Andrew Magis
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EDUCATION

Ph.D. student – Biophysics **2008-Present**
University of Illinois – Urbana-Champaign, IL
Laboratory of Nathan D. Price

Master of Science – Computer Science **2005-2007**
University of Florida – Gainesville, FL
Emphasis in Computational Biology

Bachelor of Science – Computer Science **1998-2003**
Harvey Mudd College – Claremont, CA

PROFESSIONAL EXPERIENCE

Assistant Director **May 2007-June 2008**

Structure-Based Drug Design Laboratory, University of Florida Shands Cancer Center

Integrated UF High Performance Computing center with UF Shands Cancer Center to expand computational docking services to College of Medicine.

Developed software to assist in analysis and presentation of computational docking results

Successfully solved the 3-dimensional structures of seven x-ray crystallography data sets which have been submitted to the Protein Data Bank

Assisting other researchers with computational approaches to biological problems.

Research Assistant **January 2007-May-2007**

David Ostrov, Ph.D., Department of Pathology, Immunology, and Laboratory Medicine, University of Florida

Structure-based drug design and X-ray crystallography analysis

Research Assistant / Software Developer **January 2006-August 2006**

Peter Sayeski, Ph.D., Department of Physiology and Functional Genomics, University of Florida

Perform structure-based analysis of Janus Kinase 2 protein binding sites for ligand-based inhibition. Used UF High Performance Computing supercomputer and UCSF DOCK package.

Successfully scanned over 1.2 million potential compounds for inhibitory effects.

Developed two software packages to contribute to the DOCK library: http://dock.compbio.ucsf.edu/Contributed_Code/index.htm

Network Administrator / Webmaster **June 2003-June 2008**
Tree of Life Bookstore, Seattle, WA

Network Administrator / Webmaster **June 2003-June 2005**
The 412(i) Company, Bellingham, WA

Research Assistant / Software Developer **May 2002-August 2002**
Mike Cummings, Ph.D., Marine Biology Laboratory, Woods Hole, MA

Optimized Smith-Waterman algorithm for protein-protein and DNA-DNA local sequence alignment.

Core of algorithm rewritten in assembly for MMX, SSE, and SSE2 Intel processors

PUBLICATIONS

E.V. Kurenova, D.L. Hunt, D. He, **A.T. Magis**, D.A. Ostrov, W.G. Cance. The small molecule chloropyramine hydrochloride (C4) targets the binding site of Focal Adhesion Kinase and Vascular Endothelial Growth Factor Receptor 3 and suppresses breast cancer growth *in vivo*. *J. Med. Chem.* (2009). *In Press.*

C.P. Ojano-Dirain, **A.T. Magis**, D.A. Ostrov, P.W. Stacpoole. Structure-based Drug Design in the Search for New Treatment of Mitochondrial Diseases. *Mitochondrian*. 9(1): 68 (2009).

A.T. Magis, K.M. Bailey, E.V. Kurenova, J.A. Hernandez Prada, W.G. Cance, D.A. Ostrov. Crystallization of the focal adhesion kinase targeting (FAT) domain in a primitive orthorhombic space group. *Acta Crystallographica*. F64: 564-6 (2008).

J.P. Cannon, R.N. Haire, **A.T. Magis**, D.D. Eason, K.N. Winfrey, J.A. Hernandez Prada, K.M. Bailey, J. Jakoncic, G.W. Litman and D.A. Ostrov. A bony fish immunological receptor of the NITR multigene family mediates allogeneic recognition. *Immunity.* 29(2): 228-37. (2008).

V.M. Golubovskaya, C. Nyberg, M. Zheng, F. Kweh, **A. Magis**, D. Ostrov, and W.G. Cance. A small molecule inhibitor, 1,2,4,5-benzenetetraamine tetrahydrochloride, targeting the Y397 site of focal adhesion kinase decreases tumor growth. *J. Med. Chem*. 51(23): 7405-16 (2008).

J. Sayyah, **A. Magis**, D.A. Ostrov, R.W. Allen, R.C. Braylan and P.P. Sayeski. Z3, a novel Jak2 tyrosine kinase small-molecule inhibitor that suppresses Jak2-mediated pathologic cell growth. *Mol. Cancer Ther*. 7(8): 2308-18 (2008).

D.A Ostrov, J.A. Hernandez Prada, R.N. Haire, J.P. Cannon, **A.T. Magis**, K. Bailey and G.W. Litman. Crystallization and X-ray diffraction analysis of a Novel Immune-Type Receptor from *Ictalurus punctatus* and Phasing by Se Anomalous Dispersion Methods. *Acta Crystallographica*. F63: 1035-7 (2007).

Protein Data Bank submissions: 2QHL 2QJD 2QQQ 2QTE 2RA7 3B5T 3BDB

RELEVANT SOFTWARE DEVELOPMENT

VorPROT – Computational Geometry – Protein secondary structure prediction based on Voronoi diagrams.

Sphgen_cpp – University of California, San Francisco DOCK package – protein active site determination through sphere packing.

Sphere_select – University of California, San Francisco DOCK package – protein active site selection.

Parallelized Smith-Waterman algorithm – Marine Biological Laboratory – local sequence alignment of protein and DNA sequences.