

Limsoon Wong

List of Publications by Year in descending order

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Version: 2024-02-01

282
papers

10,149
citations

46918

47
h-index

45213

90
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291
all docs

291
docs citations

291
times ranked

9380
citing authors

#	ARTICLE	IF	CITATIONS
1	How doppelgänger effects in biomedical data confound machine learning. <i>Drug Discovery Today</i> , 2022, 27, 678-685.	3.2	6
2	PROTREC: A probability-based approach for recovering missing proteins based on biological networks. <i>Journal of Proteomics</i> , 2022, 250, 104392.	1.2	8
3	Proteomic datasets of HeLa and SiHa cell lines acquired by DDA-PASEF and diaPASEF. <i>Data in Brief</i> , 2022, 41, 107919.	0.5	5
4	EnsembleFam: towards more accurate protein family prediction in the twilight zone. <i>BMC Bioinformatics</i> , 2022, 23, 90.	1.2	3
5	Are batch effects still relevant in the age of big data?. <i>Trends in Biotechnology</i> , 2022, 40, 1029-1040.	4.9	10
6	Iterating on multiple collections in synchrony. <i>Journal of Functional Programming</i> , 2022, 32, .	0.5	0
7	Resolving missing protein problems using functional class scoring. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
8	What can Venn diagrams teach us about doing data science better?. <i>International Journal of Data Science and Analytics</i> , 2021, 11, 1-10.	2.4	6
9	PDR: a new genome assembly evaluation metric based on genetics concerns. <i>Bioinformatics</i> , 2021, 37, 289-295.	1.8	2
10	Identifying collateral and synthetic lethal vulnerabilities within the DNA-damage response. <i>BMC Bioinformatics</i> , 2021, 22, 250.	1.2	2
11	Mapbatch: Conservative Batch Normalization for Single Cell RNA-Sequencing Data Enables Discovery of Rare Cell Populations in a Multiple Myeloma Cohort. <i>Blood</i> , 2021, 138, 2954-2954.	0.6	2
12	Can Peripheral Blood-Derived Gene Expressions Characterize Individuals at Ultra-high Risk for Psychosis?. <i>Computational Psychiatry</i> , 2020, 1, 168.	1.1	20
13	Driving Neurogenesis in Neural Stem Cells with High Sensitivity Optogenetics. <i>NeuroMolecular Medicine</i> , 2020, 22, 139-149.	1.8	7
14	How to do quantile normalization correctly for gene expression data analyses. <i>Scientific Reports</i> , 2020, 10, 15534.	1.6	48
15	NAUTICA: classifying transcription factor interactions by positional and protein-protein interaction information. <i>Biology Direct</i> , 2020, 15, 13.	1.9	6
16	Extensions of the External Validation for Checking Learned Model Interpretability and Generalizability. <i>Patterns</i> , 2020, 1, 100129.	3.1	87
17	The Birth of Bio-data Science: Trends, Expectations, and Applications. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 5-15.	3.0	10
18	Avoid Oversimplifications in Machine Learning: Going beyond the Class-Prediction Accuracy. <i>Patterns</i> , 2020, 1, 100025.	3.1	18

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19	Allowing mutations in maximal matches boosts genome compression performance. <i>Bioinformatics</i> , 2020, 36, 4675-4681.	1.8	13
20	Turning straw into gold: building robustness into gene signature inference. <i>Drug Discovery Today</i> , 2019, 24, 31-36.	3.2	12
21	Proteomic investigation of intra-tumor heterogeneity using network-based contextualization " A case study on prostate cancer. <i>Journal of Proteomics</i> , 2019, 206, 103446.	1.2	3
22	kmcEx: memory-frugal and retrieval-efficient encoding of counted <i>k</i> -mers. <i>Bioinformatics</i> , 2019, 35, 4871-4878.	1.8	6
23	Advanced bioinformatics methods for practical applications in proteomics. <i>Briefings in Bioinformatics</i> , 2019, 20, 347-355.	3.2	19
24	Dealing with Confounders in Omics Analysis. <i>Trends in Biotechnology</i> , 2018, 36, 488-498.	4.9	22
25	Discovering pan-correlation patterns from time course data sets by efficient mining algorithms. <i>Computing (Vienna/New York)</i> , 2018, 100, 421-437.	3.2	4
26	Big data and a bewildered lay analyst. <i>Statistics and Probability Letters</i> , 2018, 136, 73-77.	0.4	5
27	SPSNet: subpopulation-sensitive network-based analysis of heterogeneous gene expression data. <i>BMC Systems Biology</i> , 2018, 12, 28.	3.0	5
28	Protein complex prediction by date hub removal. <i>Computational Biology and Chemistry</i> , 2018, 74, 407-419.	1.1	3
29	Understanding missing proteins: a functional perspective. <i>Drug Discovery Today</i> , 2018, 23, 644-651.	3.2	15
30	TICA: Transcriptional Interaction and Coregulation Analyzer. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 342-353.	3.0	6
31	Introduction to Selected Papers from GIW2018. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1802005.	0.3	0
32	Effective Response Metric: a novel tool to predict relapse in childhood acute lymphoblastic leukaemia using time-series gene expression profiling. <i>British Journal of Haematology</i> , 2018, 181, 653-663.	1.2	7
33	Implementing a Transcription Factor Interaction Prediction System Using the GenoMetric Query Language. <i>Methods in Molecular Biology</i> , 2018, 1807, 63-81.	0.4	1
34	Why breast cancer signatures are no better than random signatures explained. <i>Drug Discovery Today</i> , 2018, 23, 1818-1823.	3.2	17
35	Understanding Missing Proteins: Why Should You Care?. , 2018, , .		0
36	MapReduce for accurate error correction of next-generation sequencing data. <i>Bioinformatics</i> , 2017, 33, 3844-3851.	1.8	15

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37	Editorial "Bioinformatics development at the BGRSSB conference series: 10th anniversary. Journal of Bioinformatics and Computational Biology, 2017, 15, 1702001.	0.3	11
38	High-speed and high-ratio referential genome compression. Bioinformatics, 2017, 33, 3364-3372.	1.8	31
39	Transcriptome and functional analysis reveals hybrid vigor for oil biosynthesis in oil palm. Scientific Reports, 2017, 7, 439.	1.6	33
40	Why Batch Effects Matter in Omics Data, and How to Avoid Them. Trends in Biotechnology, 2017, 35, 498-507.	4.9	266
41	Class-paired Fuzzy SubNETs: A paired variant of the rank-based network analysis family for feature selection based on protein complexes. Proteomics, 2017, 17, e1700093.	1.3	1
42	Transcriptome Analysis Reveals Neuroprotective aspects of Human Reactive Astrocytes induced by Interleukin 1 β . Scientific Reports, 2017, 7, 13988.	1.6	41
43	OrthoGNC: A Software for Accurate Identification of Orthologs Based on Gene Neighborhood Conservation. Genomics, Proteomics and Bioinformatics, 2017, 15, 361-370.	3.0	12
44	Protein complex-based analysis is resistant to the obfuscating consequences of batch effects -- a case study in clinical proteomics. BMC Genomics, 2017, 18, 142.	1.2	18
45	NetProt: Complex-based Feature Selection. Journal of Proteome Research, 2017, 16, 3102-3112.	1.8	16
46	Redhyte: a self-diagnosing, self-correcting, and helpful hypothesis analysis platform. Journal of Information and Telecommunication, 2017, 1, 241-258.	2.2	1
47	Spectra-first feature analysis in clinical proteomics " A case study in renal cancer. Journal of Bioinformatics and Computational Biology, 2016, 14, 1644004.	0.3	3
48	Evaluating feature-selection stability in next-generation proteomics. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650029.	0.3	62
49	Advancing Clinical Proteomics via Analysis Based on Biological Complexes: A Tale of Five Paradigms. Journal of Proteome Research, 2016, 15, 3167-3179.	1.8	37
50	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.	1.5	34
51	GFS: fuzzy preprocessing for effective gene expression analysis. BMC Bioinformatics, 2016, 17, 540.	1.2	35
52	Integrating Networks and Proteomics: Moving Forward. Trends in Biotechnology, 2016, 34, 951-959.	4.9	38
53	Design principles for clinical network-based proteomics. Drug Discovery Today, 2016, 21, 1130-1138.	3.2	18
54	Efficient Mining of Pan-Correlation Patterns from Time Course Data. Lecture Notes in Computer Science, 2016, , 234-249.	1.0	1

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55	Redhyte: Towards a Self-diagnosing, Self-correcting, and Helpful Analytic Platform. Lecture Notes in Computer Science, 2016, , 3-12.	1.0	0
56	Two scenarios for overcoming drug resistance by co-targeting. International Journal of Bioinformatics Research and Applications, 2015, 11, 72.	0.1	4
57	Regularizing predicted complexes by mutually exclusive protein-protein interactions. , 2015, , .		3
58	Prediction of problematic complexes from PPI networks: sparse, embedded, and small complexes. Biology Direct, 2015, 10, 40.	1.9	23
59	Inferring synthetic lethal interactions from mutual exclusivity of genetic events in cancer. Biology Direct, 2015, 10, 57.	1.9	64
60	Quantitative proteomics signature profiling based on network contextualization. Biology Direct, 2015, 10, 71.	1.9	34
61	Methods for protein complex prediction and their contributions towards understanding the organisation, function and dynamics of complexes. FEBS Letters, 2015, 589, 2590-2602.	1.3	66
62	Supporting Exploratory Hypothesis Testing and Analysis. ACM Transactions on Knowledge Discovery From Data, 2015, 9, 1-24.	2.5	3
63	From the static interactome to dynamic protein complexes: Three challenges. Journal of Bioinformatics and Computational Biology, 2015, 13, 1571001.	0.3	30
64	Valproic acid mediates miR-124 to down-regulate a novel protein target, GNAI1. Neurochemistry International, 2015, 91, 62-71.	1.9	7
65	The floral transcriptome of ylang ylang (<i>Cananga odorata</i> var. <i>fruticosa</i>) uncovers biosynthetic pathways for volatile organic compounds and a multifunctional and novel sesquiterpene synthase. Journal of Experimental Botany, 2015, 66, 3959-3975.	2.4	50
66	Hi-Jack: a novel computational framework for pathway-based inference of host-pathogen interactions. Bioinformatics, 2015, 31, 2332-2339.	1.8	5
67	A consensus linkage map of oil palm and a major QTL for stem height. Scientific Reports, 2015, 5, 8232.	1.6	49
68	Burial Level Change Defines a High Energetic Relevance for Protein Binding Interfaces. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 410-421.	1.9	1
69	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.	0.3	30
70	John Wooley and JBCB. Journal of Bioinformatics and Computational Biology, 2015, 13, 1501001.	0.3	0
71	Comparative transcriptomics unravel biochemical specialization of leaf tissues of Stevia (<i>Stevia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62 T	2.3	17
72	PCR-based identification of Adriatic specimen of three scorpionfish species (Scorpaenidae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 T	0.7	2

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73	JBCB, the first decade. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1401001.	0.3	1
74	Using data fusion for scoring reliability of protein-protein interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450014.	0.3	2
75	Coupling Graphs, Efficient Algorithms and B-Cell Epitope Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 7-16.	1.9	6
76	Guest Editorial for the International Conference on Genome Informatics (GIW 2013). <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 5-6.	1.9	1
77	eCAMBer: efficient support for large-scale comparative analysis of multiple bacterial strains. <i>BMC Bioinformatics</i> , 2014, 15, 65.	1.2	21
78	Rule discovery and distance separation to detect reliable miRNA biomarkers for the diagnosis of lung squamous cell carcinoma. <i>BMC Genomics</i> , 2014, 15, S16.	1.2	10
79	Next generation sequencing unravels the biosynthetic ability of Spearmint (<i>Mentha spicata</i>) peltate glandular trichomes through comparative transcriptomics. <i>BMC Plant Biology</i> , 2014, 14, 292.	1.6	64
80	LipidGO: database for lipid-related GO terms and applications. <i>Bioinformatics</i> , 2014, 30, 1043-1044.	1.8	2
81	Computational proteomics: designing a comprehensive analytical strategy. <i>Drug Discovery Today</i> , 2014, 19, 266-274.	3.2	18
82	Finding consistent disease subnetworks using PFSNet. <i>Bioinformatics</i> , 2014, 30, 189-196.	1.8	49
83	Integrating water exclusion theory into $\hat{\tau}^2$ contacts to predict binding free energy changes and binding hot spots. <i>BMC Bioinformatics</i> , 2014, 15, 57.	1.2	8
84	Stringent homology-based prediction of <i>H. sapiens</i> - <i>M. tuberculosis</i> H37Rv protein-protein interactions. <i>Biology Direct</i> , 2014, 9, 5.	1.9	74
85	A Flexible Approach to Finding Representative Pattern Sets. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2014, 26, 1562-1574.	4.0	11
86	Contemporary Network Proteomics and Its Requirements. <i>Biology</i> , 2014, 3, 22-38.	1.3	8
87	GWAMAR: Genome-wide assessment of mutations associated with drug resistance in bacteria. <i>BMC Genomics</i> , 2014, 15, S10.	1.2	22
88	Discovery of small protein complexes from PPI networks with size-specific supervised weighting. <i>BMC Systems Biology</i> , 2014, 8, S3.	3.0	34
89	A semi-automated methodology for finding lipid-related GO terms. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	1
90	Enhancing the utility of Proteomics Signature Profiling (PSP) with Pathway Derived Subnets (PDSs), performance analysis and specialised ontologies. <i>BMC Genomics</i> , 2013, 14, 35.	1.2	35

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91	Random forests on Hadoop for genome-wide association studies of multivariate neuroimaging phenotypes. BMC Bioinformatics, 2013, 14, S6.	1.2	34
92	Structural analysis on mutation residues and interfacial water molecules for human TIM disease understanding. BMC Bioinformatics, 2013, 14, S11.	1.2	14
93	PROGRESS IN COMPUTATIONAL STUDIES OF HOST-PATHOGEN INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1230001.	0.3	54
94	Stringent DDI-based Prediction of H. sapiens-M. tuberculosis H37Rv Protein-Protein Interactions. BMC Systems Biology, 2013, 7, S6.	3.0	34
95	International Conference on Genome Informatics (GIW 2013) in Singapore: introduction to the systems biology contributions. BMC Systems Biology, 2013, 7, I1.	3.0	0
96	Networks in proteomics analysis of cancer. Current Opinion in Biotechnology, 2013, 24, 1122-1128.	3.3	23
97	Accurate prediction of hot spot residues through physicochemical characteristics of amino acid sequences. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1351-1362.	1.5	43
98	Integrative Toxicoproteomics Implicates Impaired Mitochondrial Glutathione Import as an Off-Target Effect of Troglitazone. Journal of Proteome Research, 2013, 12, 2933-2945.	1.8	31
99	Comparative Network-Based Recovery Analysis and Proteomic Profiling of Neurological Changes in Valproic Acid-Treated Mice. Journal of Proteome Research, 2013, 12, 2116-2127.	1.8	42
100	A performance study of three disk-based structures for indexing and querying frequent itemsets. Proceedings of the VLDB Endowment, 2013, 6, 505-516.	2.1	3
101	A dichotomy in the intensional expressive power of nested relational calculi augmented with aggregate functions and a powerset operator. , 2013, , .		2
102	Epstein-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.	3.3	61
103	PLncDB: plant long non-coding RNA database. Bioinformatics, 2013, 29, 1068-1071.	1.8	163
104	DISRUPTION OF PROTEIN COMPLEXES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341008.	0.3	12
105	AN INTRODUCTION TO SOME NEW RESULTS IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY. Journal of Bioinformatics and Computational Biology, 2013, 11, 1301001.	0.3	2
106	THE 24TH INTERNATIONAL CONFERENCE ON GENOME INFORMATICS, GIW2013, IN SINGAPORE. Journal of Bioinformatics and Computational Biology, 2013, 11, 1302003.	0.3	2
107	The Dichotomous Intensional Expressive Power of the Nested Relational Calculus with Powerset. Lecture Notes in Computer Science, 2013, , 542-556.	1.0	0
108	Finding minimum representative pattern sets. , 2012, , .		10

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109	The role of miRNAs in complex formation and control. <i>Bioinformatics</i> , 2012, 28, 453-456.	1.8	15
110	Response: an empirical comparison of several recent epistatic interaction detection methods. <i>Bioinformatics</i> , 2012, 28, 147-148.	1.8	19
111	AssocExplorer. , 2012, , .		16
112	Discovery of Protein Complexes with Core-Attachment Structures from Tandem Affinity Purification (TAP) Data. <i>Journal of Computational Biology</i> , 2012, 19, 1027-1042.	0.8	36
113	Epidemic reemergence in adaptive complex networks. <i>Physical Review E</i> , 2012, 85, 036107.	0.8	48
114	A SHORT INTRODUCTION TO SOME RECENT PROGRESS IN PHYLOGENETIC NETWORK RECONSTRUCTION, GENOME MAPPING, GENE EXPRESSION ANALYSIS, MOLECULAR DYNAMIC SIMULATION, AND OTHER PROBLEMS IN BIOINFORMATICS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1203002.	0.3	1
115	Intrinsically disordered proteins aggregate at fungal cell-to-cell channels and regulate intercellular connectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15781-15786.	3.3	69
116	A network-based maximum link approach towards MS identifies potentially important roles for undetected ARRB1/2 and ACTB in liver cancer progression. <i>International Journal of Bioinformatics Research and Applications</i> , 2012, 8, 155.	0.1	15
117	Conservation of water molecules in protein binding interfaces. <i>International Journal of Bioinformatics Research and Applications</i> , 2012, 8, 228.	0.1	3
118	Detection of Outlier Residues for Improving Interface Prediction in Protein Heterocomplexes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1155-1165.	1.9	22
119	Progressive dry-core-wet-rim hydration trend in a nested-ring topology of protein binding interfaces. <i>BMC Bioinformatics</i> , 2012, 13, 51.	1.2	7
120	Z-score biological significance of binding hot spots of protein interfaces by using crystal packing as the reference state. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1457-1467.	1.1	2
121	Proteomics Signature Profiling (PSP): A Novel Contextualization Approach for Cancer Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 1571-1581.	1.8	47
122	CMPF: Class-switching minimized pathfinding in metabolic networks. <i>BMC Bioinformatics</i> , 2012, 13, S17.	1.2	9
123	Improved statistical model checking methods for pathway analysis. <i>BMC Bioinformatics</i> , 2012, 13, S15.	1.2	19
124	B-cell epitope prediction through a graph model. <i>BMC Bioinformatics</i> , 2012, 13, S20.	1.2	29
125	An approach to identifying drug resistance associated mutations in bacterial strains. <i>BMC Genomics</i> , 2012, 13, S23.	1.2	16
126	Embracing noise to improve cross-batch prediction accuracy. <i>BMC Systems Biology</i> , 2012, 6, S3.	3.0	4

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127	Supervised maximum-likelihood weighting of composite protein networks for complex prediction. BMC Systems Biology, 2012, 6, S13.	3.0	36
128	IntPath—an integrated pathway gene relationship database for model organisms and important pathogens. BMC Systems Biology, 2012, 6, S2.	3.0	41
129	Structural and Functional Analysis of Multi-Interface Domains. PLoS ONE, 2012, 7, e50821.	1.1	5
130	How advancement in biological network analysis methods empowers proteomics. Proteomics, 2012, 12, 550-563.	1.3	58
131	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.	1.4	7
132	Evaluating Temporal Factors in Combined Interventions of Workforce Shift and School Closure for Mitigating the Spread of Influenza. PLoS ONE, 2012, 7, e32203.	1.1	18
133	Predicting Protein Functions from Protein Interaction Networks. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 50-70.	0.8	4
134	Network-Based Pipeline for Analyzing MS Data: An Application toward Liver Cancer. Journal of Proteome Research, 2011, 10, 2261-2272.	1.8	51
135	CAMBer: an approach to support comparative analysis of multiple bacterial strains. BMC Genomics, 2011, 12, S6.	1.2	22
136	Mining Iterative Generators and Representative Rules for Software Specification Discovery. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 282-296.	4.0	10
137	Determination of a molecular signature of acute T-cell-mediated renal allograft rejection using quantitative real-time RT-PCR of 45 genes on a low density array. Pathology, 2011, 43, 72-75.	0.3	0
138	Effects of fear factors in disease propagation. Journal of Physics A: Mathematical and Theoretical, 2011, 44, 355101.	0.7	7
139	Controlling false positives in association rule mining. Proceedings of the VLDB Endowment, 2011, 5, 145-156.	2.1	19
140	Temporal factors in school closure policy for mitigating the spread of influenza. Journal of Public Health Policy, 2011, 32, 180-197.	1.0	12
141	Decomposing PPI networks for complex discovery. Proteome Science, 2011, 9, S15.	0.7	26
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	Finding consistent disease subnetworks across microarray datasets. BMC Bioinformatics, 2011, 12, S15.	1.2	39
144	Comparative analysis and assessment of M. tuberculosis H37Rv protein-protein interaction datasets. BMC Genomics, 2011, 12, S20.	1.2	29

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145	Low cytosine triphosphate synthase 2 expression renders resistance to 5-fluorouracil in colorectal cancer. <i>Cancer Biology and Therapy</i> , 2011, 11, 599-608.	1.5	13
146	Using Biological Networks in Protein Function Prediction and Gene Expression Analysis. <i>Internet Mathematics</i> , 2011, 7, 274-298.	0.7	3
147	<i>eCEO</i> : an efficient Cloud Epistasis cOmputing model in genome-wide association study. <i>Bioinformatics</i> , 2011, 27, 1045-1051.	1.8	25
148	MIRACH: efficient model checker for quantitative biological pathway models. <i>Bioinformatics</i> , 2011, 27, 734-735.	1.8	7
149	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?. <i>Bioinformatics</i> , 2011, 27, 2529-2536.	1.8	8
150	CAMBerVis: visualization software to support comparative analysis of multiple bacterial strains. <i>Bioinformatics</i> , 2011, 27, 3313-3314.	1.8	2
151	INTRODUCTION " Some New Results and Tools for Protein Function Prediction, RNA Target Site Prediction, Genotype Calling, Environmental Genomics, and More. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, v-vii.	0.3	2
152	Antibody-Specified B-Cell Epitope Prediction in Line with the Principle of Context-Awareness. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1483-1494.	1.9	36
153	Towards exploratory hypothesis testing and analysis. , 2011, , .		10
154	An empirical comparison of several recent epistatic interaction detection methods. <i>Bioinformatics</i> , 2011, 27, 2936-2943.	1.8	61
155	BRIEF INTRODUCTION TO SOME NEW PAPERS ON LATERAL TRANSFER RECONSTRUCTION, DRUG CANDIDATE SCREENING, DISEASE GENE IDENTIFICATION, AND OTHER RESULTS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, v-vii.	0.3	0
156	Protein Function Prediction Using Protein-Protein Interaction Networks. , 2011, , 243-270.		0
157	Generation of arbitrary two-point correlated directed networks with given modularity. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2010, 374, 3129-3135.	0.9	11
158	Protein Interactome Analysis for Countering Pathogen Drug Resistance. <i>Journal of Computer Science and Technology</i> , 2010, 25, 124-130.	0.9	13
159	Consistency, comprehensiveness, and compatibility of pathway databases. <i>BMC Bioinformatics</i> , 2010, 11, 449.	1.2	60
160	FastTagger: an efficient algorithm for genome-wide tag SNP selection using multi-marker linkage disequilibrium. <i>BMC Bioinformatics</i> , 2010, 11, 66.	1.2	33
161	Protein complex prediction based on k-connected subgraphs in protein interaction network. <i>BMC Systems Biology</i> , 2010, 4, 129.	3.0	37
162	Weighted complex network analysis of travel routes on the Singapore public transportation system. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 5852-5863.	1.2	159

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163	Genome-wide analysis of regions similar to promoters of histone genes. BMC Systems Biology, 2010, 4, S4.	3.0	7
164	PATTERN SPACE MAINTENANCE FOR DATA UPDATES AND INTERACTIVE MINING*. Computational Intelligence, 2010, 26, 282-317.	2.1	4
165	DA 1.0: parameter estimation of biological pathways using data assimilation approach. Bioinformatics, 2010, 26, 1794-1796.	1.8	10
166	CAMBer: An approach to support comparative analysis of multiple bacterial strains. , 2010, , .		0
167	Overcoming drug resistance by co-targeting. , 2010, , .		2
168	EFFICIENT MINING OF HAPLOTYPE PATTERNS FOR LINKAGE DISEQUILIBRIUM MAPPING. Journal of Bioinformatics and Computational Biology, 2010, 08, 127-146.	0.3	2
169	WRESTLING WITH BIOMEDICAL RESEARCH RESULTS: LANGUAGE RESOURCES AND LITERATURE ANALYSIS. Journal of Bioinformatics and Computational Biology, 2010, 08, 129-130.	0.3	1
170	BRIEF INTRODUCTION TO SOME NEW RESULTS IN GENE EXPRESSION ANALYSIS, SYSTEMS BIOLOGY MODELING, MOTIF IDENTIFICATION, AND (NONCODING) RNA ANALYSIS. Journal of Bioinformatics and Computational Biology, 2010, 08, v-vii.	0.3	0
171	NEW RESULTS IN BIOLOGICAL SEQUENCE ANALYSIS, COMPLEX GENEâ€“DISEASE ASSOCIATION, qPCR CALCULATION, AND BIOLOGICAL TEXT MINING. Journal of Bioinformatics and Computational Biology, 2010, 08, v-vii.	0.3	0
172	Efficiently Finding the Best Parameter for the Emerging Pattern-Based Classifier PCL. Lecture Notes in Computer Science, 2010, , 121-133.	1.0	3
173	Brief Overview of Bioinformatics Activities in Singapore. PLoS Computational Biology, 2009, 5, e1000508.	1.5	7
174	Key node selection for containing infectious disease spread using particle swarm optimization. , 2009, , .		10
175	SIRIUS PSB: A GENERIC SYSTEM FOR ANALYSIS OF BIOLOGICAL SEQUENCES. Journal of Bioinformatics and Computational Biology, 2009, 07, 973-990.	0.3	6
176	Pharmacodynamic Effects of Seliciclib, an Orally Administered Cell Cycle Modulator, in Undifferentiated Nasopharyngeal Cancer. Clinical Cancer Research, 2009, 15, 1435-1442.	3.2	83
177	Complex discovery from weighted PPI networks. Bioinformatics, 2009, 25, 1891-1897.	1.8	434
178	Efficient mining of distance-based subspace clusters. Statistical Analysis and Data Mining, 2009, 2, 427-444.	1.4	14
179	A Probabilistic Graphâ€“Theoretic Approach to Integrate Multiple Predictions for the Proteinâ€“Protein Subnetwork Prediction Challenge. Annals of the New York Academy of Sciences, 2009, 1158, 224-233.	1.8	20
180	Non-redundant sequential rulesâ€“Theory and algorithm. Information Systems, 2009, 34, 438-453.	2.4	58

#	ARTICLE	IF	CITATIONS
181	HPCgen A Fast Generator of Contact Networks of Large Urban Cities for Epidemiological Studies. , 2009, , .		7
182	Deciphering Drug Action and Escape Pathways: An Example on Nasopharyngeal Carcinoma. Lecture Notes in Computer Science, 2009, , 199-210.	1.0	3
183	Predicting Protein Functions from Protein Interaction Networks. , 2009, , 203-222.		3
184	Maintenance of Frequent Patterns. , 2009, , 273-293.		1
185	A Preliminary Study on the Effects of Fear Factors in Disease Propagation. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2009, , 1387-1397.	0.2	0
186	Mining Conditional Contrast Patterns. , 2009, , 294-310.		4
187	A new concise representation of frequent itemsets using generators and a positive border. Knowledge and Information Systems, 2008, 17, 35-56.	2.1	29
188	Efficient mining of frequent XML query patterns with repeating-siblings. Information and Software Technology, 2008, 50, 375-389.	3.0	15
189	Increasing the reliability of protein interactomes. Drug Discovery Today, 2008, 13, 652-658.	3.2	61
190	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. Journal of Bioinformatics and Computational Biology, 2008, 06, 435-466.	0.3	123
191	Exploiting indirect neighbours and topological weight to predict protein function from protein-protein interactions. Bioinformatics, 2008, 24, 452-452.	1.8	3
192	Effective Pruning Techniques for Mining Quasi-Cliques. Lecture Notes in Computer Science, 2008, , 33-49.	1.0	66
193	Assessing and Predicting Protein Interactions Using Both Local and Global Network Topological Metrics. , 2008, , .		31
194	Manifestation and Exploitation of Invariants in Bioinformatics. , 2008, , 28-28.		0
195	An efficient strategy for extensive integration of diverse biological data for protein function prediction. Bioinformatics, 2007, 23, 3364-3373.	1.8	56
196	Mining statistically important equivalence classes and delta-discriminative emerging patterns. , 2007, , .		83
197	CPS-tree: A Compact Partitioned Suffix Tree for Disk-based Indexing on Large Genome Sequences. , 2007, , .		8
198	Distance Based Subspace Clustering with Flexible Dimension Partitioning. , 2007, , .		29

#	ARTICLE	IF	CITATIONS
199	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.	4.0	101
200	Evolution and Maintenance of Frequent Pattern Space When Transactions Are Removed. , 2007, , 489-497.		4
201	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. , 2007, , .		33
202	Using indirect protein interactions for the prediction of Gene Ontology functions. BMC Bioinformatics, 2007, 8, S8.	1.2	54
203	RECOGNITION OF POLYADENYLATION SITES FROM ARABIDOPSIS GENOMIC SEQUENCES. , 2007, , .		7
204	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.	3.2	12
205	Manifestation and Exploitation of Invariants in Bioinformatics. Lecture Notes in Computer Science, 2007, , 365-377.	1.0	0
206	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
207	Adventures of a Logician-Engineer: A Journey through Logic, Engineering, Medicine, Biology, and Statistics. , 2006, , .		0
208	Positive Borders or Negative Borders: How to Make Lossless Generator Based Representations Concise. , 2006, , .		8
209	Computational Biology in NUS School of Computing. Asia Pacific Biotech News, 2006, 10, 1483-1486.	0.5	0
210	Dragon Promoter Mapper (DPM): a Bayesian framework for modelling promoter structures. Bioinformatics, 2006, 22, 2310-2312.	1.8	4
211	Exploiting indirect neighbours and topological weight to predict protein function from protein-protein interactions. Bioinformatics, 2006, 22, 1623-1630.	1.8	533
212	Discovering motif pairs at interaction sites from protein sequences on a proteome-wide scale. Bioinformatics, 2006, 22, 989-996.	1.8	54
213	Exploring Essential Attributes for Detecting MicroRNA Precursors from Background Sequences. Lecture Notes in Computer Science, 2006, , 131-145.	1.0	10
214	Gene Expression Profiling of Paired Pre- and Post-Prednisolone (PRED) BM Samples from Childhood ALL Identifies Robust Signatures for PRED Response and Eventual Outcome.. Blood, 2006, 108, 222-222.	0.6	1
215	IDENTIFICATION OF MICRORNA PRECURSORS VIA SVM. , 2005, , .		2
216	LinkageTracker: A Discriminative Pattern Tracking Approach to Linkage Disequilibrium Mapping. Lecture Notes in Computer Science, 2005, , 30-42.	1.0	1

#	ARTICLE	IF	CITATIONS
217	Structural geography of the space of emerging patterns. <i>Intelligent Data Analysis</i> , 2005, 9, 567-588.	0.4	5
218	Use of extreme patient samples for outcome prediction from gene expression data. <i>Bioinformatics</i> , 2005, 21, 3377-3384.	1.8	28
219	DNAFSMiner: a web-based software toolbox to recognize two types of functional sites in DNA sequences. <i>Bioinformatics</i> , 2005, 21, 671-673.	1.8	45
220	Identification of Cell Cycle-regulated Genes in Fission Yeast. <i>Molecular Biology of the Cell</i> , 2005, 16, 1026-1042.	0.9	159
221	Relative risk and odds ratio. , 2005, , .		45
222	Guest Editors' Introduction: Data Mining in Bioinformatics. <i>IEEE Intelligent Systems</i> , 2005, 20, 16-18.	4.0	74
223	Selection of patient samples and genes for outcome prediction. , 2004, , 382-92.		2
224	DeEPs: A New Instance-Based Lazy Discovery and Classification System. <i>Machine Learning</i> , 2004, 54, 99-124.	3.4	93
225	Accomplishments and challenges in bioinformatics. <i>IT Professional</i> , 2004, 6, 44-50.	1.4	13
226	The Kleisli Approach to Data Transformation and Integration. , 2004, , 135-165.		3
227	Incremental recomputation in local languages. <i>Information and Computation</i> , 2003, 181, 88-98.	0.5	18
228	Discovery of significant rules for classifying cancer diagnosis data. <i>Bioinformatics</i> , 2003, 19, ii93-ii102.	1.8	99
229	Simple rules underlying gene expression profiles of more than six subtypes of acute lymphoblastic leukemia (ALL) patients. <i>Bioinformatics</i> , 2003, 19, 71-78.	1.8	106
230	DATA MINING TOOLS FOR BIOLOGICAL SEQUENCES. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 139-167.	0.3	66
231	Using Rules to Analyse Bio-medical Data: A Comparison between C4.5 and PCL. <i>Lecture Notes in Computer Science</i> , 2003, , 254-265.	1.0	28
232	Bioinformatics in Singapore. <i>Asia Pacific Biotech News</i> , 2003, 07, 88-92.	0.5	1
233	Bioinformatics Adventures in Database Research. <i>Lecture Notes in Computer Science</i> , 2003, , 31-46.	1.0	9
234	The Kleisli Query System as a Backbone for Bioinformatics Data Integration and Analysis. , 2003, , 147-187.		15

#	ARTICLE	IF	CITATIONS
235	Identifying good diagnostic gene groups from gene expression profiles using the concept of emerging patterns. <i>Bioinformatics</i> , 2002, 18, 725-734.	1.8	139
236	FIMM, a database of functional molecular immunology: update 2002. <i>Nucleic Acids Research</i> , 2002, 30, 226-229.	6.5	38
237	Accomplishments and challenges in literature data mining for biology. <i>Bioinformatics</i> , 2002, 18, 1553-1561.	1.8	229
238	Technologies for integrating biological data. <i>Briefings in Bioinformatics</i> , 2002, 3, 389-404.	3.2	40
239	Lower bounds for invariant queries in logics with counting. <i>Theoretical Computer Science</i> , 2002, 288, 153-180.	0.5	11
240	Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. <i>Cancer Cell</i> , 2002, 1, 133-143.	7.7	1,756
241	Optimal gene expression analysis by microarrays. <i>Cancer Cell</i> , 2002, 2, 353-361.	7.7	149
242	Gaps in text-based knowledge discovery for biology. <i>Drug Discovery Today</i> , 2002, 7, 897-898.	3.2	4
243	Geography of Differences between Two Classes of Data. <i>Lecture Notes in Computer Science</i> , 2002, , 325-337.	1.0	10
244	Logics with aggregate operators. <i>Journal of the ACM</i> , 2001, 48, 880-907.	1.8	58
245	BIOINFORMATICS INTEGRATION SIMPLIFIED: THE KLEISLI WAY. , 2001, , 79-90.		1
246	Kleisli, a functional query system. <i>Journal of Functional Programming</i> , 2000, 10, 19-56.	0.5	104
247	Local properties of query languages. <i>Theoretical Computer Science</i> , 2000, 239, 277-308.	0.5	20
248	FIMM, a database of functional molecular immunology. <i>Nucleic Acids Research</i> , 2000, 28, 222-224.	6.5	48
249	On the Power of Incremental Evaluation in SQL-like Languages. <i>Lecture Notes in Computer Science</i> , 2000, , 17-30.	1.0	8
250	The functional guts of the Kleisli query system. <i>ACM SIGPLAN Notices</i> , 2000, 35, 1-10.	0.2	4
251	Finitely representable nested relations. <i>Information Processing Letters</i> , 1999, 70, 165-173.	0.4	4
252	Kleisli: a new tool for data integration in biology. <i>Trends in Biotechnology</i> , 1999, 17, 351-355.	4.9	58

#	ARTICLE	IF	CITATIONS
253	CAEP: Classification by Aggregating Emerging Patterns. Lecture Notes in Computer Science, 1999, , 30-42.	1.0	247
254	Relational expressive power of constraint query languages. Journal of the ACM, 1998, 45, 1-34.	1.8	94
255	Unary quantifiers, transitive closure, and relations of large degree. Lecture Notes in Computer Science, 1998, , 183-193.	1.0	6
256	A protein patent query system powered by Kleisli. SIGMOD Record, 1998, 27, 593-595.	0.7	3
257	Incremental recomputation of recursive queries with nested sets and aggregate functions. Lecture Notes in Computer Science, 1998, , 222-238.	1.0	14
258	A Graphical Interface to Genome Multidatabases. Journal of Database Management, 1998, 9, 24-32.	1.0	2
259	Query Languages for Bags and Aggregate Functions. Journal of Computer and System Sciences, 1997, 55, 241-272.	0.9	73
260	Query languages for bags. ACM SIGACT News, 1996, 27, 30-44.	0.1	24
261	Semantic Representations and Query Languages for Or-Sets. Journal of Computer and System Sciences, 1996, 52, 125-142.	0.9	17
262	Normal Forms and Conservative Extension Properties for Query Languages over Collection Types. Journal of Computer and System Sciences, 1996, 52, 495-505.	0.9	50
263	Local properties of query languages. Lecture Notes in Computer Science, 1996, , 140-154.	1.0	13
264	A query language for multidimensional arrays. SIGMOD Record, 1996, 25, 228-239.	0.7	33
265	On representation and querying incomplete information in databases with bags. Information Processing Letters, 1995, 56, 209-214.	0.4	11
266	Polymorphic queries across sets, bags, and lists. ACM SIGPLAN Notices, 1995, 30, 39-44.	0.2	2
267	An introduction to Remy's fast polymorphic record projection. SIGMOD Record, 1995, 24, 34-39.	0.7	5
268	On two forms of structural recursion. Lecture Notes in Computer Science, 1995, , 111-124.	1.0	14
269	Conservativity of nested relational calculi with internal generic functions. Information Processing Letters, 1994, 49, 273-280.	0.4	21
270	Aggregate Functions, Conservative Extension, and Linear Orders. Workshops in Computing, 1994, , 282-294.	0.4	20

#	ARTICLE	IF	CITATIONS
271	Some Properties of Query Languages for Bags. Workshops in Computing, 1994, , 97-114.	0.4	34
272	Comprehension syntax. SIGMOD Record, 1994, 23, 87-96.	0.7	165
273	Normal forms and conservative properties for query languages over collection types. , 1993, , .		38
274	Naturally embedded query languages. Lecture Notes in Computer Science, 1992, , 140-154.	1.0	74
275	Treating failure as value. ACM SIGPLAN Notices, 1990, 25, 29-32.	0.2	4
276	Treating failure as state. ACM SIGPLAN Notices, 1990, 25, 24-26.	0.2	0
277	QUICK: graphical user interface to multiple databases. , 0, , .		1
278	Logics with aggregate operators. , 0, , .		8
279	Kleisli: its exchange format, supporting tools, and an application in protein interaction extraction. , 0, , .		12
280	Solving the fragmentation problem of decision trees by discovering boundary emerging patterns. , 0, , .		0
281	Patient Survival Prediction from Gene Expression Data. , 0, , 89-111.		0
282	On Impossibility of Decremental Recomputation of Recursive Queries in Relational Calculus and SQL. , 0, , .		9