Robert Hoehndorf

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

152 2,950 30 49 papers citations h-index g-index

1763,7685.25.82ext. papersext. citationsavg, IFL-index

#	Paper	IF	Citations
152	DeepGO: predicting protein functions from sequence and interactions using a deep ontology-aware classifier. <i>Bioinformatics</i> , 2018 , 34, 660-668	7.2	177
151	PhenomeNET: a whole-phenome approach to disease gene discovery. <i>Nucleic Acids Research</i> , 2011 , 39, e119	20.1	166
150	Text-mining solutions for biomedical research: enabling integrative biology. <i>Nature Reviews Genetics</i> , 2012 , 13, 829-39	30.1	160
149	The role of ontologies in biological and biomedical research: a functional perspective. <i>Briefings in Bioinformatics</i> , 2015 , 16, 1069-80	13.4	143
148	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	18.3	111
147	Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. <i>Nature Genetics</i> , 2015 , 47, 969-978	36.3	106
146	The Semanticscience Integrated Ontology (SIO) for biomedical research and knowledge discovery. Journal of Biomedical Semantics, 2014, 5, 14	2.2	101
145	FoodOn: a harmonized food ontology to increase global food traceability, quality control and data integration. <i>Npj Science of Food</i> , 2018 , 2, 23	6.3	83
144	DeepGOPlus: improved protein function prediction from sequence. <i>Bioinformatics</i> , 2020 , 36, 422-429	7.2	70
143	Neuro-symbolic representation learning on biological knowledge graphs. <i>Bioinformatics</i> , 2017 , 33, 2723	- 7 .230	63
142	The Units Ontology: a tool for integrating units of measurement in science. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas033	5	63
141	Analysis of the human diseasome using phenotype similarity between common, genetic, and infectious diseases. <i>Scientific Reports</i> , 2015 , 5, 10888	4.9	62
140	Mouse genetic and phenotypic resources for human genetics. <i>Human Mutation</i> , 2012 , 33, 826-36	4.7	56
139	Evaluation of research in biomedical ontologies. <i>Briefings in Bioinformatics</i> , 2013 , 14, 696-712	13.4	55
138	Aber-OWL: a framework for ontology-based data access in biology. <i>BMC Bioinformatics</i> , 2015 , 16, 26	3.6	53
137	OPA2Vec: combining formal and informal content of biomedical ontologies to improve similarity-based prediction. <i>Bioinformatics</i> , 2019 , 35, 2133-2140	7.2	48
136	Onto2Vec: joint vector-based representation of biological entities and their ontology-based annotations. <i>Bioinformatics</i> , 2018 , 34, i52-i60	7.2	43

135	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 5	2.2	42	
134	Relations as patterns: bridging the gap between OBO and OWL. <i>BMC Bioinformatics</i> , 2010 , 11, 441	3.6	42	
133	The anatomy of phenotype ontologies: principles, properties and applications. <i>Briefings in Bioinformatics</i> , 2018 , 19, 1008-1021	13.4	41	
132	Identifying aberrant pathways through integrated analysis of knowledge in pharmacogenomics. <i>Bioinformatics</i> , 2012 , 28, 2169-75	7.2	39	
131	Interoperability between phenotype and anatomy ontologies. <i>Bioinformatics</i> , 2010 , 26, 3112-8	7.2	38	
130	Integrating systems biology models and biomedical ontologies. BMC Systems Biology, 2011 , 5, 124	3.5	37	
129	Mouse model phenotypes provide information about human drug targets. <i>Bioinformatics</i> , 2014 , 30, 719	- 7 5	35	
128	Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. <i>BMC Bioinformatics</i> , 2007 , 8, 377	3.6	34	
127	An ontology approach to comparative phenomics in plants. Plant Methods, 2015, 11, 10	5.8	33	
126	Interoperability between biomedical ontologies through relation expansion, upper-level ontologies and automatic reasoning. <i>PLoS ONE</i> , 2011 , 6, e22006	3.7	32	
125	A top-level ontology of functions and its application in the Open Biomedical Ontologies. <i>Bioinformatics</i> , 2006 , 22, e66-73	7.2	32	
124	The RICORDO approach to semantic interoperability for biomedical data and models: strategy, standards and solutions. <i>BMC Research Notes</i> , 2011 , 4, 313	2.3	31	
123	Semantic Disease Gene Embeddings (SmuDGE): phenotype-based disease gene prioritization without phenotypes. <i>Bioinformatics</i> , 2018 , 34, i901-i907	7.2	30	
122	The neurobehavior ontology: an ontology for annotation and integration of behavior and behavioral phenotypes. <i>International Review of Neurobiology</i> , 2012 , 103, 69-87	4.4	29	
121	Taxon and trait recognition from digitized herbarium specimens using deep convolutional neural networks. <i>Botany Letters</i> , 2018 , 165, 377-383	1.1	28	
120	A common layer of interoperability for biomedical ontologies based on OWL EL. <i>Bioinformatics</i> , 2011 , 27, 1001-8	7.2	28	
119	Ranking adverse drug reactions with crowdsourcing. <i>Journal of Medical Internet Research</i> , 2015 , 17, e80	7.6	27	
118	Semi-Supervised Entity Alignment via Knowledge Graph Embedding with Awareness of Degree Difference 2019 ,		25	

117	Integrating phenotype ontologies with PhenomeNET. Journal of Biomedical Semantics, 2017, 8, 58	2.2	25
116	DeepPVP: phenotype-based prioritization of causative variants using deep learning. <i>BMC Bioinformatics</i> , 2019 , 20, 65	3.6	24
115	The flora phenotype ontology (FLOPO): tool for integrating morphological traits and phenotypes of vascular plants. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 65	2.2	24
114	Semantic integration of physiology phenotypes with an application to the Cellular Phenotype Ontology. <i>Bioinformatics</i> , 2012 , 28, 1783-9	7.2	22
113	Semantic prioritization of novel causative genomic variants. <i>PLoS Computational Biology</i> , 2017 , 13, e100) 5 500	21
112	FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 39	2.2	20
111	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Applied Ontology</i> , 2011 , 6, 53-89	1.4	20
110	Semantic similarity and machine learning with ontologies. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	20
109	Evaluating the effect of annotation size on measures of semantic similarity. <i>Journal of Biomedical Semantics</i> , 2017 , 8, 7	2.2	19
108	Improving disease gene prioritization by comparing the semantic similarity of phenotypes in mice with those of human diseases. <i>PLoS ONE</i> , 2012 , 7, e38937	3.7	18
107	Linking PharmGKB to phenotype studies and animal models of disease for drug repurposing. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012 , 388-99	1.3	18
106	Analyzing gene expression data in mice with the Neuro Behavior Ontology. <i>Mammalian Genome</i> , 2014 , 25, 32-40	3.2	17
105	Computational tools for comparative phenomics: the role and promise of ontologies. <i>Mammalian Genome</i> , 2012 , 23, 669-79	3.2	17
104	Systematic analysis of experimental phenotype data reveals gene functions. <i>PLoS ONE</i> , 2013 , 8, e60847	3.7	16
103	Inferring ontology graph structures using OWL reasoning. BMC Bioinformatics, 2018, 19, 7	3.6	15
102	New approaches to the representation and analysis of phenotype knowledge in human diseases and their animal models. <i>Briefings in Functional Genomics</i> , 2011 , 10, 258-65	4.9	15
101	An integrative, translational approach to understanding rare and orphan genetically based diseases. <i>Interface Focus</i> , 2013 , 3, 20120055	3.9	14
100	Data Science and symbolic AI: Synergies, challenges and opportunities. <i>Data Science</i> , 2017 , 1, 27-38	2.2	13

99	Enriched biodiversity data as a resource and service. Biodiversity Data Journal, 2014, e1125	1.8	13
98	Applying the functional abnormality ontology pattern to anatomical functions. <i>Journal of Biomedical Semantics</i> , 2010 , 1, 4	2.2	12
97	GFO-Bio: A biological core ontology. <i>Applied Ontology</i> , 2008 , 3, 219-227	1.4	12
96	A Review of Current Standards and the Evolution of Histopathology Nomenclature for Laboratory Animals. <i>ILAR Journal</i> , 2018 , 59, 29-39	1.7	12
95	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018 , 19, 77-88	13.4	11
94	In silico exploration of Red Sea Bacillus genomes for natural product biosynthetic gene clusters. <i>BMC Genomics</i> , 2018 , 19, 382	4.5	11
93	BOWiki: an ontology-based wiki for annotation of data and integration of knowledge in biology. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 5, S5	3.6	11
92	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , 2016 , 11, e0158896	3.7	11
91	DeepViral: prediction of novel virus-host interactions from protein sequences and infectious disease phenotypes. <i>Bioinformatics</i> , 2021 ,	7.2	11
90	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017 , 18, 33	4.5	10
89	Using AberOWL for fast and scalable reasoning over BioPortal ontologies. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 49	2.2	10
88	DESM: portal for microbial knowledge exploration systems. <i>Nucleic Acids Research</i> , 2016 , 44, D624-33	20.1	10
87	Logical Gene Ontology Annotations (GOAL): exploring gene ontology annotations with OWL. <i>Journal of Biomedical Semantics</i> , 2012 , 3 Suppl 1, S3	2.2	10
86	Evaluating gold standard corpora against gene/protein tagging solutions and lexical resources. Journal of Biomedical Semantics, 2013 , 4, 28	2.2	10
85	The ontology of biological sequences. <i>BMC Bioinformatics</i> , 2009 , 10, 377	3.6	10
84	EL Embeddings: Geometric Construction of Models for the Description Logic EL++ 2019 ,		10
83	An infrastructure for ontology-based information systems in biomedicine: RICORDO case study. <i>Bioinformatics</i> , 2012 , 28, 448-50	7.2	9
82	Ontology-based prediction of cancer driver genes. <i>Scientific Reports</i> , 2019 , 9, 17405	4.9	9

81	Machine learning with biomedical ontologies		8
80	Predicting candidate genes from phenotypes, functions and anatomical site of expression. <i>Bioinformatics</i> , 2021 , 37, 853-860	7.2	8
79	PathoPhenoDB, linking human pathogens to their phenotypes in support of infectious disease research. <i>Scientific Data</i> , 2019 , 6, 79	8.2	7
78	Similarity-based search of model organism, disease and drug effect phenotypes. <i>Journal of Biomedical Semantics</i> , 2015 , 6, 6	2.2	7
77	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. <i>Scientific Reports</i> , 2017 , 7, 5968	4.9	7
76	Thematic series on biomedical ontologies in JBMS: challenges and new directions. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 15	2.2	7
75	Evaluation and cross-comparison of lexical entities of biological interest (LexEBI). <i>PLoS ONE</i> , 2013 , 8, e75185	3.7	7
74	Ontology design patterns to disambiguate relations between genes and gene products in GENIA. <i>Journal of Biomedical Semantics</i> , 2011 , 2 Suppl 5, S1	2.2	7
73	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier. <i>PLoS Computational Biology</i> , 2020 , 16, e1008453	5	7
72	EMC10 homozygous variant identified in a family with global developmental delay, mild intellectual disability, and speech delay. <i>Clinical Genetics</i> , 2020 , 98, 555-561	4	7
71	Quantitative comparison of mapping methods between Human and Mammalian Phenotype Ontology. <i>Journal of Biomedical Semantics</i> , 2012 , 3 Suppl 2, S1	2.2	6
70	Drug repurposing through joint learning on knowledge graphs and literature		6
69	DeepGOPlus: Improved protein function prediction from sequence		6
68	Quantitative evaluation of ontology design patterns for combining pathology and anatomy ontologies. <i>Scientific Reports</i> , 2019 , 9, 4025	4.9	5
67	Combining lexical and context features for automatic ontology extension. <i>Journal of Biomedical Semantics</i> , 2020 , 11, 1	2.2	5
66	Ontology-based cross-species integration and analysis of Saccharomyces cerevisiae phenotypes. <i>Journal of Biomedical Semantics</i> , 2012 , 3 Suppl 2, S6	2.2	5
65	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data		5
64	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data. <i>Bioinformatics</i> , 2020 , 36, 2229-2236	7.2	5

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63	A fast, accurate, and generalisable heuristic-based negation detection algorithm for clinical text. <i>Computers in Biology and Medicine</i> , 2021 , 130, 104216	7	5
62	DermO; an ontology for the description of dermatologic disease. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 38	2.2	5
61	Ontology based text mining of gene-phenotype associations: application to candidate gene prediction. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	4
60	Best behaviour? Ontologies and the formal description of animal behaviour. <i>Mammalian Genome</i> , 2015 , 26, 540-7	3.2	4
59	DDIEM: drug database for inborn errors of metabolism. Orphanet Journal of Rare Diseases, 2020, 15, 14	64.2	4
58	Representing physiological processes and their participants with PhysioMaps. <i>Journal of Biomedical Semantics</i> , 2013 , 4 Suppl 1, S2	2.2	4
57	Towards improving phenotype representation in OWL. <i>Journal of Biomedical Semantics</i> , 2012 , 3 Suppl 2, S5	2.2	4
56	PIDO: the primary immunodeficiency disease ontology. <i>Bioinformatics</i> , 2011 , 27, 3193-9	7.2	4
55	Semantic Systems Biology: Formal Knowledge Representation in Systems Biology for Model Construction, Retrieval, Validation and Discovery 2013 , 355-373		4
54	Improved characterisation of clinical text through ontology-based vocabulary expansion		4
53	Komenti: A semantic text mining framework		4
52	What is the right sequencing approach? Solo VS extended family analysis in consanguineous populations. <i>BMC Medical Genomics</i> , 2020 , 13, 103	3.7	4
51	Towards semantic interoperability: finding and repairing hidden contradictions in biomedical ontologies. <i>BMC Medical Informatics and Decision Making</i> , 2020 , 20, 311	3.6	4
50	Improved characterisation of clinical text through ontology-based vocabulary expansion. <i>Journal of Biomedical Semantics</i> , 2021 , 12, 7	2.2	4
49	Towards similarity-based differential diagnostics for common diseases. <i>Computers in Biology and Medicine</i> , 2021 , 133, 104360	7	4
48	Comparative genomics study reveals Red Sea Bacillus with characteristics associated with potential microbial cell factories (MCFs). <i>Scientific Reports</i> , 2019 , 9, 19254	4.9	4
47	Nail abnormalities identified in an ageing study of 30 inbred mouse strains. <i>Experimental Dermatology</i> , 2019 , 28, 383-390	4	4
46	OligoPVP: Phenotype-driven analysis of individual genomic information to prioritize oligogenic disease variants. <i>Scientific Reports</i> , 2018 , 8, 14681	4.9	4

45	Ontology-based validation and identification of regulatory phenotypes. <i>Bioinformatics</i> , 2018 , 34, i857-i8	8 6 52	4
44	A Proposal for a Gene Functions Wiki. <i>Lecture Notes in Computer Science</i> , 2006 , 669-678	0.9	4
43	The Informatics of Developmental Phenotypes 2016 , 307-318		3
42	Statistical tests for associations between two directed acyclic graphs. <i>PLoS ONE</i> , 2010 , 5, e10996	3.7	3
41	A fast, accurate, and generalisable heuristic-based negation detection algorithm for clinical text		3
40	GFVO: the Genomic Feature and Variation Ontology. <i>PeerJ</i> , 2015 , 3, e933	3.1	3
39	Ontology based mining of pathogen-disease associations from literature		3
38	Ontology based mining of pathogen-disease associations from literature. <i>Journal of Biomedical Semantics</i> , 2019 , 10, 15	2.2	2
37	Hyaline Arteriolosclerosis in 30 Strains of Aged Inbred Mice. Veterinary Pathology, 2019, 56, 799-806	2.8	2
36	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020 , 9, 136	3.6	2
35	PathoPhenoDB: linking human pathogens to their disease phenotypes in support of infectious disease research		2
34	Predicting candidate genes from phenotypes, functions, and anatomical site of expression		2
33	Modeling quantitative traits for COVID-19 case reports		2
32	DeepPVP: phenotype-based prioritization of causative variants using deep learning		2
31	Quantitative evaluation of ontology design patterns for combining pathology and anatomy ontologies		2
30	Linking common human diseases to their phenotypes; development of a resource for human phenomics. <i>Journal of Biomedical Semantics</i> , 2021 , 12, 17	2.2	2
29	Towards Similarity-based Differential Diagnostics For Common Diseases		2
28	OBML - Ontologies in Biomedicine and Life Sciences. <i>Journal of Biomedical Semantics</i> , 2011 , 2 Suppl 4, I1	2.2	1

27	LINKING PHARMGKB TO PHENOTYPE STUDIES AND ANIMAL MODELS OF DISEASE FOR DRUG REPURPOSING 2011 ,		1
26	A Machine Learning Based Approach for Similarity Search on Biodiversity Knowledge Graphs. <i>Biodiversity Information Science and Standards</i> ,3,		1
25	Phenotypic, functional and taxonomic features predict host-pathogen interactions		1
24	Self-normalizing learning on biomedical ontologies using a deep Siamese neural network		1
23	Towards semantic interoperability: finding and repairing hidden contradictions in biomedical ontologie	S	1
22	Notions of similarity for computational biology models		1
21	D4: Deep Drug-drug interaction Discovery and Demystification		1
20	DeepViral: infectious disease phenotypes improve prediction of novel virusBost interactions		1
19	Exploring Binary Relations for Ontology Extension and Improved Adaptation to Clinical Text		1
18	Vec2SPARQL: integrating SPARQL queries and knowledge graph embeddings		1
17	Ontology-based prediction of cancer driver genes		1
16	Ontologies in Biology 2010 , 347-371		1
15	DTI-Voodoo: machine learning over interaction networks and ontology-based background knowledge predicts drug-target interactions. <i>Bioinformatics</i> , 2021 ,	7.2	1
14	Datamining with Ontologies. <i>Methods in Molecular Biology</i> , 2016 , 1415, 385-97	1.4	1
13	Multi-faceted semantic clustering with text-derived phenotypes. <i>Computers in Biology and Medicine</i> , 2021 , 138, 104904	7	1
12	Usage of cell nomenclature in biomedical literature. <i>BMC Bioinformatics</i> , 2017 , 18, 561	3.6	О
11	DeepGOWeb: fast and accurate protein function prediction on the (Semantic) Web. <i>Nucleic Acids Research</i> , 2021 , 49, W140-W146	20.1	О
10	Combining biomedical knowledge graphs and text to improve predictions for drug-target interactions and drug-indications <i>PeerJ</i> , 2022 , 10, e13061	3.1	О

9	Effects of Negation and Uncertainty Stratification on Text-Derived Patient Profile Similarity <i>Frontiers in Digital Health</i> , 2021 , 3, 781227	2.3
8	Evaluating semantic similarity methods for comparison of text-derived phenotype profiles <i>BMC Medical Informatics and Decision Making</i> , 2022 , 22, 33	3.6
7	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> ,8, 1677	3.6
6	Argumentation to Represent and Reason over Biological Systems. <i>Lecture Notes in Computer Science</i> , 2012 , 124-138	0.9
5	Experiences with Aber-OWL, an Ontology Repository with OWL EL Reasoning. <i>Lecture Notes in Computer Science</i> , 2016 , 81-86	0.9
4	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier 2020 , 16, e1008453	
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