DAVID BURSTEIN

307 McCone Hall
UC Berkeley Campus
Berkeley, CA 94720

davidbur@berkeley.edu

EDUCATION

2015 to date	Postdoctoral fellow under the joint supervision of Prof. Jill Banfield and Prof. Jennifer Doudna, UC Berkeley
2013 – 2015	Rothschild and EMBO Postdoctoral fellow under the supervision of Prof. Jill Banfield, UC Berkeley
2008 – 2013	Ph.D. Studies under the supervision of Prof. Tal Pupko, Tel Aviv University
2006 – 2008	M.Sc. in the Bioinformatics track (*summa cum laude*) under the supervision of Prof. Tal Pupko, Tel Aviv University
2001 – 2004	B.Sc. in Biology (*summa cum laude*) and Computer Science (*magna cum laude*), Tel Aviv University. Double major program with a specialization in Bioinformatics

TEACHING EXPERIENCE

2009 - 2012	Instructor of the course "Perl Programming for Biology", Tel Aviv University (responsible for the entire course from design to grading) *for which I received awards from the Tel-Aviv Graduate school*
2007 – 2009	Instructor of the course "Biological Sequences Analysis", Tel Aviv College (responsible for the entire course from design to grading)
2007 – 2008	Teaching assistant in the course "Introduction to Bioinformatics" in Tel Aviv University (Lectured in recitations, created and graded assignments) *for which I received awards from the Tel-Aviv Graduate school*
2005 – 2006	Teaching assistant in the course "Algorithms in Computational Biology", the Concentrated M.Sc. Track in Computer Science, Tel Aviv University (designed and graded assignments)

PUBLICATIONS

[1]   Probst A.J., Castelle C.J., Singh A., Brown, C.T., Anantharaman K., Sharon I., Hug L., Burstein D., Emerson J.B., Thomas BC., Banfield J.F. (2016) Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO2 concentrations. **Environmental Microbiology** doi:10.1111/1462-2920.13362. [Epub ahead of print]

[2]   Burstein D., Sun C.L., Brown C.T., Sharon I., Anantharaman K., Probst A.J., Thomas B.C., Banfield J.F. (2016). Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. ***Nature Communications*** 7:10613.

[3]   Anantharaman K., Brown C.T., Burstein D., Castelle C.J., Probst A.J., Thomas B.C., Williams K.H., Banfield J.F. (2016). Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. **PeerJ** 4:e1607.

[4]   Burstein D., Amaro F., Zusman T., Lifshitz Z., Cohen O., Gilbert J.A., Pupko T., Shuman H.A., Segal G. (2016) Genomic Analysis of 38 Legionella Species Identifies Large and Diverse Effector Repertoires. ***Nature Genetics*** 48: 167–175, doi:10.1038/ng.3481.

[5]   Teper D.*, Burstein D.*, Salomon D., Gershovitz M., Pupko T., Sessa G. (2015) Identification of novel *Xanthomonas euvesicatoria* type III effector proteins by a machine-learning approach. ***Molecular Plant Pathology***. doi:10.1111/mpp.12288
* These authors contributed equally

[6]   Burstein D.*, Satanower S.*, Simovitch M.*, Belnik Y., Zehavi M., Yerushalmi G., Ben-Aroyab S., Pupko T.,Banin E. (2015) Novel Type III Effectors in Pseudomonas aeruginosa. ***mBio*** 6 (2), e00161-15
* These authors contributed equally

[7]   Sharon I., Kertesz M., Hug L.A., Pushkarev D., Blauwkamp,T.A., Castelle C.J., Amirebrahimi M., Thomas B.C., Burstein D., Tringe, S.G., et al. (2015). Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. ***Genome Research***. 25, 534–543 (2015).

[8]   Burstein D.*, Satanower S.*, Simovitch M.*, Belnik Y., Zehavi M., Yerushalmi G., Ben-Aroya S., Pupko T., and Banin E. Novel Type III Effectors in Pseudomonas aeruginosa. ***mBio*** 6, e00161–15 (2015).
* These authors contributed equally

[9]   Lifshitz Z., Burstein D., Schwartz K., Shuman H.A., Pupko T., Segal G. Identification of novel *Coxiella burnetii* Icm/Dot effectors and genetic analysis of their involvement in modulating a mitogen-activated protein kinase pathway. ***Infection and immunity*** 82 (9): 3740–3752 (2014).

[10] Yosef I., Shitrit D., Goren M.G., Burstein D., Pupko T., and Qimron U. DNA motifs determining the efficiency of protospacer adaptation into the *Escherichia coli* CRISPR array. ***Proceedings of the National Academy of Sciences USA*** 110(35): 14396–14401 (2013).

[11] Cohen O., Ashkenazy H., Karin E.L., Burstein D., and Pupko T. CoPAP: Co-evolution of Presence-Absence Patterns. ***Nucleic Acids Research*** (Web Server issue): W232-W237 (2013).

[12] Lifshitz Z.*, Burstein D.*, Peeri M., Zusman T., Schwartz K., Shuman H. A., Pupko T., and Segal G. Computational modeling and experimental validation of the Legionella and Coxiella virulence-related Type IVB secretion signal. ***Proceedings of the National Academy of Sciences USA*** 110(8):E707-705 (2013).
* These authors contributed equally

[13] Cohen, O., Ashkenazy, H., Burstein, D., and Pupko, T. Uncovering the co-evolutionary network among microbial gene families. ***Bioinformatics*** 28 ECCB 2012:i389-i394 (2012).

[14] Burstein D.*, Gould S.B.*, Zimorski V., Klösges T., Kiosse F., Major P., Martin W., Pupko T., and Dagan T. A machine-learning approach to identify hydrogenosomal proteins in *Trichomonas vaginalis*. ***Eukaryotic Cell*** 11:217-228 (2012).
* These authors contributed equally

[15] Amit M., Donyo M., Hollander D., Goren A., Kim E., Gelfman S., Lev-Maor G., Burstein D., Schwartz S., Postolsky B., Pupko T., and Ast G. Differential GC content between exons and introns establishes distinct strategies of splice site recognition. ***Cell Reports*** 1(5):543-556 (2012).

[16] Gelfman S., Burstein D., Penn O., Schwartz S., Pupko T., and Ast G. Changes in exon-intron structure during vertebrate evolution affect the splicing pattern of exons. ***Genome Research*** 22(1):35-50 (2012).

[17] Barzel A., Privman E., Peeri M., Naor A., Shachar E., Burstein D., Lazary R., Gophna U., Pupko T., and Kupiec M. Native homing endonucleases can target conserved genes in humans and in animal models. ***Nucleic Acids Research*** 39(15):6646-6659 (2011).

[18] Burstein D., Zusman T., Degtyar E., Viner R., Segal G., and Pupko T. Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach. ***PLoS Pathogens*** 5(7):e1000508 (2009).

[19] Schwartz S., Silva J., Burstein D., Pupko T., Eyras E., and Ast G. Large scale comparative analysis of splicing signals and their corresponding splicing factors in eukaryotes. ***Genome Research*** 18(1):88-103 (2008).

[20] Ulitsky I., Burstein D., Tuller T., Chor B. The ACS approach to phylogenomic reconstruction. ***Journal of Computational Biology*** 13(2):336-50 (2006).

AWARDS & HONORS

2014	**EMBO Long-Term postdoctoral Fellowship**
2013	**Rothschild postdoctoral fellowship**
2012	Training scholarship for Ph.D. students - The Aharon Katzir Center, Weizmann Institute of Science
2012	**Prof. Willy Hirsch Prize for original research work conducted in the field of microbiology** (awarded by the Israel Society for Microbiology)
2012	Outstanding poster award - the 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Long Beach, California
2012	Outstanding poster award – The 14th Israeli Bioinformatics Symposium, Hebrew University of Jerusalem
2012	Best poster award – The Seventh Edmond J. Safra Bioinformatics Retreat
2012	The Anat Krauskopf Fund Travel Award
2010	Best poster award - The Annual Meeting of the Israel Society for Microbiology (ISM)
2010	Best poster award – The Fifth Edmond J. Safra Bioinformatics Retreat
2009 - 2013	**Excellence fellow from Converging Technologies Program of the Israeli Council for Higher Education**
2009	Best poster award – The 12th Israeli Bioinformatics Symposium, Weizmann Institute of Science
2008	**Wolf Foundation Award for excellent M.Sc. students** (nation-wide prize)
2008	Award from the Tel Aviv University graduate school for excellent achievements in teaching, research and studies
2006 - 2009	Excellence fellowship from Edmond J. Safra Bioinformatics Program
2003 - 2004	Exact Science Dean's honour list
2002 and 2004	Life Science Dean's honour list

PATENTS

o Barzel, A., Privman, E., <u>Burstein, D.</u>, Gophna, U., Pupko, T., and Kupiec, M. Method for searching for homing endonucleases, their genes and their targets. U.S. Patent No. 8,566,040. Issued 22 Oct. 2013.

INVITED LECTURES

o <u>Burstein D.</u>, Lifshitz Z., Peeri M., Zusman T., Segal G., and Pupko T. Deciphering the translocation signal of the virulence-related type-IVB secretion system. *The First Tel Aviv University – Freie Universität Berlin Joint Workshop (TAU-FUB)*. March 4-7, 2013, Tel Aviv, Israel

o <u>Burstein D.</u>, Zusman T., Peeri M., Lifshitz Z., Segal G., and Pupko T. Fishing for virulent factors: machine learning prediction and experimental validation of bacterial effectors. *20th Annual Conference on Intelligent Systems for Molecular Biology (ISMB)*. July 15-17, 2012, Long Beach, California, USA

o <u>Burstein D.</u>, Peeri M., Zusman T., Lifshitz Z., Segal G., and Pupko T. Fishing for virulent factors: machine learning prediction and experimental validation of bacterial effectors. *IBM research* seminar. June 10, 2012, IBM Research Haifa, Israel.

o <u>Burstein D.</u>, Zusman T., Lifshitz Z., Peeri M., Segal G., and Pupko T. Machine learning approaches to identify and characterize effector proteins in pathogenic bacteria. *Israel Society for Microbiology (ISM) Annual Meeting*. February 13-14, 2012, Bar-Ilan University, Israel. *<u>Prize lecture for original research conducted in the field of microbiology</u>*

o <u>Burstein D.</u>, Gould S.B., Zimorski V., Klösges T., Kiosse F., Major P., Martin W., Pupko T., and Dagan T. A machine-learning approach to hydrogenosomal protein identification in *Trichomonas vaginalis. Machine Learning in Systems Biology (MLSB)*. July 20-11, 2011, Vienna, Austria

o <u>Burstein D.</u>, Gould S.B., Zimorski V., Klösges T., Henze K., Martin W., Pupko T., and Dagan T. A machine-learning approach to hydrogenosomal protein identification in Trichomonas vaginalis. *Seminar in the Department of Ecology and Evolution, University of Lausanne*. July 14, 2011, Lausanne, Switzerland

o <u>Burstein D.</u>, Gould S.B., Zimorski V., Klösges T., Henze K., Martin W., Pupko T., and Dagan T. A machine learning approach to genome-scale identification of proteins targeted to the hydrogenosome in Trichomonas vaginal. *Institute of Botany III seminar, Heinrich Heine University of Düsseldorf*. July 13, 2010, Düsseldorf, Germany

o <u>Burstein D.</u>, Ulitsky I., Tuller T., and Chor B. Information theoretic approaches to whole genome phylogenomics. *The 9th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*. May 14-18, 2005, Cambridge, Massachusetts, USA

COMMUNITY INVOLVEMENT

2010 – 2011   Volunteering as a high school tutor in the Israeli Computer Science Unplugged program

2004 – 2007   Daycare teacher assistant for children of ages 1.5 – 3

2001 – 2004   Caregiver in a residential home for adults diagnosed with autism, ALUT – The Israel National Autism Association

2001   Manager of an English summer school for new immigrants, The Israel Association of Community Centres

LANGUAGE PROFICIENCY

o Hebrew: native language

o English: fluent (speaking, reading, writing)

o French: intermediate (speaking); basic (reading)