



Supporting Materials

# Theophylline: Old Drug in a New Light, Application in COVID-19 through Computational Studies

Luis M. Montaña <sup>1</sup>, Bettina Sommer <sup>2</sup>, Juan C. Gomez-Verjan <sup>3</sup>, Genaro S. Morales-Paoli <sup>3</sup>,  
Gema Lizbeth Ramírez-Salinas <sup>4,5</sup>, Héctor Solís-Chagoyán <sup>6</sup>, Zuly A. Sanchez-Florentino <sup>6</sup>,  
Eduardo Calixto <sup>7</sup>, Gloria E. Pérez-Figueroa <sup>8,9</sup>, Rohan Carter <sup>10</sup>, Ruth Jaimez-Melgoza <sup>1</sup>,  
Bianca S. Romero-Martínez <sup>1</sup> and Edgar Flores-Soto <sup>1,\*</sup>

- <sup>1</sup> Departamento de Farmacología, Facultad de Medicina, Universidad Nacional Autónoma de México, CDMX, CP 04510, Mexico; lmmr@unam.mx (L.M.M.); jaimezruth@hotmail.com (R.J.-M.); biancasromero\_@hotmail.com (B.S.R.-M.)
  - <sup>2</sup> Laboratorio de Hiperreactividad Bronquial, Instituto Nacional de Enfermedades Respiratorias “Ismael Cosío Villegas”, CDMX, CP 14080, Mexico; bsommerc@hotmail.com
  - <sup>3</sup> Dirección de Investigación, Instituto Nacional de Geriátría, CDMX, CP 10200, Mexico; jver-jan@inger.gob.mx (J.C.G.-V.); mgenas.com@hotmail.com (G.S.M.-P.)
  - <sup>4</sup> Laboratorio de Diseño y Desarrollo de Nuevos Fármacos e Innovación Biotecnológica (Laboratory for the Design and Development of New Drugs and Biotechnological Innovation), Escuela Superior de Medicina, Instituto Politécnico Nacional, Plan de San Luis y Díaz Mirón S/N, Col. Santo Tomas, CDMX, CP 11340, Mexico; gemali86@hotmail.com
  - <sup>5</sup> Departamento de Inmunología, Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Circuito Escolar s/n, CP 4510, Mexico
  - <sup>6</sup> Laboratorio de Neurofarmacología, Instituto Nacional de Psiquiatría “Ramón de la Fuente Muñiz”, CDMX, CP 14370, Mexico; hecsolch@imp.edu.mx (H.S.-C.); zulyarmandosf@gmail.com (Z.A.S.-F.)
  - <sup>7</sup> Departamento de Neurobiología, Dirección de Investigación en Neurociencias, Instituto Nacional de Psiquiatría “Ramón de la Fuente Muñiz”, CDMX, CP 14370, Mexico; ecalixto@imp.edu.mx
  - <sup>8</sup> Unidad Periférica en el Estudio de la Neuroinflamación en Patologías Neurológicas, Instituto Nacional de Neurología y Neurocirugía. CDMX, CP. 06720, Mexico; gera.pfi3@gmail.com
  - <sup>9</sup> Laboratorio de Investigación en Inmunología y Proteómica, Hospital Infantil de México Federico Gómez, CDMX, CP. 06720, Mexico
  - <sup>10</sup> FRACGP/MBBS, Murchison Outreach Service Mount Magnet Western Australia, CP 6530, Australia; kingswood71@gmail.com
- \* Correspondence: edgarfs@comunidad.unam.mx; Tel.: +52-555-6232279

## Methodology

### *Molecular modeling of the E protein from SARS-CoV-2*

Based on the primary sequence YP\_009724392 of the E protein from SARS-CoV-2, it was possible to build the E protein of this virus by employing the crystal structure PDB: 5X29, which corresponds to the E protein of SARS-CoV. The identity percentage between the sequence of the E protein of SARS-CoV-2 and the crystal structure is 91.379%. A three-dimensional model of the pentamer of the E protein of SARS-CoV-2 was built by using Modeller 10.1 Software [1]. Obtaining the three-dimensional structure of the Spike protein of SARS-CoV-2 Crystal 7WK3, downloaded from the pdb database [2], which is the Omicron variant SARS-CoV-2 Spike protein crystal; therefore, it is the crystal that we will use for the Docking.

### *Molecular docking*

For the molecular docking of theophylline with both proteins (Spike and E of SARS-CoV-2) docking was performed directed at the RBD site (Spike protein) and the ion channel (E protein) respectively. The Vina program was used, with the following parameters: num\_modes = 20, energy\_range = 6 and exhaustiveness = 25. For the case of the Spike protein: center\_x = 210.0, center\_y = 170.0, center\_z = 270.0, size\_x = 60.00, size\_y = 60.00 and

size\_z = 60.00. And for protein E: center\_x = -7.0, center\_y = 1.0, center\_z = -6.0, size\_x = 35.00, size\_y = 30.00 and size\_z = 30.0 [3].

**Table S1.** Theophylline Simulation Conditions.

Parameter	Theophylline
Lipophilicity (Log Units)	0.89
Binds To	Albumin
Fraction Unbound	0.44
Molecular Weight (g/mol)	180.17
Compound Type And Pka	Acid / 8.8
Solubility At Ref-Ph (mg/L)	14300
Ref-pH	6.5
Metabolizing Enzymes	CYP1A2
Metabolizing Enzymes Clearance (1/Min)	0.00843
Renal Clearance	0.15
Administration Protocol	Simple protocol
Administration Type	Intravenous bolus
Dose (mg/Kg)	1 and 10
Dosing Interval	Single

**Table S2.** Individuals Simulation Conditions.

	Healthy	Renal impaired
Population	Mexican American – White (NHAES, 1997)	Mexican American – White (NHAES, 1997)
Age (Years)	70	70
Gender	Male	Male
Weight (Kg)	74.43	74.43
Height (cm)	165.96	165.96
BMI (Kg/m <sup>2</sup> )	27.02	27.02
Body Surface Area (m <sup>2</sup> )	1.85	1.85
Hematocrit	0.46	0.33
EHC continuous fraction	0	1
GFR Specific (ml/min/100 g organ)	26.6	5
Metabolizing enzymes expression	CYP1A2	CYP1A2