Hiroyuki Ogata

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/762965/publications.pdf

Version: 2024-02-01

89 papers	14,612 citations	70961 41 h-index	46693 89 g-index
103 all docs	103 docs citations	103 times ranked	12934 citing authors

#	Article	IF	Citations
1	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	6.0	2,137
2	Eukaryotic plankton diversity in the sunlit ocean. Science, 2015, 348, 1261605.	6.0	1,551
3	The 1.2-Megabase Genome Sequence of Mimivirus. Science, 2004, 306, 1344-1350.	6.0	959
4	Determinants of community structure in the global plankton interactome. Science, 2015, 348, 1262073.	6.0	842
5	KofamKOALA: KEGG Ortholog assignment based on profile HMM and adaptive score threshold. Bioinformatics, 2020, 36, 2251-2252.	1.8	820
6	Plankton networks driving carbon export in the oligotrophic ocean. Nature, 2016, 532, 465-470.	13.7	670
7	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	6.0	617
8	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. Cell, 2019, 177, 1109-1123.e14.	13.5	541
9	ViPTree: the viral proteomic tree server. Bioinformatics, 2017, 33, 2379-2380.	1.8	415
10	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
11	A Holistic Approach to Marine Eco-Systems Biology. PLoS Biology, 2011, 9, e1001177.	2.6	353
12	A global ocean atlas of eukaryotic genes. Nature Communications, 2018, 9, 373.	5.8	297
13	Linking Virus Genomes with Host Taxonomy. Viruses, 2016, 8, 66.	1.5	295
14	Metagenomic <scp>16S rDNA I</scp>llumina tags are a powerful alternative to amplicon sequencing to explore diversity and structure of microbial communities. Environmental Microbiology, 2014, 16, 2659-2671.	1.8	291
15	Global Trends in Marine Plankton Diversity across Kingdoms of Life. Cell, 2019, 179, 1084-1097.e21.	13.5	271
16	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
17	Tara Oceans: towards global ocean ecosystems biology. Nature Reviews Microbiology, 2020, 18, 428-445.	13.6	227
18	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. ISME Journal, 2013, 7, 1678-1695.	4.4	185

#	ARTICLE	IF	CITATIONS
19	The ocean sampling day consortium. GigaScience, 2015, 4, 27.	3.3	185
20	Environmental characteristics of Agulhas rings affect interocean plankton transport. Science, 2015, 348, 1261447.	6.0	158
21	Mimivirus and the emerging concept of â€œgiantâ€• virus. Virus Research, 2006, 117, 133-144.	1.1	157
22	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. Scientific Data, 2017, 4, 170093.	2.4	147
23	Taxonomic distribution of large DNA viruses in the sea. Genome Biology, 2008, 9, R106.	13.9	140
24	Horizontal gene transfer of an entire metabolic pathway between a eukaryotic alga and its DNA virus. Genome Research, 2009, 19, 1441-1449.	2.4	139
25	Mimivirus Giant Particles Incorporate a Large Fraction of Anonymous and Unique Gene Products. Journal of Virology, 2006, 80, 11678-11685.	1.5	123
26	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. MSphere, 2017, 2, .	1.3	114
27	Medusavirus, a Novel Large DNA Virus Discovered from Hot Spring Water. Journal of Virology, 2019, 93, .	1.5	113
28	Mimivirus and Mimiviridae: Giant viruses with an increasing number of potential hosts, including corals and sponges. Journal of Invertebrate Pathology, 2009, 101, 172-180.	1.5	109
29	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. Communications Biology, 2021, 4, 604.	2.0	107
30	Marine mimivirus relatives are probably large algal viruses. Virology Journal, 2008, 5, 12.	1.4	104
31	Typeâ€…III Polyketide Synthases: Functional Classification and Phylogenomics. ChemBioChem, 2017, 18, 50-65.	1.3	104
32	Taxon Richness of â€œMegaviridaeâ€• Exceeds those of Bacteria and Archaea in the Ocean. Microbes and Environments, 2018, 33, 162-171.	0.7	83
33	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. Nature Ecology and Evolution, 2020, 4, 1639-1649.	3.4	78
34	Communityâ€Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. Global Biogeochemical Cycles, 2019, 33, 391-419.	1.9	76
35	Life-cycle modification in open oceans accounts for genome variability in a cosmopolitan phytoplankton. ISME Journal, 2015, 9, 1365-1377.	4.4	70
36	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. Cell Genomics, 2022, 2, 100123.	3.0	70

#	ARTICLE	IF	CITATIONS
37	Two new subfamilies of DNA mismatch repair proteins (MutS) specifically abundant in the marine environment. ISME Journal, 2011, 5, 1143-1151.	4.4	69
38	A jumbo phage infecting the phytopathogen Ralstonia solanacearum defines a new lineage of the Myoviridae family. Virology, 2010, 398, 135-147.	1.1	65
39	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. Nature Microbiology, 2021, 6, 1561-1574.	5.9	57
40	Two asian jumbo phages, Ï•RSL2 and Ï•RSF1, infect Ralstonia solanacearum and show common features of Ï•KZ-related phages. Virology, 2016, 494, 56-66.	1.1	56
41	Contrasting biogeography and diversity patterns between diatoms and haptophytes in the central Pacific Ocean. Scientific Reports, 2018, 8, 10916.	1.6	52
42	Remarkable sequence similarity between the dinoflagellate-infecting marine girus and the terrestrial pathogen African swine fever virus. Virology Journal, 2009, 6, 178.	1.4	51
43	Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. IScience, 2021, 24, 102002.	1.9	50
44	Genomeâ€•resolved viral and cellular metagenomes revealed potential key virusâ€•host interactions in a deep freshwater lake. Environmental Microbiology, 2019, 21, 4740-4754.	1.8	49
45	Xanthomonas citri jumbo phage XacN1 exhibits a wide host range and high complement of tRNA genes. Scientific Reports, 2018, 8, 4486.	1.6	47
46	Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. ISME Journal, 2018, 12, 1287-1295.	4.4	44
47	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. Biochemical and Biophysical Research Communications, 2018, 495, 273-279.	1.0	43
48	Unique genes in giant viruses: Regular substitution pattern and anomalously short size. Genome Research, 2007, 17, 1353-1361.	2.4	42
49	The transcription factor E2A activates multiple enhancers that drive <i>Rag</i> expression in developing T and B cells. Science Immunology, 2020, 5, .	5.6	41
50	Diversity and ecological footprint of Global Ocean RNA viruses. Science, 2022, 376, 1202-1208.	6.0	41
51	Characterisation of three novel giant viruses reveals huge diversity among viruses infecting Prymnesiales (Haptophyta). Virology, 2015, 476, 180-188.	1.1	35
52	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. ISME Journal, 2016, 10, 1134-1146.	4.4	35
53	A Persistent Giant Algal Virus, with a Unique Morphology, Encodes an Unprecedented Number of Genes Involved in Energy Metabolism. Journal of Virology, 2021, 95, .	1.5	31
54	Unveiling of the Diversity of Prasinoviruses (Phycodnaviridae) in Marine Samples by Using High-Throughput Sequencing Analyses of PCR-Amplified DNA Polymerase and Major Capsid Protein Genes. Applied and Environmental Microbiology, 2014, 80, 3150-3160.	1.4	30

#	ARTICLE	IF	CITATIONS
55	Evolution of Eukaryotic DNA Polymerases via Interaction Between Cells and Large DNA Viruses. Journal of Molecular Evolution, 2015, 81, 24-33.	0.8	29
56	Giant Viruses Encode Actin-Related Proteins. Molecular Biology and Evolution, 2022, 39, .	3.5	28
57	Replications of Two Closely Related Groups of Jumbo Phages Show Different Level of Dependence on Host-encoded RNA Polymerase. Frontiers in Microbiology, 2017, 8, 1010.	1.5	26
58	The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes. Nucleic Acids Research, 2022, 50, W516-W526.	6.5	26
59	Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters. Viruses, 2018, 10, 496.	1.5	25
60	Assessing the viral content of uncultured picoeukaryotes in the globalâ€ocean by single cell genomics. Molecular Ecology, 2019, 28, 4272-4289.	2.0	25
61	Development of DNA mismatch repair gene, MutS, as a diagnostic marker for detection and phylogenetic analysis of algal Megaviruses. Virology, 2014, 466-467, 123-128.	1.1	24
62	Fifteen Marseilleviruses Newly Isolated From Three Water Samples in Japan Reveal Local Diversity of Marseilleviridae. Frontiers in Microbiology, 2019, 10, 1152.	1.5	24
63	Macroscale patterns of oceanic zooplankton composition and size structure. Scientific Reports, 2021, 11, 15714.	1.6	24
64	Quantitative Assessment of Nucleocytoplasmic Large DNA Virus and Host Interactions Predicted by Co-occurrence Analyses. MSphere, 2021, 6, .	1.3	22
65	In silico Prediction of Virus-Host Interactions for Marine Bacteroidetes With the Use of Metagenome-Assembled Genomes. Frontiers in Microbiology, 2020, 11, 738.	1.5	20
66	Prasinovirus distribution in the Northwest Mediterranean Sea is affected by the environment and particularly by phosphate availability. Virology, 2014, 466-467, 146-157.	1.1	17
67	The 474-Kilobase-Pair Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> () Tj ETQq1 1 0.784314 rgBT /Overl	0.8	17
68	Discovery of Viral Myosin Genes With Complex Evolutionary History Within Plankton. Frontiers in Microbiology, 2021, 12, 683294.	1.5	17
69	Integrative analysis of gut microbiome and host transcriptomes reveals associations between treatment outcomes and immunotherapyâ€induced colitis. Molecular Oncology, 2022, 16, 1493-1507.	2.1	17
70	Mimivirus reveals Mre11/Rad50 fusion proteins with a sporadic distribution in eukaryotes, bacteria, viruses and plasmids. Virology Journal, 2011, 8, 427.	1.4	14
71	Ecological Structuring of Temperate Bacteriophages in the Inflammatory Bowel Disease-Affected Gut. Microorganisms, 2020, 8, 1663.	1.6	14
72	Draft Genome Sequence of Medusavirus Stheno, Isolated from the Tatakai River of Uji, Japan. Microbiology Resource Announcements, 2021, 10, .	0.3	14

#	ARTICLE	IF	CITATIONS
73	DNA repair genes in the Megavirales pangenome. Current Opinion in Microbiology, 2016, 31, 94-100.	2.3	13
74	The Earth Is Small for â€œLeviathansâ€ Long Distance Dispersal of Giant Viruses across Aquatic Environments. Microbes and Environments, 2019, 34, 334-339.	0.7	11
75	Mucosal microbiota and gene expression are associated with long-term remission after discontinuation of adalimumab in ulcerative colitis. Scientific Reports, 2020, 10, 19186.	1.6	10
76	Deep sequencing of amplified <scp><i>P</i></scp><i>rasinovirus</i> and host green algal genes from an <scp>I</scp>ndian <scp>O</scp>cean transect reveals interacting trophic dependencies and new genotypes. Environmental Microbiology Reports, 2015, 7, 979-989.	1.0	8
77	Diel cycling of the cosmopolitan abundant Pelagibacter virus 37â€F6: one of the most abundant viruses on earth. Environmental Microbiology Reports, 2020, 12, 214-219.	1.0	8
78	RNA Sequencing of Medusavirus Suggests Remodeling of the Host Nuclear Environment at an Early Infection Stage. Microbiology Spectrum, 2021, 9, e0006421.	1.2	8
79	Discriminating the reaction types of plant type III polyketide synthases. Bioinformatics, 2017, 33, 1937-1943.	1.8	7
80	The Evolution of Rag Gene Enhancers and Transcription Factor E and Id Proteins in the Adaptive Immune System. International Journal of Molecular Sciences, 2021, 22, 5888.	1.8	7
81	Functional Differentiation among the <i>Arabidopsis</i> Phosphatidylinositol 4-Phosphate 5-Kinase Genes <i>PIP5K1, PIP5K2</i> and <i>PIP5K3</i>. Plant and Cell Physiology, 2022, 63, 635-648.	1.5	7
82	A Ralstonia solanacearum phage Ï•RP15 is closely related to Viunalikeviruses and encodes 19 tRNA-related sequences. Virology Reports, 2016, 6, 61-73.	0.4	6
83	An Optimized Metabarcoding Method for Mimiviridae. Microorganisms, 2020, 8, 506.	1.6	6
84	Deficiency of Gankyrin in the small intestine is associated with augmented colitis accompanied by altered bacterial composition of intestinal microbiota. BMC Gastroenterology, 2020, 20, 12.	0.8	3
85	Adaptive evolution of viruses infecting marine microalgae (haptophytes), from acute infections to stable coexistence. Biological Reviews, 2021, , .	4.7	3
86	Algal Mimiviruses (Mimiviridae). , 2021, , 677-683.		3
87	Year-round dynamics of amplicon sequence variant communities differ among eukaryotes,<i>Imitervirales</i>and prokaryotes in a coastal ecosystem. FEMS Microbiology Ecology, 2022, 97, .	1.3	3
88	Tight association between microbial eukaryote and giant virus communities in the Arctic Ocean. Limnology and Oceanography, 2022, 67, 1343-1356.	1.6	3
89	The complete genomic sequence of the novel myovirus RP13 infecting Ralstonia solanacearum, the causative agent of bacterial wilt. Archives of Virology, 2021, 166, 651-654.	0.9	2