

# Arzucan Ozgur

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1617419/publications.pdf>

Version: 2024-02-01

50  
papers

2,371  
citations

361413

20  
h-index

254184

43  
g-index

51  
all docs

51  
docs citations

51  
times ranked

2658  
citing authors

#	ARTICLE	IF	CITATIONS
1	Resources for Turkish dependency parsing: introducing the BOUN Treebank and the BoAT annotation tool. <i>Language Resources and Evaluation</i> , 2022, 56, 259-307.	2.7	6
2	ChemBoost: A Chemical Language Based Approach for Protein – Ligand Binding Affinity Prediction. <i>Molecular Informatics</i> , 2021, 40, e2000212.	2.5	12
3	A novel gene selection method for gene expression data for the task of cancer type classification. <i>Biology Direct</i> , 2021, 16, 7.	4.6	9
4	Editorial: Machine Learning Methodologies to Study Molecular Interactions. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 806474.	3.5	1
5	Exploring chemical space using natural language processing methodologies for drug discovery. <i>Drug Discovery Today</i> , 2020, 25, 689-705.	6.4	68
6	Cluster-based mention typing for named entity disambiguation. <i>Natural Language Engineering</i> , 2020, , 1-37.	2.5	1
7	Statistical representation models for mutation information within genomic data. <i>BMC Bioinformatics</i> , 2019, 20, 324.	2.6	4
8	Identifying Image Related Sentences in News Articles. , 2019, , .		1
9	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
10	Linking entities through an ontology using word embeddings and syntactic re-ranking. <i>BMC Bioinformatics</i> , 2019, 20, 156.	2.6	22
11	Machine learning-based identification and rule-based normalization of adverse drug reactions in drug labels. <i>BMC Bioinformatics</i> , 2019, 20, 707.	2.6	13
12	Turkish Treebanking: Unifying and Constructing Efforts. , 2019, , .		7
13	Improving the Annotations in the Turkish Universal Dependency Treebank. , 2019, , .		5
14	A closed-domain question answering framework using reliable resources to assist students. <i>Natural Language Engineering</i> , 2018, 24, 725-762.	2.5	7
15	Segmenting hashtags and analyzing their grammatical structure. <i>Journal of the Association for Information Science and Technology</i> , 2018, 69, 675-686.	2.9	6
16	DeepDTA: deep drug–target binding affinity prediction. <i>Bioinformatics</i> , 2018, 34, i821-i829.	4.1	717
17	A novel methodology on distributed representations of proteins using their interacting ligands. <i>Bioinformatics</i> , 2018, 34, i295-i303.	4.1	31
18	Ontology-based literature mining and class effect analysis of adverse drug reactions associated with neuropathy-inducing drugs. <i>Journal of Biomedical Semantics</i> , 2018, 9, 17.	1.6	7

#	ARTICLE	IF	CITATIONS
19	Automatic query generation using word embeddings for retrieving passages describing experimental methods. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw166.	3.0	6
20	Ontology-based literature mining of E. coli vaccine-associated gene interaction networks. Journal of Biomedical Semantics, 2017, 8, 12.	1.6	13
21	BIOSSES: a semantic sentence similarity estimation system for the biomedical domain. Bioinformatics, 2017, 33, i49-i58.	4.1	97
22	Automated Neuroanatomical Relation Extraction: A Linguistically Motivated Approach with a PVT Connectivity Graph Case Study. Frontiers in Neuroinformatics, 2016, 10, 39.	2.5	5
23	The Interaction Network Ontology-supported modeling and mining of complex interactions represented with multiple keywords in biomedical literature. BioData Mining, 2016, 9, 41.	4.0	7
24	BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw121.	3.0	28
25	A comparative study of SMILES-based compound similarity functions for drug-target interaction prediction. BMC Bioinformatics, 2016, 17, 128.	2.6	99
26	Identifying Topics in Microblogs Using Wikipedia. PLoS ONE, 2016, 11, e0151885.	2.5	15
27	Ontology-Based Categorization of Bacteria and Habitat Entities using Information Retrieval Techniques. , 2016, , .		7
28	Detection and categorization of bacteria habitats using shallow linguistic analysis. BMC Bioinformatics, 2015, 16, S5.	2.6	7
29	Literature Mining and Ontology based Analysis of Host-Brucella Gene-Gene Interaction Network. Frontiers in Microbiology, 2015, 6, 1386.	3.5	9
30	GLASS: a comprehensive database for experimentally validated GPCR-ligand associations. Bioinformatics, 2015, 31, 3035-3042.	4.1	92
31	A review on computational systems biology of pathogen-host interactions. Frontiers in Microbiology, 2015, 6, 235.	3.5	93
32	Development and application of an interaction network ontology for literature mining of vaccine-associated gene-gene interactions. Journal of Biomedical Semantics, 2015, 6, 2.	1.6	23
33	Question Analysis for a Closed Domain Question Answering System. Lecture Notes in Computer Science, 2015, , 468-482.	1.3	7
34	Classification of Beta-Lactamases and Penicillin Binding Proteins Using Ligand-Centric Network Models. PLoS ONE, 2015, 10, e0117874.	2.5	41
35	Bayesian Pathway Analysis of Cancer Microarray Data. PLoS ONE, 2014, 9, e102803.	2.5	13
36	Rule-based focus extraction in Turkish question answering systems. , 2014, , .		1

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37	Improving Named Entity Recognition for Morphologically Rich Languages Using Word Embeddings. , 2014, , .		30
38	PHISTO: pathogen-host interaction search tool. Bioinformatics, 2013, 29, 1357-1358.	4.1	145
39	Identification of fever and vaccine-associated gene interaction networks using ontology-based literature mining. Journal of Biomedical Semantics, 2012, 3, 18.	1.6	26
40	U-Compare bio-event meta-service: compatible BioNLP event extraction services. BMC Bioinformatics, 2011, 12, 481.	2.6	10
41	Mining of vaccine-associated IFN- $\gamma$ gene interaction networks using the Vaccine Ontology. Journal of Biomedical Semantics, 2011, 2, S8.	1.6	54
42	Literature-Based Discovery of IFN- $\gamma$ and Vaccine-Mediated Gene Interaction Networks. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-13.	3.0	34
43	Michigan molecular interactions r2: from interacting proteins to pathways. Nucleic Acids Research, 2009, 37, D642-D646.	14.5	85
44	Introducing meta-services for biomedical information extraction. Genome Biology, 2008, 9, S6.	8.8	61
45	Identifying gene-disease associations using centrality on a literature mined gene-interaction network. Bioinformatics, 2008, 24, i277-i285.	4.1	314
46	CO-OCCURRENCE NETWORK OF REUTERS NEWS. International Journal of Modern Physics C, 2008, 19, 689-702.	1.7	22
47	Efficient indexing technique for XML-based electronic product catalogs. Electronic Commerce Research and Applications, 2006, 5, 66-77.	5.0	7
48	Classification of Skewed and Homogenous Document Corpora with Class-Based and Corpus-Based Keywords. , 2006, , 91-101.		4
49	Social Network of Co-occurrence in News Articles. Lecture Notes in Computer Science, 2004, , 688-695.	1.3	5
50	N-gram Parsing for Jointly Training a Discriminative Constituency Parser. Polibits, 0, 47, 5-12.	0.0	2