

# Rezarta Islamaj Doçsan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/311551/publications.pdf>

Version: 2024-02-01

35  
papers

2,144  
citations

430874

18  
h-index

454955

30  
g-index

35  
all docs

35  
docs citations

35  
times ranked

2449  
citing authors

#	ARTICLE	IF	CITATIONS
1	NLM-Chem, a new resource for chemical entity recognition in PubMed full text literature. <i>Scientific Data</i> , 2021, 8, 91.	5.3	26
2	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
3	Evolving use of ancestry, ethnicity, and race in genetics researchâ€”A survey spanning seven decades. <i>American Journal of Human Genetics</i> , 2021, 108, 2215-2223.	6.2	27
4	TeamTat: a collaborative text annotation tool. <i>Nucleic Acids Research</i> , 2020, 48, W5-W11.	14.5	34
5	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
6	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, .	3.0	10
7	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, .	3.0	30
8	PMC text mining subset in BioC: about three million full-text articles and growing. <i>Bioinformatics</i> , 2019, 35, 3533-3535.	4.1	51
9	The BioC-BioGRID corpus: full text articles annotated for curation of proteinâ€”protein and genetic interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw147.	3.0	24
10	BioCreative VI Precision Medicine Track: creating a training corpus for mining protein-protein interactions affected by mutations. , 2017, , .		6
11	Crowdsourcing and curation: perspectives from biology and natural language processing. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw115.	3.0	10
12	BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw121.	3.0	28
13	Natural language processing pipelines to annotate BioC collections with an application to the NCBI disease corpus. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau056-bau056.	3.0	8
14	BioC interoperability track overview. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau053-bau053.	3.0	15
15	NCBI disease corpus: A resource for disease name recognition and concept normalization. <i>Journal of Biomedical Informatics</i> , 2014, 47, 1-10.	4.3	525
16	Author name disambiguation for <scp>P</scp>ub<scp>M</scp>ed. <i>Journal of the Association for Information Science and Technology</i> , 2014, 65, 765-781.	2.9	68
17	Finding abbreviations in biomedical literature: three BioC-compatible modules and four BioC-formatted corpora. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau044-bau044.	3.0	12
18	BioC implementations in Go, Perl, Python and Ruby. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau059-bau059.	3.0	8

#	ARTICLE	IF	CITATIONS
19	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
20	DNorm: disease name normalization with pairwise learning to rank. Bioinformatics, 2013, 29, 2909-2917.	4.1	436
21	Topics in machine learning for biomedical literature analysis and text retrieval. Journal of Biomedical Semantics, 2012, 3, S1.	1.6	2
22	An Evolutionary Algorithm Approach for Feature Generation from Sequence Data and Its Application to DNA Splice Site Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1387-1398.	3.0	29
23	Semi-automatic semantic annotation of PubMed queries: A study on quality, efficiency, satisfaction. Journal of Biomedical Informatics, 2011, 44, 310-318.	4.3	68
24	Topics in machine learning for biomedical literature analysis and text retrieval. BMC Bioinformatics, 2011, 12, I1.	2.6	0
25	A context-blocks model for identifying clinical relationships in patient records. BMC Bioinformatics, 2011, 12, S3.	2.6	14
26	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.	2.6	121
27	Click-words: learning to predict document keywords from a user perspective. Bioinformatics, 2010, 26, 2767-2775.	4.1	11
28	Extracting Rx information from clinical narrative. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 536-539.	4.4	26
29	A Textual Representation Scheme for Identifying Clinical Relationships in Patient Records. , 2010, 2010, 995-998.		1
30	Understanding PubMed(R) user search behavior through log analysis. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap018-bap018.	3.0	189
31	SplicePort--An interactive splice-site analysis tool. Nucleic Acids Research, 2007, 35, W285-W291.	14.5	190
32	Characterizing RNA Secondary-Structure Features and Their Effects on Splice-Site Prediction. , 2007, , .		1
33	Structural footprinting in protein structure comparison: the impact of structural fragments. BMC Structural Biology, 2007, 7, 53.	2.3	13
34	Features generated for computational splice-site prediction correspond to functional elements. BMC Bioinformatics, 2007, 8, 410.	2.6	21
35	A Feature Generation Algorithm for Sequences with Application to Splice-Site Prediction. Lecture Notes in Computer Science, 2006, , 553-560.	1.3	8