

Shuai Cheng Li

List of Publications by Year in descending order

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Version: 2024-02-01

150
papers

4,127
citations

201674
27
h-index

149698
56
g-index

184
all docs

184
docs citations

184
times ranked

6525
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Discrepant gut microbiota markers for the classification of obesity-related metabolic abnormalities. Scientific Reports, 2019, 9, 13424.	3.3	235
4	Evaporation of Droplets on Superhydrophobic Surfaces: Surface Roughness and Small Droplet Size Effects. Physical Review Letters, 2012, 109, 116101.	7.8	176
5	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. Nature Communications, 2015, 6, 8212.	12.8	146
6	Origin and evolution of qingke barley in Tibet. Nature Communications, 2018, 9, 5433.	12.8	141
7	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. Nature Communications, 2014, 5, 3966.	12.8	124
8	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
9	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	7.8	99
10	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. Nature Communications, 2018, 9, 1276.	12.8	80
11	Coding mutations in NUS1 contribute to Parkinson's disease. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11567-11572.	7.1	78
12	Calibur: a tool for clustering large numbers of protein decoys. BMC Bioinformatics, 2010, 11, 25.	2.6	64
13	Donkey genomes provide new insights into domestication and selection for coat color. Nature Communications, 2020, 11, 6014.	12.8	63
14	A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in <i>Capsicum</i> . Scientific Reports, 2016, 6, 18919.	3.3	60
15	Fragment-HMM: A new approach to protein structure prediction. Protein Science, 2008, 17, 1925-1934.	7.6	57
16	Protein-protein binding site identification by enumerating the configurations. BMC Bioinformatics, 2012, 13, 158.	2.6	57
17	DNA Methylation Markers for Pan-Cancer Prediction by Deep Learning. Genes, 2019, 10, 778.	2.4	55
18	A draft genome assembly of the solar-powered sea slug <i>Elysia chlorotica</i> . Scientific Data, 2019, 6, 190022.	5.3	48

#	ARTICLE	IF	CITATIONS
19	Improving protein fold recognition by extracting fold-specific features from predicted residue-residue contacts. <i>Bioinformatics</i> , 2017, 33, 3749-3757.	4.1	47
20	Distinct Gut Microbiota Composition and Functional Category in Children With Cerebral Palsy and Epilepsy. <i>Frontiers in Pediatrics</i> , 2019, 7, 394.	1.9	46
21	Resilience of human gut microbial communities for the long stay with multiple dietary shifts. <i>Gut</i> , 2019, 68, 2254-2255.	12.1	45
22	Alterations of Gut Microbiota in Cholestatic Infants and Their Correlation With Hepatic Function. <i>Frontiers in Microbiology</i> , 2018, 9, 2682.	3.5	42
23	Microbiota Composition in Upper Respiratory Tracts of Healthy Children in Shenzhen, China, Differed with Respiratory Sites and Ages. <i>BioMed Research International</i> , 2018, 2018, 1-8.	1.9	40
24	SpliceFinder: ab initio prediction of splice sites using convolutional neural network. <i>BMC Bioinformatics</i> , 2019, 20, 652.	2.6	40
25	Establishing high-accuracy biomarkers for colorectal cancer by comparing fecal microbiomes in patients with healthy families. <i>Gut Microbes</i> , 2020, 11, 918-929.	9.8	38
26	The difficulty of protein structure alignment under the RMSD. <i>Algorithms for Molecular Biology</i> , 2013, 8, 1.	1.2	36
27	Altered metabolome and microbiome features provide clues in understanding irritable bowel syndrome and depression comorbidity. <i>ISME Journal</i> , 2022, 16, 983-996.	9.8	36
28	Discriminative learning for protein conformation sampling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 228-240.	2.6	35
29	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. <i>Bioinformatics</i> , 2016, 32, 462-464.	4.1	34
30	The concordance between upper and lower respiratory microbiota in children with <i>Mycoplasma pneumoniae</i> pneumonia. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-8.	6.5	29
31	Heterogeneity of immune microenvironment in ovarian cancer and its clinical significance: a retrospective study. <i>Oncolmmunology</i> , 2020, 9, 1760067.	4.6	29
32	Pedigree Reconstruction Using Identity by Descent. <i>Journal of Computational Biology</i> , 2011, 18, 1481-1493.	1.6	25
33	<i>Mycoplasma pneumoniae</i> and <i>Streptococcus pneumoniae</i> caused different microbial structure and correlation network in lung microbiota. <i>Journal of Thoracic Disease</i> , 2016, 8, 1316-1322.	1.4	23
34	The genome variation and developmental transcriptome maps reveal genetic differentiation of skeletal muscle in pigs. <i>PLoS Genetics</i> , 2021, 17, e1009910.	3.5	22
35	Indexing DNA Sequences Using q-Grams. <i>Lecture Notes in Computer Science</i> , 2005, , 4-16.	1.3	21
36	Lung Microbiota and Pulmonary Inflammatory Cytokines Expression Vary in Children With Tracheomalacia and Adenoviral or <i>Mycoplasma pneumoniae</i> Pneumonia. <i>Frontiers in Pediatrics</i> , 2019, 7, 265.	1.9	21

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37	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 867-884.	0.8	19
38	Improving residueâ€‘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
39	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. Journal of Bioinformatics and Computational Biology, 2011, 09, 15-41.	0.8	18
40	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
41	Oviz-Bio: a web-based platform for interactive cancer genomics data visualization. Nucleic Acids Research, 2020, 48, W415-W426.	14.5	17
42	Insights into the transmission of respiratory infectious diseases through empirical human contact networks. Scientific Reports, 2016, 6, 31484.	3.3	16
43	The Alteration of Nasopharyngeal and Oropharyngeal Microbiota in Children with MPP and Non-MPP. Genes, 2017, 8, 380.	2.4	16
44	An integrated respiratory microbial gene catalogue to better understand the microbial aetiology of Mycoplasma pneumoniae pneumonia. GigaScience, 2019, 8, .	6.4	16
45	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate <i>Mesodinium rubrum</i>. ISME Journal, 2021, 15, 1056-1072.	9.8	15
46	Spectral probabilities of top-down tandem mass spectra. BMC Genomics, 2014, 15, S9.	2.8	14
47	SCDevDB: A Database for Insights Into Single-Cell Gene Expression Profiles During Human Developmental Processes. Frontiers in Genetics, 2019, 10, 903.	2.3	14
48	Understanding Horizontal Gene Transfer network in human gut microbiota. Gut Pathogens, 2020, 12, 33.	3.4	14
49	PStrain: an iterative microbial strains profiling algorithm for shotgun metagenomic sequencing data. Bioinformatics, 2021, 36, 5499-5506.	4.1	14
50	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
51	Piers. SIGMOD Record, 2004, 33, 39-44.	1.2	13
52	LoopWeaver: Loop Modeling by the Weighted Scaling of Verified Proteins. Journal of Computational Biology, 2013, 20, 212-223.	1.6	13
53	Probabilistic Models for Capturing More Physicochemical Properties on Proteinâ€‘Protein Interface. Journal of Chemical Information and Modeling, 2014, 54, 1798-1809.	5.4	13
54	Parameterized BLOSUM Matrices for Protein Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 686-694.	3.0	13

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55	Identification of Glycopeptides with Multiple Hydroxylysine O-Glycosylation Sites by Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015, 14, 5099-5108.	3.7	13
56	Reconstructing directed gene regulatory network by only gene expression data. <i>BMC Genomics</i> , 2016, 17, 430.	2.8	13
57	Proteinâ€“protein interface prediction based on hexagon structure similarity. <i>Computational Biology and Chemistry</i> , 2016, 63, 83-88.	2.3	13
58	D-GPM: A Deep Learning Method for Gene Promoter Methylation Inference. <i>Genes</i> , 2019, 10, 807.	2.4	13
59	Altered nitric oxide induced by gut microbiota reveals the connection between central precocious puberty and obesity. <i>Clinical and Translational Medicine</i> , 2021, 11, e299.	4.0	13
60	Cervicovaginal Microbiome Factors in Clearance of Human Papillomavirus Infection. <i>Frontiers in Oncology</i> , 2021, 11, 722639.	2.8	13
61	Genome-Wide Investigation and Functional Analysis of <i>Sus scrofa</i> RNA Editing Sites across Eleven Tissues. <i>Genes</i> , 2019, 10, 327.	2.4	12
62	A comprehensive investigation of metagenome assembly by linked-read sequencing. <i>Microbiome</i> , 2020, 8, 156.	11.1	12
63	Different nasopharynx and oropharynx microbiota imbalance in children with <i>Mycoplasma pneumoniae</i> or influenza virus infection. <i>Microbial Pathogenesis</i> , 2020, 144, 104189.	2.9	12
64	SuperTAD: robust detection of hierarchical topologically associated domains with optimized structural information. <i>Genome Biology</i> , 2021, 22, 45.	8.8	12
65	Designing succinct structural alphabets. <i>Bioinformatics</i> , 2008, 24, i182-i189.	4.1	11
66	The SNP-set based association study identifies ITGA1 as a susceptibility gene of attention-deficit/hyperactivity disorder in Han Chinese. <i>Translational Psychiatry</i> , 2017, 7, e1201-e1201.	4.8	11
67	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. <i>BMC Genomics</i> , 2017, 18, 268.	2.8	11
68	A unified STR profiling system across multiple species with whole genome sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 671.	2.6	11
69	DeepMF: deciphering the latent patterns in omics profiles with a deep learning method. <i>BMC Bioinformatics</i> , 2019, 20, 648.	2.6	11
70	Deep learning model reveals potential risk genes for ADHD, especially Ephrin receptor gene EPHA5. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
71	Finding Largest Well-Predicted Subset of Protein Structure Models. , 2008, , 44-55.		11
72	Proteinâ€“Protein Binding Sites Prediction by 3D Structural Similarities. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 3287-3294.	5.4	10

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73	Distinct Skin Microbiota Imbalance and Responses to Clinical Treatment in Children With Atopic Dermatitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 336.	3.9	10
74	Functional organization of the maternal and paternal human 4D Nucleome. <i>IScience</i> , 2021, 24, 103452.	4.1	10
75	MHC binding prediction with KernelRLSpan and its variations. <i>Journal of Immunological Methods</i> , 2014, 406, 10-20.	1.4	9
76	Fingerprinting protein structures effectively and efficiently. <i>Bioinformatics</i> , 2014, 30, 949-955.	4.1	9
77	In silico design of MHC class I high binding affinity peptides through motifs activation map. <i>BMC Bioinformatics</i> , 2018, 19, 516.	2.6	9
78	Intestinal <i>Bacteroides</i> sp. Imbalance Associated With the Occurrence of Childhood Undernutrition in China. <i>Frontiers in Microbiology</i> , 2019, 10, 2635.	3.5	9
79	Differential perturbations of gut microbial profiles and co-occurrence networks among phases of methamphetamine-induced conditioned place preference. <i>Journal of Neuroscience Research</i> , 2021, 99, 2860-2873.	2.9	9
80	Somatic variant analysis suite: copy number variation clonal visualization online platform for large-scale single-cell genomics. <i>Briefings in Bioinformatics</i> , 2021, , .	6.5	9
81	On protein structure alignment under distance constraint. <i>Theoretical Computer Science</i> , 2011, 412, 4187-4199.	0.9	8
82	Finding Nearly Optimal GDT Scores. <i>Journal of Computational Biology</i> , 2011, 18, 693-704.	1.6	8
83	Clustering 100,000 Protein Structure Decoys in Minutes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 765-773.	3.0	8
84	Dynamic oropharyngeal and faecal microbiota during treatment in infants hospitalized for bronchiolitis compared with age-matched healthy subjects. <i>Scientific Reports</i> , 2017, 7, 11266.	3.3	8
85	Large-scale 3D chromatin reconstruction from chromosomal contacts. <i>BMC Genomics</i> , 2019, 20, 186.	2.8	8
86	LEMON: a method to construct the local strains at horizontal gene transfer sites in gut metagenomics. <i>BMC Bioinformatics</i> , 2019, 20, 702.	2.6	8
87	Transcriptome Atlas of 16 Donkey Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 682734.	2.3	8
88	Resolving complex structures at oncovirus integration loci with conjugate graph. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
89	The Tibetan-Yi region is both a corridor and a barrier for human gene flow. <i>Cell Reports</i> , 2022, 39, 110720.	6.4	8
90	Incorporating Ab Initio energy into threading approaches for protein structure prediction. <i>BMC Bioinformatics</i> , 2011, 12, S54.	2.6	7

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91	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
92	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. Journal of Computational Biology, 2013, 20, 765-779.	1.6	7
93	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
94	Alteration of the respiratory microbiome in COVID-19 patients with different severities. Journal of Genetics and Genomics, 2022, 49, 258-261.	3.9	7
95	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
96	Detecting TAD-like domains from RNA-associated interactions. Nucleic Acids Research, 2022, 50, e88-e88.	14.5	7
97	lImpute: a self-consistent method to impute single cell RNA sequencing data. BMC Genomics, 2020, 21, 618.	2.8	6
98	SpecHap: a diploid phasing algorithm based on spectral graph theory. Nucleic Acids Research, 2021, 49, e114.	14.5	6
99	P-Binder: A System for the Protein-Protein Binding Sites Identification. Lecture Notes in Computer Science, 2012, , 127-138.	1.3	6
100	Towards Reliable Automatic Protein Structure Alignment. Lecture Notes in Computer Science, 2013, , 18-32.	1.3	6
101	FragQA: predicting local fragment quality of a sequence-structure alignment. Genome Informatics, 2007, 19, 27-39.	0.4	6
102	Structural neighboring property for identifying protein-protein binding sites. BMC Systems Biology, 2015, 9, S3.	3.0	5
103	Identification of MicroRNA Targets of Capsicum spp. Using MiRTrans—a Trans-Omics Approach. Frontiers in Plant Science, 2017, 8, 495.	3.6	5
104	KDiamend: a package for detecting key drivers in a molecular ecological network of disease. BMC Systems Biology, 2018, 12, 5.	3.0	5
105	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
106	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
107	New Approximation Algorithms for Some Dynamic Storage Allocation Problems. Lecture Notes in Computer Science, 2004, , 339-348.	1.3	5
108	Finding Compact Structural Motifs. Lecture Notes in Computer Science, 2007, , 142-149.	1.3	5

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109	On Protein Structure Alignment under Distance Constraint. Lecture Notes in Computer Science, 2009, , 65-76.	1.3	5
110	PREDICTING LOCAL QUALITY OF A SEQUENCEâ€“STRUCTURE ALIGNMENT. Journal of Bioinformatics and Computational Biology, 2009, 07, 789-810.	0.8	4
111	On two open problems of 2-interval patterns. Theoretical Computer Science, 2009, 410, 2410-2423.	0.9	4
112	LysoPhD: predicting functional prophages in bacterial genomes from high-throughput sequencing. , 2019, , .		4
113	Compare local pocket and global protein structure models by small structure patterns. , 2015, , .		3
114	MIRIA: a webserver for statistical, visual and meta-analysis of RNA editing data in mammals. BMC Bioinformatics, 2019, 20, 596.	2.6	3
115	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
116	On the Complexity of the Crossing Contact Map Pattern Matching Problem. Lecture Notes in Computer Science, 2006, , 231-241.	1.3	3
117	LDscaff: LD-based scaffolding of de novo genome assemblies. BMC Bioinformatics, 2020, 21, 570.	2.6	3
118	A PTAS For The k-Consensus Structures Problem Under Squared Euclidean Distance. Algorithms, 2008, 1, 43-51.	2.1	2
119	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
120	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
121	Residue-Specific Side-Chain Polymorphisms via Particle Belief Propagation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 33-41.	3.0	2
122	Search for More Effective Microsatellite Markers for Forensics With Next-Generation Sequencing. IEEE Transactions on Nanobioscience, 2017, 16, 375-381.	3.3	2
123	Is antibiotics prescription needed in infants with topical corticosteroids treatment for moderateâ€“severe atopic dermatitis?. Dermatologic Therapy, 2020, 33, e14215.	1.7	2
124	Editorial: Computational Methods in Inferring Cancer Tissue-of-Origin and Cancer Molecular Classification. Frontiers in Genetics, 2021, 12, 644542.	2.3	2
125	LoopWeaver â€“ Loop Modeling by the Weighted Scaling of Verified Proteins. Lecture Notes in Computer Science, 2012, , 113-126.	1.3	2
126	FragQA: predicting local fragment quality of a sequence-structure alignment. , 2007, , .		2

127	Microbiome Resilience and Health Implications for People in Half-Year Travel. <i>Frontiers in Immunology</i> , 2022, 13, 848994.	4.8	2
128	Finding compact structural motifs. <i>Theoretical Computer Science</i> , 2009, 410, 2834-2839.	0.9	1
129	Finding All Longest Common Segments in Protein Structures Efficiently. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 644-655.	3.0	1
130	More accurate models for detecting gene-gene interactions from public expression compendia. , 2016, , .		1
131	Finding more effective microsatellite markers for forensics. , 2016, , .		1
132	NGS-based likelihood ratio for identifying contributors in two- and three-person DNA mixtures. <i>Computational Biology and Chemistry</i> , 2018, 74, 428-433.	2.3	1
133	Development and Validation of a Machine Learning Model for Prediction of Response to Corticosteroid Therapy In COVID-19 Patients. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
134	Whole–genome sequencing identifies novel candidate pathogenic variants associated with left ventricular non–compaction in a three–generation family. <i>Clinical and Translational Medicine</i> , 2021, 11, e501.	4.0	1
135	A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in <i>Capsicum</i> . , 0, .		1
136	Deep learning for HGT insertion sites recognition. <i>BMC Genomics</i> , 2020, 21, 893.	2.8	1
137	SCYN: single cell CNV profiling method using dynamic programming. <i>BMC Genomics</i> , 2021, 22, 651.	2.8	1
138	Over–shedding of donor–derived cell–free DNA at immune–related regions into plasma of lung transplant recipient. <i>Clinical and Translational Medicine</i> , 2022, 12, e622.	4.0	1
139	PRCTC: a machine learning model for prediction of response to corticosteroid therapy in COVID-19 patients. <i>Aging</i> , 2022, 14, 54-72.	3.1	1
140	Dynamic changes of gut microbiota and hepatic functions are different among biliary atresia patients after Kasai portoenterostomy. <i>Clinical and Translational Medicine</i> , 2022, 12, e728.	4.0	1
141	Quantifying Significance of MHC II Residues. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 17-25.	3.0	0
142	Reconstructing directed gene regulatory network by only gene expression data. , 2015, , .		0
143	Eliminating heterozygosity from reads through coverage normalization. , 2016, , .		0
144	Guest Editorial for the 15th Asia Pacific Bioinformatics Conference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1513-1514.	3.0	0

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145	CONSENSUS CONTACT PREDICTION BY LINEAR PROGRAMMING. , 2007, , .		0
146	How Accurately Can We Model Protein Structures with Dihedral Angles?. Lecture Notes in Computer Science, 2012, , 274-287.	1.3	0
147	Finding Longest Common Segments in Protein Structures in Nearly Linear Time. Lecture Notes in Computer Science, 2012, , 334-348.	1.3	0
148	Placing Segments on Parallel Arcs. Lecture Notes in Computer Science, 2018, , 298-310.	1.3	0
149	A PTAS for the k -Consensus Structures Problem Under Euclidean Squared Distance. , 2008, , 35-44.		0
150	New Algorithms for the Spaced Seeds. , 2007, , 50-61.		0