Limsoon Wong

List of Publications by Year
in descending order

282 papers	10,149 citations	47006 47 h-index	45317 90 g-index
291 all docs	291 docs citations	291 times ranked	9380 citing authors

#	Article	IF	Citations
1	Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. Cancer Cell, 2002, 1, 133-143.	16.8	1,756
2	Exploiting indirect neighbours and topological weight to predict protein function from protein-protein interactions. Bioinformatics, 2006, 22, 1623-1630.	4.1	533
3	Complex discovery from weighted PPI networks. Bioinformatics, 2009, 25, 1891-1897.	4.1	434
4	Why Batch Effects Matter in Omics Data, and How to Avoid Them. Trends in Biotechnology, 2017, 35, 498-507.	9.3	266
5	CAEP: Classification by Aggregating Emerging Patterns. Lecture Notes in Computer Science, 1999, , 30-42.	1.3	247
6	Accomplishments and challenges in literature data mining for biology. Bioinformatics, 2002, 18, 1553-1561.	4.1	229
7	Comprehension syntax. SIGMOD Record, 1994, 23, 87-96.	1.2	165
8	PLncDB: plant long non-coding RNA database. Bioinformatics, 2013, 29, 1068-1071.	4.1	163
9	Identification of Cell Cycle-regulated Genes in Fission Yeast. Molecular Biology of the Cell, 2005, 16, 1026-1042.	2.1	159
10	Weighted complex network analysis of travel routes on the Singapore public transportation system. Physica A: Statistical Mechanics and Its Applications, 2010, 389, 5852-5863.	2.6	159
11	Optimal gene expression analysis by microarrays. Cancer Cell, 2002, 2, 353-361.	16.8	149
12	Identifying good diagnostic gene groups from gene expression profiles using the concept of emerging patterns. Bioinformatics, 2002, 18, 725-734.	4.1	139
13	USING INDIRECT PROTEIN–PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. Journal of Bioinformatics and Computational Biology, 2008, 06, 435-466.	0.8	123
14	Simple rules underlying gene expression profiles of more than six subtypes of acute lymphoblastic leukemia (ALL) patients. Bioinformatics, 2003, 19, 71-78.	4.1	106
15	Kleisli, a functional query system. Journal of Functional Programming, 2000, 10, 19-56.	0.8	104
16	Maximal Biclique Subgraphs and Closed Pattern Pairs of the Adjacency Matrix: A One-to-One Correspondence and Mining Algorithms. IEEE Transactions on Knowledge and Data Engineering, 2007, 19, 1625-1637.	5.7	101
17	Discovery of significant rules for classifying cancer diagnosis data. Bioinformatics, 2003, 19, ii93-ii102.	4.1	99
18	Relational expressive power of constraint query languages. Journal of the ACM, 1998, 45, 1-34.	2.2	94

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19	DeEPs: A New Instance-Based Lazy Discovery and Classification System. Machine Learning, 2004, 54, 99-124.	5.4	93
20	Extensions of the External Validation for Checking Learned Model Interpretability and Generalizability. Patterns, 2020, 1, 100129.	5.9	87
21	Mining statistically important equivalence classes and delta-discriminative emerging patterns. , 2007, , .		83
22	Pharmacodynamic Effects of Seliciclib, an Orally Administered Cell Cycle Modulator, in Undifferentiated Nasopharyngeal Cancer. Clinical Cancer Research, 2009, 15, 1435-1442.	7.0	83
23	Guest Editors' Introduction: Data Mining in Bioinformatics. IEEE Intelligent Systems, 2005, 20, 16-18.	4.0	74
24	Stringent homology-based prediction of H. sapiens-M. tuberculosis H37Rv protein-protein interactions. Biology Direct, 2014, 9, 5.	4.6	74
25	Naturally embedded query languages. Lecture Notes in Computer Science, 1992, , 140-154.	1.3	74
26	Query Languages for Bags and Aggregate Functions. Journal of Computer and System Sciences, 1997, 55, 241-272.	1.2	73
27	Intrinsically disordered proteins aggregate at fungal cell-to-cell channels and regulate intercellular connectivity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15781-15786.	7.1	69
28	DATA MINING TOOLS FOR BIOLOGICAL SEQUENCES. Journal of Bioinformatics and Computational Biology, 2003, 01, 139-167.	0.8	66
29	Methods for protein complex prediction and their contributions towards understanding the organisation, function and dynamics of complexes. FEBS Letters, 2015, 589, 2590-2602.	2.8	66
30	Effective Pruning Techniques for Mining Quasi-Cliques. Lecture Notes in Computer Science, 2008, , 33-49.	1.3	66
31	Next generation sequencing unravels the biosynthetic ability of Spearmint (Mentha spicata) peltate glandular trichomes through comparative transcriptomics. BMC Plant Biology, 2014, 14, 292.	3.6	64
32	Inferring synthetic lethal interactions from mutual exclusivity of genetic events in cancer. Biology Direct, 2015, 10, 57.	4.6	64
33	Evaluating feature-selection stability in next-generation proteomics. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650029.	0.8	62
34	Increasing the reliability of protein interactomes. Drug Discovery Today, 2008, 13, 652-658.	6.4	61
35	An empirical comparison of several recent epistatic interaction detection methods. Bioinformatics, 2011, 27, 2936-2943.	4.1	61
36	Epsteinâ€"Barr virus nuclear antigen leader protein localizes to promoters and enhancers with cell transcription factors and EBNA2. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18537-18542.	7.1	61

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37	Consistency, comprehensiveness, and compatibility of pathway databases. BMC Bioinformatics, 2010, 11, 449.	2.6	60
38	Kleisli: a new tool for data integration in biology. Trends in Biotechnology, 1999, 17, 351-355.	9.3	58
39	Logics with aggregate operators. Journal of the ACM, 2001, 48, 880-907.	2.2	58
40	Non-redundant sequential rulesâ€"Theory and algorithm. Information Systems, 2009, 34, 438-453.	3.6	58
41	How advancement in biological network analysis methods empowers proteomics. Proteomics, 2012, 12, 550-563.	2.2	58
42	An efficient strategy for extensive integration of diverse biological data for protein function prediction. Bioinformatics, 2007, 23, 3364-3373.	4.1	56
43	Discovering motif pairs at interaction sites from protein sequences on a proteome-wide scale. Bioinformatics, 2006, 22, 989-996.	4.1	54
44	Using indirect protein interactions for the prediction of Gene Ontology functions. BMC Bioinformatics, 2007, 8, S8.	2.6	54
45	PROGRESS IN COMPUTATIONAL STUDIES OF HOSTâ€"PATHOGEN INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1230001.	0.8	54
46	Network-Based Pipeline for Analyzing MS Data: An Application toward Liver Cancer. Journal of Proteome Research, 2011, 10, 2261-2272.	3.7	51
47	Normal Forms and Conservative Extension Properties for Query Languages over Collection Types. Journal of Computer and System Sciences, 1996, 52, 495-505.	1.2	50
48	The floral transcriptome of ylang ylang (Cananga odorata var. fruticosa) uncovers biosynthetic pathways for volatile organic compounds and a multifunctional and novel sesquiterpene synthase. Journal of Experimental Botany, 2015, 66, 3959-3975.	4.8	50
49	Finding consistent disease subnetworks using PFSNet. Bioinformatics, 2014, 30, 189-196.	4.1	49
50	A consensus linkage map of oil palm and a major QTL for stem height. Scientific Reports, 2015, 5, 8232.	3.3	49
51	FIMM, a database of functional molecular immunology. Nucleic Acids Research, 2000, 28, 222-224.	14.5	48
52	Epidemic reemergence in adaptive complex networks. Physical Review E, 2012, 85, 036107.	2.1	48
53	How to do quantile normalization correctly for gene expression data analyses. Scientific Reports, 2020, 10, 15534.	3.3	48
54	Proteomics Signature Profiling (PSP): A Novel Contextualization Approach for Cancer Proteomics. Journal of Proteome Research, 2012, 11, 1571-1581.	3.7	47

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55	DNAFSMiner: a web-based software toolbox to recognize two types of functional sites in DNA sequences. Bioinformatics, 2005, 21, 671-673.	4.1	45
56	Relative risk and odds ratio. , 2005, , .		45
57	Accurate prediction of hot spot residues through physicochemical characteristics of amino acid sequences. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1351-1362.	2.6	43
58	Comparative Network-Based Recovery Analysis and Proteomic Profiling of Neurological Changes in Valproic Acid-Treated Mice. Journal of Proteome Research, 2013, 12, 2116-2127.	3.7	42
59	IntPath--an integrated pathway gene relationship database for model organisms and important pathogens. BMC Systems Biology, 2012, 6, S2.	3.0	41
60	Transcriptome Analysis Reveals Neuroprotective aspects of Human Reactive Astrocytes induced by Interleukin 1Î². Scientific Reports, 2017, 7, 13988.	3.3	41
61	Technologies for integrating biological data. Briefings in Bioinformatics, 2002, 3, 389-404.	6.5	40
62	Finding consistent disease subnetworks across microarray datasets. BMC Bioinformatics, 2011, 12, S15.	2.6	39
63	Normal forms and conservative properties for query languages over collection types. , 1993, , .		38
64	FIMM, a database of functional molecular immunology: update 2002. Nucleic Acids Research, 2002, 30, 226-229.	14.5	38
65	Integrating Networks and Proteomics: Moving Forward. Trends in Biotechnology, 2016, 34, 951-959.	9.3	38
66	Protein complex prediction based on k-connected subgraphs in protein interaction network. BMC Systems Biology, 2010, 4, 129.	3.0	37
67	Advancing Clinical Proteomics via Analysis Based on Biological Complexes: A Tale of Five Paradigms. Journal of Proteome Research, 2016, 15, 3167-3179.	3.7	37
68	Antibody-Specified B-Cell Epitope Prediction in Line with the Principle of Context-Awareness. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1483-1494.	3.0	36
69	Discovery of Protein Complexes with Core-Attachment Structures from Tandem Affinity Purification (TAP) Data. Journal of Computational Biology, 2012, 19, 1027-1042.	1.6	36
70	Supervised maximum-likelihood weighting of composite protein networks for complex prediction. BMC Systems Biology, 2012, 6, S13.	3.0	36
71	Enhancing the utility of Proteomics Signature Profiling (PSP) with Pathway Derived Subnets (PDSs), performance analysis and specialised ontologies. BMC Genomics, 2013, 14, 35.	2.8	35
72	GFS: fuzzy preprocessing for effective gene expression analysis. BMC Bioinformatics, 2016, 17, 540.	2.6	35

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73	Random forests on Hadoop for genome-wide association studies of multivariate neuroimaging phenotypes. BMC Bioinformatics, 2013, 14, S6.	2.6	34
74	Stringent DDI-based Prediction of H. sapiens-M. tuberculosis H37Rv Protein-Protein Interactions. BMC Systems Biology, 2013, 7, S6.	3.0	34
75	Discovery of small protein complexes from PPI networks with size-specific supervised weighting. BMC Systems Biology, 2014, 8, S3.	3.0	34
76	Quantitative proteomics signature profiling based on network contextualization. Biology Direct, 2015, 10, 71.	4.6	34
77	Draft genome sequence of an elite<i>Dura</i>palm and whole-genome patterns of DNA variation in oil palm. DNA Research, 2016, 23, 527-533.	3.4	34
78	Some Properties of Query Languages for Bags. Workshops in Computing, 1994, , 97-114.	0.4	34
79	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. , 2007, , .		33
80	FastTagger: an efficient algorithm for genome-wide tag SNP selection using multi-marker linkage disequilibrium. BMC Bioinformatics, 2010, 11, 66.	2.6	33
81	Transcriptome and functional analysis reveals hybrid vigor for oil biosynthesis in oil palm. Scientific Reports, 2017, 7, 439.	3.3	33
82	A query language for multidimensional arrays. SIGMOD Record, 1996, 25, 228-239.	1.2	33
83	Integrative Toxicoproteomics Implicates Impaired Mitochondrial Glutathione Import as an Off-Target Effect of Troglitazone. Journal of Proteome Research, 2013, 12, 2933-2945.	3.7	31
84	High-speed and high-ratio referential genome compression. Bioinformatics, 2017, 33, 3364-3372.	4.1	31
85	Assessing and Predicting Protein Interactions Using Both Local and Global Network Topological Metrics. , 2008, , .		31
86	From the static interactome to dynamic protein complexes: Three challenges. Journal of Bioinformatics and Computational Biology, 2015, 13, 1571001.	0.8	30
87	A quantum leap in the reproducibility, precision, and sensitivity of gene expression profile analysis even when sample size is extremely small. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550018.	0.8	30
88	Distance Based Subspace Clustering with Flexible Dimension Partitioning. , 2007, , .		29
89	A new concise representation of frequent itemsets using generators and a positive border. Knowledge and Information Systems, 2008, 17, 35-56.	3.2	29
90	Comparative analysis and assessment of M. tuberculosis H37Rv protein-protein interaction datasets. BMC Genomics, 2011, 12, S20.	2.8	29

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91	B-cell epitope prediction through a graph model. BMC Bioinformatics, 2012, 13, S20.	2.6	29
92	Using Rules to Analyse Bio-medical Data: A Comparison between C4.5 and PCL. Lecture Notes in Computer Science, 2003, , 254-265.	1.3	28
93	Use of extreme patient samples for outcome prediction from gene expression data. Bioinformatics, 2005, 21, 3377-3384.	4.1	28
94	Decomposing PPI networks for complex discovery. Proteome Science, 2011, 9, S15.	1.7	26
95	<i>eCEO</i>: an efficient Cloud Epistasis cOmputing model in genome-wide association study. Bioinformatics, 2011, 27, 1045-1051.	4.1	25
96	Query languages for bags. ACM SIGACT News, 1996, 27, 30-44.	0.1	24
97	Networks in proteomics analysis of cancer. Current Opinion in Biotechnology, 2013, 24, 1122-1128.	6.6	23
98	Prediction of problematic complexes from PPI networks: sparse, embedded, and small complexes. Biology Direct, 2015, 10, 40.	4.6	23
99	CAMBer: an approach to support comparative analysis of multiple bacterial strains. BMC Genomics, 2011, 12, S6.	2.8	22
100	Detection of Outlier Residues for Improving Interface Prediction in Protein Heterocomplexes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1155-1165.	3.0	22
101	GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria. BMC Genomics, 2014, 15, S10.	2.8	22
102	Dealing with Confounders in Omics Analysis. Trends in Biotechnology, 2018, 36, 488-498.	9.3	22
103	Conservativity of nested relational calculi with internal generic functions. Information Processing Letters, 1994, 49, 273-280.	0.6	21
104	eCAMBer: efficient support for large-scale comparative analysis of multiple bacterial strains. BMC Bioinformatics, 2014, 15, 65.	2.6	21
105	Local properties of query languages. Theoretical Computer Science, 2000, 239, 277-308.	0.9	20
106	A Probabilistic Graph–Theoretic Approach to Integrate Multiple Predictions for the Protein–Protein Subnetwork Prediction Challenge. Annals of the New York Academy of Sciences, 2009, 1158, 224-233.	3.8	20
107	Can Peripheral Blood-Derived Gene Expressions Characterize Individuals at Ultra-high Risk for Psychosis?. Computational Psychiatry, 2020, 1, 168.	2.0	20
108	Aggregate Functions, Conservative Extension, and Linear Orders. Workshops in Computing, 1994, , 282-294.	0.4	20

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109	Controlling false positives in association rule mining. Proceedings of the VLDB Endowment, 2011, 5, 145-156.	3.8	19
110	Response: an empirical comparison of several recent epistatic interaction detection methods. Bioinformatics, 2012, 28, 147-148.	4.1	19
111	Improved statistical model checking methods for pathway analysis. BMC Bioinformatics, 2012, 13, S15.	2.6	19
112	Advanced bioinformatics methods for practical applications in proteomics. Briefings in Bioinformatics, 2019, 20, 347-355.	6.5	19
113	Incremental recomputation in local languages. Information and Computation, 2003, 181, 88-98.	0.7	18
114	Computational proteomics: designing a comprehensive analytical strategy. Drug Discovery Today, 2014, 19, 266-274.	6.4	18
115	Design principles for clinical network-based proteomics. Drug Discovery Today, 2016, 21, 1130-1138.	6.4	18
116	Protein complex-based analysis is resistant to the obfuscating consequences of batch effects --- a case study in clinical proteomics. BMC Genomics, 2017, 18, 142.	2.8	18
117	Avoid Oversimplifications in Machine Learning: Going beyond the Class-Prediction Accuracy. Patterns, 2020, 1, 100025.	5.9	18
118	Evaluating Temporal Factors in Combined Interventions of Workforce Shift and School Closure for Mitigating the Spread of Influenza. PLoS ONE, 2012, 7, e32203.	2.5	18
119	Semantic Representations and Query Languages for Or-Sets. Journal of Computer and System Sciences, 1996, 52, 125-142.	1.2	17
120	Comparative transcriptomics unravel biochemical specialization of leaf tissues of Stevia (Stevia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	4.8	17
121	Why breast cancer signatures are no better than random signatures explained. Drug Discovery Today, 2018, 23, 1818-1823.	6.4	17
122	AssocExplorer. , 2012, , .		16
123	An approach to identifying drug resistance associated mutations in bacterial strains. BMC Genomics, 2012, 13, S23.	2.8	16
124	NetProt: Complex-based Feature Selection. Journal of Proteome Research, 2017, 16, 3102-3112.	3.7	16
125	Efficient mining of frequent XML query patterns with repeating-siblings. Information and Software Technology, 2008, 50, 375-389.	4.4	15
126	The role of miRNAs in complex formation and control. Bioinformatics, 2012, 28, 453-456.	4.1	15

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127	A network-based maximum link approach towards MS identifies potentially important roles for undetected ARRB1/2 and ACTB in liver cancer progression. International Journal of Bioinformatics Research and Applications, 2012, 8, 155.	0.2	15
128	MapReduce for accurate error correction of next-generation sequencing data. Bioinformatics, 2017, 33, 3844-3851.	4.1	15
129	Understanding missing proteins: a functional perspective. Drug Discovery Today, 2018, 23, 644-651.	6.4	15
130	The Kleisli Query System as a Backbone for Bioinformatics Data Integration and Analysis. , 2003, , 147-187.		15
131	Efficient mining of distance-based subspace clusters. Statistical Analysis and Data Mining, 2009, 2, 427-444.	2.8	14
132	Structural analysis on mutation residues and interfacial water molecules for human TIM disease understanding. BMC Bioinformatics, 2013, 14, S11.	2.6	14
133	On two forms of structural recursion. Lecture Notes in Computer Science, 1995, , 111-124.	1.3	14
134	Incremental recomputation of recursive queries with nested sets and aggregate functions. Lecture Notes in Computer Science, 1998, , 222-238.	1.3	14
135	Accomplishments and challenges in bioinformatics. IT Professional, 2004, 6, 44-50.	1.5	13
136	Protein Interactome Analysis for Countering Pathogen Drug Resistance. Journal of Computer Science and Technology, 2010, 25, 124-130.	1.5	13
137	Low cytosine triphosphate synthase 2 expression renders resistance to 5-fluorouracil in colorectal cancer. Cancer Biology and Therapy, 2011, 11, 599-608.	3.4	13
138	Allowing mutations in maximal matches boosts genome compression performance. Bioinformatics, 2020, 36, 4675-4681.	4.1	13
139	Local properties of query languages. Lecture Notes in Computer Science, 1996, , 140-154.	1.3	13
140	Kleisli: its exchange format, supporting tools, and an application in protein interaction extraction. , 0, , .		12
141	Temporal factors in school closure policy for mitigating the spread of influenza. Journal of Public Health Policy, 2011, 32, 180-197.	2.0	12
142	DBAC: A simple prediction method for protein binding hot spots based on burial levels and deeply buried atomic contacts. BMC Systems Biology, 2011, 5, S5.	3.0	12
143	DISRUPTION OF PROTEIN COMPLEXES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341008.	0.8	12
144	OrthoGNC: A Software for Accurate Identification of Orthologs Based on Gene Neighborhood Conservation. Genomics, Proteomics and Bioinformatics, 2017, 15, 361-370.	6.9	12

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145	Turning straw into gold: building robustness into gene signature inference. Drug Discovery Today, 2019, 24, 31-36.	6.4	12
146	Enabling more sophisticated gene expression analysis for understanding diseases and optimizing treatments. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2007, 9, 3-13.	4.0	12
147	On representation and querying incomplete information in databases with bags. Information Processing Letters, 1995, 56, 209-214.	0.6	11
148	Lower bounds for invariant queries in logics with counting. Theoretical Computer Science, 2002, 288, 153-180.	0.9	11
149	Generation of arbitrary two-point correlated directed networks with given modularity. Physics Letters, Section A: General, Atomic and Solid State Physics, 2010, 374, 3129-3135.	2.1	11
150	A Flexible Approach to Finding Representative Pattern Sets. IEEE Transactions on Knowledge and Data Engineering, 2014, 26, 1562-1574.	5.7	11
151	Editorial â€" Bioinformatics development at the BGRSSB conference series: 10th anniversary. Journal of Bioinformatics and Computational Biology, 2017, 15, 1702001.	0.8	11
152	Key node selection for containing infectious disease spread using particle swarm optimization. , 2009, , .		10
153	DA 1.0: parameter estimation of biological pathways using data assimilation approach. Bioinformatics, 2010, 26, 1794-1796.	4.1	10
154	Mining Iterative Generators and Representative Rules for Software Specification Discovery. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 282-296.	5.7	10
155	Towards exploratory hypothesis testing and analysis. , 2011, , .		10
156	Finding minimum representative pattern sets. , 2012, , .		10
157	Rule discovery and distance separation to detect reliable miRNA biomarkers for the diagnosis of lung squamous cell carcinoma. BMC Genomics, 2014, 15, S16.	2.8	10
158	The Birth of Bio-data Science: Trends, Expectations, and Applications. Genomics, Proteomics and Bioinformatics, 2020, 18, 5-15.	6.9	10
159	Exploring Essential Attributes for Detecting MicroRNA Precursors from Background Sequences. Lecture Notes in Computer Science, 2006, , 131-145.	1.3	10
160	Geography of Di.erences between Two Classes of Data. Lecture Notes in Computer Science, 2002, , 325-337.	1.3	10
161	Are batch effects still relevant in the age of big data?. Trends in Biotechnology, 2022, 40, 1029-1040.	9.3	10
162	CMPF: Class-switching minimized pathfinding in metabolic networks. BMC Bioinformatics, 2012, 13, S17.	2.6	9

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163	Bioinformatics Adventures in Database Research. Lecture Notes in Computer Science, 2003, , 31-46.	1.3	9
164	On Impossibility of Decremental Recomputation of Recursive Queries in Relational Calculus and SQL. , 0, , .		9
165	Using indirect protein-protein interactions for protein complex predication. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 97-109.	0.4	9
166	Logics with aggregate operators. , 0, , .		8
167	Positive Borders or Negative Borders: How to Make Lossless Generator Based Representations Concise. , 2006, , .		8
168	CPS-tree: A Compact Partitioned Suffix Tree for Disk-based Indexing on Large Genome Sequences. , 2007, , .		8
169	Structural analysis of the hot spots in the binding between H1N1 HA and the 2D1 antibody: do mutations of H1N1 from 1918 to 2009 affect much on this binding?. Bioinformatics, 2011, 27, 2529-2536.	4.1	8
170	Integrating water exclusion theory into $\hat{I}^2$ contacts to predict binding free energy changes and binding hot spots. BMC Bioinformatics, 2014, 15, 57.	2.6	8
171	Contemporary Network Proteomics and Its Requirements. Biology, 2014, 3, 22-38.	2.8	8
172	On the Power of Incremental Evaluation in SQL-like Languages. Lecture Notes in Computer Science, 2000, , 17-30.	1.3	8
173	PROTREC: A probability-based approach for recovering missing proteins based on biological networks. Journal of Proteomics, 2022, 250, 104392.	2.4	8
174	Brief Overview of Bioinformatics Activities in Singapore. PLoS Computational Biology, 2009, 5, e1000508.	3.2	7
175	HPCgen A Fast Generator of Contact Networks of Large Urban Cities for Epidemiological Studies. , 2009, , .		7
176	Genome-wide analysis of regions similar to promoters of histone genes. BMC Systems Biology, 2010, 4, S4.	3.0	7
177	Effects of fear factors in disease propagation. Journal of Physics A: Mathematical and Theoretical, 2011, 44, 355101.	2.1	7
178	MIRACH: efficient model checker for quantitative biological pathway models. Bioinformatics, 2011, 27, 734-735.	4.1	7
179	Progressive dry-core-wet-rim hydration trend in a nested-ring topology of protein binding interfaces. BMC Bioinformatics, 2012, 13, 51.	2.6	7
180	A Database of Annotated Promoters of Genes Associated with Common Respiratory and Related Diseases. American Journal of Respiratory Cell and Molecular Biology, 2012, 47, 112-119.	2.9	7

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181	Valproic acid mediates miR-124 to down-regulate a novel protein target, GNAI1. Neurochemistry International, 2015, 91, 62-71.	3.8	7
182	Effective Response Metric: a novel tool to predict relapse in childhood acute lymphoblastic leukaemia using time‐series gene expression profiling. British Journal of Haematology, 2018, 181, 653-663.	2.5	7
183	Driving Neurogenesis in Neural Stem Cells with High Sensitivity Optogenetics. NeuroMolecular Medicine, 2020, 22, 139-149.	3.4	7
184	RECOGNITION OF POLYADENYLATION SITES FROM ARABIDOPSIS GENOMIC SEQUENCES. , 2007, , .		7
185	Unary quantifiers, transitive closure, and relations of large degree. Lecture Notes in Computer Science, 1998, , 183-193.	1.3	6
186	SIRIUS PSB: A GENERIC SYSTEM FOR ANALYSIS OF BIOLOGICAL SEQUENCES. Journal of Bioinformatics and Computational Biology, 2009, 07, 973-990.	0.8	6
187	Coupling Graphs, Efficient Algorithms and B-Cell Epitope Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 7-16.	3.0	6
188	TICA: Transcriptional Interaction and Coregulation Analyzer. Genomics, Proteomics and Bioinformatics, 2018, 16, 342-353.	6.9	6
189	kmcEx: memory-frugal and retrieval-efficient encoding of counted <i>k</i>-mers. Bioinformatics, 2019, 35, 4871-4878.	4.1	6
190	NAUTICA: classifying transcription factor interactions by positional and protein-protein interaction information. Biology Direct, 2020, 15, 13.	4.6	6
191	What can Venn diagrams teach us about doing data science better?. International Journal of Data Science and Analytics, 2021, 11, 1-10.	4.1	6
192	How doppelgÃnger effects in biomedical data confound machine learning. Drug Discovery Today, 2022, 27, 678-685.	6.4	6
193	An introduction to Remy's fast polymorphic record projection. SIGMOD Record, 1995, 24, 34-39.	1.2	5
194	Structural geography of the space of emerging patterns. Intelligent Data Analysis, 2005, 9, 567-588.	0.9	5
195	Structural and Functional Analysis of Multi-Interface Domains. PLoS ONE, 2012, 7, e50821.	2.5	5
196	Hi-Jack: a novel computational framework for pathway-based inference of host–pathogen interactions. Bioinformatics, 2015, 31, 2332-2339.	4.1	5
197	Big data and a bewildered lay analyst. Statistics and Probability Letters, 2018, 136, 73-77.	0.7	5
198	SPSNet: subpopulation-sensitive network-based analysis of heterogeneous gene expression data. BMC Systems Biology, 2018, 12, 28.	3.0	5

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199	Proteomic datasets of HeLa and SiHa cell lines acquired by DDA-PASEF and diaPASEF. Data in Brief, 2022, 41, 107919.	1.0	5
200	Finitely representable nested relations. Information Processing Letters, 1999, 70, 165-173.	0.6	4
201	Gaps in text-based knowledge discovery for biologyâ—¾. Drug Discovery Today, 2002, 7, 897-898.	6.4	4
202	Dragon Promoter Mapper (DPM): a Bayesian framework for modelling promoter structures. Bioinformatics, 2006, 22, 2310-2312.	4.1	4
203	Evolution and Maintenance of Frequent Pattern Space When Transactions Are Removed. , 2007, , 489-497.		4
204	PATTERN SPACE MAINTENANCE FOR DATA UPDATES AND INTERACTIVE MINING*. Computational Intelligence, 2010, 26, 282-317.	3.2	4
205	Embracing noise to improve cross-batch prediction accuracy. BMC Systems Biology, 2012, 6, S3.	3.0	4
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