Yuzhen Ye

List of Publications by Citations

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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	5,965	25	76
papers	citations	h-index	g-index
76	7,265	7.8	5.71
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
63	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Research*, **2005**, 33, 5691-702	20.1	1485
62	The ecoresponsive genome of Daphnia pulex. *Science*, **2011**, 331, 555-61	33.3	924
61	FragGeneScan: predicting genes in short and error-prone reads. *Nucleic Acids Research*, **2010**, 38, e191	20.1	535
60	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. *Genome Research*, **2008**, 18, 1100-11	9.7	387
59	Flexible structure alignment by chaining aligned fragment pairs allowing twists. *Bioinformatics*, **2003**, 19 Suppl 2, ii246-55	7.2	380
58	A core human microbiome as viewed through 16S rRNA sequence clusters. *PLoS ONE*, **2012**, 7, e34242	3.7	363
57	RAPSearch2: a fast and memory-efficient protein similarity search tool for next-generation sequencing data. *Bioinformatics*, **2012**, 28, 125-6	7.2	292
56	A parsimony approach to biological pathway reconstruction/inference for genomes and metagenomes. *PLoS Computational Biology*, **2009**, 5, e1000465	5	266
55	Multiple flexible structure alignment using partial order graphs. *Bioinformatics*, **2005**, 21, 2362-9	7.2	106
54	A novel abundance-based algorithm for binning metagenomic sequences using l-tuples. *Journal of Computational Biology*, **2011**, 18, 523-34	1.7	101
53	Diverse CRISPRs evolving in human microbiomes. *PLoS Genetics*, **2012**, 8, e1002441	6	100
52	Metagenomics: Facts and Artifacts, and Computational Challenges*. *Journal of Computer Science and Technology*, **2009**, 25, 71-81	1.7	98
51	RAPSearch: a fast protein similarity search tool for short reads. *BMC Bioinformatics*, **2011**, 12, 159	3.6	92
50	Not all predicted CRISPR-Cas systems are equal: isolated cas genes and classes of CRISPR like elements. *BMC Bioinformatics*, **2017**, 18, 92	3.6	89
49	Comparative analysis of protein domain organization. *Genome Research*, **2004**, 14, 343-53	9.7	65
48	CRISPR-Cas systems target a diverse collection of invasive mobile genetic elements in human microbiomes. *Genome Biology*, **2013**, 14, R40	18.3	45
47	Subunit-specific roles of glycine-binding domains in activation of NR1/NR3 N-methyl-D-aspartate receptors. *Molecular Pharmacology*, **2007**, 71, 112-22	4.3	45

46	Database searching by flexible protein structure alignment. *Protein Science*, **2004**, 13, 1841-50	6.3	38
45	Homology modeling provides insights into the binding mode of the PAAD/DAPIN/pyrin domain, a fourth member of the CARD/DD/DED domain family. *Protein Science*, **2003**, 12, 1872-81	6.3	35
44	POSA: a user-driven, interactive multiple protein structure alignment server. *Nucleic Acids Research*, **2014**, 42, W240-5	20.1	33
43	An ORFome assembly approach to metagenomics sequences analysis. *Journal of Bioinformatics and Computational Biology*, **2009**, 7, 455-71	1	31
42	Automatic detection of subsystem/pathway variants in genome analysis. *Bioinformatics*, **2005**, 21 Suppl 1, i478-86	7.2	31
41	Allosteric inhibition of a zinc-sensing transcriptional repressor: insights into the arsenic repressor (ArsR) family. *Journal of Molecular Biology*, **2013**, 425, 1143-57	6.5	29
40	A Graph-Centric Approach for Metagenome-Guided Peptide and Protein Identification in Metaproteomics. *PLoS Computational Biology*, **2016**, 12, e1005224	5	29
39	A segment alignment approach to protein comparison. *Bioinformatics*, **2003**, 19, 742-9	7.2	28
38	Identification of diversity-generating retroelements in human microbiomes. *International Journal of Molecular Sciences*, **2014**, 15, 14234-46	6.3	23
37	Effect of permafrost thaw on plant and soil fungal community in a boreal forest: Does fungal community change mediate plant productivity response?. *Journal of Ecology*, **2019**, 107, 1737-1752	6	22
36	Gene finding in metatranscriptomic sequences. *BMC Bioinformatics*, **2014**, 15 Suppl 9, S8	3.6	22
35	Strand-specific community RNA-seq reveals prevalent and dynamic antisense transcription in human gut microbiota. *Frontiers in Microbiology*, **2015**, 6, 896	5.7	20
34	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. *Nature Communications*, **2020**, 11, 5281	17.4	19
33	Phylogenetically Structured Differences in rRNA Gene Sequence Variation among Species of Arbuscular Mycorrhizal Fungi and Their Implications for Sequence Clustering. *Applied and Environmental Microbiology*, **2016**, 82, 4921-30	4.8	18
32	Full-Spectrum Prediction of Peptides Tandem Mass Spectra using Deep Neural Network. *Analytical Chemistry*, **2020**, 92, 4275-4283	7.8	17
31	Expanding the catalog of cas genes with metagenomes. *Nucleic Acids Research*, **2014**, 42, 2448-59	20.1	17
30	Oral spirochetes implicated in dental diseases are widespread in normal human subjects and carry extremely diverse integron gene cassettes. *Applied and Environmental Microbiology*, **2012**, 78, 5288-96	4.8	16
29	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. *Nature Microbiology*, **2021**, 6, 123-135	26.6	16

28	Modeling and analyzing three-dimensional structures of human disease proteins. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2006**, 439-50	1.3	15
27	The gain and loss of chromosomal integron systems in the Treponema species. *BMC Evolutionary Biology*, **2013**, 13, 16	3	12
26	Probabilistic inference of biochemical reactions in microbial communities from metagenomic sequences. *PLoS Computational Biology*, **2013**, 9, e1002981	5	12
25	A Meta-proteogenomic Approach to Peptide Identification Incorporating Assembly Uncertainty and Genomic Variation. *Molecular and Cellular Proteomics*, **2019**, 18, S183-S192	7.6	11
24	A de Bruijn graph approach to the quantification of closely-related genomes in a microbial community. *Journal of Computational Biology*, **2012**, 19, 814-25	1.7	11
23	Stitching gene fragments with a network matching algorithm improves gene assembly for metagenomics. *Bioinformatics*, **2012**, 28, i363-i369	7.2	11
22	MyDGR: a server for identification and characterization of diversity-generating retroelements. *Nucleic Acids Research*, **2019**, 47, W289-W294	20.1	10
21	From Gene Annotation to Function Prediction for Metagenomics. *Methods in Molecular Biology*, **2017**, 1611, 27-34	1.4	9
20	Genomic and Metagenomic Analysis of Diversity-Generating Retroelements Associated with Treponema denticola. *Frontiers in Microbiology*, **2016**, 7, 852	5.7	7
19	Long reads reveal the diversification and dynamics of CRISPR reservoir in microbiomes. *BMC Genomics*, **2019**, 20, 567	4.5	6
18	Subtractive assembly for comparative metagenomics, and its application to type 2 diabetes metagenomes. *Genome Biology*, **2015**, 16, 243	18.3	6
17	A concurrent subtractive assembly approach for identification of disease associated sub-metagenomes. *Lecture Notes in Computer Science*, **2017**, 2017, 18-33	0.9	5
16	Characterization of CRISPR RNA transcription by exploiting stranded metatranscriptomic data. *Rna*, **2016**, 22, 945-56	5.8	5
15	Using high-abundance proteins as guides for fast and effective peptide/protein identification from human gut metaproteomic data. *Microbiome*, **2021**, 9, 80	16.6	5
14	CRISPRs for Strain Tracking and Their Application to Microbiota Transplantation Data Analysis. *CRISPR Journal*, **2019**, 2, 41-50	2.5	4
13	Functional association prediction by community profiling. *Methods*, **2017**, 129, 8-17	4.6	3
12	MODELING AND ANALYZING THREE-DIMENSIONAL STRUCTURES OF HUMAN DISEASE PROTEINS **2005**,		3
11	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species. *PLoS Computational Biology*, **2020**, 16, e1007951	5	2

LIST OF PUBLICATIONS

10	A repository of microbial marker genes related to human health and diseases for host phenotype prediction using microbiome data. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2019**, 24, 236-247	1.3	2
9	Comparison of CRISPR-Cas Immune Systems in Healthcare-Related Pathogens. *Frontiers in Microbiology*, **2021**, 12, 758782	5.7	2
8	Identification and Classification of Reverse Transcriptases in Bacterial Genomes and Metagenomes		2
7	A Parsimony Approach to Biological Pathway Reconstruction/Inference for Metagenomes **2011**, 453-460		1
6	An ORFome assembly approach to metagenomics sequences analysis. *Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference*, **2008**, 7, 3-13		1
5	Metaproteomics as a tool for studying the protein landscape of human-gut bacterial species.. *PLoS Computational Biology*, **2022**, 18, e1009397	5	1
4	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species **2020**, 16, e1007951		
3	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species **2020**, 16, e1007951		
2	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species **2020**, 16, e1007951		
1	Model-based and phylogenetically adjusted quantification of metabolic interaction between microbial species **2020**, 16, e1007951		