

Ting-Fung Chan

List of Publications by Year in descending order

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Version: 2024-02-01

173
papers

6,862
citations

61687

45
h-index

87275

74
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189
all docs

189
docs citations

189
times ranked

11841
citing authors

#	ARTICLE	IF	CITATIONS
1	SOX4 is a novel phenotypic regulator of endothelial cells in atherosclerosis revealed by single-cell analysis. <i>Journal of Advanced Research</i> , 2023, 43, 187-203.	4.4	13
2	Integrative omics analysis reveals the protective role of vitamin C on perfluorooctanoic acid-induced hepatotoxicity. <i>Journal of Advanced Research</i> , 2022, 35, 279-294.	4.4	7
3	Analyzing the synergistic adverse effects of BPA and its substitute, BHPF, on ulcerative colitis through comparative metabolomics. <i>Chemosphere</i> , 2022, 287, 132160.	4.2	12
4	A tRNA-derived fragment from Chinese yew suppresses ovarian cancer growth via targeting TRPA1. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 718-732.	2.3	19
5	Differential microRNA expression, microRNA arm switching, and microRNA:long noncoding RNA interaction in response to salinity stress in soybean. <i>BMC Genomics</i> , 2022, 23, 65.	1.2	13
6	miRNA-mRNA Integrative Analysis Reveals the Roles of miRNAs in Hypoxia-Altered Embryonic Development- and Sex Determination-Related Genes of Medaka Fish. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	1
7	Type 2 innate immunity drives distinct neonatal immune profile conducive for heart regeneration. <i>Theranostics</i> , 2022, 12, 1161-1172.	4.6	6
8	Nonalbuminuric Diabetic Kidney Disease and Risk of All-Cause Mortality and Cardiovascular and Kidney Outcomes in Type 2 Diabetes: Findings From the Hong Kong Diabetes Biobank. <i>American Journal of Kidney Diseases</i> , 2022, 80, 196-206.e1.	2.1	12
9	The Identification of MATE Antisense Transcripts in Soybean Using Strand-Specific RNA-Seq Datasets. <i>Genes</i> , 2022, 13, 228.	1.0	1
10	Integrated Omics Approaches Revealed the Osmotic Stress-Responsive Genes and Microbiota in Gill of Marine Medaka. <i>MSystems</i> , 2022, 7, e0004722.	1.7	10
11	Network Pharmacology and Comparative Transcriptome Reveals Biotargets and Mechanisms of Curcumin Treating Lung Adenocarcinoma Patients With COVID-19. <i>Frontiers in Nutrition</i> , 2022, 9, 870370.	1.6	13
12	Single-Cell Atlas of the Drosophila Leg Disc Identifies a Long Non-Coding RNA in Late Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6796.	1.8	4
13	Genetic architecture of wild soybean (<i>Glycine soja</i> Sieb. and Zucc.) populations originating from different East Asian regions. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1577-1588.	0.8	2
14	Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. <i>Communications Biology</i> , 2021, 4, 83.	2.0	31
15	Pan-cancer investigation reveals mechanistic insights of planar cell polarity gene Fuz in carcinogenesis. <i>Aging</i> , 2021, 13, 7259-7283.	1.4	10
16	Investigating the role of <i>dachshund b</i> in the development of the pancreatic islet in zebrafish. <i>Journal of Diabetes Investigation</i> , 2021, 12, 710-727.	1.1	2
17	Authentication of Hedyotis products by adaptor ligation-mediated PCR and metabarcoding. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 196, 113920.	1.4	7
18	RNA G-quadruplexes (rG4s): genomics and biological functions. <i>Nucleic Acids Research</i> , 2021, 49, 5426-5450.	6.5	86

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19	Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. <i>BMC Genomics</i> , 2021, 22, 313.	1.2	11
20	Proteomic Response of the Brain to Hypoxic Stress in Marine Medaka Fish (<i>Oryzias melastigma</i>). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
21	Differentially expressed microRNAs that target functional genes in mature soybean nodules. <i>Plant Genome</i> , 2021, 14, e20103.	1.6	8
22	CAG RNAs induce DNA damage and apoptosis by silencing <i>NUDT16</i> expression in polyglutamine degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	17
23	Increased copy number of <i>gibberellin 2-oxidase 8</i> genes reduced trailing growth and shoot length during soybean domestication. <i>Plant Journal</i> , 2021, 107, 1739-1755.	2.8	24
24	Low-Dose Radiation Can Cause Epigenetic Alterations Associated With Impairments in Both Male and Female Reproductive Cells. <i>Frontiers in Genetics</i> , 2021, 12, 710143.	1.1	9
25	Detrimental effects of microplastic exposure on normal and asthmatic pulmonary physiology. <i>Journal of Hazardous Materials</i> , 2021, 416, 126069.	6.5	60
26	Changes of the intestinal microbiota along the gut of Japanese Eel (<i>Anguilla japonica</i>). <i>Letters in Applied Microbiology</i> , 2021, 73, 529-541.	1.0	3
27	Characterization of PFOS toxicity on in-vivo and ex-vivo mouse pancreatic islets. <i>Environmental Pollution</i> , 2021, 289, 117857.	3.7	15
28	Smad3 deficiency promotes beta cell proliferation and function in <i>db/db</i> mice <i>via</i> restoring Pax6 expression. <i>Theranostics</i> , 2021, 11, 2845-2859.	4.6	16
29	Identification of Smad3-related transcriptomes in type 2 diabetic nephropathy by whole transcriptome RNA sequencing. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 2052-2068.	1.6	5
30	G-quadruplex RNA motifs influence gene expression in the malaria parasite <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2021, 49, 12486-12501.	6.5	11
31	Toward haplotype studies in polyploid plants to assist breeding. <i>Molecular Plant</i> , 2021, 14, 1969-1972.	3.9	6
32	Integratome analysis of adipose tissues reveals abnormal epigenetic regulation of adipogenesis, inflammation, and insulin signaling in obese individuals with type 2 diabetes. <i>Clinical and Translational Medicine</i> , 2021, 11, e596.	1.7	4
33	Terpenes and Terpenoids in Plants: Interactions with Environment and Insects. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7382.	1.8	172
34	In-silico Exploration of Channel Type and Efflux Silicon Transporters and Silicification Proteins in 80 Sequenced Viridiplantae Genomes. <i>Plants</i> , 2020, 9, 1612.	1.6	7
35	Advances in optical mapping for genomic research. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2051-2062.	1.9	71
36	Multi-omic approach provides insights into osmoregulation and osmoconformation of the crab <i>Scylla paramamosain</i> . <i>Scientific Reports</i> , 2020, 10, 21771.	1.6	19

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37	rG4-seeker enables high-confidence identification of novel and non-canonical rG4 motifs from rG4-seq experiments. <i>RNA Biology</i> , 2020, 17, 903-917.	1.5	14
38	Hypoxia causes sex-specific hepatic toxicity at the transcriptome level in marine medaka (<i>Oryzias latipes</i>). <i>Overlook</i> , 2020, 10, 11.	1.9	11
39	Integrative omics analyses uncover the mechanism underlying the immunotoxicity of perfluorooctanesulfonate in human lymphocytes. <i>Chemosphere</i> , 2020, 256, 127062.	4.2	15
40	Micro-RNA Clusters Integrate Evolutionary Constraints on Expression and Target Affinities: The miR-6/5/4/286/3/309 Cluster in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2955-2965.	3.5	2
41	Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. <i>Nature Communications</i> , 2020, 11, 3051.	5.8	47
42	Korean Wild Soybeans (<i>Glycine soja</i> Sieb & Zucc.): Geographic Distribution and Germplasm Conservation. <i>Agronomy</i> , 2020, 10, 214.	1.3	14
43	Transcriptomic analysis reveals the oncogenic role of S6K1 in hepatocellular carcinoma. <i>Journal of Cancer</i> , 2020, 11, 2645-2655.	1.2	8
44	Analysis of Soybean Long Non-Coding RNAs Reveals a Subset of Small Peptide-Coding Transcripts. <i>Plant Physiology</i> , 2020, 182, 1359-1374.	2.3	46
45	Osmotic stress induces gut microbiota community shift in fish. <i>Environmental Microbiology</i> , 2020, 22, 3784-3802.	1.8	31
46	A crustacean annotated transcriptome (CAT) database. <i>BMC Genomics</i> , 2020, 21, 32.	1.2	13
47	Millipede genomes reveal unique adaptations during myriapod evolution. <i>PLoS Biology</i> , 2020, 18, e3000636.	2.6	18
48	SCRaMBLE-in: A Fast and Efficient Method to Diversify and Improve the Yields of Heterologous Pathways in Synthetic Yeast. <i>Methods in Molecular Biology</i> , 2020, 2205, 305-327.	0.4	0
49	Monochorionic twins with selective fetal growth restriction: insight from placental whole-transcriptome analysis. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 223, 749.e1-749.e16.	0.7	3
50	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
51	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
52	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
53	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
54	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0

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55	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
56	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
57	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
58	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
59	OMMA enables population-scale analysis of complex genomic features and phylogenomic relationships from nanochannel-based optical maps. <i>GigaScience</i> , 2019, 8, .	3.3	5
60	Systematic evaluation and optimization of the experimental steps in RNA G-quadruplex structure sequencing. <i>Scientific Reports</i> , 2019, 9, 8091.	1.6	13
61	LncRNAs with miRNAs in regulation of gastric, liver, and colorectal cancers: updates in recent years. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4649-4677.	1.7	99
62	Genome maps across 26 human populations reveal population-specific patterns of structural variation. <i>Nature Communications</i> , 2019, 10, 1025.	5.8	123
63	Hypoxia Causes Transgenerational Impairment of Ovarian Development and Hatching Success in Fish. <i>Environmental Science & Technology</i> , 2019, 53, 3917-3928.	4.6	39
64	Endothelial TFEB (Transcription Factor EB) Restrains IKK (Î ^Î B Kinase)-p65 Pathway to Attenuate Vascular Inflammation in Diabetic <i>db/db</i> Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 719-730.	1.1	50
65	A Small RNA Transforms the Multidrug Resistance of <i>Pseudomonas aeruginosa</i> to Drug Susceptibility. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 218-228.	2.3	13
66	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	5.8	183
67	Reference-Based Identification of Long Noncoding RNAs in Plants with Strand-Specific RNA-Sequencing Data. <i>Methods in Molecular Biology</i> , 2019, 1933, 245-255.	0.4	1
68	A Targeted Gene Panel That Covers Coding, Non-coding and Short Tandem Repeat Regions Improves the Diagnosis of Patients With Neurodegenerative Diseases. <i>Frontiers in Neuroscience</i> , 2019, 13, 1324.	1.4	4
69	Characterization of Hepatocellular Carcinoma Cell Lines Using a Fractionation-Then-Sequencing Approach Reveals Nuclear-Enriched HCC-Associated lncRNAs. <i>Frontiers in Genetics</i> , 2019, 10, 1081.	1.1	12
70	Replication Study for the Association of GWAS-associated Loci With Adolescent Idiopathic Scoliosis Susceptibility and Curve Progression in a Chinese Population. <i>Spine</i> , 2019, 44, 464-471.	1.0	19
71	Progression of diabetic kidney disease and trajectory of kidney function decline in Chinese patients with Type 2 diabetes. <i>Kidney International</i> , 2019, 95, 178-187.	2.6	105
72	Characterization of Cellulose Synthase A (CESA) Gene Family in Eudicots. <i>Biochemical Genetics</i> , 2019, 57, 248-272.	0.8	16

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73	Transcriptomic reprogramming in soybean seedlings under salt stress. <i>Plant, Cell and Environment</i> , 2019, 42, 98-114.	2.8	111
74	524-P: RNA-Sequencing of Laser-Microdissected Glomeruli and Tubules Reveal Differentially Expressed Genes in Diabetic Kidney Disease. <i>Diabetes</i> , 2019, 68, .	0.3	0
75	Comparative transcriptomics of multidrug-resistant <i>Acinetobacter baumannii</i> in response to antibiotic treatments. <i>Scientific Reports</i> , 2018, 8, 3515.	1.6	53
76	A comprehensive web tool for toehold switch design. <i>Bioinformatics</i> , 2018, 34, 2862-2864.	1.8	31
77	Transcriptomic analysis reveals transgenerational effect of hypoxia on the neural control of testicular functions. <i>Aquatic Toxicology</i> , 2018, 195, 41-48.	1.9	11
78	High-quality assembly of <i>Dermatophagoides pteronyssinus</i> genome and transcriptome reveals a wide range of novel allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2268-2271.e8.	1.5	34
79	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018, 67, 1414-1427.	0.3	136
80	Comparative transcriptomic characterization of a new <i>mib</i> mutant allele, <i>mib</i> , in zebrafish. <i>Gene</i> , 2018, 642, 51-57.	1.0	0
81	Fine-tuning carbapenem resistance by reducing porin permeability of bacteria activated in the selection process of conjugation. <i>Scientific Reports</i> , 2018, 8, 15248.	1.6	19
82	miRNA-Mediated Interactions in and between Plants and Insects. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3239.	1.8	23
83	Transcriptomic and methylomic analysis reveal the toxicological effect of 2,3,7,8-Tetrachlorodibenzodioxin on human embryonic stem cell. <i>Chemosphere</i> , 2018, 206, 663-673.	4.2	13
84	Coordinated regulation of core and accessory genes in the multipartite genome of <i>Sinorhizobium fredii</i> . <i>PLoS Genetics</i> , 2018, 14, e1007428.	1.5	50
85	Identification of Plasmid-Encoded sRNAs in a bla _{NDM-1} -Harboring Multidrug-Resistance Plasmid pNDM-HK in Enterobacteriaceae. <i>Frontiers in Microbiology</i> , 2018, 9, 532.	1.5	5
86	Planar cell polarity gene <i>Fuz</i> triggers apoptosis in neurodegenerative disease models. <i>EMBO Reports</i> , 2018, 19, .	2.0	18
87	High-quality assembly of <i>Dermatophagoides pteronyssinus</i> genome and transcriptome reveals a wide range of novel allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, AB286.	1.5	0
88	OMBlast: alignment tool for optical mapping using a seed-and-extend approach. <i>Bioinformatics</i> , 2017, 33, 311-319.	1.8	39
89	Transcriptome sequencing reveals prenatal PFOS exposure on liver disorders. <i>Environmental Pollution</i> , 2017, 223, 416-425.	3.7	30
90	Using genetics to inform new therapeutics for diabetes. <i>Expert Review of Endocrinology and Metabolism</i> , 2017, 12, 159-169.	1.2	0

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91	OMTools: a software package for visualizing and processing optical mapping data. <i>Bioinformatics</i> , 2017, 33, 2933-2935.	1.8	28
92	A comparison of transcriptomic profiles in endometrium during window of implantation between women with unexplained recurrent implantation failure and recurrent miscarriage. <i>Reproduction</i> , 2017, 153, 749-758.	1.1	62
93	The CTX-M-14 plasmid pHK01 encodes novel small RNAs and influences host growth and motility. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	12
94	Transcriptomic and Functional Analyses on the Effects of Dioxin on Insulin Secretion of Pancreatic Islets and β^2 -Cells. <i>Environmental Science & Technology</i> , 2017, 51, 11390-11400.	4.6	8
95	MicroRNAs regulate the sesquiterpenoid hormonal pathway in <i>Drosophila</i> and other arthropods. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171827.	1.2	20
96	Effects of in Utero PFOS Exposure on Transcriptome, Lipidome, and Function of Mouse Testis. <i>Environmental Science & Technology</i> , 2017, 51, 8782-8794.	4.6	51
97	An iterative algorithm for de novo optical map assembly. , 2017, , .		1
98	Systematic Selection of Reference Genes for the Normalization of Circulating RNA Transcripts in Pregnant Women Based on RNA-Seq Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1709.	1.8	26
99	Efforts and Challenges in Engineering the Genetic Code. <i>Life</i> , 2017, 7, 12.	1.1	17
100	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. <i>Genome Biology</i> , 2017, 18, 230.	3.8	28
101	Transcriptomic profiles in peripheral blood between women with unexplained recurrent implantation failure and recurrent miscarriage and the correlation with endometrium: A pilot study. <i>PLoS ONE</i> , 2017, 12, e0189159.	1.1	11
102	Comparison of Small RNA Profiles of Glycine max and Glycine soja at Early Developmental Stages. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2043.	1.8	7
103	Transcriptomic alterations in <i>Daphnia magna</i> embryos from mothers exposed to hypoxia. <i>Aquatic Toxicology</i> , 2016, 177, 454-463.	1.9	13
104	Whole-genome sequencing of two probands with hereditary spastic paraplegia reveals novel splice-donor region variant and known pathogenic variant in <i>SPG11</i> . <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001248.	0.5	7
105	Interactome-transcriptome analysis discovers signatures complementary to GWAS Loci of Type 2 Diabetes. <i>Scientific Reports</i> , 2016, 6, 35228.	1.6	20
106	Genome-wide association study in Chinese identifies new susceptibility loci associated with chronic kidney disease in type 2 diabetes. <i>Diabetes Research and Clinical Practice</i> , 2016, 120, S49-S50.	1.1	0
107	Pathogenesis of POLR1C-dependent Type 3 Treacher Collins Syndrome revealed by a zebrafish model. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1147-1158.	1.8	38
108	Oncogenic mutations and dysregulated pathways in obesity-associated hepatocellular carcinoma. <i>Oncogene</i> , 2016, 35, 6271-6280.	2.6	28

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109	Fatty liver disease induced by perfluorooctane sulfonate: Novel insight from transcriptome analysis. <i>Chemosphere</i> , 2016, 159, 166-177.	4.2	43
110	Transcriptomic responses of marine medaka's ovary to hypoxia. <i>Aquatic Toxicology</i> , 2016, 177, 476-483.	1.9	21
111	Hypoxia alters testicular functions of marine medaka through microRNAs regulation. <i>Aquatic Toxicology</i> , 2016, 180, 266-273.	1.9	34
112	Hypoxia causes transgenerational impairments in reproduction of fish. <i>Nature Communications</i> , 2016, 7, 12114.	5.8	134
113	Towards a More Accurate Error Model for BioNano Optical Maps. <i>Lecture Notes in Computer Science</i> , 2016, , 67-79.	1.0	8
114	Discovery and functional characterization of novel miRNAs in the marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2016, 175, 106-116.	1.9	13
115	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. <i>Genetics</i> , 2016, 202, 351-362.	1.2	126
116	Differential responses of female and male brains to hypoxia in the marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2016, 172, 36-43.	1.9	13
117	Hypoxia alters steroidogenesis in female marine medaka through miRNAs regulation. <i>Aquatic Toxicology</i> , 2016, 172, 1-8.	1.9	49
118	Ancestral whole-genome duplication in the marine chelicerate horseshoe crabs. <i>Heredity</i> , 2016, 116, 190-199.	1.2	114
119	Transcriptomic analysis reveals specific osmoregulatory adaptive responses in gill mitochondria-rich cells and pavement cells of the Japanese eel. <i>BMC Genomics</i> , 2015, 16, 1072.	1.2	28
120	Small RNAs in Plant Responses to Abiotic Stresses: Regulatory Roles and Study Methods. <i>International Journal of Molecular Sciences</i> , 2015, 16, 24532-24554.	1.8	42
121	Genome of the Rusty Millipede, <i>Trigoniulus corallinus</i> , Illuminates Diplopod, Myriapod, and Arthropod Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 1280-1295.	1.1	21
122	How did arthropod sesquiterpenoids and ecdysteroids arise? Comparison of hormonal pathway genes in non-insect arthropod genomes. <i>Genome Biology and Evolution</i> , 2015, 7, evv120.	1.1	64
123	The draft genome, transcriptome, and microbiome of <i>Dermatophagoides farinae</i> reveal a broad spectrum of dust mite allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 539-548.	1.5	172
124	Transcriptomic responses of corpuscle of Stannius gland of Japanese eels (<i>Anguilla japonica</i>) to Changes in Water Salinity. <i>Scientific Reports</i> , 2015, 5, 9836.	1.6	21
125	A new mib allele with a chromosomal deletion covering <i>foxc1a</i> exhibits anterior somite specification defect. <i>Scientific Reports</i> , 2015, 5, 10673.	1.6	10
126	Hypoxia induces miR-210, leading to anti-apoptosis in ovarian follicular cells of marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2015, 165, 189-196.	1.9	29

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127	Hepatocellular carcinoma-derived exosomes promote motility of immortalized hepatocyte through transfer of oncogenic proteins and RNAs. <i>Carcinogenesis</i> , 2015, 36, 1008-1018.	1.3	213
128	Tissue-specific transcriptome assemblies of the marine medaka <i>Oryzias melastigma</i> and comparative analysis with the freshwater medaka <i>Oryzias latipes</i> . <i>BMC Genomics</i> , 2015, 16, 135.	1.2	47
129	Draft Genome Sequence of Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Strain CUAB1 from a Patient in Hong Kong, China. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
130	Identification of putative ecdysteroid and juvenile hormone pathway genes in the shrimp <i>Neocaridina denticulata</i> . <i>General and Comparative Endocrinology</i> , 2015, 214, 167-176.	0.8	74
131	Using RNA-Seq Data to Evaluate Reference Genes Suitable for Gene Expression Studies in Soybean. <i>PLoS ONE</i> , 2015, 10, e0136343.	1.1	64
132	The Essential Component in DNA-Based Information Storage System: Robust Error-Tolerating Module. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 49.	2.0	18
133	Genomic Sequence and Experimental Tractability of a New Decapod Shrimp Model, <i>Neocaridina denticulata</i> . <i>Marine Drugs</i> , 2014, 12, 1419-1437.	2.2	77
134	Mutations Enabling Displacement of Tryptophan by 4-Fluorotryptophan as a Canonical Amino Acid of the Genetic Code. <i>Genome Biology and Evolution</i> , 2014, 6, 629-641.	1.1	31
135	Draft Genome Sequence of <i>Clostridium butyricum</i> Strain NOR 33234, Isolated from an Elderly Patient with Diarrhea. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
136	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. <i>Bioinformatics</i> , 2014, 30, 1049-1055.	1.8	5
137	A novel missense mutation in <i>CCDC88C</i> activates the JNK pathway and causes a dominant form of spinocerebellar ataxia. <i>Journal of Medical Genetics</i> , 2014, 51, 590-595.	1.5	64
138	Viral-Human Chimeric Transcript Predisposes Risk to Liver Cancer Development and Progression. <i>Cancer Cell</i> , 2014, 25, 335-349.	7.7	254
139	Monitoring bacterial growth using tunable resistive pulse sensing with a pore-based technique. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 855-862.	1.7	60
140	Transcriptome sequencing of Chinese and Caucasian population identifies ethnic-associated differential transcript abundance of heterogeneous nuclear ribonucleoprotein K (hnRNPK). <i>Genomics</i> , 2014, 103, 56-64.	1.3	20
141	Integrative Identification of Epstein-Barr Virus-Associated Mutations and Epigenetic Alterations in Gastric Cancer. <i>Gastroenterology</i> , 2014, 147, 1350-1362.e4.	0.6	90
142	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014, 15, 408.	3.8	173
143	De Novo Transcriptome Sequencing of the Snail <i>Echinolittorina malaccana</i> : Identification of Genes Responsive to Thermal Stress and Development of Genetic Markers for Population Studies. <i>Marine Biotechnology</i> , 2014, 16, 547-559.	1.1	43
144	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	5.8	332

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145	Familial Young-Onset Diabetes, Pre-Diabetes and Cardiovascular Disease Are Associated with Genetic Variants of DACH1 in Chinese. PLoS ONE, 2014, 9, e84770.	1.1	16
146	Genome-wide association study in a Chinese population identifies a susceptibility locus for type 2 diabetes at 7q32 near PAX4. Diabetologia, 2013, 56, 1291-1305.	2.9	94
147	Identification of small RNAs in <i>Mycobacterium smegmatis</i> using heterologous Hfq. Rna, 2013, 19, 74-84.	1.6	25
148	Parallel architecture for DNA sequence inexact matching with Burrows-Wheeler Transform. Microelectronics Journal, 2013, 44, 670-682.	1.1	16
149	Deep sequencing of small RNA transcriptome reveals novel non-coding RNAs in hepatocellular carcinoma. Journal of Hepatology, 2013, 58, 1165-1173.	1.8	160
150	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. Briefings in Bioinformatics, 2013, 14, 548-555.	3.2	8
151	Experimental verification of microRNA targets is essential, prediction alone is insufficient. Carcinogenesis, 2013, 34, 723-723.	1.3	1
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