David Burstein

The Shmunis School of Biomedicine and Cancer Research
George S. Wise Faculty of Life Sciences, Tel Aviv University
Email: davidbur@tauex.tau.ac.il
Lab website: https://burstein-lab.github.io/

I study interactions within microbial communities using integrated computational and experimental approaches. My work centers on CRISPR-Cas systems, mobile genetic elements, and antimicrobial resistance, exploring both fundamental questions and translational applications in medicine and biotechnology.

Personal Details

Citizenship: Israeli/French

Employment and Positions

2024 –	Associate Professor, The Shmunis School of Biomedicine and Cancer Research George S. Wise Faculty of Life Sciences, Tel Aviv University
2025 –	Visiting Professor (Sabbatical), Department of Microbiology & Immunology, UBC
2018 – 2023	Senior Lecturer (Assistant Professor equiv.), The Department of Molecular Microbiology and Biotechnology, George S. Wise Faculty of Life Sciences, Tel Aviv University
2015 – 2018	Postdoctoral fellow, The California Institute for Quantitative Biosciences, University of California, Berkeley (Advisor: Jennifer A. Doudna)
2013 – 2015	EMBO fellow, Earth and Planetary Sciences, University of California, Berkeley (Advisor: Jill F. Banfield)

Education

2008 – 2013	PhD., Department of Cell Research and Immunology, Tel Aviv University (Advisor: Tal Pupko)
2006 – 2008	MSc., Department of Cell Research and Immunology, Tel Aviv University (Advisor: Tal Pupko)
2001 – 2004	BSc. Double major in Life Sciences and Computer Science

Publications

Metrics:

h-index: 37 (Google Scholar), 31 (Scopus), 31 (Web of Science)

Total citations: 8,738 (Google Scholar), 5,956 (Scopus), 5,454 (WoS, without self-citations)

Self in bold; Students/personnel under my supervision underlined

* Equal contribution

✉ Corresponding author

Peer-Reviewed Publications

1. Rannon E., **Burstein, D✉.** Optimizing Protein Tokenization: Reduced Amino Acid Al-phabets for Efficient and Accurate Protein Language Models. ***Bioinformatics***. 2026, *accepted,*
   Preprint of accepted version:

2. Fraikin, N., Samuel, B., **Burstein, D✉**, Lesterlin, C✉. Strategies for zygotic gene expression during plasmid establishment. ***Plasmid***. 2025, June; Vol. 134: pp 102754

3. Rannon E., Shashua, S., **Burstein, D✉.** DRAMMA: A multifaceted machine learning approach for novel antimicrobial resistance gene detection in metagenomic data. ***Microbiome***. 2025, March; Vol. 13: pp. 67

4. Samuel, B., Mittelman, K., Croitoru, S. Y., Ben-Haim, M., **Burstein, D✉**. Diverse anti-defense systems are encoded in the leading region of plasmids. ***Nature***. 2024, October; Vol. 635: pp. 186–192 .

5. Hershko Y., Rannon E., Adler A., **Burstein D.**, and Barkan D. WarA, a remote *Nocardia wallacei* homolog of NpmA and KamB, confers broad spectrum aminoglycoside resistance in Nocardia and Mycobacteria. ***International Journal of Antimicrobial Agents****.* 2024, February; Vol: 63(2), 107089. .

6. Miller. D., Arias, O., **Burstein, D✉.** GeNLP: An interactive web application for microbial gene exploration and prediction. ***Bioinformatics***. 2024, January; Vol:40(2), btae034 .

7. Harari, S., Miller, D., Fleishon, S., **Burstein, D.**, and Stern, A. Using big sequencing data to identify chronic SARS-Coronavirus-2 infections. ***Nature Communications****.* 2024, January; Vol. 15: pp. 648 .

8. Alon, D. M., Mittelman, K., Stibbe, E., Countryman, S., Stodieck, L., Shankini Doraisingam, Martin, D. M. L., Hamo, Pines, G✉., **Burstein D✉**.CRISPR-based genetic diagnostics in microgravity. ***Biosensors & Bioelectronics***. 2023, October Vol: 237, 115479

9. Hershko, Y., Levytskyi, K., Rannon, E., Assous, M. V., Ken-Dror, S., Amit, S., Ben-Zvi, H., Sagi, O., Schwartz, O., Sorek, N., Szwarcwort, M., Barkan, D., **Burstein, D.,** and Adler, A. Phenotypic and genotypic analysis of antimicrobial resistance in Nocardia species. ***Journal of Antimicrobial Chemotherapy***. 2023, September; Vol: 78(9): pp. 2783.

10. Miller, D., Stern, A., **Burstein, D✉.** Deciphering microbial gene function using natural language processing. ***Nature Communications***. 2022, September; Vol. 13: pp. 5731.

11. Alon, D. M., Partosh, T., **Burstein, D.**, Pines, G. Rapid and sensitive on-site genetic diagnostics of pest fruit flies using CRISPR-Cas12a. ***Pest Management Science*** 2022, September; Vol 79(1), pp. 68–75.

12. Tsuchida, C. A., Zhang, S., Doost, M. S., Zhao Y., Wang, J., O'Brien, E., Fang, H., Li, C. P., Li, D., Hai, Z. Y., Chuck, J., Brötzmann, J., Vartoumian, A., **Burstein, D.**, Chen, X. W., Nogales, E., Doudna, J. A., Liu J. J. G. Chimeric CRISPR-CasX enzymes and guide RNAs for improved genome editing activity. ***Molecular Cell.*** 2022, March; Vol .82: pp 1199–1209.

13. Nahmad, A. D., Raviv, Y., Horovitz-Fried, M., Sofer, I., Akriv, T., Nataf, D., Dotan, I., Carmi, Y., **Burstein, D.**, Wine, Y., Benhar, I., Barzel, A. Engineered B cells expressing an anti-HIV antibody enable memory retention, isotype switching and clonal expansion. ***Nature Communications***. 2020, November; Vol. 11: pp. 5851.

14. Harrington, L. B., Ma, E., Chen, J. S., Witte, I. P., Gertz, D., Paez-Espino, D., Al-Shayeb, B., Kyrpides, N. C., **Burstein, D.**, Banfield, J. F., and Doudna, J. A. A scoutRNA Is required for some Type V CRISPR-Cas systems. ***Molecular Cell***. 2020, July; Vol. 79: pp. 416–424.e5

15. Méheust, R., **Burstein, D.**, Castelle, C. J., and Banfield, J. F. The distinction of CPR bacteria from other bacteria based on protein family content. ***Nature Communications***. 2019, September; Vol. 10: pp. 4173.

16. Diamond, S., Andeer, P. F., Li, Z., Crits-Christoph, A., **Burstein, D.**, Anantharaman, K., Lane, K. R., Thomas, B. C., Pan, C., Northen, T. R., and Banfield, J. F. Mediterranean grassland soil C–N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. ***Nature Microbiology***. 2019, August; Vol. 4: pp. 1356–1367.

17. Wright, A. V., Wang, J. Y., **Burstein, D.,** Harrington, L. B., Paez-Espino, D., Kyrpides, N. C., Iavarone, A. T., Banfield, J. F., and Doudna, J. A. A functional mini-Integrase in a two-protein type V-C CRISPR system. ***Molecular Cell***. 2019, February; Vol. 73: pp. 727-737.e3.

18. Carnevali, P. B. M., Schulz, F., Castelle, C. J., Kantor, R. S., Shih, P. M., Sharon, I., Santini, J. M., Olm, M. R., Amano, Y., Thomas, B. C., Anantharaman, K., **Burstein, D.**, Becraft, E. D., Stepanauskas, R., Woyke, T., and Banfield, J. F. Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. ***Nature Communications***. 2019, January; Vol. 10: pp. 463.

19. Harrington, L. B.*, **Burstein, D.*,** Chen, J. S., Paez-Espino, D., Ma, E., Witte, I. P., Cofsky, J. C., Kyrpides, N. C., Banfield, J. F., and Doudna, J. A. Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. ***Science***. 2018, November; Vol. 362: pp. 839–842.

20. Dudek, N. K., Sun, C. L., **Burstein, D.**, Kantor, R. S., Aliaga Goltsman, D. S., Bik, E. M., Thomas, B. C., Banfield, J. F., and Relman, D. A. Novel microbial diversity and functional potential in the marine mammal oral microbiome. ***Current Biology***. 2017, December; Vol. 27: pp. 3752-3762.e6.

21. Hernsdorf, A. W., Amano, Y., Miyakawa, K., Ise, K., Suzuki, Y., Anantharaman, K., Probst, A., **Burstein, D.**, Thomas, B. C., and Banfield, J. F. Potential for microbial H_2 and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. ***The ISME Journal***. 2017, August; Vol. 11: pp. 1915–1929.

22. Paul, B. G., **Burstein, D.**, Castelle, C. J., Handa, S., Arambula, D., Czornyj, E., Thomas, B. C., Ghosh, P., Miller, J. F., Banfield, J. F., and Valentine, D. L. Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. ***Nature Microbiology***. 2017, June; Vol. 2: pp. 17045.

23. East-Seletsky, A., O'Connell, M. R., **Burstein, D.**, Knott, G. J., and Doudna, J. A. RNA Targeting by functionally orthogonal type VI-A CRISPR-Cas enzymes. ***Molecular Cell***. 2017, May; Vol. 66: pp. 373-383.e3.

24. Olm, M. R., Brown, C. T., Brooks, B., Firek, B., Baker, R., **Burstein, D.**, Soenjoyo, K., Thomas, B. C., Morowitz, M., and Banfield, J. F. Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. ***Genome Research***. 2017, April; Vol. 27: pp. 601–612.

25. **Burstein, D.***, Harrington, L. B.*, Strutt, S. C., Probst, A. J., Anantharaman, K., Thomas, B. C., Doudna, J. A., and Banfield, J. F. New CRISPR–Cas systems from uncultivated microbes. ***Nature***. 2017, February; Vol. 542: pp. 237–241.

26. Probst, A. J., Castelle, C. J., Singh, A., Brown, C. T., Anantharaman, K., Sharon, I., Hug, L. A., **Burstein, D.**, Emerson, J. B., Thomas, B. C., and Banfield, J. F. Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO_2 concentrations. ***Environmental Microbiology***. 2017, February; Vol. 19: pp. 459–474.

27. East-Seletsky, A.*, O'Connell, M. R.*, Knight, S. C., **Burstein, D.,** Cate, J. H. D., Tjian, R., and Doudna, J. A. Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. ***Nature***. 2016, October; Vol. 538: pp. 270–273.

28. **Burstein, D.**, Sun, C. L., Brown, C. T., Sharon, I., Anantharaman, K., Probst, A. J., Thomas, B. C., and Banfield, J. F. Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. ***Nature Communications***. 2016, February; Vol. 7: pp. 10613.

29. **Burstein, D.**, Amaro, F., Zusman, T., Lifshitz, Z., Cohen, O., Gilbert, J. A., Pupko, T., Shuman, H. A., and Segal, G. Genomic analysis of 38 *Legionella* species identifies large and diverse effector repertoires. ***Nature Genetics***. 2016, February; Vol. 48: pp. 167–175.

30. Teper, D.*, **Burstein, D.***, Salomon, D., Gershovitz, M., Pupko, T., and Sessa, G. Identification of novel *Xanthomonas euvesicatoria* type III effector proteins by a machine-learning approach. ***Molecular Plant Pathology***. 2016, April; Vol. 17: pp. 398–411.

31. Anantharaman, K., Brown, C. T., **Burstein, D.**, Castelle, C. J., Probst, A. J., Thomas, B. C., Williams, K. H., and Banfield, J. F. Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. ***PeerJ***. 2016, January; Vol. 4: pp. e1607.

32. **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***. 2015, May; Vol. 6: pp. e00161-15.

33. 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., Williams, K. H., and Banfield, J. F. Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. ***Genome Research***. 2015, April; Vol. 25: pp. 534–543.

34. Lifshitz, Z., **Burstein, D.**, Schwartz, K., Shuman, H. A., Pupko, T., and 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***. 2014, September; Vol. 82: pp. 3740–3752.

35. Yosef, I., Shitrit, D., Goren, M. G., **Burstein, D.,** Pupko, T., and Qimron, U. DNA motifs determining the efficiency of adaptation into the *Escherichia coli* CRISPR array. ***Proceedings of the National Academy of Sciences***. 2013, August; Vol. 110: pp. 14396–14401.

36. Cohen, O., Ashkenazy, H., Levy Karin, E., **Burstein, D.**, and Pupko, T. CoPAP: Coevolution of presence-absence patterns. ***Nucleic Acids Research***. 2013, July; Vol. 41: pp. W232–W237.

37. 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***. 2013, February; Vol. 110: pp. E707–E715.

38. Cohen, O., Ashkenazy, H., **Burstein, D.**, and Pupko, T. Uncovering the co-evolutionary network among prokaryotic genes. ***Bioinformatics***. 2012, September; Vol. 28: pp. i389–i394.

39. 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***. 2012, May; Vol. 1:

pp. 543–556.

40. **Burstein, D.***, Gould, S. B.*, Zimorski, V., Kloesges, T., Kiosse, F., Major, P., Martin, W. F., Pupko, T., and Dagan, T. A machine learning approach to identify hydrogenosomal proteins in *Trichomonas vaginalis*. ***Eukaryotic Cell***. 2012, February; Vol. 11: pp. 217–228.

41. Gelfman, S., **Burstein, D.**, Penn, O., Savchenko, A., Amit, M., Schwartz, S., Pupko, T., and Ast, G. Changes in exon–intron structure during vertebrate evolution affect the splicing pattern of exons. ***Genome Research***. 2012, January; Vol. 22: pp. 35–50.

42. 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***. 2011, August; Vol. 39: pp. 6646–6659.

43. **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***. 2009, July; Vol. 5: pp. e1000508.

44. 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***. 2008, January; Vol. 18: pp. 88–103.

45. Ulitsky, I., **Burstein, D.**, Tuller, T., and Chor, B. The average common substring approach to phylogenomic reconstruction. ***Journal of Computational Biology***. 2006, March; Vol. 13: pp. 336–350.

Peer-Reviewed Proceeding

46. **Burstein, D.**, Ulitsky, I., Tuller, T., and Chor, B. Information theoretic approaches to whole genome phylogenies. Journal of Computational Biology. ***International Conference on Research in Computational Molecular Biology (RECOMB)***. Cambridge, MA, USA. 2005.

Invited Highlight Papers (Non-Peer-Reviewed)

47. Mittelman, K., and **Burstein, D✉.** Tiny hidden genes within our microbiome. ***Cell***. 2019, August; Vol. 178: pp. 1034–1035

Papers under review

48. Rannon, E., **Burstein, D✉.** Leveraging Natural Language Processing to Unravel the Mystery of Life: A Review of NLP Approaches in Genomics, Transcriptomics, and Proteomics. 2026, *under review in Genome Biology.*

49. Solan, Y., Shur, G., **Burstein, D✉.** Global-scale analysis of the taxonomic and ecological distribution of key pathogenic secretion systems. 2026, *under revision in mSystems.*

Patents

Granted Patents:

2025 US12227753B2: CasY compositions and methods of use, *The Regents of the University of California*.

2025 US12264314B1: CasZ compositions and methods of use, *The Regents of the University of California*.

2024 US11970719B2: Class 2 CRISPR/Cas compositions and methods of use, *The Regents of the University of California*.

2023 US11795472B2: RNA-guided nucleic acid modifying enzymes and methods of use thereof, *The Regents of the University of California*.

2023 GB2582100B: Cas12c Compositions and methods of use, *The Regents of the University of California*.

Pending Patents:

2024 WO2024166096A1 Methods and Constructs for Improving Conjugation Efficiency, *Ramot at Tel Aviv University Ltd*.

Grant Funding

2025 European Research Council (ERC) Consolidator Grant, *“Systematic Investigation of Anti-Defense Function and Regulation in Bacterial Conjugation” (DEFCONJ)*.
PI, 60 months, 2,275,000 Euro (~3,680,000 CAD)

2025 Ministry of Defence, “An LLM-based approach to predict the function of genes and design tailored pathways and genomic segments”
Co-PI, 12 months, 600,000 NIS (~264,000 CAD)

2024 TAU Center for Artificial Intelligence & Data Science (TAD), *“Genomic Language Models Integrating Hierarchical Biological Knowledge”*.
PI, 12 months 120,000 NIS (~52,000 CAD)

2023 Israel Science Foundation (ISF) *“Natural language models for predicting gene function in microbes”*.
PI, 60 months, 1,350,000 NIS (~595,000 CAD)

2023 Ministry of Defence, *“Language model approaches for detection of genome editing events”*.
PI, 24 months, 572,000 NIS (~252,000 CAD)

2020 Ministry of Defence, *“Detection of Antimicrobial Resistance Genes using Computational Approaches and Metagenomic Data Analysis”*.
PI, 36 months, 800,000 NIS (~353,000 CAD)

2020 Israel Innovation Authority, *“CRISPR-IL consortium: AI-based Infrastructure for Improving Accuracy and Efficiency of Genome Editing using CRISPR Technology”*.

Co-PI, part of a joint academic and industry consortium, 18 months, 37 million NIS (~16.3 million CAD), out of which 500,000 NIS to my lab (~220,000 CAD)

2019 Mammoth Biosciences (Sponsored Research) , *"Expansion of class 2 CRISPR-Cas systems repertoire"*.
PI, 30 months, 588,000 USD (~818,000 CAD)

2018 Israel Council for Higher Education, *"Metagenomic and Machine Learning Approaches for Discovery of CRISPR Systems and Resistance Genes"*.
PI, 170,000 NIS (~75,000 CAD)

2018 Israel Science Foundation (ISF), *"Discovery and characterization of novel CRISPR-Cas systems"*.
PI, 60 months, 1,675,000 NIS (~739,000 CAD)

Awards and Fellowships

2018 Alon Fellowship for Outstanding Young Faculty, Israel Council for Higher Education
2014 Long-Term Postdoctoral Fellowship, European Molecular Biology Organization (EMBO)
2013 Rothschild Postdoctoral Fellowship, Yad Hanadiv
2012 Prof. Willy Hirsch Prize for Original Research in Microbiology, Israel Society for Microbiology
2009 Excellence Fellowship, Converging Technologies Program, Israeli Council for Higher Education (48 months)
2008 Wolf Foundation Award for excellent MSc students
2006 Excellence Fellowship, Edmond J. Safra Bioinformatics Center (36 months)

Presentations (showing 2018 – present)

2027 EMBO Symposium, Immune System of Bacteria, University of Cambridge. *Invited Speaker*

2026 Gordon Research Conference, Microbiome Editing, Pomona. *Invited Speaker*
Conference Symposium, CSHL meeting on Microbiomes, Cold Spring Harbor. *Invited Speaker*
Conference Symposium, ILANIT/FISEB Experimental Biology. Eilat. *Invited Speaker*

2025 Conference Symposium, Israel Data Science and AI Initiative annual meeting. *Invited Speaker*
Conference Symposium, Center for AI and Data Science, Tel Aviv University. *Invited Speaker*
Seminar, Department of Microbiology & Immunology, University of British Columbia
Seminar, The Shmunis School of Biomedicine and Cancer Research, Tel Aviv University
Seminar, Department of Biochemistry & Molecular Biology, Tel Aviv University

2024 Conference Symposium, Doudna Lab 30 Year Symposium. UC Berkeley. *Invited Speaker*
Conference Symposium, UC Berkeley-TAU Initiative in Computational Biology and Bioinformatics. Center for Regulatory Genomics (CRG), Barcelona. *Invited Speaker*

Seminar, Department of Life Sciences, Ben-Gurion University

2023 Conference Symposium, Bacterial Genetics and Ecology, Copenhagen. *Speaker*
Conference Symposium, Israeli Bioinformatics Symposium. *Invited Speaker*
EMBO Symposium, Immune System of Bacteria. Weizmann Institute. *Speaker*
Conference Symposium, ILANIT Experimental Biology Conference. Eilat. *Speaker*
Seminar, Department of Microbiology, Immunology, and Genetics, Ben-Gurion University
Seminar, The Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan University
Seminar, Plant & Environmental Sciences. Weizmann Institute of Science
Seminar, Plant and Environmental Sciences, Hebrew University of Jerusalem

2021 Conference Symposium, Paradigm Changes in the Management of Early Pregnancy and Pregnancy Loss. Dubai (delivered virtually). *Invited Speaker*
Online Workshop, Bioinformatic tools for biological insight. University of Bergen. *Invited Speaker*
Seminar, Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem
Seminar, Israel Institute for Biological Research
Seminar, The Horizon community of educators, Israel Space Agency
Seminar, Google Israel

2020 Online Symposium, Israeli Society of Evolutionary Biology annual meeting. *Invited Speaker*
Conference Symposium, Synthetic Biology. Israel Institute for Biological Research *Invited Speaker*
Seminar, School of Computer Science and Engineering, The Hebrew University of Jerusalem

2019 Conference Symposium, Harvey Prize Symposium, Technion. *Invited Speaker*
Conference Symposium, UC Berkeley-TAU Initiative in Computational Biology and Bioinformatics. Tel Aviv University. *Invited Speaker*
Online Workshop, Microbiome Metagenomics. College of Health Sciences, Uganda Virus Research Institute, Makerere University. *Invited Speaker*
Conference Symposium, The Israeli Society for Microbiology Meeting. Weizmann Institute of Science. *Invited Speaker*
Conference Symposium, Annual Broad-ISF Symposium, Jerusalem. *Invited Speaker*
Conference Symposium, Workshop on Nanoscience and Nanotechnology. Center for Nanoscience & Nanotechnology, Tel Aviv University. *Invited Speaker*
Seminar, Gynaecology and Maternity Center, Sheba Hospital
Seminar, Institute of Evolution, University of Haifa

2018 Conference Symposium, UC Berkeley-TAU Initiative in Computational Biology and Bioinformatics. UC Berkeley. *Invited Speaker*

Conference Symposium, The Israeli Society for Microbiology Meeting. Ben Gurion University
Invited Speaker

Seminar, Faculty of Life Science, Bar Ilan University

Seminar, Department of Life Science, Ben Gurion University

Supervision

I have supervised nine PhD students (five currently active), nine MSc students (two currently active), and 18 undergraduates.

Asaf Zorea (2024 – 2030), Life Sciences, TAU, PhD student
Ori Ben Shir (2025 – 2030), Life Sciences, TAU, PhD student
Ella Rannon (2024 – 2029), Life Sciences, TAU, PhD student
Chen Agassy (2024 – 2026), TAU, Bioinformatics MSc
Nadav Shalev (2024 – 2026), TAU, Bioinformatics MSc
Guy Shur (2023 – 2028), Life Sciences, TAU, PhD student
Ori Ben-Shir (2023 – 2024), TAU, Bioinformatics MSc
Shirley Croitoru (2022 – 2027), Life Sciences, TAU, PhD student
Edan Gabay (2022 – 2025), TAU, Bioinformatics MSc
Maya Ben-Haim (2021 – 2024), TAU, Mathematical and Theoretical Biology MSc
Ella Rannon (2021 – 2024), TAU, Bioinformatics MSc
Adi Yanni (2020 – 2023), Life Sciences, TAU, PhD student (with Dr. Johann Elbaz, TAU)
Dr. Dan Mark Alon (2020 – 2023), Life Sciences, TAU, PhD student (with Dr. Gur Pines, AGRI)
Yatir Solan (2020 – 2023), TAU, Mathematical and Theoretical Biology MSc
Dr. Bruria Samuel (2019 – 2025), Direct PhD Track, Life Sciences, TAU, PhD student
Dr. Danielle Miller (2019 – 2024), Life Sciences, TAU, PhD student (with Prof. Adi Stern, TAU)
Dov Gertz (2019 – 2021), TAU, Bioinformatics MSc
Sagi Shaashua (2019 – 2021), TAU, Bioinformatics MSc

Additional personnel

Ortal Peretz (2022 – 2024), TAU, Bioinformatician
Yael Gershon (2022 – 2023), TAU, Lab Technician
Dr. Roy Rabinowitz (2022 – 2023), TAU, Researcher
Tomer Parket (2021 – 2024), TAU, Data Analyst
Ofir Arias (2020 – 2023), TAU, Software Specialist
Yuval Cohen (2020 – 2021), TAU, Programmer
Dr. Karin Mittelman (2018 – present), TAU, Research Associate

Teaching (since 2018)

2024 – 2025	Data Games, Co-Director, 2nd- and 3rd-year undergraduate and graduate student Project-Based Learning course, Life Science Faculty, TAU (~30 students)
2019 – 2025	Introduction to Bioinformatics, Co-Director, 2nd-year mandatory course, Life Science Faculty, TAU (~300 students)
2019 – 2025	Computational Genomics, Co-Director, 3rd-year and graduate student course, Computer Science School, TAU (~50 students)
2020 – 2023	Scientific Literacy, Director, 2nd-year mandatory course, Life Science Faculty, TAU (~20 students)

Teaching Excellence

Dean's Excellence Award and Top 100 Lecturers at Tel Aviv University, annually 2019–2024

Professional Service

Journals: Nature Microbiology, Nature Methods, Nature Reviews Microbiology, Nature Communications, Scientific Reports, Microbiome, Proceedings of the National Academy of Sciences (PNAS), FEMS Microbial Ecology, Bioinformatics, iScience, PLoS Computational Biology, Nucleic Acid Research (NAR), Molecular Biology and Evolution (MBE), The ISME Journal, Philosophical Transactions of the Royal Society B, mBio, PLoS One, Scientific Reports, GigaScience, The CRISPR journal, Genome and Biology Evolution (GBE), Protein Science

Funding Agencies: Dutch Research Council (NWO), Swiss National Science Foundation (SNSF), French National Research Agency (ANR), US-Israel Binational Science Foundation (BSF), Israel Science Foundation (ISF), Tel Aviv University Center for Combating Pandemics (TCCP), Koret-Berkeley-TAU (KBT)

2023 – present	Board Member, The Israeli Society for Bioinformatics and Computational Biology (ISBCB).
2023 – present	Edmond J. Safra Center for Bioinformatics, Steering Committee
2023 – 2025	Chair of the BSc. Bioinformatics program
2018 – 2023	Chair of the Life Science MSc. Bioinformatics program