

CURRICULUM VITAE: EYAL AKIVA

CONTACT DETAILS

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EDUCATION

- 2012- Post-doctoral researcher, UCSF (Department of Bioengineering and Therapeutic Sciences, prof. Patricia Babbitt's lab)
- 2010-2011 Post-doctoral researcher, UCSF (Department of Bioengineering and Therapeutic Sciences, prof. Tanja Kortemme's lab)
- 2004-2010 PhD studies in bioinformatics, The Hebrew University of Jerusalem, Israel (prof. Hanah Margalit's lab), "Various Aspects of Modularity in Protein-Protein Interaction"
- 2001-2004 MSc studies in bioinformatics and genetics, The Hebrew University of Jerusalem, Israel (prof. Shmuel Ben-Sasson's lab), "Exploiting the Exploiters: Identification of Virus-Host Peptide Mimicry as a Source for Modules of Functional Significance". Final grade: 94.44 (*MAGNA CUM LAUDE*)
- 1997-2000 BSc studies in biology (major) and computer science (minor), Bar-Ilan University, Israel. Final project advisor: Dr. Ramit Mehr "Modeling the Evolution of the Immune System: a Simulation of the Evolution of Genes that Encode the Variable Regions of Immunoglobulins". Final grade: 88.7 (*MAGNA CUM LAUDE*)
- 1996-1997 First year of "Industrial Engineering and Management" studies, Tel-Aviv University, Israel

OTHER EXPERIENCE

- 2000-01 Researcher at "Do-coop technologies", a company engaged with the development of biological applications of proprietary nano-particles. Most of the work was carried out in the lab of Prof. Eshel Ben-Jacob at the Tel-Aviv University.

HONORS AND AWARDS

- 2016 ILANIT (FISEB) 2017 conference Travel Award.
- 2015 ASBMB 2015 Graduate/Postdoctoral Travel Award.
- 2009 BioSapiens travel fellowship for the ISMB/ECCB 2009 conference held in Stockholm.
- 2006-2010 Excellence scholarship (Faculty of Medicine, The Hebrew University).
- 2006 Excellence mark for my job as a teaching assistant in "Structure and function of proteins" course, taught by Prof. Ora Schueler-Furman.
- 1999 One-year tuition scholarship for academic achievements.
- 1998 Dean's excellence mark for second year of BSc studies.

KEYWORDS/AREAS OF INTEREST

Rational enzyme design; Enzyme function prediction; Metagenomic Data Analysis; Metabolic pathway discovery; Nitroreductases; Sirtuins; Alkaline phosphatases; Tautomerase; Protein classification; Protein structure modeling; Ancestral gene reconstruction; Host-pathogen interactions; Domain-motif interactions; Protein disorder; Phosphorylation.

TEACHING, MENTORING AND TEACHING-RELATED EDUCATION

- 2016 Science Teaching Effectiveness Program for Upcoming Professors (STEP-UP) Introduction to Pedagogy course (UCSF)
- 2016 Student mentorship: Two periods of mentoring Audrey Huang, a visiting student from Prof. Frances Arnold's lab from Caltech; "Sequence-Function studies of NfsA enzymes from the FMN-dependent nitroreductase superfamily" (6 weeks), and "Studying one million nitroreductases from metagenomic surveys" (9 weeks).
- 2015 Lecturer: "Function prediction mini-course" (2015, UCSF), with Prof. Patsy Babbitt
- 2014 Bay Area Postdocs: Workshop on Scientific Teaching (held in SFSU).
- 2013 Graduate student mentorship: "Mapping the Functional Evolution of Group II Chaperonins", of a shared student between the Babbitt and Kortemme labs (Samuel Thompson)
- 2013 Teaching assistance in "Bioinformatics and Computational Biology" course, taught by Prof. Patricia Babbitt (one guest lecture).
- 2013 Promoting Interactive Learning through Audience Response Systems (Workshop in UCSF).
- 2009-10 Student supervision: "The Code of Phosphorylation", Final project of Computer science/Life science student Michal Chorev.
- 2005-09 Teaching assistant in "Structure and function of proteins" course, taught by Prof. Ora Schueler-Furman. Included also website design and conversion of course platform from InSight molecular visualization program to Swiss-PDB Viewer (<http://courses.md.huji.ac.il/81817/>).

ACTIVE COLLABORATIONS AND PROJECTS

1. Prof. Nobu Tokuriki, University of British Columbia, Canada: *Mapping reaction specificity in the FMN-dependent nitroreductases superfamily.*
2. Prof. Dan Herschlag, Stanford, CA, USA: *Evolution of enzyme function in the Alkaline phosphatase superfamily.*
3. Prof. Amir Aharoni, Ben Gurion university, Israel: *Evolution of substrate specificity of human Siruin-1.*

4. Prof. Chris Whitman, U. Texas at Austin: *Tracking the evolution of functional divergence in the Tautomerase superfamily.*
5. Prof. Shimon Bershtein, Ben Gurion university, Israel: *Ancestral gene reconstruction as a gateway to trace enzyme evolution.*
6. Joint genome institute (Department of energy): *Utilizing metagenomic sequences for enzyme function prediction* (link: <http://jgi.doe.gov/doi-user-facilities-figs-join-forces-to-tackle-biology-big-data/>).

PUBLICATIONS

1. **Akiva E***, Copp NJ*, Tokuriki N and Babbitt PC, *Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily.* Under revisions. (*equal contribution).
2. Davidson R, Baas B, **Akiva E**, Holliday GL, Polacco BJ, LeVieux J, Pullara CR, Zhang YJ, Whitman CP and Babbitt PC: *A global view of structure-function relationships in the tautomerase superfamily.* Submitted.
3. Holliday GL, Brown SD, **Akiva E**, Mischel D, Hicks MA, Morris J, Huang C, Meng E, Pegg S, Ferrin T and Babbitt PC, *Biocuration in the Structure-Function Linkage Database: The Anatomy of a Superfamily*, DATABASE (Oxford), 2017(1), 2017 (DOI 10.1093/database/bax006).
4. Holliday GL, Davidson R, **Akiva E**, Babbitt PC, *Evaluating functional annotations of enzymes using the Gene Ontology.* In Dessimoz C & Škunca N (Eds.), The Gene Ontology Handbook (pp. 111-132). New York, NY: Springer (Humana Press), 2016, DOI 10.1007/978-1-4939-3743-1.
5. **Akiva E**, Babbitt PC, *Evolutionary Reprogramming of Protein-Protein Interaction Specificity*, Cell [a preview paper], 163 (3), 535-537, 2015.
6. Betz NJ, Boswell NW, Fugate CJ, Ghose S, **Akiva E**, Holliday GL, Babbitt PC, Peters JW, Shepard EM and Broderick JB, *[FeFe]-Hydrogenase Maturation: Insights into the role HydE plays in dithiomethylamine biosynthesis*, Biochemistry, 54(9):1807–1818, 2015.
7. Zhao S, Sakai A, Zhang X, Vetting M, Kumar R, Hillerich B, San Francisco B, Solbiati J, Steeves A, Brown S, **Akiva E**, Barber AE 2nd, Seidel R, Cronan JE, Babbitt PC, Almo SC, Gerlt JA and Jacobson MP, *Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks.* eLife, e03275, 2014.
8. Mashiyama TS, Malabanan MM, **Akiva E**, Bhosle R, Branch MC, Hillerich B, Jagessar B, Kim J, Patskovsky Y, Seidel RD, Stead M, Toro R, Vetting MW, Almo SC, Armstrong RN and Babbitt PC. *Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere*, PLoS Biology, 12(4):e1001843, 2014.
9. **Akiva E***, Brown SD*, Almonacid DE, Barber AE 2nd, Custer AF, Hicks MA, Huang CC, Lauck F, Mashiyama ST, Meng EC, Mischel D, Morris JH, Ojha S, Schnoes AM, Stryke D, Yunes JM, Ferrin TE, Holliday GL and Babbitt PC. *The Structure-Function Linkage Database*, Nucleic Acid Research, 42(D):521-30, 2014. (*equal contribution).

10. Humphris EL*, **Akiva E***, Varela R, O'Connor S and Kortemme T. *Prediction of viral mutational tolerance using flexible backbone protein design*, PLoS Computational Biology, 8:e1002639, 2012. (*equal contribution).
11. **Akiva E**, Friedlander G, Itzhaki Z and Margalit H. *A dynamic view of domain-motif interactions*, PLoS Computational Biology, 8:e1002341, 2012.
12. Jäger S, Cimermancic P, Gulbahce N, Johnson J, Clarke S, Shales M, Mercenne G, Pache L, Li K, Hernandez H, Jang G, Roth S, **Akiva E**, Marlett J, Stephens M, D'Orso I, Fernandes J, Fahey M, Mahon C, ODonoghue A, Todorovic A, Morris J, Maltby D, Alber T, Cagney G, Bushman F, Young J, Chanda S, Sundquist W, Kortemme T, Hernandez R, Craik C, Burlingame A, Sali A, Frankel A, and Krogan NJ. *Global Landscape of HIV-Human Protein Complexes*, Nature, 481(7381):365-70, 2011.
13. Itzhaki Z, **Akiva E** and Margalit H. *Preferential use of protein domain-pairs as interaction mediators: order and transitivity*, Bioinformatics, 26(20):2564-70, 2010.
14. **Akiva E**, Itzhaki Z and Margalit H. *Built-in loops allow versatility in domain-domain interactions: lessons from self-interacting domains*, Proc Natl Acad Sci U S A., 105:36(13292-7), 2008.
15. Itzhaki Z, **Akiva E**, Altuvia Y and Margalit H. *Evolutionary conservation of domain-domain interactions*, Genome Biol. 7(12):R125, 2006.

INVITED TALKS

1. **Akiva E**, Copp NJ, Tokuriki N and Babbitt PC, From “big data” to enzyme chemical function: The nitroreductase superfamily as a model system. 254th ACS (American Chemical Society) meeting, Washington DC, USA, 2017.
2. **Akiva E**, Copp NJ, Tokuriki N and Babbitt PC, How natural variation can guide rational enzyme design? Lessons from the functionally diverse nitroreductase enzyme superfamily. *12th Annual DOE Joint Genome Institute Genomics of Energy & Environment Meeting (Synthetic Biology Workshop)*. Joint Genome institute, Walnut creek, CA, USA, 2017.
3. **Akiva E**, Hendler A, Babbitt PC and Aharoni A, Evolution of protein-protein interaction multi-specificity. ILANIT/FISEB (Federation of the Israeli Societies of Experimental Biology) conference, Eilat, Israel, 2017.
4. **Eyal Akiva**, Patricia C. Babbitt, Mapping sequence-function space of enzymes using protein similarity networks. *Machine learning meets DNA*, Workshop held in DNA2.0, Menlo Park, CA, USA, 2015.
5. **Eyal Akiva**, Patricia C. Babbitt, Cherry-picking sequences for multiple sequence alignments using protein similarity networks. *Multiple Sequence Alignment Workshop*. Institute of Pure and Applied Mathematics, UCLA, Los Angeles, CA, USA, 2015.
6. **Eyal Akiva**, Patricia C. Babbitt, Unraveling new protein functions and pathways using sequence similarity networks and genomic context information. *Conference on Predicting Cell Metabolism and Phenotypes*, SRI international, Menlo Park, CA, USA, 2013.
7. Gemma L. Holliday, **Eyal Akiva** and Patricia C. Babbitt, Protein function curation: linking sequence & chemical reaction spaces in the SFLD. *The Conference of the International Society for Biocuration*, Cambridge, UK, 2013.
8. **Eyal Akiva**, Shoshana Brown, Patricia C. Babbitt, A yearly update on the Enzyme Function Initiative Superfamily/Genome core. *Enzyme Function Initiative yearly meeting*, New Rochelle,

New York, USA, 2013.

9. Hanah Margalit and **Eyal Akiva**, A dynamic view of domain-motif interaction networks, *Systems Biology: Networks, A Cold Spring Harbor Laboratory conference*, Hinxton, UK (2010).
10. **Eyal Akiva**, Zohar Itzhaki, Hanah Margalit, Built-in loops allow versatility in domain-domain interactions: Lessons from self-interacting domains. *European Conference of Computational Biology*, Stockholm, Sweden (2009).
11. **Eyal Akiva**, Zohar Itzhaki, Hanah Margalit. *Network Biology: Cold Spring Harbor Laboratory meeting*, Hinxton, UK (2008).

POSTERS PRESENTED IN CONFERENCES AND MEETINGS

1. **Eyal Akiva**, Shoshana D Brown, Gemma L. Holliday and Patricia C. Babbitt, Enzyme “Social” Networks: Tracking Sequence / Function Relationships to Elucidate Determinants of Enzyme Specificity and Mechanism. *The American Society for Biochemistry and Molecular Biology (ASBMB) annual meeting*, Boston, MA, USA (2015)
2. **Eyal Akiva**, Patricia C. Babbitt, Cherry-picking sequences for multiple sequence alignments using protein similarity networks. *Multiple Sequence Alignment Workshop*. Institute of Pure and Applied Mathematics, UCLA, Los Angeles, CA, USA (2015).
3. **Eyal Akiva**, Susan T. Mashiyama, M. Merced Malabanan, Richard N. Armstrong and Patricia C. Babbitt, Tracking Enzyme Sequence/Function Divergence Using Protein Similarity Networks: Applications for Discovery of New Functions, *The 27th Symposium Of The Protein Society*, Cambridge, MA, USA (2013).
4. **Eyal Akiva** and Patricia C. Babbitt, Discovering novel protein function using genomic context: The GST superfamily as a test case, *Enzyme Function Initiative Meeting*, San Francisco, USA (2012).
5. **Eyal Akiva**, Elisabeth Humphris, Rocco Valera and Tanja Kortemme, Prediction of protein mutational tolerance using flexible backbone protein design, *Rosetta conference*, Leavenworth, Washington, USA (2011).
6. Zohar Itzhaki, **Eyal Akiva**, Yael Altuvia and Hanah Margalit, Evolutionary Conservation of Domain-Domain Interactions, *The European Conference of Computational Biology conference*, Eilat, Israel (2008).
7. **Eyal Akiva**, Zohar Itzhaki and Hanah MArgalit, Built-in Loops Allow Versatility in Domain-domain Interactions, *The Israeli Bioinformatics symposium*, Tel Aviv, Israel (2008).
8. **Eyal Akiva**, Amir Orlev, Shmuel S Ben Sasson, Exploiting the Exploiters: Identification of Pathogen-Host Peptide, Mimicry as a Source for Modules of Functional Significance. *The Israeli Bioinformatics symposium*, Tel Aviv, Israel (2004).

NON-RESEARCH ACTIVITY, OTHER INTEREST

1. During the past two years I gave science-related classes (centered around proteins) to elementary school pupils.
2. Non-academic interests: Bread baking and 3D-printing.