

Hiroyuki Ogata

List of Publications by Year in descending order

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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	Integrative analysis of gut microbiome and host transcriptomes reveals associations between treatment outcomes and immunotherapy-induced colitis. <i>Molecular Oncology</i> , 2022, 16, 1493-1507.	2.1	17
2	Giant Viruses Encode Actin-Related Proteins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	28
3	Year-round dynamics of amplicon sequence variant communities differ among eukaryotes, <i>Imitervirales</i> and prokaryotes in a coastal ecosystem. <i>FEMS Microbiology Ecology</i> , 2022, 97, .	1.3	3
4	Functional Differentiation among the <i>Arabidopsis</i> Phosphatidylinositol 4-Phosphate 5-Kinase Genes <i>PIP5K1</i> , <i>PIP5K2</i> and <i>PIP5K3</i> . <i>Plant and Cell Physiology</i> , 2022, 63, 635-648.	1.5	7
5	Tight association between microbial eukaryote and giant virus communities in the Arctic Ocean. <i>Limnology and Oceanography</i> , 2022, 67, 1343-1356.	1.6	3
6	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
7	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	3.0	70
8	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	6.0	41
9	The complete genomic sequence of the novel myovirus RP13 infecting <i>Ralstonia solanacearum</i> , the causative agent of bacterial wilt. <i>Archives of Virology</i> , 2021, 166, 651-654.	0.9	2
10	Draft Genome Sequence of Medusavirus Stheno, Isolated from the Tatakai River of Uji, Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	14
11	Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , 2021, 24, 102002.	1.9	50
12	A Persistent Giant Algal Virus, with a Unique Morphology, Encodes an Unprecedented Number of Genes Involved in Energy Metabolism. <i>Journal of Virology</i> , 2021, 95, .	1.5	31
13	Quantitative Assessment of Nucleocytoplasmic Large DNA Virus and Host Interactions Predicted by Co-occurrence Analyses. <i>MSphere</i> , 2021, 6, .	1.3	22
14	The Evolution of Rag Gene Enhancers and Transcription Factor E and Id Proteins in the Adaptive Immune System. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5888.	1.8	7
15	Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021, 4, 604.	2.0	107
16	Discovery of Viral Myosin Genes With Complex Evolutionary History Within Plankton. <i>Frontiers in Microbiology</i> , 2021, 12, 683294.	1.5	17
17	Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021, 11, 15714.	1.6	24
18	RNA Sequencing of Medusavirus Suggests Remodeling of the Host Nuclear Environment at an Early Infection Stage. <i>Microbiology Spectrum</i> , 2021, 9, e0006421.	1.2	8

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19	Adaptive evolution of viruses infecting marine microalgae (haptophytes), from acute infections to stable coexistence. <i>Biological Reviews</i> , 2021, , .	4.7	3
20	Algal Mimiviruses (Mimiviridae). , 2021, , 677-683.		3
21	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
22	KofamKOALA: KEGG Ortholog assignment based on profile HMM and adaptive score threshold. <i>Bioinformatics</i> , 2020, 36, 2251-2252.	1.8	820
23	Diel cycling of the cosmopolitan abundant Pelagibacter virus 37â€œ6: one of the most abundant viruses on earth. <i>Environmental Microbiology Reports</i> , 2020, 12, 214-219.	1.0	8
24	Ecological Structuring of Temperate Bacteriophages in the Inflammatory Bowel Disease-Affected Gut. <i>Microorganisms</i> , 2020, 8, 1663.	1.6	14
25	The transcription factor E2A activates multiple enhancers that drive <i>Rag</i> expression in developing T and B cells. <i>Science Immunology</i> , 2020, 5, .	5.6	41
26	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
27	Mucosal microbiota and gene expression are associated with long-term remission after discontinuation of adalimumab in ulcerative colitis. <i>Scientific Reports</i> , 2020, 10, 19186.	1.6	10
28	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	13.6	227
29	In silico Prediction of Virus-Host Interactions for Marine Bacteroidetes With the Use of Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 738.	1.5	20
30	Deficiency of Gankyrin in the small intestine is associated with augmented colitis accompanied by altered bacterial composition of intestinal microbiota. <i>BMC Gastroenterology</i> , 2020, 20, 12.	0.8	3
31	An Optimized Metabarcoding Method for Mimiviridae. <i>Microorganisms</i> , 2020, 8, 506.	1.6	6
32	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
33	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	13.5	271
34	Genomeâ€œresolved viral and cellular metagenomes revealed potential key virusâ€œhost interactions in a deep freshwater lake. <i>Environmental Microbiology</i> , 2019, 21, 4740-4754.	1.8	49
35	Assessing the viral content of uncultured picoeukaryotes in the globalâ€œocean by single cell genomics. <i>Molecular Ecology</i> , 2019, 28, 4272-4289.	2.0	25
36	Fifteen Marseilleviruses Newly Isolated From Three Water Samples in Japan Reveal Local Diversity of Marseilleviridae. <i>Frontiers in Microbiology</i> , 2019, 10, 1152.	1.5	24

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37	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
38	Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
39	Medusavirus, a Novel Large DNA Virus Discovered from Hot Spring Water. <i>Journal of Virology</i> , 2019, 93, .	1.5	113
40	The Earth Is Small for "Leviathans": Long Distance Dispersal of Giant Viruses across Aquatic Environments. <i>Microbes and Environments</i> , 2019, 34, 334-339.	0.7	11
41	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
42	Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. <i>ISME Journal</i> , 2018, 12, 1287-1295.	4.4	44
43	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
44	<i>Xanthomonas citri</i> jumbo phage XacN1 exhibits a wide host range and high complement of tRNA genes. <i>Scientific Reports</i> , 2018, 8, 4486.	1.6	47
45	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 273-279.	1.0	43
46	Degenerate PCR Primers to Reveal the Diversity of Giant Viruses in Coastal Waters. <i>Viruses</i> , 2018, 10, 496.	1.5	25
47	Taxon Richness of "Megaviridae" Exceeds those of Bacteria and Archaea in the Ocean. <i>Microbes and Environments</i> , 2018, 33, 162-171.	0.7	83
48	Contrasting biogeography and diversity patterns between diatoms and haptophytes in the central Pacific Ocean. <i>Scientific Reports</i> , 2018, 8, 10916.	1.6	52
49	Discriminating the reaction types of plant type III polyketide synthases. <i>Bioinformatics</i> , 2017, 33, 1937-1943.	1.8	7
50	ViPTree: the viral proteomic tree server. <i>Bioinformatics</i> , 2017, 33, 2379-2380.	1.8	415
51	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. <i>MSphere</i> , 2017, 2, .	1.3	114
52	Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017, 4, 170093.	2.4	147
53	Type III Polyketide Synthases: Functional Classification and Phylogenomics. <i>ChemBioChem</i> , 2017, 18, 50-65.	1.3	104
54	Replications of Two Closely Related Groups of Jumbo Phages Show Different Level of Dependence on Host-encoded RNA Polymerase. <i>Frontiers in Microbiology</i> , 2017, 8, 1010.	1.5	26

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55	Linking Virus Genomes with Host Taxonomy. <i>Viruses</i> , 2016, 8, 66.	1.5	295
56	Two asian jumbo phages, Φ RSL2 and Φ RSF1, infect <i>Ralstonia solanacearum</i> and show common features of Φ KZ-related phages. <i>Virology</i> , 2016, 494, 56-66.	1.1	56
57	DNA repair genes in the Megavirales pangenome. <i>Current Opinion in Microbiology</i> , 2016, 31, 94-100.	2.3	13
58	A <i>Ralstonia solanacearum</i> phage Φ RP15 is closely related to Viunlikeviruses and encodes 19 tRNA-related sequences. <i>Virology Reports</i> , 2016, 6, 61-73.	0.4	6
59	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
60	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. <i>ISME Journal</i> , 2016, 10, 1134-1146.	4.4	35
61	Deep sequencing of amplified <i>P</i> and <i>rasinivirus</i> and host green algal genes from an Indian Ocean transect reveals interacting trophic dependencies and new genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 979-989.	1.0	8
62	The 474-Kilobase-Pair Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> (<i>Haptophyta</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	17
63	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	6.0	842
64	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
65	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
66	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
67	Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015, 348, 1261447.	6.0	158
68	Characterisation of three novel giant viruses reveals huge diversity among viruses infecting Prymnesiales (Haptophyta). <i>Virology</i> , 2015, 476, 180-188.	1.1	35
69	Evolution of Eukaryotic DNA Polymerases via Interaction Between Cells and Large DNA Viruses. <i>Journal of Molecular Evolution</i> , 2015, 81, 24-33.	0.8	29
70	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	3.3	185
71	Life-cycle modification in open oceans accounts for genome variability in a cosmopolitan phytoplankton. <i>ISME Journal</i> , 2015, 9, 1365-1377.	4.4	70
72	Prasinovirus distribution in the Northwest Mediterranean Sea is affected by the environment and particularly by phosphate availability. <i>Virology</i> , 2014, 466-467, 146-157.	1.1	17

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73	Development of DNA mismatch repair gene, MutS, as a diagnostic marker for detection and phylogenetic analysis of algal Megaviruses. <i>Virology</i> , 2014, 466-467, 123-128.	1.1	24
74	Metagenomic <scp>16S rDNA I</scp>llumina 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
75	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. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3150-3160.	1.4	30
76	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. <i>ISME Journal</i> , 2013, 7, 1678-1695.	4.4	185
77	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
78	Two new subfamilies of DNA mismatch repair proteins (MutS) specifically abundant in the marine environment. <i>ISME Journal</i> , 2011, 5, 1143-1151.	4.4	69
79	Mimivirus reveals Mre11/Rad50 fusion proteins with a sporadic distribution in eukaryotes, bacteria, viruses and plasmids. <i>Virology Journal</i> , 2011, 8, 427.	1.4	14
80	A jumbo phage infecting the phytopathogen <i>Ralstonia solanacearum</i> defines a new lineage of the Myoviridae family. <i>Virology</i> , 2010, 398, 135-147.	1.1	65
81	Horizontal gene transfer of an entire metabolic pathway between a eukaryotic alga and its DNA virus. <i>Genome Research</i> , 2009, 19, 1441-1449.	2.4	139
82	Mimivirus and Mimiviridae: Giant viruses with an increasing number of potential hosts, including corals and sponges. <i>Journal of Invertebrate Pathology</i> , 2009, 101, 172-180.	1.5	109
83	Remarkable sequence similarity between the dinoflagellate-infecting marine virus and the terrestrial pathogen African swine fever virus. <i>Virology Journal</i> , 2009, 6, 178.	1.4	51
84	Marine mimivirus relatives are probably large algal viruses. <i>Virology Journal</i> , 2008, 5, 12.	1.4	104
85	Taxonomic distribution of large DNA viruses in the sea. <i>Genome Biology</i> , 2008, 9, R106.	13.9	140
86	Unique genes in giant viruses: Regular substitution pattern and anomalously short size. <i>Genome Research</i> , 2007, 17, 1353-1361.	2.4	42
87	Mimivirus and the emerging concept of "giant" virus. <i>Virus Research</i> , 2006, 117, 133-144.	1.1	157
88	Mimivirus Giant Particles Incorporate a Large Fraction of Anonymous and Unique Gene Products. <i>Journal of Virology</i> , 2006, 80, 11678-11685.	1.5	123
89	The 1.2-Megabase Genome Sequence of Mimivirus. <i>Science</i> , 2004, 306, 1344-1350.	6.0	959