

Kian Mau Goh

List of Publications by Year in descending order

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74
papers

1,571
citations

377584

21
h-index

388640

36
g-index

75
all docs

75
docs citations

75
times ranked

2176
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of key bacterial players during successful full-scale soil field bioremediation in Antarctica. <i>International Biodeterioration and Biodegradation</i> , 2022, 168, 105354.	1.9	5
2	A Bibliometric Analysis and Review of Pullulan-Degrading Enzymes—Past and Current Trends. <i>Catalysts</i> , 2022, 12, 143.	1.6	11
3	Genome Analysis of <i>Celeribacter</i> sp. PS-C1 Isolated from Sekinchan Beach in Selangor, Malaysia, Reveals Its β -Glucosidase and Licheninase Activities. <i>Microorganisms</i> , 2022, 10, 410.	1.6	4
4	Thermophiles and carbohydrate-active enzymes (CAZymes) in biofilm microbial consortia that decompose lignocellulosic plant litters at high temperatures. <i>Scientific Reports</i> , 2022, 12, 2850.	1.6	17
5	Editorial: Genetics, Genomics and -omics of Thermophiles, Volume II. <i>Frontiers in Microbiology</i> , 2022, 13, 879450.	1.5	1
6	Draft Genome Sequence of <i>Microaerobacter geothermalis</i> Nad S1 ^T , a Microaerophilic Bacterium Isolated from Tenusia Hot Spring. <i>Microbiology Resource Announcements</i> , 2022, , e0008822.	0.3	0
7	Genome sequence of an uncharted halophilic bacterium <i>Robertkochia marina</i> with deciphering its phosphate-solubilizing ability. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 251-256.	0.8	5
8	Metagenomics and Culture Dependent Insights into the Distribution of Firmicutes across Two Different Sample Types Located in the Black Hills Region of South Dakota, USA. <i>Microorganisms</i> , 2021, 9, 113.	1.6	8
9	Draft Genome Sequence of <i>Roseovarius</i> sp. PS-C2, Isolated from Sekinchan Beach in Selangor, Malaysia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0067321.	0.3	2
10	Draft Genome Sequence of <i>Cellulomonas</i> sp. PS-H5, Isolated from Sekinchan Beach in Selangor, Malaysia. <i>Microbiology Resource Announcements</i> , 2021, 10, e0095621.	0.3	1
11	Genomic analysis of a lignocellulose degrading strain from the underexplored genus <i>Meridianimaribacter</i> . <i>Genomics</i> , 2020, 112, 952-960.	1.3	20
12	Meta-Analysis of Microbial Communities in Hot Springs: Recurrent Taxa and Complex Shaping Factors beyond pH and Temperature. <i>Microorganisms</i> , 2020, 8, 906.	1.6	27
13	Global Transcriptomic Responses of <i>Roseithermus sacchariphilus</i> Strain RA in Media Supplemented with Beechwood Xylan. <i>Microorganisms</i> , 2020, 8, 976.	1.6	2
14	Environmental Remediation of Antineoplastic Drugs: Present Status, Challenges, and Future Directions. <i>Processes</i> , 2020, 8, 747.	1.3	10
15	<i>Robertkochia solimangrovi</i> sp. nov., isolated from mangrove soil, and emended description of the genus <i>Robertkochia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1769-1776.	0.8	13
16	Heterologous expression, purification and biochemical characterization of a new endo-1,4- β -xylanase from <i>Rhodothermaceae</i> bacterium RA. <i>Protein Expression and Purification</i> , 2019, 164, 105464.	0.6	18
17	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019, 10, 4574.	5.8	90
18	Current Status and Potential Applications of Underexplored Prokaryotes. <i>Microorganisms</i> , 2019, 7, 468.	1.6	17

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19	Editorial: Recent Advances in Bioremediation/Biodegradation by Extreme Microorganisms. <i>Frontiers in Microbiology</i> , 2019, 10, 1851.	1.5	14
20	Characterizing a Halo-Tolerant GH10 Xylanase from <i>Roseithermus sacchariphilus</i> Strain RA and Its CBM-Truncated Variant. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2284.	1.8	26
21	Genome analysis of a thermophilic exopolysaccharide-producing bacterium - <i>Geobacillus</i> sp. WSUCF1. <i>Scientific Reports</i> , 2019, 9, 1608.	1.6	24
22	<i>Aquella oligotrophicagen. nov. sp. nov.</i> : A new member of the family <i>Neisseriaceae</i> isolated from laboratory tap water. <i>MicrobiologyOpen</i> , 2019, 8, e793.	1.2	12
23	Draft Genome Sequences of <i>Longimonas halophila</i> KCTC 42399 and <i>Longibacter salinarum</i> KCTC 52045. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
24	Microbial diversity of thermophiles with biomass deconstruction potential in a foliage-rich hot spring. <i>MicrobiologyOpen</i> , 2018, 7, e00615.	1.2	27
25	Genomic analyses of five <i>Roseivirga</i> species: Insights into marine adaptation. <i>Marine Genomics</i> , 2018, 38, 97-101.	0.4	2
26	<i>Vibrio coralliirubri</i> sp. nov., a new species isolated from mucus of red coral (<i>Corallium rubrum</i>) collected at Procida island, Italy. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1105-1115.	0.7	18
27	Purification and characterization of a novel GH1 beta-glucosidase from <i>Jeotgalibacillus malaysiensis</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 115, 1094-1102.	3.6	43
28	Draft genome sequence of <i>Vitellibacter aquimaris</i> D-24 T isolated from seawater. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 10-12.	0.8	3
29	Complete genome sequence of <i>Rhodothermaceae</i> bacterium RA with cellulolytic and xylanolytic activities. <i>3 Biotech</i> , 2018, 8, 376.	1.1	14
30	Direct Cellulase Gene Amplification From Hot Spring Using the Guidance of 16S rRNA Amplicon Metagenomics. , 2018, , 309-325.		1
31	Effects of single and co-immobilization on the product specificity of type I pullulanase from <i>Anoxybacillus</i> sp. SK3-4. <i>International Journal of Biological Macromolecules</i> , 2017, 104, 322-332.	3.6	17
32	Use of Megaprimer and Overlapping Extension PCR (OE-PCR) to Mutagenize and Enhance Cyclodextrin Glucosyltransferase (CGTase) Function. <i>Methods in Molecular Biology</i> , 2017, 1498, 385-396.	0.4	7
33	Global transcriptomic response of <i>Anoxybacillus</i> sp. SK 3-4 to aluminum exposure. <i>Journal of Basic Microbiology</i> , 2017, 57, 151-161.	1.8	7
34	Editorial: Genetics, Genomics and “Omics of Thermophiles. <i>Frontiers in Microbiology</i> , 2017, 8, 560.	1.5	5
35	Effects of Physiochemical Factors on Prokaryotic Biodiversity in Malaysian Circumneutral Hot Springs. <i>Frontiers in Microbiology</i> , 2017, 8, 1252.	1.5	49
36	Genome Analysis of a New <i>Rhodothermaceae</i> Strain Isolated from a Hot Spring. <i>Frontiers in Microbiology</i> , 2016, 7, 1109.	1.5	18

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37	Immobilization of α -Amylase from <i>Anoxybacillus</i> sp. SK3-4 on ReliZyme and Immobead Supports. <i>Molecules</i> , 2016, 21, 1196.	1.7	26
38	Draft Genome Sequence of the Sulfate-Reducing Bacterium <i>Desulfotomaculum copahuensis</i> Strain CINDEF11 Isolated from the Geothermal Copahue System, Neuqu�n, Argentina. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
39	Crystal structure of <i>Anoxybacillus</i> α -amylase provides insights into maltose binding of a new glycosyl hydrolase subclass. <i>Scientific Reports</i> , 2016, 6, 23126.	1.6	31
40	Genome sequence of <i>Roseivirga</i> sp. strain D-25 and its potential applications from the genomic aspect. <i>Marine Genomics</i> , 2016, 28, 29-31.	0.4	7
41	Characterization of a type I pullulanase from <i>Anoxybacillus</i> sp. SK3-4 reveals an unusual substrate hydrolysis. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6291-6307.	1.7	19
42	Characterization of a glucose-tolerant β -glucosidase from <i>Anoxybacillus</i> sp. DT3-1. <i>Biotechnology for Biofuels</i> , 2016, 9, 174.	6.2	51
43	Characterization of the mechanism of prolonged adaptation to osmotic stress of <i>Jeotgalibacillus malaysiensis</i> via genome and transcriptome sequencing analyses. <i>Scientific Reports</i> , 2016, 6, 33660.	1.6	57
44	<i>Vitellibacter aquimaris</i> sp. nov., a marine bacterium isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3662-3668.	0.8	21
45	Proposal to reclassify <i>Roseivirga ehrenbergii</i> (Nedashkovskaya et al., 2008) as <i>Roseivirga seohaensis</i> comb. nov., description of <i>Roseivirga seohaensis</i> subsp. <i>aquiponti</i> subsp. nov. and emendation of the genus <i>Roseivirga</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5537-5543.	0.8	17
46	Genome sequence of <i>Anoxybacillus ayderensis</i> ABO4T isolated from the Ayder hot spring in Turkey. <i>Standards in Genomic Sciences</i> , 2015, 10, 70.	1.5	14
47	Draft Genome Sequence of Yellow Pigmented <i>Jeotgalibacillus alimentarius</i> JY-13 T , the First Halophile Strain of the Genus <i>Jeotgalibacillus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	2
48	ISOLATION AND CHARACTERIZATION OF BIOTECHNOLOGY RELEVANT BACTERIA FROM MARINE ENVIRONMENT. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2015, 77, .	0.3	0
49	Draft genome of <i>Jeotgalibacillus campisalis</i> SF-57T, a moderate halophilic bacterium isolated from marine saltern. <i>Marine Genomics</i> , 2015, 23, 59-60.	0.4	4
50	Draft Genome Sequence of <i>Erythrobacter vulgaris</i> Strain O1, a Glycosyl Hydrolase-Producing Bacterium. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
51	Genome Sequence of <i>Anoxybacillus thermarum</i> AF/04 ^T , Isolated from the Euganean Hot Springs in Abano Terme, Italy. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
52	Draft Genome Sequence of <i>Jeotgalibacillus soli</i> DSM 23228, a Bacterium Isolated from Alkaline Sandy Soil. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
53	Characterization of aluminum resistant <i>Anoxybacillus</i> sp. SK 3-4 isolated from a hot spring. <i>Journal of Basic Microbiology</i> , 2015, 55, 514-519.	1.8	7
54	Diversity of thermophiles in a Malaysian hot spring determined using 16S rRNA and shotgun metagenome sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 177.	1.5	161

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55	Complete genome of <i>Jeotgalibacillus malaysiensis</i> D5 T consisting of a chromosome and a circular megaplasmid. <i>Journal of Biotechnology</i> , 2015, 204, 13-14.	1.9	8
56	Thermophiles in the genomic era: Biodiversity, science, and applications. <i>Biotechnology Advances</i> , 2015, 33, 633-647.	6.0	125
57	Draft genome sequence of <i>Vitellibacter vladivostokensis</i> KMM 3516T: A protease-producing bacterium. <i>Marine Genomics</i> , 2015, 23, 49-50.	0.4	5
58	Isolation of <i>Jeotgalibacillus malaysiensis</i> sp. nov. from a sandy beach, and emended description of the genus <i>Jeotgalibacillus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2215-2221.	0.8	18
59	Complete genome of the potential thermozyyme producer <i>Anoxybacillus gonensis</i> G2T isolated from the Gnen hot springs in Turkey. <i>Journal of Biotechnology</i> , 2015, 212, 65-66.	1.9	7
60	Analysis of <i>Anoxybacillus</i> Genomes from the Aspects of Lifestyle Adaptations, Prophage Diversity, and Carbohydrate Metabolism. <i>PLoS ONE</i> , 2014, 9, e90549.	1.1	56
61	Protein engineering of selected residues from conserved sequence regions of a novel <i>Anoxybacillus</i> �-amylase. <i>Scientific Reports</i> , 2014, 4, 5850.	1.6	33
62	Recent discoveries and applications of <i>Anoxybacillus</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1475-1488.	1.7	94
63	A High Molecular-Mass <i>Anoxybacillus</i> sp. SK3-4 Amylopullulanase: Characterization and Its Relationship in Carbohydrate Utilization. <i>International Journal of Molecular Sciences</i> , 2013, 14, 11302-11318.	1.8	31
64	Trends and Tips in Protein Engineering, A Review. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013, 59, .	0.3	0
65	Application of Statistical Experimental Design for Optimization of Novel �-amylase Production by <i>Anoxybacillus</i> Species. <i>Journal of Biological Sciences</i> , 2013, 13, 605-613.	0.1	3
66	Rational Mutagenesis of Cyclodextrin Glucanotransferase at the Calcium Binding Regions for Enhancement of Thermostability. <i>International Journal of Molecular Sciences</i> , 2012, 13, 5307-5323.	1.8	18
67	Isolation and characterization of pullulan-degrading <i>Anoxybacillus</i> species isolated from Malaysian hot springs. <i>Environmental Technology (United Kingdom)</i> , 2012, 33, 1231-1238.	1.2	23
68	Domain replacement to elucidate the role of B domain in CGTase thermostability and activity. <i>Process Biochemistry</i> , 2012, 47, 2123-2130.	1.8	7
69	Cloning and characterization of two new thermostable and alkali-tolerant �-amylases from the <i>Anoxybacillus</i> species that produce high levels of maltose. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 731-741.	1.4	48
70	<i>Meiothermus</i> sp. SK3-2: A potential source for the production of trehalose from maltose. <i>African Journal of Biotechnology</i> , 2011, 10, 12745-12753.	0.3	3
71	A predominant �-CGTase G1 engineered to elucidate the relationship between protein structure and product specificity. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2009, 57, 270-277.	1.8	27
72	Cloning, extracellular expression and characterization of a predominant �-CGTase from <i>Bacillus</i> sp. G1 in <i>E. coli</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2008, 35, 1705-1714.	1.4	47

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73	Molecular Modeling of a Predominant \hat{I}^2 -CGTase G1 and Analysis of Ionic Interaction in CGTase. <i>Biotechnology</i> , 2008, 7, 418-429.	0.5	11
74	The effects of reaction conditions on the production of \hat{I}^3 -cyclodextrin from tapioca starch by using a novel recombinant engineered CGTase. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2007, 49, 118-126.	1.8	27