

Shinichi Sunagawa

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8648217/shinichi-sunagawa-publications-by-year.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , 2022 ,	21.6	14
122	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome.. <i>Science</i> , 2022 , 376, 156-162	33.3	9
121	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022 , 2, 100123		6
120	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , 2021 ,	50.4	8
119	The rumen microbiome inhibits methane formation through dietary choline supplementation. <i>Scientific Reports</i> , 2021 , 11, 21761	4.9	0
118	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
117	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine learning toolbox. <i>Genome Biology</i> , 2021 , 22, 93	18.3	26
116	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021 , 4, 604	6.7	17
115	A general non-self response as part of plant immunity. <i>Nature Plants</i> , 2021 , 7, 696-705	11.5	7
114	miR-802 regulates Paneth cell function and enterocyte differentiation in the mouse small intestine. <i>Nature Communications</i> , 2021 , 12, 3339	17.4	4
113	The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. <i>Nature Microbiology</i> , 2021 , 6, 852-864	26.6	8
112	Space, time and microdiversity: towards a resolution revolution in microbiomics. <i>Environmental Microbiology Reports</i> , 2021 , 13, 31-35	3.7	
111	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021 , 9, e10911	3.1	14
110	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
109	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021 , 11, 15714	4.9	2
108	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021 , 1, e218		2
107	A roadmap for metagenomic enzyme discovery. <i>Natural Product Reports</i> , 2021 , 38, 1994-2023	15.1	17

106	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020 , 18, 428-445	22.2	60
105	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
104	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020 , 14, 1247-1259	11.9	23
103	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
102	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
101	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
100	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
99	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
98	Escherichia coli limits Salmonella Typhimurium infections after diet shifts and fat-mediated microbiota perturbation in mice. <i>Nature Microbiology</i> , 2019 , 4, 2164-2174	26.6	46
97	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
96	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019 , 68, 1781-1790	19.2	33
95	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
94	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019 , 177, 1109-1123.e14	56.2	256
93	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019 , 33, 391-419	5.9	42
92	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
91	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
90	Marine DNA Viral Macro-and Micro-Diversity From Pole to Pole. <i>SSRN Electronic Journal</i> , 2019 ,	1	3
89	Synthetic microbiota reveal priority effects and keystone strains in the Arabidopsis phyllosphere. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1445-1454	12.3	99

88	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019 , 179, 1068-1083.e21	56.2	113
87	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019 , 179, 1084-1097.e21	56.2	108
86	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019 , 8,	8.9	158
85	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
84	Scaling of species distribution explains the vast potential marine prokaryote diversity. <i>Scientific Reports</i> , 2019 , 9, 18710	4.9	7
83	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
82	Natural noncanonical protein splicing yields products with diverse amino acid residues. <i>Science</i> , 2018 , 359, 779-782	33.3	52
81	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018 , 9, 310	17.4	55
80	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018 , 9, 373	17.4	168
79	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
78	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018 , 560, 233-237	50.4	654
77	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , 2018 , 8, e021682	3	23
76	Microbiota stability in healthy individuals after single-dose lactulose challenge-A randomized controlled study. <i>PLoS ONE</i> , 2018 , 13, e0206214	3.7	11
75	The Ocean Gene Atlas: exploring the biogeography of plankton genes online. <i>Nucleic Acids Research</i> , 2018 , 46, W289-W295	20.1	61
74	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
73	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
72	Marine microbial diversity. <i>Current Biology</i> , 2017 , 27, R489-R494	6.3	38
71	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355

70	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , 2017 , 12, e0182392	3.7	64
69	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017 , 4, 170093	8.2	89
68	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017 , 13, 960	12.2	69
67	Salt-responsive gut commensal modulates T17 axis and disease. <i>Nature</i> , 2017 , 551, 585-589	50.4	553
66	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017 , 45, D529-D534	20.1	74
65	RNase H As Gene Modifier, Driver of Evolution and Antiviral Defense. <i>Frontiers in Microbiology</i> , 2017 , 8, 1745	5.7	26
64	Quantitative 3D-imaging for cell biology and ecology of environmental microbial eukaryotes. <i>ELife</i> , 2017 , 6,	8.9	20
63	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016 , 537, 689-693	50.4	400
62	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016 , 535, 376-81	50.4	977
61	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
60	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016 , 532, 465-470	50.4	392
59	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
58	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. <i>PLoS ONE</i> , 2016 , 11, e0155362	3.7	147
57	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016 , 32, 2520-3.2	3.2	117
56	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016 , 352, 586-9	33.3	326
55	Global genetic capacity for mixotrophy in marine picocyanobacteria. <i>ISME Journal</i> , 2016 , 10, 2946-2957	11.9	53
54	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015 , 16, 82	18.3	107
53	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107

52	Open science resources for the discovery and analysis of Tara Oceans data. <i>Scientific Data</i> , 2015 , 2, 150083	198
51	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (Sebastes). <i>BMC Genomics</i> , 2015 , 16, 656	4.5 6
50	Ocean plankton. Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015 , 348, 1262073	33.3 496
49	Ocean plankton. Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015 , 348, 1261498	33.3 421
48	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359	33.3 1261
47	Ocean plankton. Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015 , 348, 1261605	33.3 990
46	Ocean plankton. Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015 , 348, 1261447	33.3 100
45	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , 2015 , 16, 73	18.3 108
44	A fair comparison. <i>Nature Methods</i> , 2014 , 11, 359	21.6 33
43	Metagenomic insights into the human gut resistome and the forces that shape it. <i>BioEssays</i> , 2014 , 36, 316-29	4.1 57
42	Classification and quantification of bacteriophage taxa in human gut metagenomes. <i>ISME Journal</i> , 2014 , 8, 1391-402	11.9 102
41	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
40	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5 1088
39	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
38	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014 , 10, 766	12.2 575
37	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
36	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013 , 10, 881-4	21.6 234
35	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4 2584

34	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
33	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013 , 23, 1163-9	9.7	269
32	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
31	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013 , 7, 1678-95	11.9	142
30	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013 , 2, 120	0.8	1
29	Transcriptomic responses to darkness stress point to common coral bleaching mechanisms. <i>Coral Reefs</i> , 2012 , 31, 215-228	4.2	45
28	MOCAT: a metagenomics assembly and gene prediction toolkit. <i>PLoS ONE</i> , 2012 , 7, e47656	3.7	143
27	Assessment of metagenomic assembly using simulated next generation sequencing data. <i>PLoS ONE</i> , 2012 , 7, e31386	3.7	157
26	Symbiodinium transcriptomes: genome insights into the dinoflagellate symbionts of reef-building corals. <i>PLoS ONE</i> , 2012 , 7, e35269	3.7	178
25	A holistic approach to marine eco-systems biology. <i>PLoS Biology</i> , 2011 , 9, e1001177	9.7	265
24	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
23	Rapid evolution of coral proteins responsible for interaction with the environment. <i>PLoS ONE</i> , 2011 , 6, e20392	3.7	74
22	Coral host transcriptomic states are correlated with Symbiodinium genotypes. <i>Molecular Ecology</i> , 2010 , 19, 1174-86	5.7	105
21	The porcelain crab transcriptome and PCAD, the porcelain crab microarray and sequence database. <i>PLoS ONE</i> , 2010 , 5, e9327	3.7	19
20	Threatened corals provide underexplored microbial habitats. <i>PLoS ONE</i> , 2010 , 5, e9554	3.7	219
19	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
18	The host transcriptome remains unaltered during the establishment of coral-algal symbioses. <i>Molecular Ecology</i> , 2009 , 18, 1823-33	5.7	112
17	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

16	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
15	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
14	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
13	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
12	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
11	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
10	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
9	Ecogenomics and biogeochemical impacts of uncultivated globally abundant ocean viruses		5
8	Microbiome meta-analysis and cross-disease comparison enabled by the SIAMCAT machine-learning toolbox		3
7	Ecogenomics of key prokaryotes in the arctic ocean		5
6	The Ocean Gene Atlas: exploring the biogeography of plankton genes online		1
5	Metabolic Architecture of the Deep Ocean Microbiome		17
4	Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems		20
3	Uncharted biosynthetic potential of the ocean microbiome		6
2	Airborne bacteria over the oceans shed light on global biogeodiversity patterns		1
1	Biosynthetic potential of the global ocean microbiome. <i>Nature</i> ,	50.4	6