

# Ling Luo

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17  
papers

351  
citations

8  
h-index

18  
g-index

22  
ext. papers

560  
ext. citations

6.7  
avg, IF

3.57  
L-index

#	Paper	IF	Citations
17	An attention-based BiLSTM-CRF approach to document-level chemical named entity recognition. <i>Bioinformatics</i> , <b>2018</b> , 34, 1381-1388	7.2	130
16	Drug drug interaction extraction from biomedical literature using syntax convolutional neural network. <i>Bioinformatics</i> , <b>2016</b> , 32, 3444-3453	7.2	78
15	An attention-based effective neural model for drug-drug interactions extraction. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 445	3.6	41
14	Disease named entity recognition from biomedical literature using a novel convolutional neural network. <i>BMC Medical Genomics</i> , <b>2017</b> , 10, 73	3.7	21
13	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> , <b>2019</b> , 2019,	5	18
12	A neural network-based joint learning approach for biomedical entity and relation extraction from biomedical literature. <i>Journal of Biomedical Informatics</i> , <b>2020</b> , 103, 103384	10.2	15
11	Artificial Intelligence in Action: Addressing the COVID-19 Pandemic with Natural Language Processing. <i>Annual Review of Biomedical Data Science</i> , <b>2021</b> , 4, 313-339	5.6	11
10	LitSuggest: a web-based system for literature recommendation and curation using machine learning. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W352-W358	20.1	9
9	Exploiting sequence labeling framework to extract document-level relations from biomedical texts. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 125	3.6	8
8	A neural network approach to chemical and gene/protein entity recognition in patents. <i>Journal of Cheminformatics</i> , <b>2018</b> , 10, 65	8.6	5
7	KGHC: a knowledge graph for hepatocellular carcinoma. <i>BMC Medical Informatics and Decision Making</i> , <b>2020</b> , 20, 135	3.6	3
6	ML-CNN: A novel deep learning based disease named entity recognition architecture <b>2016</b> ,		3
5	A multi-task learning based approach to biomedical entity relation extraction <b>2018</b> ,		3
4	Document triage for identifying protein-protein interactions affected by mutations: a neural network ensemble approach. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2018</b> , 2018,	5	3
3	HMNPPID-human malignant neoplasm protein-protein interaction database. <i>Human Genomics</i> , <b>2019</b> , 13, 44	6.8	1
2	PhenoTagger: A Hybrid Method for Phenotype Concept Recognition using Human Phenotype Ontology. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
1	PhenoRerank: a re-ranking model for phenotypic concept recognition pre-trained on human phenotype ontology.. <i>Journal of Biomedical Informatics</i> , <b>2022</b> , 104059	10.2	

