

# Itai Sharon – Curriculum Vitae

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## RESEARCH AND ACADEMIC EXPERIENCE

**Principle Investigator**, MIGAL – Galilee Research Institute, 08/2015 – present  
Research focuses on the development of computational and other tools for microbial ecology

**Senior Lecturer**, Tel-Hai College, 10/2015 – present  
Teaches basic and advanced courses at the Computer Science Department

**Postdoctoral Researcher**, University of California, Berkeley, 2010 – 2015  
Research focus: dynamics and structure of microbial communities across different environments  
Advisor: Prof. Jillian Banfield

**Short postdoc**, Technion, Israel Institute of Technology, 04 – 08/2010  
Research focus: analysis of next generation sequencing  
Affiliation: Laboratory of Dr. Itai Yanai

**Algorithm developer**, NDS Technologies, Haifa, Israel, 1998 – 2007  
Developed algorithms and software for image analysis and understanding

## EDUCATION

**PhD**, Technion – Israel Institute of Technology, Computer Science, 2010  
Dissertation title: Computational methods for metagenomic analysis  
Advisors: Prof. Oded Béjà and Prof. Ron Pinter

**MSc**, Technion – Israel Institute of Technology, Computer Science, 2005  
Research focus: similarity detection for low complexity and remotely related proteins  
Advisors: Dr. Golan Yona and Assoc. Prof. Ran El-Yaniv

**BSc**, Technion – Israel Institute of Technology, Computer Science, 1998  
GPA: 89.6

## REFEREED PUBLICATIONS

1. Fridman, S., Flores-Uribe, J., Larom, S., Alalouf, O., Liran, O., Yacoby, I., Salama, F., Bailleul, B., Rappaport, F., Ziv, T., **Sharon, I.**, Cornejo-Castillo, F.M., Philosof, A., Dupont, C.L., Sanchez, P., Acinas, S.G., Rohwer, F., Lindell, D. and Bèjà, O. (2017). A myovirus encoding both photosystem-I and II proteins enhances cyclic electron flow in infected *Prochlorococcus* cells. *Nature Microbiol.* accepted.
2. Philosof, A., Yutin, N., Flores-Uribe, J., **Sharon, I.**, Koonin, E.V., Bèjà, O. (2017). Novel abundant oceanic viruses of uncultured marine group II Euryarchaeota. *Current Biology*, 27(9), 1362-1368.
3. 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., Banfield, J.F. (2017). Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO<sub>2</sub> concentrations. *Environ Microbiol*, 19(2), 459-474.
4. Raveh-Sadka, T., Firek, B., **Sharon, I.**, Baker, R., Brown, C.T., Thomas, B.C., Morowitz, M.J., Banfield, J.F. (2016). Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. **ISME J.**, doi: 10.1038/ismej.2016.83.
5. Wrighton, K.C., Castelle, C.J., Varaljay, V.A., Satagopan, S., Brown, C.T., Wilkins, M.J., Thomas, B.C., **Sharon, I.**, Williams, K.H., Tabita, F.R., Banfield, J.F. (2016). RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. **ISME J.**, doi: 10.1038/ismej.2016.53.
6. 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., Banfield, J.F. (2016). Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO<sub>2</sub> concentrations. **Environ Microbiol**, doi: 10.1111/1462-2920.13362
7. 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. **Nat Commun**, doi: 10.1038/ncomms10613
8. Hug, L.A., Thomas, B.C., **Sharon, I.**, Brown, C.T., Sharma, R., Hettich, R.L., Wilkins, M.J., Williams, K.H., Singh, A., Banfield, J.F. (2016). Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. **Environ Microbiol**, 18(1), 159-173
9. Brown, C.T., Hug, L.A., Thomas, B.C., **Sharon, I.**, Castelle, C.J., Singh, A., Wilkins, M.J., Wrighton, K.C., Williams, K.H. and Banfield, J.F. (2015). Unusual biology across a group comprising more than 15% of domain Bacteria. *Nature*, doi:10.1038/nature14486
10. Hug, L.A., Thomas, B.C., **Sharon, I.**, Brown, C.T., Sharma, R., Hettich, R.L., Wilkins, M.J., Williams, K.H., Singh, A., Banfield, J.F. (2015). Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. *Environ Microbiol*, doi: 10.1111/1462-2920.12930
11. Paez-Espino, D., **Sharon, I.**, Morovic, W., Stahl, B., Thomas, B.C., Barrangou, R., Banfield, J.F. (2015). CRISPR immunity drives rapid phage genome evolution. *mBio*, 6(2), e00262-15
12. **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., Banfield, J.F. (2015). Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. *Genome Res*, 25, 534-543
13. Raveh-Sadka, T., Thomas, B.C., Singh, A., Firek, B., Brooks, B., Castelle, C.J., **Sharon, I.**, Baker, R., Good, M., Morowitz, M.J., Banfield, J.F. (2015). Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. *eLife*, 4, e05477

14. Wrighton, K.C., Castelle, C.J., Wilkins, M.J., Hug, L.A., **Sharon, I.**, Thomas, B.C., Handley, K.M., Mullin, S.W., Nicora, C.D., Singh, A., Lipton, M.S., Long, P.E., Williams, K.H., Banfield, J.F. (2014). Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. *ISME J*, 8(7), 1452-1463
15. Brooks, B., Firek, B.A., Miller, C.S., **Sharon, I.**, Thomas, B.C., Baker, R., Morowitz, M.J., Banfield, J.F. (2014). Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. *Microbiome*, 2(1)
16. **Sharon, I.**, Banfield, J.F. (2013). Genomes from metagenomics. *Science*, 342(6162), 1057-1058
17. Di Rienzi, S.C.\*, **Sharon, I.\***, Wrighton, K.C., Koren, O., Hug, L.A., Thomas, B.C., Goodrich, J.K., Bell, J.T., Spector, T.D., Banfield, J.F., Ley, R.E. (2013). The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. *eLife*, 2, e01102
18. Brown, C.T., **Sharon, I.**, Thomas, B.C., Castelle, C.J., Morowitz, M.J., Banfield, J.F. (2013). Genome resolved analysis of a premature infant gut microbial community reveals a *Varibaculum cambriense* genome and a shift towards fermentation-based metabolism during the third week of life. *Microbiome*, 1(30)
19. Kantor, R.S., Wrighton, K.C., Handley, K.M., **Sharon, I.**, Hug, L.A., Castelle, C.J., Thomas, B.C., Banfield, J.F. (2013). Small genomes and sparse metabolisms of sediment-associated bacteria from four candidate phyla. *mBio*, 4(5), e00708-13
20. **Sharon, I.**, Morowitz, M.J., Thomas, B.C., Costello, E.K., Relman, D.A., Banfield, J.F. (2013). Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. *Genome Res*, 23(1), 111-120
21. Hug, L.A., Castelle, C.J., Wrighton, K.C., Thomas, B.C., **Sharon, I.**, Frischkorn, K.R., Williams, K.H., Tringe, S.G., Banfield, J.F. (2013). Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. *Microbiome*, 1(22)
22. Wrighton, K.C., Thomas, B.C., **Sharon, I.**, Miller, C.S., Castelle, C.J., VerBerkmoes, N.C., Wilkins, M.J., Hettich, R.J., Lipton, M.S., Williams, K.H., Long, P.E., Banfield, J.F. (2012). Fermentation, Hydrogen and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. *Science*, 337(6102), 1661-1665
23. Avrani, S., Wurtzel, O., **Sharon, I.**, Sorek, R., Lindell, D. (2011). Genomic island variability facilitates *Prochlorococcus*-virus coexistence. *Nature*, 474, 604-608
24. Handley, K.M., VerBerkmoes, N.C., Steefel, C.I., Williams, K.H., **Sharon, I.**, Miller, C.S., Frischkorn, K.R., Chourey, K., Thomas, B.C., Shah, M.B., Long, P.E., Hettich, R.L., Banfield, J.F. (2012). Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. *ISME J*, 7(4), 800-816
25. **Sharon, I.**, Battchikova, N., Aro, E.-M., Giglione, C., Meinel, T., Glaser, F., Pinter, R.Y., Breitbart, M., Rohwer, F., Béjà, O. (2011). Comparative metagenomics of microbial traits within oceanic viral communities. *ISME J*, 5(7), 1178-1190
26. Atamna-Ismaeel, N., Finkel, O.M., Glaser, F., **Sharon, I.**, Schneider, R., Post, A.F., Spudich, J.L., von Mering, C., Vorholt, J.A., Iluz, D., Béjà, O., Belkin, S. (2011). Microbial rhodopsins on leaf surfaces of terrestrial plants. *Environ Microbiol*, 14(1), 140-146
27. Alperovitch, A.\*, **Sharon, I.\***, Rohwer, F., Aro, E.M., Milo, R., Nelson, N., Béjà, O. (2011). Reconstructing a puzzle: Existence of cyanophages containing both photosystem-I & photosystem-II gene-suites inferred from oceanic metagenomic datasets. *Environ Microbiol*, 13, 24-32
28. **Sharon, I.\***, Bercovici, S.\*, Pinter, R., Shlomi, T. (2010). Pathway-based functional analysis of metagenomes. *J Comput Biol*, 18(3), 495-505 (RECOMB 2010 issue)

29. Bodaker, I.\*, **Sharon, I.\***, Suzuki, M.T., Feingersch, R., Shmoish, M., Andreishcheva, E., Sogin, M.L., Rosenberg, M., Maguire, M.E., Belkin, S., Oren, O., Bèjà, O. (2010). Comparative community genomics in the Dead Sea, an increasingly extreme environment. *ISME J*, 4(3), 399-407
  30. **Sharon, I.\***, Alperovitch, A.\*, Rohwer, F., Haynes, M., Glaser, F., Atamna-Ismaeel, N., Pinter, R.Y., Partensky, F., Koonin, E.V., Wolf, Y.I., Nelson, N., Bèjà, O. (2009). Photosystem I gene cassettes are present in marine virus genomes. *Nature*, 461, 258-262
  31. Feingersch, R., Suzuki, M.T., Shmoish, M., **Sharon, I.**, Sabehi, G., Partensky, F., Bèjà, O. (2009). Microbial community genomics in eastern Mediterranean Sea surface waters. *ISME J*, 4(1), 78-87
  32. **Sharon, I.**, Pati, A., Markowitz, V.M., Pinter, R.Y. (2009). A statistical framework for the functional analysis of metagenomes. *Proceedings of 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, LNCS, 5541:496-511
  33. **Sharon, I.**, Davis, J.V. and Yona, G. (2009). Book chapter: Prediction of protein-protein Interactions: a study on the co-evolution model. *Methods Mol Biol: Computational Systems Biology*, 61-88, Springer-Verlag
  34. Loy, A., Duller, S., Baranyi, C., Mußmann, M., Ott, J., **Sharon, I.**, Bèjà, O., Le Paslier, D., Dahl, C., Wagner, M.(2008). Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. *Environ Microbiol*, 11(2), 289-299
  35. Atamna-Ismaeel, N., Sabehi, G., **Sharon, I.**, Witzel, K-P., Labrenz, M., Jurgens, K., Barkay, T., Stomp, M., Huisman, J., Bèjà, O. (2008). Widespread distribution of proteorhodopsins in freshwater and brackish ecosystems. *ISME J*, 2(6), 656-662
  36. Kagan, J., **Sharon, I.**, Bèjà, O., Kuhn, J. (2008). The tryptophan pathway genes of the Sargasso Sea metagenome: new operon structure. *Genome Biol*, 9(1), R20
  37. **Sharon, I.\***, Tzahor, S.\*, Williamson, S.\*, Shmoish, M., Man-Aharonovich, D., Rusch, D.B., Yooseph, S., Zeidner, G., Golden, S.S., Mackey, S.R., Adir, N., Weingart, U., Horn, D., Venter, J.C., Mandel-Gutfreund, Y., Bèjà, O. (2007). Viral photosynthetic reaction center genes and transcripts in the marine environment. *ISME J*, 1(6), 492-501
  38. **Sharon, I.**, Birkland, A., Chang, K., El-Yaniv, R., Yona, G. (2005). Correcting BLAST e-values for low-complexity segments. *J Comput Biol*, 12(7), 978-1001
- \* equal contribution

## ACADEMIC ACTIVITY

- Session chair, ISM 2017
- Program committee, ISMB/ECCB 2013
- Reviewer for *Nature Biotechnology*, *Genome Research*, *PLoS Genetics*, *ISME J*, *Applied and Environmental Microbiology*, *Proceedings of the Royal Society B*, *BMC Evolutionary Biology*, *Bioinformatics*, *PLOS ONE*, *BMC Bioinformatics*, *Nature Scientific Reports*, the Israel Science Foundation (ISF)
- Reviews for the 9<sup>th</sup>, 12<sup>th</sup>, and 14<sup>th</sup> RECOMB conferences, and the Genome Informatics Workshop (GIW) 2009

## SELECTED AWARDS AND FELLOWSHIPS

- 2012            **InnoCentive \$10k prize for the challenge “Microbial Strain Identification from a Mixture of Genetic Material”**  
Single winner out of 139 solvers
- 2010-2012      **The European Molecular Biology Organization (EMBO) Long Term Postdoctoral Fellowship**  
Acceptance rate: 13%
- 2010            **Mark of Distinction in Teaching, Faculty of Computer Science, Technion**  
Awarded to top 10% of lecturers based on student surveys
- 2010            **Technion Graduate School Award for Excellent Journal Publication**  
Awarded annually to 3 publications at the Technion
- 2008, 2010     **Excellence Fellowship, Faculty of Computer Science, Technion**
- 2009            **Jacobs Fellowship, Jacobs Graduate School, Technion**  
Awarded annually, one of two recipients at the Faculty of Computer Science
- 2006            **Excellent Teaching Assistant Award, Faculty of Computer Science, Technion**  
Awarded to top 10% of teaching assistants based on student surveys

## TEACHING EXPERIENCE

- Lecturer  
(Tel Hai)
- i. Introduction to Systems Programming (2 semester)
  - ii. Big Data (2 semester)
  - iii. Algorithms I (1 semester)
  - iv. Next Generation Sequencing Data Analysis (workshop, summer 2017)
- Lecturer  
(Technion)
- i. Introduction to Computers (CS234112, 1 semester)
  - ii. Introduction to Computer Science (CS234114, 2 semesters)
  - iii. Introduction to Systems Programming (CS234122, 1 semester)
- Teaching  
Assistant  
(Technion)
- i. Topics in Microarray Data Analysis, (CS236632, 1 semester)
  - ii. Algorithms in Computational Biology (CS236522, 1 semester)
  - iii. Introduction to Computer Science (CS234114, 2 semesters)
  - iv. Object Oriented Programming (CS236703, 5 semesters)

## SELECTED INVITED AND CONFERENCE TALKS

- 2017 **Israeli Society for Bioinformatics General Meeting (IBS 2017)**  
“Uncovering Earth microbiome, thousands of genomes at a time”. **Invited.**
- 2016 **Israeli Society for Microbiology General Meeting (ISM 2016)**  
“Strain variation in microbial communities”. **Invited.**
- 2015 **Newe Ya’ar**  
“Strain variation in microbial populations and its impact on community resilience”.  
**Invited.**
- 2015 **Illumina**  
“Accurate, multi-kb Illumina Truseq synthetic reads resolve complex microbial populations and detect rare microorganisms”. **Invited.**
- 2014 **Joint Genome Institute (JGI) User meeting**  
“Multi-kb Illumina reads reveal significant strain variation and rare organisms in aquifer sediment microbial communities”. **Contributed.**
- 2014 **Joint Genome Institute (JGI) MGM Workshop**  
“Metagenomic binning”. **Invited.**
- 2012 **UC Berkeley**  
“Reconstructing complete genomes from metagenomic data and the way to community genomics”. **Invited.**
- 2012 **American Society for Microbiology General Meeting (ASM 2012)**  
“Microbial species and strain variations during infant gut colonization”. **Invited.**
- 2011 **University of Haifa**  
“Metagenomics based study of microbial genes in phages”. **Invited.**
- 2010 **Research in Computational Molecular Biology (RECOMB 2010)**  
“Pathway-based functional analysis of metagenomes”. **Contributed.**
- 2009 **Research in Computational Molecular Biology (RECOMB 2009)**  
“A statistical framework for the functional analysis of metagenomes”. **Contributed.**
- 2009 **Israeli Society for Microbiology General Meeting (ISM 2009)**  
“Studying genes and gene organizations from metagenomic data”. **Invited.**