

C u r r i c u l u m V i t a e

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Present Address:

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Research Interests

Computational protein function prediction
Evolution of protein function
Operon evolution
Protein structure-function relationships
Metagenomics

Academic Employment

2009- Assistant Professor, Departments of Microbiology and Computer Science & Software Engineering (affiliate) Miami University Oxford, Ohio USA. Research in my lab deals with the evolution of bacterial gene clusters, computational metagenomics, and prediction of protein function. Teaching: developed an upper-division bioinformatics course; undergraduate seminar; graduate seminar; freshman introduction to ecology and evolution.

2007- 2009 Research Associate, bioinformatics core, marine microbial ecology, California Institute for Telecommunications and Information Technology, University of California, San Diego. Research in metagenomic data. Develop new methods for functional classification and analysis of metagenomes. Locate and analyze functional clusters of genes on metagenomic assemblies. I also lead a four person team implementing the acquisition of metagenomic data and metadata into a semantic database.

2002-2007 Postdoctoral associate at Adam Godzik's lab. Program in Bioinformatics and Systems Biology, Sanford-Burnham Institute, La Jolla, CA, USA. Research in structural

bioinformatics, including protein classification, function prediction and function based target selection for structural genomics.

1997-2002 Teaching assistant. Faculty of Medicine, The Hebrew University of Jerusalem, Israel. Taught a lab course in introductory bioinformatics for advanced undergraduate and graduate students.

Education

1997-2002 Ph.D .student at Dr. Hanah Margalit's lab, Dept. of Molecular Genetics and Biotechnology, The Hebrew University - Hadassah Medical School, Jerusalem. I investigated proteins displaying a low pairwise identity, but a high overall structural similarity. Finding the structural parameters for such a phenomenon, and investigating its evolutionary implications in various protein families were the two chief goals of my research. Thesis title: "Sequence-Structure Relationship in Proteins: a Computational Analysis of Proteins that Differ in Sequence but Share the Same Fold".

1995-1996 Masters' studies in Structural & Molecular Biochemistry at the Biological Chemistry dept., Institute of Life-Sciences, The Hebrew University, Jerusalem, Israel. Advisors: Prof. Joseph Orly & Dr. Aryeh Weiss. Graduated January 1997, Magna cum Laude. Thesis subject: "Immunofluorescent Quantitative Protein Analysis of Cultured Cells: Use of a Digital Microscopy Workstation".

1991-1994 B.Sc. in Biology, The Hebrew University, Jerusalem, Israel. Graduated 1994, Magna cum Laude.

Publications

(Select publications marked with a *)

1. Bielewicz S, Bell E, Kong W, Friedberg I, Priscu JC, Morgan-Kiss RM **Protist diversity in a permanently ice-covered Antarctic lake during the polar night transition** (2011) *ISME Journal* 3/2011
2. Kelly RJ, Vincent DE and Friedberg I **IPRStats: visualization of the functional potential of an InterProScan run** (2010) *BMC Bioinformatics* 1(Suppl2):S13
3. Wooley JC, Godzik A and Friedberg I **A Primer on Metagenomics** *PLoS Computational Biology* (2010)
4. Cock PJ, Antao T, Chang JT, Chapman BA, Cox CJ, Dalke A, Friedberg I, Hamelryck T, Kauff F, Wilczynski B, de Hoon MJ. **Biopython: freely available Python tools for computational molecular biology and bioinformatics** *Bioinformatics* (2009) Mar 20

5. Godzik A., Jambon M. and Friedberg I. **The Assessment of Protein Function Predictions** *Cellular and Molecular Life Sciences* (2007) (19-20):2505-11
6. Friedberg Ilan, Nika K., Tautz L., Saito K., Cerignoli F., Friedberg Iddo, Godzik A. and Mustelin T **Identification and characterization of Dusp27, a novel dual-specific protein phosphatase** (2007) *FEBS Letters* May 29;581(13):2527-33
7. * Friedberg I. and Godzik A. **Functional Differentiation of Proteins: Implications for Structural Genomics** (2007) *Structure* 15(4):405-415
8. * Friedberg I., Harder T., Kolodny R., Sitbon E., Li Z. and Godzik A. **Using an alignment of fragment strings for comparing protein structures** *Bioinformatics* (2007) 23: e219-e224
9. * Friedberg I. **Automated Function Prediction: the Genomic Challenge** *Briefings in Bioinformatics* (2006) Sep;7(3):225-42 (Invited Review)
10. Friedberg I., Harder T. and Godzik A. **JAFa: a Protein Function Annotation Meta-Server** *Nucleic Acids Research* (2006) Jul 1;34:W379-80
11. * Friedberg I. and Godzik, A. **Connecting the Protein Structure Universe by Using Sparse Recurring Fragments** *Structure (Camb.)* (2005) Aug;13(8):1213-24
12. Friedberg I. and Godzik A. **Fragnostic: walking through protein structure space** *Nucleic Acids Research* (2005) 33:W249-W251
13. Friedberg I., Jaroszewski L., Ye Y. and Godzik A. **The interplay of fold recognition and experimental structure determination in structural genomics** *Current Opinion in Structural Biology* (2004) 14:307-312 1
14. Alonso A., Sasin J., Bottini N., Friedberg I., Friedberg I., Osterman A., Godzik A., Hunter T., Dixon J., and Mustelin T. **Protein Tyrosine Phosphatases in the Human Genome** *Cell* (2004) Jun 11;117(6):699-711
15. Bourne P.E., Allerston C.K.J., Krebs W., Li W., Shindyalov I.N., Godzik, A., Friedberg I., Liu T., Wild D., Hwang S., Gharamani Z., Chen L., and Westbrook J. **The Status of Structural Genomics Defined through the Analysis of Current Targets and Structures** *Pac. Sym. Biocomp.* (2004) 375-386
16. Friedberg I. and Margalit H: **PeCoP: automatic determination of persistently conserved positions in protein families** (2002) *Bioinformatics* 18 (9):1276-1277
17. Friedberg I. and Margalit H.: **Persistently Conserved Positions in Structurally-Similar, Sequence Dissimilar Proteins: Roles in Preserving Protein Fold and Function** (2002) *Protein Science* 11(2):350-360
18. Friedberg I., Kaplan T, and Margalit H: **Evaluation of PSI-BLAST alignment**

- Accuracy in Comparison to Structural Alignments.** (2000) *Protein Science*, Nov;9(11):2278-84
19. Friedberg I, Kaplan T. and Margalit H.: **Glimmers in the Midnight Zone: Characterization of Aligned Identical Residues in Sequence-Dissimilar Proteins Sharing a Common Fold** (2000) *Proc. Int. Sys. Comp. Biol.* 2000: 162-170 (Now *Bioinformatics*)
20. Cherradi N, Rossier MF, Vallotton MB, Timberg R, Friedberg I, Orly J, Wang XJ, Stocco DM, Capponi AM: **Submitochondrial distribution of three key steroidogenic proteins (steroidogenic acute regulatory protein and cytochrome p450scc and 3beta-hydroxysteroid dehydrogenase isomerase enzymes) upon stimulation by intracellular calcium in adrenal glomerulosa cells.** *J. Biol. Chem.* 1997 Mar 21;272(12):7899-7907

Manuscripts in Preparation or Submitted:

1. Schwartz, S, Friedberg I, Ivanov IV, Davidson LA, Goldsby JS, Dahl DB, Damir H, Wang M, Donovan SM and Chapkin RS **Mutualism between gut microbiota and the host as revealed in a comparative study of breast-fed versus formula-fed infants** (submitted, *Genome Biology*)
2. Ream DC, Wohlever M and Friedberg I: **The event driven model for operon evolution**
3. Repo S, Ng P, Friedberg I, *et al* **Critical Assessment of Genomic Interpretation**
4. Radivojac P,.....,Mooney S and Friedberg I **A Critical Assessment of Function Annotations**

Editorials and opinion pieces in scientific journals:

1. Bourne PE, Friedberg I (2006) **Ten Simple Rules for Selecting a Postdoctoral Position.** *PLoS Comp Biol* 2(11): e1
2. Rodrigues A, Grant B, Godzik A and Friedberg I. **The 2006 Automated Function Prediction Meeting BMC Bioinformatics** 8(Suppl 4)
3. Friedberg I., Jambon M. and Godzik A. **New Avenues in Protein Function Prediction** *Protein Science* (2006) Jun;15(6):1527-9

Select Conference Publications and Invited Talks

1. **Glimmers in the Midnight Zone** (Lecture) 8th Intelligent Systems in Computational Biology conference, San Diego, CA USA (2000)

2. **Generation and Use of Substitution Matrices in Biopython.** Bioinformatics Open Source Conference (BOSC) 2001, Copenhagen, poster & lecture: **Friedberg I & Chapman B.**
3. **Use of Fragments for Mapping Protein Structure Space (Lecture)**
University of California, San Diego, Weizmann Institute of Science, Israel 8/2004, Tel Aviv University 8/2004, Ben Gurion University, Israel 8/2004, Compugen, Israel 8/2004
4. **The Assessment of Function Prediction Servers (Lecture)**
First Automated Function Prediction Special Interest Group meeting 7/2005.
5. **Using an alignment of fragment strings for comparing protein structures**
European Conference for Computational Biology 2006 (Lecture. Declined due to last minute travel cancellation).
6. **Structural Biology as a Data Rich Science (Lecture)**
University of California, Riverside; University of California, Merced; University of Virginia; George Mason University
7. **Function Based Target Selection for Structural Genomics (Lecture)**
ISMB/ECCB 2007 (August 2007)
2008: Technion, Israel, Hebrew University Jerusalem, Israel; Tel Aviv University, Israel; Texas A&M University, TX USA; University of Kansas, KS USA; Ontario Institute for Cancer Research, ON Canada
8. **Protein Function Differentiation: Structural Genomics and Metagenomics Connections (Lecture)**
Computational Systems Bioinformatics 2007, La Jolla California
9. **Visualization of the Functional Potential of Metagenomes (Lecture)**
Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2010
10. **Assessing Functional Predictions, Critical Assessment for Function Annotations (Lecture)** 18th Microbial Genomics Meeting, Lake Arrowhead, CA September 2010
11. **Handling the Metagenomic Data Deluge (Lecture)**
Texas A&M, October 2010
12. **Assessing Functional Predictions (Lecture)** Critical Assessment of Genome Interpretation, University of California Berkeley, CA December 2010
13. **Metagenomic Networks: an invited tutorial**
MITACS Workshop on Biological Networks and Systems Biology, Simon Fraser University Harbor Center, Vancouver January, 2011
14. **The Event-Driven Model of Operon Evolution (Lecture)**
Annual meeting of the Ohio Chapter of the American Society of Microbiology, March 2011.
15. **Future directions for CAGI and Genome Interpretation** (Invited panelist) ISMB 2011

- 16. The Human gut Ecosystem: Gut Microbiome and Host Transcriptome in Breast-fed vs. Formula-fed Infant (Lecture)** ISMB 2011 (late breaking research track).
- 17. The Mycoplasma Online Genome Database, Microscopy & Genomics (Lecture)**
Ontario Institute for Cancer Research, Toronto.
- 18. The Critical Assessment of Function Annotations (Lecture)** Cold Spring Harbor
Symposium on Genome Informatics

Teaching

2009-2010: Courses taught at Miami University:

BMZ 115 Introductory biology

MBI/BOT/ZOO 485/585 Principles of Bioinformatics (developed by me).

MBI 690 Graduate Seminar

MBI 490 Senior Seminar

2009-2011: employed twelve undergraduate students in independent studies. Six of the students were engaged in an inter-institutional competition organized by Texas A&M university. The competition involved rigorous annotation of protein sequences in UniProtKB, and taught the students detailed reading of scientific papers, the proper use of Gene Ontology based annotation, and application of critical thinking and detail-oriented skills towards protein annotation.

2009-present Mentor of one graduate students (PhD candidate) in the Microbiology Program, at Miami University.

2005-2006 Tutored an exchange graduate student in part of his thesis project. Mr. Tim Harder and I co-authored papers #8 and #10 in the publications list.

1999-2002 Teaching assistant, *Bioinformatics: computational sequence analysis of biological macromolecules*. Undergraduate senior/post graduate course, The Hebrew University, Jerusalem

1996 GNA-VSNS Biocomputing course. Contributed instructional software to one of the first distance learning course in bioinformatics, coordinated at the University of Bielefeld, Germany. <http://www.techfak.uni-bielefeld.de/bcd/welcome.html>

1996-1997 GNA-VSNS Principles of Protein Structure course: structural biology and bioinformatics distance learning course from Birkbeck College, London, UK.
<http://www.crist.bb.k.ac.uk/PPS/>

Other Academic Service Activities

2011 Associate Editor, *BMC Bioinformatics*

2010 Developed assessment methods for the Critical Assessment of Genome Interpretation Experiment led by Steven E. Brenner, University of California Berkeley.

(Manuscript in preparation). <http://genomeinterpretation.org>

2010-present Editorial board member, *Microbial Informatics and Experimentation*

2009 Grant reviewer, Binational Science Foundation

2008 Grant reviewer, National Science Foundation Plant Genome Research Program

2008-present Academic Editor, *PLoS ONE*

2008 Guest Editor, *PLoS Computational Biology*

2007 Book proposal reviewer for CRC press

2007 Guest editor *BMC Bioinformatics* special section on automated function prediction, published May, 2007

2007 Organizer and co-chair, metagenomics workshop, Computational Systems Bioinformatics conference 2007, La Jolla, California

2006, 2007 Program committee member, Pacific Symposium of Biocomputing.

2006 Guest editor, *Protein Science* special section on automated protein function prediction. June, 2006.

Program committee member, Intelligent Systems in Molecular Biology (ISMB) 2003, 2005, 2006

2005- present Founder, co-organizer and co-chair of the Automated Function

Prediction meetings <http://BioFunctionPrediction.org> This activity has recently been funded by the NIH (\$20,000) and US-DOE (\$5,000). The meeting now hosts a biannual community-driven critical assessment experiment in which research teams are evaluated for their ability to predict the function of proteins given their sequence.

2002-present Manuscript referee for the following publications: *Bioinformatics*; *Proteins: structure function and bioinformatics*; *Nucleic Acids Research*; *BMC Bioinformatics*; *BMC Genomics*; *Protein Science*; *PLoS Computational Biology*; *PLoS One*; *Genome Biology*; *Drug Discovery Today*; *Trends in Genetics*; *Journal of Molecular Biology*;

Other activities

2005: Project coordinator Biopython. As project coordinator, I was responsible for monitoring CVS deposits, coordination among developers (see below), and compiling a version release.

2000- I have been involved as a programmer with several open-source bioinformatics projects. Most notably the Biopython (<http://biopython.org>) project aiming at providing basic tools for bioinformatics in the Python programming language.

Memberships

International Society of Computational Biology

The Protein Society

Life Sciences Society

Sigma Xi (Full Member)

The American Association for the Advancement of Science

Fellowships and Awards

Hirsch & Braine Raskin Foundation Student Endowment Fund, 2000/2001

Katzir Travel Award: 2001

International Society for Computational Biology Conference Travel Award: 2001,2002, 2005, 2006

Protein Society Travel Award: 2003

Grants

Funded:

Miami University Shoupp Award for Industry / Academia collaboration. "Applying Workflows to Field Programmable Gate Array Technology" (2009) \$5,000 (awarded)

Miami University College of Arts & Science Summer Research Award (\$5,000).

Miami University Committee on Faculty Research grant (\$20,000) (PI)

US Department of Energy "Critical Assessment of Function Annotation Conference" \$5,000 (PI)

NIH R13 "Conference: Critical Assessment of Function Annotation" (Co investigator, PI: Predrag Radivojac, Indiana University) (\$20,000)

Unfunded:

NSF/ABI "ABI Innovation: a comprehensive approach to tracking operon evolution" (\$642,729) (PI) ([In resubmission](#))

NIH R21/BISTI "Analysis of Gene Cluster Evolution Using an Event-Driven Approach" (NIGMS) (PI) (\$386,000)

Pending:

NSF/ABI "ABI Innovation:Recovery of Pathways from Genome context Analysis of Metagenomic Data" (PI) (\$450,000)

NIH "Genetic Mechanisms Regulating Physical Activity Behavior in Mice" (Role: Co-PI; PI: Tim Lightfoot, Texas A&M). (\$55,000 requested for the Friedberg lab).