Christopher J Mungall

List of Publications by Year
in descending order

169	44,691	11639 70	5986 160
papers	citations	h-index	g-index

199	199	199	59940
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome sequence of the human malaria parasite Plasmodium falciparum. Nature, 2002, 419, 498-511.	13.7	3,881
2	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	6.5	3,474
3	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	6.5	2,416
4	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	13.7	2,269
5	The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. Nature Biotechnology, 2007, 25, 1251-1255.	9.4	1,955
6	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	13.7	1,838
7	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	6.5	1,838
8	AmiGO: online access to ontology and annotation data. Bioinformatics, 2009, 25, 288-289.	1.8	1,647
9	Comparative Genomics of the Eukaryotes. Science, 2000, 287, 2204-2215.	6.0	1,573
10	The Bioperl Toolkit: Perl Modules for the Life Sciences. Genome Research, 2002, 12, 1611-1618.	2.4	1,427
11	The Generic Genome Browser: A Building Block for a Model Organism System Database. Genome Research, 2002, 12, 1599-1610.	2.4	1,006
12	The Gene Ontology (GO) project in 2006. Nucleic Acids Research, 2006, 34, D322-D326.	6.5	923
13	Tools for neuroanatomy and neurogenetics in Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9715-9720.	3.3	902
14	Creating the Gene Ontology Resource: Design and Implementation. Genome Research, 2001, 11, 1425-1433.	2.4	881
15	Relations in biomedical ontologies. Genome Biology, 2005, 6, R46.	13.9	737
16	JBrowse: A next-generation genome browser. Genome Research, 2009, 19, 1630-1638.	2.4	724
17	GOATOOLS: A Python library for Gene Ontology analyses. Scientific Reports, 2018, 8, 10872.	1.6	717
18	The Human Phenotype Ontology in 2017. Nucleic Acids Research, 2017, 45, D865-D876.	6.5	699

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19	The Human Phenotype Ontology project: linking molecular biology and disease through phenotype data. Nucleic Acids Research, 2014, 42, D966-D974.	6.5	698
20	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	3.8	687
21	The Human Phenotype Ontology in 2021. Nucleic Acids Research, 2021, 49, D1207-D1217.	6.5	652
22	The Sequence Ontology: a tool for the unification of genome annotations. Genome Biology, 2005, 6, R44.	13.9	638
23	Uberon, an integrative multi-species anatomy ontology. Genome Biology, 2012, 13, R5.	13.9	545
24	Expansion of the Human Phenotype Ontology (HPO) knowledge base and resources. Nucleic Acids Research, 2019, 47, D1018-D1027.	6.5	539
25	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	6.0	517
26	Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. Nucleic Acids Research, 2015, 43, D1071-D1078.	6.5	498
27	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	9.4	456
28	The Gene Ontology in 2010: extensions and refinements. Nucleic Acids Research, 2010, 38, D331-D335.	6.5	450
29	The Matchmaker Exchange: A Platform for Rare Disease Gene Discovery. Human Mutation, 2015, 36, 915-921.	1.1	390
30	The FlyBase database of the Drosophila genome projects and community literature. Nucleic Acids Research, 2003, 31, 172-175.	6.5	372
31	Annotation of the Drosophila melanogaster euchromatic genome: a systematic review. Genome Biology, 2002, 3, research0083.1.	13.9	308
32	The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic Acids Research, 2017, 45, D712-D722.	6.5	306
33	Improved exome prioritization of disease genes through cross-species phenotype comparison. Genome Research, 2014, 24, 340-348.	2.4	300
34	Linking Human Diseases to Animal Models Using Ontology-Based Phenotype Annotation. PLoS Biology, 2009, 7, e1000247.	2.6	247
35	The environment ontology: contextualising biological and biomedical entities. Journal of Biomedical Semantics, 2013, 4, 43.	0.9	244
36	Integrating phenotype ontologies across multiple species. Genome Biology, 2010, 11, R2.	13.9	232

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37	A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. American Journal of Human Genetics, 2016, 99, 595-606.	2.6	223
38	A Chado case study: an ontology-based modular schema for representing genome-associated biological information. Bioinformatics, 2007, 23, i337-i346.	1.8	216
39	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
40	How many rare diseases are there?. Nature Reviews Drug Discovery, 2020, 19, 77-78.	21.5	204
41	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	2.6	203
42	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. Journal of Biomedical Semantics, 2016, 7, 44.	0.9	201
43	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	6.5	191
44	The Release 5.1 Annotation of Drosophila melanogaster Heterochromatin. Science, 2007, 316, 1586-1591.	6.0	181
45	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	2.6	178
46	The Monarch Initiative in 2019: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic Acids Research, 2020, 48, D704-D715.	6.5	178
47	The environment ontology in 2016: bridging domains with increased scope, semantic density, and interoperation. Journal of Biomedical Semantics, 2016, 7, 57.	0.9	173
48	High-performance web services for querying gene and variant annotation. Genome Biology, 2016, 17, 91.	3.8	166
49	Global biotic interactions: An open infrastructure to share and analyze species-interaction datasets. Ecological Informatics, 2014, 24, 148-159.	2.3	161
50	National Center for Biomedical Ontology: Advancing Biomedicine through Structured Organization of Scientific Knowledge. OMICS A Journal of Integrative Biology, 2006, 10, 185-198.	1.0	149
51	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. PLoS Computational Biology, 2009, 5, e1000431.	1.5	148
52	Alliance of Genome Resources Portal: unified model organism research platform. Nucleic Acids Research, 2020, 48, D650-D658.	6.5	145
53	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	3.8	144
54	The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. Nucleic Acids Research, 2018, 46, D1168-D1180.	6.5	133

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55	The Plant Ontology as a Tool for Comparative Plant Anatomy and Genomic Analyses. Plant and Cell Physiology, 2013, 54, e1-e1.	1.5	131
56	Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. Journal of Biomedical Semantics, 2014, 5, 21.	0.9	121
57	Logical Development of the Cell Ontology. BMC Bioinformatics, 2011, 12, 6.	1.2	117
58	Phenotype ontologies: the bridge between genomics and evolution. Trends in Ecology and Evolution, 2007, 22, 345-350.	4.2	116
59	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. Nucleic Acids Research, 2017, 45, D737-D743.	6.5	116
60	PhenoDigm: analyzing curated annotations to associate animal models with human diseases. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat025-bat025.	1.4	115
61	Ontology engineering. Nature Biotechnology, 2010, 28, 128-130.	9.4	113
62	Ontobee: A linked ontology data server to support ontology term dereferencing, linkage, query and integration. Nucleic Acids Research, 2017, 45, D347-D352.	6.5	110
63	ROBOT: A Tool for Automating Ontology Workflows. BMC Bioinformatics, 2019, 20, 407.	1.2	97
64	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414.	2.6	97
65	Cross-product extensions of the Gene Ontology. Journal of Biomedical Informatics, 2011, 44, 80-86.	2.5	96
66	Standardized description of scientific evidence using the Evidence Ontology (ECO). Database: the Journal of Biological Databases and Curation, 2014, 2014, bau075-bau075.	1.4	95
67	On the Use of Gene Ontology Annotations to Assess Functional Similarity among Orthologs and Paralogs: A Short Report. PLoS Computational Biology, 2012, 8, e1002386.	1.5	91
68	CLO: The cell line ontology. Journal of Biomedical Semantics, 2014, 5, 37.	0.9	89
69	Computational evaluation of exome sequence data using human and model organism phenotypes improves diagnostic efficiency. Genetics in Medicine, 2016, 18, 608-617.	1.1	85
70	Obol: Integrating Language and Meaning in Bio-Ontologies. Comparative and Functional Genomics, 2004, 5, 509-520.	2.0	82
71	Ontologies as integrative tools for plant science. American Journal of Botany, 2012, 99, 1263-1275.	0.8	79
72	A method for increasing expressivity of Gene Ontology annotations using a compositional approach. BMC Bioinformatics, 2014, 15, 155.	1.2	78

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73	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	77
74	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. Nature Genetics, 2019, 51, 1429-1433.	9.4	76
75	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	72
76	Large-Scale Trends in the Evolution of Gene Structures within 11 Animal Genomes. PLoS Computational Biology, 2006, 2, e15.	1.5	69
77	Evolution of the Sequence Ontology terms and relationships. Journal of Biomedical Informatics, 2011, 44, 87-93.	2.5	68
78	Entity/quality-based logical definitions for the human skeletal phenome using PATO. , 2009, 2009, 7069-72.		67
79	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. Nucleic Acids Research, 2019, 47, D1186-D1194.	6.5	67
80	Navigating the Phenotype Frontier: The Monarch Initiative. Genetics, 2016, 203, 1491-1495.	1.2	65
81	The ARKdb: genome databases for farmed and other animals. Nucleic Acids Research, 2001, 29, 106-110.	6.5	64
82	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	64
83	KG-COVID-19: A Framework to Produce Customized Knowledge Graphs for COVID-19 Response. Patterns, 2021, 2, 100155.	3.1	62
84	MIRO: guidelines for minimum information for the reporting of an ontology. Journal of Biomedical Semantics, 2018, 9, 6.	0.9	55
85	MouseFinder: Candidate disease genes from mouse phenotype data. Human Mutation, 2012, 33, 858-866.	1.1	53
86	The Ontologies Community of Practice: A CGIAR Initiative for Big Data in Agrifood Systems. Patterns, 2020, 1, 100105.	3.1	53
87	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
88	Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 2022, 220, .	1.2	52
89	Survey-based naming conventions for use in OBO Foundry ontology development. BMC Bioinformatics, 2009, 10, 125.	1.2	50
90	The Matchmaker Exchange API: Automating Patient Matching Through the Exchange of Structured Phenotypic and Genotypic Profiles. Human Mutation, 2015, 36, 922-927.	1.1	50

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91	Formalization of taxon-based constraints to detect inconsistencies in annotation and ontology development. BMC Bioinformatics, 2010, 11, 530.	1.2	48
92	Dovetailing biology and chemistry: integrating the Gene Ontology with the ChEBI chemical ontology. BMC Genomics, 2013, 14, 513.	1.2	45
93	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. Nature Reviews Nephrology, 2020, 16, 686-696.	4.1	45
94	The Gene Ontology (GO) Cellular Component Ontology: integration with SAO (Subcellular Anatomy) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	44
95	Phenotypic overlap in the contribution of individual genes to CNV pathogenicity revealed by cross-species computational analysis of single-gene mutations in humans, mice and zebrafish. DMM Disease Models and Mechanisms, 2013, 6, 358-72.	1.2	43
96	The National Microbiome Data Collaborative: enabling microbiome science. Nature Reviews Microbiology, 2020, 18, 313-314.	13.6	42
97	A Unified Anatomy Ontology of the Vertebrate Skeletal System. PLoS ONE, 2012, 7, e51070.	1.1	40
98	Dead simple OWL design patterns. Journal of Biomedical Semantics, 2017, 8, 18.	0.9	39
99	Semantic integration of clinical laboratory tests from electronic health records for deep phenotyping and biomarker discovery. Npj Digital Medicine, 2019, 2, .	5.7	39
100	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	9.4	38
101	Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. Clinical and Translational Science, 2022, 15, 1848-1855.	1.5	38
102	Novel sequence feature variant type analysis of the HLA genetic association in systemic sclerosis. Human Molecular Genetics, 2010, 19, 707-719.	1.4	37
103	Use of Model Organism and Disease Databases to Support Matchmaking for Human Disease Gene Discovery. Human Mutation, 2015, 36, 979-984.	1.1	36
104	The Plant Ontology Facilitates Comparisons of Plant Development Stages Across Species. Frontiers in Plant Science, 2019, 10, 631.	1.7	36
105	Hematopoietic cell types: Prototype for a revised cell ontology. Journal of Biomedical Informatics, 2011, 44, 75-79.	2.5	35
106	Capturing phenotypes for precision medicine. Journal of Physical Education and Sports Management, 2015, 1, a000372.	0.5	32
107	Nose to tail, roots to shoots: spatial descriptors for phenotypic diversity in the Biological Spatial Ontology. Journal of Biomedical Semantics, 2014, 5, 34.	0.9	31
108	Mapping between the OBO and OWL ontology languages. Journal of Biomedical Semantics, 2011, 2, S3.	0.9	30

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109	TermGenie â€“ a web-application for pattern-based ontology class generation. Journal of Biomedical Semantics, 2014, 5, 48.	0.9	30
110	An improved ontological representation of dendritic cells as a paradigm for all cell types. BMC Bioinformatics, 2009, 10, 70.	1.2	29
111	Improving ontologies by automatic reasoning and evaluation of logical definitions. BMC Bioinformatics, 2011, 12, 418.	1.2	29
112	A Census of Disease Ontologies. Annual Review of Biomedical Data Science, 2018, 1, 305-331.	2.8	29
113	Encoding Clinical Data with the Human Phenotype Ontology for Computational Differential Diagnostics. Current Protocols in Human Genetics, 2019, 103, e92.	3.5	29
114	A strategy for building neuroanatomy ontologies. Bioinformatics, 2012, 28, 1262-1269.	1.8	28
115	Plain-language medical vocabulary for precision diagnosis. Nature Genetics, 2018, 50, 474-476.	9.4	28
116	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborativeâ€™s Workshop and Follow-On Activities. MSystems, 2021, 6, .	1.7	28
117	Ontologies for Biologists: A Community Model for the Annotation of Genomic Data. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 227-236.	2.0	27
118	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Applied Ontology, 2011, 6, 53-89.	1.0	23
119	Clinical interpretation of CNVs with cross-species phenotype data. Journal of Medical Genetics, 2014, 51, 766-772.	1.5	23
120	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	23
121	FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. Journal of Biomedical Semantics, 2016, 7, 39.	0.9	22
122	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. Mammalian Genome, 2009, 20, 457-461.	1.0	21
123	VO: Vaccine Ontology. Nature Precedings, 0, , .	0.1	21
124	ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic Acids Research, 2022, 50, D1515-D1521.	6.5	21
125	Disease insights through cross-species phenotype comparisons. Mammalian Genome, 2015, 26, 548-555.	1.0	19
126	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	1.8	19

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127	NSAID use and clinical outcomes in COVID-19 patients: a 38-center retrospective cohort study. Virology Journal, 2022, 19, 84.	1.4	19
128	The health care and life sciences community profile for dataset descriptions. PeerJ, 2016, 4, e2331.	0.9	18
129	Genome-Wide Analysis of Human Disease Alleles Reveals That Their Locations Are Correlated in Paralogous Proteins. PLoS Computational Biology, 2008, 4, e1000218.	1.5	17
130	Representing Kidney Development Using the Gene Ontology. PLoS ONE, 2014, 9, e99864.	1.1	17
131	Phenotypeâ€driven approaches to enhance variant prioritization and diagnosis of rare disease. Human Mutation, 2022, 43, 1071-1081.	1.1	17
132	Novel and Emerging Capabilities that Can Provide a Holistic Understanding of the Plant Root Microbiome. Phytobiomes Journal, 2021, 5, 122-132.	1.4	16
133	Emerging semantics to link phenotype and environment. PeerJ, 2015, 3, e1470.	0.9	15
134	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	1.8	14
135	Ontology based molecular signatures for immune cell types via gene expression analysis. BMC Bioinformatics, 2013, 14, 263.	1.2	13
136	FAIR principles and the IEDB: short-term improvements and a long-term vision of OBO-foundry mediated machine-actionable interoperability. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	13
137	The Porifera Ontology (PORO): enhancing sponge systematics with an anatomy ontology. Journal of Biomedical Semantics, 2014, 5, 39.	0.9	12
138	Transforming the study of organisms: Phenomic data models and knowledge bases. PLoS Computational Biology, 2020, 16, e1008376.	1.5	12
139	Modeling biochemical pathways in the gene ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw126.	1.4	11
140	A Logical Model of Homology for Comparative Biology. Systematic Biology, 2020, 69, 345-362.	2.7	11
141	The influence of disease categories on gene candidate predictions from model organism phenotypes. Journal of Biomedical Semantics, 2014, 5, S4.	0.9	9
142	From SNOMED CT to Uberon: Transferability of evaluation methodology between similarly structured ontologies. Artificial Intelligence in Medicine, 2017, 79, 9-14.	3.8	9
143	A knowledge based approach to matching human neurodegenerative disease and animal models. Frontiers in Neuroinformatics, 2013, 7, 7.	1.3	8
144	ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. BMC Bioinformatics, 2010, 11, S8.	1.2	7

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145	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. Open Biology, 2020, 10, 200149.	1.5	7
146	Experiences Using Logic Programming in Bioinformatics. Lecture Notes in Computer Science, 2009, , 1-21.	1.0	7
147	SvAnna: efficient and accurate pathogenicity prediction of coding and regulatory structural variants in long-read genome sequencing. Genome Medicine, 2022, 14, 44.	3.6	7
148	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. Frontiers in Bioinformatics, 2022, 1, .	1.0	6
149	OPPL-Galaxy, a Galaxy tool for enhancing ontology exploitation as part of bioinformatics workflows. Journal of Biomedical Semantics, 2013, 4, 2.	0.9	5
150	BioMake: a GNU make-compatible utility for declarative workflow management. Bioinformatics, 2017, 33, 3502-3504.	1.8	5
151	Sequence Ontology terminology for gene regulation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194745.	0.9	5
152	Muscle Logic: New Knowledge Resource for Anatomy Enables Comprehensive Searches of the Literature on the Feeding Muscles of Mammals. PLoS ONE, 2016, 11, e0149102.	1.1	5
153	Supervised learning with word embeddings derived from PubMed captures latent knowledge about protein kinases and cancer. NAR Genomics and Bioinformatics, 2021, 3, lqab113.	1.5	4
154	Evolution of the Sequence Ontology terms and relationships. Nature Precedings, 2009, , .	0.1	3
155	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Nature Precedings, 2009, , .	0.1	3
156	Distributed Cognition and Process Management Enabling Individualized Translational Research: The NIH Undiagnosed Diseases Program Experience. Frontiers in Medicine, 2016, 3, 39.	1.2	3
157	String of PURLsÂâ€“ frugal migration and maintenance of persistent identifiers. Data Science, 2020, 3, 3-13.	0.7	3
158	The gene regulation knowledge commons: the action area of GREEKC. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194768.	0.9	3
159	Cross-Product Extensions of the Gene Ontology. Nature Precedings, 2009, , .	0.1	2
160	Taking shortcuts with OWL using safe macros. Nature Precedings, 2010, , .	0.1	2
161	INVESTIGATING THE IMPORTANCE OF ANATOMICAL HOMOLOGY FOR CROSS-SPECIES PHENOTYPE COMPARISONS USING SEMANTIC SIMILARITY. , 2016, , .		2
162	Development of an Ontology of Microbial Phenotypes (OMP). Nature Precedings, 2009, , .	0.1	1

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163	Taking shortcuts with OWL using safe macros. Nature Precedings, 2011, , .	0.1	1
164	What is an anatomy ontology?. Anatomical Record, 2013, 296, 1797-1799.	0.8	1
165	Knowledge Beacons: Web services for data harvesting of distributed biomedical knowledge. PLoS ONE, 2021, 16, e0231916.	1.1	1
166	Hematopoietic Cell Types: Prototype for a Revised Cell Ontology. Nature Precedings, 2009, , .	0.1	0
167	Modularization for the Cell Ontology. Nature Precedings, 2011, , .	0.1	0
168	Use of animal models for exome prioritization of rare disease genes. Orphanet Journal of Rare Diseases, 2014, 9, O19.	1.2	0
169	Tools for exploring mouse models of human disease. Drug Discovery Today: Disease Models, 2016, 20, 21-26.	1.2	0