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	ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic Acids Research, 2022, 50, D1515-D1521.	6.5	21
2	The gene regulation knowledge commons: the action area of GREEKC. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194768.	0.9	3
3	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. Frontiers in Bioinformatics, 2022, 1, .	1.0	6
4	Harmonizing model organism data in the Alliance of Genome Resources. Genetics, 2022, 220, .	1.2	52
5	Phenotypeâ€driven approaches to enhance variant prioritization and diagnosis of rare disease. Human Mutation, 2022, 43, 1071-1081.	1.1	17
6	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
7	NSAID use and clinical outcomes in COVID-19 patients: a 38-center retrospective cohort study. Virology Journal, 2022, 19, 84.	1.4	19
8	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	23
9	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	9.4	38
10	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
11	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	1.8	14
12	KG-COVID-19: A Framework to Produce Customized Knowledge Graphs for COVID-19 Response. Patterns, 2021, 2, 100155.	3.1	62
13	The Human Phenotype Ontology in 2021. Nucleic Acids Research, 2021, 49, D1207-D1217.	6.5	652
14	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborativeâ€™s Workshop and Follow-On Activities. MSystems, 2021, 6, .	1.7	28
15	Knowledge Beacons: Web services for data harvesting of distributed biomedical knowledge. PLoS ONE, 2021, 16, e0231916.	1.1	1
16	Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics, 2021, 37, 3343-3348.	1.8	19
17	Sequence Ontology terminology for gene regulation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194745.	0.9	5
18	Novel and Emerging Capabilities that Can Provide a Holistic Understanding of the Plant Root Microbiome. Phytobiomes Journal, 2021, 5, 122-132.	1.4	16

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19	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	6.5	2,416
20	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	77
21	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
22	Alliance of Genome Resources Portal: unified model organism research platform. Nucleic Acids Research, 2020, 48, D650-D658.	6.5	145
23	A Logical Model of Homology for Comparative Biology. Systematic Biology, 2020, 69, 345-362.	2.7	11
24	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
25	The Ontologies Community of Practice: A CGIAR Initiative for Big Data in Agrifood Systems. Patterns, 2020, 1, 100105.	3.1	53
26	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
27	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. Nature Reviews Nephrology, 2020, 16, 686-696.	4.1	45
28	String of PURLsÂâ€“ frugal migration and maintenance of persistent identifiers. Data Science, 2020, 3, 3-13.	0.7	3
29	The National Microbiome Data Collaborative: enabling microbiome science. Nature Reviews Microbiology, 2020, 18, 313-314.	13.6	42
30	How many rare diseases are there?. Nature Reviews Drug Discovery, 2020, 19, 77-78.	21.5	204
31	Transforming the study of organisms: Phenomic data models and knowledge bases. PLoS Computational Biology, 2020, 16, e1008376.	1.5	12
32	ROBOT: A Tool for Automating Ontology Workflows. BMC Bioinformatics, 2019, 20, 407.	1.2	97
33	Encoding Clinical Data with the Human Phenotype Ontology for Computational Differential Diagnostics. Current Protocols in Human Genetics, 2019, 103, e92.	3.5	29
34	The Plant Ontology Facilitates Comparisons of Plant Development Stages Across Species. Frontiers in Plant Science, 2019, 10, 631.	1.7	36
35	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
36	Semantic integration of clinical laboratory tests from electronic health records for deep phenotyping and biomarker discovery. Npj Digital Medicine, 2019, 2, .	5.7	39

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37	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	6.5	3,474
38	Expansion of the Human Phenotype Ontology (HPO) knowledge base and resources. Nucleic Acids Research, 2019, 47, D1018-D1027.	6.5	539
39	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. Nucleic Acids Research, 2019, 47, D1186-D1194.	6.5	67
40	Plain-language medical vocabulary for precision diagnosis. Nature Genetics, 2018, 50, 474-476.	9.4	28
41	The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. Nucleic Acids Research, 2018, 46, D1168-D1180.	6.5	133
42	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
43	A Census of Disease Ontologies. Annual Review of Biomedical Data Science, 2018, 1, 305-331.	2.8	29
44	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
45	GOATOOLS: A Python library for Gene Ontology analyses. Scientific Reports, 2018, 8, 10872.	1.6	717
46	MIRO: guidelines for minimum information for the reporting of an ontology. Journal of Biomedical Semantics, 2018, 9, 6.	0.9	55
47	The Human Phenotype Ontology in 2017. Nucleic Acids Research, 2017, 45, D865-D876.	6.5	699
48	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	6.5	1,838
49	BioMake: a GNU make-compatible utility for declarative workflow management. Bioinformatics, 2017, 33, 3502-3504.	1.8	5
50	From SNOMED CT to Uberon: Transferability of evaluation methodology between similarly structured ontologies. Artificial Intelligence in Medicine, 2017, 79, 9-14.	3.8	9
51	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
52	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	9.4	456
53	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
54	Dead simple OWL design patterns. Journal of Biomedical Semantics, 2017, 8, 18.	0.9	39

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55	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
56	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
57	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
58	Distributed Cognition and Process Management Enabling Individualized Translational Research: The NIH Undiagnosed Diseases Program Experience. Frontiers in Medicine, 2016, 3, 39.	1.2	3
59	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. Journal of Biomedical Semantics, 2016, 7, 44.	0.9	201
60	The environment ontology in 2016: bridging domains with increased scope, semantic density, and interoperation. Journal of Biomedical Semantics, 2016, 7, 57.	0.9	173
61	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
62	Navigating the Phenotype Frontier: The Monarch Initiative. Genetics, 2016, 203, 1491-1495.	1.2	65
63	Tools for exploring mouse models of human disease. Drug Discovery Today: Disease Models, 2016, 20, 21-26.	1.2	0
64	FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. Journal of Biomedical Semantics, 2016, 7, 39.	0.9	22
65	Modeling biochemical pathways in the gene ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw126.	1.4	11
66	High-performance web services for querying gene and variant annotation. Genome Biology, 2016, 17, 91.	3.8	166
67	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
68	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
69	The health care and life sciences community profile for dataset descriptions. PeerJ, 2016, 4, e2331.	0.9	18
70	INVESTIGATING THE IMPORTANCE OF ANATOMICAL HOMOLOGY FOR CROSS-SPECIES PHENOTYPE COMPARISONS USING SEMANTIC SIMILARITY. , 2016, , .		2
71	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
72	Use of Model Organism and Disease Databases to Support Matchmaking for Human Disease Gene Discovery. Human Mutation, 2015, 36, 979-984.	1.1	36

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73	Capturing phenotypes for precision medicine. Journal of Physical Education and Sports Management, 2015, 1, a000372.	0.5	32
74	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	6.0	517
75	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	3.8	687
76	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	2.6	178
77	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	2.6	203
78	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
79	Disease insights through cross-species phenotype comparisons. Mammalian Genome, 2015, 26, 548-555.	1.0	19
80	The Matchmaker Exchange: A Platform for Rare Disease Gene Discovery. Human Mutation, 2015, 36, 915-921.	1.1	390
81	Emerging semantics to link phenotype and environment. PeerJ, 2015, 3, e1470.	0.9	15
82	Representing Kidney Development Using the Gene Ontology. PLoS ONE, 2014, 9, e99864.	1.1	17
83	The Porifera Ontology (PORO): enhancing sponge systematics with an anatomy ontology. Journal of Biomedical Semantics, 2014, 5, 39.	0.9	12
84	Clinical interpretation of CNVs with cross-species phenotype data. Journal of Medical Genetics, 2014, 51, 766-772.	1.5	23
85	Global biotic interactions: An open infrastructure to share and analyze species-interaction datasets. Ecological Informatics, 2014, 24, 148-159.	2.3	161
86	Improved exome prioritization of disease genes through cross-species phenotype comparison. Genome Research, 2014, 24, 340-348.	2.4	300
87	TermGenie â€“ a web-application for pattern-based ontology class generation. Journal of Biomedical Semantics, 2014, 5, 48.	0.9	30
88	Use of animal models for exome prioritization of rare disease genes. Orphanet Journal of Rare Diseases, 2014, 9, O19.	1.2	0
89	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	3.8	144
90	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

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91	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	13.7	1,838
92	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	13.7	2,269
93	The Human Phenotype Ontology project: linking molecular biology and disease through phenotype data. Nucleic Acids Research, 2014, 42, D966-D974.	6.5	698
94	Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. Journal of Biomedical Semantics, 2014, 5, 21.	0.9	121
95	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
96	CLO: The cell line ontology. Journal of Biomedical Semantics, 2014, 5, 37.	0.9	89
97	The influence of disease categories on gene candidate predictions from model organism phenotypes. Journal of Biomedical Semantics, 2014, 5, S4.	0.9	9
98	A method for increasing expressivity of Gene Ontology annotations using a compositional approach. BMC Bioinformatics, 2014, 15, 155.	1.2	78
99	OPPL-Galaxy, a Galaxy tool for enhancing ontology exploitation as part of bioinformatics workflows. Journal of Biomedical Semantics, 2013, 4, 2.	0.9	5
100	The Gene Ontology (GO) Cellular Component Ontology: integration with SAO (Subcellular Anatomy) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	44
101	Ontology based molecular signatures for immune cell types via gene expression analysis. BMC Bioinformatics, 2013, 14, 263.	1.2	13
102	Dovetailing biology and chemistry: integrating the Gene Ontology with the ChEBI chemical ontology. BMC Genomics, 2013, 14, 513.	1.2	45
103	The Plant Ontology as a Tool for Comparative Plant Anatomy and Genomic Analyses. Plant and Cell Physiology, 2013, 54, e1-e1.	1.5	131
104	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
105	What is an anatomy ontology?. Anatomical Record, 2013, 296, 1797-1799.	0.8	1
106	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
107	The environment ontology: contextualising biological and biomedical entities. Journal of Biomedical Semantics, 2013, 4, 43.	0.9	244
108	A knowledge based approach to matching human neurodegenerative disease and animal models. Frontiers in Neuroinformatics, 2013, 7, 7.	1.3	8

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109	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	72
110	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	64
111	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
112	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	6.5	191
113	Ontologies as integrative tools for plant science. American Journal of Botany, 2012, 99, 1263-1275.	0.8	79
114	Uberon, an integrative multi-species anatomy ontology. Genome Biology, 2012, 13, R5.	13.9	545
115	A strategy for building neuroanatomy ontologies. Bioinformatics, 2012, 28, 1262-1269.	1.8	28
116	MouseFinder: Candidate disease genes from mouse phenotype data. Human Mutation, 2012, 33, 858-866.	1.1	53
117	A Unified Anatomy Ontology of the Vertebrate Skeletal System. PLoS ONE, 2012, 7, e51070.	1.1	40
118	Taking shortcuts with OWL using safe macros. Nature Precedings, 2011, , .	0.1	1
119	Modularization for the Cell Ontology. Nature Precedings, 2011, , .	0.1	0
120	Mapping between the OBO and OWL ontology languages. Journal of Biomedical Semantics, 2011, 2, S3.	0.9	30
121	Hematopoietic cell types: Prototype for a revised cell ontology. Journal of Biomedical Informatics, 2011, 44, 75-79.	2.5	35
122	Cross-product extensions of the Gene Ontology. Journal of Biomedical Informatics, 2011, 44, 80-86.	2.5	96
123	Evolution of the Sequence Ontology terms and relationships. Journal of Biomedical Informatics, 2011, 44, 87-93.	2.5	68
124	Improving ontologies by automatic reasoning and evaluation of logical definitions. BMC Bioinformatics, 2011, 12, 418.	1.2	29
125	Logical Development of the Cell Ontology. BMC Bioinformatics, 2011, 12, 6.	1.2	117
126	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Applied Ontology, 2011, 6, 53-89.	1.0	23

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127	Formalization of taxon-based constraints to detect inconsistencies in annotation and ontology development. BMC Bioinformatics, 2010, 11, 530.	1.2	48
128	ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. BMC Bioinformatics, 2010, 11, S8.	1.2	7
129	Ontology engineering. Nature Biotechnology, 2010, 28, 128-130.	9.4	113
130	Taking shortcuts with OWL using safe macros. Nature Precedings, 2010, , .	0.1	2
131	Novel sequence feature variant type analysis of the HLA genetic association in systemic sclerosis. Human Molecular Genetics, 2010, 19, 707-719.	1.4	37
132	The Gene Ontology in 2010: extensions and refinements. Nucleic Acids Research, 2010, 38, D331-D335.	6.5	450
133	Integrating phenotype ontologies across multiple species. Genome Biology, 2010, 11, R2.	13.9	232
134	Evolution of the Sequence Ontology terms and relationships. Nature Precedings, 2009, , .	0.1	3
135	Cross-Product Extensions of the Gene Ontology. Nature Precedings, 2009, , .	0.1	2
136	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Nature Precedings, 2009, , .	0.1	3
137	Hematopoietic Cell Types: Prototype for a Revised Cell Ontology. Nature Precedings, 2009, , .	0.1	0
138	Development of an Ontology of Microbial Phenotypes (OMP). Nature Precedings, 2009, , .	0.1	1
139	Entity/quality-based logical definitions for the human skeletal phenome using PATO. , 2009, 2009, 7069-72.		67
140	AmiGO: online access to ontology and annotation data. Bioinformatics, 2009, 25, 288-289.	1.8	1,647
141	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. PLoS Computational Biology, 2009, 5, e1000431.	1.5	148
142	Linking Human Diseases to Animal Models Using Ontology-Based Phenotype Annotation. PLoS Biology, 2009, 7, e1000247.	2.6	247
143	Survey-based naming conventions for use in OBO Foundry ontology development. BMC Bioinformatics, 2009, 10, 125.	1.2	50
144	An improved ontological representation of dendritic cells as a paradigm for all cell types. BMC Bioinformatics, 2009, 10, 70.	1.2	29

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145	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. Mammalian Genome, 2009, 20, 457-461.	1.0	21
146	JBrowse: A next-generation genome browser. Genome Research, 2009, 19, 1630-1638.	2.4	724
147	Experiences Using Logic Programming in Bioinformatics. Lecture Notes in Computer Science, 2009, , 1-21.	1.0	7
148	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
149	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
150	The Release 5.1 Annotation of Drosophila melanogaster Heterochromatin. Science, 2007, 316, 1586-1591.	6.0	181
151	A Chado case study: an ontology-based modular schema for representing genome-associated biological information. Bioinformatics, 2007, 23, i337-i346.	1.8	216
152	Phenotype ontologies: the bridge between genomics and evolution. Trends in Ecology and Evolution, 2007, 22, 345-350.	4.2	116
153	The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. Nature Biotechnology, 2007, 25, 1251-1255.	9.4	1,955
154	The Gene Ontology (GO) project in 2006. Nucleic Acids Research, 2006, 34, D322-D326.	6.5	923
155	Large-Scale Trends in the Evolution of Gene Structures within 11 Animal Genomes. PLoS Computational Biology, 2006, 2, e15.	1.5	69
156	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
157	The Sequence Ontology: a tool for the unification of genome annotations. Genome Biology, 2005, 6, R44.	13.9	638
158	Relations in biomedical ontologies. Genome Biology, 2005, 6, R46.	13.9	737
159	Obol: Integrating Language and Meaning in Bio-Ontologies. Comparative and Functional Genomics, 2004, 5, 509-520.	2.0	82
160	The FlyBase database of the Drosophila genome projects and community literature. Nucleic Acids Research, 2003, 31, 172-175.	6.5	372
161	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
162	The Generic Genome Browser: A Building Block for a Model Organism System Database. Genome Research, 2002, 12, 1599-1610.	2.4	1,006

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163	The Bioperl Toolkit: Perl Modules for the Life Sciences. Genome Research, 2002, 12, 1611-1618.	2.4	1,427
164	Annotation of the Drosophila melanogaster euchromatic genome: a systematic review. Genome Biology, 2002, 3, research0083.1.	13.9	308
165	Genome sequence of the human malaria parasite Plasmodium falciparum. Nature, 2002, 419, 498-511.	13.7	3,881
166	Creating the Gene Ontology Resource: Design and Implementation. Genome Research, 2001, 11, 1425-1433.	2.4	881
167	The ARKdb: genome databases for farmed and other animals. Nucleic Acids Research, 2001, 29, 106-110.	6.5	64
168	Comparative Genomics of the Eukaryotes. Science, 2000, 287, 2204-2215.	6.0	1,573
169	VO: Vaccine Ontology. Nature Precedings, 0, , .	0.1	21