

# Darren A Natale

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/387603/publications.pdf>

Version: 2024-02-01

74  
papers

49,613  
citations

81434

41  
h-index

93651

72  
g-index

78  
all docs

78  
docs citations

78  
times ranked

75744  
citing authors

#	ARTICLE	IF	CITATIONS
1	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	6.5	1,385
2	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	6.5	4,709
3	COVID-19 biomarkers and their overlap with comorbidities in a disease biomarker data model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	11
4	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
5	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	77
6	GlyGen: Computational and Informatics Resources for Glycoscience. <i>Glycobiology</i> , 2020, 30, 72-73.	1.3	123
7	Protein ontology on the semantic web for knowledge discovery. <i>Scientific Data</i> , 2020, 7, 337.	2.4	9
8	BpForms and BcForms: a toolkit for concretely describing non-canonical polymers and complexes to facilitate global biochemical networks. <i>Genome Biology</i> , 2020, 21, 117.	3.8	8
9	UniRule: a unified rule resource for automatic annotation in the UniProt Knowledgebase. <i>Bioinformatics</i> , 2020, 36, 4643-4648.	1.8	42
10	GlyGen data model and processing workflow. <i>Bioinformatics</i> , 2020, 36, 3941-3943.	1.8	22
11	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
12	UniProt: a worldwide hub of protein knowledge. <i>Nucleic Acids Research</i> , 2019, 47, D506-D515.	6.5	6,185
13	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	6.5	3,474
14	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
15	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. <i>Scientific Reports</i> , 2018, 8, 6518.	1.6	31
16	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	6.5	1,838
17	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
18	Protein Ontology (PRO): enhancing and scaling up the representation of protein entities. <i>Nucleic Acids Research</i> , 2017, 45, D339-D346.	6.5	73

#	ARTICLE	IF	CITATIONS
19	Tutorial on Protein Ontology Resources. <i>Methods in Molecular Biology</i> , 2017, 1558, 57-78.	0.4	2
20	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 24.	0.9	10
21	The development of non-coding RNA ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 214.	0.1	9
22	OmniSearch: a semantic search system based on the Ontology for MicroRNA Target (OMIT) for microRNA-target gene interaction data. <i>Journal of Biomedical Semantics</i> , 2016, 7, 25.	0.9	27
23	Computational clustering for viral reference proteomes: Table 1.. <i>Bioinformatics</i> , 2016, 32, 2041-2043.	1.8	3
24	Scalable Text Mining Assisted Curation of Post-Translationally Modified Proteoforms in the Protein Ontology. <i>CEUR Workshop Proceedings</i> , 2016, 1747, .	2.3	0
25	Toll-Like Receptor Signaling in Vertebrates: Testing the Integration of Protein, Complex, and Pathway Data in the Protein Ontology Framework. <i>PLoS ONE</i> , 2015, 10, e0122978.	1.1	2
26	A semantic approach for knowledge capture of MicroRNA-Target gene interactions. , 2015, , .		10
27	A domain ontology for the Non-Coding RNA field. , 2015, , .		0
28	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
29	OMIT: Dynamic, Semi-Automated Ontology Development for the microRNA Domain. <i>PLoS ONE</i> , 2014, 9, e100855.	1.1	18
30	Protein Ontology: a controlled structured network of protein entities. <i>Nucleic Acids Research</i> , 2014, 42, D415-D421.	6.5	63
31	Activities at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2014, 42, D191-D198.	6.5	1,162
32	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. <i>Frontiers in Genetics</i> , 2013, 4, 62.	1.1	7
33	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012, 40, D71-D75.	6.5	1,196
34	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
35	The representation of protein complexes in the Protein Ontology (PRO). <i>BMC Bioinformatics</i> , 2011, 12, 371.	1.2	14
36	The Protein Ontology: a structured representation of protein forms and complexes. <i>Nucleic Acids Research</i> , 2011, 39, D539-D545.	6.5	102

#	ARTICLE	IF	CITATIONS
37	Protein-Centric Data Integration for Functional Analysis of Comparative Proteomics Data. <i>Methods in Molecular Biology</i> , 2011, 694, 323-339.	0.4	3
38	Structure-Guided Rule-Based Annotation of Protein Functional Sites in UniProt Knowledgebase. <i>Methods in Molecular Biology</i> , 2011, 694, 91-105.	0.4	7
39	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. <i>PLoS ONE</i> , 2011, 6, e18910.	1.1	94
40	Community annotation in biology. <i>Biology Direct</i> , 2010, 5, 12.	1.9	21
41	Novel sequence feature variant type analysis of the HLA genetic association in systemic sclerosis. <i>Human Molecular Genetics</i> , 2010, 19, 707-719.	1.4	37
42	The Universal Protein Resource (UniProt) in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D142-D148.	6.5	1,131
43	Quantitative Organelle Proteomics of MCF-7 Breast Cancer Cells Reveals Multiple Subcellular Locations for Proteins in Cellular Functional Processes. <i>Journal of Proteome Research</i> , 2010, 9, 495-508.	1.8	32
44	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
45	TGF-beta signaling proteins and the Protein Ontology. <i>BMC Bioinformatics</i> , 2009, 10, S3.	1.2	9
46	A procedure to recruit members to enlarge protein family databases - the building of UECOG (UniRef-Enriched COG Database) as a model. <i>Genetics and Molecular Research</i> , 2008, 7, 910-924.	0.3	6
47	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2007, 35, D193-D197.	6.5	488
48	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2007, 36, D190-D195.	6.5	852
49	Framework for a Protein Ontology. <i>BMC Bioinformatics</i> , 2007, 8, S1.	1.2	78
50	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006, 34, D187-D191.	6.5	961
51	Framework for a protein ontology. , 2006, , .		1
52	Computational identification of strain-, species- and genus-specific proteins. <i>BMC Bioinformatics</i> , 2005, 6, 279.	1.2	16
53	PIRSF: family classification system at the Protein Information Resource. <i>Nucleic Acids Research</i> , 2004, 32, 112D-114.	6.5	193
54	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2004, 33, D154-D159.	6.5	1,681

#	ARTICLE	IF	CITATIONS
55	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004, 32, 115D-119.	6.5	2,994
56	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. <i>Genome Biology</i> , 2004, 5, R7.	13.9	814
57	The COG database: an updated version includes eukaryotes. <i>BMC Bioinformatics</i> , 2003, 4, 41.	1.2	3,913
58	Evolution of Eukaryotic Gene Repertoire and Gene Structure: Discovering the Unexpected Dynamics of Genome Evolution. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 293-302.	2.0	6
59	The complete genome of hyperthermophile <i>Methanopyrus kandleri</i> AV19 and monophyly of archaeal methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4644-4649.	3.3	283
60	Congruent evolution of different classes of non-coding DNA in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002, 30, 4264-4271.	6.5	99
61	Independent Evolution of Heavy Metal-Associated Domains in Copper Chaperones and Copper-Transporting ATPases. <i>Journal of Molecular Evolution</i> , 2001, 53, 622-633.	0.8	27
62	The COG database: new developments in phylogenetic classification of proteins from complete genomes. <i>Nucleic Acids Research</i> , 2001, 29, 22-28.	6.5	1,733
63	Initiation of eukaryotic DNA replication: conservative or liberal?. <i>Journal of Cellular Physiology</i> , 2000, 184, 139-150.	2.0	80
64	Copper chaperones in bacteria: association with copper-transporting ATPases. <i>Trends in Biochemical Sciences</i> , 2000, 25, 480-481.	3.7	13
65	Towards understanding the first genome sequence of a crenarchaeon by genome annotation using clusters of orthologous groups of proteins (COGs). <i>Genome Biology</i> , 2000, 1, research0009.1.	13.9	96
66	The COG database: a tool for genome-scale analysis of protein functions and evolution. <i>Nucleic Acids Research</i> , 2000, 28, 33-36.	6.5	3,734
67	Selective instability of Orc1 protein accounts for the absence of functional origin recognition complexes during the M-G1 transition in mammals. <i>EMBO Journal</i> , 2000, 19, 2728-2738.	3.5	80
68	Using the COG database to improve gene recognition in complete genomes. <i>Genetica</i> , 2000, 108, 9-17.	0.5	79
69	Selective activation of pre-replication complexes in vitro at specific sites in mammalian nuclei. <i>Journal of Cell Science</i> , 2000, 113 ( Pt 5), 887-98.	1.2	19
70	A specialized version of the HD hydrolase domain implicated in signal transduction. <i>Journal of Molecular Microbiology and Biotechnology</i> , 1999, 1, 303-5.	1.0	75
71	Absence of an Unusual "Densely Methylated Island" at the Hamster dhfr ori-1 <sup>2</sup> . <i>Journal of Biological Chemistry</i> , 1997, 272, 10021-10029.	1.6	20
72	Ease of DNA unwinding is a conserved property of yeast replication origins. <i>Nucleic Acids Research</i> , 1993, 21, 555-560.	6.5	118

#	ARTICLE	IF	CITATIONS
73	DNA helical stability accounts for mutational defects in a yeast replication origin.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 2654-2658.	3.3	111
74	Stable DNA unwinding, not "breathing," accounts for single-strand-specific nuclease hypersensitivity of specific A+T-rich sequences.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 9464-9468.	3.3	173