

# Shinichi Sunagawa

## List of Publications by Year in descending order

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124  
papers

43,047  
citations

12330  
69  
h-index

17105  
122  
g-index

146  
all docs

146  
docs citations

146  
times ranked

43677  
citing authors

#	ARTICLE	IF	CITATIONS
1	metaSNV v2: detection of SNVs and subspecies in prokaryotic metagenomes. <i>Bioinformatics</i> , 2022, 38, 1162-1164.	4.1	11
2	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	27.8	85
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
4	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
5	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.	14.5	26
6	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	6.5	70
7	Terrestrial and marine influence on atmospheric bacterial diversity over the north Atlantic and Pacific Oceans. <i>Communications Earth &amp; Environment</i> , 2022, 3, .	6.8	13
8	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , 2022, 607, 111-118.	27.8	128
9	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	13.3	27
10	Space, time and microdiversity: towards a resolution revolution in microbiomics. <i>Environmental Microbiology Reports</i> , 2021, 13, 31-35.	2.4	0
11	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021, 9, e10911.	2.0	44
12	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.	11.1	20
13	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. <i>Genome Biology</i> , 2021, 22, 93.	8.8	122
14	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	4.4	107
15	A general non-self response as part of plant immunity. <i>Nature Plants</i> , 2021, 7, 696-705.	9.3	50
16	miR-802 regulates Paneth cell function and enterocyte differentiation in the mouse small intestine. <i>Nature Communications</i> , 2021, 12, 3339.	12.8	16
17	The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. <i>Nature Microbiology</i> , 2021, 6, 852-864.	13.3	70
18	mTAGs: taxonomic profiling using degenerate consensus reference sequences of ribosomal RNA genes. <i>Bioinformatics</i> , 2021, 38, 270-272.	4.1	5

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19	Macroscale patterns of oceanic zooplankton composition and size structure. Scientific Reports, 2021, 11, 15714.	3.3	24
20	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. Current Protocols, 2021, 1, e218.	2.9	8
21	A roadmap for metagenomic enzyme discovery. Natural Product Reports, 2021, 38, 1994-2023.	10.3	76
22	The rumen microbiome inhibits methane formation through dietary choline supplementation. Scientific Reports, 2021, 11, 21761.	3.3	3
23	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. Nature Microbiology, 2021, 6, 1561-1574.	13.3	57
24	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	14.5	60
25	Consistent host and organ occupancy of phyllosphere bacteria in a community of wild herbaceous plant species. ISME Journal, 2020, 14, 245-258.	9.8	75
26	Tara Pacific Expedition's Atmospheric Measurements of Marine Aerosols across the Atlantic and Pacific Oceans: Overview and Preliminary Results. Bulletin of the American Meteorological Society, 2020, 101, E536-E554.	3.3	9
27	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. Nature Ecology and Evolution, 2020, 4, 1639-1649.	7.8	78
28	Tara Oceans: towards global ocean ecosystems biology. Nature Reviews Microbiology, 2020, 18, 428-445.	28.6	227
29	Import of Aspartate and Malate by DcuABC Drives H <sub>2</sub> /Fumarate Respiration to Promote Initial Salmonella Gut-Lumen Colonization in Mice. Cell Host and Microbe, 2020, 27, 922-936.e6.	11.0	58
30	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. ISME Journal, 2020, 14, 1247-1259.	9.8	74
31	A multiproducer microbiome generates chemical diversity in the marine sponge <i>Mycale hentscheli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9508-9518.	7.1	71
32	Synthetic microbiota reveal priority effects and keystone strains in the Arabidopsis phyllosphere. Nature Ecology and Evolution, 2019, 3, 1445-1454.	7.8	234
33	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	28.9	268
34	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	28.9	271
35	Escherichia coli limits Salmonella Typhimurium infections after diet shifts and fat-mediated microbiota perturbation in mice. Nature Microbiology, 2019, 4, 2164-2174.	13.3	88
36	The Tara Pacific expedition's A pan-ecosystemic approach of the 'omics' complexity of coral reef holobionts across the Pacific Ocean. PLoS Biology, 2019, 17, e3000483.	5.6	48

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37	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	12.1	73
38	Gut microbial beta-glucuronidase and glycerol/diol dehydratase activity contribute to dietary heterocyclic amine biotransformation. <i>BMC Microbiology</i> , 2019, 19, 99.	3.3	42
39	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
40	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	4.9	76
41	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	12.8	298
42	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	30.7	734
43	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019, , .	0.4	4
44	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, .	2.5	42
45	Scaling of species distribution explains the vast potential marine prokaryote diversity. <i>Scientific Reports</i> , 2019, 9, 18710.	3.3	8
46	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
47	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	6.0	313
48	Natural noncanonical protein splicing yields products with diverse $\beta$ -amino acid residues. <i>Science</i> , 2018, 359, 779-782.	12.6	87
49	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	12.8	101
50	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	12.8	297
51	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
52	Microbiota stability in healthy individuals after single-dose lactulose challengeâ€“A randomized controlled study. <i>PLoS ONE</i> , 2018, 13, e0206214.	2.5	18
53	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018, 46, W289-W295.	14.5	126
54	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	27.8	1,370

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55	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018, 8, e021682.	1.9	31
56	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.	3.4	69
57	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.	8.2	420
58	Marine microbial diversity. <i>Current Biology</i> , 2017, 27, R489-R494.	3.9	69
59	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
60	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	5.3	147
61	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	7.2	115
62	Salt-responsive gut commensal modulates TH17 axis and disease. <i>Nature</i> , 2017, 551, 585-589.	27.8	896
63	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	14.5	131
64	RNase H As Gene Modifier, Driver of Evolution and Antiviral Defense. <i>Frontiers in Microbiology</i> , 2017, 8, 1745.	3.5	49
65	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , 2017, 12, e0182392.	2.5	92
66	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. <i>ELife</i> , 2017, 6, .	6.0	45
67	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. <i>PLoS ONE</i> , 2016, 11, e0155362.	2.5	249
68	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	4.1	172
69	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	12.6	461
70	Global genetic capacity for mixotrophy in marine picocyanobacteria. <i>ISME Journal</i> , 2016, 10, 2946-2957.	9.8	82
71	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
72	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	27.8	1,506

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73	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016, 7, 11071.	12.8	72
74	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	27.8	670
75	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.	14.5	1,937
76	Open science resources for the discovery and analysis of Tara Oceans data. <i>Scientific Data</i> , 2015, 2, 150023.	5.3	330
77	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (Sebastes). <i>BMC Genomics</i> , 2015, 16, 656.	2.8	8
78	Computational eco-systems biology in Tara Oceans: translating data into knowledge. <i>Molecular Systems Biology</i> , 2015, 11, 809.	7.2	16
79	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	12.6	842
80	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	12.6	617
81	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
82	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
83	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	12.6	158
84	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , 2015, 16, 73.	8.8	143
85	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015, 16, 82.	8.8	184
86	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	27.8	1,627
87	Metagenomics of the Coral Holobiont. , 2015, , 354-358.		0
88	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	7.2	991
89	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.	3.8	291
90	A fair comparison. <i>Nature Methods</i> , 2014, 11, 359-359.	19.0	64

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91	Metagenomic insights into the human gut resistome and the forces that shape it. BioEssays, 2014, 36, 316-329.	2.5	76
92	Classification and quantification of bacteriophage taxa in human gut metagenomes. ISME Journal, 2014, 8, 1391-1402.	9.8	127
93	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909
94	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	17.5	1,664
95	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . ISME Journal, 2014, 8, 2411-2422.	9.8	80
96	Accurate and universal delineation of prokaryotic species. Nature Methods, 2013, 10, 881-884.	19.0	311
97	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
98	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	19.0	442
99	Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 1163-1169.	5.5	356
100	Genomic variation landscape of the human gut microbiome. Nature, 2013, 493, 45-50.	27.8	783
101	Exploring nucleocytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. ISME Journal, 2013, 7, 1678-1695.	9.8	185
102	Metagenomics of the Coral Holobiont. , 2013, , 1-5.		0
103	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
104	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. PLoS ONE, 2012, 7, e47656.	2.5	208
105	Transcriptomic responses to darkness stress point to common coral bleaching mechanisms. Coral Reefs, 2012, 31, 215-228.	2.2	67
106	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. PLoS ONE, 2012, 7, e31386.	2.5	214
107	Symbiodinium Transcriptomes: Genome Insights into the Dinoflagellate Symbionts of Reef-Building Corals. PLoS ONE, 2012, 7, e35269.	2.5	221
108	A Holistic Approach to Marine Eco-Systems Biology. PLoS Biology, 2011, 9, e1001177.	5.6	353

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109	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
110	Rapid Evolution of Coral Proteins Responsible for Interaction with the Environment. <i>PLoS ONE</i> , 2011, 6, e20392.	2.5	114
111	Coral host transcriptomic states are correlated with <i>Symbiodinium</i> genotypes. <i>Molecular Ecology</i> , 2010, 19, 1174-1186.	3.9	136
112	The Porcelain Crab Transcriptome and PCAD, the Porcelain Crab Microarray and Sequence Database. <i>PLoS ONE</i> , 2010, 5, e9327.	2.5	21
113	Threatened Corals Provide Underexplored Microbial Habitats. <i>PLoS ONE</i> , 2010, 5, e9554.	2.5	273
114	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.	1.9	191
115	The host transcriptome remains unaltered during the establishment of coral-algal symbioses. <i>Molecular Ecology</i> , 2009, 18, 1823-1833.	3.9	130
116	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.	9.8	364
117	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.	1.0	34
118	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.	1.1	42
119	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.	2.8	169
120	Identification and Gene Expression Analysis of a Taxonomically Restricted Cysteine-Rich Protein Family in Reef-Building Corals. <i>PLoS ONE</i> , 2009, 4, e4865.	2.5	62
121	Differential gene expression during thermal stress and bleaching in the Caribbean coral <i>Montastraea faveolata</i> . <i>Molecular Ecology</i> , 2008, 17, 3952-3971.	3.9	379
122	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.	1.6	33
123	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
124	Import of Aspartate and Malate by DcuABC Drives H <sub>2</sub> /Fumarate Respiration to Promote <i>Salmonella</i> Gut-Luminal Colonization. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1