

# Jin Sun

## List of Publications by Year in descending order

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92  
papers

3,004  
citations

172457

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docs citations

95  
times ranked

3204  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic and metatranscriptomic analyses reveal minor-yet-crucial roles of gut microbiome in deep-sea hydrothermal vent snail. <i>Animal Microbiome</i> , 2022, 4, 3.	3.8	7
2	Comparative transcriptomic analysis of in situ and onboard fixed deep-sea limpets reveals sample preparation-related differences. <i>IScience</i> , 2022, 25, 104092.	4.1	6
3	Delineating biogeographic regions in Indian Ocean deep-sea vents and implications for conservation. <i>Diversity and Distributions</i> , 2022, 28, 2858-2870.	4.1	13
4	Endosymbiont population genomics sheds light on transmission mode, partner specificity, and stability of the scaly-foot snail holobiont. <i>ISME Journal</i> , 2022, 16, 2132-2143.	9.8	6
5	Host-Endosymbiont Genome Integration in a Deep-Sea Chemosymbiotic Clam. <i>Molecular Biology and Evolution</i> , 2021, 38, 502-518.	8.9	46
6	Hologenome analysis reveals dual symbiosis in the deep-sea hydrothermal vent snail <i>Gigantopelta aegis</i> . <i>Nature Communications</i> , 2021, 12, 1165.	12.8	38
7	Phylogenetic Relationships and Adaptation in Deep-Sea Mussels: Insights from Mitochondrial Genomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1900.	4.1	20
8	Mutanofactin promotes adhesion and biofilm formation of cariogenic <i>Streptococcus mutans</i> . <i>Nature Chemical Biology</i> , 2021, 17, 576-584.	8.0	28
9	Molluscan phylogenomics requires strategically selected genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200161.	4.0	14
10	Benchmarking Oxford Nanopore read assemblers for high-quality molluscan genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200160.	4.0	22
11	Optimal Design for Higher Resistance to Thermal Impulse: A Lesson Learned from the Shells of Deep-Sea Hydrothermal-Vent Snails. <i>Jom</i> , 2021, 73, 1714-1722.	1.9	3
12	Genomic Signatures Supporting the Symbiosis and Formation of Chitinous Tube in the Deep-Sea Tubeworm <i>Paraescarpia echinospica</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 4116-4134.	8.9	37
13	Hidden Historical Habitat-Linked Population Divergence and Contemporary Gene Flow of a Deep-Sea Patellogastropod Limpet. <i>Molecular Biology and Evolution</i> , 2021, 38, 5640-5654.	8.9	12
14	Structure and Connectivity of Hydrothermal Vent Communities Along the Mid-Ocean Ridges in the West Indian Ocean: A Review. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	7
15	Culture Enrichment Combined With Long-Read Sequencing Facilitates Genomic Understanding of Hadal Sediment Microbes. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	5
16	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. <i>ISME Journal</i> , 2020, 14, 135-150.	9.8	41
17	Insights into the strategy of micro-environmental adaptation: Transcriptomic analysis of two alvinocaridid shrimps at a hydrothermal vent. <i>PLoS ONE</i> , 2020, 15, e0227587.	2.5	8
18	Exploring the Influence of Signal Molecules on Marine Biofilms Development. <i>Frontiers in Microbiology</i> , 2020, 11, 571400.	3.5	16

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19	Population Genetic Structure and Gene Expression Plasticity of the Deep-Sea Vent and Seep Squat Lobster <i>Shinkaia crosnieri</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	16
20	Proteomic Comparison of the Cytotoxicology of Two Diastereomers of Citreamicin Reveals Differentially Activation of NF- $\kappa$ B Pathway. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	0
21	Nearest vent, dearest friend: biodiversity of Tiancheng vent field reveals cross-ridge similarities in the Indian Ocean. <i>Royal Society Open Science</i> , 2020, 7, 200110.	2.4	31
22	Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. <i>Nature Communications</i> , 2020, 11, 3051.	12.8	47
23	Hemocyanin of the caenogastropod <i>Pomacea canaliculata</i> exhibits evolutionary differences among gastropod clades. <i>PLoS ONE</i> , 2020, 15, e0228325.	2.5	9
24	The Scaly-foot Snail genome and implications for the origins of biomineralised armour. <i>Nature Communications</i> , 2020, 11, 1657.	12.8	64
25	Insights into the Synthesis, Secretion and Curing of Barnacle Cyprid Adhesive via Transcriptomic and Proteomic Analyses of the Cement Gland. <i>Marine Drugs</i> , 2020, 18, 186.	4.6	10
26	The mitochondrial genome of the deep-sea limpet <i>Bathycypraea nipponica</i> (Patellogastropoda). <i>Genome Biology and Evolution</i> , 2020, 12, 1077.	0.4	7
27	Comparative Proteomics on Deep-Sea Amphipods after in Situ Copper Exposure. <i>Environmental Science &amp; Technology</i> , 2019, 53, 13981-13991.	10.0	9
28	Complex factors shape phenotypic variation in deep-sea limpets. <i>Biology Letters</i> , 2019, 15, 20190504.	2.3	20
29	Potential Interactions between Clade SUP05 Sulfur-Oxidizing Bacteria and Phages in Hydrothermal Vent Sponges. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	22
30	Marine biofilms constitute a bank of hidden microbial diversity and functional potential. <i>Nature Communications</i> , 2019, 10, 517.	12.8	100
31	Non-digestible proteins and protease inhibitors: implications for defense of the colored eggs of the freshwater apple snail <i>Pomacea canaliculata</i> . <i>Canadian Journal of Zoology</i> , 2019, 97, 558-566.	1.0	9
32	Signatures of Divergence, Invasiveness, and Terrestrialization Revealed by Four Apple Snail Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1507-1520.	8.9	65
33	Quantitative Proteomic Analysis to Understand the Mechanisms of Zinc Oxide Nanoparticle Toxicity to <i>Daphnia pulex</i> (Crustacea: Daphniidae): Comparing with Bulk Zinc Oxide and Zinc Salt. <i>Environmental Science &amp; Technology</i> , 2019, 53, 5436-5444.	10.0	32
34	Host-Symbiont Interactions in Deep-Sea Chemosymbiotic Vesicomymid Clams: Insights From Transcriptome Sequencing. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	17
35	Understanding the transition from water to land: Insights from multi-omic analyses of the perivitelline fluid of apple snail eggs. <i>Journal of Proteomics</i> , 2019, 194, 79-88.	2.4	11
36	Gut Microbial Divergence between Two Populations of the Hadal Amphipod <i>Hirondellea gigas</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	19

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37	The mitochondrial genome of the deep-sea tubeworm <i>Paraescarpia echinospica</i> (Siboglinidae). <i>Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 50 62</i>	0.4	33
38	Phylogeny, evolution and mitochondrial gene order rearrangement in scale worms (Aphroditiformia). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62</i>	2.7	67
39	AmpuBase: a transcriptome database for eight species of apple snails (Gastropoda: Ampullariidae). <i>BMC Genomics</i> , 2018, 19, 179.	2.8	20
40	Comparative proteomics and codon substitution analysis reveal mechanisms of differential resistance to hypoxia in congeneric snails. <i>Journal of Proteomics</i> , 2018, 172, 36-48.	2.4	9
41	Identification of Barnacle Shell Proteins by Transcriptome and Proteomic Approaches. , 2018, , 105-112.		2
42	Genome Reduction in <i>Psychromonas</i> Species within the Gut of an Amphipod from the Ocean's Deepest Point. <i>MSystems</i> , 2018, 3, .	3.8	21
43	De novo transcriptome assembly and positive selection analysis of an individual deep-sea fish. <i>BMC Genomics</i> , 2018, 19, 394.	2.8	49
44	Population genetic structure of the deep-sea mussel <i>Bathymodiolus platifrons</i> (Bivalvia). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62</i>	3.1	30
45	Genome-wide discovery of single nucleotide polymorphisms (SNPs) and single nucleotide variants (SNVs) in deep-sea mussels: Potential use in population genomics and cross-species application. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 318-326.	1.4	31
46	An integrated proteomic and transcriptomic analysis of perivitelline fluid proteins in a freshwater gastropod laying aerial eggs. <i>Journal of Proteomics</i> , 2017, 155, 22-30.	2.4	27
47	Molecular adaptation in the world's deepest-living animal: Insights from transcriptome sequencing of the hadal amphipod <i>Hirondellea gigas</i> . <i>Molecular Ecology</i> , 2017, 26, 3732-3743.	3.9	69
48	Adaptation and evolution of deep-sea scale worms (Annelida: Polynoidae): insights from transcriptome comparison with a shallow-water species. <i>Scientific Reports</i> , 2017, 7, 46205.	3.3	31
49	Adaptation to deep-sea chemosynthetic environments as revealed by mussel genomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 121.	7.8	250
50	Molecular pathology of skeletal growth anomalies in the brain coral <i>Platygyra carnosa</i> : A meta-transcriptomic analysis. <i>Marine Pollution Bulletin</i> , 2017, 124, 660-667.	5.0	17
51	Dataset for the proteomic and transcriptomic analyses of perivitelline fluid proteins in Pomacea snail eggs. <i>Data in Brief</i> , 2017, 15, 203-207.	1.0	6
52	Metagenomic analysis reveals a green sulfur bacterium as a potential coral symbiont. <i>Scientific Reports</i> , 2017, 7, 9320.	3.3	29
53	Comparative Transcriptomic Analysis Reveals Candidate Genes and Pathways Involved in Larval Settlement of the Barnacle <i>Megabalanus volcano</i> . <i>International Journal of Molecular Sciences</i> , 2017, 18, 2253.	4.1	11
54	The mitochondrial genome of the deep-sea glass sponge <i>Lophophysema eversa</i> (Porifera). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62</i>	0.6	4

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55	Environmental switching during biofilm development in a cold seep system and functional determinants of species sorting. <i>Molecular Ecology</i> , 2016, 25, 1958-1971.	3.9	5
56	Characterization of Arginine Kinase in the Barnacle <i>Amphibalanus Amphitrite</i> and Its Role in the Larval Settlement. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2016, 326, 237-249.	1.3	5
57	The deep-sea glass sponge <i>Lophophysema eversa</i> harbours potential symbionts responsible for the nutrient conversions of carbon, nitrogen and sulfur. <i>Environmental Microbiology</i> , 2016, 18, 2481-2494.	3.8	64
58	The deepest mitochondrial genome sequenced from Mariana Trench <i>Hirondellea gigas</i> (Amphipoda). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 802-803.	0.4	13
59	Post-translational modifications are enriched within protein functional groups important to bacterial adaptation within a deep-sea hydrothermal vent environment. <i>Microbiome</i> , 2016, 4, 49.	11.1	35
60	Secretory locations of SIPC in <i>Amphibalanus amphitrite</i> cyprids and a novel function of SIPC in biomineralization. <i>Scientific Reports</i> , 2016, 6, 29376.	3.3	9
61	The mitochondrial genome of the deep-sea snail <i>Provanna</i> sp. (Gastropoda: Provannidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4026-4027.	0.7	8
62	Cochliomycin A inhibits the larval settlement of <i>Amphibalanus amphitrite</i> by activating the NO/cGMP pathway. <i>Biofouling</i> , 2016, 32, 35-44.	2.2	14
63	High-throughput transcriptome sequencing of the cold seep mussel <i>Bathymodiolus platifrons</i> . <i>Scientific Reports</i> , 2015, 5, 16597.	3.3	78
64	Extracellular matrix-associated proteins form an integral and dynamic system during <i>Pseudomonas aeruginosa</i> biofilm development. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 40.	3.9	48
65	Insights from an Integrated View of the Biology of Apple Snails (Caenogastropoda: Ampullariidae). <i>Malacologia</i> , 2015, 58, 245-302.	0.4	161
66	Hepatic Proteomic Responses in Marine Medaka ( <i>Oryzias melastigma</i> ) Chronically Exposed to Antifouling Compound Butenolide [5-octylfuran-2(5H)-one] or 4,5-Dichloro-2-N-Octyl-4-Isothiazolin-3-One (DCOIT). <i>Environmental Science &amp; Technology</i> , 2015, 49, 1851-1859.	10.0	41
67	Genetic Basis of Differential Heat Resistance between Two Species of Congeneric Freshwater Snails: Insights from Quantitative Proteomics and Base Substitution Rate Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 4296-4308.	3.7	30
68	Integration of Transcriptomic and Proteomic Approaches Provides a Core Set of Genes for Understanding of Scallop Attachment. <i>Marine Biotechnology</i> , 2015, 17, 523-532.	2.4	43
69	Data for transcriptomic and iTRAQ proteomic analysis of <i>Anguilla japonica</i> gills in response to osmotic stress. <i>Data in Brief</i> , 2015, 3, 120-125.	1.0	2
70	Proteomic Basis of Stress Responses in the Gills of the Pacific Oyster <i>Crassostrea gigas</i> . <i>Journal of Proteome Research</i> , 2015, 14, 304-317.	3.7	96
71	Proteomic changes in brain tissues of marine medaka ( <i>Oryzias melastigma</i> ) after chronic exposure to two antifouling compounds: Butenolide and 4,5-dichloro-2-n-octyl-4-isothiazolin-3-one (DCOIT). <i>Aquatic Toxicology</i> , 2014, 157, 47-56.	4.0	29
72	Proteomic profiling during the pre-competent to competent transition of the biofouling polychaete <i>Hydroides elegans</i> . <i>Biofouling</i> , 2014, 30, 921-928.	2.2	2

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73	iTRAQ-based quantitative proteomic analysis reveals acute hypo-osmotic responsive proteins in the gills of the Japanese eel ( <i>Anguilla japonica</i> ). <i>Journal of Proteomics</i> , 2014, 105, 133-143.	2.4	21
74	Proteomic analysis identifies proteins related to carotenoid accumulation in Yesso scallop ( <i>Patinopecten yessoensis</i> ). <i>Food Chemistry</i> , 2014, 147, 111-116.	8.2	23
75	Transcriptomic and iTRAQ proteomic approaches reveal novel short-term hyperosmotic stress responsive proteins in the gill of the Japanese eel ( <i>Anguilla japonica</i> ). <i>Journal of Proteomics</i> , 2013, 89, 81-94.	2.4	47
76	Understanding the Regulation of Estivation in a Freshwater Snail through iTRAQ-Based Comparative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 5271-5280.	3.7	47
77	Transcriptome and Quantitative Proteome Analysis Reveals Molecular Processes Associated with Larval Metamorphosis in the Polychaete <i>Pseudopolydora vexillosa</i> . <i>Journal of Proteome Research</i> , 2013, 12, 1344-1358.	3.7	13
78	Novel Animal Defenses against Predation: A Snail Egg Neurotoxin Combining Lectin and Pore-Forming Chains That Resembles Plant Defense and Bacteria Attack Toxins. <i>PLoS ONE</i> , 2013, 8, e63782.	2.5	62
79	PcarnBase: Development of a Transcriptomic Database for the Brain Coral <i>Platygyra carnosus</i> . <i>Marine Biotechnology</i> , 2013, 15, 244-251.	2.4	47
80	iTRAQ-Based Proteomic Profiling of the Barnacle <i>Balanus amphitrite</i> in Response to the Antifouling Compound Meleagrin. <i>Journal of Proteome Research</i> , 2013, 12, 2090-2100.	3.7	50
81	Complete mitochondrial genome of the brain coral <i>Platygyra carnosus</i> . <i>Mitochondrial DNA</i> , 2013, 24, 194-195.	0.6	11
82	Characterization of the Proteomic Profiles of the Brown Tide Alga <i>Aureoumbra lagunensis</i> under Phosphate- and Nitrogen-Limiting Conditions and of Its Phosphate Limitation-Specific Protein with Alkaline Phosphatase Activity. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2025-2033.	3.1	31
83	De novo assembly of the transcriptome of an invasive snail and its multiple ecological applications. <i>Molecular Ecology Resources</i> , 2012, 12, 1133-1144.	4.8	32
84	First Proteome of the Egg Perivitelline Fluid of a Freshwater Gastropod with Aerial Oviposition. <i>Journal of Proteome Research</i> , 2012, 11, 4240-4248.	3.7	54
85	Transcriptomic Analysis of Neuropeptides and Peptide Hormones in the Barnacle <i>Balanus amphitrite</i> : Evidence of Roles in Larval Settlement. <i>PLoS ONE</i> , 2012, 7, e46513.	2.5	44
86	Consumption, survival and growth in the invasive freshwater snail <i>Pomacea canaliculata</i> : does food freshness matter?. <i>Journal of Molluscan Studies</i> , 2011, 77, 189-195.	1.2	31
87	Phylogenetic diversity and community structure of sponge-associated bacteria from mangroves of the Caribbean Sea. <i>Aquatic Microbial Ecology</i> , 2011, 62, 231-240.	1.8	18
88	lip2, a novel lipase gene cloned from <i>Aspergillus niger</i> exhibits enzymatic characteristics distinct from its previously identified family member. <i>Biotechnology Letters</i> , 2010, 32, 951-956.	2.2	8
89	Protein expression during the embryonic development of a gastropod. <i>Proteomics</i> , 2010, 10, 2701-2711.	2.2	30
90	2D Gel-Based Multiplexed Proteomic Analysis during Larval Development and Metamorphosis of the Biofouling Polychaete Tubeworm <i>Hydroides elegans</i> . <i>Journal of Proteome Research</i> , 2010, 9, 4851-4860.	3.7	27

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91	Estuarine nutrient loading affects phytoplankton growth and microzooplankton grazing at two contrasting sites in Hong Kong coastal waters. <i>Marine Ecology - Progress Series</i> , 2009, 379, 77-90.	1.9	70
92	Diversity and spatial distribution of sediment ammonia-oxidizing crenarchaeota in response to estuarine and environmental gradients in the Changjiang Estuary and East China Sea. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2084-2095.	1.8	146