Cecilia N Arighi

List of Publications by Year
in descending order

82 papers	25,685 citations	117625 34 h-index	74163 75 g-index
88 all docs	88 docs citations	88 times ranked	43695 citing authors

#	Article	IF	Citations
1	UniProt: a worldwide hub of protein knowledge. Nucleic Acids Research, 2019, 47, D506-D515.	14.5	6,185
2	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	14.5	4,709
3	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	14.5	3,474
4	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
5	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	14.5	1,838
6	Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198.	14.5	1,162
7	The Universal Protein Resource (UniProt) in 2010. Nucleic Acids Research, 2010, 38, D142-D148.	14.5	1,131
8	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 36, D190-D195.	14.5	852
9	Role of the mammalian retromer in sorting of the cation-independent mannose 6-phosphate receptor. Journal of Cell Biology, 2004, 165, 123-133.	5.2	549
10	The Universal Protein Resource (UniProt) 2009. Nucleic Acids Research, 2009, 37, D169-D174.	14.5	548
11	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 35, D193-D197.	14.5	488
12	Divalent interaction of the GGAs with the Rabaptin-5-Rabex-5 complex. EMBO Journal, 2003, 22, 78-88.	7.8	135
13	Text mining for the biocuration workflow. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas020-bas020.	3.0	132
14	iPTMnet: an integrated resource for protein post-translational modification network discovery. Nucleic Acids Research, 2018, 46, D542-D550.	14.5	120
15	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	6.5	110
16	The Protein Ontology: a structured representation of protein forms and complexes. Nucleic Acids Research, 2011, 39, D539-D545.	14.5	102
17	On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.	4.1	91
18	Overview of the BioCreative III Workshop. BMC Bioinformatics, 2011, 12, S1.	2.6	88

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19	Framework for a Protein Ontology. BMC Bioinformatics, 2007, 8, S1.	2.6	78
20	A crowdsourcing open platform for literature curation in UniProt. PLoS Biology, 2021, 19, e3001464.	5.6	74
21	Protein Ontology (PRO): enhancing and scaling up the representation of protein entities. Nucleic Acids Research, 2017, 45, D339-D346.	14.5	73
22	An overview of the BioCreative 2012 Workshop Track III: interactive text mining task. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas056-bas056.	3.0	68
23	Structural mechanism for ubiquitinated-cargo recognition by the Golgi-localized, Â-ear-containing, ADP-ribosylation-factor-binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2334-2339.	7.1	66
24	BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4.	2.6	65
25	Protein Ontology: a controlled structured network of protein entities. Nucleic Acids Research, 2014, 42, D415-D421.	14.5	63
26	Expert curation in UniProtKB: a case study on dealing with conflicting and erroneous data. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau016-bau016.	3.0	56
27	miRTex: A Text Mining System for miRNA-Gene Relation Extraction. PLoS Computational Biology, 2015, 11, e1004391.	3.2	50
28	Overview of the gene ontology task at BioCreative IV. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau086-bau086.	3.0	45
29	BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039.	3.0	43
30	RLIMS-P 2.0: A Generalizable Rule-Based Information Extraction System for Literature Mining of Protein Phosphorylation Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 17-29.	3.0	42
31	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. Bioinformatics, 2020, 36, 4643-4648.	4.1	42
32	BC4GO: a full-text corpus for the BioCreative IV GO task. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau074-bau074.	3.0	36
33	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
34	PIRSF Family Classification System for Protein Functional and Evolutionary Analysis. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	35
35	Murine Oviductosomes (OVS) microRNA profiling during the estrous cycle: Delivery of OVS-borne microRNAs to sperm where miR-34c-5p localizes at the centrosome. Scientific Reports, 2018, 8, 16094.	3.3	35
36	PIRSF family classification system for protein functional and evolutionary analysis. Evolutionary Bioinformatics, 2007, 2, 197-209.	1.2	35

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37	Temperature-Induced Conformational Transition of Intestinal Fatty Acid Binding Protein Enhancing Ligand Binding:â€‰ A Functional, Spectroscopic, and Molecular Modeling Study. Biochemistry, 1998, 37, 16802-16814.	2.5	31
38	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. Scientific Reports, 2018, 8, 6518.	3.3	31
39	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
40	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. Frontiers in Bioscience - Landmark, 2007, 12, 5071.	3.0	30
41	An improved ontological representation of dendritic cells as a paradigm for all cell types. BMC Bioinformatics, 2009, 10, 70.	2.6	29
42	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
43	iPTMnet: Integrative Bioinformatics for Studying PTM Networks. Methods in Molecular Biology, 2017, 1558, 333-353.	0.9	26
44	RLIMS-P: an online text-mining tool for literature-based extraction of protein phosphorylation information. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau081-bau081.	3.0	23
45	Construction of phosphorylation interaction networks by text mining of full-length articles using the eFIP system. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	23
46	iTextMine: integrated text-mining system for large-scale knowledge extraction from the literature. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	22
47	The eFIP system for text mining of protein interaction networks of phosphorylated proteins. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas044-bas044.	3.0	20
48	BioCreative-2012 Virtual Issue. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas049-bas049.	3.0	19
49	Temperature-Induced Conformational Switch in Intestinal Fatty Acid Binding Protein (IFABP) Revealing an Alternative Mode for Ligand Binding. Biochemistry, 2003, 42, 7539-7551.	2.5	18
50	A framework for biomedical figure segmentation towards image-based document retrieval. BMC Systems Biology, 2013, 7, S8.	3.0	16
51	Construction of protein phosphorylation networks by data mining, text mining and ontology integration: analysis of the spindle checkpoint. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat038.	3.0	15
52	An effective biomedical document classification scheme in support of biocuration: addressing class imbalance. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
53	An evolutionarily conserved motif is required for Plasmodesmata-located protein 5 to regulate cell-to-cell movement. Communications Biology, 2020, 3, 291.	4.4	15
54	The representation of protein complexes in the Protein Ontology (PRO). BMC Bioinformatics, 2011, 12, 371.	2.6	14

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55	pGenN, a Gene Normalization Tool for Plant Genes and Proteins in Scientific Literature. PLoS ONE, 2015, 10, e0135305.	2.5	12
56	Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PLoS ONE, 2015, 10, e0141773.	2.5	12
57	emiRIT: a text-mining-based resource for microRNA information. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	10
58	eFIP: A Tool for Mining Functional Impact of Phosphorylation from Literature. Methods in Molecular Biology, 2011, 694, 63-75.	0.9	10
59	TGF-beta signaling proteins and the Protein Ontology. BMC Bioinformatics, 2009, 10, S3.	2.6	9
60	An Automatic System for Extracting Figures and Captions in Biomedical PDF Documents. , 2011, , .		9
61	Protein ontology on the semantic web for knowledge discovery. Scientific Data, 2020, 7, 337.	5.3	9
62	Utilizing image and caption information for biomedical document classification. Bioinformatics, 2021, 37, i468-i476.	4.1	8
63	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. Frontiers in Genetics, 2013, 4, 62.	2.3	7
64	A Coordinated Approach by Public Domain Bioinformatics Resources to Aid the Fight Against Alzheimerâ€™s Disease Through Expert Curation of Key Protein Targets. Journal of Alzheimer's Disease, 2020, 77, 257-273.	2.6	7
65	UPCLASS: a deep learning-based classifier for UniProtKB entry publications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	7
66	Analysis of Protein Phosphorylation and Its Functional Impact on Proteinâ€“Protein Interactions via Text Mining of the Scientific Literature. Methods in Molecular Biology, 2017, 1558, 213-232.	0.9	7
67	Robust segmentation of biomedical figures for image-based document retrieval. , 2012, , .		6
68	BioC-compatible full-text passage detection for proteinâ€“protein interactions using extended dependency graph. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw072.	3.0	6
69	eGenPub, a text mining system for extending computationally mapped bibliography for UniProt Knowledgebase by capturing centrality. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	6
70	PIRSitePredict for protein functional site prediction using position-specific rules. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	5
71	A Tutorial on Protein Ontology Resources for Proteomic Studies. Methods in Molecular Biology, 2011, 694, 77-90.	0.9	4
72	Micellar Lipoproteins as the Possible Storage and Translocation Form of Intracellular Diacylglycerol. Biochemical and Biophysical Research Communications, 1998, 243, 669-673.	2.1	3

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73	Pathway curation: Application of text-mining tools eGIFT and RLIMS-P. , 2012, , .		2
74	Toll-Like Receptor Signaling in Vertebrates: Testing the Integration of Protein, Complex, and Pathway Data in the Protein Ontology Framework. PLoS ONE, 2015, 10, e0122978.	2.5	2
75	Tutorial on Protein Ontology Resources. Methods in Molecular Biology, 2017, 1558, 57-78.	0.9	2
76	An Image-Text Approach for Extracting Experimental Evidence of Protein-Protein Interactions in the Biomedical Literature. , 2013, , .		1
77	Text Mining of Protein Phosphorylation Information Using a Generalizable Rule-Based Approach. , 2013, , .		1
78	Mining impact of protein modifications on protein-protein interactions from literature. , 2009, , .		0
79	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	0
80	Scalable Text Mining Assisted Curation of Post-Translationally Modified Proteoforms in the Protein Ontology. CEUR Workshop Proceedings, 2016, 1747, .	2.3	0
81	Hagit Shatkay-Reshef 1965â€“2022. Bioinformatics Advances, 2022, 2, .	2.4	0
82	ANIMO: Annotation of Biomed Image Modalities. , 2021, , .		0