

# CITATION REPORT

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**HPOSim: an R package for phenotypic similarity measure and enrichment analysis based on the human phenotype ontology**

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#	Paper	IF	Citations
46	Fusing literature and full network data improves disease similarity computation. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 326	3.6	9
45	Datamining with Ontologies. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1415, 385-97	1.4	1
44	Future Directions. <b>2016</b> , 281-294		0
43	Exploiting HPO to Predict a Ranked List of Phenotype Categories for LiverTox Case Reports. <i>Lecture Notes in Computer Science</i> , <b>2017</b> , 3-9	0.9	
42	A comprehensive global genotype-phenotype database for rare diseases. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2017</b> , 5, 66-75	2.3	45
41	The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. <i>Nature Genetics</i> , <b>2017</b> , 49, 36-45	36.3	172
40	Investigations on factors influencing HPO-based semantic similarity calculation. <i>Journal of Biomedical Semantics</i> , <b>2017</b> , 8, 34	2.2	2
39	Measuring phenotype-phenotype similarity through the interactome. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 114	3.6	26
38	Exploring Disease Similarity by Integrating Multiple Data Sources. <b>2018</b> ,		2
37	HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences. <i>PeerJ</i> , <b>2018</b> , 6, e5298	3.1	12
36	An online tool for measuring and visualizing phenotype similarities using HPO. <i>BMC Genomics</i> , <b>2018</b> , 19, 571	4.5	3
35	PubCaseFinder: A Case-Report-Based, Phenotype-Driven Differential-Diagnosis System for Rare Diseases. <i>American Journal of Human Genetics</i> , <b>2018</b> , 103, 389-399	11	17
34	Phenotype-driven gene prioritization for rare diseases using graph convolution on heterogeneous networks. <i>BMC Medical Genomics</i> , <b>2018</b> , 11, 57	3.7	14
33	A new method to measure the semantic similarity from query phenotypic abnormalities to diseases based on the human phenotype ontology. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 162	3.6	5
32	Disease classification: from phenotypic similarity to integrative genomics and beyond. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1769-1780	13.4	11
31	HPO2Vec+: Leveraging heterogeneous knowledge resources to enrich node embeddings for the Human Phenotype Ontology. <i>Journal of Biomedical Informatics</i> , <b>2019</b> , 96, 103246	10.2	13
30	Computational Methods for Identifying Similar Diseases. <i>Molecular Therapy - Nucleic Acids</i> , <b>2019</b> , 18, 590-604	10.7	69

29	Drug repositioning of herbal compounds via a machine-learning approach. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 247	3.6	19
28	A Recurrent Missense Variant in AP2M1 Impairs Clathrin-Mediated Endocytosis and Causes Developmental and Epileptic Encephalopathy. <i>American Journal of Human Genetics</i> , <b>2019</b> , 104, 1060-1072 <sup>11</sup>		39
27	Predicting disease-related phenotypes using an integrated phenotype similarity measurement based on HPO. <i>BMC Systems Biology</i> , <b>2019</b> , 13, 34	3.5	4
26	Curation and bioinformatic analysis of strabismus genes supports functional heterogeneity and proposes candidate genes with connections to RASopathies. <i>Gene</i> , <b>2019</b> , 697, 213-226	3.8	3
25	MultiSourcDSim: an integrated approach for exploring disease similarity. <i>BMC Medical Informatics and Decision Making</i> , <b>2019</b> , 19, 269	3.6	4
24	Phenotype-genotype comorbidity analysis of patients with rare disorders provides insight into their pathological and molecular bases. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1009054	6	5
23	Evaluation of standard and semantically-augmented distance metrics for neurology patients. <i>BMC Medical Informatics and Decision Making</i> , <b>2020</b> , 20, 203	3.6	3
22	Network based approach for discovering novel gene-phenotypic association and disease co morbidities using ontological data. <i>Procedia Computer Science</i> , <b>2020</b> , 167, 819-829	1.6	1
21	UFO: A tool for unifying biomedical ontology-based semantic similarity calculation, enrichment analysis and visualization. <i>PLoS ONE</i> , <b>2020</b> , 15, e0235670	3.7	6
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16	autoHGPEC: Automated prediction of novel disease-gene and disease-disease associations and evidence collection based on a random walk on heterogeneous network. <i>F1000Research</i> , 7, 658	3.6	1
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10	Biomedical data, computational methods and tools for evaluating disease-disease associations.. <i>Briefings in Bioinformatics</i> , <b>2022</b> ,	13.4	2
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8	Missense variants in ANKRD11 cause KBG syndrome by impairment of stability or transcriptional activity of the encoded protein.		1
7	Gene-SCOUT: identifying genes with similar continuous trait fingerprints from phenome-wide association analyses.. <i>Nucleic Acids Research</i> , <b>2022</b> ,	20.1	1
6	Clinical diagnosis of metabolic disorders using untargeted metabolomic profiling and disease-specific networks learned from profiling data.. <i>Scientific Reports</i> , <b>2022</b> , 12, 6556	4.9	1
5	Missense variants in ANKRD11 cause KBG syndrome by impairment of stability or transcriptional activity of the encoded protein. <i>Genetics in Medicine</i> , <b>2022</b> ,	8.1	0
4	Klarigi: Characteristic explanations for semantic biomedical data. <b>2022</b> , 106425		0
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