

# Kazuharu Arakawa

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/3781078/kazuharu-arakawa-publications-by-year.pdf>

**Version:** 2024-04-28

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.

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	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
101	Desiccation-induced fibrous condensation of CAHS protein from an anhydrobiotic tardigrade. <i>Scientific Reports</i> , <b>2021</b> , 11, 21328	4.9	7
100	Multiomics 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
99	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	2.1	1
98	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
97	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
96	Complete Genome Sequence of <i>Adlercreutzia equolifaciens</i> subsp. DSM 18785. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10,	1.3	2
95	RNA sequencing data for gamma radiation response in the extremotolerant tardigrade. <i>Data in Brief</i> , <b>2021</b> , 36, 107111	1.2	1
94	Complete Genome Sequence of Bacterium Strain P1, Isolated from Mouse Feces. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0062721	1.3	
93	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
92	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
91	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
90	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	
89	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
88	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
87	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
86	The complete mitochondrial genome of (Araneae: Araneidae). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2986-2988	0.5	

85	Transcriptomic data during development of a two-spotted cricket. <i>Data in Brief</i> , <b>2021</b> , 38, 107388	1.2	2
84	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
83	Spider silk self-assembly via modular liquid-liquid phase separation and nanofibrillation. <i>Science Advances</i> , <b>2020</b> , 6,	14.3	24
82	Complete Genome Sequence of sp. Strain KH172YL63, Isolated from Deep-Sea Sediment. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
81	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
80	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
79	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
78	Complete Genome Sequence of Bifidobacterium longum Strain Jih1, Isolated from Human Feces. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
77	Pre-treatment with D942, a furancarboxylic acid derivative, increases desiccation tolerance in an anhydrobiotic tardigrade Hypsibius exemplaris. <i>FEBS Open Bio</i> , <b>2020</b> , 10, 1774-1781	2.7	4
76	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
75	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
74	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
73	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
72	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
71	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
70	AMPK activity is required for the induction of anhydrobiosis in a tardigrade Hypsibius exemplaris, and its potential up-regulator is PP2A. <i>Genes To Cells</i> , <b>2019</b> , 24, 768-780	2.3	5
69	Orb-weaving spider Araneus ventricosus genome elucidates the spidroin gene catalogue. <i>Scientific Reports</i> , <b>2019</b> , 9, 8380	4.9	41
68	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

67	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
66	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
65	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
64	Nanopore sequencing: Review of potential applications in functional genomics. <i>Development Growth and Differentiation</i> , <b>2019</b> , 61, 316-326	3	125
63	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
62	Horizontal Gene Transfer in Metazoa: Examples and Methods <b>2019</b> , 203-226		3
61	Complete Genome Sequence of Halophilic Deep-Sea Bacterium <i>Halomonas axialensis</i> Strain Althf1. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
60	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
59	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
58	Comparison of the transcriptomes of two tardigrades with different hatching coordination. <i>BMC Developmental Biology</i> , <b>2019</b> , 19, 24	3.1	4
57	Ultralow Input Genome Sequencing Library Preparation from a Single Tardigrade Specimen. <i>Journal of Visualized Experiments</i> , <b>2018</b> ,	1.6	6
56	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
55	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
54	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
53	The complete mitochondrial genome of (Lepidoptera: Psychidae). <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 812-813	0.5	5
52	The complete mitochondrial genome of (Heterotardigrada: Echiniscidae). <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 810-811	0.5	3
51	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
50	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

49	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
48	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
47	Genome sequencing of a single tardigrade <i>Hypsibius dujardini</i> individual. <i>Scientific Data</i> , <b>2016</b> , 3, 1600638.2		37
46	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
45	Rearing and observation of immature stages of the hoverfly (Diptera, Syrphidae). <i>Biodiversity Data Journal</i> , <b>2016</b> , e10185	1.8	2
44	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
43	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
42	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
41	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
40	Undesigned selection for replication termination of bacterial chromosomes. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 2918-27	6.5	8
39	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
38	G-Links: a gene-centric link acquisition service. <i>F1000Research</i> , <b>2014</b> , 3, 285	3.6	3
37	G-Links: a gene-centric link acquisition service. <i>F1000Research</i> , <b>2014</b> , 3, 285	3.6	2
36	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
35	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
34	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
33	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
32	Validation of bacterial replication termination models using simulation of genomic mutations. <i>PLoS ONE</i> , <b>2012</b> , 7, e34526	3.7	10

31	Two novel heat-soluble protein families abundantly expressed in an anhydrobiotic tardigrade. <i>PLoS ONE</i> , <b>2012</b> , 7, e44209	3.7	70
30	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
29	Metabolic flux analysis and visualization. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 3313-23	5.6	26
28	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
27	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
26	Comprehensive prediction of chromosome dimer resolution sites in bacterial genomes. <i>BMC Genomics</i> , <b>2011</b> , 12, 19	4.5	51
25	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
24	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
23	Genome Projector: zoomable genome map with multiple views. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 31	3.6	32
22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	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
14	GEM System: automatic prototyping of cell-wide metabolic pathway models from genomes. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 168	3.6	36

13	On the interplay of gene positioning and the role of rho-independent terminators in Escherichia coli. <i>FEBS Letters</i> , <b>2006</b> , 580, 6909-14	3.8	7
12	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
11	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
10	MEGU: pathway mapping web-service based on KEGG and SVG. <i>In Silico Biology</i> , <b>2006</b> , 6, 621-5	2	9
9	KEGG-based pathway visualization tool for complex omics data. <i>In Silico Biology</i> , <b>2005</b> , 5, 419-23	2	63
8	Multiomics study of a heterotardigrade, <i>Echiniscus testudo</i> , suggests convergent evolution of anhydrobiosis-related proteins in Tardigrada		1
7	A novel Mn-dependent peroxidase contributes to tardigrade anhydrobiosis		2
6	Comparative genomics of the tardigrades <i>Hypsibius dujardini</i> and <i>Ramazzottius varieornatus</i>		6
5	Genome sequencing of a single tardigrade <i>Hypsibius dujardini</i> individual		2
4	Multicomponent nature underlies the extraordinary mechanical properties of spider dragline silk		1
3	Desiccation-induced fibrous condensation of CAHS protein from an anhydrobiotic tardigrade		1
2	Darwin's bark spider shares a spidroin repertoire with <i>Caerostris extrusa</i> but achieves extraordinary silk toughness through gene expression		1
1	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