

Tomasz Osinski

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Education

2016 PhD in Bioinformatics

Adam Mickiewicz University in Poznan, Poland

“Determination of the spatial structure and comparative analysis of selected inhaled allergens and their complexes with antibodies” *Advisors: Prof. Janusz M. Bujnicki and Prof. Wladek Minor (University of Virginia)*

2008 MSc in Biology (spec. Bioinformatics)

Adam Mickiewicz University in Poznan, Poland

“Use of the Machine Learning Approach in the Prediction of RNA Tertiary Structures”
Advisor: Prof. Janusz M. Bujnicki

2006 BSc. in Biology (spec. Bioinformatics)

Adam Mickiewicz University in Poznan, Poland & Polish Academy of Sciences in Poznan, Poland

“Rules for Designing of the siRNA Reagents as Tools for Genetic Diseases Therapy”
Advisors: Prof. Wlodzimierz J. Krzyzosiak and Prof. Artur Jarmolowski

Qualifications

- Extensive experience in providing computing support at various stages of research projects
- Advanced **Python/shell** programming and workflow automation
- In-depth knowledge in general IT, scientific computing, **HPC (GPGPU, OpenMP, slurm)** - including system design and setup of **cluster system** (workstations, servers and low-latency networking)
- Ability to identify and resolve system performance problems and bottlenecks
- Ability to optimize Cryo Electron Microscopy data workflow
- Ability to analyze 3D data from Cryo Electron Microscopy
- Many years of experience with teaching, explaining and presenting computational workflow to non-technical audience
- Ability to properly set and follow timelines for particular tasks, as well as provide the details about the possible/actual delays
- Ability to improve existing systems performance, often by going above and beyond to achieve best in-class standards; always paying attention to details, while having the bigger picture in mind

Experiences

5/2016 University of Virginia; Postdoctoral Research Associate

– *Department of Molecular Physiology and Biological Physics and*

present *Department of Biochemistry and Molecular Genetics*

- design, setup and deployment of the cluster for hosting of web services (**Proxmox, LXC, KVM virtualization, NFS, ZFS**) with High Availability capabilities

- successful migration of the existing infrastructure to the containers (**LXC, NFS**):
 - CSGID: <https://csgid.org>
 - IRRMC: <https://proteindiffraction.org>
- successful disaster recoveries during hardware failures of disk arrays (controller/disk failure)
- Automatization of the computational workflow for Cryo Electron Microscopy (CryoEM) lab (**Python, shell scripts**):
 - Data maintenance - deduplication
 - Data archival – compression and transfer to cold storage
- 3D protein structural data visualization
- design, optimization and delivery of **HPC** for **CryoEM** (use of **GPGPU** and **OpenMP**) and computing resources for X-ray crystallography
- design, setup and administration of disk arrays for CryoEM data storage (1.5PB total; **ZFS**; 40GigE net)
- design, setup and administration of 15 HPC Linux workstations for CryoEM data processing (each 2x18core CPU, 2xGPU, 768GB RAM, 10GbE net)
- design and setup of a low-latency network for data transfers to CryoEM HPC workstations (**pfsense**, 10/40GbE network)

10/2014 University of Virginia, Laboratory Specialist

– *Department of Molecular Physiology and Biological Physics*

- 5/2016**
- design and deployment of a backup/recovery system (based on ZFS features)
 - management and deployment of large-scale filesystems (ZFS; over 0.5PB total)
 - successful disaster recoveries during various failures of disk arrays (controller/disk failure)
 - successful migration of the existing infrastructure to new equipment and systems
 - research on solving structures of protein complexes with X-ray crystallography
 - designing and providing computing resources for X-ray crystallography

9/2008 University of Virginia, Visiting Graduate Student

– *Department of Molecular Physiology and Biological Physics*

- 12/2013**
- computing support work for High Throughput X-ray crystallography laboratory
 - sysadmin of >30 workstations for X-ray protein crystallography data analysis
 - providing the backend for Structural Genomics projects (some do not exist anymore):
 - Center for Structural Genomics of Infectious Diseases (<https://csgid.org>)
 - New York Center for Structural Genomics (project discontinued by NIH)
 - Midwest Center for Structural Genomics (project discontinued by NIH)
 - design and assembly of multiple (>10) servers and disk arrays for handling and serving X-ray crystallography data through websites

Other activities

2017 – present | Membership in the American Biophysical Society

2013 – present | Membership in the American Crystallography Association

Publications

1 • Structures of filamentous viruses infecting hyperthermophilic archaea explain DNA stabilization in extreme environments.

Wang F, Baquero DP, Beltran LC, Su Z, **Osinski T**, Zheng W, Prangishvili D, Krupovic M, Egelman EH.
Proc Natl Acad Sci U S A. 2020 Aug 18 doi: 10.1073/pnas.2011125117

2 • Structure of a filamentous virus uncovers familial ties within the archaeal virosphere

Wang F, Baquero DP, Su Z, **Osinski T**, Prangishvili D, Egelman EH, Krupovic M.
Virus Evol. 2020 Apr 29 doi: 10.1093/ve/veaa023

3 • The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years.

Grabowski M, Cymborowski M, Porebski PJ, **Osinski T**, Shabalin IG, Cooper DR, Minor W.
Struct Dyn. 2019 Nov 22;6(6):064301. doi: 10.1063/1.5128672

4 • Ambidextrous helical nanotubes from self-assembly of designed helical hairpin motifs.

Hughes SA, Wang F, Wang S, Kreutzberger MAB, **Osinski T**, Orlova A, Wall JS, Zuo X, Egelman EH, Conticello VP.
Proc Natl Acad Sci U S A. 2019 Jul 1. pii: 201903910. doi: 10.1073/pnas.1903910116

5 • An extensively glycosylated archaeal pilus survives extreme conditions.

Wang F, Cvirkaite-Krupovic V, Kreutzberger MAB, Su Z, de Oliveira GAP, **Osinski T**, Sherman N, DiMaio F, Wall JS, Prangishvili D, Krupovic M, Egelman EH.
Nat Microbiol. 2019 May 20. doi: 10.1038/s41564-019-0458-x

6 • Structural conservation in a membrane-enveloped filamentous virus infecting a hyperthermophilic acidophile.

Liu Y, **Osinski T**, Wang F, Krupovic M, Schouten S, Kasson P, Prangishvili D, Egelman EH.
Nat Commun. 2018 Aug 22;9(1):3360. doi: 10.1038/s41467-018-05684-6

7 • Cryoelectron Microscopy Reconstructions of the Pseudomonas aeruginosa and Neisseria gonorrhoeae Type IV Pili at Sub-nanometer Resolution.

Wang F, Coureuil M, **Osinski T**, Orlova A, Altindal T, Gesbert G, Nassif X, Egelman EH, Craig L.
Structure. 2017 Sep 5;25(9):1423-1435.e4. doi: 10.1016/j.str.2017.07.016

8 • Antigenic Determinants of Der p 1: Specificity and Cross-Reactivity Associated with IgE Antibody Recognition.

Glesner J, Vailes LD, Schlachter C, Mank N, Minor W, **Osinski T**, Chruszcz M, Chapman MD, Pomés A.
J Immunol. 2017 Feb 1;198(3):1334-1344. doi: 10.4049/jimmunol.1600072

9 • Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria.

Majorek KA, **Osinski T**, Tran DT, Revilla A, Anderson WF, Minor W, Kuhn ML.
Biochim Biophys Acta Proteins Proteom. 2017 Jan;1865(1):55-64. doi: 10.1016/j.bbapap.2016.10.011

10 • Dissecting the Structural Elements for the Activation of β -Ketoacyl-(Acyl Carrier Protein) Reductase from *Vibrio cholerae*.

Hou J, Zheng H, Chruszcz M, Zimmerman MD, Shumilin IA, **Osinski T**, Demas M, Grimshaw S, Minor W. *J Bacteriol.* 2015 Nov 9;198(3):463-76. doi: 10.1128/JB.00360-15

11 • Structural analysis of Der p 1-antibody complexes and comparison with complexes of proteins or peptides with monoclonal antibodies

Osinski T, Pomés A, Majorek KA, Glesner J, Offermann LR, Vailes LD, Chapman MD, Minor W, Chruszcz M. *J Immunol.* 2015 Jul 1;195(1):307-16. doi: 10.4049/jimmunol.1402199

12 • The major cockroach allergen Bla g 4 binds tyramine and octopamine.

Offermann LR, Chan SL, **Osinski T**, Tan YW, Chew FT, Sivaraman J, Mok YK, Minor W, Chruszcz M. *Mol Immunol.* 2014 Jul;60(1):86-94. doi: 10.1016/j.molimm.2014.03.016

13 • Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins.

Chruszcz M, Ciardiello MA, **Osinski T**, Majorek KA, Giangrieco I, Font J, Breiteneder H, Thalassinou K, Minor W.

Mol Immunol. 2013 Dec;56(4):794-803. doi: 10.1016/j.molimm.2013.07.004

14 • *Alternaria alternata* allergen Alt a 1: a unique β -barrel protein dimer found exclusively in fungi.

Chruszcz M, Chapman MD, **Osinski T**, Solberg R, Demas M, Porebski PJ, Majorek KA, Pomés A, Minor W. *J Allergy Clin Immunol.* 2012 Jul;130(1):241-7.e9. doi: 10.1016/j.jaci.2012.03.047

15 • Molecular determinants for antibody binding on group 1 house dust mite allergens.

Chruszcz M, Pomés A, Glesner J, Vailes LD, **Osinski T**, Porebski PJ, Majorek KA, Heymann PW, Platts-Mills TA, Minor W, Chapman MD.

J Biol Chem. 2012 Mar 2;287(10):7388-98. doi: 10.1074/jbc.M111.311159

16 • Unmet challenges of structural genomics.

Chruszcz M, Domagalski M, **Osinski T**, Wlodawer A, Minor W.

Curr Opin Struct Biol. 2010 Oct;20(5):587-97. doi: 10.1016/j.sbi.2010.08.001

Electron Microscopy Map Deposits in EM Data Bank (8 maps)

EMD-21094, EMD-20083, EMD-0252, EMD-9136, , EMD-7797, EMD-8739, EMD-8740

Protein Structure Deposits in Protein Data Bank (39 structures)

6HQE, 6D5F, 5VCO, 4VCN, 5JPH, 4POZ, 4IHR, 3P7M, 3III, 4WEQ, 4U13, 4N7C, 4N7D, 4N18, 4MOU, 4IGV, 4IGW, 4IGX, 4IGY, 4IHO, 4IH2, 4KUB, 4JYK, 4JXQ, 4JRO, 4JFR, 4IJK, 4IIV, 4IIU, 4IIN, 4I08, 4H31, 4GQA, 3V0R, 3TZH, 3TL2, 3RSH, 3RRO, 3IB3