Zhiyong Lu

List of Publications by Year
in descending order

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	LitCovid: an open database of COVID-19 literature. Nucleic Acids Research, 2021, 49, D1534-D1540.	14.5	189
2	Recent advances of automated methods for searching and extracting genomic variant information from biomedical literature. Briefings in Bioinformatics, 2021, 22, .	6.5	13
3	NLM-Chem, a new resource for chemical entity recognition in PubMed full text literature. Scientific Data, 2021, 8, 91.	5.3	26
4	LitSuggest: a web-based system for literature recommendation and curation using machine learning. Nucleic Acids Research, 2021, 49, W352-W358.	14.5	28
5	NLM-Gene, a richly annotated gold standard dataset for gene entities that addresses ambiguity and multi-species gene recognition. Journal of Biomedical Informatics, 2021, 118, 103779.	4.3	9
6	Artificial Intelligence in Action: Addressing the COVID-19 Pandemic with Natural Language Processing. Annual Review of Biomedical Data Science, 2021, 4, 313-339.	6.5	38
7	Editor's introduction to the special section on the 7th Biomedical Linked Annotation Hackathon (BLAH7). Genomics and Informatics, 2021, 19, e20.	0.8	0
8	Benchmarking Effectiveness and Efficiency of Deep Learning Models for Semantic Textual Similarity in the Clinical Domain: Validation Study. JMIR Medical Informatics, 2021, 9, e27386.	2.6	5
9	Ten tips for a text-mining-ready article: How to improve automated discoverability and interpretability. PLoS Biology, 2020, 18, e3000716.	5.6	10
10	TeamTat: a collaborative text annotation tool. Nucleic Acids Research, 2020, 48, W5-W11.	14.5	34
11	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.	3.0	15
12	BioConceptVec: Creating and evaluating literature-based biomedical concept embeddings on a large scale. PLoS Computational Biology, 2020, 16, e1007617.	3.2	43
13	LitSense: making sense of biomedical literature at sentence level. Nucleic Acids Research, 2019, 47, W594-W599.	14.5	37
14	Tracking human genes along the translational continuum. Npj Genomic Medicine, 2019, 4, 25.	3.8	2
15	PMC text mining subset in BioC: about three million full-text articles and growing. Bioinformatics, 2019, 35, 3533-3535.	4.1	51
16	PubTator central: automated concept annotation for biomedical full text articles. Nucleic Acids Research, 2019, 47, W587-W593.	14.5	248
17	tmVar 2.0: integrating genomic variant information from literature with dbSNP and ClinVar for precision medicine. Bioinformatics, 2018, 34, 80-87.	4.1	79
18	How user intelligence is improving PubMed. Nature Biotechnology, 2018, 36, 937-945.	17.5	46

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19	Best Match: New relevance search for PubMed. PLoS Biology, 2018, 16, e2005343.	5.6	90
20	LitVar: a semantic search engine for linking genomic variant data in PubMed and PMC. Nucleic Acids Research, 2018, 46, W530-W536.	14.5	96
21	ezTag: tagging biomedical concepts via interactive learning. Nucleic Acids Research, 2018, 46, W523-W529.	14.5	27
22	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. PLoS Computational Biology, 2018, 14, e1006390.	3.2	33
23	MeSH-based dataset for measuring the relevance of text retrieval. , 2018, , .		5
24	Towards PubMed 2.0. ELife, 2017, 6, .	6.0	86
25	On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.	4.1	91
26	Text Mining Genotype-Phenotype Relationships from Biomedical Literature for Database Curation and Precision Medicine. PLoS Computational Biology, 2016, 12, e1005017.	3.2	81
27	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
28	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
29	TaggerOne: joint named entity recognition and normalization with semi-Markov Models. Bioinformatics, 2016, 32, 2839-2846.	4.1	221
30	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw161.	3.0	30
31	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	6.1	166
32	GNormPlus: An Integrative Approach for Tagging Genes, Gene Families, and Protein Domains. BioMed Research International, 2015, 2015, 1-7.	1.9	155
33	SimConcept: A Hybrid Approach for Simplifying Composite Named Entities in Biomedical Text. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 1385-1391.	6.3	18
34	Hybrid curation of geneâ€"mutation relations combining automated extraction and crowdsourcing. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	3.0	35
35	NCBI disease corpus: A resource for disease name recognition and concept normalization. Journal of Biomedical Informatics, 2014, 47, 1-10.	4.3	525
36	Accessing Biomedical Literature in the Current Information Landscape. Methods in Molecular Biology, 2014, 1159, 11-31.	0.9	32

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37	PubTator: a web-based text mining tool for assisting biocuration. Nucleic Acids Research, 2013, 41, W518-W522.	14.5	523
38	tmVar: a text mining approach for extracting sequence variants in biomedical literature. Bioinformatics, 2013, 29, 1433-1439.	4.1	197
39	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
40	DNorm: disease name normalization with pairwise learning to rank. Bioinformatics, 2013, 29, 2909-2917.	4.1	436
41	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.	3.0	67
42	SR4GN: A Species Recognition Software Tool for Gene Normalization. PLoS ONE, 2012, 7, e38460.	2.5	71
43	The gene normalization task in BioCreative III. BMC Bioinformatics, 2011, 12, S2.	2.6	101
44	Overview of BioCreative II gene normalization. Genome Biology, 2008, 9, S3.	9.6	237