

# Gary Xie

## List of Publications by Year in descending order

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58  
papers

7,022  
citations

101384

36  
h-index

143772

57  
g-index

60  
all docs

60  
docs citations

60  
times ranked

10157  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i> ) Tj ETQq1 1 0.784314 rgBT /Over	9.4	1516
2	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	1.4	804
3	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
4	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012, 6, 1-10.	4.4	320
5	Assembling the Marine Metagenome, One Cell at a Time. <i>PLoS ONE</i> , 2009, 4, e5299.	1.1	320
6	The complete genome sequence of <i>Moorella thermoacetica</i> (f. <i>Clostridium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td (therm	1.8	256
7	Molecular Characterization of a Novel Botulinum Neurotoxin Type H Gene. <i>Journal of Infectious Diseases</i> , 2014, 209, 192-202.	1.9	239
8	Capturing Single Cell Genomes of Active Polysaccharide Degraders: An Unexpected Contribution of Verrucomicrobia. <i>PLoS ONE</i> , 2012, 7, e35314.	1.1	236
9	Novel Features of the Polysaccharide-Digesting Gliding Bacterium <i>Flavobacterium johnsoniae</i> as Revealed by Genome Sequence Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6864-6875.	1.4	212
10	Genome Sequence of the Cellulolytic Gliding Bacterium <i>Cytophaga hutchinsonii</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 3536-3546.	1.4	208
11	Pathogenomic Sequence Analysis of <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> Isolates Closely Related to <i>Bacillus anthracis</i> . <i>Journal of Bacteriology</i> , 2006, 188, 3382-3390.	1.0	191
12	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. <i>Ecology</i> , 2014, 95, 3190-3202.	1.5	174
13	Accurate, Rapid Taxonomic Classification of Fungal Large-Subunit rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1523-1533.	1.4	160
14	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	13.7	156
15	Analysis of the Neurotoxin Complex Genes in <i>Clostridium botulinum</i> A1-A4 and B1 Strains: BoNT/A3, /Ba4 and /B1 Clusters Are Located within Plasmids. <i>PLoS ONE</i> , 2007, 2, e1271.	1.1	154
16	Recombination and insertion events involving the botulinum neurotoxin complex genes in <i>Clostridium botulinum</i> types A, B, E and F and <i>Clostridium butyricum</i> type E strains. <i>BMC Biology</i> , 2009, 7, 66.	1.7	141
17	Ancient Origin of the Tryptophan Operon and the Dynamics of Evolutionary Change. <i>Microbiology and Molecular Biology Reviews</i> , 2003, 67, 303-342.	2.9	125
18	Genomic Comparison of <i>Escherichia coli</i> O104:H4 Isolates from 2009 and 2011 Reveals Plasmid, and Prophage Heterogeneity, Including Shiga Toxin Encoding Phage stx2. <i>PLoS ONE</i> , 2012, 7, e48228.	1.1	118

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19	Complete Genome Sequence of the Chemolithoautotrophic Marine Magnetotactic Coccus Strain MC-1. Applied and Environmental Microbiology, 2009, 75, 4835-4852.	1.4	114
20	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
21	Dynamics of <i>Streptococcus mutans</i> Transcriptome in Response to Starch and Sucrose during Biofilm Development. PLoS ONE, 2010, 5, e13478.	1.1	106
22	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
23	Common bacterial responses in six ecosystems exposed to 10 years of elevated atmospheric carbon dioxide. Environmental Microbiology, 2012, 14, 1145-1158.	1.8	79
24	Community and gene composition of a human dental plaque microbiota obtained by metagenomic sequencing. Molecular Oral Microbiology, 2010, 25, 391-405.	1.3	78
25	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
26	The Complete Genome Sequence of <i>Bacillus thuringiensis</i> Al Hakam. Journal of Bacteriology, 2007, 189, 3680-3681.	1.0	71
27	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. BMC Genomics, 2016, 17, 180.	1.2	71
28	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
29	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
30	Biological Consequences of Ancient Gene Acquisition and Duplication in the Large Genome of <i>Candidatus Solibacter usitatus</i> Ellin6076. PLoS ONE, 2011, 6, e24882.	1.1	60
31	A 360-kb interchromosomal duplication of the human HYDIN locus. Genomics, 2006, 88, 762-771.	1.3	52
32	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
33	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
34	Complete Genome Sequence of <i>Francisella tularensis</i> Subspecies <i>holarctica</i> FTNF002-00. PLoS ONE, 2009, 4, e7041.	1.1	47
35	<i>Clostridium botulinum</i> Strain Af84 Contains Three Neurotoxin Gene Clusters: <i>bont/A2</i> , <i>bont/F4</i> and <i>bont/F5</i> . PLoS ONE, 2013, 8, e61205.	1.1	44
36	Complete Genome Sequence of <i>Haemophilus somnus</i> ( <i>Histophilus somni</i> ) Strain 129Pt and Comparison to <i>Haemophilus ducreyi</i> 35000HP and <i>Haemophilus influenzae</i> Rd. Journal of Bacteriology, 2007, 189, 1890-1898.	1.0	42

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37	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. <i>Briefings in Functional Genomics</i> , 2011, 10, 322-333.	1.3	41
38	Complete Genome Sequence of a thermotolerant sporogenic lactic acid bacterium, <i>Bacillus coagulans</i> strain 36D1. <i>Standards in Genomic Sciences</i> , 2011, 5, 331-340.	1.5	28
39	The Alternative Translational Profile That Underlies the Immune-Evasive State of Persistence in <i>Chlamydiaceae</i> Exploits Differential Tryptophan Contents of the Protein Repertoire. <i>Microbiology and Molecular Biology Reviews</i> , 2012, 76, 405-443.	2.9	28
40	Lateral gene transfer and ancient paralogy of operons containing redundant copies of tryptophan-pathway genes in <i>Xylella</i> species and in heterocystous cyanobacteria. <i>Genome Biology</i> , 2003, 4, R14.	13.9	27
41	An attenuated strain of <i>Bacillus anthracis</i> (CDC 684) has a large chromosomal inversion and altered growth kinetics. <i>BMC Genomics</i> , 2011, 12, 477.	1.2	24
42	Inter-genomic displacement via lateral gene transfer of bacterial trp operons in an overall context of vertical genealogy. <i>BMC Biology</i> , 2004, 2, 15.	1.7	18
43	Genome Sequence of <i>Kingella kingae</i> Septic Arthritis Isolate PYKK081. <i>Journal of Bacteriology</i> , 2012, 194, 3017-3017.	1.0	17
44	Complete genome sequence of <i>Arthrobacter</i> sp. strain FB24. <i>Standards in Genomic Sciences</i> , 2013, 9, 106-116.	1.5	17
45	Comparative analysis of <i>Pseudomonas aeruginosa</i> penicillin-binding protein 7 in the context of its membership in the family of low-molecular-mass PBPs. <i>Microbiology (United Kingdom)</i> , 1998, 144, 975-983.	0.7	13
46	Large Direct Repeats Flank Genomic Rearrangements between a New Clinical Isolate of <i>Francisella tularensis</i> subsp. <i>tularensis</i> A1 and Schu S4. <i>PLoS ONE</i> , 2010, 5, e9007.	1.1	12
47	A Probable Mixed-Function Supraoperon in <i>Pseudomonas</i> Exhibits Gene Organization Features of Both Intergenomic Conservation and Gene Shuffling. <i>Journal of Molecular Evolution</i> , 1999, 49, 108-121.	0.8	11
48	The Distinctive Evolution of orfX <i>Clostridium parbotulinum</i> Strains and Their Botulinum Neurotoxin Type A and F Gene Clusters Is Influenced by Environmental Factors and Gene Interactions via Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 566908.	1.5	11
49	Genomic Characterization of Newly Completed Genomes of Botulinum Neurotoxin-Producing Species from Argentina, Australia, and Africa. <i>Genome Biology and Evolution</i> , 2020, 12, 229-242.	1.1	8
50	Recruiting Human Microbiome Shotgun Data to Site-Specific Reference Genomes. <i>PLoS ONE</i> , 2014, 9, e84963.	1.1	6
51	Hidden Markov Model: a shortest unique representative approach to detect the protein toxins, virulence factors and antibiotic resistance genes. <i>BMC Research Notes</i> , 2021, 14, 122.	0.6	4
52	Genomics for Key Players in the N Cycle. <i>Methods in Enzymology</i> , 2011, 496, 289-318.	0.4	3
53	Comparative genomic and phenotypic characterization of invasive non-typhoidal <i>Salmonella</i> isolates from Siaya, Kenya. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008991.	1.3	3
54	Genome Sequence of <i>Staphylococcus pettenkoferi</i> Strain SMA0010-04 (UGA20), a Clinical Isolate from Siaya County Referral Hospital in Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2

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55	Genome Sequence of a <i>Staphylococcus xylosus</i> Clinical Isolate, Strain SMA0341-04 (UGA5), from Siaya County Referral Hospital in Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
56	Genome Sequences of a <i>Staphylococcus aureus</i> Clinical Isolate, Strain SMA0034-04 (UGA22), from Siaya County Referral Hospital in Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
57	A Probable Mixed-Function Supraoperon in <i>Pseudomonas</i> Exhibits Gene Organization Features of Both Intergenomic Conservation and Gene Shuffling. <i>Journal of Molecular Evolution</i> , 2000, 50, 202-202.	0.8	0
58	Draft Genome Sequences of Two <i>Staphylococcus warneri</i> Clinical Isolates, Strains SMA0023-04 (UGA3) and SMA0670-05 (UGA28), from Siaya County Referral Hospital, Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0