BIOGRAPHICAL SKETCH

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NAME: Eisenberg, David

eRA COMMONS USER NAME (credential, e.g., agency login): EISENBERG2

POSITION TITLE: Paul D. Boyer Professor of Biochemistry & Molecular Biology

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
Harvard College, Cambridge, MA (J.T. Edsall)	A.B.	06/1961	Biochemical Sciences
Oxford University, Oxford, UK (C.A. Coulson)	D. Phil.	10/1964	Theoretical Chemistry

A. Personal Statement

Understanding biology through structure and computation has been my career-long interest. Starting with computation and x-ray diffraction, I later added the tools of TEM, and more recently micro-electron diffraction and cryoEM. I have focused increasingly on proteins associated with amyloid and prion diseases. These are diseases of protein oligomerization and fibrillation. By newly developed methods of microcrystallography and microelectron diffraction, our lab has been able to determine the atomic structures of some 200 of disease related fibril structures. In the past year, we have determined structures of 10 amyloid fibrils by cryoEM. Google Scholar citations: n > 100,000; h >140

In laboratory training, I have supervised dozens of undergraduates, over 76 Ph.D. theses, and some 80 postdoctoral fellows, most of who are carrying out research in structural and computational biology in universities, research institutes, and industries. Former trainees work in at least a dozen countries. With regard to education, I have coauthored ~350 research papers and reviews, and two books: a monograph on the structure and properties of water [~5500 citations] and a text on physical chemistry for the life sciences. Both are still in print after 50 and 40 years, respectively. I also established and direct a user-friendly facility for determination of atomic structures by x-ray and EM methods which has welcomed and helped scores of student users from UCLA, other research institutions and industry professionals. I strive to provide a lab environment that is inclusive, safe and supportive. I set high expectations for rigorous scientific training and I offer candid constructive feedback to my mentees. My trainees receive extensive computational and quantitative training to facilitate their research goals. I meet often with my trainees to align research expectations and provide advice and career connections as they prepare to enter independent careers. Students in my lab routinely graduate in under 5 years, with a few exceptions. All my students attend the joint UCLA Structure meetings where they present their research and receive feedback on their research approach, data analysis and data interpretation. This is also a place where they learn about rigorous experimental design, methodologies, and data analyses.

B. Positions and Honors

Princeton University, Princeton	Postdoc	1964-1966	Water, H-bonding	(Walter Kauzmann)
Caltech, Pasadena	Postdoc	1966-1969	Structural Biology	(R.E. Dickerson)
UCLA, Los Angeles	Asst. Prof-Prof	1969-present	Chemistry & Biochemistry	
UCLA, Los Angeles	Director	1993-2014	UCLA-DOE Institute	
Howard Hughes Medical Institute	Investigator	2001-present	Investigator	
Paul Boyer Chair		2009-present		

Selected Memberships and Awards

L.J. Henderson Prize, 1961 for best undergraduate thesis in Biochemical Sciences; Rhodes Scholarship, 1961-1964; Alfred P. Sloan Fellowship, 1969-1971; USPHS Career Development Award, 1972-1977; UCLA Distinguished Teaching Award, 1975; McCoy Award of the UCLA Department of Chemistry and Biochemistry for

innovative research, 1982 (with R.E. Dickerson); Guggenheim Fellowship, 1985; UCLA Faculty Research Lectureship, 1989; National Academy of Sciences, 1989; American Academy of Arts & Sciences, 1991; Pierce Award of the Immunotoxin Society, 1992; Protein Society Stein & Moore Award, 1996; American Chemical Society Repligen Award in Molecular Biology, 1998; Fellow, Biophysical Society Inaugural Year Fellow, 1999; Amgen Award of the Protein Society, 2000; Institute of Medicine 2002; American Philosophical Society, 2003; UCLA Seaborg Medal, 2004; Harvard Westheimer Medal, 2005; Harvey International Prize in Human Health, 2009; Biophysical Society, Emily Gray Award, 2009; Honorary Fellow, Queen's College, Oxford, 2010; ISMB Accomplishment by a Senior Scientist Award, 2013; Inaugural Switzer Price for Biomedical Discovery, 2014; ASBMB Bert and Natalie Vallee Award in Biomedical Science, 2015; Fellow, American Crystallographic Assoc, 2015, MBI Legacy Award, 2015; Vallee Visiting Professor, 2016; UCSF Andrew Braisted Award Lecturer, 2016; Paul Sigler Prize, Yale University, 2017. NAS Strategic Planning Committee, 2019. Passano Laureate, 2020.

C. Contribution to Science

1. Structural biology of the amyloid state of proteins: Prior to our atomic-resolution crystallographic studies of amyloid-forming proteins, only low-resolution information from EM and fiber diffraction were available. Papers a, b, and c describe the common spine of amyloid fibers: a pair of beta-sheets, closely mating by interdigitation of their sidechains, termed a steric zipper. Paper a was the first atomic resolution structure of the amyloid state. Paper b showed that numerous amyloid fibrils have steric-zipper spines, and classified the possible symmetries of this structural motif. Paper c includes a cyoEM structure for a 27-protofilament amyloid fibril formed by a segment of protein TDP-43. Paper d reveals a new type of protein interaction—termed LARKS—between low-complexity domains, responsible for multivalent networks and gels, such as those found in membrane-less organelles.

a. Nelson R, Sawaya MR, Balbirnie M, Madsen AO, Riekel C, Grothe R, **Eisenberg D.** Structure of the cross-beta spine of amyloid-like fibrils. *Nature.* **435**, 773-8 (2005). PMCID: PMC1479801 [>2200 citations]
b. Sawaya MR, Sambashivan S, Nelson R, Ivanova MI, Sievers SA, Apostol MI, Thompson MJ, Balbirnie M, Wiltzius JJ, McFarlane HT, Madsen AØ, Riekel C, **Eisenberg D.** Atomic structures of amyloid cross-beta spines reveal varied steric zippers. *Nature.* **447**, 453-7 (2007). PMID: 17468747 [~2100 citations]
c. Guenther EL, Ge P, Trinh H, Sawaya MR, Cascio D, Boyer DR, Gonen T, Zhou ZH, **Eisenberg D**. Atomic-level evidence for packing and positional amyloid polymorphism by segment from TDP-43 RRM2. *NSMB* **25**:311-319 (2018) doi: 10.1038/s41594-018-0045-5
d. Michael P. Hughes, Michael R. Sawaya, David R. Boyer, Lukasz Goldschmidt, Jose A. Rodriguez, Duilio Cascio, Lisa Chong, Tamir Gonen, **David S. Eisenberg**. Atomic structures of low-complexity protein segments reveal kinked β-sheets that assemble into networks. *Science.* **359***, 698-701* (2018).

2. Inhibition of formation of amyloid fibrils and of amyloid cytotoxicity: Dozens of human diseases are associated with amyloid fibrils. We have been able to inhibit amyloid formation both by structure-based design (papers e-h). Paper h reports improved inhibitors of the aggregation of tau (at the root of Alzheimer's, CTE, and 25 other tauopathies) and of the intercellular prion-like spread of tau fibrils.

e. Sievers SA, Karanicolas J, Chang HW, Zhao A, Jiang L, Zirafi O, Stevens JT, Munch J, Baker D, **Eisenberg D**. Structure-based design of non-natural amino-acid inhibitors of amyloid fibril formation. *Nature.* **475**, 96-100 (2011). PMCID: PMC4073670 [400 citations]
f. Jiang L, Liu C, Leibly D, Landau M, Zhao M, Hughes MP, **Eisenberg DS**. Structure-based discovery of fiber-binding compounds that reduce the cytotoxicity of amyloid beta. *Elife*. (2013). 2:e00857. DOI: 10.7554/eLife.00857 PMCID: PMC3713518 [120 citations]
g. Saelices L, Chung K, Lee JH, Benson MD, Bijzet J., Cohn W, Whitelegge, JP, **Eisenberg D**. Amyloid seeding of transthyretin by ex vivo cardiac fibrils: inhibition and implications. *PNAS*, 115, E6741-E6750 www.pnas.org/cgi/doi/10.1073/pnas.1805131115 (2018)
h. Seidler, PM, Boyer, DR, Rodriguez,JA, Sawaya,MR, Cascio,D, Murray,K, Gonen,T, **Eisenberg, DS**. Structure-based inhibitors of tau aggregation. *Nature Chemistry*. **10**, 170-176 (2018). DOI:10.1038/NCHEM.2889 (2017). PMCID: PMC5784779 (120 citations)

3. Computational analysis of amino acid sequences and protein structures: As protein sequences and structures became readily available in the 1980s and 1990s, I developed new methods to extract information from sequences and structures. Paper i describes a new property of proteins—the hydrophobic moment, which has been widely applied to detect periodicities in proteins. Paper j introduced atomic solvation parameters, used subsequently by many to estimate free energy changes of protein folding and binding. Paper k introduced the Profile method for detection of distantly related protein sequences. It was later coded by others into the powerful PsiBlast algorithm. Paper l invented threading of sequences on to structures to identify new proteins having previously determined folds. This method has also been widely applied.

i. **D. Eisenberg**, RM Weiss, TC Terwilliger. The hydrophobic moment detects periodicity in protein hydrophobicity. *Proc. Natl. Acad. Sci. U.S.A.* **81**, 140-144 (1984). PMCID: PMC344626 [1000 citations]
j. **D. Eisenberg**, A.D. McLachlan. Solvation energy in protein folding and binding. *Nature.* **319**,199-203 (1986). PMID: 3945310 [2200 citations]
k. M Gribskov, AD McLachlan, **D Eisenberg**. Profile analysis: detection of distantly related proteins. *Proc. Natl. Acad. Sci. U.S.A.* **84**, 4355-4358 (1987). PMCID: PMC305087 [1600 citations]
l. JU Bowie, R Luthy, **D Eisenberg**. A method to identify protein sequences that fold into a known 3D structure. *Science.* **253**, 164-170 (1991). PMID: 1853201 [3100 citations]

4. Methods for inferring protein interactions and functions from genome sequences. The advent of genome sequencing brought the puzzle of how to infer from this mass of information the function of proteins and the pathways and complexes formed by proteins. Our group, together with the group of Todd Yeates, worked out several methods described in papers m, n, and o. We also began a database of protein interactions described in paper o.

m. Marcotte EM, Pellegrini M, Ng HL, Rice DW, Yeates TO, **Eisenberg D**. Detecting protein function and protein-protein interactions from genome sequences. *Science.* **285**, 751-3 (1999). PMID: 10427000 [2000 citations]
n. Marcotte EM, Pellegrini M, Thompson MJ, Yeates TO, **Eisenberg D.** A combined algorithm for genome-wide prediction of protein function. *Nature.* **402**, 83-6 (1999). PMID: 10573421 [1100 citations]
o. Xenarios I, Salwínski L, Duan XJ, Higney P, Kim SM, **Eisenberg D**. DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. *Nucleic Acids Res.* **30**, 303-5 (2002). PMCID: PMC99070 [1900 citations]

5. Electron microscopy and micro-electron diffraction:

p. Frank J, Goldfarb W, **Eisenberg D**, Baker TS. Reconstruction of glutamine synthetase using computer averaging. [The first report of TEM single particle averaging] *Ultramicroscopy*. **3**, 283-90 (1978). PMCID: PMC4167717 [215 citations]
q. Jose A. Rodriguez, Magdalena Ivanova, Michael R. Sawaya, Duilio Cascio, Francis Reyes, Dan Shi, Smriti Sangwan, Elizabeth Guenther, Lisa Johnson, Meng Zhang, Lin Jiang, Mark Arbing, Julian Whitelegge, Johan Hattne, Brent Nannega, Aaron S. Brewster, Marc Messerschmidt, Sébastien Boutet, Nicholas K. Sauter, Tamir Gonen, **David Eisenberg**. Structure of the toxic core of α-synuclein from invisible crystals *Nature.* **525**, 486-90 (2015). PMCID: PMC4791177 [169 citations]
r. Michael R. Sawaya, Jose Rodriguez, Duilio Cascio, Michael J. Collazo, Dan Shi, Francis E. Reyes, Johan Hattnef, Tamir Gonen, **David S. Eisenberg**. Ab Initio structure determination from prion nanocrystals at atomic resolution by MicroED *PNAS*, **113**, 11232-11236 (2016). 9. PMCID: PMC5056061 [19 citations]
s. de la Cruz, M. Jason; Hattne, Johan; Shi, Dan; Seidler, Paul; Rodriguez, Jose; Reyes, Francis; Sawaya, Michael R.; Cascio, Duilio; Weiss, Simon C.; Kim, Sun Kyung; Hinck, Cynthia S.; Hinck, Andrew P.; Calero, Guillermo; **Eisenberg, David**; Gonen, Tamir Atomic-resolution structures from fragmented protein crystals with the cryoEM method MicroED *Nature Methods.* **14**, 399-402 (2017). PCMID: PMC5376236 [27 citations]

BIOGRAPHICAL SKETCH

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NAME: Sawaya, Michael R.

eRA COMMONS USER NAME (credential, e.g., agency login): sawaya2

POSITION TITLE: Bioinformatics Specialist III

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)	END DATE MM/YYYY	FIELD OF STUDY
San Diego State University, San Diego, California	BS	08/1989	Chemistry
University of California, San Diego, San Diego, California	PHD	12/1994	Biochemistry
Harvard Medical School, Boston, Massachusetts	Postdoctoral Fellow	01/2000	Structural Biology

A. Personal Statement

I have been passionate about imaging biological molecules since 1989, when I learned that a molecule's image can reveal the one thing that distinguishes an inanimate collection of atoms from a life-giving molecule: its structure. At that time, the best technology available to see these biological molecules was X-ray crystallography, so I devoted my graduate and postdoctoral careers to mastering it. Early success awakened in me a second passion -- to share this technology with others. I joined the UCLA-DOE Technology Center in 2000, where my role has been to assist students and postdocs in biological structure determination via formal classes, one-on-one interactions, and authoring tutorials published on the web, in journals, and in books. In this endeavor, I have also been successful. Over my career, I have assisted scientists in over 40 research groups in acquiring images of over 520 biological molecules, resulting in 203 peer-reviewed publications. Occasionally, weak data or limited samples threatened to obscure our view of these molecules. To overcome these problems, I collaborated in the development of new software and technologies, which we have made freely available via web servers and publications. Most recently, advances in electron microscopy have made it possible to illuminate larger pieces of life at the atomic level than previously feasible. The prospect of new discoveries fills me with a new sense of excitement, and I feel compelled to catalyze the spread of this new wave of biological imaging.

1. McPartland L, Heller DM, Eisenberg DS, Hochschild A, Sawaya MR. Atomic insights into the genesis of cellular filaments by globular proteins. Nat Struct Mol Biol. 2018 Aug;25(8):705-714. PubMed PMID: 30076408.
2. Colletier JP, Sawaya MR, Gingery M, Rodriguez JA, Cascio D, Brewster AS, Michels-Clark T, Hice RH, Coquelle N, Boutet S, Williams GJ, Messerschmidt M, DePonte DP, Sierra RG, Laksmono H, Koglin JE, Hunter MS, Park HW, Uervirojnangkoorn M, Bideshi DK, Brunger AT, Federici BA, Sauter NK, Eisenberg DS. De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. Nature. 2016 Nov 3;539(7627):43-47. PubMed PMID: 27680699; PubMed Central PMCID: PMC5161637.
3. Sawaya MR, Rodriguez J, Cascio D, Collazo MJ, Shi D, Reyes FE, Hattne J, Gonen T, Eisenberg DS. Ab initio structure determination from prion nanocrystals at atomic resolution by MicroED. Proc Natl Acad Sci U S A. 2016 Oct 4;113(40):11232-11236. PubMed PMID: 27647903; PubMed Central PMCID: PMC5056061.
4. Sawaya MR, Cascio D, Gingery M, Rodriguez J, Goldschmidt L, Colletier JP, Messerschmidt MM, Boutet S, Koglin JE, Williams GJ, Brewster AS, Nass K, Hattne J, Botha S, Doak RB, Shoeman RL, DePonte DP, Park HW, Federici BA, Sauter NK, Schlichting I, Eisenberg DS. Protein crystal structure obtained at 2.9 Å resolution from injecting bacterial cells into an X-ray free-electron laser beam. Proc Natl Acad Sci U S A. 2014 Sep 2;111(35):12769-74. PubMed PMID: 25136092; PubMed Central PMCID: PMC4156696.

B. Positions and Honors

Positions and Employment

2000 - 2002	Research Faculty, University of California, Los Angeles, Los Angeles, CA
2002 -	Bioinformatics Specialist III, Howard Hughes Medical Institute, UCLA, Los Angeles, CA

Other Experience and Professional Memberships

2010 - 2020	Member, American Crystallographic Association

Honors

2004	Chemical Technologies Advancement Award, University of California, Los Angeles
2005	Herbert Newby McCoy award for outstanding research, University of California, Los Angeles
2006	Herbert Newby McCoy award for outstanding research, University of California, Los Angeles

C. Contribution to Science

1. Molecular Imaging Tutorials and Courses: At any given time, dozens of students are engaged in structural biology projects at UCLA and seek me for guidance. Some questions arise repeatedly regarding basic crystallographic tasks. To address many of these questions, I wrote crystallographic tutorials. Two of these are freely available on the internet, http://people.mbi.ucla.edu/sawaya/tutorials/tutorials.html, and https://pymolwiki.org/index.php/PLoS . For incoming graduate students, I organized a crystallography laboratory course with my colleague, Duilio Cascio, which we teach every winter quarter at UCLA, Chemistry M230D, http://people.mbi.ucla.edu/sawaya/m230d/m230d.html . The students get hand-on experience in every step of structure determination, from crystallization to structure validation. I also deliver a series of lectures in structural biology to an undergraduate audience in a course entitled “Structure, Patterns and Polyhedra,” Chemistry M117, and a lecture in how to illustrate molecules in Chemistry 258, an important skill for successful grant writing.

    a. Mura C, McCrimmon CM, Vertrees J, Sawaya MR. An introduction to biomolecular graphics. PLoS Comput Biol. 2010 Aug 26;6(8)PubMed PMID: 20865174; PubMed Central PMCID: PMC2928806.
    b. Sawaya MR. Characterizing a crystal from an initial native dataset. Methods Mol Biol. 2007;364:95-120. PubMed PMID: 17172762.
    c. Sawaya MR. Crystal Structure Refinement. 1 ed. Muller P, editor. New York: Oxford University Press; 2006. Chapter 11, Protein structure (cross)validation; p.187-196. 213p.
    d. Leslie M. EDUCATION: The Crystallographer's Companion. Science (New York, N.Y.). 2004 July 02; 305(5680):23.

2. A Web Tool to Overcome Severe Anisotropy: The diffraction signal that we measure from a biological molecule in order to acquire its image is often anisotropic, meaning it is strong in some direction(s) of the molecule and weaker in one or two other directions. This anisotropy can cause the image of the molecule to appear featureless, especially in one or two particular dimensions, making it difficult to interpret the structural arrangement of atoms. In 2005, we encountered a case of anisotropy so severe, that we could not complete building an atomic model into the map. After some research, we developed a protocol for scaling and sharpening the signal, which revealed clear details of the molecule’s shape. We assembled a pipeline to perform these tasks and made it available to others as a web server, http://services.mbi.ucla.edu/anisoscale/. The server runs over 3000 jobs per year. Many high-profile structures have benefited from the diffraction anisotropy server. Our paper which first described these methods received 436 citations.

    a. Sawaya MR. Methods to refine macromolecular structures in cases of severe diffraction anisotropy. Methods Mol Biol. 2014;1091:205-14. PubMed PMID: 24203335.
    b. Strong M, Sawaya MR, Wang S, Phillips M, Cascio D, Eisenberg D. Toward the structural genomics of complexes: crystal structure of a PE/PPE protein complex from Mycobacterium tuberculosis. Proc Natl

Acad Sci U S A. 2006 May 23;103(21):8060-5. PubMed PMID: 16690741; PubMed Central PMCID: PMC1472429.

3. New Methods to Image Biological Molecules: The invention of the X-ray free-electron laser in 2010 enabled the production of x-ray pulses one billion times brighter than conventional X-ray radiation sources, thereby opening diffraction-based imaging to smaller samples (crystals) than previously feasible. Sample size is often a limiting factor, especially if the sample is derived from a human, such as an Alzheimer's patient. New developments in electron beam hardware have made it feasible to harness the large scattering cross-section of electrons to image similarly small samples. I advanced both these fields, by developing methods used to acquire phase information, the missing component in the imaging-by-diffraction experiment. We successfully applied heavy atom soaking methods for de novo phasing with the X-ray laser, and *ab inito* phasing with the electron beam. Our work has motivated progress in structural biology labs around the world.

    a. Colletier JP, Sawaya MR, Gingery M, Rodriguez JA, Cascio D, Brewster AS, Michels-Clark T, Hice RH, Coquelle N, Boutet S, Williams GJ, Messerschmidt M, DePonte DP, Sierra RG, Laksmono H, Koglin JE, Hunter MS, Park HW, Uervirojnangkoorn M, Bideshi DK, Brunger AT, Federici BA, Sauter NK, Eisenberg DS. De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure. Nature. 2016 Nov 3;539(7627):43-47. PubMed PMID: 27680699; PubMed Central PMCID: PMC5161637.
    b. Sawaya MR, Rodriguez J, Cascio D, Collazo MJ, Shi D, Reyes FE, Hattne J, Gonen T, Eisenberg DS. Ab initio structure determination from prion nanocrystals at atomic resolution by MicroED. Proc Natl Acad Sci U S A. 2016 Oct 4;113(40):11232-11236. PubMed PMID: 27647903; PubMed Central PMCID: PMC5056061.
    c. Rodriguez JA, Ivanova MI, Sawaya MR, Cascio D, Reyes FE, Shi D, Sangwan S, Guenther EL, Johnson LM, Zhang M, Jiang L, Arbing MA, Nannenga BL, Hattne J, Whitelegge J, Brewster AS, Messerschmidt M, Boutet S, Sauter NK, Gonen T, Eisenberg DS. Structure of the toxic core of α-synuclein from invisible crystals. Nature. 2015 Sep 24;525(7570):486-90. PubMed PMID: 26352473; PubMed Central PMCID: PMC4791177.
    d. Sawaya MR, Cascio D, Gingery M, Rodriguez J, Goldschmidt L, Colletier JP, Messerschmidt MM, Boutet S, Koglin JE, Williams GJ, Brewster AS, Nass K, Hattne J, Botha S, Doak RB, Shoeman RL, DePonte DP, Park HW, Federici BA, Sauter NK, Schlichting I, Eisenberg DS. Protein crystal structure obtained at 2.9 Å resolution from injecting bacterial cells into an X-ray free-electron laser beam. Proc Natl Acad Sci U S A. 2014 Sep 2;111(35):12769-74. PubMed PMID: 25136092; PubMed Central PMCID: PMC4156696.

4. Amyloid Atlas Database: Recent technological advances in solid state NMR and especially cryoEM have suddenly brought the hidden world of amyloid biology into atomic level focus. Over the last 3.5 years the number of full-length amyloid fibril structures more than quadrupled from just 17 to over 80. Using this vastly improved coverage, we expertly illustrate the physical and energetic properties of these structures in a comprehensive database (https://people.mbi.ucla.edu/sawaya/amyloidatlas/). Patterns revealed here suggest that some functional amyloid-like fibrils to be far less stable than pathogenic fibrils.

    e. Michael R. Sawaya, Michael P. Hughes, Jose A. Rodriguez, Roland Riek, David S. Eisenberg. The Expanding Amyloid Family: Pathogenesis, Function, Structure, and Energetics. In preparation.

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/myncbi/michael.sawaya.1/bibliography/public/

D. Additional Information: Research Support and/or Scholastic Performance

Completed Research Support

F32 GM19790-01, National Institutes of Health
Sawaya, Michael (PI)
01/01/99-01/26/00
Crystallization of DNA Replication Proteins

Crystallographic structure determination of gp4 DNA helicase/primase from T7 bacteriophage
Role: PDC

BIOGRAPHICAL SKETCH

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NAME: Jiang, Yi Xiao

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

POSITION TITLE: Ph.D. Candidate

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
McGill University, Montréal, Canada	B.S.	06/2018	Biochemistry
University of California, Los Angeles, Los Angeles, California	Ph.D.	In progress	Molecular Biology

A. Personal Statement

My passion for the basic sciences was cultivated early in my undergraduate career, where I pursued diverse research experiences at McGill University. I joined in Dr. William Muller's group, who was interested in the role of the ErbB2/HER2 proto-oncogene in the development of breast cancer. I designed, experimentally tested, and identified shRNAs that knocked down ErbB2ΔEx16, an oncogenically potent splice variant of ErbB2/HER2. Under the supervision of Dr. Martin Schmeing, I completed my undergraduate honors thesis with the support of an NSERC Undergraduate Student Research Award. I studied microbial mega-enzyme complexes called polyketide synthases (PKSs), which are composed of modular domains and synthesize valuable biomolecules from simple substrates. Using a combination of x-ray crystallography and organic chemistry, I investigated the mechanisms of substrate selection by the gatekeeping thioesterase domain. From this project, I became fascinated by how the structure of proteins enable their life-sustaining functions.

In my graduate studies at UCLA, I am working in Dr. David Eisenberg's laboratory to study proteins associated with amyloid diseases. Dr. Eisenberg is a world-renowned physical biochemist and has an extensive record of mentoring predoctoral and postdoctoral scientists who continue onto prolific careers in academic and industry research. My technical training focuses on computational and structural biology, including x-ray crystallography and cryo-EM. By applying biophysical methods to visualize prion-like protein structures, I seek to understand the molecular mechanisms underlying disorders of protein misfolding and aggregation. I am excited about translating the information learned from atomic-resolution images of pathological protein assemblies into the design of structure-based therapeutics. In addition to my research, I am honing my skills in science teaching and communication by serving as a teaching assistant in undergraduate courses, and presenting my research discoveries at group meetings, conferences, and outreach programs.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2016 Research Assistant, Rosalind & Morris Goodman Cancer Research Center, Montréal, Canada

Other Experiences and Professional Memberships

2015-2017 Council Executive, McGill Biochemistry Undergraduate Society
2017-2018 President, McGill Biochemistry Undergraduate Society
2019-present Member, UCLA Science Policy Group

Honors

2015 Keyfitz Scholar, McGill University
2017 Undergraduate Student Research Award, The Natural Sciences and Engineering Research Council
2017 NSERC Bursary Supplement, Fonds de Recherche du Québec Nature et Technologies
2018 First Class Honours in Biochemistry, McGill University

D. Additional Information: Research Support and/or Scholastic Performance

Scholastic Performance

YEAR	COURSE TITLE	GRADE
	MCGILL UNIVERSITY	
2015	Molecular Biology	B
2015	Introduction to Organic Chemistry I	A
2015	Calculus II	A
2015	Introduction to Physics – Mechanics	A
2016	Molecular Mechanisms of Cell Function	A-
2016	Laboratory Methods in Biochemistry and Molecular Biology I	A
2016	Physical Chemistry in Biological Science I	B-
2016	Introduction to Organic Chemistry II	A-
2016	Introduction to Physics – Electromagnetism	A
2016	Foundations of Programming	A
2016	Metabolic Biochemistry	A
2016	Laboratory Methods in Biochemistry and Molecular Biology II	A-
2016	Introduction to Organic Chemistry III	A-
2016	Principles of Statistics I	A
2016	Mammalian Physiology	A
2017	Introduction to Molecular and Cell Biology	A-
2017	Biochemistry of Macromolecules	B+
2017	Undergraduate Research Project	A
2017	Basic Genetics	A
2017	Advanced Organic Chemistry Laboratory	A
2017	Protein Structure and Function	A-
2017	Nucleic Acids	B+
2017	Research Laboratory in Biochemistry	A
2017	International Migration	A
2018	Science of Storms	A-
2018	Biophysical Methods in Biochemistry	B+
2018	Independent Research	A
2018	Physical Chemistry in Biological Science II	A
	UNIVERSITY OF CALIFORNIA, LOS ANGELES	
2018	Structure, Function and Dynamics of Macromolecular Assemblies	B
2018	Mitochondria, Proteostasis and Neurodegenerative Diseases	A-
2019	Structural Molecular Biology	A-
2019	Structural Molecular Biology Laboratory	A
2019	Scientific Writing	A
2019	Proteomics and Protein Mass Spectrometry	A
2020	Applied Bioinformatics Laboratory for Biologists	A+