Shuai Cheng Li

List of Publications by Citations

148 papers	2,498 citations	22 h-index	46 g-index
184 ext. papers	3,420 ext. citations	5.7 avg, IF	4.68 L-index

#	Paper	IF	Citations
148	Whole-genome sequencing of cultivated and wild peppers provides insights into Capsicum domestication and specialization. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 5135-40	11.5	466
147	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, 158-63	36.3	264
146	Evaporation of droplets on superhydrophobic surfaces: surface roughness and small droplet size effects. *Physical Review Letters*, **2012**, 109, 116101	7.4	137
145	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. *Nature Communications*, **2015**, 6, 8212	17.4	111
144	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. *Nature Communications*, **2014**, 5, 3966	17.4	101
143	Discrepant gut microbiota markers for the classification of obesity-related metabolic abnormalities. *Scientific Reports*, **2019**, 9, 13424	4.9	99
142	Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. *American Journal of Human Genetics*, **2016**, 98, 256-74	11	87
141	Origin and evolution of qingke barley in Tibet. *Nature Communications*, **2018**, 9, 5433	17.4	65
140	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. *Nature Ecology and Evolution*, **2017**, 1, 59	12.3	61
139	Calibur: a tool for clustering large numbers of protein decoys. *BMC Bioinformatics*, **2010**, 11, 25	3.6	53
138	Coding mutations in contribute to Parkinson's disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 11567-11572	11.5	50
137	Fragment-HMM: a new approach to protein structure prediction. *Protein Science*, **2008**, 17, 1925-34	6.3	48
136	A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in Capsicum. *Scientific Reports*, **2016**, 6, 18919	4.9	43
135	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. *Nature Communications*, **2018**, 9, 1276	17.4	37
134	Protein-protein binding site identification by enumerating the configurations. *BMC Bioinformatics*, **2012**, 13, 158	3.6	33
133	Improving protein fold recognition by extracting fold-specific features from predicted residue-residue contacts. *Bioinformatics*, **2017**, 33, 3749-3757	7.2	31
132	A draft genome assembly of the solar-powered sea slug Elysia chlorotica. *Scientific Data*, **2019**, 6, 190022	3.2	30

131	Discriminative learning for protein conformation sampling. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 228-40	4.2	30
130	Resilience of human gut microbial communities for the long stay with multiple dietary shifts. *Gut*, **2019**, 68, 2254-2255	19.2	28
129	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. *Bioinformatics*, **2016**, 32, 462-4	7.2	25
128	Distinct Gut Microbiota Composition and Functional Category in Children With Cerebral Palsy and Epilepsy. *Frontiers in Pediatrics*, **2019**, 7, 394	3.4	22
127	Pedigree reconstruction using identity by descent. *Journal of Computational Biology*, **2011**, 18, 1481-93	1.7	22
126	Microbiota Composition in Upper Respiratory Tracts of Healthy Children in Shenzhen, China, Differed with Respiratory Sites and Ages. *BioMed Research International*, **2018**, 2018, 6515670	3	20
125	DNA Methylation Markers for Pan-Cancer Prediction by Deep Learning. *Genes*, **2019**, 10,	4.2	19
124	The difficulty of protein structure alignment under the RMSD. *Algorithms for Molecular Biology*, **2013**, 8, 1	1.8	19
123	Alterations of Gut Microbiota in Cholestatic Infants and Their Correlation With Hepatic Function. *Frontiers in Microbiology*, **2018**, 9, 2682	5.7	19
122	SpliceFinder: ab initio prediction of splice sites using convolutional neural network. *BMC Bioinformatics*, **2019**, 20, 652	3.6	17
121	Indexing DNA Sequences Using q-Grams. *Lecture Notes in Computer Science*, **2005**, 4-16	0.9	16
120	Mycoplasma pneumoniae and Streptococcus pneumoniae caused different microbial structure and correlation network in lung microbiota. *Journal of Thoracic Disease*, **2016**, 8, 1316-22	2.6	16
119	Improving residue-residue contact prediction via low-rank and sparse decomposition of residue correlation matrix. *Biochemical and Biophysical Research Communications*, **2016**, 472, 217-22	3.4	16
118	Heterogeneity of immune microenvironment in ovarian cancer and its clinical significance: a retrospective study. *OncoImmunology*, **2020**, 9, 1760067	7.2	15
117	Protein secondary structure prediction using NMR chemical shift data. *Journal of Bioinformatics and Computational Biology*, **2010**, 8, 867-84	1	15
116	Error tolerant NMR backbone resonance assignment and automated structure generation. *Journal of Bioinformatics and Computational Biology*, **2011**, 9, 15-41	1	15
115	Donkey genomes provide new insights into domestication and selection for coat color. *Nature Communications*, **2020**, 11, 6014	17.4	15
114	Establishing high-accuracy biomarkers for colorectal cancer by comparing fecal microbiomes in patients with healthy families. *Gut Microbes*, **2020**, 11, 918-929	8.8	14

113	The concordance between upper and lower respiratory microbiota in children with Mycoplasma pneumoniae pneumonia. *Emerging Microbes and Infections*, **2018**, 7, 92	18.9	14
112	Insights into the transmission of respiratory infectious diseases through empirical human contact networks. *Scientific Reports*, **2016**, 6, 31484	4.9	13
111	Protein-protein interface prediction based on hexagon structure similarity. *Computational Biology and Chemistry*, **2016**, 63, 83-88	3.6	13
110	Probabilistic models for capturing more physicochemical properties on protein-protein interface. *Journal of Chemical Information and Modeling*, **2014**, 54, 1798-809	6.1	13
109	LoopWeaver: loop modeling by the weighted scaling of verified proteins. *Journal of Computational Biology*, **2013**, 20, 212-23	1.7	13
108	Spectral probabilities of top-down tandem mass spectra. *BMC Genomics*, **2014**, 15 Suppl 1, S9	4.5	12
107	Parameterized BLOSUM Matrices for Protein Alignment. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2015**, 12, 686-94	3	10
106	Reconstructing directed gene regulatory network by only gene expression data. *BMC Genomics*, **2016**, 17 Suppl 4, 430	4.5	10
105	Finding Largest Well-Predicted Subset of Protein Structure Models **2008**, 44-55		10
104	Lung Microbiota and Pulmonary Inflammatory Cytokines Expression Vary in Children With Tracheomalacia and Adenoviral or Pneumonia. *Frontiers in Pediatrics*, **2019**, 7, 265	3.4	9
103	Protein-protein binding sites prediction by 3D structural similarities. *Journal of Chemical Information and Modeling*, **2011**, 51, 3287-94	6.1	9
102	Piers. *SIGMOD Record*, **2004**, 33, 39-44	1.1	9
101	Genome-Wide Investigation and Functional Analysis of RNA Editing Sites across Eleven Tissues. *Genes*, **2019**, 10,	4.2	8
100	Identification of Glycopeptides with Multiple Hydroxylysine O-Glycosylation Sites by Tandem Mass Spectrometry. *Journal of Proteome Research*, **2015**, 14, 5099-108	5.6	8
99	MHC binding prediction with KernelRLSpan and its variations. *Journal of Immunological Methods*, **2014**, 406, 10-20	2.5	8
98	Designing succinct structural alphabets. *Bioinformatics*, **2008**, 24, i182-9	7.2	8
97	The Alteration of Nasopharyngeal and Oropharyngeal Microbiota in Children with MPP and Non-MPP. *Genes*, **2017**, 8,	4.2	7
96	SCDevDB: A Database for Insights Into Single-Cell Gene Expression Profiles During Human Developmental Processes. *Frontiers in Genetics*, **2019**, 10, 903	4.5	7

95	Detecting protein conformational changes in interactions via scaling known structures. *Journal of Computational Biology*, **2013**, 20, 765-79	1.7	7
94	Clustering 100,000 protein structure decoys in minutes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 765-73	3	7
93	An integrated respiratory microbial gene catalogue to better understand the microbial aetiology of Mycoplasma pneumoniae pneumonia. *GigaScience*, **2019**, 8,	7.6	6
92	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	8.6	6
91	On protein structure alignment under distance constraint. *Theoretical Computer Science*, **2011**, 412, 4187-4199	1.4	6
90	Publisher 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,	7.4	6
89	Pedigree Reconstruction Using Identity by Descent. *Lecture Notes in Computer Science*, **2011**, 136-152	0.9	6
88	P-Binder: A System for the Protein-Protein Binding Sites Identification. *Lecture Notes in Computer Science*, **2012**, 127-138	0.9	6
87	DeepMF: deciphering the latent patterns in omics profiles with a deep learning method. *BMC Bioinformatics*, **2019**, 20, 648	3.6	6
86	In silico design of MHC class I high binding affinity peptides through motifs activation map. *BMC Bioinformatics*, **2018**, 19, 516	3.6	6
85	D-GPM: A Deep Learning Method for Gene Promoter Methylation Inference. *Genes*, **2019**, 10,	4.2	5
84	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. *BMC Genomics*, **2017**, 18, 268	4.5	5
83	Structural neighboring property for identifying protein-protein binding sites. *BMC Systems Biology*, **2015**, 9 Suppl 5, S3	3.5	5
82	Fingerprinting protein structures effectively and efficiently. *Bioinformatics*, **2014**, 30, 949-55	7.2	5
81	Finding nearly optimal GDT scores. *Journal of Computational Biology*, **2011**, 18, 693-704	1.7	5
80	Towards Reliable Automatic Protein Structure Alignment. *Lecture Notes in Computer Science*, **2013**, 18-32	0.9	5
79	Understanding Horizontal Gene Transfer network in human gut microbiota. *Gut Pathogens*, **2020**, 12, 33	5.4	5
78	LEMON: a method to construct the local strains at horizontal gene transfer sites in gut metagenomics. *BMC Bioinformatics*, **2019**, 20, 702	3.6	5

77	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate Mesodinium rubrum. *ISME Journal*, **2021**, 15, 1056-1072	11.9	5
76	FragQA: predicting local fragment quality of a sequence-structure alignment. *Genome Informatics*, **2007**, 19, 27-39		5
75	Large-scale 3D chromatin reconstruction from chromosomal contacts. *BMC Genomics*, **2019**, 20, 186	4.5	4
74	Dynamic oropharyngeal and faecal microbiota during treatment in infants hospitalized for bronchiolitis compared with age-matched healthy subjects. *Scientific Reports*, **2017**, 7, 11266	4.9	4
73	Incorporating Ab Initio energy into threading approaches for protein structure prediction. *BMC Bioinformatics*, **2011**, 12 Suppl 1, S54	3.6	4
72	Predicting local quality of a sequence-structure alignment. *Journal of Bioinformatics and Computational Biology*, **2009**, 7, 789-810	1	4
71	On two open problems of 2-interval patterns. *Theoretical Computer Science*, **2009**, 410, 2410-2423	1.1	4
70	Altered metabolome and microbiome features provide clues in understanding irritable bowel syndrome and depression comorbidity. *ISME Journal*, **2021**,	11.9	4
69	Functional organization of the maternal and paternal human 4D Nucleome. *IScience*, **2021**, 24, 103452	6.1	4
68	New Approximation Algorithms for Some Dynamic Storage Allocation Problems. *Lecture Notes in Computer Science*, **2004**, 339-348	0.9	4
67	Finding Compact Structural Motifs. *Lecture Notes in Computer Science*, **2007**, 142-149	0.9	4
66	A comprehensive investigation of metagenome assembly by linked-read sequencing. *Microbiome*, **2020**, 8, 156	16.6	4
65	Intestinal sp. Imbalance Associated With the Occurrence of Childhood Undernutrition in China. *Frontiers in Microbiology*, **2019**, 10, 2635	5.7	4
64	PStrain: An Iterative Microbial Strains Profiling Algorithm for Shotgun Metagenomic Sequencing Data. *Bioinformatics*, **2020**,	7.2	4
63	Analysis and comparison of long non-coding RNAs expressed in the ovaries of Meishan and Yorkshire pigs. *Animal Genetics*, **2019**, 50, 660-669	2.5	3
62	Identification of MicroRNA Targets of spp. Using MiRTrans-a Trans-Omics Approach. *Frontiers in Plant Science*, **2017**, 8, 495	6.2	3
61	Compare local pocket and global protein structure models by small structure patterns **2015**,		3
60	Alteration of the respiratory microbiome in COVID-19 patients with different severities. *Journal of Genetics and Genomics*, **2021**,	4	3

59	Somatic variant analysis suite: copy number variation clonal visualization online platform for large-scale single-cell genomics. *Briefings in Bioinformatics*, **2021**,	13.4	3
58	On Protein Structure Alignment under Distance Constraint. *Lecture Notes in Computer Science*, **2009**, 65-76	0.9	3
57	Functional Organization of the Maternal and Paternal Human 4D Nucleome		3
56	Breastfeeding restored the gut microbiota in caesarean section infants and lowered the infection risk in early life. *BMC Pediatrics*, **2020**, 20, 532	2.6	3
55	Distinct Skin Microbiota Imbalance and Responses to Clinical Treatment in Children With Atopic Dermatitis. *Frontiers in Cellular and Infection Microbiology*, **2020**, 10, 336	5.9	3
54	Deep learning model reveals potential risk genes for ADHD, especially Ephrin receptor gene EPHA5. *Briefings in Bioinformatics*, **2021**, 22,	13.4	3
53	LysoPhD: predicting functional prophages in bacterial genomes from high-throughput sequencing **2019**,		3
52	Development and validation of an online model to predict critical COVID-19 with immune-inflammatory parameters. *Journal of Intensive Care*, **2021**, 9, 19	7	3
51	Oviz-Bio: a web-based platform for interactive cancer genomics data visualization. *Nucleic Acids Research*, **2020**, 48, W415-W426	20.1	2
50	Residue-Specific Side-Chain Polymorphisms via Particle Belief Propagation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2014**, 11, 33-41	3	2
49	Residues with similar hexagon neighborhoods share similar side-chain conformations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 240-8	3	2
48	A PTAS For The k-Consensus Structures Problem Under Squared Euclidean Distance. *Algorithms*, **2008**, 1, 43-51	1.8	2
47	Periodontal and Peri-Implant Microbiome Dysbiosis Is Associated With Alterations in the Microbial Community Structure and Local Stability.. *Frontiers in Microbiology*, **2021**, 12, 785191	5.7	2
46	LDscaff: LD-based scaffolding of de novo genome assemblies. *BMC Bioinformatics*, **2020**, 21, 570	3.6	2
45	The genome variation and developmental transcriptome maps reveal genetic differentiation of skeletal muscle in pigs. *PLoS Genetics*, **2021**, 17, e1009910	6	2
44	LoopWeaver ‖Loop Modeling by the Weighted Scaling of Verified Proteins. *Lecture Notes in Computer Science*, **2012**, 113-126	0.9	2
43	SCYN: Single cell CNV profiling method using dynamic programming		2
42	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. *Lecture Notes in Computer Science*, **2013**, 58-74	0.9	2

41	Longitudinal virological changes and underlying pathogenesis in hospitalized COVID-19 patients in Guangzhou, China. *Science China Life Sciences*, **2021**, 1	8.5	2
40	Altered nitric oxide induced by gut microbiota reveals the connection between central precocious puberty and obesity. *Clinical and Translational Medicine*, **2021**, 11, e299	5.7	2
39	Transcriptome Atlas of 16 Donkey Tissues. *Frontiers in Genetics*, **2021**, 12, 682734	4.5	2
38	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	4.4	2
37	On the Complexity of the Crossing Contact Map Pattern Matching Problem. *Lecture Notes in Computer Science*, **2006**, 231-241	0.9	2
36	Finding All Longest Common Segments in Protein Structures Efficiently. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2015**, 12, 644-55	3	1
35	Different nasopharynx and oropharynx microbiota imbalance in children with Mycoplasma pneumoniae or influenza virus infection. *Microbial Pathogenesis*, **2020**, 144, 104189	3.8	1
34	KDiamend: a package for detecting key drivers in a molecular ecological network of disease. *BMC Systems Biology*, **2018**, 12, 5	3.5	1
33	NGS-based likelihood ratio for identifying contributors in two- and three-person DNA mixtures. *Computational Biology and Chemistry*, **2018**, 74, 428-433	3.6	1
32	Protein Structure Idealization: How accurately is it possible to model protein structures with dihedral angles?. *Algorithms for Molecular Biology*, **2013**, 8, 5	1.8	1
31	Finding compact structural motifs. *Theoretical Computer Science*, **2009**, 410, 2834-2839	1.1	1
30	Consensus Approaches to Protein Structure Prediction189-208		1
29	Deep learning for HGT insertion sites recognition. *BMC Genomics*, **2020**, 21, 893	4.5	1
28	D-GPM: a deep learning method for gene promoter methylation inference		1
27	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	5.7	1
26	Is antibiotics prescription needed in infants with topical corticosteroids treatment for moderate-to-severe atopic dermatitis?. *Dermatologic Therapy*, **2020**, 33, e14215	2.2	1
25	scSVAS: CNV clonal visualization online platform for large scale single-cell genomics		1
24	Cervicovaginal Microbiome Factors in Clearance of Human Papillomavirus Infection. *Frontiers in Oncology*, **2021**, 11, 722639	5.3	1

#	Title	IF	Citations
23	More accurate models for detecting gene-gene interactions from public expression compendia **2016**,		1
22	MIRIA: a webserver for statistical, visual and meta-analysis of RNA editing data in mammals. *BMC Bioinformatics*, **2019**, 20, 596	3.6	1
21	A unified STR profiling system across multiple species with whole genome sequencing data. *BMC Bioinformatics*, **2019**, 20, 671	3.6	1
20	SuperTAD: robust detection of hierarchical topologically associated domains with optimized structural information. *Genome Biology*, **2021**, 22, 45	18.3	1
19	SpecHap: a diploid phasing algorithm based on spectral graph theory. *Nucleic Acids Research*, **2021**, 49, e114	20.1	1
18	Both Simulation and Sequencing Data Reveal Multiple SARS-CoV-2 Variants Coinfection in COVID-19 Pandemic		1
17	Microbiome Resilience and Health Implications for People in Half-Year Travel.. *Frontiers in Immunology*, **2022**, 13, 848994	8.4	1
16	Search for More Effective Microsatellite Markers for Forensics With Next-Generation Sequencing. *IEEE Transactions on Nanobioscience*, **2017**, 16, 375-381	3.4	0
15	A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in Capsicum		0
14	I-Impute: a self-consistent method to impute single cell RNA sequencing data. *BMC Genomics*, **2020**, 21, 618	4.5	0
13	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	6.8	0
12	The Tibetan-Yi region is both a corridor and a barrier for human gene flow.. *Cell Reports*, **2022**, 39, 110720	10.6	0
11	Quantifying Significance of MHC II Residues. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2014**, 11, 17-25	3	
10	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	5.7	
9	A PTAS for the k-Consensus Structures Problem Under Euclidean Squared Distance **2008**, 35-44		
8	New Algorithms for the Spaced Seeds **2007**, 50-61		
7	SCYN: single cell CNV profiling method using dynamic programming. *BMC Genomics*, **2021**, 22, 651	4.5	
6	Placing Segments on Parallel Arcs. *Lecture Notes in Computer Science*, **2018**, 298-310	0.9	

5   On the Near-Linear Correlation of the Eigenvalues Across BLOSUM Matrices. *Lecture Notes in Computer Science*, **2015**, 199-210   0.9

4   How Accurately Can We Model Protein Structures with Dihedral Angles?. *Lecture Notes in Computer Science*, **2012**, 274-287   0.9

3   Finding Longest Common Segments in Protein Structures in Nearly Linear Time. *Lecture Notes in Computer Science*, **2012**, 334-348   0.9

2   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   5.7

1   Dynamic changes of gut microbiota and hepatic functions are different among biliary atresia patients after Kasai portoenterostomy.. *Clinical and Translational Medicine*, **2022**, 12, e728   5.7