

Zhiyong Lu

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

4,792
citations

172457

29
h-index

265206

42
g-index

45
all docs

45
docs citations

45
times ranked

3998
citing authors

#	ARTICLE	IF	CITATIONS
1	NCBI disease corpus: A resource for disease name recognition and concept normalization. Journal of Biomedical Informatics, 2014, 47, 1-10.	4.3	525
2	PubTator: a web-based text mining tool for assisting biocuration. Nucleic Acids Research, 2013, 41, W518-W522.	14.5	523
3	DNorm: disease name normalization with pairwise learning to rank. Bioinformatics, 2013, 29, 2909-2917.	4.1	436
4	BioCreative V CDR task corpus: a resource for chemical disease relation extraction. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw068.	3.0	350
5	PubTator central: automated concept annotation for biomedical full text articles. Nucleic Acids Research, 2019, 47, W587-W593.	14.5	248
6	Overview of BioCreative II gene normalization. Genome Biology, 2008, 9, S3.	9.6	237
7	TaggerOne: joint named entity recognition and normalization with semi-Markov Models. Bioinformatics, 2016, 32, 2839-2846.	4.1	221
8	tmVar: a text mining approach for extracting sequence variants in biomedical literature. Bioinformatics, 2013, 29, 1433-1439.	4.1	197
9	LitCovid: an open database of COVID-19 literature. Nucleic Acids Research, 2021, 49, D1534-D1540.	14.5	189
10	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	6.1	166
11	GNormPlus: An Integrative Approach for Tagging Genes, Gene Families, and Protein Domains. BioMed Research International, 2015, 2015, 1-7.	1.9	155
12	BioC: a minimalist approach to interoperability for biomedical text processing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat064-bat064.	3.0	123
13	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, .	3.0	123
14	The gene normalization task in BioCreative III. BMC Bioinformatics, 2011, 12, S2.	2.6	101
15	LitVar: a semantic search engine for linking genomic variant data in PubMed and PMC. Nucleic Acids Research, 2018, 46, W530-W536.	14.5	96
16	On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.	4.1	91
17	Best Match: New relevance search for PubMed. PLoS Biology, 2018, 16, e2005343.	5.6	90
18	Towards PubMed 2.0. ELife, 2017, 6, .	6.0	86

#	ARTICLE	IF	CITATIONS
19	Text Mining Genotype-Phenotype Relationships from Biomedical Literature for Database Curation and Precision Medicine. <i>PLoS Computational Biology</i> , 2016, 12, e1005017.	3.2	81
20	tmVar 2.0: integrating genomic variant information from literature with dbSNP and ClinVar for precision medicine. <i>Bioinformatics</i> , 2018, 34, 80-87.	4.1	79
21	SR4GN: A Species Recognition Software Tool for Gene Normalization. <i>PLoS ONE</i> , 2012, 7, e38460.	2.5	71
22	Biocuration workflows and text mining: overview of the BioCreative 2012 Workshop Track II. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas043-bas043.	3.0	67
23	PMC text mining subset in BioC: about three million full-text articles and growing. <i>Bioinformatics</i> , 2019, 35, 3533-3535.	4.1	51
24	How user intelligence is improving PubMed. <i>Nature Biotechnology</i> , 2018, 36, 937-945.	17.5	46
25	BioConceptVec: Creating and evaluating literature-based biomedical concept embeddings on a large scale. <i>PLoS Computational Biology</i> , 2020, 16, e1007617.	3.2	43
26	Artificial Intelligence in Action: Addressing the COVID-19 Pandemic with Natural Language Processing. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 313-339.	6.5	38
27	LitSense: making sense of biomedical literature at sentence level. <i>Nucleic Acids Research</i> , 2019, 47, W594-W599.	14.5	37
28	Hybrid curation of gene-mutation relations combining automated extraction and crowdsourcing. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	3.0	35
29	TeamTat: a collaborative text annotation tool. <i>Nucleic Acids Research</i> , 2020, 48, W5-W11.	14.5	34
30	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. <i>PLoS Computational Biology</i> , 2018, 14, e1006390.	3.2	33
31	Accessing Biomedical Literature in the Current Information Landscape. <i>Methods in Molecular Biology</i> , 2014, 1159, 11-31.	0.9	32
32	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw161.	3.0	30
33	LitSuggest: a web-based system for literature recommendation and curation using machine learning. <i>Nucleic Acids Research</i> , 2021, 49, W352-W358.	14.5	28
34	ezTag: tagging biomedical concepts via interactive learning. <i>Nucleic Acids Research</i> , 2018, 46, W523-W529.	14.5	27
35	NLM-Chem, a new resource for chemical entity recognition in PubMed full text literature. <i>Scientific Data</i> , 2021, 8, 91.	5.3	26
36	SimConcept: A Hybrid Approach for Simplifying Composite Named Entities in Biomedical Text. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2015, 19, 1385-1391.	6.3	18

#	ARTICLE	IF	CITATIONS
37	Deep learning with sentence embeddings pre-trained on biomedical corpora improves the performance of finding similar sentences in electronic medical records. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 73.	3.0	15
38	Recent advances of automated methods for searching and extracting genomic variant information from biomedical literature. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	13
39	Ten tips for a text-mining-ready article: How to improve automated discoverability and interpretability. <i>PLoS Biology</i> , 2020, 18, e3000716.	5.6	10
40	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.	4.3	9
41	MeSH-based dataset for measuring the relevance of text retrieval. , 2018, , .		5
42	Benchmarking Effectiveness and Efficiency of Deep Learning Models for Semantic Textual Similarity in the Clinical Domain: Validation Study. <i>JMIR Medical Informatics</i> , 2021, 9, e27386.	2.6	5
43	Tracking human genes along the translational continuum. <i>Npj Genomic Medicine</i> , 2019, 4, 25.	3.8	2
44	Editorâ€™s introduction to the special section on the 7th Biomedical Linked Annotation Hackathon (BLAH7). <i>Genomics and Informatics</i> , 2021, 19, e20.	0.8	0