

BECKMAN YOUNG INVESTIGATOR BIOKSKETCH FORM

NAME OF APPLICANT Armache, Jean-Paul	POSITION TITLE Assistant Professor
INSTITUTION Pennsylvania State University	DATE OF APPOINTMENT: 04/01/2019

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY
Technical University of Lodz, Poland	M.Sc.	2006	<u>Field:</u> Computer Science (Artificial Intelligence) <u>Dissertation:</u> "Evolution of speciation in a system of n -agents performing common tasks" <u>Advisors:</u> Mariusz Zubert and Andrzej Napieralski;
Ludwig-Maximilians-University of Munich, Germany	Ph.D.	2011	<u>Field:</u> Biochemistry (Structural Biology); <u>Dissertation:</u> "5.5Å Structure of the Eukaryotic Ribosome" <u>Advisor:</u> Roland Beckmann;
University of California San Francisco	Postdoctoral scholar	2019	<u>Field:</u> Biochemistry and Biophysics (Structural Biology). <u>Advisor:</u> Yifan Cheng

A. Personal Statement -

- Briefly describe why your experience and qualifications make you particularly well-suited to conduct the proposed research:

I am an expert in computational biology, having worked in the field of structural biology for the past thirteen years. I received a M.Sc. in Computer Science with a major in Artificial Intelligence and Software Engineering. I have a strong algorithmic base, excellent understanding of the methods applied in structural biology and digital signal processing and I always stay on top of the new technology. This is why method development has always been a strong part of what I envisioned to pursue in my lab. In the past, during my postdoctoral research, I participated in the development of MotionCor2, the most popular motion-correction software in the world. As a structural biologist, I am very aware of the benefits and deficiencies of current high-resolution technologies and I will use this knowledge to develop techniques to overcome these insufficiencies. In my laboratory, we work also on the ATP-dependent chromatin remodeling complexes, that will be perfect testbed for optimizing the technology. My lab will build the platform and will use it to study the dynamics of chromatin remodeling using AFM under varying solution conditions.

- How is the proposed research unique/novel/cutting edge:

The project will represent a paradigm shift in our ability to simultaneously elucidate the structure and dynamics of macromolecules. We will use machine learning and state-of-the-art image analysis algorithms and will use some of the techniques applied in the field of cryo-EM. Furthermore, we will use the IBM Watson complex data mining and natural language processing to parse millions of publications to extract information and overlay it on our visual layers. We will process and generate molecular movies with minimal noise from AFM images and use this to generate constraints for molecular dynamics refinement. We will simplify dynamics measurements and will correlate them with other structural and non-structural information from a plethora of sources. Finally, we will provide for the first time ever the complete picture of chromatin remodeling process, during the ATP hydrolysis and in the presence and absence of a variety of factors.

- Briefly describe your current research project(s):

Our lab is currently working on a number of projects. In March 2020 we were awarded a Covid19 Seed Grant to study translation and modulation of viral and host proteins in the host cell. This project is ongoing, and we expect the results to show a paradigm shift in understanding Coronavirus translation.

We have two ongoing ATP-dependent chromatin-remodeling projects that will lead us to high-resolution cryo-EM maps, but will also allow us to optimize the single-particle AFM technique.

Finally, we are investigating two membrane proteins, one in bacteria and another in Eukarya and we hope that the proposed technology development project will also benefit our studies in this field.

B. Positions and Honors

List in chronological order previous positions, concluding with the present position.

ACTIVITY/OCCUPATION	BEGINNING DATE (MM/DD/YYYY)	ENDING DATE (MM/DD/YYYY)	FIELD	INSTITUTION/COMPANY	SUPERVISOR/EMPLOYER
Graduate Student	02/15/07	07/31/11	Biochemistry	Ludwig-Maximilians-University of Munich	Roland Beckmann
Postdoctoral scholar	08/01/11	03/31/13	Biochemistry	Ludwig-Maximilians-University of Munich	Roland Beckmann
Postdoctoral scholar	05/01/13	03/31/19	Biochemistry	University of California San Francisco	Yifan Cheng
Assistant Professor	04/01/19	-	Biochemistry	Pennsylvania State University	Wendy Hanna-Rose

Academic and Professional Honors

List any honors. Include memberships.

2017-2018 Member of Biophysical Society
2015-2016 Member of American Heart Association
2011 Römer Award, Ludwig-Maximilians-University of Munich, Munich, Germany
2011 Ph.D. *Summa cum laude* in Biochemistry, Ludwig-Maximilians-University of Munich, Munich, Germany
2006 M.Sc. awarded with distinction in computer science, Technical University of Lodz, Lodz, Poland

C. Publications

Total number of peer-reviewed journal publications: 23 + 2 review articles (Complete list of published work in MyBibliography: <https://www.ncbi.nlm.nih.gov/sites/myncbi/1N3onuzkv59kL/collections/59025012/public/>)

List **ALL** articles in peer-reviewed journal publications in which you were the first/second and/or senior author (* marks "contributed equally; underlining of the name is there only to make it more readable for the reviewers)

1. Armache JP, Cheng Y. *Single-particle cryo-EM: beyond the resolution*. Natl Sci Rev. 2019 Oct;6(5):864-866. doi: 10.1093/nsr/nwz127. Epub 2019 Sep 2. PMID: 31867130; PMCID: PMC6911652.
2. Armache JP*, Gamarra N*, Johnson SL, Leonard JD, Wu S, Narlikar GJ, Cheng Y. *Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome*. Elife. 2019 Jun 18;8:e46057. doi: 10.7554/eLife.46057. PMID: 31210637; PMCID: PMC6611695.
3. Valencia-Sánchez MI, De Ioannes P, Wang M, Vasilyev N, Chen R, Nudler E, Armache JP, Armache KJ. *Structural Basis of Dot1L Stimulation by Histone H2B Lysine 120 Ubiquitination*. Mol Cell. 2019 Jun 6;74(5):1010-1019.e6. doi: 10.1016/j.molcel.2019.03.029. Epub 2019 Apr 10. PMID: 30981630; PMCID: PMC7009778.
4. Nguyen NX, Armache JP, Lee C, Yang Y, Zeng W, Mootha VK, Cheng Y, Bai XC, Jiang Y. *Cryo-EM structure of a fungal mitochondrial calcium uniporter*. Nature. 2018 Jul;559(7715):570-574. doi: 10.1038/s41586-018-0333-6. Epub 2018 Jul 11. PMCID: PMC6063787.
5. Wu S, Armache JP, Cheng Y. *Single-particle cryo-EM data acquisition by using direct electron detection camera*. Microscopy (Oxf). 2016 Feb;65(1):35-41. doi: 10.1093/jmicro/dfv355. Epub 2015 Nov 6. PMID: 26546989; PMCID: PMC4749049.
6. Paulsen CE*, Armache JP*, Gao Y, Cheng Y, Julius D. *Structure of the TRPA1 ion channel suggests regulatory mechanisms*. Nature. 2015 Apr 23;520(7548):511-7. doi: 10.1038/nature14367. Epub 2015 Apr 8. PMCID: PMC4409540.
7. Anger AM*, Armache JP*, Berninghausen O, Habeck M, Subklewe M, Wilson DN, Beckmann R. *Structures of the human and Drosophila 80S ribosome*. Nature. 2013 May 2;497(7447):80-5. doi: 10.1038/nature12104. PMID: 23636399.
8. Armache JP*, Anger AM*, Márquez V, Franckenberg S, Fröhlich T, Villa E, Berninghausen O, Thomm M, Arnold GJ, Beckmann R, Wilson DN. *Promiscuous behaviour of archaeal ribosomal proteins: implications for eukaryotic ribosome*

evolution. Nucleic Acids Res. 2013 Jan;41(2):1284-93. doi: 10.1093/nar/gks1259. Epub 2012 Dec 6. PMID: 23222135; PMCID: PMC3553981.

9. Becker T, Armache JP, Jarasch A, Anger AM, Villa E, Sieber H, Motaal BA, Mielke T, Berninghausen O, Beckmann R. *Structure of the no-go mRNA decay complex Dom34-Hbs1 bound to a stalled 80S ribosome*. Nat Struct Mol Biol. 2011 Jun;18(6):715-20. doi: 10.1038/nsmb.2057. Epub 2011 May 29. PMID: 21623367.
10. Armache JP*, Jarasch A*, Anger AM*, Villa E, Becker T, Bhushan S, Jossinet F, Habeck M, Dindar G, Franckenberg S, Marquez V, Mielke T, Thomm M, Berninghausen O, Beatrix B, Söding J, Westhof E, Wilson DN, Beckmann R. *Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution*. Proc Natl Acad Sci U S A. 2010 Nov 16;107(46):19748-53. doi: 10.1073/pnas.1009999107. Epub 2010 Oct 27. PMID: 20980660; PMCID: PMC2993355.
11. Armache JP*, Jarasch A*, Anger AM*, Villa E, Becker T, Bhushan S, Jossinet F, Habeck M, Dindar G, Franckenberg S, Marquez V, Mielke T, Thomm M, Berninghausen O, Beatrix B, Söding J, Westhof E, Wilson DN, Beckmann R. *Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome*. Proc Natl Acad Sci U S A. 2010 Nov 16;107(46):19754-9. doi: 10.1073/pnas.1010005107. Epub 2010 Oct 25. PMID: 20974910; PMCID: PMC2993421.