

Shinichi Sunagawa

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

43,047
citations

12303

69
h-index

17055

122
g-index

146
all docs

146
docs citations

146
times ranked

43677
citing authors

#	ARTICLE	IF	CITATIONS
1	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
2	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
3	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
4	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	6.5	1,937
5	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
6	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
7	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
8	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
9	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	13.7	1,370
10	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	3.2	991
11	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
12	Salt-responsive gut commensal modulates TH17 axis and disease. <i>Nature</i> , 2017, 551, 585-589.	13.7	896
13	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	6.0	842
14	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
15	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
16	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
17	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
18	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629

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19	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
20	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
21	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
22	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	6.0	461
23	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
24	Functional implications of microbial and viral gut metagenome changes in early stage L-DOPA-naïve Parkinson's disease patients. <i>Genome Medicine</i> , 2017, 9, 39.	3.6	420
25	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
26	Differential gene expression during thermal stress and bleaching in the Caribbean coral <i>Montastraea faveolata</i> . <i>Molecular Ecology</i> , 2008, 17, 3952-3971.	2.0	379
27	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , 2009, 3, 512-521.	4.4	364
28	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013, 23, 1163-1169.	2.4	356
29	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
30	Open science resources for the discovery and analysis of Tara Oceans data. <i>Scientific Data</i> , 2015, 2, 150023.	2.4	330
31	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	2.8	313
32	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013, 10, 881-884.	9.0	311
33	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
34	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
35	Metagenomic 16S rDNA Illumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. <i>Environmental Microbiology</i> , 2014, 16, 2659-2671.	1.8	291
36	Threatened Corals Provide Underexplored Microbial Habitats. <i>PLoS ONE</i> , 2010, 5, e9554.	1.1	273

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37	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
38	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
39	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. <i>PLoS ONE</i> , 2016, 11, e0155362.	1.1	249
40	Synthetic microbiota reveal priority effects and keystone strains in the <i>Arabidopsis</i> phyllosphere. <i>Nature Ecology and Evolution</i> , 2019, 3, 1445-1454.	3.4	234
41	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	13.6	227
42	Symbiodinium Transcriptomes: Genome Insights into the Dinoflagellate Symbionts of Reef-Building Corals. <i>PLoS ONE</i> , 2012, 7, e35269.	1.1	221
43	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e31386.	1.1	214
44	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	1.1	208
45	Transcriptomic responses to heat stress and bleaching in the elkhorn coral <i>Acropora palmata</i> . <i>Marine Ecology - Progress Series</i> , 2010, 402, 97-113.	0.9	191
46	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	4.4	185
47	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015, 16, 82.	3.8	184
48	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	1.8	172
49	Generation and analysis of transcriptomic resources for a model system on the rise: the sea anemone <i>Aiptasia pallida</i> and its dinoflagellate endosymbiont. <i>BMC Genomics</i> , 2009, 10, 258.	1.2	169
50	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	6.0	158
51	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	2.4	147
52	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , 2015, 16, 73.	3.8	143
53	Coral host transcriptomic states are correlated with <i>Symbiodinium</i> genotypes. <i>Molecular Ecology</i> , 2010, 19, 1174-1186.	2.0	136
54	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133

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55	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	6.5	131
56	The host transcriptome remains unaltered during the establishment of coral-algal symbioses. <i>Molecular Ecology</i> , 2009, 18, 1823-1833.	2.0	130
57	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	13.7	128
58	Classification and quantification of bacteriophage taxa in human gut metagenomes. <i>ISME Journal</i> , 2014, 8, 1391-1402.	4.4	127
59	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018, 46, W289-W295.	6.5	126
60	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	6.0	124
61	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. <i>Genome Biology</i> , 2021, 22, 93.	3.8	122
62	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	3.2	115
63	Rapid Evolution of Coral Proteins Responsible for Interaction with the Environment. <i>PLoS ONE</i> , 2011, 6, e20392.	1.1	114
64	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
65	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	5.8	101
66	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , 2017, 12, e0182392.	1.1	92
67	<i>Escherichia coli</i> limits <i>Salmonella Typhimurium</i> infections after diet shifts and fat-mediated microbiota perturbation in mice. <i>Nature Microbiology</i> , 2019, 4, 2164-2174.	5.9	88
68	Natural noncanonical protein splicing yields products with diverse β -amino acid residues. <i>Science</i> , 2018, 359, 779-782.	6.0	87
69	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
70	Global genetic capacity for mixotrophy in marine picocyanobacteria. <i>ISME Journal</i> , 2016, 10, 2946-2957.	4.4	82
71	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . <i>ISME Journal</i> , 2014, 8, 2411-2422.	4.4	80
72	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. <i>Nature Ecology and Evolution</i> , 2020, 4, 1639-1649.	3.4	78

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73	Metagenomic insights into the human gut resistome and the forces that shape it. <i>BioEssays</i> , 2014, 36, 316-329.	1.2	76
74	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
75	A roadmap for metagenomic enzyme discovery. <i>Natural Product Reports</i> , 2021, 38, 1994-2023.	5.2	76
76	Consistent host and organ occupancy of phyllosphere bacteria in a community of wild herbaceous plant species. <i>ISME Journal</i> , 2020, 14, 245-258.	4.4	75
77	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
78	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	6.1	73
79	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	5.8	72
80	A multiproducer microbiome generates chemical diversity in the marine sponge <i>Mycale hentscheli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9508-9518.	3.3	71
81	The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. <i>Nature Microbiology</i> , 2021, 6, 852-864.	5.9	70
82	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
83	Gut microbiota differs between children with Inflammatory Bowel Disease and healthy siblings in taxonomic and functional composition: a metagenomic analysis. <i>American Journal of Physiology - Renal Physiology</i> , 2017, 312, G327-G339.	1.6	69
84	Marine microbial diversity. <i>Current Biology</i> , 2017, 27, R489-R494.	1.8	69
85	Transcriptomic responses to darkness stress point to common coral bleaching mechanisms. <i>Coral Reefs</i> , 2012, 31, 215-228.	0.9	67
86	A fair comparison. <i>Nature Methods</i> , 2014, 11, 359-359.	9.0	64
87	Identification and Gene Expression Analysis of a Taxonomically Restricted Cysteine-Rich Protein Family in Reef-Building Corals. <i>PLoS ONE</i> , 2009, 4, e4865.	1.1	62
88	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, D621-D625.	6.5	60
89	Import of Aspartate and Malate by DcuABC Drives H ₂ /Fumarate Respiration to Promote Initial <i>Salmonella</i> Gut-Lumen Colonization in Mice. <i>Cell Host and Microbe</i> , 2020, 27, 922-936.e6.	5.1	58
90	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	5.9	57

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91	A general non-self response as part of plant immunity. <i>Nature Plants</i> , 2021, 7, 696-705.	4.7	50
92	RNase H As Gene Modifier, Driver of Evolution and Antiviral Defense. <i>Frontiers in Microbiology</i> , 2017, 8, 1745.	1.5	49
93	The Tara Pacific expeditionâ€™A pan-ecosystemic approach of the â€™omicsâ€™-complexity of coral reef holobionts across the Pacific Ocean. <i>PLoS Biology</i> , 2019, 17, e3000483.	2.6	48
94	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. <i>ELife</i> , 2017, 6, .	2.8	45
95	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021, 9, e10911.	0.9	44
96	Gene expression microarray analysis encompassing metamorphosis and the onset of calcification in the scleractinian coral <i>Montastraea faveolata</i> . <i>Marine Genomics</i> , 2009, 2, 149-159.	0.4	42
97	Gut microbial beta-glucuronidase and glycerol/diol dehydratase activity contribute to dietary heterocyclic amine biotransformation. <i>BMC Microbiology</i> , 2019, 19, 99.	1.3	42
98	Expanding Tara Oceans Protocols for Underway, Ecosystemic Sampling of the Ocean-Atmosphere Interface During Tara Pacific Expedition (2016â€™2018). <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	42
99	Evolutionary analysis of orthologous cDNA sequences from cultured and symbiotic dinoflagellate symbionts of reef-building corals (Dinophyceae: Symbiodinium). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 67-74.	0.4	34
100	Hyperthermic stress-induced increase in the expression of glutamate-cysteine ligase and glutathione levels in the symbiotic sea anemone <i>Aiptasia pallida</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2008, 151, 133-138.	0.7	33
101	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018, 8, e021682.	0.8	31
102	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	5.9	27
103	The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes. <i>Nucleic Acids Research</i> , 2022, 50, W516-W526.	6.5	26
104	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	1.6	24
105	The Porcelain Crab Transcriptome and PCAD, the Porcelain Crab Microarray and Sequence Database. <i>PLoS ONE</i> , 2010, 5, e9327.	1.1	21
106	High throughput sequencing provides exact genomic locations of inducible prophages and accurate phage-to-host ratios in gut microbial strains. <i>Microbiome</i> , 2021, 9, 77.	4.9	20
107	Microbiota stability in healthy individuals after single-dose lactulose challengeâ€™A randomized controlled study. <i>PLoS ONE</i> , 2018, 13, e0206214.	1.1	18
108	Computational ecoâ€™systems biology in <i>Tara Oceans</i> : translating data into knowledge. <i>Molecular Systems Biology</i> , 2015, 11, 809.	3.2	16

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109	miR-802 regulates Paneth cell function and enterocyte differentiation in the mouse small intestine. <i>Nature Communications</i> , 2021, 12, 3339.	5.8	16
110	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. <i>Communications Earth & Environment</i> , 2022, 3, .	2.6	13
111	metaSNV v2: detection of SNVs and subspecies in prokaryotic metagenomes. <i>Bioinformatics</i> , 2022, 38, 1162-1164.	1.8	11
112	Tara Pacific Expedition's Atmospheric Measurements of Marine Aerosols across the Atlantic and Pacific Oceans: Overview and Preliminary Results. <i>Bulletin of the American Meteorological Society</i> , 2020, 101, E536-E554.	1.7	9
113	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (Sebastes). <i>BMC Genomics</i> , 2015, 16, 656.	1.2	8
114	Scaling of species distribution explains the vast potential marine prokaryote diversity. <i>Scientific Reports</i> , 2019, 9, 18710.	1.6	8
115	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021, 1, e218.	1.3	8
116	Variation in cell densities and pigment concentrations of symbiotic dinoflagellates in the coral <i>Pavona clavus</i> in the eastern Pacific (Costa Rica). <i>Ciencias Marinas</i> , 2008, 34, 113-123.	0.4	7
117	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013, 2, 120.	0.6	6
118	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. <i>Bioinformatics</i> , 2021, 38, 270-272.	1.8	5
119	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
120	The rumen microbiome inhibits methane formation through dietary choline supplementation. <i>Scientific Reports</i> , 2021, 11, 21761.	1.6	3
121	Import of Aspartate and Malate by DcuABC Drives H ₂ /Fumarate Respiration to Promote <i>Salmonella</i> Gut-Luminal Colonization. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
122	Space, time and microdiversity: towards a resolution revolution in microbiomics. <i>Environmental Microbiology Reports</i> , 2021, 13, 31-35.	1.0	0
123	Metagenomics of the Coral Holobiont. , 2013, , 1-5.		0
124	Metagenomics of the Coral Holobiont. , 2015, , 354-358.		0