

Yuzhen Ye

List of Publications by Year in Descending Order

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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.

63

papers

5,965

citations

25

h-index

76

g-index

76

ext. papers

7,265

ext. citations

7.8

avg. IF

5.71

L-index

#	Paper	IF	Citations
63	Metaproteomics as a tool for studying the protein landscape of human-gut bacterial species.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009397	5	1
62	Comparison of CRISPR-Cas Immune Systems in Healthcare-Related Pathogens. <i>Frontiers in Microbiology</i> , 2021 , 12, 758782	5.7	2
61	Using high-abundance proteins as guides for fast and effective peptide/protein identification from human gut metaproteomic data. <i>Microbiome</i> , 2021 , 9, 80	16.6	5
60	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021 , 6, 123-135	26.6	16
59	Full-Spectrum Prediction of Peptides Tandem Mass Spectra using Deep Neural Network. <i>Analytical Chemistry</i> , 2020 , 92, 4275-4283	7.8	17
58	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species. <i>PLoS Computational Biology</i> , 2020 , 16, e1007951	5	2
57	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020 , 11, 5281	17.4	19
56	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species 2020 , 16, e1007951		
55	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species 2020 , 16, e1007951		
54	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species 2020 , 16, e1007951		
53	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species 2020 , 16, e1007951		
52	Effect of permafrost thaw on plant and soil fungal community in a boreal forest: Does fungal community change mediate plant productivity response?. <i>Journal of Ecology</i> , 2019 , 107, 1737-1752	6	22
51	A Meta-proteogenomic Approach to Peptide Identification Incorporating Assembly Uncertainty and Genomic Variation. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S183-S192	7.6	11
50	MyDGR: a server for identification and characterization of diversity-generating retroelements. <i>Nucleic Acids Research</i> , 2019 , 47, W289-W294	20.1	10
49	Long reads reveal the diversification and dynamics of CRISPR reservoir in microbiomes. <i>BMC Genomics</i> , 2019 , 20, 567	4.5	6
48	A repository of microbial marker genes related to human health and diseases for host phenotype prediction using microbiome data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019 , 24, 236-247	1.3	2
47	CRISPRs for Strain Tracking and Their Application to Microbiota Transplantation Data Analysis. <i>CRISPR Journal</i> , 2019 , 2, 41-50	2.5	4

46	Not all predicted CRISPR-Cas systems are equal: isolated cas genes and classes of CRISPR like elements. <i>BMC Bioinformatics</i> , 2017 , 18, 92	3.6	89
45	A concurrent subtractive assembly approach for identification of disease associated sub-metagenomes. <i>Lecture Notes in Computer Science</i> , 2017 , 2017, 18-33	0.9	5
44	From Gene Annotation to Function Prediction for Metagenomics. <i>Methods in Molecular Biology</i> , 2017 , 1611, 27-34	1.4	9
43	Functional association prediction by community profiling. <i>Methods</i> , 2017 , 129, 8-17	4.6	3
42	Characterization of CRISPR RNA transcription by exploiting stranded metatranscriptomic data. <i>Rna</i> , 2016 , 22, 945-56	5.8	5
41	Phylogenetically Structured Differences in rRNA Gene Sequence Variation among Species of Arbuscular Mycorrhizal Fungi and Their Implications for Sequence Clustering. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 4921-30	4.8	18
40	A Graph-Centric Approach for Metagenome-Guided Peptide and Protein Identification in Metaproteomics. <i>PLoS Computational Biology</i> , 2016 , 12, e1005224	5	29
39	Genomic and Metagenomic Analysis of Diversity-Generating Retroelements Associated with <i>Treponema denticola</i> . <i>Frontiers in Microbiology</i> , 2016 , 7, 852	5.7	7
38	Strand-specific community RNA-seq reveals prevalent and dynamic antisense transcription in human gut microbiota. <i>Frontiers in Microbiology</i> , 2015 , 6, 896	5.7	20
37	Subtractive assembly for comparative metagenomics, and its application to type 2 diabetes metagenomes. <i>Genome Biology</i> , 2015 , 16, 243	18.3	6
36	Gene finding in metatranscriptomic sequences. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 9, S8	3.6	22
35	POSA: a user-driven, interactive multiple protein structure alignment server. <i>Nucleic Acids Research</i> , 2014 , 42, W240-5	20.1	33
34	Identification of diversity-generating retroelements in human microbiomes. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 14234-46	6.3	23
33	Expanding the catalog of cas genes with metagenomes. <i>Nucleic Acids Research</i> , 2014 , 42, 2448-59	20.1	17
32	CRISPR-Cas systems target a diverse collection of invasive mobile genetic elements in human microbiomes. <i>Genome Biology</i> , 2013 , 14, R40	18.3	45
31	The gain and loss of chromosomal integron systems in the <i>Treponema</i> species. <i>BMC Evolutionary Biology</i> , 2013 , 13, 16	3	12
30	Allosteric inhibition of a zinc-sensing transcriptional repressor: insights into the arsenic repressor (ArsR) family. <i>Journal of Molecular Biology</i> , 2013 , 425, 1143-57	6.5	29
29	Probabilistic inference of biochemical reactions in microbial communities from metagenomic sequences. <i>PLoS Computational Biology</i> , 2013 , 9, e1002981	5	12

28	Oral spirochetes implicated in dental diseases are widespread in normal human subjects and carry extremely diverse integron gene cassettes. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5288-96	4.8	16
27	Diverse CRISPRs evolving in human microbiomes. <i>PLoS Genetics</i> , 2012 , 8, e1002441	6	100
26	RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 125-6	7.2	292
25	A de Bruijn graph approach to the quantification of closely-related genomes in a microbial community. <i>Journal of Computational Biology</i> , 2012 , 19, 814-25	1.7	11
24	Stitching gene fragments with a network matching algorithm improves gene assembly for metagenomics. <i>Bioinformatics</i> , 2012 , 28, i363-i369	7.2	11
23	A core human microbiome as viewed through 16S rRNA sequence clusters. <i>PLoS ONE</i> , 2012 , 7, e34242	3.7	363
22	A Parsimony Approach to Biological Pathway Reconstruction/Inference for Metagenomes 2011 , 453-460		1
21	The ecoresponsive genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011 , 331, 555-61	33.3	924
20	RAPSearch: a fast protein similarity search tool for short reads. <i>BMC Bioinformatics</i> , 2011 , 12, 159	3.6	92
19	A novel abundance-based algorithm for binning metagenomic sequences using l-tuples. <i>Journal of Computational Biology</i> , 2011 , 18, 523-34	1.7	101
18	FragGeneScan: predicting genes in short and error-prone reads. <i>Nucleic Acids Research</i> , 2010 , 38, e191	20.1	535
17	An ORFome assembly approach to metagenomics sequences analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2009 , 7, 455-71	1	31
16	A parsimony approach to biological pathway reconstruction/inference for genomes and metagenomes. <i>PLoS Computational Biology</i> , 2009 , 5, e1000465	5	266
15	Metagenomics: Facts and Artifacts, and Computational Challenges*. <i>Journal of Computer Science and Technology</i> , 2009 , 25, 71-81	1.7	98
14	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008 , 18, 1100-11	9.7	387
13	An ORFome assembly approach to metagenomics sequences analysis. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008 , 7, 3-13		1
12	Subunit-specific roles of glycine-binding domains in activation of NR1/NR3 N-methyl-D-aspartate receptors. <i>Molecular Pharmacology</i> , 2007 , 71, 112-22	4.3	45
11	Modeling and analyzing three-dimensional structures of human disease proteins. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006 , 439-50	1.3	15

10	MODELING AND ANALYZING THREE-DIMENSIONAL STRUCTURES OF HUMAN DISEASE PROTEINS 2005,		3
9	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. <i>Nucleic Acids Research</i> , 2005 , 33, 5691-702	20.1	1485
8	Multiple flexible structure alignment using partial order graphs. <i>Bioinformatics</i> , 2005 , 21, 2362-9	7.2	106
7	Automatic detection of subsystem/pathway variants in genome analysis. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i478-86	7.2	31
6	Comparative analysis of protein domain organization. <i>Genome Research</i> , 2004 , 14, 343-53	9.7	65
5	Database searching by flexible protein structure alignment. <i>Protein Science</i> , 2004 , 13, 1841-50	6.3	38
4	A segment alignment approach to protein comparison. <i>Bioinformatics</i> , 2003 , 19, 742-9	7.2	28
3	Homology modeling provides insights into the binding mode of the PAAD/DAPIN/pyrin domain, a fourth member of the CARD/DD/DED domain family. <i>Protein Science</i> , 2003 , 12, 1872-81	6.3	35
2	Flexible structure alignment by chaining aligned fragment pairs allowing twists. <i>Bioinformatics</i> , 2003 , 19 Suppl 2, ii246-55	7.2	380
1	Identification and Classification of Reverse Transcriptases in Bacterial Genomes and Metagenomes		2