Shuai Cheng Li

List of Publications by Year
in descending order

150	4,127	201674	149698
papers	citations	27	56
		h-index	g-index

184	184	184	6525
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Altered metabolome and microbiome features provide clues in understanding irritable bowel syndrome and depression comorbidity. ISME Journal, 2022, 16, 983-996.	9.8	36
2	Alteration of the respiratory microbiome in COVID-19 patients with different severities. Journal of Genetics and Genomics, 2022, 49, 258-261.	3.9	7
3	Over‐shedding of donor‐derived cell‐free DNA at immune‐related regions into plasma of lung transplant recipient. Clinical and Translational Medicine, 2022, 12, e622.	4.0	1
4	PRCTC: a machine learning model for prediction of response to corticosteroid therapy in COVID-19 patients. Aging, 2022, 14, 54-72.	3.1	1
5	Both simulation and sequencing data reveal coinfections with multiple SARS-CoV-2 variants in the COVID-19 pandemic. Computational and Structural Biotechnology Journal, 2022, 20, 1389-1401.	4.1	7
6	Microbiome Resilience and Health Implications for People in Half-Year Travel. Frontiers in Immunology, 2022, 13, 848994.	4.8	2
7	Dynamic changes of gut microbiota and hepatic functions are different among biliary atresia patients after Kasai portoenterostomy. Clinical and Translational Medicine, 2022, 12, e728.	4.0	1
8	Detecting TAD-like domains from RNA-associated interactions. Nucleic Acids Research, 2022, 50, e88-e88.	14.5	7
9	The Tibetan-Yi region is both a corridor and a barrier for human gene flow. Cell Reports, 2022, 39, 110720.	6.4	8
10	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate *Mesodinium rubrum*. ISME Journal, 2021, 15, 1056-1072.	9.8	15
11	PStrain: an iterative microbial strains profiling algorithm for shotgun metagenomic sequencing data. Bioinformatics, 2021, 36, 5499-5506.	4.1	14
12	SuperTAD: robust detection of hierarchical topologically associated domains with optimized structural information. Genome Biology, 2021, 22, 45.	8.8	12
13	Altered nitric oxide induced by gut microbiota reveals the connection between central precocious puberty and obesity. Clinical and Translational Medicine, 2021, 11, e299.	4.0	13
14	Development and validation of an online model to predict critical COVID-19 with immune-inflammatory parameters. Journal of Intensive Care, 2021, 9, 19.	2.9	7
15	Editorial: Computational Methods in Inferring Cancer Tissue-of-Origin and Cancer Molecular Classification. Frontiers in Genetics, 2021, 12, 644542.	2.3	2
16	Longitudinal virological changes and underlying pathogenesis in hospitalized COVID-19 patients in Guangzhou, China. Science China Life Sciences, 2021, 64, 2129-2143.	4.9	3
17	Deep learning model reveals potential risk genes for ADHD, especially Ephrin receptor gene EPHA5. Briefings in Bioinformatics, 2021, 22, .	6.5	11
18	Cervicovaginal Microbiome Factors in Clearance of Human Papillomavirus Infection. Frontiers in Oncology, 2021, 11, 722639.	2.8	13

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19	Transcriptome Atlas of 16 Donkey Tissues. Frontiers in Genetics, 2021, 12, 682734.	2.3	8
20	SpecHap: a diploid phasing algorithm based on spectral graph theory. Nucleic Acids Research, 2021, 49, e114.	14.5	6
21	Whole‐genome sequencing identifies novel candidate pathogenic variants associated with left ventricular non‐compaction in a three‐generation family. Clinical and Translational Medicine, 2021, 11, e501.	4.0	1
22	Resolving complex structures at oncovirus integration loci with conjugate graph. Briefings in Bioinformatics, 2021, 22, .	6.5	8
23	Differential perturbations of gut microbial profiles and co‐occurrence networks among phases of methamphetamine‐induced conditioned place preference. Journal of Neuroscience Research, 2021, 99, 2860-2873.	2.9	9
24	Somatic variant analysis suite: copy number variation clonal visualization online platform for large-scale single-cell genomics. Briefings in Bioinformatics, 2021, , .	6.5	9
25	SCYN: single cell CNV profiling method using dynamic programming. BMC Genomics, 2021, 22, 651.	2.8	1
26	The genome variation and developmental transcriptome maps reveal genetic differentiation of skeletal muscle in pigs. PLoS Genetics, 2021, 17, e1009910.	3.5	22
27	Functional organization of the maternal and paternal human 4D Nucleome. IScience, 2021, 24, 103452.	4.1	10
28	Periodontal and Peri-Implant Microbiome Dysbiosis Is Associated With Alterations in the Microbial Community Structure and Local Stability. Frontiers in Microbiology, 2021, 12, 785191.	3.5	14
29	Understanding Horizontal Gene Transfer network in human gut microbiota. Gut Pathogens, 2020, 12, 33.	3.4	14
30	I-Impute: a self-consistent method to impute single cell RNA sequencing data. BMC Genomics, 2020, 21, 618.	2.8	6
31	Breastfeeding restored the gut microbiota in caesarean section infants and lowered the infection risk in early life. BMC Pediatrics, 2020, 20, 532.	1.7	17
32	Donkey genomes provide new insights into domestication and selection for coat color. Nature Communications, 2020, 11, 6014.	12.8	63
33	A comprehensive investigation of metagenome assembly by linked-read sequencing. Microbiome, 2020, 8, 156.	11.1	12
34	Distinct Skin Microbiota Imbalance and Responses to Clinical Treatment in Children With Atopic Dermatitis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 336.	3.9	10
35	CIRPMC: An online model with simplified inflammatory signature to predict the occurrence of critical illness in patients with COVID‐19. Clinical and Translational Medicine, 2020, 10, e210.	4.0	5
36	Is antibiotics prescription needed in infants with topical corticosteroids treatment for moderate‐to‐severe atopic dermatitis?. Dermatologic Therapy, 2020, 33, e14215.	1.7	2

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37	Heterogeneity of immune microenvironment in ovarian cancer and its clinical significance: a retrospective study. OncoImmunology, 2020, 9, 1760067.	4.6	29
38	Oviz-Bio: a web-based platform for interactive cancer genomics data visualization. Nucleic Acids Research, 2020, 48, W415-W426.	14.5	17
39	Establishing high-accuracy biomarkers for colorectal cancer by comparing fecal microbiomes in patients with healthy families. Gut Microbes, 2020, 11, 918-929.	9.8	38
40	Different nasopharynx and oropharynx microbiota imbalance in children with Mycoplasma pneumoniae or influenza virus infection. Microbial Pathogenesis, 2020, 144, 104189.	2.9	12
41	LDscaff: LD-based scaffolding of de novo genome assemblies. BMC Bioinformatics, 2020, 21, 570.	2.6	3
42	Deep learning for HGT insertion sites recognition. BMC Genomics, 2020, 21, 893.	2.8	1
43	An integrated respiratory microbial gene catalogue to better understand the microbial aetiology of Mycoplasma pneumoniae pneumonia. GigaScience, 2019, 8, .	6.4	16
44	Lung Microbiota and Pulmonary Inflammatory Cytokines Expression Vary in Children With Tracheomalacia and Adenoviral or Mycoplasma pneumoniae Pneumonia. Frontiers in Pediatrics, 2019, 7, 265.	1.9	21
45	SCDevDB: A Database for Insights Into Single-Cell Gene Expression Profiles During Human Developmental Processes. Frontiers in Genetics, 2019, 10, 903.	2.3	14
46	D-GPM: A Deep Learning Method for Gene Promoter Methylation Inference. Genes, 2019, 10, 807.	2.4	13
47	DNA Methylation Markers for Pan-Cancer Prediction by Deep Learning. Genes, 2019, 10, 778.	2.4	55
48	A draft genome assembly of the solar-powered sea slug Elysia chlorotica. Scientific Data, 2019, 6, 190022.	5.3	48
49	Analysis and comparison of long non‐codingRNAs expressed in the ovaries of Meishan and Yorkshire pigs. Animal Genetics, 2019, 50, 660-669.	1.7	5
50	Distinct Gut Microbiota Composition and Functional Category in Children With Cerebral Palsy and Epilepsy. Frontiers in Pediatrics, 2019, 7, 394.	1.9	46
51	Discrepant gut microbiota markers for the classification of obesity-related metabolic abnormalities. Scientific Reports, 2019, 9, 13424.	3.3	235
52	Genome-Wide Investigation and Functional Analysis of Sus scrofa RNA Editing Sites across Eleven Tissues. Genes, 2019, 10, 327.	2.4	12
53	Large-scale 3D chromatin reconstruction from chromosomal contacts. BMC Genomics, 2019, 20, 186.	2.8	8
54	LysoPhD: predicting functional prophages in bacterial genomes from high-throughput sequencing. , 2019, , .		4

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55	LEMON: a method to construct the local strains at horizontal gene transfer sites in gut metagenomics. BMC Bioinformatics, 2019, 20, 702.	2.6	8
56	Intestinal Bacteroides sp. Imbalance Associated With the Occurrence of Childhood Undernutrition in China. Frontiers in Microbiology, 2019, 10, 2635.	3.5	9
57	MIRIA: a webserver for statistical, visual and meta-analysis of RNA editing data in mammals. BMC Bioinformatics, 2019, 20, 596.	2.6	3
58	A unified STR profiling system across multiple species with whole genome sequencing data. BMC Bioinformatics, 2019, 20, 671.	2.6	11
59	DeepMF: deciphering the latent patterns in omics profiles with a deep learning method. BMC Bioinformatics, 2019, 20, 648.	2.6	11
60	SpliceFinder: ab initio prediction of splice sites using convolutional neural network. BMC Bioinformatics, 2019, 20, 652.	2.6	40
61	Resilience of human gut microbial communities for the long stay with multiple dietary shifts. Gut, 2019, 68, 2254-2255.	12.1	45
62	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. Nature Communications, 2018, 9, 1276.	12.8	80
63	KDiamend: a package for detecting key drivers in a molecular ecological network of disease. BMC Systems Biology, 2018, 12, 5.	3.0	5
64	NGS-based likelihood ratio for identifying contributors in two- and three-person DNA mixtures. Computational Biology and Chemistry, 2018, 74, 428-433.	2.3	1
65	In silico design of MHC class I high binding affinity peptides through motifs activation map. BMC Bioinformatics, 2018, 19, 516.	2.6	9
66	Guest Editorial for the 15th Asia Pacific Bioinformatics Conference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1513-1514.	3.0	0
67	Origin and evolution of qingke barley in Tibet. Nature Communications, 2018, 9, 5433.	12.8	141
68	Alterations of Gut Microbiota in Cholestatic Infants and Their Correlation With Hepatic Function. Frontiers in Microbiology, 2018, 9, 2682.	3.5	42
69	Coding mutations inNUS1contribute to Parkinson's disease. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11567-11572.	7.1	78
70	The concordance between upper and lower respiratory microbiota in children with <i>Mycoplasma pneumoniae</i> pneumonia. Emerging Microbes and Infections, 2018, 7, 1-8.	6.5	29
71	Microbiota Composition in Upper Respiratory Tracts of Healthy Children in Shenzhen, China, Differed with Respiratory Sites and Ages. BioMed Research International, 2018, 2018, 1-8.	1.9	40
72	Placing Segments on Parallel Arcs. Lecture Notes in Computer Science, 2018, , 298-310.	1.3	0

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73	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	7.8	99
74	Search for More Effective Microsatellite Markers for Forensics With Next-Generation Sequencing. IEEE Transactions on Nanobioscience, 2017, 16, 375-381.	3.3	2
75	Improving protein fold recognition by extracting fold-specific features from predicted residue–residue contacts. Bioinformatics, 2017, 33, 3749-3757.	4.1	47
76	Dynamic oropharyngeal and faecal microbiota during treatment in infants hospitalized for bronchiolitis compared with age-matched healthy subjects. Scientific Reports, 2017, 7, 11266.	3.3	8
77	The SNP-set based association study identifies ITGA1 as a susceptibility gene of attention-deficit/hyperactivity disorder in Han Chinese. Translational Psychiatry, 2017, 7, e1201-e1201.	4.8	11
78	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. BMC Genomics, 2017, 18, 268.	2.8	11
79	Identification of MicroRNA Targets of Capsicum spp. Using MiRTrans–a Trans-Omics Approach. Frontiers in Plant Science, 2017, 8, 495.	3.6	5
80	The Alteration of Nasopharyngeal and Oropharyngeal Microbiota in Children with MPP and Non-MPP. Genes, 2017, 8, 380.	2.4	16
81	Mycoplasma pneumoniae and Streptococcus pneumoniae caused different microbial structure and correlation network in lung microbiota. Journal of Thoracic Disease, 2016, 8, 1316-1322.	1.4	23
82	Eliminating heterozygosity from reads through coverage normalization. , 2016, , .		0
83	More accurate models for detecting gene-gene interactions from public expression compendia. , 2016, , .		1
84	Finding more effective microsatellite markers for forensics. , 2016, , .		1
85	Improving residue–residue contact prediction via low-rank and sparse decomposition of residue correlation matrix. Biochemical and Biophysical Research Communications, 2016, 472, 217-222.	2.1	19
86	A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in Capsicum. Scientific Reports, 2016, 6, 18919.	3.3	60
87	Insights into the transmission of respiratory infectious diseases through empirical human contact networks. Scientific Reports, 2016, 6, 31484.	3.3	16
88	Reconstructing directed gene regulatory network by only gene expression data. BMC Genomics, 2016, 17, 430.	2.8	13
89	Protein–protein interface prediction based on hexagon structure similarity. Computational Biology and Chemistry, 2016, 63, 83-88.	2.3	13
90	Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. American Journal of Human Genetics, 2016, 98, 256-274.	6.2	109

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91	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. Bioinformatics, 2016, 32, 462-464.	4.1	34
92	Structural neighboring property for identifying protein-protein binding sites. BMC Systems Biology, 2015, 9, S3.	3.0	5
93	Compare local pocket and global protein structure models by small structure patterns. , 2015, , .		3
94	Reconstructing directed gene regulatory network by only gene expression data. , 2015, , .		0
95	Genome-wide profiling of HPV integration in cervical cancer identifies clustered genomic hot spots and a potential microhomology-mediated integration mechanism. Nature Genetics, 2015, 47, 158-163.	21.4	393
96	Parameterized BLOSUM Matrices for Protein Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 686-694.	3.0	13
97	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. Nature Communications, 2015, 6, 8212.	12.8	146
98	Identification of Glycopeptides with Multiple Hydroxylysine O-Glycosylation Sites by Tandem Mass Spectrometry. Journal of Proteome Research, 2015, 14, 5099-5108.	3.7	13
99	Finding All Longest Common Segments in Protein Structures Efficiently. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 644-655.	3.0	1
100	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5135-5140.	7.1	674
101	MHC binding prediction with KernelRLSpan and its variations. Journal of Immunological Methods, 2014, 406, 10-20.	1.4	9
102	Fingerprinting protein structures effectively and efficiently. Bioinformatics, 2014, 30, 949-955.	4.1	9
103	Spectral probabilities of top-down tandem mass spectra. BMC Genomics, 2014, 15, S9.	2.8	14
104	Probabilistic Models for Capturing More Physicochemical Properties on Protein–Protein Interface. Journal of Chemical Information and Modeling, 2014, 54, 1798-1809.	5.4	13
105	Quantifying Significance of MHC II Residues. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 17-25.	3.0	0
106	Residue-Specific Side-Chain Polymorphisms via Particle Belief Propagation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 33-41.	3.0	2
107	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	12.8	124
108	Protein Structure Idealization: How accurately is it possible to model protein structures with dihedral angles?. Algorithms for Molecular Biology, 2013, 8, 5.	1.2	2

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109	The difficulty of protein structure alignment under the RMSD. Algorithms for Molecular Biology, 2013, 8, 1.	1.2	36
110	LoopWeaver: Loop Modeling by the Weighted Scaling of Verified Proteins. Journal of Computational Biology, 2013, 20, 212-223.	1.6	13
111	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. Journal of Computational Biology, 2013, 20, 765-779.	1.6	7
112	Towards Reliable Automatic Protein Structure Alignment. Lecture Notes in Computer Science, 2013, , 18-32.	1.3	6
113	Evaporation of Droplets on Superhydrophobic Surfaces: Surface Roughness and Small Droplet Size Effects. Physical Review Letters, 2012, 109, 116101.	7.8	176
114	Publisher's Note: Evaporation of Droplets on Superhydrophobic Surfaces: Surface Roughness and Small Droplet Size Effects [Phys. Rev. Lett.109, 116101 (2012)]. Physical Review Letters, 2012, 109, .	7.8	7
115	Clustering 100,000 Protein Structure Decoys in Minutes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 765-773.	3.0	8
116	Protein-protein binding site identification by enumerating the configurations. BMC Bioinformatics, 2012, 13, 158.	2.6	57
117	Residues with Similar Hexagon Neighborhoods Share Similar Side-Chain Conformations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 240-248.	3.0	2
118	LoopWeaver – Loop Modeling by the Weighted Scaling of Verified Proteins. Lecture Notes in Computer Science, 2012, , 113-126.	1.3	2
119	P-Binder: A System for the Protein-Protein Binding Sites Identification. Lecture Notes in Computer Science, 2012, , 127-138.	1.3	6
120	How Accurately Can We Model Protein Structures with Dihedral Angles?. Lecture Notes in Computer Science, 2012, , 274-287.	1.3	0
121	Finding Longest Common Segments in Protein Structures in Nearly Linear Time. Lecture Notes in Computer Science, 2012, , 334-348.	1.3	0
122	Protein–Protein Binding Sites Prediction by 3D Structural Similarities. Journal of Chemical Information and Modeling, 2011, 51, 3287-3294.	5.4	10
123	On protein structure alignment under distance constraint. Theoretical Computer Science, 2011, 412, 4187-4199.	0.9	8
124	Incorporating Ab Initio energy into threading approaches for protein structure prediction. BMC Bioinformatics, 2011, 12, S54.	2.6	7
125	Pedigree Reconstruction Using Identity by Descent. Journal of Computational Biology, 2011, 18, 1481-1493.	1.6	25
126	Finding Nearly Optimal GDT Scores. Journal of Computational Biology, 2011, 18, 693-704.	1.6	8

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127	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. Journal of Bioinformatics and Computational Biology, 2011, 09, 15-41.	0.8	18
128	Calibur: a tool for clustering large numbers of protein decoys. BMC Bioinformatics, 2010, 11, 25.	2.6	64
129	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 867-884.	0.8	19
130	PREDICTING LOCAL QUALITY OF A SEQUENCEâ€"STRUCTURE ALIGNMENT. Journal of Bioinformatics and Computational Biology, 2009, 07, 789-810.	0.8	4
131	Finding compact structural motifs. Theoretical Computer Science, 2009, 410, 2834-2839.	0.9	1
132	On two open problems of 2-interval patterns. Theoretical Computer Science, 2009, 410, 2410-2423.	0.9	4
133	On Protein Structure Alignment under Distance Constraint. Lecture Notes in Computer Science, 2009, , 65-76.	1.3	5
134	Discriminative learning for protein conformation sampling. Proteins: Structure, Function and Bioinformatics, 2008, 73, 228-240.	2.6	35
135	Fragmentâ€HMM: A new approach to protein structure prediction. Protein Science, 2008, 17, 1925-1934.	7.6	57
136	Designing succinct structural alphabets. Bioinformatics, 2008, 24, i182-i189.	4.1	11
137	A PTAS For The k-Consensus Structures Problem Under Squared Euclidean Distance. Algorithms, 2008, 1, 43-51.	2.1	2
138	Finding Largest Well-Predicted Subset of Protein Structure Models. , 2008, , 44-55.		11
139	A PTAS for the k-Consensus Structures Problem Under Euclidean Squared Distance. , 2008, , 35-44.		0
140	Finding Compact Structural Motifs. Lecture Notes in Computer Science, 2007, , 142-149.	1.3	5
141	FragQA: predicting local fragment quality of a sequence-structure alignment. , 2007, , .		2
142	CONSENSUS CONTACT PREDICTION BY LINEAR PROGRAMMING. , 2007, , .		0
143	New Algorithms for the Spaced Seeds. , 2007, , 50-61.		0
144	FragQA: predicting local fragment quality of a sequence-structure alignment. Genome Informatics, 2007, 19, 27-39.	0.4	6

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145	On the Complexity of the Crossing Contact Map Pattern Matching Problem. Lecture Notes in Computer Science, 2006, , 231-241.	1.3	3
146	Indexing DNA Sequences Using q-Grams. Lecture Notes in Computer Science, 2005, , 4-16.	1.3	21
147	Piers. SIGMOD Record, 2004, 33, 39-44.	1.2	13
148	New Approximation Algorithms for Some Dynamic Storage Allocation Problems. Lecture Notes in Computer Science, 2004, , 339-348.	1.3	5
149	Development and Validation of a Machine Learning Model for Prediction of Response to Corticosteroid Therapy In COVID-19 Patients. SSRN Electronic Journal, 0, , .	0.4	1
150	A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in Capsicum. , 0, .		1