

Robert Hoehndorf

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1508983/robert-hoehndorf-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

152
papers

2,950
citations

30
h-index

49
g-index

176
ext. papers

3,768
ext. citations

5.2
avg, IF

5.82
L-index

#	Paper	IF	Citations
152	Evaluating semantic similarity methods for comparison of text-derived phenotype profiles.. <i>BMC Medical Informatics and Decision Making</i> , 2022 , 22, 33	3.6	
151	Combining biomedical knowledge graphs and text to improve predictions for drug-target interactions and drug-indications.. <i>PeerJ</i> , 2022 , 10, e13061	3.1	0
150	Effects of Negation and Uncertainty Stratification on Text-Derived Patient Profile Similarity.. <i>Frontiers in Digital Health</i> , 2021 , 3, 781227	2.3	
149	Semantic similarity and machine learning with ontologies. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	20
148	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
147	DeepViral: prediction of novel virus-host interactions from protein sequences and infectious disease phenotypes. <i>Bioinformatics</i> , 2021 ,	7.2	11
146	Improved characterisation of clinical text through ontology-based vocabulary expansion. <i>Journal of Biomedical Semantics</i> , 2021 , 12, 7	2.2	4
145	DeepGOWeb: fast and accurate protein function prediction on the (Semantic) Web. <i>Nucleic Acids Research</i> , 2021 , 49, W140-W146	20.1	0
144	Towards similarity-based differential diagnostics for common diseases. <i>Computers in Biology and Medicine</i> , 2021 , 133, 104360	7	4
143	DTI-Voodoo: machine learning over interaction networks and ontology-based background knowledge predicts drug-target interactions. <i>Bioinformatics</i> , 2021 ,	7.2	1
142	Predicting candidate genes from phenotypes, functions and anatomical site of expression. <i>Bioinformatics</i> , 2021 , 37, 853-860	7.2	8
141	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
140	Multi-faceted semantic clustering with text-derived phenotypes. <i>Computers in Biology and Medicine</i> , 2021 , 138, 104904	7	1
139	DDIEM: drug database for inborn errors of metabolism. <i>Orphanet Journal of Rare Diseases</i> , 2020 , 15, 1464.2		4
138	Combining lexical and context features for automatic ontology extension. <i>Journal of Biomedical Semantics</i> , 2020 , 11, 1	2.2	5
137	DeepGOPlus: improved protein function prediction from sequence. <i>Bioinformatics</i> , 2020 , 36, 422-429	7.2	70
136	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020 , 9, 136	3.6	2

135	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier. <i>PLoS Computational Biology</i> , 2020 , 16, e1008453	5	7
134	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
133	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data. <i>Bioinformatics</i> , 2020 , 36, 2229-2236	7.2	5
132	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
131	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
130	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier 2020 , 16, e1008453		
129	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier 2020 , 16, e1008453		
128	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier 2020 , 16, e1008453		
127	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier 2020 , 16, e1008453		
126	Ontology based mining of pathogen-disease associations from literature. <i>Journal of Biomedical Semantics</i> , 2019 , 10, 15	2.2	2
125	PathoPhenoDB, linking human pathogens to their phenotypes in support of infectious disease research. <i>Scientific Data</i> , 2019 , 6, 79	8.2	7
124	Semi-Supervised Entity Alignment via Knowledge Graph Embedding with Awareness of Degree Difference 2019 ,		25
123	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
122	Quantitative evaluation of ontology design patterns for combining pathology and anatomy ontologies. <i>Scientific Reports</i> , 2019 , 9, 4025	4.9	5
121	DeepPVP: phenotype-based prioritization of causative variants using deep learning. <i>BMC Bioinformatics</i> , 2019 , 20, 65	3.6	24
120	Hyaline Arteriosclerosis in 30 Strains of Aged Inbred Mice. <i>Veterinary Pathology</i> , 2019 , 56, 799-806	2.8	2
119	EL Embeddings: Geometric Construction of Models for the Description Logic EL++ 2019 ,		10
118	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

117	Ontology-based prediction of cancer driver genes. <i>Scientific Reports</i> , 2019 , 9, 17405	4.9	9
116	Comparative genomics study reveals Red Sea <i>Bacillus</i> with characteristics associated with potential microbial cell factories (MCFs). <i>Scientific Reports</i> , 2019 , 9, 19254	4.9	4
115	OPA2Vec: combining formal and informal content of biomedical ontologies to improve similarity-based prediction. <i>Bioinformatics</i> , 2019 , 35, 2133-2140	7.2	48
114	Nail abnormalities identified in an ageing study of 30 inbred mouse strains. <i>Experimental Dermatology</i> , 2019 , 28, 383-390	4	4
113	Taxon and trait recognition from digitized herbarium specimens using deep convolutional neural networks. <i>Botany Letters</i> , 2018 , 165, 377-383	1.1	28
112	The anatomy of phenotype ontologies: principles, properties and applications. <i>Briefings in Bioinformatics</i> , 2018 , 19, 1008-1021	13.4	41
111	DeepGO: predicting protein functions from sequence and interactions using a deep ontology-aware classifier. <i>Bioinformatics</i> , 2018 , 34, 660-668	7.2	177
110	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018 , 19, 77-88	13.4	11
109	Onto2Vec: joint vector-based representation of biological entities and their ontology-based annotations. <i>Bioinformatics</i> , 2018 , 34, i52-i60	7.2	43
108	Inferring ontology graph structures using OWL reasoning. <i>BMC Bioinformatics</i> , 2018 , 19, 7	3.6	15
107	In silico exploration of Red Sea <i>Bacillus</i> genomes for natural product biosynthetic gene clusters. <i>BMC Genomics</i> , 2018 , 19, 382	4.5	11
106	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
105	OligoPVP: Phenotype-driven analysis of individual genomic information to prioritize oligogenic disease variants. <i>Scientific Reports</i> , 2018 , 8, 14681	4.9	4
104	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
103	Semantic Disease Gene Embeddings (SmuDGE): phenotype-based disease gene prioritization without phenotypes. <i>Bioinformatics</i> , 2018 , 34, i901-i907	7.2	30
102	Ontology-based validation and identification of regulatory phenotypes. <i>Bioinformatics</i> , 2018 , 34, i857-i865	7.2	4
101	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017 , 18, 33	4.5	10
100	Neuro-symbolic representation learning on biological knowledge graphs. <i>Bioinformatics</i> , 2017 , 33, 2723-2730	7.2	63

99	Semantic prioritization of novel causative genomic variants. <i>PLoS Computational Biology</i> , 2017 , 13, e1005500	2.1	21
98	Integrating phenotype ontologies with PhenomeNET. <i>Journal of Biomedical Semantics</i> , 2017 , 8, 58	2.2	25
97	Usage of cell nomenclature in biomedical literature. <i>BMC Bioinformatics</i> , 2017 , 18, 561	3.6	0
96	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. <i>Scientific Reports</i> , 2017 , 7, 5968	4.9	7
95	Evaluating the effect of annotation size on measures of semantic similarity. <i>Journal of Biomedical Semantics</i> , 2017 , 8, 7	2.2	19
94	Data Science and symbolic AI: Synergies, challenges and opportunities. <i>Data Science</i> , 2017 , 1, 27-38	2.2	13
93	The Informatics of Developmental Phenotypes 2016 , 307-318		3
92	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
91	Using AberOWL for fast and scalable reasoning over BioPortal ontologies. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 49	2.2	10
90	DESM: portal for microbial knowledge exploration systems. <i>Nucleic Acids Research</i> , 2016 , 44, D624-33	20.1	10
89	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , 2016 , 11, e0158896	3.7	11
88	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
87	DermO; an ontology for the description of dermatologic disease. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 38	2.2	5
86	Datamining with Ontologies. <i>Methods in Molecular Biology</i> , 2016 , 1415, 385-97	1.4	1
85	Experiences with Aber-OWL, an Ontology Repository with OWL EL Reasoning. <i>Lecture Notes in Computer Science</i> , 2016 , 81-86	0.9	
84	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
83	Best behaviour? Ontologies and the formal description of animal behaviour. <i>Mammalian Genome</i> , 2015 , 26, 540-7	3.2	4
82	Analysis of the human diseasome using phenotype similarity between common, genetic, and infectious diseases. <i>Scientific Reports</i> , 2015 , 5, 10888	4.9	62

81	Aber-OWL: a framework for ontology-based data access in biology. <i>BMC Bioinformatics</i> , 2015 , 16, 26	3.6	53
80	An ontology approach to comparative phenomics in plants. <i>Plant Methods</i> , 2015 , 11, 10	5.8	33
79	Similarity-based search of model organism, disease and drug effect phenotypes. <i>Journal of Biomedical Semantics</i> , 2015 , 6, 6	2.2	7
78	The role of ontologies in biological and biomedical research: a functional perspective. <i>Briefings in Bioinformatics</i> , 2015 , 16, 1069-80	13.4	143
77	Ranking adverse drug reactions with crowdsourcing. <i>Journal of Medical Internet Research</i> , 2015 , 17, e80	7.6	27
76	GFVO: the Genomic Feature and Variation Ontology. <i>PeerJ</i> , 2015 , 3, e933	3.1	3
75	Analyzing gene expression data in mice with the Neuro Behavior Ontology. <i>Mammalian Genome</i> , 2014 , 25, 32-40	3.2	17
74	Mouse model phenotypes provide information about human drug targets. <i>Bioinformatics</i> , 2014 , 30, 719-25	7.5	35
73	The Semanticscience Integrated Ontology (SIO) for biomedical research and knowledge discovery. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 14	2.2	101
72	Thematic series on biomedical ontologies in JBMS: challenges and new directions. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 15	2.2	7
71	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
70	Enriched biodiversity data as a resource and service. <i>Biodiversity Data Journal</i> , 2014 , e1125	1.8	13
69	Representing physiological processes and their participants with PhysioMaps. <i>Journal of Biomedical Semantics</i> , 2013 , 4 Suppl 1, S2	2.2	4
68	Evaluation of research in biomedical ontologies. <i>Briefings in Bioinformatics</i> , 2013 , 14, 696-712	13.4	55
67	Evaluating gold standard corpora against gene/protein tagging solutions and lexical resources. <i>Journal of Biomedical Semantics</i> , 2013 , 4, 28	2.2	10
66	An integrative, translational approach to understanding rare and orphan genetically based diseases. <i>Interface Focus</i> , 2013 , 3, 20120055	3.9	14
65	Systematic analysis of experimental phenotype data reveals gene functions. <i>PLoS ONE</i> , 2013 , 8, e60847	3.7	16
64	Evaluation and cross-comparison of lexical entities of biological interest (LexEBI). <i>PLoS ONE</i> , 2013 , 8, e75185	3.7	7

63	Semantic Systems Biology: Formal Knowledge Representation in Systems Biology for Model Construction, Retrieval, Validation and Discovery 2013 , 355-373		4
62	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
61	Text-mining solutions for biomedical research: enabling integrative biology. <i>Nature Reviews Genetics</i> , 2012 , 13, 829-39	30.1	160
60	Computational tools for comparative phenomics: the role and promise of ontologies. <i>Mammalian Genome</i> , 2012 , 23, 669-79	3.2	17
59	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
58	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
57	Ontology-based cross-species integration and analysis of <i>Saccharomyces cerevisiae</i> phenotypes. <i>Journal of Biomedical Semantics</i> , 2012 , 3 Suppl 2, S6	2.2	5
56	Towards improving phenotype representation in OWL. <i>Journal of Biomedical Semantics</i> , 2012 , 3 Suppl 2, S5	2.2	4
55	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
54	Mouse genetic and phenotypic resources for human genetics. <i>Human Mutation</i> , 2012 , 33, 826-36	4.7	56
53	An infrastructure for ontology-based information systems in biomedicine: RICORDO case study. <i>Bioinformatics</i> , 2012 , 28, 448-50	7.2	9
52	Semantic integration of physiology phenotypes with an application to the Cellular Phenotype Ontology. <i>Bioinformatics</i> , 2012 , 28, 1783-9	7.2	22
51	Identifying aberrant pathways through integrated analysis of knowledge in pharmacogenomics. <i>Bioinformatics</i> , 2012 , 28, 2169-75	7.2	39
50	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
49	Argumentation to Represent and Reason over Biological Systems. <i>Lecture Notes in Computer Science</i> , 2012 , 124-138	0.9	
48	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
47	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
46	Interoperability between biomedical ontologies through relation expansion, upper-level ontologies and automatic reasoning. <i>PLoS ONE</i> , 2011 , 6, e22006	3.7	32

45	OBML - Ontologies in Biomedicine and Life Sciences. <i>Journal of Biomedical Semantics</i> , 2011 , 2 Suppl 4, I1	2.2	1
44	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
43	Integrating systems biology models and biomedical ontologies. <i>BMC Systems Biology</i> , 2011 , 5, 124	3.5	37
42	LINKING PHARMGKB TO PHENOTYPE STUDIES AND ANIMAL MODELS OF DISEASE FOR DRUG REPURPOSING 2011 ,		1
41	PIDO: the primary immunodeficiency disease ontology. <i>Bioinformatics</i> , 2011 , 27, 3193-9	7.2	4
40	PhenomeNET: a whole-phenome approach to disease gene discovery. <i>Nucleic Acids Research</i> , 2011 , 39, e119	20.1	166
39	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
38	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Applied Ontology</i> , 2011 , 6, 53-89	1.4	20
37	A common layer of interoperability for biomedical ontologies based on OWL EL. <i>Bioinformatics</i> , 2011 , 27, 1001-8	7.2	28
36	Statistical tests for associations between two directed acyclic graphs. <i>PLoS ONE</i> , 2010 , 5, e10996	3.7	3
35	Interoperability between phenotype and anatomy ontologies. <i>Bioinformatics</i> , 2010 , 26, 3112-8	7.2	38
34	Relations as patterns: bridging the gap between OBO and OWL. <i>BMC Bioinformatics</i> , 2010 , 11, 441	3.6	42
33	Applying the functional abnormality ontology pattern to anatomical functions. <i>Journal of Biomedical Semantics</i> , 2010 , 1, 4	2.2	12
32	Ontologies in Biology 2010 , 347-371		1
31	The ontology of biological sequences. <i>BMC Bioinformatics</i> , 2009 , 10, 377	3.6	10
30	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
29	GFO-Bio: A biological core ontology. <i>Applied Ontology</i> , 2008 , 3, 219-227	1.4	12
28	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

27	A top-level ontology of functions and its application in the Open Biomedical Ontologies. <i>Bioinformatics</i> , 2006 , 22, e66-73	7.2	32
26	A Proposal for a Gene Functions Wiki. <i>Lecture Notes in Computer Science</i> , 2006 , 669-678	0.9	4
25	A fast, accurate, and generalisable heuristic-based negation detection algorithm for clinical text		3
24	A Machine Learning Based Approach for Similarity Search on Biodiversity Knowledge Graphs. <i>Biodiversity Information Science and Standards</i> , 3,		1
23	PathoPhenoDB: linking human pathogens to their disease phenotypes in support of infectious disease research		2
22	Phenotypic, functional and taxonomic features predict host-pathogen interactions		1
21	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 8, 1677	3.6	
20	Self-normalizing learning on biomedical ontologies using a deep Siamese neural network		1
19	Towards semantic interoperability: finding and repairing hidden contradictions in biomedical ontologies		1
18	Notions of similarity for computational biology models		1
17	Predicting candidate genes from phenotypes, functions, and anatomical site of expression		2
16	D4: Deep Drug-drug interaction Discovery and Demystification		1
15	DeepViral: infectious disease phenotypes improve prediction of novel virus-host interactions		1
14	Machine learning with biomedical ontologies		8
13	Modeling quantitative traits for COVID-19 case reports		2
12	Improved characterisation of clinical text through ontology-based vocabulary expansion		4
11	Komenti: A semantic text mining framework		4
10	Exploring Binary Relations for Ontology Extension and Improved Adaptation to Clinical Text		1

9	DeepPVP: phenotype-based prioritization of causative variants using deep learning	2
8	Quantitative evaluation of ontology design patterns for combining pathology and anatomy ontologies	2
7	Drug repurposing through joint learning on knowledge graphs and literature	6
6	Ontology based mining of pathogen-disease associations from literature	3
5	Vec2SPARQL: integrating SPARQL queries and knowledge graph embeddings	1
4	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data	5
3	Ontology-based prediction of cancer driver genes	1
2	DeepGOPlus: Improved protein function prediction from sequence	6
1	Towards Similarity-based Differential Diagnostics For Common Diseases	2