Gary Xie

List of Publications by Year
in descending order

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58
papers

7,022
citations

101384
36
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60
all docs

60
docs citations

60
times ranked

10157
citing authors

#	Article	IF	Citations
1	Comparative genomic and phenotypic characterization of invasive non-typhoidal Salmonella isolates from Siaya, Kenya. PLoS Neglected Tropical Diseases, 2021, 15, e0008991.	1.3	3
2	The Distinctive Evolution of orfX Clostridium parabotulinum Strains and Their Botulinum Neurotoxin Type A and F Gene Clusters Is Influenced by Environmental Factors and Gene Interactions via Mobile Genetic Elements. Frontiers in Microbiology, 2021, 12, 566908.	1.5	11
3	Hidden Markov Model: a shortest unique representative approach to detect the protein toxins, virulence factors and antibiotic resistance genes. BMC Research Notes, 2021, 14, 122.	0.6	4
4	Genomic Characterization of Newly Completed Genomes of Botulinum Neurotoxin-Producing Species from Argentina, Australia, and Africa. Genome Biology and Evolution, 2020, 12, 229-242.	1.1	8
5	Draft Genome Sequences of Two Staphylococcus warneri Clinical Isolates, Strains SMA0023-04 (UGA3) and SMA0670-05 (UGA28), from Siaya County Referral Hospital, Siaya, Kenya. Microbiology Resource Announcements, 2019, 8, .	0.3	0
6	Genome Sequence of Staphylococcus pettenkoferi Strain SMA0010-04 (UGA20), a Clinical Isolate from Siaya County Referral Hospital in Siaya, Kenya. Microbiology Resource Announcements, 2019, 8, .	0.3	2
7	Genome Sequence of a Staphylococcus xylosus Clinical Isolate, Strain SMA0341-04 (UGA5), from Siaya County Referral Hospital in Siaya, Kenya. Microbiology Resource Announcements, 2019, 8, .	0.3	2
8	Genome Sequences of a Staphylococcus aureus Clinical Isolate, Strain SMA0034-04 (UGA22), from Siaya County Referral Hospital in Siaya, Kenya. Microbiology Resource Announcements, 2019, 8, .	0.3	1
9	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. BMC Genomics, 2016, 17, 180.	1.2	71
10	Genomic sequences of six botulinum neurotoxin-producing strains representing three clostridial species illustrate the mobility and diversity of botulinum neurotoxin genes. Infection, Genetics and Evolution, 2015, 30, 102-113.	1.0	70
11	Recruiting Human Microbiome Shotgun Data to Site-Specific Reference Genomes. PLoS ONE, 2014, 9, e84963.	1.1	6
12	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. Ecology, 2014, 95, 3190-3202.	1.5	174
13	From Genus to Phylum: Large-Subunit and Internal Transcribed Spacer rRNA Operon Regions Show Similar Classification Accuracies Influenced by Database Composition. Applied and Environmental Microbiology, 2014, 80, 829-840.	1.4	88
14	Molecular Characterization of a Novel Botulinum Neurotoxin Type H Gene. Journal of Infectious Diseases, 2014, 209, 192-202.	1.9	239
15	Complete genome sequence of Arthrobacter sp. strain FB24. Standards in Genomic Sciences, 2013, 9, 106-116.	1.5	17
16	Metagenome Sequence Analysis of Filamentous Microbial Communities Obtained from Geochemically Distinct Geothermal Channels Reveals Specialization of Three Aquificales Lineages. Frontiers in Microbiology, 2013, 4, 84.	1.5	73
17	Clostridium botulinum Strain Af84 Contains Three Neurotoxin Gene Clusters: Bont/A2, bont/F4 and bont/F5. PLoS ONE, 2013, 8, e61205.	1.1	44
18	The AlternativeTranslational Profile That Underlies the Immune-Evasive State of Persistence in Chlamydiaceae Exploits Differential Tryptophan Contents of the Protein Repertoire. Microbiology and Molecular Biology Reviews, 2012, 76, 405-443.	2.9	28

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19	Genomic Comparison of Escherichia coli O104:H4 Isolates from 2009 and 2011 Reveals Plasmid, and Prophage Heterogeneity, Including Shiga Toxin Encoding Phage stx2. PLoS ONE, 2012, 7, e48228.	1.1	118
20	Genome Sequence of Kingella kingae Septic Arthritis Isolate PYKK081. Journal of Bacteriology, 2012, 194, 3017-3017.	1.0	17
21	Saliva microbiomes distinguish caries-active from healthy human populations. ISME Journal, 2012, 6, 1-10.	4.4	320
22	Capturing Single Cell Genomes of Active Polysaccharide Degraders: An Unexpected Contribution of Verrucomicrobia. PLoS ONE, 2012, 7, e35314.	1.1	236
23	Accurate, Rapid Taxonomic Classification of Fungal Large-Subunit rRNA Genes. Applied and Environmental Microbiology, 2012, 78, 1523-1533.	1.4	160
24	Common bacterial responses in six ecosystems exposed to 10 years of elevated atmospheric carbon dioxide. Environmental Microbiology, 2012, 14, 1145-1158.	1.8	79
25	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. Briefings in Functional Genomics, 2011, 10, 322-333.	1.3	41
26	Complete Genome Sequence of a thermotolerant sporogenic lactic acid bacterium, Bacillus coagulans strain 36D1. Standards in Genomic Sciences, 2011, 5, 331-340.	1.5	28
27	An attenuated strain of Bacillus anthracis (CDC 684) has a large chromosomal inversion and altered growth kinetics. BMC Genomics, 2011, 12, 477.	1.2	24
28	Genomics for Key Players in the N Cycle. Methods in Enzymology, 2011, 496, 289-318.	0.4	3
29	Biological Consequences of Ancient Gene Acquisition and Duplication in the Large Genome of Candidatus Solibacter usitatus Ellin6076. PLoS ONE, 2011, 6, e24882.	1.1	60
30	Large Direct Repeats Flank Genomic Rearrangements between a New Clinical Isolate of Francisella tularensis subsp. tularensis A1 and Schu S4. PLoS ONE, 2010, 5, e9007.	1.1	12
31	Comparative genomics of clinical and environmental <i>Vibrio mimicus</i>. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21134-21139.	3.3	52
32	Community and gene composition of a human dental plaque microbiota obtained by metagenomic sequencing. Molecular Oral Microbiology, 2010, 25, 391-405.	1.3	78
33	Dynamics of Streptococcus mutans Transcriptome in Response to Starch and Sucrose during Biofilm Development. PLoS ONE, 2010, 5, e13478.	1.1	106
34	Complete genome of the cellulolytic thermophile <i>Acidothermus cellulolyticus</i> 11B provides insights into its ecophysiological and evolutionary adaptations. Genome Research, 2009, 19, 1033-1043.	2.4	109
35	Cohesion Group Approach for Evolutionary Analysis of Aspartokinase, an Enzyme That Feeds a Branched Network of Many Biochemical Pathways. Microbiology and Molecular Biology Reviews, 2009, 73, 594-651.	2.9	62
36	Novel Features of the Polysaccharide-Digesting Gliding Bacterium <i>Flavobacterium johnsoniae</i> as Revealed by Genome Sequence Analysis. Applied and Environmental Microbiology, 2009, 75, 6864-6875.	1.4	212

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37	Recombination and insertion events involving the botulinum neurotoxin complex genes in Clostridium botulinum types A, B, E and F and Clostridium butyricumtype E strains. BMC Biology, 2009, 7, 66.	1.7	141
38	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1954-1959.	3.3	530
39	Three Genomes from the Phylum<i>Acidobacteria</i>Provide Insight into the Lifestyles of These Microorganisms in Soils. Applied and Environmental Microbiology, 2009, 75, 2046-2056.	1.4	804
40	Complete Genome Sequence of the Chemolithoautotrophic Marine Magnetotactic Coccus Strain MC-1. Applied and Environmental Microbiology, 2009, 75, 4835-4852.	1.4	114
41	Assembling the Marine Metagenome, One Cell at a Time. PLoS ONE, 2009, 4, e5299.	1.1	320
42	Complete Genome Sequence of Francisella tularensis Subspecies holarctica FTNF002-00. PLoS ONE, 2009, 4, e7041.	1.1	47
43	Genome sequencing and analysis of the biomass-degrading fungus Trichoderma reesei (syn. Hypocrea) Tj ETQq1 1 0.784314 rgBT /Over	9.4	1,116
44	The complete genome sequence of<i>Moorella thermoacetica</i>(f.<i>Clostridium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (therm	1.8	256
45	The Complete Genome Sequence of Bacillus thuringiensis Al Hakam. Journal of Bacteriology, 2007, 189, 3680-3681.	1.0	71
46	Genome Sequence of the Cellulolytic Gliding Bacterium Cytophaga hutchinsonii. Applied and Environmental Microbiology, 2007, 73, 3536-3546.	1.4	208
47	Complete Genome Sequence of Haemophilus somnus (Histophilus somni) Strain 129Pt and Comparison to Haemophilus ducreyi 35000HP and Haemophilus influenzae Rd. Journal of Bacteriology, 2007, 189, 1890-1898.	1.0	42
48	Analysis of the Neurotoxin Complex Genes in Clostridium botulinum A1-A4 and B1 Strains: BoNT/A3, /Ba4 and /B1 Clusters Are Located within Plasmids. PLoS ONE, 2007, 2, e1271.	1.1	154
49	Pathogenomic Sequence Analysis of Bacillus cereus and Bacillus thuringiensis Isolates Closely Related to Bacillus anthracis. Journal of Bacteriology, 2006, 188, 3382-3390.	1.0	191
50	A 360-kb interchromosomal duplication of the human HYDIN locus. Genomics, 2006, 88, 762-771.	1.3	52
51	The sequence and analysis of duplication-rich human chromosome 16. Nature, 2004, 432, 988-994.	13.7	156
52	Inter-genomic displacement via lateral gene transfer of bacterial trp operons in an overall context of vertical genealogy. BMC Biology, 2004, 2, 15.	1.7	18
53	Lateral gene transfer and ancient paralogy of operons containing redundant copies of tryptophan-pathway genes in Xylella species and in heterocystous cyanobacteria. Genome Biology, 2003, 4, R14.	13.9	27
54	Ancient Origin of the Tryptophan Operon and the Dynamics of Evolutionary Change. Microbiology and Molecular Biology Reviews, 2003, 67, 303-342.	2.9	125

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55	Dynamic diversity of the tryptophan pathway in chlamydiae: reductive evolution and a novel operon for tryptophan recapture. Genome Biology, 2002, 3, research0051.1.	13.9	50
56	A Probable Mixed-Function Supraoperon in Pseudomonas Exhibits Gene Organization Features of Both Intergenomic Conservation and Gene Shuffling. Journal of Molecular Evolution, 2000, 50, 202-202.	0.8	0
57	A Probable Mixed-Function Supraoperon in Pseudomonas Exhibits Gene Organization Features of Both Intergenomic Conservation and Gene Shuffling. Journal of Molecular Evolution, 1999, 49, 108-121.	0.8	11
58	Comparative analysis of Pseudomonas aeruginosa penicillin-binding protein 7 in the context of its membership in the family of low-molecular-mass PBPs. Microbiology (United Kingdom), 1998, 144, 975-983.	0.7	13