Joel Subach mjsubach@alumni.ncsu.edu

CAREER OBJECTIVE: Position in Academia or Research Science Focusing on Nano-Biomedical Engineering (Computational Protein Engineering)

OCCUPATIONAL EXPERIENCE:

- > 25 Years Experience Teaching-Developed/Implemented lesson plans for Biology, Chemistry, Physics, and Math through lectures and laboratories in Private/Public High Schools and private tutoring (College/University level) in Connecticut and Los Angeles California; 1989-2012
- 1-2017-5-2017, Manhattan College, Science Instructor (Chemistry, Physics, Earth Science, Biology, Nanotechnology), Riverdale, New York City, New York
- Experience in Teaching in a Multi-Ethnic Environment, Canvas LMS Savvy
- 1-2020-Present, Pannexin1 Pharmacophore Discovery; Computational Approach; Self-Employment
- o 12-2022-Present, Editor; Journal of Nanomedicine & Nanotechnology; Research Paper Assessment

ACADEMIC EDUCATION:

- **BA Degree**, Physical Anthropology; Central Connecticut State University; 1990 Honor Roll, CCSU 1989-90; Junior & Senior years of BA GPA 3.0 1989-1990
- Post–Graduate, 1991-2012; Science; UCLA; Post Baccalaureate Science
 Certificate; GPA 3.315
- **MS Degree**, Nano-Engineering; NCSU, 2014, Specialization in Biomedical Sciences and Technical Electives in Advanced Mathematics for Scientists and Engineers I and II, GPA 3.5
- Ph.D; Biomedical Informatics/Nano-Medicine; Rutgers University, 2014-2020, New Jersey, GPA 3.964
- Spanish Speaking Certified Level B1.1

PUBLISHED WORKS:

o Doctoral Dissertation, Title: Pannexin-1 In Silico Modeling Towards Physiological and Pathological Functioning; Year Published 2020, link below: (Computational Molecular Protein Design of Uncrystallized Protein via Homology Protein Modeling and Ligand-Docking)

Rutgers University Repository Link:

https://rucore.libraries.rutgers.edu/rutgers-lib/62581/

Rutgers University Dissertation PDF Link:

https://rucore.libraries.rutgers.edu/rutgers-lib/62581/PDF/1/play/

COMPUTATIONAL SKILL-SET:

• Protein Modeling:

MODELLER: Homology Protein Modeling, Missing Residue (Loop) Modeling **AlphaFold:** Protein Structure Modeling Monomer and Multimer (COSMIC2)

GalaxyWeb: Protein Oligomer Modeling **COSMIC2:** Oligomer Modeling, ColabFold

• Protein Receptor Docking:

MedusaDock: Ligand Receptor Docking

• Template Selection:

NCBI, Phyre² BLAST: Template Selection

○ Alignment Prediction:

Clustal, PROMALS3D, Phyre², RaptorX/CNFpred

Topology Prediction:

TMpred, TMHMM, SOSUI, RaptorX, Phyre²

Molecular Dynamic Simulation Prediction:

GROMACS: Membrane Protein-Ligand Complex Umbrella Sampling, Protein Ligand Interactions-Dynamics/Energy, CHARM-GUI Membrane Builder

- Python Coding Skills, MATLAB, Xmgrace, Linux, Cloud Computing Force Field Development Understanding
- Ligand Optimization:

Force Field Toolkit (ffTK); Parameterizing Small Molecules i.e. ORCA (QM)

Visual Software:

Pymol, VMD, Avogadro: Visual Analysis, RMSD, Distances, Residue Analysis

Dr. Joel Subach

To whom it may concern,

My current holding of a Ph.D. in Biomedical Informatics and Nanomedicine at Rutgers University will offer your learning institution an eclectic academic background towards Biomedical Engineering instruction, my *in silico* molecular design software skills will moreover contribute to innovative molecular modeling research. Computationally my experience encompasses novel 3-D *in silico* protein design and nanoparticle ligand-receptor dynamic simulation dockings. My future endeavors include bringing a novel nano-medical *in silico* engineering design/approach to a lab performing cutting-edge research within my area of interest, nanoparticle ligand-receptor engineering. Moreover I wish to share this insightful research to students encouraging, challenging and enriching the next generations. (Since 2020 I have been independently investigating Panx1 simulation towards pharmacophore development.)

I am available for an interview at your convenience, thank you for your time and considerations and may we enjoy each others success.

Respectfully yours,

Joel Subach