Melissa Anne Haendel

List of Publications by Year
in descending order

173 papers	14,326 citations	26610 56 h-index	27389 106 g-index

213 all docs	213 docs citations	213 times ranked	20245 citing authors

#	Article	IF	Citations
1	Synergies between centralized and federated approaches to data quality: a report from the national COVID cohort collaborative. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 609-618.	2.2	39
2	Long-term use of immunosuppressive medicines and in-hospital COVID-19 outcomes: a retrospective cohort study using data from the National COVID Cohort Collaborative. Lancet Rheumatology, The, 2022, 4, e33-e41.	2.2	96
3	Sleep and circadian informatics data harmonization: a workshop report from the Sleep Research Society and Sleep Research Network. Sleep, 2022, 45, .	0.6	8
4	Association Between COVID-19 and Mortality in Hip Fracture Surgery in the National COVID Cohort Collaborative (N3C): A Retrospective Cohort Study. Journal of the American Academy of Orthopaedic Surgeons Global Research and Reviews, 2022, 6, .	0.4	9
5	Characteristics, Outcomes, and Severity Risk Factors Associated With SARS-CoV-2 Infection Among Children in the US National COVID Cohort Collaborative. JAMA Network Open, 2022, 5, e2143151.	2.8	102
6	Association Between Immune Dysfunction and COVID-19 Breakthrough Infection After SARS-CoV-2 Vaccination in the US. JAMA Internal Medicine, 2022, 182, 153.	2.6	182
7	Ankle Fracture and Length of Stay in US Adult Population Using Data From the National COVID Cohort Collaborative. Foot & Ankle Orthopaedics, 2022, 7, 24730114221077282.	0.1	4
8	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. JAMA Network Open, 2022, 5, e223890.	2.8	31
9	Implementation of Zebrafish Ontologies for Toxicology Screening. Frontiers in Toxicology, 2022, 4, 817999.	1.6	4
10	Ensuring a safe(r) harbor: Excising personally identifiable information from structured electronic health record data. Journal of Clinical and Translational Science, 2022, 6, e10.	0.3	2
11	The Clinical Variant Analysis Tool: Analyzing the evidence supporting reported genomic variation in clinical practice. Genetics in Medicine, 2022, 24, 1512-1522.	1.1	4
12	Harmonizing units and values of quantitative data elements in a very large nationally pooled electronic health record (EHR) dataset. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1172-1182.	2.2	11
13	Acute Upper Airway Disease in Children With the Omicron (B.1.1.529) Variant of SARS-CoV-2â€"A Report From the US National COVID Cohort Collaborative. JAMA Pediatrics, 2022, 176, 819.	3.3	41
14	Lumping versus splitting: How to approach defining a disease to enable accurate genomic curation. Cell Genomics, 2022, 2, 100131.	3.0	11
15	Risk of newâ€onset psychiatric sequelae of <scp>COVID</scp>â€19 in the early and late postâ€acute phase. World Psychiatry, 2022, 21, 319-320.	4.8	15
16	NSAID use and clinical outcomes in COVID-19 patients: a 38-center retrospective cohort study. Virology Journal, 2022, 19, 84.	1.4	19
17	Identifying who has long COVID in the USA: a machine learning approach using N3C data. The Lancet Digital Health, 2022, 4, e532-e541.	5.9	104
18	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	23

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19	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	9.4	38
20	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
21	Is authorship sufficient for todayâ€™s collaborative research? A call for contributor roles. Accountability in Research, 2021, 28, 23-43.	1.6	40
22	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 427-443.	2.2	342
23	KG-COVID-19: A Framework to Produce Customized Knowledge Graphs for COVID-19 Response. Patterns, 2021, 2, 100155.	3.1	62
24	The Human Phenotype Ontology in 2021. Nucleic Acids Research, 2021, 49, D1207-D1217.	6.5	652
25	The landscape of nutri-informatics: a review of current resources and challenges for integrative nutrition research. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	15
26	Underrepresentation of Phenotypic Variability of 16p13.11 Microduplication Syndrome Assessed With an Online Self-Phenotyping Tool (Phenotypr): Cohort Study. Journal of Medical Internet Research, 2021, 23, e21023.	2.1	4
27	From Reductionism to Reintegration: Solving societyâ€™s most pressing problems requires building bridges between data types across the life sciences. PLoS Biology, 2021, 19, e3001129.	2.6	6
28	Sharing biological data: why, when, and how. FEBS Letters, 2021, 595, 847-863.	1.3	26
29	Association Between Glucagon-Like Peptide 1 Receptor Agonist and Sodiumâ€“Glucose Cotransporter 2 Inhibitor Use and COVID-19 Outcomes. Diabetes Care, 2021, 44, 1564-1572.	4.3	43
30	Outcomes of SARS-CoV-2 Infection in Patients With Chronic Liver Disease and Cirrhosis: A National COVID Cohort Collaborative Study. Gastroenterology, 2021, 161, 1487-1501.e5.	0.6	79
31	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. JAMA Network Open, 2021, 4, e2116901.	2.8	179
32	One is the loneliest number: genotypic matchmaking using the electronic health record. Genetics in Medicine, 2021, 23, 1830-1832.	1.1	6
33	Interpretable prioritization of splice variants in diagnostic next-generation sequencing. American Journal of Human Genetics, 2021, 108, 1564-1577.	2.6	36
34	The IDeaS initiative: pilot study to assess the impact of rare diseases on patients and healthcare systems. Orphanet Journal of Rare Diseases, 2021, 16, 429.	1.2	31
35	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	77
36	Associations between HIV infection and clinical spectrum of COVID-19: a population level analysis based on US National COVID Cohort Collaborative (N3C) data. Lancet HIV,the, 2021, 8, e690-e700.	2.1	106

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37	The Data Use Ontology to streamline responsible access to human biomedical datasets. Cell Genomics, 2021, 1, 100028.	3.0	31
38	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
39	Characterizing Long COVID: Deep Phenotype of a Complex Condition. EBioMedicine, 2021, 74, 103722.	2.7	127
40	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
41	The case for open science: rare diseases. JAMIA Open, 2020, 3, 472-486.	1.0	33
42	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. Nature Reviews Nephrology, 2020, 16, 686-696.	4.1	45
43	Ontologies, Knowledge Representation, and Machine Learning for Translational Research: Recent Contributions. Yearbook of Medical Informatics, 2020, 29, 159-162.	0.8	14
44	Structuring, reuse and analysis of electronic dental data using the Oral Health and Disease Ontology. Journal of Biomedical Semantics, 2020, 11, 8.	0.9	4
45	Interpretable Clinical Genomics with a Likelihood Ratio Paradigm. American Journal of Human Genetics, 2020, 107, 403-417.	2.6	56
46	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	9.4	104
47	How many rare diseases are there?. Nature Reviews Drug Discovery, 2020, 19, 77-78.	21.5	204
48	Community Approaches for Integrating Environmental Exposures into Human Models of Disease. Environmental Health Perspectives, 2020, 128, 125002.	2.8	11
49	Transforming the study of organisms: Phenomic data models and knowledge bases. PLoS Computational Biology, 2020, 16, e1008376.	1.5	12
50	A phenome-wide association study of 26 mendelian genes reveals phenotypic expressivity of common and rare variants within the general population. PLoS Genetics, 2020, 16, e1008802.	1.5	12
51	Title is missing!. , 2020, 16, e1008802.		0
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55	Title is missing!. , 2020, 16, e1008802.		0
56	Title is missing!. , 2020, 16, e1008802.		0
57	A comprehensive iterative approach is highly effective in diagnosing individuals who are exome negative. Genetics in Medicine, 2019, 21, 161-172.	1.1	60
58	Encoding Clinical Data with the Human Phenotype Ontology for Computational Differential Diagnostics. Current Protocols in Human Genetics, 2019, 103, e92.	3.5	29
59	De Novo Variants in WDR37 Are Associated with Epilepsy, Colobomas, Dysmorphism, Developmental Delay, Intellectual Disability, and Cerebellar Hypoplasia. American Journal of Human Genetics, 2019, 105, 413-424.	2.6	43
60	Data-driven method to enhance craniofacial and oral phenotype vocabularies. Journal of the American Dental Association, 2019, 150, 933-939.e2.	0.7	7
61	De Novo Pathogenic Variants in N-cadherin Cause a Syndromic Neurodevelopmental Disorder with Corpus Callosum, Axon, Cardiac, Ocular, and Genital Defects. American Journal of Human Genetics, 2019, 105, 854-868.	2.6	29
62	New models for human disease from the International Mouse Phenotyping Consortium. Mammalian Genome, 2019, 30, 143-150.	1.0	57
63	Ten quick tips for biocuration. PLoS Computational Biology, 2019, 15, e1006906.	1.5	21
64	Enabling Global Clinical Collaborations on Identifiable Patient Data: The Minerva Initiative. Frontiers in Genetics, 2019, 10, 611.	1.1	14
65	Lysosomal Storage and Albinism Due to Effects of a De Novo CLCN7 Variant on Lysosomal Acidification. American Journal of Human Genetics, 2019, 104, 1127-1138.	2.6	59
66	Semantic integration of clinical laboratory tests from electronic health records for deep phenotyping and biomarker discovery. Npj Digital Medicine, 2019, 2, .	5.7	39
67	The Global academic research organization network: Data sharing to cure diseases and enable learning health systems. Learning Health Systems, 2019, 3, e10073.	1.1	11
68	An analysis and metric of reusable data licensing practices for biomedical resources. PLoS ONE, 2019, 14, e0213090.	1.1	10
69	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	3.1	57
70	Bi-allelic Variants in TONSL Cause SPONASTRIME Dysplasia and a Spectrum of Skeletal Dysplasia Phenotypes. American Journal of Human Genetics, 2019, 104, 422-438.	2.6	27
71	FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. Cell Systems, 2019, 9, 417-421.	2.9	33
72	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	14

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73	The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. Genes, 2019, 10, 960.	1.0	6
74	Representing glycophenotypes: semantic unification of glycobiology resources for disease discovery. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	5
75	Expanding the Spectrum of BAF-Related Disorders: De Novo Variants in SMARCC2 Cause a Syndrome with Intellectual Disability and Developmental Delay. American Journal of Human Genetics, 2019, 104, 164-178.	2.6	59
76	Expansion of the Human Phenotype Ontology (HPO) knowledge base and resources. Nucleic Acids Research, 2019, 47, D1018-D1027.	6.5	539
77	Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. American Journal of Human Genetics, 2018, 102, 494-504.	2.6	59
78	Plain-language medical vocabulary for precision diagnosis. Nature Genetics, 2018, 50, 474-476.	9.4	28
79	matchbox: An open-source tool for patient matching via the Matchmaker Exchange. Human Mutation, 2018, 39, 1827-1834.	1.1	20
80	Classification, Ontology, and Precision Medicine. New England Journal of Medicine, 2018, 379, 1452-1462.	13.9	220
81	ClinGen advancing genomic dataâ€sharing standards as a GA4GH driver project. Human Mutation, 2018, 39, 1686-1689.	1.1	15
82	A Census of Disease Ontologies. Annual Review of Biomedical Data Science, 2018, 1, 305-331.	2.8	29
83	OpenVIVO: Transparency in Scholarship. Frontiers in Research Metrics and Analytics, 2018, 2, .	0.9	11
84	IRF2BPL Is Associated with Neurological Phenotypes. American Journal of Human Genetics, 2018, 103, 245-260.	2.6	69
85	The Human Phenotype Ontology in 2017. Nucleic Acids Research, 2017, 45, D865-D876.	6.5	699
86	The Undiagnosed Diseases Network: Accelerating Discovery about Health and Disease. American Journal of Human Genetics, 2017, 100, 185-192.	2.6	142
87	A Recurrent De Novo Variant in NACC1 Causes a Syndrome Characterized by Infantile Epilepsy, Cataracts, and Profound Developmental Delay. American Journal of Human Genetics, 2017, 100, 343-351.	2.6	35
88	MARRVEL: Integration of Human and Model Organism Genetic Resources to Facilitate Functional Annotation of the Human Genome. American Journal of Human Genetics, 2017, 100, 843-853.	2.6	181
89	Sharing Clinical and Genomic Data on Cancer â€" The Need for Global Solutions. New England Journal of Medicine, 2017, 376, 2006-2009.	13.9	35
90	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 2017, 169, 6-12.	13.5	103

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91	A Syndromic Neurodevelopmental Disorder Caused by De Novo Variants in EBF3. American Journal of Human Genetics, 2017, 100, 128-137.	2.6	96
92	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
93	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.	0.4	92
94	Matchmaker Exchange. Current Protocols in Human Genetics, 2017, 95, 9.31.1-9.31.15.	3.5	47
95	Improved Diagnosis and Care for Rare Diseases through Implementation of Precision Public Health Framework. Advances in Experimental Medicine and Biology, 2017, 1031, 55-94.	0.8	20
96	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
97	Gold-standard ontology-based anatomical annotation in the CRAFT Corpus. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	4
98	Defining Disease, Diagnosis, and Translational Medicine within a Homeostatic Perturbation Paradigm: The National Institutes of Health Undiagnosed Diseases Program Experience. Frontiers in Medicine, 2017, 4, 62.	1.2	23
99	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
100	Reproducible and reusable research: are journal data sharing policies meeting the mark?. PeerJ, 2017, 5, e3208.	0.9	108
101	Laying a Community-Based Foundation for Data-Driven Semantic Standards in Environmental Health Sciences. Environmental Health Perspectives, 2016, 124, 1136-1140.	2.8	21
102	Distributed Cognition and Process Management Enabling Individualized Translational Research: The NIH Undiagnosed Diseases Program Experience. Frontiers in Medicine, 2016, 3, 39.	1.2	3
103	The Ontology for Biomedical Investigations. PLoS ONE, 2016, 11, e0154556.	1.1	217
104	Reproducibility and conflicts in immune epitope data. Immunology, 2016, 147, 349-354.	2.0	4
105	INNOVATIVE APPROACHES TO COMBINING GENOTYPE, PHENOTYPE, EPIGENETIC, AND EXPOSURE DATA FOR PRECISION DIAGNOSTICS. , 2016, , .		0
106	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. Journal of Biomedical Semantics, 2016, 7, 44.	0.9	201
107	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
108	Navigating the Phenotype Frontier: The Monarch Initiative. Genetics, 2016, 203, 1491-1495.	1.2	65

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109	Tools for exploring mouse models of human disease. Drug Discovery Today: Disease Models, 2016, 20, 21-26.	1.2	0
110	The Resource Identification Initiative: A Cultural Shift in Publishing. Neuroinformatics, 2016, 14, 169-182.	1.5	26
111	The Resource Identification Initiative: A cultural shift in publishing. Journal of Comparative Neurology, 2016, 524, 8-22.	0.9	32
112	The Resource Identification Initiative: a cultural shift in publishing. Brain and Behavior, 2016, 6, e00417.	1.0	37
113	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
114	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
115	The health care and life sciences community profile for dataset descriptions. PeerJ, 2016, 4, e2331.	0.9	18
116	Dealing with Data: A Case Study on Information and Data Management Literacy. , 2016, , 3-12.		0
117	PhenomeCentral: A Portal for Phenotypic and Genotypic Matchmaking of Patients with Rare Genetic Diseases. Human Mutation, 2015, 36, 931-940.	1.1	107
118	Use of Model Organism and Disease Databases to Support Matchmaking for Human Disease Gene Discovery. Human Mutation, 2015, 36, 979-984.	1.1	36
119	Capturing phenotypes for precision medicine. Journal of Physical Education and Sports Management, 2015, 1, a000372.	0.5	32
120	Next-generation diagnostics and disease-gene discovery with the Exomiser. Nature Protocols, 2015, 10, 2004-2015.	5.5	296
121	Finding Our Way through Phenotypes. PLoS Biology, 2015, 13, e1002033.	2.6	178
122	Summarizing and visualizing structural changes during the evolution of biomedical ontologies using a Diff Abstraction Network. Journal of Biomedical Informatics, 2015, 56, 127-144.	2.5	14
123	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	2.6	203
124	Disease insights through cross-species phenotype comparisons. Mammalian Genome, 2015, 26, 548-555.	1.0	19
125	The Matchmaker Exchange: A Platform for Rare Disease Gene Discovery. Human Mutation, 2015, 36, 915-921.	1.1	390
126	The Resource Identification Initiative: A cultural shift in publishing. F1000Research, 2015, 4, 134.	0.8	47

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127	The Resource Identification Initiative: A cultural shift in publishing. F1000Research, 2015, 4, 134.	0.8	42
128	Achieving human and machine accessibility of cited data in scholarly publications. PeerJ Computer Science, 2015, 1, e1.	2.7	89
129	The Porifera Ontology (PORO): enhancing sponge systematics with an anatomy ontology. Journal of Biomedical Semantics, 2014, 5, 39.	0.9	12
130	Clinical interpretation of CNVs with cross-species phenotype data. Journal of Medical Genetics, 2014, 51, 766-772.	1.5	23
131	Improved exome prioritization of disease genes through cross-species phenotype comparison. Genome Research, 2014, 24, 340-348.	2.4	300
132	Use of animal models for exome prioritization of rare disease genes. Orphanet Journal of Rare Diseases, 2014, 9, O19.	1.2	0
133	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	3.8	144
134	Effective diagnosis of genetic disease by computational phenotype analysis of the disease-associated genome. Science Translational Medicine, 2014, 6, 252ra123.	5.8	223
135	Thematic series on biomedical ontologies in JBMS: challenges and new directions. Journal of Biomedical Semantics, 2014, 5, 15.	0.9	8
136	The Human Phenotype Ontology project: linking molecular biology and disease through phenotype data. Nucleic Acids Research, 2014, 42, D966-D974.	6.5	698
137	Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. Journal of Biomedical Semantics, 2014, 5, 21.	0.9	121
138	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
139	CLO: The cell line ontology. Journal of Biomedical Semantics, 2014, 5, 37.	0.9	89
140	The zebrafish anatomy and stage ontologies: representing the anatomy and development of Danio rerio. Journal of Biomedical Semantics, 2014, 5, 12.	0.9	53
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	Computing on the anatomical form for disease discovery (338.1). FASEB Journal, 2014, 28, 338.1.	0.2	0
143	Ontology based molecular signatures for immune cell types via gene expression analysis. BMC Bioinformatics, 2013, 14, 263.	1.2	13
144	An overview of the BioCreative 2012 Workshop Track III: interactive text mining task. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas056-bas056.	1.4	68

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145	What is an anatomy ontology?. Anatomical Record, 2013, 296, 1797-1799.	0.8	1
146	On the reproducibility of science: unique identification of research resources in the biomedical literature. PeerJ, 2013, 1, e148.	0.9	216
147	An ontology-based method for secondary use of electronic dental record data. AMIA Summits on Translational Science Proceedings, 2013, 2013, 234-8.	0.4	6
148	Dealing with Data: A Case Study on Information and Data Management Literacy. PLoS Biology, 2012, 10, e1001339.	2.6	49
149	Preface. International Review of Neurobiology, 2012, 103, xi-xii.	0.9	0
150	Research resources: curating the new eagle-i discovery system. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar067-bar067.	1.4	31
151	Uberon, an integrative multi-species anatomy ontology. Genome Biology, 2012, 13, R5.	13.9	545
152	Lost and Found in Behavioral Informatics. International Review of Neurobiology, 2012, 103, 1-18.	0.9	1
153	A Unified Anatomy Ontology of the Vertebrate Skeletal System. PLoS ONE, 2012, 7, e51070.	1.1	40
154	Modularization for the Cell Ontology. Nature Precedings, 2011, , .	0.1	0
155	eagle-i: An Ontology-Driven Framework For Biomedical Resource Curation And Discovery. Nature Precedings, 2010, , .	0.1	0
156	The Teleost Anatomy Ontology: Anatomical Representation for the Genomics Age. Systematic Biology, 2010, 59, 369-383.	2.7	76
157	Integrating phenotype ontologies across multiple species. Genome Biology, 2010, 11, R2.	13.9	232
158	Uberon: towards a comprehensive multi-species anatomy ontology. Nature Precedings, 2009, , .	0.1	11
159	Linking Human Diseases to Animal Models Using Ontology-Based Phenotype Annotation. PLoS Biology, 2009, 7, e1000247.	2.6	247
160	An F-domain introduced by alternative splicing regulates activity of the zebrafish thyroid hormone receptor Î±. General and Comparative Endocrinology, 2008, 155, 176-189.	0.8	34
161	CARO â€“ The Common Anatomy Reference Ontology. Computational Biology, 2008, , 327-349.	0.1	45
162	OBO-Edit an ontology editor for biologists. Bioinformatics, 2007, 23, 2198-2200.	1.8	250

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163	The Zebrafish Information Network: the zebrafish model organism database provides expanded support for genotypes and phenotypes. Nucleic Acids Research, 2007, 36, D768-D772.	6.5	137
164	Phenotype ontologies: the bridge between genomics and evolution. Trends in Ecology and Evolution, 2007, 22, 345-350.	4.2	116
165	Connecting evolutionary morphology to genomics using ontologies: a case study from Cypriniformes including zebrafish. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 655-668.	0.6	46
166	The Zebrafish Information Network: the zebrafish model organism database. Nucleic Acids Research, 2006, 34, D581-D585.	6.5	263
167	Leukaemia inhibitory factor (LIF) is functionally linked to axotrophin and both LIF and axotrophin are linked to regulatory immune tolerance. FEBS Letters, 2005, 579, 609-614.	1.3	31
168	Developmental Toxicity of the Dithiocarbamate Pesticide Sodium Metam in Zebrafish. Toxicological Sciences, 2004, 81, 390-400.	1.4	102
169	Slow degeneration of zebrafish Rohon-Beard neurons during programmed cell death. Developmental Dynamics, 2004, 229, 30-41.	0.8	88
170	Gene Trapping in Embryonic Stem Cells In Vitro to Identify Novel Developmentally Regulated Genes in the Mouse. , 2000, 136, 297-307.		2
171	In VitroPreselection of Gene-Trapped Embryonic Stem Cell Clones for Characterizing Novel Developmentally Regulated Genes in the Mouse. Developmental Biology, 1997, 185, 201-214.	0.9	72
172	Cytoskeletal changes during neurogenesis in cultures of avian neural crest cells. Journal of Neurocytology, 1996, 25, 289-301.	1.6	27
173	Modularization for the Cell Ontology. Nature Precedings, 0, , .	0.1	1