Weizhong Li

List of Publications by Year
in descending order

65	47,371	117453	106150
papers	citations	34	65
		h-index	g-index

68	68	68	67870
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Molecular Systems Biology, 2011, 7, 539.	3.2	12,778
2	Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. Bioinformatics, 2006, 22, 1658-1659.	1.8	8,965
3	CD-HIT: accelerated for clustering the next-generation sequencing data. Bioinformatics, 2012, 28, 3150-3152.	1.8	7,030
4	InterProScan 5: genome-scale protein function classification. Bioinformatics, 2014, 30, 1236-1240.	1.8	6,553
5	CD-HIT Suite: a web server for clustering and comparing biological sequences. Bioinformatics, 2010, 26, 680-682.	1.8	2,254
6	A new bioinformatics analysis tools framework at EMBL-EBI. Nucleic Acids Research, 2010, 38, W695-W699.	6.5	1,553
7	Analysis Tool Web Services from the EMBL-EBI. Nucleic Acids Research, 2013, 41, W597-W600.	6.5	1,483
8	The EMBL-EBI bioinformatics web and programmatic tools framework. Nucleic Acids Research, 2015, 43, W580-W584.	6.5	934
9	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	2.6	736
10	FFAS03: a server for profile-profile sequence alignments. Nucleic Acids Research, 2005, 33, W284-W288.	6.5	522
11	Interplay between the human gut microbiome and host metabolism. Nature Communications, 2019, 10, 4505.	5.8	450
12	Deep Learning and Its Applications in Biomedicine. Genomics, Proteomics and Bioinformatics, 2018, 16, 17-32.	3.0	420
13	Coping with cold: An integrative, multitissue analysis of the transcriptome of a poikilothermic vertebrate. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16970-16975.	3.3	410
14	Ultrafast clustering algorithms for metagenomic sequence analysis. Briefings in Bioinformatics, 2012, 13, 656-668.	3.2	403
15	Community cyberinfrastructure for Advanced Microbial Ecology Research and Analysis: the CAMERA resource. Nucleic Acids Research, 2011, 39, D546-D551.	6.5	291
16	Alterations in the Porcine Colon Microbiota Induced by the Gastrointestinal Nematode Trichuris suis. Infection and Immunity, 2012, 80, 2150-2157.	1.0	208
17	Identification of ribosomal RNA genes in metagenomic fragments. Bioinformatics, 2009, 25, 1338-1340.	1.8	207
18	Genomic signatures of mitonuclear coevolution across populations of Tigriopus californicus. Nature Ecology and Evolution, 2018, 2, 1250-1257.	3.4	154

#	Article	IF	Citations
19	Occurrence of phosphate acquisition genes in *Prochlorococcus* cells from different ocean regions. Environmental Microbiology, 2009, 11, 1340-1347.	1.8	149
20	Seasonally hibernating phenotype assessed through transcript screening. Physiological Genomics, 2006, 24, 13-22.	1.0	138
21	Worm Burden-Dependent Disruption of the Porcine Colon Microbiota by Trichuris suis Infection. PLoS ONE, 2012, 7, e35470.	1.1	138
22	The effect of helminth infection on the microbial composition and structure of the caprine abomasal microbiome. Scientific Reports, 2016, 6, 20606.	1.6	129
23	Analysis and comparison of very large metagenomes with fast clustering and functional annotation. BMC Bioinformatics, 2009, 10, 359.	1.2	114
24	Impact of intrapartum and postnatal antibiotics on the gut microbiome and emergence of antimicrobial resistance in infants. Scientific Reports, 2019, 9, 10635.	1.6	106
25	A Unique Substrate Recognition Profile for Matrix Metalloproteinase-2. Journal of Biological Chemistry, 2002, 277, 4485-4491.	1.6	103
26	A Unique Substrate Binding Mode Discriminates Membrane Type-1 Matrix Metalloproteinase from Other Matrix Metalloproteinases. Journal of Biological Chemistry, 2002, 277, 23788-23793.	1.6	84
27	FR-HIT, a very fast program to recruit metagenomic reads to homologous reference genomes. Bioinformatics, 2011, 27, 1704-1705.	1.8	76
28	In search for more accurate alignments in the twilight zone. Protein Science, 2009, 11, 1702-1713.	3.1	72
29	Web services at the European Bioinformatics Institute-2009. Nucleic Acids Research, 2009, 37, W6-W10.	6.5	65
30	Cutaneous immune responses in the common carp detected using transcript analysis. Molecular Immunology, 2007, 44, 1664-1679.	1.0	64
31	Deep learning-based six-type classifier for lung cancer and mimics from histopathological whole slide images: a retrospective study. BMC Medicine, 2021, 19, 80.	2.3	61
32	Transcriptome Characterization by RNA-seq Unravels the Mechanisms of Butyrate-Induced Epigenomic Regulation in Bovine Cells. PLoS ONE, 2012, 7, e36940.	1.1	44
33	A Residue in the S2 Subsite Controls Substrate Selectivity of Matrix Metalloproteinase-2 and Matrix Metalloproteinase-9. Journal of Biological Chemistry, 2003, 278, 17158-17163.	1.6	43
34	Gene identification and protein classification in microbial metagenomic sequence data via incremental clustering. BMC Bioinformatics, 2008, 9, 182.	1.2	42
35	Vertical Transmission of Gut Microbiome and Antimicrobial Resistance Genes in Infants Exposed to Antibiotics at Birth. Journal of Infectious Diseases, 2021, 224, 1236-1246.	1.9	41
36	Benchmarking variant callers in next-generation and third-generation sequencing analysis. Briefings in Bioinformatics, 2021, 22, .	3.2	40

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37	The EBI Search engine: providing search and retrieval functionality for biological data from EMBL-EBI. Nucleic Acids Research, 2015, 43, W585-W588.	6.5	37
38	Content discovery and retrieval services at the European Nucleotide Archive. Nucleic Acids Research, 2015, 43, D23-D29.	6.5	36
39	PSI-Search: iterative HOE-reduced profile SSEARCH searching. Bioinformatics, 2012, 28, 1650-1651.	1.8	34
40	Assembly information services in the European Nucleotide Archive. Nucleic Acids Research, 2014, 42, D38-D43.	6.5	33
41	A segment alignment approach to protein comparison. Bioinformatics, 2003, 19, 742-749.	1.8	31
42	Probing Metagenomics by Rapid Cluster Analysis of Very Large Datasets. PLoS ONE, 2008, 3, e3375.	1.1	30
43	Computational resources associating diseases with genotypes, phenotypes and exposures. Briefings in Bioinformatics, 2019, 20, 2098-2115.	3.2	27
44	ncRPheno: a comprehensive database platform for identification and validation of disease related noncoding RNAs. RNA Biology, 2020, 17, 943-955.	1.5	23
45	A Fast Clustering Algorithm for Analyzing Highly Similar Compounds of Very Large Libraries. Journal of Chemical Information and Modeling, 2006, 46, 1919-1923.	2.5	20
46	Identification of a cytokine-dominated immunosuppressive class in squamous cell lung carcinoma with implications for immunotherapy resistance. Genome Medicine, 2022, 14, .	3.6	20
47	Query-seeded iterative sequence similarity searching improves selectivity 5â€"20-fold. Nucleic Acids Research, 2017, 45, e46-e46.	6.5	19
48	MicroPhenoDB Associates Metagenomic Data with Pathogenic Microbes, Microbial Core Genes, and Human Disease Phenotypes. Genomics, Proteomics and Bioinformatics, 2020, 18, 760-772.	3.0	19
49	Transcriptomic Sequencing Reveals a Set of Unique Genes Activated by Butyrate-Induced Histone Modification. Gene Regulation and Systems Biology, 2016, 10, GRSB.S35607.	2.3	18
50	Using EMBLâ€"EBI Services via Web Interface and Programmatically via Web Services. Current Protocols in Bioinformatics, 2014, 48, 3.12.1-50.	25.8	17
51	The Annotation-enriched non-redundant patent sequence databases. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat005.	1.4	15
52	Alternative Splicing Regulated by Butyrate in Bovine Epithelial Cells. PLoS ONE, 2012, 7, e39182.	1.1	13
53	Metagenomic Insights into the RDX-Degrading Potential of the Ovine Rumen Microbiome. PLoS ONE, 2014, 9, e110505.	1.1	13
54	ncRNAVar: A Manually Curated Database for Identification of Noncoding RNA Variants Associated with Human Diseases. Journal of Molecular Biology, 2021, 433, 166727.	2.0	12

#	Article	IF	Citations
55	A whole-slide image (WSI)-based immunohistochemical feature prediction system improves the subtyping of lung cancer. Lung Cancer, 2022, 165, 18-27.	0.9	12
56	VISSA: a program to visualize structural features from structure sequence alignment. Bioinformatics, 2006, 22, 887-888.	1.8	11
57	Non-redundant patent sequence databases with value-added annotations at two levels. Nucleic Acids Research, 2010, 38, D52-D56.	6.5	11
58	Web-based bioinformatics workflows for end-to-end RNA-seq data computation and analysis in agricultural animal species. BMC Genomics, 2016, 17, 761.	1.2	11
59	Cytokine storm promoting T cell exhaustion in severe COVID-19 revealed by single cell sequencing data analysis. Precision Clinical Medicine, 2022, 5, .	1.3	11
60	Splice variants and regulatory networks associated with host resistance to the intestinal worm Cooperia oncophora in cattle. Veterinary Parasitology, 2015, 211, 241-250.	0.7	6
61	Microbial Species that Initially Colonize the Human Gut at Birth or in Early Childhood Can Stay in Human Body for Lifetime. Microbial Ecology, 2021, 82, 1074-1079.	1.4	6
62	CanImmunother: a manually curated database for identification of cancer immunotherapies associating with biomarkers, targets, and clinical effects. OncoImmunology, 2021, 10, 1944553.	2.1	5
63	Application of ESTs in Microarray Analysis. Methods in Molecular Biology, 2009, 533, 289-309.	0.4	3
64	ExprAlign - the identification of ESTs in non-model species by alignment of cDNA microarray expression profiles. BMC Genomics, 2009, 10, 560.	1.2	1
65	Combined alignments of sequences and domains characterize unknown proteins with remotely related protein search PSISearch2D. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	1