BIOGRAPHICAL SKETCH

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NAME: **Elizabeth D'Lauro**

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

POSITION TITLE: **Graduate Student – 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)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Alvernia University, Reading, PA	BS	08/2016	05/2020	Biochemistry, Minor in Mathematics
Drexel University, Philadelphia, PA	Ph.D.	08/2020	05/2026 (Projected)	Biochemistry

A. Personal Statement

Antibiotic resistance is a growing burden on our health care system, threatening the efficacy of our antibiotics. The goal of my research proposal is to investigate the sensing and activation mechanism of a set of clinically threatening pathogens, namely vancomycin-resistant enterococci (VRE). My Ph.D. thesis research aims to study the molecular and structural features of the VRE sensing protein VanS, to discover insights into ways alleviate this public health crisis. Funding for this project will support the training I need to investigate the question of how these pathogens maintain resistance.

Prior to attending university, I had a passion for science and always performed well academically. Yet, with no family or friends in the science field, my path towards science was very self-motivated and independent. It was during my undergrad years when I found a scientific community that allowed me the space to thrive. I joined several science clubs and educational outreach programs that only furthered my desire for a career in science. To gain research experience, my advisor, Dr. David Shoup, helped me construct a project that combined my interests in biomedical research and math. I used computational tools to model and solve complex problems related to pharmaceutical companies to optimize specific constraints in drug development, saving them both time and costs prior to drug production. With this experience, I gained many useful skills in computational modeling, independent thinking, and problem solving. This research also prompted my interest in biomedical research, specifically with drugs, to apply some of the computational knowledge I had acquired to a lab setting. This multidisciplinary background and support from advisors inspired my interest in pursuing graduate training and has provided me with a wide range of skill sets to help me succeed.

As a current graduate student, I quickly gained the necessary skills for bench research. I received individualized training and guidance from professors who promoted my bench skills while encouraging independent thinking. Within my rotations, I excelled in various techniques from computational modeling, protein expression and purification, microbial techniques, and mass spectrometry, all necessary for my proposed research. These rotations allowed me to experience a range of biochemical tools and techniques, allowing me to become a more versatile scientist and researcher.

My current research project combines various biochemical techniques that I have acquired throughout my scientific training. In my thesis lab of Dr. Patrick Loll, I am gaining a deeper understanding of membrane protein purification, structural biology techniques, such as X-ray crystallography and cryo-EM, as well as protein-protein interactions. Dr. Loll is an expert crystallographer with expertise in membrane proteins for both structural and functional studies. Given my proposed goals of studying the molecular and structural features of the VanS sensor protein, Dr. Loll is an excellent mentor to provide guidance for this project. Additionally, I have begun an amazing opportunity to gain first-hand training in cryo-EM at Thomas Jefferson University, under the guidance of Dr. Gino

Cingolani, one of my thesis committee members. This technique is directly applicable to my proposed research and provides individualized training to further my research goals.

During my Ph.D., I seek to investigate the mechanism of activation for VRE and develop into an independent researcher and thinker to aid in my contribution to the scientific community. This project encompasses both structural and functional work, both essential skills for a training biochemist. I plan to use this training to continue to grow my scientific communication skills, such as attending conferences, presenting talks and posters, and publishing my findings. Ultimately, these skills will develop me as a well-rounded scientist with a skill set suitable for a career in either academia or industry.

B. Positions and Honors

Positions and Employment

2016-2018 **Sustainability Outreach Educator***, Alvernia University, Reading, PA*.

2018 **Summer Undergraduate Research Fellow (SURF)**, *Alvernia University*, Project advised by Dr. David Shoup.

2020 **Laboratory Intern at Industrial Metal Plating**, *Reading, PA*.

Academic and Scientific Honors and Awards

2016 - 2020 **Trustees Scholarship**, *Alvernia University*. Awarded to students based on merit prior to beginning school.

2016 – 2020 **Dean's List**, *Alvernia University*. Awarded to students with a cumulative GPA of 3.50 or higher.

2018 – 2020 **Beta Kappa Chi Honor Society**, *Alvernia University*. A national honor society recognizing academic achievement of students in the fields of science and mathematics.

2020 **Summa Cum Laude**, *Alvernia University*. Awarded to graduating students with a cumulative GPA of 3.90 or higher.

2023 **Protein Science Young Investigator Travel Award Recipient** – The Protein Society's Annual Symposium

2023 **Honorable Mention in the Poster Competition** - The Protein Society's Annual Symposium

2023 **Department Seminar** presented to the Department of Biochemistry and Molecular Biology at Drexel University

2024 **Trainee at NCCAT's Annual Single Particle Analysis Short Course Workshop**

2024 **Dean's Travel Award Recipient**

Professional Memberships

2022 – present Member, The Protein Society

2022 – present Member, The American Crystallographic Association (ACA)

2021 – 2022 Member, American Society for Biochemistry and Molecular Biology (ASBMB)

C. Contributions to Science

1. **Summer Undergraduate Research Fellow (SURF) Research Student – 2018** - During my undergraduate career, I was selected for a mathematics-focused summer research project. My advisor, Dr. David Shoup, and I created a project that investigated optimization techniques in pharmaceutical industries. Specifically, my project sought to create an algorithm that would optimize certain constraints within pharmaceutical companies' drug composition, such as drug friability and disintegration. We used reference data of common over-the-counter drugs to select specific restraints to optimize and determine the most effective solution to meet those constraints. We used drug properties and composition from acetaminophen and minimized the amount of disintegration of the pill while still maintaining other drug properties. We used a nonlinear regression method to determine the best-fit equation that computes the best possible solution. Pharmaceutical companies can use these modeling techniques to create complex, nonlinear regression functions to help optimize their workflow in drug development, such as cost constraints.
2. **Graduate Research – 2020** – My first graduate rotation was completed remotely with computational modeling due to COVID, however my previous computational modeling skills aided me in this project. I completed this rotation with Dr. Shae Padrick where we utilized modeling to identify the molecular kinetics that occur in a biological system, given certain parameters. We studied the relationship between actin and a polymerizing complex comprised of Arp2/3 and WASP proteins. We sought to model this

polymerizing interaction by including thermodynamic parameters to model data that would reflect what we see experimentally. We modelled multiple iterations of a range of parameter estimations of the interaction between these proteins with rate laws considered. We expanded this study into the lab to investigate if these results match experimental data.

3. **Graduate Research – 2021** – My third graduate lab rotation was in the lab of Drs. Joris Beld and Amy Ma. During this rotation, my project sought to identify and characterize the biosynthetic pathway of cobamides in two anaerobic species. With previous data identifying three unique pathways responsible for salvaging, remodeling, and synthesizing cobamides (Vitamin B_{12}), my project sought to extend this to unstudied anaerobic species. We used two genera of bacteria isolated from the human gut microbiome, *Prevotella* and *Bacteroides*. Using mass spectrometry, we showed preliminary data that suggests that *Prevotella* can take up supplemented cobamide variants and use its biosynthetic pathways to salvage and remodel cobamide. Identifying the exact mechanism these bacteria utilize for cobamide synthesis will explain how anaerobic bacteria in the gut are able to resource share within distinct bacterial communities.

D. Publications

1. Grasty KC, Guzik C, **D'Lauro EJ**, Padrick SB, Beld J, Loll PJ. “Structure of VanS from vancomycin-resistant enterococci: A sensor kinase with weak ATP binding.” J Biol Chem. 2023 Mar. doi: 10.1016/j.jbc.2023.103001.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Loll, Patrick John

eRA COMMONS USER NAME (credential, e.g., agency login): PLOLL1

POSITION TITLE: Professor of Biochemistry and 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
Catholic University of America, Washington DC	BChE, *Summa cum laude*	05/1981	Chemical Engineering
Johns Hopkins University School of Medicine, Baltimore MD	PhD	05/1989	Biophysics
University of Chicago, Chicago IL	Post-doctoral	05/1995	Membrane Protein Structural Biology

A. Personal Statement

I am a protein biochemist, structural biologist, and protein biophysicist, with experience in a wide range of biochemical and biophysical techniques. Throughout my career,I have studied many proteins and other biomolecules. In particular, I began working with membrane proteins during my post-doctoral fellowship, and have continued studying them ever since. In addition to working with membrane proteins themselves, we also work with various membrane mimetics, including liposomes, lipidic cubic phases, nanodiscs, and SMALPs, and have access to all the instrumentation necessary to characterize these different membrane species. Our lipid expertise has been directly transferable to this collaboration with Dr. Burns, allowing us to readily develop protocols for generating and characterizing lipid nanoparticles.

I received my PhD training with the biophysicist and crystallographer Eaton Lattman, and have continued to work in structural biology and protein biophysics since that time. During my post-doctoral training with Michael Garavito, I obtained extensive training with membrane protein purification and crystallization, and was part of the team that determined the first crystal structure of a eukaryotic membrane protein, COX-1. When I started my own research group, we began our work with natural product antibiotics, while continuing to work in protein chemistry, expression, and purification, and in particular on membrane protein crystallization. As a PI I have been funded by NIH, NASA, the American Heart Association, and the American Cancer Society. Together with Eaton Lattman, I have produced a popular introductory crystallography text. My lab has worked with a wide variety of proteins, ranging from small soluble proteins to membrane proteins to large macromolecular assemblies. Dr. Burns and I have been close colleagues for over twenty years, during which time I have sat on many of his students' thesis committees. I am excited to contribute our expertise to this new vaccine initiative.

Publications I would like to highlight:

1. **Loll, P. J.**, Bevivino, A. E., Korty, B. D., & Axelsen, P. H. (1997) "Simultaneous recognition of a carboxylate-containing ligand and an intramolecular surrogate ligand in the crystal structure of an asymmetric vancomycin dimer." *J. Am. Chem. Soc.* **119**: 1516-1522.
2. Economou, N. J., Nahoum, V., Weeks, S. D., Grasty, K. C., Zentner, I. J., Townsend, T. M., Bhuiya, M. W., Cocklin, S., **Loll, P. J.** (2012) "A carrier protein strategy yields the structure of dalbavancin." *J. Am. Chem. Soc*. **134**: 4637-4645. PMCID: 3304006.

3. Maciunas, L. J., Porter, N., Lee, P. J., Gupta, K., and **Loll, P. J.** (2021) "Structures of full-length VanR from *S. coelicolor* in both the inactive and activated states." *Acta Crystallogr. D,* **77**: 1027-1039. DOI: 10.1107/S2059798321006288. PMCID: 8329863.
4. Grasty, K. C., Guzik, C., D'Lauro, E.J., Padrick, S.B., Beld, J., **Loll, P.J.** (2023) "Structure of VanS from vancomycin-resistant Enterococci: A sensor kinase with weak ATP binding." *J Biol Chem.* in press. doi: 10.1016/j.jbc.2023.103001. PMCID in process.

B. Positions, Scientific Appointments, and Honors

Positions and employment

2007-present	Professor of Biochemistry & Molecular Biology (with tenure) Drexel University College of Medicine, Philadelphia, PA
2001-2007	Associate Professor of Biochemistry & Molecular Biology (with tenure) Drexel University College of Medicine, Philadelphia, PA
1995–2001	Assistant Professor of Pharmacology, University of Pennsylvania School of Medicine, Philadelphia, PA

Other experience and professional memberships

2022	Reviewer, INSERM
2018-present	Member, Editorial Board, Journal of Biological Chemistry
2016	Instructor, SLAC workshop: "Crystallization: Focus on micro and nano crystals & high throughput methods, Stanford University
2012-2018	Regular Member, NIH Macromolecular Structure and Function-B Study Section
2012-2013	Reviewer, Quebec Consortium for Drug Discovery
2012, 2014	Reviewer, Canada Foundation for Innovation
2007, 2009	Member, NIH Membrane Protein Structural Biology Roadmap Study Section
2005-2010	Instructor, NSLS Membrane Protein Crystallization Workshop
2004-2015	External Advisory Board, Membrane Protein Production and Characterization Center of Biomedical Research Excellence, University of Delaware.
2004-2012	Co-editor, Acta Crystallographic Section F
1998-2004	Reviewer, Macromolecular Crystallography Panel, Advanced Light Source
1998-2002	Reviewer, NASA Microgravity Research Program
1987-present	Member, American Crystallographic Association (Secretary, 2012-2014)

Honors

2022	Julian Marsh Faculty Scholar Award, Drexel University
2016	Faculty Teaching Award: PhD Programs, Drexel Graduate School of Biomedical Sciences and Professional Studies
2013	Visiting Professor, Université d'Avignon et des Pays de Vaucluse
2009, 2011	Graduate Student Association Excellence in Teaching Award
2001	Drexel University 10^6 Club Award
1999	Dean's Award for Excellence in Graduate Student Training
1997	Young Researchers' International Aspirin Award
1997	Michael S. Brown Junior Research Award
1995	American Cancer Society Institutional Research Award
1995	University of Pennsylvania Research Foundation Award
1993-1994	Syntex post-doctoral fellowship
1990-1993	Damon Runyon-Walter Winchell Cancer Research Fund fellowship

C. Contributions to Science

1. **Mechanisms of natural-product antibiotics; antibiotic resistance.** Most clinically important antibiotics are derived from natural products; a subset of these molecules are large, peptide-based macrocycles that recognize and sequester components of the bacterium's membrane or cell wall. Importantly, because these antibiotics' targets are not genomically encoded, bacteria cannot directly alter the target's structure via

mutations in the bacterial genome. This feature drastically slows the development of resistance, and makes these compounds particularly interesting as scaffolds for the development of new therapeutics. My laboratory has been a leader in the study of target recognition by large natural-product antibiotics, starting from our determination of the first crystal structure for vancomycin in 1997. Since that time, we have determined structures for a series of vancomycin-ligand complexes and for the vancomycin aglycon, and determined the first crystal structures for ristocetin, teicoplanin, and dalbavancin. We developed a novel carrier protein strategy to facilitate structure determination for such antibiotic-target complexes, and expanded our studies to other antibiotics, publishing the first crystal structures for ramoplanin, tyrocidine, and bacitracin.More recently, we expanded our focus to include the regulation of vancomycin resistance, which is mediated by the VanRS two-component system. The largest open question in this field is how the VanS sensor kinase recognizes the antibiotic, and we have recently been able to answer this question for one of the most common types of vancomycin-resistant enterococci (manuscript in preparation). Our work in this area has sparked our interest in microbial physiology, leading to our excitement about the TonB-ExbD project.

Hamburger, J. B., Hoertz, A. J., Lee, A., Senturia, R. J. McCafferty, D. G., & **Loll, P. J.** (2009) "A crystal structure of a dimer of the antibiotic ramoplanin illustrates membrane positioning and a potential Lipid II docking interface." *Proc. Nat. Acad. Sci. USA*, **106**: 13759-64; PMCID: PMC2728967.

Economou, N. J., Cocklin, S., **Loll, P. J.** (2013) "A high resolution crystal structure reveals the molecular details of target recognition by bacitracin." *Proc. Nat. Acad. Sci. USA*, **110**:14207-14212; PMCID: PMC3761639.

Loll, P. J., Upton, E. C., Nahoum, V., Economou, N. J., & Cocklin, S. (2014) "The high resolution structure of tyrocidine A reveals an amphipathic dimer." *Biochim. Biophys. Acta* **1838**:1199-1207. DOI: 10.1016/j.bbamem.2014.01.033

Upton E. C., Maciunas L. J., **Loll P. J.** (2019) "Vancomycin does not affect the enzymatic activities of purified $VanS_A$." *PLoS One.* **14**(1):e0210627. doi: 10.1371/journal.pone.0210627. PMCID: PMC6345502.

2. **Membrane protein structural biology.** Since my early work on the membrane protein COX-1, I have retained an interest in membrane protein crystallization. Motivated by the conviction that a more comprehensive understanding of the physical forces mediating crystal growth, we have extended the pioneering work of Bill Wilson on the crystallization slot to demonstrate that the second osmotic virial coefficient (B_{22}) is a robust indicator of crystallization for membrane proteins, as well as for soluble proteins. We further showed that the detergent component of the protein-detergent complex is a primary driver of the complex's self-interaction behavior, suggesting that mapping how a detergent's B_{22} values respond to various precipitants could demarcate defined regions of experimental space that would be the most fruitful areas to screen for crystallization of *any* protein solubilized in that detergent; we also developed high-throughput methods to carry out such mapping experiments. These ideas have been picked up by others and contribute to membrane protein screens currently used in some high-throughput screening labs.

Hitscherich, C. Jr., Kaplan, J., Allaman, M., Wiencek, J., & **Loll, P. J.** (2000) "Static Light Scattering Studies of OmpF Porin: Implications for Integral Membrane Protein Crystallization." *Protein Science,* **9**: 1559-1566.

Mattoon, D., Gupta, K., Doyon, J., Loll, **P. J.**, & DiMaio, D. (2001) "Identification of the transmembrane dimer interface of the bovine papillomavirus E5 transforming protein." *Oncogene*, **20**: 3824-3834.

Loll, P. J., Hitscherich, C. Jr., Aseyev, V., Allaman, M., & Weincek, J. (2002) "Assessing Micellar Interaction and Growth in Detergent Solutions Used to Crystallize Integral Membrane Proteins." *Crystal Growth & Design* **2:** 533-539.

Loll, P. J. (2014) "Membrane proteins, detergents, and crystals: What is the state of the art?" *Acta Crystallogr.* **F70**:1576-83. DOI: 10.1107/S2053230X14025035; PMID: 25484203.

3. **Recognition of anesthetics by proteins**. For many years we collaborated with Roderick Eckenhoff in the Department of Anesthesiology and Critical Care at the University of Pennsylvania to investigate the biophysical basis of anesthetic recognition by proteins. Much of this work has been devoted to analysis of anesthetic binding by the model protein apoferritin, which is the highest affinity anesthetic-binding protein currently known. This work has yielded high-resolution structures of the binding sites for halothane, isoflurane,

propofol, and barbiturates, providing insights into the features that control anesthetic recognition and suggesting avenues for the discovery of new anesthetics. More recently, this work has shifted focus toward characterization of anesthestics' interactions with more physiologically relevant ion-channel targets; this initiative is currently funded by a P01 award, and as part of that award we are actively engaged in expressing and purifying potassium channel proteins for structural analysis.

Vedula, L. S., Brannigan, G., Economou, N. J., Xi, J., Hall, M. A., Liu, R., Rossi, M. J., Dailey, W. P., Grasty, K. C., Klein, M. L., Eckenhoff, R. G., & **Loll, P. J.** (2009) "A unitary anesthetic-binding site at high resolution." *J. Biol. Chem*. **284**: 24176-84; PMCID: PMC2782011.

Oakley, S., Vedula, S. L., Bu, W., Meng, Q. C., Xi, J., Liu, R., Eckenhoff, R. G., & **Loll, P. J.** (2012) "Recognition of Anesthetic Barbiturates by a Protein Binding Site: A High Resolution Structural Analysis." *PLoS One* 7: e32070; PMCID: PMC3281113.

Loll, P. J. (2018) "Structural Analysis of Anesthetics in Complex with Soluble Proteins." *Methods Enzymol.* **603**:3-20. PMID: 29673532.

Yang, E., Bu, W., Suma, A., Carnevale, V., Grasty, K.C., **Loll, P. J.**, Woll, K., Bhanu, K., Garcia, B. A., Eckenhoff, R. G., & Covarrubias, M. (2021) "Binding Sites and the Mechanism of Action of Propofol and a Photoreactive Analog in Prokaryotic Voltage-Gated Sodium Channels." *ACS Chem. Neurosci.* **12**: 3898-3914. PMID 34607428.

4. **Josephin family of deubiquitinating enzymes.** The four Josephin proteins make up the smallest of the five human families of deubiquitinating enzymes. The best-studied member of this family, ataxin-3, contains a poly-glutamine repeat, and expansion of this repeat gives rise to the neurodegenerative disease Machado-Joseph disease (spinocerebellar ataxia-type 3). Our group was among the first to characterize aggregation and fibril formation by ataxin-3. We demonstrated that proteolysis of ataxin-3 was not required for fibrillogenesis, as had previously been suggested, and proposed a parallel beta-strand model for fibril structure that has subsequently been found in a variety of amyloid species. More recently, we have determined the crystal structure of the related ataxin-3-like protein (ATXN3L) in complex with a ubiquitin substrate, and characterized the enzymatic activities of all four Josephins, showing that while ataxin-3 and ATXN3L are highly similar structurally, the latter protein possesses a much higher intrinsic activity, suggesting that evolutionary constraints may have kept the activity of ataxin-3 at a low level. As part of our efforts to relate the structure of the poly-ubiquitin substrate to the activities of the various deubiquitinating enzymes, we were also one of several groups to demonstrate that K63-linked polyubiquitin adopts an extended conformation that differs significantly from that of K48-linked ubiquitin chains.

Bevivino, A. E. & **Loll, P. J.** (2001) "An expanded glutamine repeat destabilizes native ataxin-3 structure and mediates formation of parallel beta fibrils." *Proc. Nat. Acad. Sci. USA*, **98**: 11955-11960; PMCID: PMC59749.

Weeks, S. D., Grasty, K. C., Hernandez-Cuebas, L., & **Loll, P. J.** (2011) "Crystal structure of a Josephin-ubiquitin complex: Evolutionary restraints on ataxin-3 deubiquitinating activity." *J. Biol. Chem.* **286**, 4555-4565; PMCID: PMC3039388.

Rao M. V., Williams D. R., Cocklin S., **Loll P. J.** (2017) "Interaction between the AAA+ ATPase p97 and its cofactor ataxin3 in health and disease: Nucleotide-induced conformational changes regulate cofactor binding." *J Biol Chem.* **292**:18392-18407. PMCID: PMC5682953.

Grasty, K. C., Weeks, S. D., & **Loll, P. J.** (2019) "Structural insights into the activity and regulation of human Josephin-2." *J Struct Biol X* **3**:100011. DOI: 10.1016/j.yjsbx.2019.100011. PMCID PMC7337049.

5. **COX-1 and NSAIDs.** The rate-limiting step in the biosynthesis of prostaglandins and related eicosanoid hormones is the conversion of arachidonic acid to prostaglandin H_2, and is catalyzed by the membrane-bound enzyme COX-1 (also known as prostaglandin H_2 synthase). This enzyme is the target of the class of compounds known as non-steroidal antiiflammatory drugs (NSAIDs), which includes such widely used therapeutics as aspirin, ibuprofen, naproxen, and diclofenac. As a post-doctoral fellow in Michael Garavito's laboratory, I participated in the first structure determination of COX-1, which represented the first-ever crystal structure for a eukaryotic membrane protein. I also determined the structure of the enzyme as acetylated by aspirin, thereby providing structural insight into the action of one of the most widely used medications in the

world. After starting my own laboratory, I continued to probe the interactions between NSAIDs and COX-1, resolving a long-standing controversy about the structural basis for different modes of inhibition kinetics (slow tight-binding vs. reversible), characterizing the interaction between the enzyme and novel NSAID derivatives, and producing the highest resolution structure recorded for any COX-1 enzyme.

Picot, D., **Loll, P. J.**, & Garavito, R. M. (1994) "The X-ray crystal structure of the membrane protein prostaglandin H2 synthase-1." *Nature* 367: 243-249.

Loll, P. J., Picot, D., &. Garavito, R. M (1995) "The structural basis of aspirin activity inferred from the crystal structure of inactivated prostaglandin H_2 synthase." *Nat. Struct. Biol.* **2**: 637-643.

Selinsky, B. S., Kupta, K., Sharkey, C. T., & **Loll, P. J.** (2001) "Structural analysis of NSAID binding by prostaglandin H_2 synthase: Time-dependent and time-independent inhibitors elicit identical enzyme conformations." *Biochemistry*, 40: 5172-5180.

Gupta, K., Selinsky, B. S., Kaub, C. J., Katz, A. K., & **Loll, P. J.** (2004) "The 2.0 Å resolution crystal structure of Prostaglandin H_2 Synthase-1: Structural insights into an unusual peroxidase." *J. Mol. Biol.*, **335**: 503-518.

FULL LIST OF PUBLISHED WORK:

http://www.ncbi.nlm.nih.gov/sites/myncbi/patrick.loll.1/bibliography/41557635/public/?sort=date&direction=descending