

## Piotr Zenon Kozbial, Ph.D.

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### Career objective

Next Generation Sequencing. Epigenetic, Architectural, and Transcriptome Strategies of Regulated Gene Expression Programs.

### Skills

- Expertise in **biochemical analysis** (DNA, RNA, and protein) and computational analysis of the relationships between sequence, molecular structure, and protein function.
- **Postdoctoral experience in structural genomics, bioinformatics, wiki-based collaboration platforms, and Linux-based research computing.**
- Seven years of **teaching experience**. Organized and taught courses in Plant Molecular Biology and Plant Molecular Biotechnology to third- and fourth-year students at Warsaw University and directed three graduate students in their M.Sc. research projects.
- Expert in computational inference of protein function, analysis of molecular interactions, modeling of protein, and RNA structure. Annotated about 160 novel proteins and identified components of several metabolic pathways from fungi, human microbiome, and environmental metagenome dataset. Characterized proteins with potential application in biotechnology (cellulose and xylose degrading enzymes, starch-binding homologs of SusD, dye decolorizing peroxidases, O-antigen biosynthesis proteins, proteases, and methyltransferases).
- **Hands-on experience in molecular biology, biochemistry, and genetics**, including design, expression, purification, and characterization of recombinant proteins; analysis of **protein interactions in chromatin**; subcellular localization of engineered proteins (fluorescent microscopy); analysis of post-translational modifications (immunodetection, autoradiography, and mass spectrometry); enzymatic manipulation and analysis of DNA and RNA; construction and screening of recombinant cDNA libraries; genetic transformation; genotyping (PCR and Southern blot hybridization); and discovery and analysis of differentially expressed genes (RT-PCR and northern blot).
- Experience in **chromatin biology**, comparative fungal genomics, metagenomics, epigenetics, and factors affecting plant cell wall thickening.
- Excellent ability to multitask, usually working on 2–3 projects at the same time.
- Ability to rapidly assimilate and **mine scientific literature** in the life sciences and bioinformatics.
- Highly **collaborative** and **self-directed**.

### Education

- **2003, Ph.D. in Molecular Biology**, University of Warsaw, Poland. Research supervisor: Andrzej Jerzmanowski, **Howard Hughes Medical Institute** International Research Scholar; Web site: <http://www.hhmi.org/research/scholars/jerz.html>
- **1995, M.Sc. in Molecular Biology**, University of Warsaw, Poland.

### Other Information

- **U.S. Permanent Resident** legally authorized to work for any employer in the United States. Citizen of Poland legally authorized to work and travel within the majority of European countries.
- Willing to relocate within the U.S. for an attractive opportunity.

## Professional experience

### Senior Statistician

06/2009-current

University of California San Diego, La Jolla, CA, USA, Department of Medicine

- Investigate regulatory, architectural, and integrative strategies responsible for orchestrating nuclear programs of genome-wide transcriptional responses to diverse signaling pathways.

### Postdoctoral Associate

04/2006–04/2009

Burnham Institute for Medical Research, La Jolla, CA, USA, Joint Center for Structural Genomics, Bioinformatics Core headed by Prof. Adam Godzik.

- Published **six research papers over the last two years** exploring:
  - (a) ten novel families of RNA-binding LSm/Sm-like proteins of putative viral origin,
  - (b) three regulatory proteins involved in bacterial cell division and sporulation,
  - (c) heme binding in two novel dye-decolorizing peroxidases,
  - (d) ADP-ribosylated protein.
- Annotated ~160 novel proteins with structures solved by the Joint Center for Structural Genomics. PDB codes: 3ffr, 3ff0, 3f9t, 3f6t, 3f1z, 3ezu, 3egr, etc.
- Prepared over 120 protein structure summaries for **www.topsan.org**.
- Developed computational analysis pipeline for protein structure analysis on a computer cluster.

### Postdoctoral Research Associate

06/2003–04/2006

Stowers Institute for Medical Research, Kansas City, MO, USA, Bioinformatics Center headed by Prof. Arcady Mushegian.

- Predicted conserved non-protein coding regions in fungal genomes.
- Published thorough examination of all S-adenosyl-L-methionine-binding proteins. This work was cited 32 times and is **one of BMC Structural Biology's most-viewed articles of all time**.
- Co-authored publication about SWI3 protein. This work was cited 20 times by other scientists investigating chromatin remodeling, epigenetic regulators of development, and retinoblastoma orthologs.
- Presented research at the International Conference on Modeling of Protein Interactions in Genomes, Lawrence, KS, USA.
- Participated in CASP6 competition (Critical Assessment of Techniques for Protein Structure Prediction).

### Predoctoral Associate

10/1995–05/2003

University of Warsaw, Poland, Laboratory of Plant Molecular Biology headed by Prof. Andrzej Jerzmanowski. Thesis title: "Differential analysis of gene expression in *Nicotiana tabacum* with a reduced level of major histone H1 variants."

- Published three research papers.

- **Trained third- and fourth-year students** in molecular biology techniques by organizing and teaching practical courses. Directed graduate students in their M.Sc. research projects.
- Was awarded Grant BW (1996, 1998, and 2000).
- Obtained **6 years of experience in administration of Linux/Windows computer network** in Laboratory of Plant Molecular Biology.

## Publications

1. Das D, **Kozbial P**, et al. (2009) 'Crystal structure of a novel Sm-like protein of putative cyanophage origin at 2.60 Å resolution.' *Proteins: Structure, Function, and Bioinformatics*. 75(2):296-307.
2. Xu Q, et al. (2009) 'A Structural Basis for the Regulatory Inactivation of DnaA.' *J Mol Biol*. 385(2):368-380.
3. **Kozbial P**, Xu Q, Chiu HJ, et al. (2008) 'Crystal structures of MW1337R and lin2004: Representatives of a novel protein family that adopt a four-helical bundle fold.' *Proteins: Structure, Function, and Bioinformatics*. 71(3):1589-1596.
4. Xu Q, **Kozbial P**, et al. (2008) 'Crystal structure of an ADP-ribosylated protein with a cytidine deaminase-like fold, but unknown function (TM1506), from *Thermotoga maritima* at 2.70 Å resolution.' *Proteins: Structure, Function, and Bioinformatics*. 71(3):1546-1552.
5. Zubieta C, Krishna SS, Kapoor M, **Kozbial P**, et al. (2007) 'Crystal Structures of Two Novel Dye-decolorizing Peroxidases Reveal a β-barrel Fold with a Conserved Heme-binding Motif.' *Proteins: Structure, Function, and Bioinformatics*. 69(2):223-33.
6. Zubieta C, et al. (2007) 'Identification and Structural Characterization of Heme Binding in a Novel Dye-decolorizing Peroxidase, TyrA.' *Proteins: Structure, Function, and Bioinformatics*. 69(2):234-43.
7. **Kozbial PZ**, and Mushegian AR. (2005) 'Natural history of S-adenosylmethionine-binding proteins.' *BMC Struct Biol*. 5:19.
8. Sarnowski TJ, et al. (2005) 'SWI3 Subunits of Putative SWI/SNF Chromatin-Remodeling Complexes Play Distinct Roles during *Arabidopsis* Development.' *Plant Cell*. (9):2454-72.
9. Calikowski T, **Kozbial P**, Kuras M, and Jerzmanowski A. (2000) 'Perturbation in linker histone content has no effect on the cell cycle but affects the cell size of suspension grown tobacco BY-2 cells.' *Plant Sci*. 157:51-63.
10. **Kozbial PZ**, Jerzmanowski A, Shirsat AH and Kacperska A. (1998) 'Transient freezing regulates expression of extensin-type genes in winter oilseed rape.' *Physiologia Plantarum* 103:264-270.
11. Shirsat AH, Wiczorek D, and **Kozbial P** (1996) 'A gene for *Brassica napus* extensin is differentially expressed on wounding.' *Plant Mol. Biol*. 30: 1291-1300.

## Selected presentations

**2008**—International Conference on Metagenomics, La Jolla, CA, USA. "Annotation of an Sm-like Protein from the Environmental Metagenome Dataset."

**2008**—Protein Structure Initiative "Bottlenecks" Workshop, Bethesda, MD, USA.  
"Improving the Accuracy of High-Throughput Protein Structure Annotation."

**2008**—Workshop on the Biological Annotation of Novel Proteins, San Diego, CA, USA.  
"Exploring the Unknown Regions of Protein Structure Space."

**2006**—2<sup>nd</sup> Automated Function Prediction Meeting, University of California, San Diego, CA, USA. "The Open Protein Structure Annotation Network."

**2005**—International Conference on Modeling of Protein Interactions in Genomes, Lawrence, KS, USA. "Natural History of S-adenosylmethionine Binding Proteins: Structural, Functional, and Evolutionary Relationships."