

# Claire O'Donovan

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

11,052  
citations

196777

29  
h-index

214428

50  
g-index

54  
all docs

54  
docs citations

54  
times ranked

19333  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolomics: The Stethoscope for the Twenty-First Century. <i>Medical Principles and Practice</i> , 2021, 30, 301-310.	1.1	46
2	ISA API: An open platform for interoperable life science experimental metadata. <i>GigaScience</i> , 2021, 10, .	3.3	19
3	The Enzyme Portal: an integrative tool for enzyme information and analysis. <i>FEBS Journal</i> , 2021, , .	2.2	2
4	Progress towards an OECD reporting framework for transcriptomics and metabolomics in regulatory toxicology. <i>Regulatory Toxicology and Pharmacology</i> , 2021, 125, 105020.	1.3	46
5	The growing need for controlled data access models in clinical proteomics and metabolomics. <i>Nature Communications</i> , 2021, 12, 5787.	5.8	17
6	MetaboLights: a resource evolving in response to the needs of its scientific community. <i>Nucleic Acids Research</i> , 2020, 48, D440-D444.	6.5	435
7	Dissemination and analysis of the quality assurance (QA) and quality control (QC) practices of LC-MS based untargeted metabolomics practitioners. <i>Metabolomics</i> , 2020, 16, 113.	1.4	56
8	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
9	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, .	3.3	60
10	Towards quality assurance and quality control in untargeted metabolomics studies. <i>Metabolomics</i> , 2019, 15, 4.	1.4	101
11	Automated assembly of species metabolomes through data submission into a public repository. <i>GigaScience</i> , 2017, 6, 1-4.	3.3	9
12	From the research laboratory to the database: the <i>Caenorhabditis elegans</i> kinome in UniProtKB. <i>Biochemical Journal</i> , 2017, 474, 493-515.	1.7	9
13	UniProt Tools. <i>Current Protocols in Bioinformatics</i> , 2016, 53, 1.29.1-1.29.15.	25.8	150
14	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. <i>Bioinformatics</i> , 2016, 32, 2264-2271.	1.8	37
15	Minimizing proteome redundancy in the UniProt Knowledgebase. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw139.	1.4	24
16	Searching and Navigating UniProt Databases. <i>Current Protocols in Bioinformatics</i> , 2015, 50, 1.27.1-1.27.10.	25.8	72
17	The GOA database: Gene Ontology annotation updates for 2015. <i>Nucleic Acids Research</i> , 2015, 43, D1057-D1063.	6.5	493
18	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	1.5	13

#	ARTICLE	IF	CITATIONS
19	Representing Kidney Development Using the Gene Ontology. <i>PLoS ONE</i> , 2014, 9, e99864.	1.1	17
20	Expert curation in UniProtKB: a case study on dealing with conflicting and erroneous data. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau016-bau016.	1.4	56
21	Understanding how and why the Gene Ontology and its annotations evolve: the GO within UniProt. <i>GigaScience</i> , 2014, 3, 4.	3.3	70
22	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
23	The EBI enzyme portal. <i>Nucleic Acids Research</i> , 2013, 41, D773-D780.	6.5	19
24	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas062.	1.4	17
25	DATABASE, <i>The Journal of Biological Databases and Curation</i> , is now the official journal of the International Society for Biocuration. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat077-bat077.	1.4	1
26	Biocurators and Biocuration: surveying the 21st century challenges. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar059-bar059.	1.4	59
27	AntiFam: a tool to help identify spurious ORFs in protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas003-bas003.	1.4	38
28	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. <i>Nucleic Acids Research</i> , 2012, 41, D483-D489.	6.5	238
29	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , 2012, 40, D565-D570.	6.5	349
30	A Guide to UniProt for Protein Scientists. <i>Methods in Molecular Biology</i> , 2011, 694, 25-35.	0.4	15
31	The Impact of Focused Gene Ontology Curation of Specific Mammalian Systems. <i>PLoS ONE</i> , 2011, 6, e27541.	1.1	23
32	Solving the Problem: Genome Annotation Standards before the Data Deluge. <i>Standards in Genomic Sciences</i> , 2011, 5, 168-193.	1.5	61
33	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB "complete proteome" sets. <i>Proteomics</i> , 2011, 11, 4434-4438.	1.3	25
34	QuickGO: a user tutorial for the web-based Gene Ontology browser. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap010.	1.4	42
35	The GOA database in 2009--an integrated Gene Ontology Annotation resource. <i>Nucleic Acids Research</i> , 2009, 37, D396-D403.	6.5	497
36	QuickGO: a web-based tool for Gene Ontology searching. <i>Bioinformatics</i> , 2009, 25, 3045-3046.	1.8	789

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37	The Protein Feature Ontology: a tool for the unification of protein feature annotations. <i>Bioinformatics</i> , 2008, 24, 2767-2772.	1.8	19
38	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
39	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	6.5	57
40	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006, 34, D187-D191.	6.5	961
41	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2004, 33, D154-D159.	6.5	1,681
42	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
43	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003, 31, 365-370.	6.5	3,096
44	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003, 31, 43-50.	6.5	56
45	Managing core resources for genomics and proteomics. <i>Pharmacogenomics</i> , 2003, 4, 343-350.	0.6	4
46	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , 2002, 3, 275-284.	3.2	273
47	The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , 2001, 19, 178-181.	4.9	87
48	The role SWISS-PROT and TrEMBL play in the genome research environment. <i>Journal of Biotechnology</i> , 2000, 78, 221-234.	1.9	23
49	Removing redundancy in SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 1999, 15, 258-259.	1.8	32
50	Glycosyltransferases in SWISS-PROT. , 1998, 15, 507-509.		0