

Shinichi Sunagawa

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

123
papers

27,001
citations

60
h-index

146
g-index

146
ext. papers

36,953
ext. citations

17.7
avg, IF

6.33
L-index

#	Paper	IF	Citations
123	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
122	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
121	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359	33.3	1261
120	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016 , 44, D286-93	20.1	1211
119	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
118	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
117	Ocean plankton. Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015 , 348, 1261605	33.3	990
116	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016 , 535, 376-81	50.4	977
115	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018 , 560, 233-237	50.4	654
114	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
113	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014 , 10, 766	12.2	575
112	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
111	Salt-responsive gut commensal modulates T17 axis and disease. <i>Nature</i> , 2017 , 551, 585-589	50.4	553
110	Ocean plankton. Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015 , 348, 1262073	33.3	496
109	Ocean plankton. Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015 , 348, 1261498	33.3	421
108	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016 , 537, 689-693	50.4	400
107	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016 , 532, 465-470	50.4	392

106	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
105	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355
104	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019 , 25, 679-689	50.5	353
103	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
102	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016 , 352, 586-9	33.3	326
101	Differential gene expression during thermal stress and bleaching in the Caribbean coral <i>Montastraea faveolata</i> . <i>Molecular Ecology</i> , 2008 , 17, 3952-71	5.7	304
100	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , 2009 , 3, 512-21	11.9	287
99	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	14.4	274
98	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013 , 23, 1163-9	9.7	269
97	A holistic approach to marine eco-systems biology. <i>PLoS Biology</i> , 2011 , 9, e1001177	9.7	265
96	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019 , 177, 1109-1123.e14	56.2	256
95	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013 , 10, 881-4	21.6	234
94	Threatened corals provide underexplored microbial habitats. <i>PLoS ONE</i> , 2010 , 5, e9554	3.7	219
93	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, 2659-71	5.2	200
92	Open science resources for the discovery and analysis of Tara Oceans data. <i>Scientific Data</i> , 2015 , 2, 150083	3.7	198
91	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
90	Symbiodinium transcriptomes: genome insights into the dinoflagellate symbionts of reef-building corals. <i>PLoS ONE</i> , 2012 , 7, e35269	3.7	178
89	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018 , 9, 373	17.4	168

88	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019 , 8,	8.9	158
87	Assessment of metagenomic assembly using simulated next generation sequencing data. <i>PLoS ONE</i> , 2012 , 7, e31386	3.7	157
86	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. <i>PLoS ONE</i> , 2016 , 11, e0155362	3.7	147
85	MOCAT: a metagenomics assembly and gene prediction toolkit. <i>PLoS ONE</i> , 2012 , 7, e47656	3.7	143
84	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013 , 7, 1678-95	11.9	142
83	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
82	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	2.6	126
81	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016 , 32, 2520-3.2	3.2	117
80	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019 , 179, 1068-1083.e21	56.2	113
79	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	4.5	113
78	The host transcriptome remains unaltered during the establishment of coral-algal symbioses. <i>Molecular Ecology</i> , 2009 , 18, 1823-33	5.7	112
77	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019 , 179, 1084-1097.e21	56.2	108
76	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , 2015 , 16, 73	18.3	108
75	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015 , 16, 82	18.3	107
74	Coral host transcriptomic states are correlated with Symbiodinium genotypes. <i>Molecular Ecology</i> , 2010 , 19, 1174-86	5.7	105
73	Classification and quantification of bacteriophage taxa in human gut metagenomes. <i>ISME Journal</i> , 2014 , 8, 1391-402	11.9	102
72	Ocean plankton. Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015 , 348, 1261447	33.3	100
71	Synthetic microbiota reveal priority effects and keystone strains in the <i>Arabidopsis</i> phyllosphere. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1445-1454	12.3	99

70	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017 , 4, 170093	8.2	89
69	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017 , 45, D529-D534	20.1	74
68	Rapid evolution of coral proteins responsible for interaction with the environment. <i>PLoS ONE</i> , 2011 , 6, e20392	3.7	74
67	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017 , 13, 960	12.2	69
66	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , 2017 , 12, e0182392	3.7	64
65	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . <i>ISME Journal</i> , 2014 , 8, 2411-22	11.9	63
64	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018 , 46, W289-W295	20.1	61
63	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020 , 18, 428-445	22.2	60
62	Metagenomic insights into the human gut resistome and the forces that shape it. <i>BioEssays</i> , 2014 , 36, 316-29	4.1	57
61	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018 , 9, 310	17.4	55
60	Identification and gene expression analysis of a taxonomically restricted cysteine-rich protein family in reef-building corals. <i>PLoS ONE</i> , 2009 , 4, e4865	3.7	53
59	Global genetic capacity for mixotrophy in marine picocyanobacteria. <i>ISME Journal</i> , 2016 , 10, 2946-2957	11.9	53
58	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	5.1	52
57	Natural noncanonical protein splicing yields products with diverse amino acid residues. <i>Science</i> , 2018 , 359, 779-782	33.3	52
56	Cyanobacterial symbionts diverged in the late Cretaceous towards lineage-specific nitrogen fixation factories in single-celled phytoplankton. <i>Nature Communications</i> , 2016 , 7, 11071	17.4	51
55	Consistent host and organ occupancy of phyllosphere bacteria in a community of wild herbaceous plant species. <i>ISME Journal</i> , 2020 , 14, 245-258	11.9	47
54	<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	26.6	46
53	Transcriptomic responses to darkness stress point to common coral bleaching mechanisms. <i>Coral Reefs</i> , 2012 , 31, 215-228	4.2	45

52	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019 , 33, 391-419	5.9	42
51	Marine microbial diversity. <i>Current Biology</i> , 2017 , 27, R489-R494	6.3	38
50	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, 149-59	1.9	37
49	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019 , 68, 1781-1790	19.2	33
48	A fair comparison. <i>Nature Methods</i> , 2014 , 11, 359	21.6	33
47	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	2	31
46	Import of Aspartate and Malate by DcuABC Drives H/Fumarate Respiration to Promote Initial Salmonella Gut-Lumen Colonization in Mice. <i>Cell Host and Microbe</i> , 2020 , 27, 922-936.e6	23.4	28
45	A multiproducer microbiome generates chemical diversity in the marine sponge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 9508-9518	11.5	27
44	RNase H As Gene Modifier, Driver of Evolution and Antiviral Defense. <i>Frontiers in Microbiology</i> , 2017 , 8, 1745	5.7	26
43	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. <i>Genome Biology</i> , 2021 , 22, 93	18.3	26
42	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. <i>Nature Ecology and Evolution</i> , 2020 , 4, 1639-1649	12.3	25
41	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, 133-8	2.3	24
40	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020 , 14, 1247-1259	11.9	23
39	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018 , 8, e021682	3	23
38	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	20.1	21
37	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. <i>ELife</i> , 2017 , 6,	8.9	20
36	Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems		20
35	The porcelain crab transcriptome and PCAD, the porcelain crab microarray and sequence database. <i>PLoS ONE</i> , 2010 , 5, e9327	3.7	19

34	Expanding Tara Oceans Protocols for Underway, Ecosystemic Sampling of the Ocean-Atmosphere Interface During Tara Pacific Expedition (2016-2018). <i>Frontiers in Marine Science</i> , 2019 , 6,	4.5	18
33	The Tara Pacific expedition-A pan-ecosystemic approach of the "-omics" complexity of coral reef holobionts across the Pacific Ocean. <i>PLoS Biology</i> , 2019 , 17, e3000483	9.7	17
32	Metabolic Architecture of the Deep Ocean Microbiome		17
31	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021 , 4, 604	6.7	17
30	A roadmap for metagenomic enzyme discovery. <i>Natural Product Reports</i> , 2021 , 38, 1994-2023	15.1	17
29	Gut microbial beta-glucuronidase and glycerol/diol dehydratase activity contribute to dietary heterocyclic amine biotransformation. <i>BMC Microbiology</i> , 2019 , 19, 99	4.5	16
28	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021 , 9, e10911	3.1	14
27	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , 2022 ,	21.6	14
26	Microbiota stability in healthy individuals after single-dose lactulose challenge-A randomized controlled study. <i>PLoS ONE</i> , 2018 , 13, e0206214	3.7	11
25	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021 , 6, 1561-1574	26.6	9
24	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome.. <i>Science</i> , 2022 , 376, 156-162	33.3	9
23	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , 2021 ,	50.4	8
22	The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. <i>Nature Microbiology</i> , 2021 , 6, 852-864	26.6	8
21	A general non-self response as part of plant immunity. <i>Nature Plants</i> , 2021 , 7, 696-705	11.5	7
20	Scaling of species distribution explains the vast potential marine prokaryote diversity. <i>Scientific Reports</i> , 2019 , 9, 18710	4.9	7
19	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (Sebastes). <i>BMC Genomics</i> , 2015 , 16, 656	4.5	6
18	Uncharted biosynthetic potential of the ocean microbiome		6
17	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022 , 2, 100123		6

16	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> ,	50.4	6
15	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	1.7	5
14	Ecogenomics and biogeochemical impacts of uncultivated globally abundant ocean viruses		5
13	Ecogenomics of key prokaryotes in the arctic ocean		5
12	Tara Pacific Expedition—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	6.1	5
11	miR-802 regulates Paneth cell function and enterocyte differentiation in the mouse small intestine. <i>Nature Communications</i> , 2021 , 12, 3339	17.4	4
10	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019 ,	1	3
9	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine-learning toolbox		3
8	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	16.6	3
7	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021 , 11, 15714	4.9	2
6	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021 , 1, e218		2
5	The Ocean Gene Atlas: exploring the biogeography of plankton genes online		1
4	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013 , 2, 120	0.8	1
3	Airborne bacteria over the oceans shed light on global biogeodiversity patterns		1
2	The rumen microbiome inhibits methane formation through dietary choline supplementation. <i>Scientific Reports</i> , 2021 , 11, 21761	4.9	0
1	Space, time and microdiversity: towards a resolution revolution in microbiomics. <i>Environmental Microbiology Reports</i> , 2021 , 13, 31-35	3.7	