Claire O'Donovan

List of Publications by Year
in descending order

50 papers	11,052 citations	172457 29 h-index	189892 50 g-index
54 all docs	54 docs citations	54 times ranked	17156 citing authors

#	Article	IF	Citations
1	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. Nucleic Acids Research, 2003, 31, 365-370.	14.5	3,096
2	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2004, 33, D154-D159.	14.5	1,681
3	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
4	QuickGO: a web-based tool for Gene Ontology searching. Bioinformatics, 2009, 25, 3045-3046.	4.1	789
5	The GOA database in 2009--an integrated Gene Ontology Annotation resource. Nucleic Acids Research, 2009, 37, D396-D403.	14.5	497
6	The GOA database: Gene Ontology annotation updates for 2015. Nucleic Acids Research, 2015, 43, D1057-D1063.	14.5	493
7	MetaboLights: a resource evolving in response to the needs of its scientific community. Nucleic Acids Research, 2020, 48, D440-D444.	14.5	435
8	The UniProt-GO Annotation database in 2011. Nucleic Acids Research, 2012, 40, D565-D570.	14.5	349
9	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
10	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. Briefings in Bioinformatics, 2002, 3, 275-284.	6.5	273
11	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
12	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. Nucleic Acids Research, 2012, 41, D483-D489.	14.5	238
13	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. Genome Research, 2007, 17, 175-183.	5.5	218
14	UniProt Tools. Current Protocols in Bioinformatics, 2016, 53, 1.29.1-1.29.15.	25.8	150
15	Towards quality assurance and quality control in untargeted metabolomics studies. Metabolomics, 2019, 15, 4.	3.0	101
16	The human proteomics initiative (HPI). Trends in Biotechnology, 2001, 19, 178-181.	9.3	87
17	Searching and Navigating UniProt Databases. Current Protocols in Bioinformatics, 2015, 50, 1.27.1-1.27.10.	25.8	72
18	Understanding how and why the Gene Ontology and its annotations evolve: the GO within UniProt. GigaScience, 2014, 3, 4.	6.4	70

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19	Solving the Problem: Genome Annotation Standards before the Data Deluge. Standards in Genomic Sciences, 2011, 5, 168-193.	1.5	61
20	PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, .	6.4	60
21	Biocurators and Biocuration: surveying the 21st century challenges. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar059-bar059.	3.0	59
22	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. Nucleic Acids Research, 2007, 36, D793-D799.	14.5	57
23	The European Bioinformatics Institute's data resources. Nucleic Acids Research, 2003, 31, 43-50.	14.5	56
24	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
25	Dissemination and analysis of the quality assurance (QA) and quality control (QC) practices of LCâ€"MS based untargeted metabolomics practitioners. Metabolomics, 2020, 16, 113.	3.0	56
26	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
27	Metabolomics: The Stethoscope for the Twenty-First Century. Medical Principles and Practice, 2021, 30, 301-310.	2.4	46
28	Progress towards an OECD reporting framework for transcriptomics and metabolomics in regulatory toxicology. Regulatory Toxicology and Pharmacology, 2021, 125, 105020.	2.7	46
29	QuickGO: a user tutorial for the web-based Gene Ontology browser. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap010.	3.0	42
30	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	3.0	38
31	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	4.1	37
32	Removing redundancy in SWISS-PROT and TrEMBL. Bioinformatics, 1999, 15, 258-259.	4.1	32
33	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB â€œcomplete proteomeâ€•sets. Proteomics, 2011, 11, 4434-4438.	2.2	25
34	Minimizing proteome redundancy in the UniProt Knowledgebase. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw139.	3.0	24
35	The role SWISS-PROT and TrEMBL play in the genome research environment. Journal of Biotechnology, 2000, 78, 221-234.	3.8	23
36	The Impact of Focused Gene Ontology Curation of Specific Mammalian Systems. PLoS ONE, 2011, 6, e27541.	2.5	23

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37	The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772.	4.1	19
38	The EBI enzyme portal. Nucleic Acids Research, 2013, 41, D773-D780.	14.5	19
39	ISA API: An open platform for interoperable life science experimental metadata. GigaScience, 2021, 10, .	6.4	19
40	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas062.	3.0	17
41	Representing Kidney Development Using the Gene Ontology. PLoS ONE, 2014, 9, e99864.	2.5	17
42	The growing need for controlled data access models in clinical proteomics and metabolomics. Nature Communications, 2021, 12, 5787.	12.8	17
43	A Guide to UniProt for Protein Scientists. Methods in Molecular Biology, 2011, 694, 25-35.	0.9	15
44	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	2.6	13
45	Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4.	6.4	9
46	From the research laboratory to the database: the Caenorhabditis elegans kinome in UniProtKB. Biochemical Journal, 2017, 474, 493-515.	3.7	9
47	Managing core resources for genomics and proteomics. Pharmacogenomics, 2003, 4, 343-350.	1.3	4
48	The Enzyme Portal: an integrative tool for enzyme information and analysis. FEBS Journal, 2021, , .	4.7	2
49	DATABASE, The Journal of Biological Databases and Curation, is now the official journal of the International Society for Biocuration. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat077-bat077.	3.0	1
50	Glycosyltransferases in SWISS-PROT. , 1998, 15, 507-509.		0