

Han Ming Gan

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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.

194
papers

2,583
citations

26
h-index

40
g-index

230
ext. papers

3,562
ext. citations

3.3
avg, IF

5.39
L-index

#	Paper	IF	Citations
194	Deciphering chicken gut microbial dynamics based on high-throughput 16S rRNA metagenomics analyses. <i>Gut Pathogens</i> , 2015 , 7, 4	5.4	155
193	High-resolution bacterial 16S rRNA gene profile meta-analysis and biofilm status reveal common colorectal cancer consortia. <i>Npj Biofilms and Microbiomes</i> , 2017 , 3, 34	8.2	145
192	DNA metabarcoding of insects and allies: an evaluation of primers and pipelines. <i>Bulletin of Entomological Research</i> , 2015 , 105, 717-27	1.7	90
191	Helicobacter pylori Eradication Causes Perturbation of the Human Gut Microbiome in Young Adults. <i>PLoS ONE</i> , 2016 , 11, e0151893	3.7	82
190	Integrated shotgun sequencing and bioinformatics pipeline allows ultra-fast mitogenome recovery and confirms substantial gene rearrangements in Australian freshwater crayfishes. <i>BMC Evolutionary Biology</i> , 2014 , 14, 19	3	80
189	Microbial succession and the functional potential during the fermentation of Chinese soy sauce brine. <i>Frontiers in Microbiology</i> , 2014 , 5, 556	5.7	52
188	Biodegradation of 4-aminobenzenesulfonate by <i>Ralstonia</i> sp. PBA and <i>Hydrogenophaga</i> sp. PBC isolated from textile wastewater treatment plant. <i>Chemosphere</i> , 2011 , 82, 507-13	8.4	52
187	Finding Nemo: hybrid assembly with Oxford Nanopore and Illumina reads greatly improves the clownfish (<i>Amphiprion ocellaris</i>) genome assembly. <i>GigaScience</i> , 2018 , 7, 1-6	7.6	50
186	Genome sequence of <i>Pichia kudriavzevii</i> M12, a potential producer of bioethanol and phytase. <i>Eukaryotic Cell</i> , 2012 , 11, 1300-1		50
185	ORDER within the chaos: Insights into phylogenetic relationships within the Anomura (Crustacea: Decapoda) from mitochondrial sequences and gene order rearrangements. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 127, 320-331	4.1	50
184	Comparative genomic analysis of six bacteria belonging to the genus <i>Novosphingobium</i> : insights into marine adaptation, cell-cell signaling and bioremediation. <i>BMC Genomics</i> , 2013 , 14, 431	4.5	43
183	MitoPhAST, a new automated mitogenomic phylogeny tool in the post-genomic era with a case study of 89 decapod mitogenomes including eight new freshwater crayfish mitogenomes. <i>Molecular Phylogenetics and Evolution</i> , 2015 , 85, 180-8	4.1	42
182	Analysis of anoxybacillus genomes from the aspects of lifestyle adaptations, prophage diversity, and carbohydrate metabolism. <i>PLoS ONE</i> , 2014 , 9, e90549	3.7	42
181	De novo genome assembly and annotation of Australia's largest freshwater fish, the Murray cod (<i>Maccullochella peelii</i>), from Illumina and Nanopore sequencing read. <i>GigaScience</i> , 2017 , 6, 1-6	7.6	40
180	Microbiome analysis of Pacific white shrimp gut and rearing water from Malaysia and Vietnam: implications for aquaculture research and management. <i>PeerJ</i> , 2018 , 6, e5826	3.1	40
179	Expansion and systematics redefinition of the most threatened freshwater mussel family, the Margaritiferidae. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 127, 98-118	4.1	37
178	A horizon scan of priorities for coastal marine microbiome research. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1509-1520	12.3	37

177	Impact of dengue virus (DENV) co-infection on clinical manifestations, disease severity and laboratory parameters. <i>BMC Infectious Diseases</i> , 2016 , 16, 406	4	34
176	Comparative mitogenomics of the Decapoda reveals evolutionary heterogeneity in architecture and composition. <i>Scientific Reports</i> , 2019 , 9, 10756	4.9	32
175	Effects of condensed tannin fractions of different molecular weights on population and diversity of bovine rumen methanogenic archaea in vitro , as determined by high-throughput sequencing. <i>Animal Feed Science and Technology</i> , 2016 , 216, 146-160	3	31
174	Whole Genome Sequencing of the Asian Arowana (<i>Scleropages formosus</i>) Provides Insights into the Evolution of Ray-Finned Fishes. <i>Genome Biology and Evolution</i> , 2015 , 7, 2885-95	3.9	30
173	Taxonomic Classification of 373 Genomes Reveals Species Misidentification and New Genospecies within the Genus. <i>Frontiers in Microbiology</i> , 2017 , 8, 1296	5.7	30
172	Whole genome sequencing and analysis reveal insights into the genetic structure, diversity and evolutionary relatedness of luxI and luxR homologs in bacteria belonging to the Sphingomonadaceae family. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014 , 4, 188	5.9	29
171	Signatures of polygenic adaptation associated with climate across the range of a threatened fish species with high genetic connectivity. <i>Molecular Ecology</i> , 2017 , 26, 6253-6269	5.7	26
170	Digging deeper: new gene order rearrangements and distinct patterns of codons usage in mitochondrial genomes among shrimps from the Axiidea, Gebiidea and Caridea (Crustacea: Decapoda). <i>PeerJ</i> , 2017 , 5, e2982	3.1	26
169	Field calibration of blowfly-derived DNA against traditional methods for assessing mammal diversity in tropical forests. <i>Genome</i> , 2016 , 59, 1008-1022	2.4	26
168	Climate-driven mitochondrial selection: A test in Australian songbirds. <i>Molecular Ecology</i> , 2018 , 27, 898-918	5.18	25
167	Elucidating the diet of the island flying fox () in Peninsular Malaysia through Illumina Next-Generation Sequencing. <i>PeerJ</i> , 2017 , 5, e3176	3.1	24
166	Purifying selection and genetic drift shaped Pleistocene evolution of the mitochondrial genome in an endangered Australian freshwater fish. <i>Heredity</i> , 2017 , 118, 466-476	3.6	22
165	Identification of genes involved in the 4-aminobenzenesulfonate degradation pathway of <i>Hydrogenophaga</i> sp. PBC via transposon mutagenesis. <i>FEMS Microbiology Letters</i> , 2011 , 318, 108-114	2.9	22
164	Metabolomics and 16S rRNA sequencing of human colorectal cancers and adjacent mucosa. <i>PLoS ONE</i> , 2018 , 13, e0208584	3.7	21
163	Rapid recovery of nuclear and mitochondrial genes by genome skimming from Northern Hemisphere freshwater crayfish. <i>Zoologica Scripta</i> , 2017 , 46, 718-728	2.5	20
162	Genome sequence of <i>Hydrogenophaga</i> sp. strain PBC, a 4-aminobenzenesulfonate-degrading bacterium. <i>Journal of Bacteriology</i> , 2012 , 194, 4759-60	3.5	20
161	Characterization of an autotrophic bioreactor microbial consortium degrading thiocyanate. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 5889-5901	5.7	18
160	Crustal fluid and ash alteration impacts on the biosphere of Shikoku Basin sediments, Nankai Trough, Japan. <i>Geobiology</i> , 2015 , 13, 562-80	4.3	18

159	Identification of an rsh gene from a <i>Novosphingobium</i> sp. necessary for quorum-sensing signal accumulation. <i>Journal of Bacteriology</i> , 2009 , 191, 2551-60	3.5	18
158	Genome sequence and comparative pathogenomics analysis of a <i>Salmonella enterica</i> Serovar Typhi strain associated with a typhoid carrier in Malaysia. <i>Journal of Bacteriology</i> , 2012 , 194, 5970-1	3.5	18
157	Global MLST of <i>Salmonella</i> Typhi Revisited in Post-genomic Era: Genetic Conservation, Population Structure, and Comparative Genomics of Rare Sequence Types. <i>Frontiers in Microbiology</i> , 2016 , 7, 270	5.7	18
156	The male and female complete mitochondrial genome sequences of the Endangered freshwater mussel <i>Potomida littoralis</i> (Cuvier, 1798) (Bivalvia: Unionidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3571-2	1.3	17
155	Complete genome sequence of <i>Novosphingobium resinovorum</i> SA1, a versatile xenobiotic-degrading bacterium capable of utilizing sulfanilic acid. <i>Journal of Biotechnology</i> , 2017 , 241, 76-80	3.7	17
154	Nanopore Long-Read Guided Complete Genome Assembly of , and Genomic Insights into 4-Aminobenzenesulfonate, -Aminobenzoic Acid and Hydrogen Metabolism in the Genus. <i>Frontiers in Microbiology</i> , 2017 , 8, 1880	5.7	17
153	Whole-genome sequences of 13 endophytic bacteria isolated from shrub willow (<i>salix</i>) grown in geneva, new york. <i>Genome Announcements</i> , 2014 , 2,		17
152	Whole-Genome Sequences of Five Oligotrophic Bacteria Isolated from Deep within Lechuguilla Cave, New Mexico. <i>Genome Announcements</i> , 2014 , 2,		17
151	Phylogeography of red muntjacs reveals three distinct mitochondrial lineages. <i>BMC Evolutionary Biology</i> , 2017 , 17, 34	3	16
150	In Situ Stimulation of Thiocyanate Biodegradation through Phosphate Amendment in Gold Mine Tailings Water. <i>Environmental Science & Technology</i> , 2017 , 51, 13353-13362	10.3	16
149	First comprehensive multi-tissue transcriptome of <i>Cherax quadricarinatus</i> (Decapoda: Parastacidae) reveals unexpected diversity of endogenous cellulase. <i>Organisms Diversity and Evolution</i> , 2016 , 16, 185-200	1.7	16
148	The complete genome sequence of EC1-UPM, a novel N4-like bacteriophage that infects <i>Escherichia coli</i> O78:K80. <i>Virology Journal</i> , 2013 , 10, 308	6.1	16
147	Quorum-sensing signal production by <i>Agrobacterium vitis</i> strains and their tumor-inducing and tartrate-catabolic plasmids. <i>FEMS Microbiology Letters</i> , 2009 , 296, 102-9	2.9	16
146	Genome sequence of <i>Aureobasidium pullulans</i> AY4, an emerging opportunistic fungal pathogen with diverse biotechnological potential. <i>Eukaryotic Cell</i> , 2012 , 11, 1419-20		16
145	The first Margaritiferidae male (M-type) mitogenome: mitochondrial gene order as a potential character for determining higher-order phylogeny within Unionida (Bivalvia). <i>Journal of Molluscan Studies</i> , 2017 , 83, 249-252	1.1	15
144	Whole genome sequencing of isolated from the chewing stick (): insights into phylogeny, mitogenome dynamics and carotenoid biosynthesis. <i>PeerJ</i> , 2017 , 5, e4030	3.1	15
143	Pleistocene divergence across a mountain range and the influence of selection on mitogenome evolution in threatened Australian freshwater cod species. <i>Heredity</i> , 2016 , 116, 506-15	3.6	15
142	Comparative genomics of closely related <i>Salmonella enterica</i> serovar Typhi strains reveals genome dynamics and the acquisition of novel pathogenic elements. <i>BMC Genomics</i> , 2014 , 15, 1007	4.5	15

141	Improved genomic resources for the black tiger prawn (<i>Penaeus monodon</i>). <i>Marine Genomics</i> , 2020 , 52, 100751	1.9	14
140	Genome sequence of <i>Methylobacterium</i> sp. strain GXF4, a xylem-associated bacterium isolated from <i>Vitis vinifera</i> L. grapevine. <i>Journal of Bacteriology</i> , 2012 , 194, 5157-8	3.5	14
139	High-throughput terrestrial biodiversity assessments: mitochondrial metabarcoding, metagenomics or metatranscriptomics?. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019 , 30, 60-67	1.3	14
138	Genomic evidence of neo-sex chromosomes in the eastern yellow robin. <i>GigaScience</i> , 2019 , 8,	7.6	13
137	Absence of evidence is not evidence of absence: Nanopore sequencing and complete assembly of the European lobster (<i>Homarus gammarus</i>) mitogenome uncovers the missing nad2 and a new major gene cluster duplication. <i>BMC Genomics</i> , 2019 , 20, 335	4.5	13
136	Phaeophyceae (Brown Algal) Extracts Activate Plant Defense Systems in Challenged With. <i>Frontiers in Plant Science</i> , 2020 , 11, 852	6.2	13
135	The complete mitogenome of the hermit crab <i>Clibanarius infraspinus</i> (Hilgendorf, 1869), (Crustacea; Decapoda; Diogenidae) - a new gene order for the Decapoda. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4099-4100	1.3	13
134	The complete mitogenome of <i>Cherax monticola</i> (Crustacea: Decapoda: Parastacidae), a large highland crayfish from New Guinea. <i>Mitochondrial DNA</i> , 2016 , 27, 337-8		13
133	iDNA at Sea: Recovery of Whale Shark (<i>Rhincodon typus</i>) Mitochondrial DNA Sequences from the Whale Shark Copepod (<i>Pandarus rhincodonicus</i>) Confirms Global Population Structure. <i>Frontiers in Marine Science</i> , 2017 , 4,	4.5	13
132	L,L-diaminopimelate aminotransferase (DapL): a putative target for the development of narrow-spectrum antibacterial compounds. <i>Frontiers in Microbiology</i> , 2014 , 5, 509	5.7	13
131	Mesozoic mitogenome rearrangements and freshwater mussel (Bivalvia: Unionoidea) macroevolution. <i>Heredity</i> , 2020 , 124, 182-196	3.6	13
130	AdeR, a PucR-type transcription factor, activates expression of L-alanine dehydrogenase and is required for sporulation of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 4995-5001	3.5	12
129	Whole-genome sequence of <i>Cupriavidus</i> sp. strain BIS7, a heavy-metal-resistant bacterium. <i>Journal of Bacteriology</i> , 2012 , 194, 6324	3.5	12
128	Modulatory effects of condensed tannin fractions of different molecular weights from a <i>Leucaena leucocephala</i> hybrid on the bovine rumen bacterial community in vitro. <i>Journal of the Science of Food and Agriculture</i> , 2016 , 96, 4565-74	4.3	12
127	The complete mitogenome of the red claw crayfish <i>Cherax quadricarinatus</i> (Von Martens, 1868) (Crustacea: Decapoda: Parastacidae). <i>Mitochondrial DNA</i> , 2016 , 27, 385-6		11
126	Whole-Genome Sequences of Two Carbapenem-Resistant Strains Isolated from a Tertiary Hospital in Johor, Malaysia. <i>Genome Announcements</i> , 2017 , 5,		11
125	Genome sequence of <i>Novosphingobium</i> sp. strain Rr 2-17, a nopaline crown gall-associated bacterium isolated from <i>Vitis vinifera</i> L. grapevine. <i>Journal of Bacteriology</i> , 2012 , 194, 5137-8	3.5	11
124	Draft genome sequence of <i>Pantoea</i> sp. strain A4, a <i>Rafflesia</i> -associated bacterium that produces N-acylhomoserine lactones as quorum-sensing molecules. <i>Journal of Bacteriology</i> , 2012 , 194, 6610	3.5	11

123	Genome sequence of <i>Roseomonas</i> sp. strain B5, a quorum-quenching N-acylhomoserine lactone-degrading bacterium isolated from Malaysian tropical soil. <i>Journal of Bacteriology</i> , 2012 , 194, 6681-2	3.5	11
122	The complete mitogenome of the freshwater crayfish <i>Cherax cainii</i> (Crustacea: Decapoda: Parastacidae). <i>Mitochondrial DNA</i> , 2016 , 27, 126-7		10
121	A Giant Genome for a Giant Crayfish () With Insights Into Pseudogenes in Decapod Genomes. <i>Frontiers in Genetics</i> , 2020 , 11, 201	4.5	10
120	More evolution underground: Accelerated mitochondrial substitution rate in Australian burrowing freshwater crayfishes (Decapoda: Parastacidae). <i>Molecular Phylogenetics and Evolution</i> , 2018 , 118, 88-98	4.1	10
119	Cloning and functional analysis of the genes coding for 4-aminobenzenesulfonate 3,4-dioxygenase from <i>Hydrogenophaga</i> sp. PBC. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1933-1941	2.9	10
118	Genome sequence of <i>Citrobacter</i> sp. strain A1, a dye-degrading bacterium. <i>Journal of Bacteriology</i> , 2012 , 194, 5485-6	3.5	10
117	Best Foot Forward: Nanopore Long Reads, Hybrid Meta-Assembly, and Haplotig Purging Optimizes the First Genome Assembly for the Southern Hemisphere Blacklip Abalone (). <i>Frontiers in Genetics</i> , 2019 , 10, 889	4.5	10
116	Genetic diversity of <i>Enterococcus faecalis</i> isolated from environmental, animal and clinical sources in Malaysia. <i>Journal of Infection and Public Health</i> , 2017 , 10, 617-623	7.4	9
115	Disentangling the Taxonomy of the Mahseers (<i>Tor</i> spp.) of Malaysia: An Integrated Approach Using Morphology, Genetics and Historical Records. <i>Reviews in Fisheries Science and Aquaculture</i> , 2017 , 25, 171-183	8.3	9
114	Transcriptome-Guided Identification of Carbohydrate Active Enzymes (CAZy) from the Christmas Island Red Crab, <i>Gecarcoidea natalis</i> and a Vote for the Inclusion of Transcriptome-Derived Crustacean CAZys in Comparative Studies. <i>Marine Biotechnology</i> , 2018 , 20, 654-665	3.4	9
113	Variability of mitochondrial ORFans hints at possible differences in the system of doubly uniparental inheritance of mitochondria among families of freshwater mussels (Bivalvia: Unionida). <i>BMC Evolutionary Biology</i> , 2019 , 19, 229	3	9
112	More limbs on the tree: mitogenome characterisation and systematic position of living fossil species <i>Neoglyphea inopinata</i> and <i>Laurentaeglyphea neocaledonica</i> (Decapoda : Glypheidea : Glypheidae). <i>Invertebrate Systematics</i> , 2018 , 32, 448	1.2	9
111	A glimpse into the genetic basis of symbiosis between and their helper strains in the biodegradation of 4-aminobenzenesulfonate. <i>Journal of Genomics</i> , 2017 , 5, 77-82	0.9	8
110	Whole Genome Assembly of the Snout Otter Clam, , Using Nanopore and Illumina Data, Benchmarked Against Bivalve Genome Assemblies. <i>Frontiers in Genetics</i> , 2019 , 10, 1158	4.5	8
109	Genome sequence of <i>Ralstonia</i> sp. strain PBA, a bacterium involved in the biodegradation of 4-aminobenzenesulfonate. <i>Journal of Bacteriology</i> , 2012 , 194, 5139-40	3.5	8
108	Changes in rumen protozoal community by condensed tannin fractions of different molecular weights from a <i>Leucaena leucocephala</i> hybrid in vitro. <i>Journal of Applied Microbiology</i> , 2017 , 123, 41-53	4.7	7
107	Two reads to rule them all: Nanopore long read-guided assembly of the iconic Christmas Island red crab, <i>Gecarcoidea natalis</i> (Pocock, 1888), mitochondrial genome and the challenges of AT-rich mitogenomes. <i>Marine Genomics</i> , 2019 , 45, 64-71	1.9	7
106	The complete mitochondrial genome of the invasive house crow <i>Corvus splendens</i> (Passeriformes: Corvidae). <i>Mitochondrial DNA</i> , 2016 , 27, 974-5		7

105	The complete mitogenome of the crayfish <i>Cherax glaber</i> (Crustacea: Decapoda: Parastacidae). <i>Mitochondrial DNA</i> , 2016 , 27, 220-1		7
104	The complete mitogenome of the giant clam <i>Tridacna squamosa</i> (Heterodonta: Bivalvia: Tridacnidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3220-1	1.3	7
103	Draft Genome Sequence of <i>Clostridium perfringens</i> Strain JJC, a Highly Efficient Hydrogen Producer Isolated from Landfill Leachate Sludge. <i>Genome Announcements</i> , 2014 , 2,		7
102	The complete mitogenome of the rock pool prawn <i>Palaemon serenus</i> (Heller, 1862) (Crustacea: Decapoda: Palaemonidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3155-6	1.3	6
101	New Sequence Types of Isolated from a Malaysian Aquaculture Pond, as Revealed by Whole-Genome Sequencing. <i>Genome Announcements</i> , 2017 , 5,		6
100	Insight Into the Microbial Co-occurrence and Diversity of 73 Grapevine () Crown Galls Collected Across the Northern Hemisphere. <i>Frontiers in Microbiology</i> , 2019 , 10, 1896	5.7	6
99	One More Decade of <i>Agrobacterium</i> Taxonomy. <i>Current Topics in Microbiology and Immunology</i> , 2018 , 418, 1-14	3.3	6
98	The complete mitogenome of purple mottled shore crab <i>Cyclograpsus granulosus</i> H. Milne-Edwards, 1853 (Crustacea: Decapoda: Grapsoidea). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3981-3982	1.3	6
97	Whole-Genome Sequence and Classification of 11 Endophytic Bacteria from Poison Ivy (<i>Toxicodendron radicans</i>). <i>Genome Announcements</i> , 2015 , 3,		6
96	Draft Genome Sequence of <i>Clostridium bifermentans</i> Strain WYM, a Promising Biohydrogen Producer Isolated from Landfill Leachate Sludge. <i>Genome Announcements</i> , 2014 , 2,		6
95	Genome sequence of <i>Enterococcus</i> sp. strain C1, an azo dye decolorizer. <i>Journal of Bacteriology</i> , 2012 , 194, 5716-7	3.5	6
94	Health and saliva microbiomes of a semi-urbanized indigenous tribe in Peninsular Malaysia. <i>F1000Research</i> , 2019 , 8, 175	3.6	6
93	Rapid genotyping of tilapia lake virus (TiLV) using Nanopore sequencing. <i>Journal of Fish Diseases</i> , 2021 , 44, 1491-1502	2.6	6
92	The complete mitogenome of the Australian land crayfish <i>Engaeus lyelli</i> (Clark 1936) (Crustacea: Decapoda: Parastacidae). <i>Mitochondrial DNA</i> , 2016 , 27, 595-6		5
91	The Influence of Modernization and Disease on the Gastric Microbiome of Orang Asli, Myanmar and Modern Malaysians. <i>Microorganisms</i> , 2019 , 7,	4.9	5
90	De Novo assembly and characterisation of the greentail prawn (<i>Metapenaeus bennettiae</i>) hepatopancreas transcriptome - identification of stress response and detoxification transcripts. <i>Marine Genomics</i> , 2019 , 47, 100677	1.9	5
89	Whole-Genome Sequence and Annotation of Octopine-Utilizing <i>Pseudomonas kilonensis</i> (Previously <i>P. fluorescens</i>) Strain 1855-344. <i>Genome Announcements</i> , 2015 , 3,		5
88	The complete mitogenome of the whale shark parasitic copepod <i>Pandarus rhincodoniscus norman</i> , Newbound & Knott (Crustacea; Siphonostomatoida; Pandaridae)—a new gene order for the copepoda. <i>Mitochondrial DNA</i> , 2016 , 27, 694-5		5

87	Genomic characterization of eight strains isolated from pristine caves and a whole genome phylogeny of. <i>Journal of Genomics</i> , 2017 , 5, 12-15	0.9	5
86	Temporal changes in arthropod activity in tropical anthropogenic forests. <i>Bulletin of Entomological Research</i> , 2018 , 108, 792-799	1.7	5
85	The complete mitogenome of the endangered white-clawed freshwater crayfish <i>Austropotamobius pallipes</i> (Lereboullet, 1858) (Crustacea: Decapoda: Astacidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3329-30	1.3	5
84	Characterisation of 12 microsatellite loci in the Vietnamese commercial clam <i>Lutraria rhynchaena</i> Jonas 1844 (Heterodonta: Bivalvia: Mactridae) through next-generation sequencing. <i>Molecular Biology Reports</i> , 2016 , 43, 391-6	2.8	5
83	The complete mitogenome of the porcelain crab <i>Petrolisthes haswelli</i> Miers, 1884 (Crustacea: Decapoda: Anomura). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3983-3984	1.3	5
82	The complete mitogenome of the marine bivalve <i>Lutraria rhynchaena</i> Jonas 1844 (Heterodonta: Bivalvia: Mactridae). <i>Mitochondrial DNA</i> , 2016 , 27, 335-6		5
81	The complete mitogenome of the Australian spiny crayfish <i>Euastacus yarraensis</i> (McCoy, 1888) (Crustacea: Decapoda: Parastacidae). <i>Mitochondrial DNA</i> , 2016 , 27, 929-30		5
80	The complete mitogenome of the swimming crab <i>Thalamita crenata</i> (Rüppell, 1830) (Crustacea; Decapoda; Portunidae). <i>Mitochondrial DNA</i> , 2016 , 27, 1275-6		5
79	The complete mitogenome of the ghost crab <i>Ocypode ceratophthalmus</i> (Pallas, 1772) (Crustacea: Decapoda: Ocypodidae). <i>Mitochondrial DNA</i> , 2016 , 27, 2123-4		5
78	Genome sequence of multidrug-resistant <i>Escherichia coli</i> EC302/04, isolated from a human tracheal aspirate. <i>Journal of Bacteriology</i> , 2012 , 194, 6691-2	3.5	5
77	Genome sequence and comparative genomics analysis of a <i>Vibrio cholerae</i> O1 strain isolated from a cholera patient in Malaysia. <i>Journal of Bacteriology</i> , 2012 , 194, 6933	3.5	5
76	Genome sequencing-assisted identification and the first functional validation of N-acyl-homoserine-lactone synthases from the Sphingomonadaceae family. <i>PeerJ</i> , 2016 , 4, e2332	3.1	5
75	Mitogenomic phylogeny and fossil-calibrated mutation rates for all F- and M-type mtDNA genes of the largest freshwater mussel family, the Unionidae (Bivalvia). <i>Zoological Journal of the Linnean Society</i> ,	2.4	5
74	First genomic insights into carbapenem-resistant <i>Klebsiella pneumoniae</i> from Malaysia. <i>Journal of Global Antimicrobial Resistance</i> , 2020 , 20, 153-159	3.4	5
73	Mitochondrial genomes of the jungle crow <i>Corvus macrorhynchos</i> (Passeriformes: Corvidae) from shed feathers and a phylogenetic analysis of genus <i>Corvus</i> using mitochondrial protein-coding genes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 2668-70	1.3	4
72	Genome Sequence of subsp. Strain K27, a Marine Bacterium Isolated from Sponge (). <i>Genome Announcements</i> , 2018 , 6,		4
71	The complete mitogenome of the invasive spiny-cheek crayfish <i>Orconectes limosus</i> (Rafinesque, 1817) (Crustacea: Decapoda: Cambaridae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3181-3	1.3	4
70	The complete mitogenome of the Norway lobster <i>Nephrops norvegicus</i> (Linnaeus, 1758) (Crustacea: Decapoda: Nephropidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3179-80	1.3	4

69	The complete mitogenome of the Macquarie perch, <i>Macquaria australasica</i> Cuvier, 1830 (Teleostei: Percichthyidae). <i>Mitochondrial DNA</i> , 2016 , 27, 383-4		4
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54	Draft genome of <i>Jeotgalibacillus campisalis</i> SF-57(T), a moderate halophilic bacterium isolated from marine saltern. <i>Marine Genomics</i> , 2015 , 23, 59-60	1.9	3
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