BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Taylor, Lily

eRA COMMONS USER NAME (credential, e.g., agency login): lilytaylor

POSITION TITLE: Graduate Student Research Assistant

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
University of Arizona	BS	08/2016	05/2020	Biochemistry
UC Los Angeles (UCLA)	PHD	07/2020	In Progress	Biochemistry, Molecular and Structural Biology

A. Personal Statement

My primary research interests involve the application of methods in synthetic and structural biology to assess the relationship between protein sequence and function. My interest in ascribing the functional properties of a protein to its encoded sequence parallels my undergraduate research experiences in which I modeled the structural properties of small molecular dimers under the guidance of Professor Stephen Kukolich at the University of Arizona to define key interactions between the molecules of interest. In doing so, I became well-versed in computational chemistry methods and appreciative of the vast information gained from a thorough structural understanding of a particular system. Upon the completion of my undergraduate degree, I entered the Biochemistry, Molecular and Structural Biology PhD program at UCLA where I now apply computational and structural methods to biological systems as an avenue to study how viruses exploit sequence-function relationships to gain broader pathogenic properties, and how this information can be used to predict the scope of their functional sequence landscapes. Under the advisement of Professor Jose Rodriguez at UCLA, I plan to explore the functional and structural effects of sequence variation of viral machinery implicated in serious human disease - information that will ultimately be utilized for the development of therapeutics and to gain a greater understanding of the molecular properties that govern their pathogenicity.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2020 – Present Graduate Student Researcher, UC Los Angeles
2018 – 2020 Undergraduate Student Researcher, University of Arizona

Honors

2025-2026 Dissertation Year Award, UC Los Angeles
2025 Arnold J. Berk Research Achievement Award, UC Los Angeles
2025 John M. Jordan Excellence in Research Award, UC Los Angeles
2022 – 2024 Cellular and Molecular Biology Training Fellowship, UC Los Angeles
2017 – 2020 Silver and Sage Scholarship Award, University of Arizona
2016 – 2020 Arizona Excellence Scholarship Award, University of Arizona
2016 – 2020 Honors Program Member, University of Arizona

C. Contributions to Science

Undergraduate Research: As an undergraduate at the University of Arizona I worked in the lab of Professor Stephen Kukolich where I studied the properties of concerted proton-tunneling interactions in hydrogen-bonded networks. I worked towards defining the tunneling frequencies of proton exchanges between symmetrically hydrogen-bonded acids using microwave spectroscopy and high-performance computing. I also applied these methods to obtain precise structural models of transition metal complexes and small molecular dimers.

Graduate Research: My ongoing predoctoral research is focused on studying the structural and functional consequences of sequence variation of New World Hemorrhagic Fever Mammarenavirus (NWM) glycoproteins. While all pathogenic NWMs bind the same cellular receptor to initiate infection, the sequences across the receptor-binding domains of NWM glycoproteins differ substantially, with sequence identities ranging from 25-46%. This sequence variability curtails efforts to develop broadly neutralizing therapeutics against these deadly pathogens and limits our ability to prepare for and identify emerging strains that may pose a serious risk to human health. My work aims to elucidate the structural and functional effects of sequence variation of the NWM glycoproteins to build a comprehensive understanding of the sequence-level factors which regulate their pathogenic properties. This information will be extracted by first mapping the paths that traverse the functional sequence landscape between human infection-causing strains, determining the sites of structural variability across these functional variants, and using this information to identify key sites that can be exploited to inform the rational design of proteins and inhibitors that modulate viral infectivity.

1. Taylor, L. J., Sawaya, M. R., Westover, J.B., Wang, C., Jimenez F., Munoz, A.J., Whitelegge, J., Gowen, B.B., Helguera, G.F., Castells-Graells, R., Rodriguez, J. A. (2025) *In situ* insights into antibody-mediated neutralization of a pre-fusion Junin virus glycoprotein complex. Publication *in press* at Cell Reports.
2. Taylor, L. J., Rodriguez, J. A. (2024) Approaches to Characterize *In Situ* Viral Glycoprotein Structure and Function. Poster presented at: American Crystallographic Association; July 2024; Denver, OH.
3. Taylor, L. J., Rodriguez, J. A. (2024) Evaluating the Functional Implications of Sequence Variation Across New World Hemorrhagic Fever Mammarenavirus Glycoproteins. Poster presented at: American Society for Virology; June 2024; Columbus, OH.
4. Taylor, L. J., Rodriguez, J. A. (2023) Toward Structural Insights into New World Hemorrhagic Fever Mammarenavirus Glycoprotein-Mediated Infection. Poster presented at: West Coast Structural Biology Workshop; 2023 March; Pacific Grove, CA.
5. Taylor, L. J., Ferrero, S., Helguera, G., Rodriguez, J. A. (2022) Predicting the Function of New World Hemorrahgic Fever Mammarenavirus Glycoprotein Variants. Poster presented at: Seaborg Symposium; 2022 August; Los Angeles, CA and Sigman Symposium; 2022 October; Los Angeles, CA.

D. Scholastic Performance

YEAR	COURSE TITLE	GRADE
	UNIVERSITY OF ARIZONA	
2016	Honors Fundamentals of Chemistry	B
2016	Honors Fundamental Techniques of Chemistry	B
2016	Honors Advanced First-Year Composition	A
2016	Honors Special Topics in Science	A
2016	Calculus 1	B
2016	Spanish 1	A
2017	Honors Quest	A
2017	Honors Colloquium	A
2017	Calculus 2	C
2017	Spanish 2	A
2017	Minority Biomedical Research Colloquium	A

2017	Honors Organic Chemistry	B
2017	Honors Organic Chemistry Lab	A
2017	Mathematical Physics for Chemistry	B
2017	General Biology Lab	A
2017	General Biology	C
2017	The Pursuit of Happiness	A
2018	Introduction to Biochemical Research	A
2018	Honors Organic Chemistry 2	B
2018	Honors Organic Chemistry Lab 2	A
2018	Dance Appreciation	A
2018	General Biology 2	A
2018	General Biology 2 Lab	A
2018	Nutrition, Food and You	A
2018	Introduction to African American Literature	A
2018	Biochemistry 1	A
2018	Ecology	A
2018	Medical Ethics	A

YEAR	COURSE TITLE	GRADE
2018	Introductory Mechanics	A
2019	Biochemistry 2	A
2019	Biochemistry Lab Techniques	A
2019	Honors Colloquium	A
2019	Environmental Ethics	A
2019	Introductory Electricity and Magnetism	B
2019	Physical Chemistry 1	A
2019	Word Roots: Science and Medical Terms	A
2019	Introductory Biostatistics	B
2019	Introductory Biotechnology	A
2020	Honors Water Use and Sustainability	A
2020	Biochemistry of Nucleic Acids	A
2020	Honors Thesis 2	A
2020	Physical Chemistry 2	A
2020	Plants and Our World	A
	UC LOS ANGELES	
2020	Biochemistry Research Seminar	A
2020	Protein Structure	A
2020	Biocatalysts and Bioenergetics	A
2020	Nucleic Acid Structure	A
2020	Gene Expression	A
2020	Biomolecular Structure and Regulation	A
2021	Structural Biology	A
2021	Structural Molecular Biology	A
2021	Structural Molecular Biology Lab	A
2021	Protein Mass Spectroscopy	A
2021	Stem Cell Seminar	S
2022	Chemistry of Biology	S
2022	Organic Colloquium	A
2023	Core Principles in Cell and Molecular Biology	A
2023	Skills Development for Cell & Molecular Biologists	S

2023	Advanced Topics and Approaches in Cell and Molecular Biology	S
2023	Ethics and Accountability in Biomedical Research	S

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NAME: Rodriguez, Jose A

eRA COMMONS USER NAME (credential, e.g., agency login): JRODRIGUEZ2

POSITION TITLE: Associate Professor, Department of Chemistry & Biochemistry, UCLA

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of California, Los Angeles (UCLA)	B.S.	06/2007	Biophysics
University of California, Los Angeles (UCLA)	Ph.D.	09/2012	Molecular Biology
University of California, Los Angeles (UCLA)	Postdoctoral	07/2016	Biological Chemistry

A. Personal Statement

My research is aimed at understanding fundamental aspects of molecular structure. This includes an improved understanding of the relationship between biological structure and function, the development of new tools and approaches that advance our knowledge of biochemistry, and the discovery of new treatments to combat devastating and incurable diseases.

My formative scientific experiences have allowed me to contribute to several important areas of biomedical science including (1) characterization of the millisecond timescale swimming behavior of *Trypanosoma brucei*, the parasitic pathogen responsible for African sleeping sickness, (2) use of high brilliance X-ray sources to uncover the three dimensional structure of the *Neospora caninum* cell (3) development of antibody-based immunotherapies to treat cancer, (4) development of inhibitors of infection by New World Arenaviruses – etiological agents of deadly South American hemorrhagic fevers, (5) determination of the structures of insecticidal toxins critical for future pesticide development and vector control for tropical disease eradication, and (6) determination of structures of toxic segments of amyloid forming proteins, including those that cause Parkinson's, Alzheimer's and Prion disease.

My scientific vision has been shaped by an early introduction to methods development in imaging including the use and application of high-powered instruments including brilliant X-ray and electron sources. I have applied these instruments to address pressing questions in aging research. As an example of this, in 2015 I helped advance the new cryo-electron microscopy technique known as electron micro-diffraction (MicroED) by determining a structure of the toxic core of alpha-synuclein fibrils, the cause of Parkinson's disease - the first novel structure determined by MicroED. Since 2015, my group has been at the forefront of electron diffraction developments; we have established ED as a growing scientific field for both small molecule and protein nanocrystals. My group has further leveraged emerging cryoEM and cryoET approaches. In particular we have invested in the application of correlative light and electron microscopy of cells by fluorescence-guided cryogenic Focused Ion Beam (FIB) milling and cryoET. Our efforts have been carried out both at UCLA facilities and at NIH-sponsored cryoEM and cryoET national centers.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2021-present Associate Professor, Department of Chemistry and Biochemistry, UCLA
2016-2021 Assistant Professor, Department of Chemistry and Biochemistry, UCLA
2014-2017 Visiting Scientist, Biophysics with Tamir Gonen in Janelia Research Campus
2013-2016 Giannini Post-Doctoral Fellow, Biological Chemistry with David Eisenberg at UCLA

2013-2015 Lecturer, Physics in the UCLA Department of Physics and Astronomy
2013-2014 Visiting Scientist, Spring-8 in RIKEN Harima Institute
2012-2013 HHMI Post-Doctoral Associate, Biological Chemistry with David Eisenberg at UCLA
2010-2012 Graduate Student Mentor, Undergrad Research Center, Tama Hasson at UCLA
2007-2012 Graduate Student Researcher, Molecular Biology with Manuel L. Penichet at UCLA

Other Experience and Professional Memberships

2020-present Microscopy Society, Member
2020-present USNC/Cr EM representative
2018-present American Chemical Society, Member
2017-present Biophysical Society, Member
2006-2012 American Association for Cancer Research (AACR), Student Member

Honors

2020 Sloan Fellowship
2019-2021 Packard Fellowship
2019 UCLA Chem & Biochemistry McCoy Award
2018 American Chemical Society, Chemistry & Engineering News Talented 12
2018-2022 Pew Scholar Award
2017-2020 Searle Foundation Scholar Award
2017-2021 Beckman Young Investigator Award
2015 Parvin Foundation Award for Post-Doctoral Research
2013-2016 Giannini Foundation Post-Doctoral Fellowship
2011 UCLA AMGEN Molecular Biology Institute Dissertation Year Award
2007-2007 NSF-AGEP Competitive Edge Graduate Summer Research Fellowship
2007-2012 Howard Hughes Medical Institute Gilliam Fellowship for Graduate Studies
2007-2011 UCLA Whitcome Fellowship for Graduate Study in Molecular Biology
2006-2007 American Association for Cancer Research Thomas J. Bardos Award
2005 HHMI Excellent Research Opportunities Program
2005-2007 Minority Access to Research Careers (MARC) trainee, UCLA

C. Contributions to Science

1. *Biophysics of Emerging Pathogens and Prions*

A principal goal of my group's work is to identify the structures and functions of pathogen-associated, and to develop therapeutic interventions on the basis of newfound structural knowledge. We have effectively done this with emerging viral pathogens such as pathogenic New World Hemorrhagic Fever Mammarenavirus viruses, finding the structural basis for their neutralization by potent antibodies. Most recently, we have also developed technical advances to more quickly and effectively determine the structures of small molecules bound to their pathogen-associated protein targets, including beta lactamases associated with bacterial resistance. In the 'pathogens' category, I include not only conventional (nucleic acid-based) disease-causing vectors, but also, the infectious proteinaceous assemblies referred to as 'prions'. Alongside my trainees and colleagues, over the past decade, I have learned and applied methods in structural biology to help determine the structures of prions or prion-like assemblies in the context of normal and pathological processes. The select list of articles, below, describes my efforts in applying novel approaches for structural and biophysical investigation of infectious agents.

A. Taylor, L.J., Sawaya, M.R., Westover, J.B., Wang, C., Jimenez, F., Muñoz, A.J., Whitelegge, J., Gowen, B.B., Helguera, G.F., Castells-Graells, R., **Rodriguez, J.A.** (2025) *In situ* insights into antibody-mediated neutralization of a pre-fusion Junin virus glycoprotein complex. **Cell Reports** (*in press*).
B. Vlahakis, N.V., Flowers, C.W., Liu, M., Agdanowski, M., Johnson, S., Summers, J.A., Keyser, C., Russell, P., Rose, S., Orlans, J., Adhami, N., Chen, Y., Sawaya, M.R., Basu, S., de Sanctis, D., Wakatsuki, S., Nelson, H.M., Loo, J.A., Tang, Y., **Rodriguez, J.A.** (2025) Combining MicroED and native mass spectrometry for structural discovery of enzyme-small molecule complexes. **PNAS** (*in press*).

C. Glynn, C., Hernandez, E., Gallagher-Jones, M., Miao, J., Sigurdson, C. and **Rodriguez, J.A.** (2022) Structural consequences of sequence variation in mammalian prion b2a2 loop segments. **Front. in Neuroscience**, 16.
D. Glynn, C., Sawaya, M.R., Ge P., Gallagher-Jones, M., Short, C.W., Bowman, R., Apostol, M., Zhou, Z.H., Eisenberg, D.S., **Rodriguez, J.A.** (2020) Cryo-EM structure of a human prion fibril with a hydrophobic, protease-resistant core. **Nature SMB**. doi: 10.1038/s41594-020-0403-y.

2. *Structures Relevant to Functional and Pathogenic Amyloids*

My interest in amyloid-related degenerative diseases is closely related to my work on pathogenic prions. Over the past decade I have contributed to our understanding of the amyloid state of proteins, beyond that of prions. In both normal biological function and in the case of disease, the function of amyloids remains poorly understood. To help illuminate amyloid structures, my trainees, colleagues and I have leveraged cryoEM approaches, determining structures of segments and full proteins in amyloid assemblies. These generally appear as fibrils formed by many repeat peptide or protein units in beta sheet-rich configurations. Our understanding of their structures has also allowed our analysis of their function and structure in cells. Most recently, we have also developed new AI-driven algorithms to expand our understanding of amyloid-propensity across entire proteomes. Overall, our work has resulted in a number of original research articles including some recently accepted articles that are included as preprints, highlighted below.

A. Zink, S., Qu1, S., Holton, T., Shankar, E., Stanley, P., Eisenberg, D.S., Sawaya, M.R., and **Rodriguez, J.A**. (2025) Leveraging Structure-Informed Machine Learning for Fast Steric Zipper Propensity Prediction Across Whole Proteomes. **PLOS Comp. Biol.** (*under review*)
B. Flores, M.D., Sawaya, M.R., Boyer, D.R., Zink, S., Tovmasyan, S., Saucedo, A., Zee, C., Cardenas, J., Fioriti, L., **Rodriguez, J.A**. (2025) Structure of a reversible amyloid fibril formed by the CPEB3 prion-like domain reveals a core sequence involved in translational regulation. **Structure** S0969-2126(25)00185-6.
C. Hazari, A., Sawaya, M.R., Sajimon, M., Vlahakis N., **Rodriguez, J.**, Eisenberg, D., Raskatov, J.A. (2024) Racemic Peptides from Amyloid β and Amylin Form Rippled β-Sheets Rather Than Pleated β-Sheets. **Journal of the American Chemical Society** 47, 25917-25926.
D. Richards, L.S., Flores, M.D., Zink, S., Schibrowsky, N.A., Sawaya, M.R., **Rodriguez, J.A**. (2023) Cryo-EM Structure of a Human LECT2 Amyloid Fibril Reveals a Network of Polar Ladders at its Core. **Structure** 31, 1386–1393.

3. *Cryo Electron Microscopy and Electron Crystallography*

The revolution in cryogenic electron microscopy has now led to a major shift in our understanding of biomolecular structures. As a consequence, we can visualize molecules and assemblies with molecular or atomic resolution, even when they are unable to form large perfect crystals. Taking advantage of recent technological and computational improvements, I have helped further expand and apply cryoEM and micro electron diffraction (MicroED) methodologies. The four articles presented below encapsulate some of those efforts in addition to highlighting their application to pressing biomedical problems through the determination of novel macromolecular structures.

A. Richards LS, Flores MD, Millán C, Glynn C, Zee C, Sawaya MR, Gallagher-Jones M, Borges RJ, Usón I, **Rodriguez JA**. (2023) Fragment-Based Ab Initio Phasing of Peptidic Nanocrystals by MicroED. *ACS Bio Med Chem Au*. doi: 10.1021/acsbiomedchemau.2c00082.
B. Kim, L.J., Ohashi, M., Tan, D., Asay, M., Cascio, D., **Rodriguez, J.A**., Tang, Y., Nelson, H. (2021) Prospecting for natural products by genome mining and microcrystal electron diffraction. *Nature Chem Bio*. 17, 872–877.
C. Jones, C.G., Martynowycz, M.W., Hattne, J., Fulton, T.J., Stoltz, B.M., **Rodriguez, J.A.,** Nelson, H. and Gonen, T. (2018) The CryoEM Method MicroED as a Powerful Tool for Small Molecule Structure Determination. *ACS Central Sci*. *4* (11), 1587–1592.

4. *X-ray Crystallography & Diffraction Methods*

Over the course of my career, I have benefitted from the application of diffraction theory in many ways, but none more tangible than through its use in crystallography and in the development of novel imaging methods. These have enabled me and my collaborators to visualize the structures of molecules and cells with unprecedented details. I have leveraged X-ray free electron lasers to image nanoparticles and to study the structures of cell grown crystals. I have used electron diffraction to determine novel atomic structures from crystalline only hundreds of molecules thick, applied these methods to rapidly

and accurately investigate small molecule structures. The four articles below illustrate some of those efforts including the use of serial crystallography for the determination of entirely novel structures, and studies to improve the interpretation of electron diffraction data.

A. Treteau, G., *et al*. (2022) *De novo* determination of mosquitocidal Cry11Aa and Cry11Ba structures from naturally-occurring nanocrystals. *Nature Comms*. 13 (1), 1-18.
B. Richards LS, Millán C, Miao J, Martynowycz MW, Sawaya MR, Gonen T, Borges RJ, Usón I, **Rodriguez JA**. Fragment-based determination of a proteinase K structure from MicroED data using ARCIMBOLDO_SHREDDER. *Acta Crystallogr D Struct Biol*. 2020 Aug 1;76(Pt 8):703-712. doi: 10.1107/S2059798320008049. Epub 2020 Jul 27. PMID: 32744252; PMCID: PMC7397493
C. Jones CG, Asay M, Kim LJ, Kleinsasser JF, Saha A, Fulton TJ, Berkley KR, Cascio D, Malyutin AG, Conley MP, Stoltz BM, Lavallo V, **Rodríguez JA**, Nelson HM. Characterization of Reactive Organometallic Species via MicroED. *ACS Cent Sci*. 2019 Sep 25;5(9):1507-1513. doi: 10.1021/acscentsci.9b00403. epub 2019 Sep 6. PMID: 31572777; PMCID: PMC6764211
D. Colletier, J.P., Sawaya, M.R., Gingery, M., **Rodriguez, J.A.**, Cascio, D., Brewster, A.S., Boutet, S., Williams, G.J., Messerschmidt, M., DePonte, D.P., Sierra, R.G., Laksmono, H., Koglin, J., Hunter, M.S., Park, H.W., Uervirojnangkoorn, M., Bideshi, D.K., Brunger, A.T., Federici, B.A., Sauter, N.K., Eisenberg, D.S. (2016) A potent mosquito larvicide revealed by *de novo* phasing with an X-ray free-electron laser. *Nature*. DOI 10.1038/nature19825.

Comprehensive List of Published Work:
https://www.ncbi.nlm.nih.gov/sites/myncbi/1RGFUfHRv5957/collections/51179380/public/