

## EYAL AKIVA, PhD

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## EDUCATION

- 2012-2017 Post-doctoral fellowship at UCSF, Dept. Of Bioengineering and Therapeutic Sciences. Host: Prof. Patricia Babbitt.
- 2010-2012 Post-doctoral fellowship at UCSF, Dept. Of Bioengineering and Therapeutic Sciences. Host: Prof. Tanja Kortemme.
- 2004-2010 PhD at The Hebrew University of Jerusalem (Israel), bioinformatics. Host: Prof. Hanah Margalit. "Various Aspects of Modularity in Protein-Protein Interaction".
- 2001-2004 MSc at The Hebrew University of Jerusalem (Israel), bioinformatics and human genetics. Host: Prof. Muli Ben-Sasson. "Exploiting the Exploiters: Identification of Virus-Host Peptide Mimicry as a Source for Modules of Functional Significance". *MAGNA CUM LAUDE*.
- 1997-2000 BSc at Bar-Ilan University (Israel), biology (major) and computer science (minor). Final project advisor: Prof. Ramit Mehr "Modeling the Evolution of the Immune System: a Simulation of the Evolution of Genes that Encode the Variable Regions of Immunoglobulins". *MAGNA CUM LAUDE*.
- 1996-1997 First year of "Industrial Engineering and Management" studies, Tel-Aviv University, Israel.

## OTHER WORK EXPERIENCE

- 2000-01 'Do-coop technologies': Team leader and chemistry/microbiology researcher; development of biological applications and manufacture of proprietary nanoparticles (Or Yehuda, Israel and Tel-Aviv University (Prof. Eshel Ben-Jacob's lab at the school of physics)).

## FUNDING, HONORS AND AWARDS

- 2017 **Grant:** Co-PI, "Utilizing metagenomic sequences for enzyme function prediction", Joint Genome Institute (US Department of Energy) (<http://jgi.doe.gov/doi-user-facilities-figs-join-forces-to-tackle-biology-big-data/>).
- 2017 **Travel award:** Federation of all the Israel Societies for Experimental Biology (ILANIT) conference (Eilat, Israel).
- 2015 **Travel award:** Am. Soc. for Bioch. & Mol Biol. (ASBMB) annual meeting (Boston, MA).
- 2009 **Travel award:** Eur. Con. for Comput. Biol. (ECCB) annual meeting (Stockholm, Sweden).
- 2006-2010 **Excellence scholarship** (stipend) (Faculty of Medicine, The Hebrew University, Israel).
- 2006 **Teaching assistance excellence mark** (The Hebrew University, Israel).
- 1999 One year **Tuition scholarship** for academic achievements (Bar Ilan University, Israel).
- 1998 Dean's **excellence mark** for second year of BSc studies (Bar Ilan University, Israel).

## PUBLICATIONS

1. 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*. Accepted to **JBC**.
2. **Akiva E\***, Copp NJ\*, Tokuriki N and Babbitt PC (2017). *Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily*, **PNAS**, 114(45):E9549-E9558. (\*equal contribution).
3. Holliday GL, Brown SD, **Akiva E**, Mischel D, Hicks MA, Morris J, Huang C, Meng E, Pegg S, Ferrin T and Babbitt PC (2017). *Biocuration in the Structure-Function Linkage Database: The Anatomy of a Superfamily*, **DATABASE (Oxford)**, 2017(1).
4. Holliday GL, Davidson R, **Akiva E**, Babbitt PC (2016). *Evaluating functional annotations of enzymes using the Gene Ontology*, in **The Gene Ontology Handbook**, pp. 111-132, Dessimoz C & Škunca N (Eds.), Springer (Humana Press), New York. DOI 10.1007/978-1-4939-3743-1.
5. **Akiva E**, Babbitt PC (2015). *Evolutionary Reprogramming of Protein-Protein Interaction Specificity*, **Cell**, 163 (3), 535-537. [A preview paper]
6. Betz NJ, Boswell NW, Fugate CJ, Ghose S, **Akiva E**, Holliday GL, Babbitt PC, Peters JW, Shepard EM and Broderick JB (2015). *[FeFe]-Hydrogenase Maturation: Insights into the role HydE plays in dithiomethylamine biosynthesis*, **Biochemistry**, 54(9):1807–1818.
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 (2014). *Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks*, **eLife**, e03275.7.725.
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 (2014). *Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere*, **PLoS Biology**, 12(4):e1001843.
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 (2014). *The Structure-Function Linkage Database*, **Nucleic Acids Research**, 42(D):521-30. (\*equal contribution).
10. Humphris EL\*, **Akiva E\***, Varela R, O'Connor S and Kortemme T (2012). *Prediction of viral mutational tolerance using flexible backbone protein design*, **PLoS Computational Biology**, 8:e1002639. (\*equal contribution).
11. **Akiva E**, Friedlander G, Itzhaki Z and Margalit H (2012). *A dynamic view of domain-motif interactions*, **PLoS Computational Biology**, 8:e1002341.
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 (2011). *Global Landscape of HIV-Human Protein Complexes*, **Nature**, 481(7381):365-70.

13. Itzhaki Z, **Akiva E** and Margalit H (2010). *Preferential use of protein domain-pairs as interaction mediators: order and transitivity*, **Bioinformatics**, 26(20):2564-70.
14. **Akiva E**, Itzhaki Z and Margalit H (2008). *Built-in loops allow versatility in domain-domain interactions: lessons from self-interacting domains*, **PNAS**, 105:36(13292-7).
15. Itzhaki Z, **Akiva E**, Altuvia Y and Margalit H (2006). *Evolutionary conservation of domain-domain interactions*, **Genome Biol.** 7(12):R125.

## TEACHING EXPERIENCE

- 2017      **Mentorship:** Tomer Achler (undergraduate student) from The Ben Gurion University (Israel), “Ancestral gene reconstruction as a gateway for tracing enzyme evolution” (6 weeks) [UCSF].
- 2016      **Learning about teaching:** Science Teaching Effectiveness 4-days Program - Introduction to pedagogy course [UCSF].
- 2016      **Mentorship:** Audrey Huang (undergraduate student) from Prof. Frances Arnold’s lab (Caltech), “Sequence-Function studies of NfsA enzymes from the nitroreductase superfamily” (6 weeks), and “Studying one million nitroreductases from metagenomic surveys” (9 weeks) [UCSF].
- 2015      **Teaching:** “Function prediction mini-course”, with Prof. Patsy Babbitt; lecturing, developing exercises, evaluating projects [UCSF].
- 2014      **Learning about teaching:** Bay Area Postdocs: Workshop on Scientific Teaching [held in San Francisco State University].
- 2013      **Mentorship:** Samuel Thompson (graduate student) from the Babbitt and Kortemme labs, “Mapping the Functional Evolution of Group II Chaperonins” (4 weeks) [UCSF].
- 2013      **Teaching:** Teaching assistance in “Bioinformatics and Computational Biology” course, taught by Prof. Patricia Babbitt; one guest lecture [UCSF].
- 2013      **Learning about teaching:** Promoting Interactive Learning through Audience Response Systems [Workshop in UCSF]
- 2009-10   **Mentorship:** Michal Chorev (Undergraduate student), “The Code of Phosphorylation” (6 weeks) [The Hebrew University, Israel]
- 2005-09   **Teaching:** Teaching assistant "Structure and function of proteins" course, taught by Prof. Ora Furman and Prof. Hanah Margalit. Delivered weekly exercises, evaluated student works, developed exercises in protein structure visualization (<http://courses.md.huji.ac.il/81817>). I got an excellence mark for teaching (class of 2006) [The Hebrew University, Israel].

## INVITED TALKS

1. **Eyal Akiva**, Janine N. Copp, Nobuhiko Tokuriki and Patricia C. Babbitt, 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. **Eyal Akiva**, Janine N. Copp, Nobuhiko Tokuriki and Patricia C. Babbitt, 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. **Eyal Akiva**, Adi Hendler, Patricia C. Babbitt and Amir Aharoni, Evolution of protein-protein interaction multi-specificity. *ILANIT/FISEB (Federation of the Israeli Societies of Experimental Biology) conference*, Eilat, Israel, 2017.
4. **Eyal Akiva** and Patricia C. Babbitt, Mapping sequence-function space of enzymes using protein similarity networks. *Machine learning meets DNA*, Workshop held in DNA2.0, San Francisco, CA, USA, 2015.
5. **Eyal Akiva** and 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** and 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 and 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. **Eyal Akiva** and Hanah Margalit, 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 and 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 and Hanah Margalit, *Network Biology: Cold Spring Harbor Laboratory meeting*, Hinxton, UK, 2008.

## SELECTED POSTER PRESENTATIONS

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. **Eyal Akiva**, Zohar Itzhaki and Hanah Margalit, Built-in Loops Allow Versatility in Domain-domain Interactions, *The Israeli Bioinformatics symposium*, Tel Aviv, Israel (2008).
7. **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).

## **SERVICE AND OUTREACH**

- 2012-present    Reviewer - personally invited to review papers from Nature Communications, Nucleic Acids Research, PLoS Computational Biology, Bioinformatics, BMC Bioinformatics, BMC Evolutionary Biology, The FEBS Journal and PLoS One.
- 2014-present    JewCSF- organized and initiated activities for Jewish students and postdocs at UCSF.
- 2012-2016       Science-related classes (centered around proteins) given to elementary school pupils.