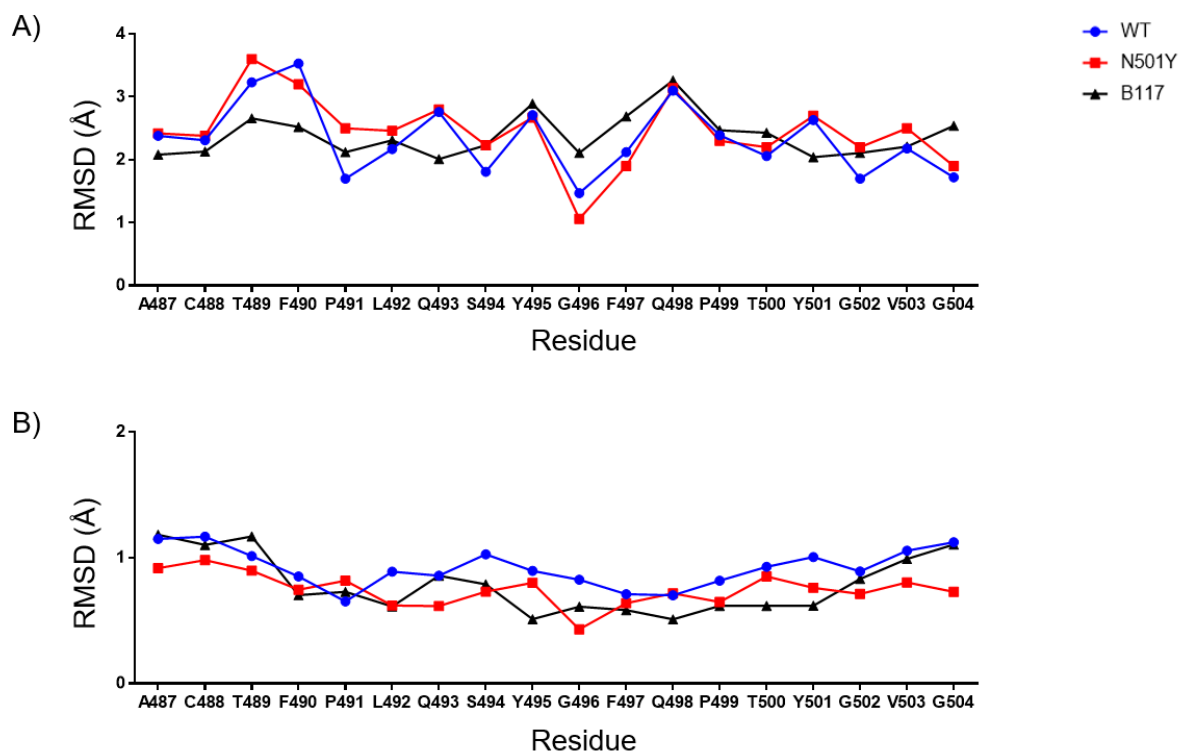
E-mail: [hrangel2006@gmail.com](mailto:hrangel2006@gmail.com)

Beata Jastrzebska, Ph.D., Department of Pharmacology, Cleveland Center for  
Membrane and Structural Biology, School of Medicine, Case Western Reserve University,  
10900 Euclid Ave, Cleveland, OH 44106-4965, USA; Phone: 216-368-4631;

Fax: 216-368-1300; E-mail: [bxj27@case.edu](mailto:bxj27@case.edu)

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**Supplementary Figure 1:** The root-mean-square-deviation (RMSD) of the protein C $\alpha$  atoms with the respect to the initial structure for the evaluated spike protein-ACE2 complex was obtained by molecular docking. **A)** The analysis performed with the VegaZZ software and **B)** The analysis performed with the CABS-Flex software.