

Cecilia N Arighi

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

25,685
citations

117453

34
h-index

74018

75
g-index

88
all docs

88
docs citations

88
times ranked

43695
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Hagit Shatkay-Reshef 1965â€“2022. <i>Bioinformatics Advances</i> , 2022, 2, . | 0.9 | 0 |
| 2 | Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663. | 3.2 | 110 |
| 3 | UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489. | 6.5 | 4,709 |
| 4 | emiRIT: a text-mining-based resource for microRNA information. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, . | 1.4 | 10 |
| 5 | Utilizing image and caption information for biomedical document classification. <i>Bioinformatics</i> , 2021, 37, i468-i476. | 1.8 | 8 |
| 6 | The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334. | 6.5 | 2,416 |
| 7 | A crowdsourcing open platform for literature curation in UniProt. <i>PLoS Biology</i> , 2021, 19, e3001464. | 2.6 | 74 |
| 8 | ANIMO: Annotation of Biomed Image Modalities. , 2021, , . | | 0 |
| 9 | Protein ontology on the semantic web for knowledge discovery. <i>Scientific Data</i> , 2020, 7, 337. | 2.4 | 9 |
| 10 | A Coordinated Approach by Public Domain Bioinformatics Resources to Aid the Fight Against Alzheimerâ€™s Disease Through Expert Curation of Key Protein Targets. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 257-273. | 1.2 | 7 |
| 11 | UPCLASS: a deep learning-based classifier for UniProtKB entry publications. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, . | 1.4 | 7 |
| 12 | UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. <i>Bioinformatics</i> , 2020, 36, 4643-4648. | 1.8 | 42 |
| 13 | An evolutionarily conserved motif is required for Plasmodesmata-located protein 5 to regulate cell-to-cell movement. <i>Communications Biology</i> , 2020, 3, 291. | 2.0 | 15 |
| 14 | OUP accepted manuscript. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, . | 1.4 | 0 |
| 15 | An effective biomedical document classification scheme in support of biocuration: addressing class imbalance. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, . | 1.4 | 15 |
| 16 | PIRSitePredict for protein functional site prediction using position-specific rules. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, . | 1.4 | 5 |
| 17 | UniProt: a worldwide hub of protein knowledge. <i>Nucleic Acids Research</i> , 2019, 47, D506-D515. | 6.5 | 6,185 |
| 18 | The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338. | 6.5 | 3,474 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | iTextMine: integrated text-mining system for large-scale knowledge extraction from the literature. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 1.4 | 22 |
| 20 | 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. | 1.6 | 35 |
| 21 | iPTMnet: an integrated resource for protein post-translational modification network discovery. Nucleic Acids Research, 2018, 46, D542-D550. | 6.5 | 120 |
| 22 | 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. | 1.6 | 31 |
| 23 | Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338. | 6.5 | 1,838 |
| 24 | Protein Ontology (PRO): enhancing and scaling up the representation of protein entities. Nucleic Acids Research, 2017, 45, D339-D346. | 6.5 | 73 |
| 25 | 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, . | 1.4 | 6 |
| 26 | On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460. | 1.8 | 91 |
| 27 | Analysis of Protein Phosphorylation and Its Functional Impact on Protein-Protein Interactions via Text Mining of the Scientific Literature. Methods in Molecular Biology, 2017, 1558, 213-232. | 0.4 | 7 |
| 28 | iPTMnet: Integrative Bioinformatics for Studying PTM Networks. Methods in Molecular Biology, 2017, 1558, 333-353. | 0.4 | 26 |
| 29 | Tutorial on Protein Ontology Resources. Methods in Molecular Biology, 2017, 1558, 57-78. | 0.4 | 2 |
| 30 | BioC-compatible full-text passage detection for protein-protein interactions using extended dependency graph. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw072. | 1.4 | 6 |
| 31 | Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119. | 1.4 | 36 |
| 32 | BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw121. | 1.4 | 28 |
| 33 | Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw161. | 1.4 | 30 |
| 34 | Scalable Text Mining Assisted Curation of Post-Translationally Modified Proteoforms in the Protein Ontology. CEUR Workshop Proceedings, 2016, 1747, . | 2.3 | 0 |
| 35 | 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, . | 1.4 | 23 |
| 36 | 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. | 1.1 | 2 |

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|----|--|-----|-----------|
| 37 | miRTex: A Text Mining System for miRNA-Gene Relation Extraction. PLoS Computational Biology, 2015, 11, e1004391. | 1.5 | 50 |
| 38 | 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. | 1.9 | 42 |
| 39 | pGenN, a Gene Normalization Tool for Plant Genes and Proteins in Scientific Literature. PLoS ONE, 2015, 10, e0135305. | 1.1 | 12 |
| 40 | Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PLoS ONE, 2015, 10, e0141773. | 1.1 | 12 |
| 41 | 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. | 1.4 | 23 |
| 42 | Overview of the gene ontology task at BioCreative IV. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau086-bau086. | 1.4 | 45 |
| 43 | 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. | 1.4 | 56 |
| 44 | Protein Ontology: a controlled structured network of protein entities. Nucleic Acids Research, 2014, 42, D415-D421. | 6.5 | 63 |
| 45 | BC4GO: a full-text corpus for the BioCreative IV GO task. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau074-bau074. | 1.4 | 36 |
| 46 | Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198. | 6.5 | 1,162 |
| 47 | BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039. | 1.4 | 43 |
| 48 | A framework for biomedical figure segmentation towards image-based document retrieval. BMC Systems Biology, 2013, 7, S8. | 3.0 | 16 |
| 49 | An Image-Text Approach for Extracting Experimental Evidence of Protein-Protein Interactions in the Biomedical Literature. , 2013, , . | | 1 |
| 50 | Text Mining of Protein Phosphorylation Information Using a Generalizable Rule-Based Approach. , 2013, , . | | 1 |
| 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. | 1.4 | 15 |
| 52 | 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. | 1.4 | 68 |
| 53 | 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. | 1.1 | 7 |
| 54 | 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. | 1.4 | 20 |

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|----|--|-----|-----------|
| 55 | Text mining for the biocuration workflow. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas020-bas020. | 1.4 | 132 |
| 56 | Pathway curation: Application of text-mining tools eGIFT and RLIMS-P. , 2012, , . | | 2 |
| 57 | BioCreative-2012 Virtual Issue. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas049-bas049. | 1.4 | 19 |
| 58 | Robust segmentation of biomedical figures for image-based document retrieval. , 2012, , . | | 6 |
| 59 | An Automatic System for Extracting Figures and Captions in Biomedical PDF Documents. , 2011, , . | | 9 |
| 60 | The representation of protein complexes in the Protein Ontology (PRO). BMC Bioinformatics, 2011, 12, 371. | 1.2 | 14 |
| 61 | Overview of the BioCreative III Workshop. BMC Bioinformatics, 2011, 12, S1. | 1.2 | 88 |
| 62 | BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4. | 1.2 | 65 |
| 63 | The Protein Ontology: a structured representation of protein forms and complexes. Nucleic Acids Research, 2011, 39, D539-D545. | 6.5 | 102 |
| 64 | eFIP: A Tool for Mining Functional Impact of Phosphorylation from Literature. Methods in Molecular Biology, 2011, 694, 63-75. | 0.4 | 10 |
| 65 | A Tutorial on Protein Ontology Resources for Proteomic Studies. Methods in Molecular Biology, 2011, 694, 77-90. | 0.4 | 4 |
| 66 | The Universal Protein Resource (UniProt) in 2010. Nucleic Acids Research, 2010, 38, D142-D148. | 6.5 | 1,131 |
| 67 | The Universal Protein Resource (UniProt) 2009. Nucleic Acids Research, 2009, 37, D169-D174. | 6.5 | 548 |
| 68 | An improved ontological representation of dendritic cells as a paradigm for all cell types. BMC Bioinformatics, 2009, 10, 70. | 1.2 | 29 |
| 69 | TGF-beta signaling proteins and the Protein Ontology. BMC Bioinformatics, 2009, 10, S3. | 1.2 | 9 |
| 70 | Mining impact of protein modifications on protein-protein interactions from literature. , 2009, , . | | 0 |
| 71 | The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 35, D193-D197. | 6.5 | 488 |
| 72 | The Universal Protein Resource (UniProt). Nucleic Acids Research, 2007, 36, D190-D195. | 6.5 | 852 |

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|----|--|-----|-----------|
| 73 | Framework for a Protein Ontology. BMC Bioinformatics, 2007, 8, S1. | 1.2 | 78 |
| 74 | Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. Frontiers in Bioscience - Landmark, 2007, 12, 5071. | 3.0 | 30 |
| 75 | PIRSF family classification system for protein functional and evolutionary analysis. Evolutionary Bioinformatics, 2007, 2, 197-209. | 0.6 | 35 |
| 76 | PIRSF Family Classification System for Protein Functional and Evolutionary Analysis. Evolutionary Bioinformatics, 2006, 2, 117693430600200. | 0.6 | 35 |
| 77 | Structural mechanism for ubiquitinated-cargo recognition by the Golgi-localized, \hat{A} -ear-containing, ADP-ribosylation-factor-binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2334-2339. | 3.3 | 66 |
| 78 | Role of the mammalian retromer in sorting of the cation-independent mannose 6-phosphate receptor. Journal of Cell Biology, 2004, 165, 123-133. | 2.3 | 549 |
| 79 | Divalent interaction of the GGAs with the Rabaptin-5-Rabex-5 complex. EMBO Journal, 2003, 22, 78-88. | 3.5 | 135 |
| 80 | Temperature-Induced Conformational Switch in Intestinal Fatty Acid Binding Protein (IFABP) Revealing an Alternative Mode for Ligand Binding. Biochemistry, 2003, 42, 7539-7551. | 1.2 | 18 |
| 81 | Micellar Lipoproteins as the Possible Storage and Translocation Form of Intracellular Diacylglycerol. Biochemical and Biophysical Research Communications, 1998, 243, 669-673. | 1.0 | 3 |
| 82 | Temperature-Induced Conformational Transition of Intestinal Fatty Acid Binding Protein Enhancing Ligand Binding: \hat{A} Functional, Spectroscopic, and Molecular Modeling Study. Biochemistry, 1998, 37, 16802-16814. | 1.2 | 31 |