

# Kazuharu Arakawa

## 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.

102  
papers

2,321  
citations

24  
h-index

46  
g-index

114  
ext. papers

3,040  
ext. citations

4.6  
avg, IF

5.31  
L-index

#	Paper	IF	Citations
102	Multiple high-throughput analyses monitor the response of <i>E. coli</i> to perturbations. <i>Science</i> , <b>2007</b> , 316, 593-7	33.3	574
101	Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein. <i>Nature Communications</i> , <b>2016</b> , 7, 12808	17.4	160
100	Nanopore sequencing: Review of potential applications in functional genomics. <i>Development Growth and Differentiation</i> , <b>2019</b> , 61, 316-326	3	125
99	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i> . <i>PLoS Biology</i> , <b>2017</b> , 15, e2002266	9.7	107
98	Two novel heat-soluble protein families abundantly expressed in an anhydrobiotic tardigrade. <i>PLoS ONE</i> , <b>2012</b> , 7, e44209	3.7	70
97	Pathway projector: web-based zoomable pathway browser using KEGG atlas and Google Maps API. <i>PLoS ONE</i> , <b>2009</b> , 4, e7710	3.7	68
96	Base editors for simultaneous introduction of C-to-T and A-to-G mutations. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 865-869	44.5	63
95	KEGG-based pathway visualization tool for complex omics data. <i>In Silico Biology</i> , <b>2005</b> , 5, 419-23	2	63
94	De novo assembly and comparative transcriptome analysis of <i>Euglena gracilis</i> in response to anaerobic conditions. <i>BMC Genomics</i> , <b>2016</b> , 17, 182	4.5	60
93	Novel mitochondria-targeted heat-soluble proteins identified in the anhydrobiotic Tardigrade improve osmotic tolerance of human cells. <i>PLoS ONE</i> , <b>2015</b> , 10, e0118272	3.7	54
92	Analysis of DNA repair and protection in the Tardigrade <i>Ramazzottius varieornatus</i> and <i>Hypsibius dujardini</i> after exposure to UVC radiation. <i>PLoS ONE</i> , <b>2013</b> , 8, e64793	3.7	53
91	Comprehensive prediction of chromosome dimer resolution sites in bacterial genomes. <i>BMC Genomics</i> , <b>2011</b> , 12, 19	4.5	51
90	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , <b>2014</b> , 5, 5	2.2	42
89	No evidence for extensive horizontal gene transfer from the draft genome of a tardigrade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E3057	11.5	42
88	Orb-weaving spider <i>Araneus ventricosus</i> genome elucidates the spidroin gene catalogue. <i>Scientific Reports</i> , <b>2019</b> , 9, 8380	4.9	41
87	Genome sequencing of a single tardigrade <i>Hypsibius dujardini</i> individual. <i>Scientific Data</i> , <b>2016</b> , 3, 1600638.2		37
86	GEM System: automatic prototyping of cell-wide metabolic pathway models from genomes. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 168	3.6	36

85	Analysis of repetitive amino acid motifs reveals the essential features of spider dragline silk proteins. <i>PLoS ONE</i> , <b>2017</b> , 12, e0183397	3.7	34
84	Glucan synthase-like 2 is indispensable for paramylon synthesis in <i>Euglena gracilis</i> . <i>FEBS Letters</i> , <b>2017</b> , 591, 1360-1370	3.8	32
83	Genome Projector: zoomable genome map with multiple views. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 31	3.6	32
82	Evaluation of the impact of RNA preservation methods of spiders for de novo transcriptome assembly. <i>Molecular Ecology Resources</i> , <b>2016</b> , 16, 662-72	8.4	26
81	Metabolic flux analysis and visualization. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 3313-23	5.6	26
80	G-language System as a platform for large-scale analysis of high-throughput omics data. <i>Journal of Pesticide Sciences</i> , <b>2006</b> , 31, 282-288	2.7	26
79	Spider silk self-assembly via modular liquid-liquid phase separation and nanofibrillation. <i>Science Advances</i> , <b>2020</b> , 6,	14.3	24
78	Quantitative analysis of replication-related mutation and selection pressures in bacterial chromosomes and plasmids using generalised GC skew index. <i>BMC Genomics</i> , <b>2009</b> , 10, 640	4.5	24
77	The GC skew index: a measure of genomic compositional asymmetry and the degree of replicational selection. <i>Evolutionary Bioinformatics</i> , <b>2007</b> , 3, 159-68	1.9	24
76	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , <b>2013</b> , 4, 6	2.2	22
75	An integrative description of <i>Macrobiotus shonaicus</i> sp. nov. (Tardigrada: Macrobiotidae) from Japan with notes on its phylogenetic position within the hufelandi group. <i>PLoS ONE</i> , <b>2018</b> , 13, e0192210	3.7	19
74	The bagworm genome reveals a unique fibroin gene that provides high tensile strength. <i>Communications Biology</i> , <b>2019</b> , 2, 148	6.7	18
73	A new redescription of , supported by transcriptome, provides resources for describing concealed species diversity within the monotypic genus (Eutardigrada). <i>Zoological Letters</i> , <b>2020</b> , 6, 2	3	17
72	Merging multiple omics datasets in silico: statistical analyses and data interpretation. <i>Methods in Molecular Biology</i> , <b>2013</b> , 985, 459-70	1.4	15
71	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , <b>2011</b> , 2, 4	2.2	15
70	Measures of compositional strand bias related to replication machinery and its applications. <i>Current Genomics</i> , <b>2012</b> , 13, 4-15	2.6	15
69	Validating the significance of genomic properties of Chi sites from the distribution of all octamers in <i>Escherichia coli</i> . <i>Gene</i> , <b>2007</b> , 392, 239-46	3.8	15
68	Noise-reduction filtering for accurate detection of replication termini in bacterial genomes. <i>FEBS Letters</i> , <b>2007</b> , 581, 253-8	3.8	15

67	Multicomponent nature underlies the extraordinary mechanical properties of spider dragline silk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	15
66	Spidroin profiling of cribellate spiders provides insight into the evolution of spider prey capture strategies. <i>Scientific Reports</i> , <b>2020</b> , 10, 15721	4.9	14
65	Molecular palaeontology illuminates the evolution of ecdysozoan vision. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2018</b> , 285,	4.4	13
64	G-language genome analysis environment with REST and SOAP web service interfaces. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W700-5	20.1	12
63	GEMBASSY: an EMBOSS associated software package for comprehensive genome analyses. <i>Source Code for Biology and Medicine</i> , <b>2013</b> , 8, 17	1.9	11
62	Patterns of population structure and complex haplotype sharing among field isolates of the green alga <i>Chlamydomonas reinhardtii</i> . <i>Molecular Ecology</i> , <b>2019</b> , 28, 3977-3993	5.7	10
61	Validation of bacterial replication termination models using simulation of genomic mutations. <i>PLoS ONE</i> , <b>2012</b> , 7, e34526	3.7	10
60	Accelerated Laboratory Evolution Reveals the Influence of Replication on the GC Skew in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 3110-3117	3.9	9
59	MEGU: pathway mapping web-service based on KEGG and SVG. <i>In Silico Biology</i> , <b>2006</b> , 6, 621-5	2	9
58	Undesigned selection for replication termination of bacterial chromosomes. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 2918-27	6.5	8
57	Restauro-G: a rapid genome re-annotation system for comparative genomics. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2007</b> , 5, 53-8	6.5	7
56	On the interplay of gene positioning and the role of rho-independent terminators in <i>Escherichia coli</i> . <i>FEBS Letters</i> , <b>2006</b> , 580, 6909-14	3.8	7
55	Desiccation-induced fibrous condensation of CAHS protein from an anhydrobiotic tardigrade. <i>Scientific Reports</i> , <b>2021</b> , 11, 21328	4.9	7
54	Reconsidering the "glass transition" hypothesis of intrinsically unstructured CAHS proteins in desiccation tolerance of tardigrades. <i>Molecular Cell</i> , <b>2021</b> , 81, 409-410	17.6	7
53	Ultralow Input Genome Sequencing Library Preparation from a Single Tardigrade Specimen. <i>Journal of Visualized Experiments</i> , <b>2018</b> ,	1.6	6
52	Multomics study of a heterotardigrade, <i>Echiniscus testudo</i> , suggests the possibility of convergent evolution of abundant heat-soluble proteins in Tardigrada. <i>BMC Genomics</i> , <b>2021</b> , 22, 813	4.5	6
51	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i>		6
50	AMPK activity is required for the induction of anhydrobiosis in a tardigrade <i>Hypsibius exemplaris</i> , and its potential up-regulator is PP2A. <i>Genes To Cells</i> , <b>2019</b> , 24, 768-780	2.3	5

49	Hybridization between Japanese and North American <i>Chlamydomonas reinhardtii</i> (Volvocales, Chlorophyceae). <i>Phycological Research</i> , <b>2014</b> , 62, 232-236	1.3	5
48	The Unique Antimicrobial Recognition and Signaling Pathways in Tardigrades with a Comparison Across Ecdysozoa. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 1137-1148	3.2	5
47	Selection effects on the positioning of genes and gene structures from the interplay of replication and transcription in bacterial genomes. <i>Evolutionary Bioinformatics</i> , <b>2007</b> , 3, 279-86	1.9	5
46	The complete mitochondrial genome of (Lepidoptera: Psychidae). <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 812-813	0.5	5
45	The balance of crystalline and amorphous regions in the fibroin structure underpins the tensile strength of bagworm silk. <i>Zoological Letters</i> , <b>2021</b> , 7, 11	3	5
44	Darwin's bark spider shares a spidroin repertoire with but achieves extraordinary silk toughness through gene expression.. <i>Open Biology</i> , <b>2021</b> , 11, 210242	7	5
43	Simultaneous Metabarcoding of Eukaryotes and Prokaryotes to Elucidate the Community Structures within Tardigrade Microhabitats. <i>Diversity</i> , <b>2020</b> , 12, 110	2.5	4
42	Pre-treatment with D942, a furancarboxylic acid derivative, increases desiccation tolerance in an anhydrobiotic tardigrade <i>Hypsibius exemplaris</i> . <i>FEBS Open Bio</i> , <b>2020</b> , 10, 1774-1781	2.7	4
41	A web server for interactive and zoomable Chaos Game Representation images. <i>Source Code for Biology and Medicine</i> , <b>2009</b> , 4, 6	1.9	4
40	Comparison of the transcriptomes of two tardigrades with different hatching coordination. <i>BMC Developmental Biology</i> , <b>2019</b> , 19, 24	3.1	4
39	Complete Genome Sequence of sp. Strain KH172YL61, Isolated from Deep-Sea Sediments in the Nankai Trough, Japan. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	3
38	Horizontal Gene Transfer in Metazoa: Examples and Methods <b>2019</b> , 203-226		3
37	KBWS: an EMBOSS associated package for accessing bioinformatics web services. <i>Source Code for Biology and Medicine</i> , <b>2011</b> , 6, 8	1.9	3
36	G-Links: a gene-centric link acquisition service. <i>F1000Research</i> , <b>2014</b> , 3, 285	3.6	3
35	Proteomic evidence for the silk fibroin genes of spider mites (Order Trombidiformes: Family Tetranychidae). <i>Journal of Proteomics</i> , <b>2021</b> , 239, 104195	3.9	3
34	Comparative proteomic analysis of mitochondria isolated from <i>Euglena gracilis</i> under aerobic and hypoxic conditions. <i>PLoS ONE</i> , <b>2019</b> , 14, e0227226	3.7	3
33	The complete mitochondrial genome of (Heterotardigrada: Echiniscidae). <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 810-811	0.5	3
32	Complete Genome Sequence of <i>Halomonas olivaria</i> , a Moderately Halophilic Bacterium Isolated from Olive Processing Effluents, Obtained by Nanopore Sequencing. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2

31	Complete Genome Sequence of . Strain MN05-02, a UV-Resistant Bacterium from a Manganese Deposit in the Sonoran Desert. <i>Journal of Genomics</i> , <b>2019</b> , 7, 18-25	0.9	2
30	Complete Genome Sequence of Halophilic Deep-Sea Bacterium Halomonas axialensis Strain Althf1. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
29	A novel Mn-dependent peroxidase contributes to tardigrade anhydrobiosis		2
28	Rearing and observation of immature stages of the hoverfly (Diptera, Syrphidae). <i>Biodiversity Data Journal</i> , <b>2016</b> , e10185	1.8	2
27	Complete Genome Sequence of Halomonas meridiana Strain Eplume2, Isolated from a Hydrothermal Plume in the Northeast Pacific Ocean. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	2
26	G-Links: a gene-centric link acquisition service. <i>F1000Research</i> , <b>2014</b> , 3, 285	3.6	2
25	Genome sequencing of a single tardigrade Hypsibius dujardini individual		2
24	Complete Genome Sequence of Adlercreutzia equolifaciens subsp. DSM 18785. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10,	1.3	2
23	Systematics of tardigrada: A reanalysis of tardigrade taxonomy with specific reference to Guil et al. (2019). <i>Zoologica Scripta</i> , <b>2021</b> , 50, 376-382	2.5	2
22	Transcriptomic data during development of a two-spotted cricket. <i>Data in Brief</i> , <b>2021</b> , 38, 107388	1.2	2
21	GPAC: benchmarking the sensitivity of genome informatics analysis to genome annotation completeness. <i>In Silico Biology</i> , <b>2006</b> , 6, 49-60	2	2
20	Examples of Extreme Survival: Tardigrade Genomics and Molecular Anhydrobiology.. <i>Annual Review of Animal Biosciences</i> , <b>2022</b> , 10, 17-37	13.7	2
19	Complete Genome Sequence of Halomonas sulfidaeris Strain Esulfide1 Isolated from a Metal Sulfide Rock at a Depth of 2,200 Meters, Obtained Using Nanopore Sequencing. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1
18	Complete Genome Sequence of sp. Strain KH172YL63, Isolated from Deep-Sea Sediment. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
17	Complete Genome Sequence of Halomonas meridiana Strain Slthf1, Isolated from a Deep-Sea Thermal Vent. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
16	Complete Genome Sequence of Halomonas hydrothermalis Strain Slthf2, a Halophilic Bacterium Isolated from a Deep-Sea Hydrothermal-Vent Environment. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
15	Complete Genome Sequence of Bifidobacterium longum Strain Jih1, Isolated from Human Feces. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
14	Complete Genome Sequences of Two Cutibacterium acnes Strains Isolated from an Orthopedic Surgical Site. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1

13	Multiomics study of a heterotardigrade, <i>Echiniscus testudo</i> , suggests convergent evolution of anhydrobiosis-related proteins in Tardigrada		1
12	Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian Tetragnatha spiders. <i>Bmc Ecology and Evolution</i> , <b>2021</b> , 21, 48	21	1
11	Multicomponent nature underlies the extraordinary mechanical properties of spider dragline silk		1
10	Complete Genome Sequence of sp. Strain SVR, an Antimonate-Reducing Bacterium Isolated from Antimony-Rich Mine Soil. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10,	1.3	1
9	RNA sequencing data for gamma radiation response in the extremotolerant tardigrade. <i>Data in Brief</i> , <b>2021</b> , 36, 107111	1.2	1
8	Desiccation-induced fibrous condensation of CAHS protein from an anhydrobiotic tardigrade		1
7	Darwin's bark spider shares a spidroin repertoire with <i>Caerostris extrusa</i> but achieves extraordinary silk toughness through gene expression		1
6	Complete Genome Sequence of <i>Sphingomonas paucimobilis</i> Strain Kira, Isolated from Human Neuroblastoma SH-SY5Y Cell Cultures Supplemented with Retinoic Acid. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10,	1.3	1
5	Tardigrade Secretory-Abundant Heat-Soluble Protein Has a Flexible $\beta$ Barrel Structure in Solution and Keeps This Structure in Dehydration. <i>Journal of Physical Chemistry B</i> , <b>2021</b> , 125, 9145-9154	3.4	1
4	Complete Genome Sequences of Four Bacteria Isolated from the Gut of a Spiny Ant ( <i>Polyrhachis lamellidens</i> ). <i>Microbiology Resource Announcements</i> ,	1.3	1
3	Complete Genome Sequence of Bacterium Strain P1, Isolated from Mouse Feces. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0062721	1.3	
2	Complete Genome Sequences of Two Strains, Isolated from Seawater () and Soil () in South Korea. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0033721	1.3	
1	The complete mitochondrial genome of (Araneae: Araneidae). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2986-2988	0.5	