

# Itai Sharon

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

10,063  
citations

94381

37  
h-index

197736

49  
g-index

53  
all docs

53  
docs citations

53  
times ranked

11995  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	13.7	1,050
2	Personalized Gut Mucosal Colonization Resistance to Empiric Probiotics Is Associated with Unique Host and Microbiome Features. <i>Cell</i> , 2018, 174, 1388-1405.e21.	13.5	1,015
3	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
4	Post-Antibiotic Gut Mucosal Microbiome Reconstitution Is Impaired by Probiotics and Improved by Autologous FMT. <i>Cell</i> , 2018, 174, 1406-1423.e16.	13.5	752
5	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. <i>Science</i> , 2012, 337, 1661-1665.	6.0	637
6	Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. <i>Microbiome</i> , 2013, 1, 22.	4.9	493
7	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. <i>Microbiome</i> , 2014, 2, 1.	4.9	437
8	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. <i>Genome Research</i> , 2013, 23, 111-120.	2.4	409
9	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. <i>ELife</i> , 2013, 2, e01102.	2.8	355
10	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. <i>MBio</i> , 2013, 4, e00708-13.	1.8	298
11	Genomic island variability facilitates <i>Prochlorococcus</i> –virus coexistence. <i>Nature</i> , 2011, 474, 604-608.	13.7	267
12	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
13	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO <sub>2</sub> concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
14	Photosystem I gene cassettes are present in marine virus genomes. <i>Nature</i> , 2009, 461, 258-262.	13.7	195
15	A distinct abundant group of microbial rhodopsins discovered using functional metagenomics. <i>Nature</i> , 2018, 558, 595-599.	13.7	190
16	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	4.4	170
17	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016, 18, 159-173.	1.8	164
18	Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. <i>Environmental Microbiology</i> , 2009, 11, 289-299.	1.8	162

#	ARTICLE	IF	CITATIONS
19	CRISPR Immunity Drives Rapid Phage Genome Evolution in <i>Streptococcus thermophilus</i> . <i>MBio</i> , 2015, 6, .	1.8	151
20	Genomes from Metagenomics. <i>Science</i> , 2013, 342, 1057-1058.	6.0	149
21	Comparative metagenomics of microbial traits within oceanic viral communities. <i>ISME Journal</i> , 2011, 5, 1178-1190.	4.4	135
22	Viral photosynthetic reaction center genes and transcripts in the marine environment. <i>ISME Journal</i> , 2007, 1, 492-501.	4.4	122
23	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	2.4	121
24	Neonatal antibiotic exposure impairs child growth during the first six years of life by perturbing intestinal microbial colonization. <i>Nature Communications</i> , 2021, 12, 443.	5.8	113
25	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. <i>ELife</i> , 2015, 4, .	2.8	111
26	Comparative community genomics in the Dead Sea: an increasingly extreme environment. <i>ISME Journal</i> , 2010, 4, 399-407.	4.4	101
27	Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. <i>ISME Journal</i> , 2013, 7, 800-816.	4.4	98
28	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016, 10, 2702-2714.	4.4	98
29	Widespread distribution of proteorhodopsins in freshwater and brackish ecosystems. <i>ISME Journal</i> , 2008, 2, 656-662.	4.4	97
30	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	5.8	87
31	Novel Abundant Oceanic Viruses of Uncultured Marine Group II Euryarchaeota. <i>Current Biology</i> , 2017, 27, 1362-1368.	1.8	81
32	Microbial rhodopsins on leaf surfaces of terrestrial plants. <i>Environmental Microbiology</i> , 2012, 14, 140-146.	1.8	78
33	A myovirus encoding both photosystem I and II proteins enhances cyclic electron flow in infected <i>Prochlorococcus</i> cells. <i>Nature Microbiology</i> , 2017, 2, 1350-1357.	5.9	74
34	Highly active rubiscos discovered by systematic interrogation of natural sequence diversity. <i>EMBO Journal</i> , 2020, 39, e104081.	3.5	72
35	Microbial community genomics in eastern Mediterranean Sea surface waters. <i>ISME Journal</i> , 2010, 4, 78-87.	4.4	66
36	Genome resolved analysis of a premature infant gut microbial community reveals a <i>Varibaculum cambriense</i> genome and a shift towards fermentation-based metabolism during the third week of life. <i>Microbiome</i> , 2013, 1, 30.	4.9	50

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37	Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. <i>ISME Journal</i> , 2016, 10, 2817-2830.	4.4	47
38	Reconstructing a puzzle: existence of cyanophages containing both photosystemâ€” and photosystemâ€” gene suites inferred from oceanic metagenomic datasets. <i>Environmental Microbiology</i> , 2011, 13, 24-32.	1.8	46
39	Cyanophage-encoded lipid desaturases: oceanic distribution, diversity and function. <i>ISME Journal</i> , 2018, 12, 343-355.	4.4	23
40	Pathway-Based Functional Analysis of Metagenomes. <i>Journal of Computational Biology</i> , 2011, 18, 495-505.	0.8	21
41	The Core Human Microbiome: Does It Exist and How Can We Find It? A Critical Review of the Concept. <i>Nutrients</i> , 2022, 14, 2872.	1.7	16
42	The tryptophan pathway genes of the Sargasso Sea metagenome: new operon structures and the prevalence of non-operon organization. <i>Genome Biology</i> , 2008, 9, R20.	13.9	15
43	A Statistical Framework for the Functional Analysis of Metagenomes. <i>Lecture Notes in Computer Science</i> , 2009, , 496-511.	1.0	15
44	A novel uncultured marine cyanophage lineage with lysogenic potential linked to a putative marine <i>Synechococcus</i> â€” relicâ€” prophage. <i>Environmental Microbiology Reports</i> , 2019, 11, 598-604.	1.0	13
45	Correcting BLAST e-Values for Low-Complexity Segments. <i>Journal of Computational Biology</i> , 2005, 12, 980-1003.	0.8	10
46	Origins of bloodstream infections following fecal microbiota transplantation: a strain-level analysis. <i>Blood Advances</i> , 2022, 6, 568-573.	2.5	8
47	Prediction of Proteinâ€”Protein Interactions: A Study of the Co-evolution Model. <i>Methods in Molecular Biology</i> , 2009, 541, 61-88.	0.4	6
48	Pathway-Based Functional Analysis of Metagenomes. <i>Lecture Notes in Computer Science</i> , 2010, , 50-64.	1.0	0