

Zhiyong

List of Publications by Year in descending order

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Version: 2024-02-01

191
papers

18,606
citations

25014

57
h-index

20343

116
g-index

196
all docs

196
docs citations

196
times ranked

18455
citing authors

#	ARTICLE	IF	CITATIONS
1	Database resources of the national center for biotechnology information. <i>Nucleic Acids Research</i> , 2022, 50, D20-D26.	6.5	887
2	Global-Local attention network with multi-task uncertainty loss for abnormal lymph node detection in MR images. <i>Medical Image Analysis</i> , 2022, 77, 102345.	7.0	13
3	DeepLensNet: Deep Learning Automated Diagnosis and Quantitative Classification of Cataract Type and Severity. <i>Ophthalmology</i> , 2022, 129, 571-584.	2.5	23
4	Predicting myocardial infarction through retinal scans and minimal personal information. <i>Nature Machine Intelligence</i> , 2022, 4, 55-61.	8.3	30
5	Detecting visually significant cataract using retinal photograph-based deep learning. <i>Nature Aging</i> , 2022, 2, 264-271.	5.3	14
6	PhenoRerank: A re-ranking model for phenotypic concept recognition pre-trained on human phenotype ontology. <i>Journal of Biomedical Informatics</i> , 2022, 129, 104059.	2.5	2
7	Machine Learning Approach to Facilitate Knowledge Synthesis at the Intersection of Liver Cancer, Epidemiology, and Health Disparities Research. <i>JCO Clinical Cancer Informatics</i> , 2022, , .	1.0	0
8	Recent advances in biomedical literature mining. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	59
9	LitCovid: an open database of COVID-19 literature. <i>Nucleic Acids Research</i> , 2021, 49, D1534-D1540.	6.5	189
10	COVID-19-CT-CXR: A Freely Accessible and Weakly Labeled Chest X-Ray and CT Image Collection on COVID-19 From Biomedical Literature. <i>IEEE Transactions on Big Data</i> , 2021, 7, 3-12.	4.4	55
11	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2021, 49, D10-D17.	6.5	545
12	Recent advances of automated methods for searching and extracting genomic variant information from biomedical literature. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
13	PhenoTagger: a hybrid method for phenotype concept recognition using human phenotype ontology. <i>Bioinformatics</i> , 2021, 37, 1884-1890.	1.8	18
14	NLM-Chem, a new resource for chemical entity recognition in PubMed full text literature. <i>Scientific Data</i> , 2021, 8, 91.	2.4	26
15	Learning Few-Shot Chest X-Ray Diagnosis Using Images From The Published Scientific Literature. , 2021, , .		3
16	Multimodal, multitask, multiattention (M3) deep learning detection of reticular pseudodrusen: Toward automated and accessible classification of age-related macular degeneration. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 1135-1148.	2.2	11
17	LitSuggest: a web-based system for literature recommendation and curation using machine learning. <i>Nucleic Acids Research</i> , 2021, 49, W352-W358.	6.5	28
18	NLM-Gene, a richly annotated gold standard dataset for gene entities that addresses ambiguity and multi-species gene recognition. <i>Journal of Biomedical Informatics</i> , 2021, 118, 103779.	2.5	9

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19	Artificial Intelligence in Action: Addressing the COVID-19 Pandemic with Natural Language Processing. Annual Review of Biomedical Data Science, 2021, 4, 313-339.	2.8	38
20	Improving Interpretability in Machine Diagnosis. Ophthalmology Science, 2021, 1, 100038.	1.0	8
21	Editorâ€™s introduction to the special section on the 7th Biomedical Linked Annotation Hackathon (BLAH7). Genomics and Informatics, 2021, 19, e20.	0.4	0
22	BERT-GT: cross-sentence <i>n</i>-ary relation extraction with BERT and Graph Transformer. Bioinformatics, 2021, 36, 5678-5685.	1.8	19
23	Artificial Intelligence in Age-Related Macular Degeneration (AMD). , 2021, , 101-112.		3
24	Evolving use of ancestry, ethnicity, and race in genetics researchâ€™A survey spanning seven decades. American Journal of Human Genetics, 2021, 108, 2215-2223.	2.6	27
25	Benchmarking Effectiveness and Efficiency of Deep Learning Models for Semantic Textual Similarity in the Clinical Domain: Validation Study. JMIR Medical Informatics, 2021, 9, e27386.	1.3	5
26	Multi-task deep learning-based survival analysis on the prognosis of late AMD using the longitudinal data in AREDS.. AMIA ... Annual Symposium proceedings, 2021, 2021, 506-515.	0.2	0
27	FullMeSH: improving large-scale MeSH indexing with full text. Bioinformatics, 2020, 36, 1533-1541.	1.8	26
28	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2020, 48, D9-D16.	6.5	381
29	Better synonyms for enriching biomedical search. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1894-1902.	2.2	6
30	Predicting risk of late age-related macular degeneration using deep learning. Npj Digital Medicine, 2020, 3, 111.	5.7	33
31	Ten tips for a text-mining-ready article: How to improve automated discoverability and interpretability. PLoS Biology, 2020, 18, e3000716.	2.6	10
32	TeamTat: a collaborative text annotation tool. Nucleic Acids Research, 2020, 48, W5-W11.	6.5	34
33	Deep learning with sentence embeddings pre-trained on biomedical corpora improves the performance of finding similar sentences in electronic medical records. BMC Medical Informatics and Decision Making, 2020, 20, 73.	1.5	15
34	BioConceptVec: Creating and evaluating literature-based biomedical concept embeddings on a large scale. PLoS Computational Biology, 2020, 16, e1007617.	1.5	43
35	Deep Learning Automated Detection of Reticular Pseudodrusen from Fundus Autofluorescence Images or Color Fundus Photographs in AREDS2. Ophthalmology, 2020, 127, 1674-1687.	2.5	19
36	Keep up with the latest coronavirus research. Nature, 2020, 579, 193-193.	13.7	230

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37	Automated abnormality classification of chest radiographs using deep convolutional neural networks. <i>Npj Digital Medicine</i> , 2020, 3, 70.	5.7	133
38	An Empirical Study of Multi-Task Learning on BERT for Biomedical Text Mining. , 2020, , .		49
39	PDC - a probabilistic distributional clustering algorithm: a case study on suicide articles in PubMed. <i>AMIA Summits on Translational Science Proceedings</i> , 2020, 2020, 259-268.	0.4	0
40	LitSense: making sense of biomedical literature at sentence level. <i>Nucleic Acids Research</i> , 2019, 47, W594-W599.	6.5	37
41	ML-Net: multi-label classification of biomedical texts with deep neural networks. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 1279-1285.	2.2	83
42	PubMed Text Similarity Model and its application to curation efforts in the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	10
43	Coinheritance of generalized pustular psoriasis and familial Behçet's-like autoinflammatory syndrome with variants in <i>IL36RN</i> and <i>TNFAIP3</i> in the heterozygous state. <i>Journal of Dermatology</i> , 2019, 46, 907-910.	0.6	7
44	A Deep Learning Approach for Automated Detection of Geographic Atrophy from Color Fundus Photographs. <i>Ophthalmology</i> , 2019, 126, 1533-1540.	2.5	55
45	BioWordVec, Improving biomedical word embeddings with subword information and MeSH. <i>Scientific Data</i> , 2019, 6, 52.	2.4	268
46	Tracking human genes along the translational continuum. <i>Npj Genomic Medicine</i> , 2019, 4, 25.	1.7	2
47	Fine-Grained Lesion Annotation in CT Images With Knowledge Mined From Radiology Reports. , 2019, , .		0
48	A Text-Mining System for Concept Annotation in Biomedical Full Text Articles. , 2019, , .		1
49	Biomedical Mention Disambiguation using a Deep Learning Approach. , 2019, , .		9
50	Overview of the BioCreative VI Precision Medicine Track: mining protein interactions and mutations for precision medicine. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	30
51	PMC text mining subset in BioC: about three million full-text articles and growing. <i>Bioinformatics</i> , 2019, 35, 3533-3535.	1.8	51
52	PubTator central: automated concept annotation for biomedical full text articles. <i>Nucleic Acids Research</i> , 2019, 47, W587-W593.	6.5	248
53	Exploring semi-supervised variational autoencoders for biomedical relation extraction. <i>Methods</i> , 2019, 166, 112-119.	1.9	45
54	Text Mining for Drug Discovery. <i>Methods in Molecular Biology</i> , 2019, 1939, 231-252.	0.4	30

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55	Using deep learning to identify translational research in genomic medicine beyond bench to bedside. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	4
56	BioSentVec: creating sentence embeddings for biomedical texts. , 2019, , .		91
57	A self-attention based deep learning method for lesion attribute detection from CT reports. , 2019, , .		14
58	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2019, 47, D23-D28.	6.5	502
59	DeepSeeNet: A Deep Learning Model for Automated Classification of Patient-based Age-related Macular Degeneration Severity from Color Fundus Photographs. Ophthalmology, 2019, 126, 565-575.	2.5	220
60	ChestX-ray: Hospital-Scale Chest X-ray Database and Benchmarks on Weakly Supervised Classification and Localization of Common Thorax Diseases. Advances in Computer Vision and Pattern Recognition, 2019, , 369-392.	0.9	45
61	Transfer Learning in Biomedical Natural Language Processing: An Evaluation of BERT and ELMo on Ten Benchmarking Datasets. , 2019, , .		360
62	Introduction to BLAH5 special issue: recent progress on interoperability of biomedical text mining. Genomics and Informatics, 2019, 17, e12.	0.4	0
63	A multi-task deep learning model for the classification of Age-related Macular Degeneration. AMIA Summits on Translational Science Proceedings, 2019, 2019, 505-514.	0.4	8
64	Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.	1.5	1,282
65	Generalizing biomedical relation classification with neural adversarial domain adaptation. Bioinformatics, 2018, 34, 2973-2981.	1.8	30
66	tmVar 2.0: integrating genomic variant information from literature with dbSNP and ClinVar for precision medicine. Bioinformatics, 2018, 34, 80-87.	1.8	79
67	A Deep Phenotype Association Study Reveals Specific Phenotype Associations with Genetic Variants in Age-related Macular Degeneration. Ophthalmology, 2018, 125, 559-568.	2.5	30
68	TieNet: Text-Image Embedding Network for Common Thorax Disease Classification and Reporting in Chest X-Rays. , 2018, , .		261
69	How user intelligence is improving PubMed. Nature Biotechnology, 2018, 36, 937-945.	9.4	46
70	Sentence Similarity Measures Revisited. , 2018, , .		5
71	PubMed Labs: an experimental system for improving biomedical literature search. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	15
72	Assisting document triage for human kinome curation via machine learning. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	2

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73	Overview of the BioCreative VI text-mining services for Kinome Curation Track. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	3
74	Best Match: New relevance search for PubMed. PLoS Biology, 2018, 16, e2005343.	2.6	90
75	LitVar: a semantic search engine for linking genomic variant data in PubMed and PMC. Nucleic Acids Research, 2018, 46, W530-W536.	6.5	96
76	PubMed Phrases, an open set of coherent phrases for searching biomedical literature. Scientific Data, 2018, 5, 180104.	2.4	13
77	A Fast Deep Learning Model for Textual Relevance in Biomedical Information Retrieval. , 2018, , .		25
78	ezTag: tagging biomedical concepts via interactive learning. Nucleic Acids Research, 2018, 46, W523-W529.	6.5	27
79	Extracting chemicalâ€“protein relations with ensembles of SVM and deep learning models. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	85
80	A Field Sensor: computing the composition and intent of PubMed queries. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	4
81	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. PLoS Computational Biology, 2018, 14, e1006390.	1.5	33
82	PSB 2019 Workshop on Text Mining and Visualization for Precision Medicine. , 2018, , .		0
83	NegBio: a high-performance tool for negation and uncertainty detection in radiology reports. AMIA Summits on Translational Science Proceedings, 2018, 2017, 188-196.	0.4	18
84	Bridging the gap: Incorporating a semantic similarity measure for effectively mapping PubMed queries to documents. Journal of Biomedical Informatics, 2017, 75, 122-127.	2.5	33
85	DIGNiFI: Discovering causative genes for orphan diseases using protein-protein interaction networks. BMC Systems Biology, 2017, 11, 23.	3.0	12
86	MeSH Now: automatic MeSH indexing at PubMed scale via learning to rank. Journal of Biomedical Semantics, 2017, 8, 15.	0.9	57
87	ChestX-Ray8: Hospital-Scale Chest X-Ray Database and Benchmarks on Weakly-Supervised Classification and Localization of Common Thorax Diseases. , 2017, , .		2,038
88	Towards PubMed 2.0. ELife, 2017, 6, .	2.8	86
89	On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.	1.8	91
90	Deep learning for extracting protein-protein interactions from biomedical literature. , 2017, , .		61

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91	BioCreative VI Precision Medicine Track: creating a training corpus for mining protein-protein interactions affected by mutations. , 2017, , .		6
92	Deep Learning for Biomedical Information Retrieval: Learning Textual Relevance from Click Logs. , 2017, , .		16
93	Mining Related Articles for Automatic Journal Cataloging. Journal of Data and Information Science, 2017, 1, 45-59.	0.5	0
94	DIGNiFI. , 2016, , .		0
95	Text Mining Genotype-Phenotype Relationships from Biomedical Literature for Database Curation and Precision Medicine. PLoS Computational Biology, 2016, 12, e1005017.	1.5	81
96	Discovering biomedical semantic relations in PubMed queries for information retrieval and database curation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw025.	1.4	5
97	BioCreative V CDR task corpus: a resource for chemical disease relation extraction. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw068.	1.4	350
98	Improving chemical disease relation extraction with rich features and weakly labeled data. Journal of Cheminformatics, 2016, 8, 53.	2.8	62
99	Text mining for precision medicine: automating disease-mutation relationship extraction from biomedical literature. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 766-772.	2.2	52
100	Text Mining for Precision Medicine: Bringing Structure to EHRs and Biomedical Literature to Understand Genes and Health. Advances in Experimental Medicine and Biology, 2016, 939, 139-166.	0.8	46
101	Assessing the state of the art in biomedical relation extraction: overview of the BioCreative V chemical-disease relation (CDR) task. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	1.4	123
102	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	1.4	36
103	TaggerOne: joint named entity recognition and normalization with semi-Markov Models. Bioinformatics, 2016, 32, 2839-2846.	1.8	221
104	Mining chemical patents with an ensemble of open systems. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw065.	1.4	12
105	Crowdsourcing in biomedicine: challenges and opportunities. Briefings in Bioinformatics, 2016, 17, 23-32.	3.2	82
106	Beyond accuracy: creating interoperable and scalable text-mining web services. Bioinformatics, 2016, 32, 1907-1910.	1.8	37
107	A survey of current trends in computational drug repositioning. Briefings in Bioinformatics, 2016, 17, 2-12.	3.2	459
108	Community challenges in biomedical text mining over 10 years: success, failure and the future. Briefings in Bioinformatics, 2016, 17, 132-144.	3.2	161

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109	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. Database: the Journal of Biological Databases and Curation, 2016, 2016, bau161.	1.4	30
110	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	2.8	166
111	tmChem: a high performance approach for chemical named entity recognition and normalization. Journal of Cheminformatics, 2015, 7, S3.	2.8	203
112	Scaling drug indication curation through crowdsourcing. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	34
113	GNormPlus: An Integrative Approach for Tagging Genes, Gene Families, and Protein Domains. BioMed Research International, 2015, 2015, 1-7.	0.9	155
114	Text Mining for Translational Bioinformatics. BioMed Research International, 2015, 2015, 1-2.	0.9	4
115	Identifying named entities from PubMed® for enriching semantic categories. BMC Bioinformatics, 2015, 16, 57.	1.2	10
116	Challenges in clinical natural language processing for automated disorder normalization. Journal of Biomedical Informatics, 2015, 57, 28-37.	2.5	125
117	SimConcept: A Hybrid Approach for Simplifying Composite Named Entities in Biomedical Text. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 1385-1391.	3.9	18
118	Crowdsourcing and mining crowd data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 267-9.	0.7	2
119	LabeledIn: Cataloging labeled indications for human drugs. Journal of Biomedical Informatics, 2014, 52, 448-456.	2.5	35
120	Text mining tools for assisting literature curation. , 2014, , .		2
121	Overview of the gene ontology task at BioCreative IV. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau086-bau086.	1.4	45
122	SimConcept. , 2014, 2014, 138-146.		13
123	tmBioC: improving interoperability of text-mining tools with BioC. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	8
124	Hybrid curation of gene-mutation relations combining automated extraction and crowdsourcing. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	35
125	BioC interoperability track overview. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau053-bau053.	1.4	15
126	BC4GO: a full-text corpus for the BioCreative IV GO task. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau074-bau074.	1.4	36

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127	NCBI disease corpus: A resource for disease name recognition and concept normalization. Journal of Biomedical Informatics, 2014, 47, 1-10.	2.5	525
128	Author name disambiguation for <scp>P</scp>ub<scp>M</scp>ed. Journal of the Association for Information Science and Technology, 2014, 65, 765-781.	1.5	68
129	CROWDSOURCING AND MINING CROWD DATA. , 2014, , .		3
130	BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039.	1.4	43
131	Accessing Biomedical Literature in the Current Information Landscape. Methods in Molecular Biology, 2014, 1159, 11-31.	0.4	32
132	Automated Disease Normalization with Low Rank Approximations. , 2014, , .		8
133	Automatic extraction of drug indications from FDA drug labels. AMIA ... Annual Symposium proceedings, 2014, 2014, 787-94.	0.2	4
134	Pathway-based drug repositioning using causal inference. BMC Bioinformatics, 2013, 14, S3.	1.2	71
135	PubTator: a web-based text mining tool for assisting biocuration. Nucleic Acids Research, 2013, 41, W518-W522.	6.5	523
136	tmVar: a text mining approach for extracting sequence variants in biomedical literature. Bioinformatics, 2013, 29, 1433-1439.	1.8	197
137	An overview of the BioCreative 2012 Workshop Track III: interactive text mining task. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas056-bas056.	1.4	68
138	BioC: a minimalist approach to interoperability for biomedical text processing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat064-bat064.	1.4	123
139	Toward Creating a Gold Standard of Drug Indications from FDA Drug Labels. , 2013, , .		5
140	DNorm: disease name normalization with pairwise learning to rank. Bioinformatics, 2013, 29, 2909-2917.	1.8	436
141	Developing Topic-specific Search Filters for PubMed with Click-through Data. Methods of Information in Medicine, 2013, 52, 395-402.	0.7	9
142	Large-Scale Event Extraction from Literature with Multi-Level Gene Normalization. PLoS ONE, 2013, 8, e55814.	1.1	83
143	Predicting clicks of PubMed articles. AMIA ... Annual Symposium proceedings, 2013, 2013, 947-56.	0.2	0
144	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2012, 40, D13-D25.	6.5	510

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145	Prioritizing PubMed articles for the Comparative Toxicogenomic Database utilizing semantic information. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas042-bas042.	1.4	12
146	Biocuration workflows and text mining: overview of the BioCreative 2012 Workshop Track II. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas043-bas043.	1.4	67
147	Linking multiple disease-related resources through UMLS. , 2012, , .		9
148	Improving Online Access to Drug-Related Information. , 2012, , .		1
149	BioCreative-2012 Virtual Issue. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas049-bas049.	1.4	19
150	Accelerating literature curation with text-mining tools: a case study of using PubTator to curate genes in PubMed abstracts. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas041-bas041.	1.4	83
151	Systematic identification of pharmacogenomics information from clinical trials. Journal of Biomedical Informatics, 2012, 45, 870-878.	2.5	26
152	A Network Approach for Computational Drug Repositioning. , 2012, , .		0
153	A new method for computational drug repositioning using drug pairwise similarity. , 2012, 2012, 1-4.		63
154	Improving links between literature and biological data with text mining: a case study with GEO, PDB and MEDLINE. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas026.	1.4	21
155	Automatic identification and normalization of dosage forms in drug monographs. BMC Medical Informatics and Decision Making, 2012, 12, 9.	1.5	2
156	SR4GN: A Species Recognition Software Tool for Gene Normalization. PLoS ONE, 2012, 7, e38460.	1.1	71
157	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2011, 39, D38-D51.	6.5	582
158	Semi-automatic semantic annotation of PubMed queries: A study on quality, efficiency, satisfaction. Journal of Biomedical Informatics, 2011, 44, 310-318.	2.5	68
159	A context-blocks model for identifying clinical relationships in patient records. BMC Bioinformatics, 2011, 12, S3.	1.2	14
160	Overview of the BioCreative III Workshop. BMC Bioinformatics, 2011, 12, S1.	1.2	88
161	The gene normalization task in BioCreative III. BMC Bioinformatics, 2011, 12, S2.	1.2	101
162	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. BMC Bioinformatics, 2011, 12, S3.	1.2	121

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163	BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4.	1.2	65
164	Recommending MeSH terms for annotating biomedical articles. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 660-667.	2.2	107
165	Extraction of data deposition statements from the literature: a method for automatically tracking research results. Bioinformatics, 2011, 27, 3306-3312.	1.8	27
166	PubMed and beyond: a survey of web tools for searching biomedical literature. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq036-baq036.	1.4	375
167	Click-words: learning to predict document keywords from a user perspective. Bioinformatics, 2010, 26, 2767-2775.	1.8	11
168	Extracting Rx information from clinical narrative. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 536-539.	2.2	26
169	Automatic integration of drug indications from multiple health resources. , 2010, , .		24
170	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2010, 38, D5-D16.	6.5	417
171	A Textual Representation Scheme for Identifying Clinical Relationships in Patient Records. , 2010, 2010, 995-998.		1
172	Summarizing Documents by Measuring the Importance of a Subset of Vertices within a Graph. , 2009, 1, 267-272.		4
173	Identifying related journals through log analysis. Bioinformatics, 2009, 25, 3038-3039.	1.8	15
174	Understanding PubMed(R) user search behavior through log analysis. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap018-bap018.	1.4	189
175	Improving accuracy for identifying related PubMed queries by an integrated approach. Journal of Biomedical Informatics, 2009, 42, 831-838.	2.5	14
176	Evaluation of query expansion using MeSH in PubMed. Information Retrieval, 2009, 12, 69-80.	1.6	139
177	Evaluating Relevance Ranking Strategies for MEDLINE Retrieval. Journal of the American Medical Informatics Association: JAMIA, 2009, 16, 32-36.	2.2	45
178	Towards automatic generation of gene summary. , 2009, , .		7
179	Exploring two biomedical text genres for disease recognition. , 2009, , .		8
180	Finding query suggestions for PubMed. AMIA ... Annual Symposium proceedings, 2009, 2009, 396-400.	0.2	16

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181	Semantic role labeling for protein transport predicates. BMC Bioinformatics, 2008, 9, 277.	1.2	19
182	OpenDMAP: An open source, ontology-driven concept analysis engine, with applications to capturing knowledge regarding protein transport, protein interactions and cell-type-specific gene expression. BMC Bioinformatics, 2008, 9, 78.	1.2	112
183	Overview of BioCreative II gene normalization. Genome Biology, 2008, 9, S3.	13.9	237
184	Concept recognition for extracting protein interaction relations from biomedical text. Genome Biology, 2008, 9, S9.	3.8	34
185	Evaluating relevance ranking strategies for MEDLINE retrieval. AMIA ... Annual Symposium proceedings, 2008, , 439.	0.2	2
186	GeneRIF QUALITY ASSURANCE AS SUMMARY REVISION. , 2006, , 269-80.		45
187	Finding GeneRIFs via gene ontology annotations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 52-63.	0.7	15
188	EVALUATION OF LEXICAL METHODS FOR DETECTING RELATIONSHIPS BETWEEN CONCEPTS FROM MULTIPLE ONTOLOGIES. , 2005, , .		23
189	FINDING GENERIFS VIA GENE ONTOLOGY ANNOTATIONS. , 2005, , .		14
190	Proteome Analyst: custom predictions with explanations in a web-based tool for high-throughput proteome annotations. Nucleic Acids Research, 2004, 32, W365-W371.	6.5	93
191	Automatic Extraction of Clusters from Hierarchical Clustering Representations. Lecture Notes in Computer Science, 2003, , 75-87.	1.0	64