Marco Roos

List of Publications by Year in Descending Order

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Version: 2024-04-25

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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.

63 papers	5,727 citations	20 h-index	75 g-index
76 ext. papers	8,277 ext. citations	5 avg, IF	4.48 L-index

#	Paper	IF	Citations
63	Huntington Disease Gene Expression Signatures in Blood Compared to Brain of YAC128 Mice as Candidates for Monitoring of Pathology.. *Molecular Neurobiology*, **2022**, 1	6.2	
62	Semantic modelling of common data elements for rare disease registries, and a prototype workflow for their deployment over registry data.. *Journal of Biomedical Semantics*, **2022**, 13, 9	2.2	0
61	Applying the FAIR principles to data in a hospital: challenges and opportunities in a pandemic.. *Journal of Biomedical Semantics*, **2022**, 13, 12	2.2	1
60	Enabling FAIR Discovery of Rare Disease Digital Resources. *Studies in Health Technology and Informatics*, **2021**, 279, 144-146	0.5	
59	ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. *EMBO Journal*, **2021**, 40, e107409	13	11
58	How Patient Organizations Can Drive FAIR Data Efforts to Facilitate Research and Health Care: A Report of the Virtual Second International Meeting on Duchenne Data Sharing, March 3, 2021. *Journal of Neuromuscular Diseases*, **2021**, 8, 1097-1108	5	0
57	The de novo FAIRification process of a registry for vascular anomalies. *Orphanet Journal of Rare Diseases*, **2021**, 16, 376	4.2	2
56	De-novo FAIRification via an Electronic Data Capture system by automated transformation of filled electronic Case Report Forms into machine-readable data. *Journal of Biomedical Informatics*, **2021**, 122, 103897	10.2	4
55	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. *Scientific Data*, **2021**, 8, 10	8.2	4
54	FAIR Principles: Interpretations and Implementation Considerations. *Data Intelligence*, **2020**, 2, 10-29	3	66
53	A Generic Workflow for the Data FAIRification Process. *Data Intelligence*, **2020**, 2, 56-65	3	30
52	Making FAIR Easy with FAIR Tools: From Creolization to Convergence. *Data Intelligence*, **2020**, 2, 87-95	3	16
51	The □□f FAIR □As Open as Possible, as Closed as Necessary. *Data Intelligence*, **2020**, 2, 47-55	3	18
50	Applying the FAIR Data Principles to the Registry of Vascular Anomalies (VASCA). *Studies in Health Technology and Informatics*, **2020**, 271, 115-116	0.5	3
49	The case for open science: rare diseases. *JAMIA Open*, **2020**, 3, 472-486	2.9	17
48	Drug prioritization using the semantic properties of a knowledge graph. *Scientific Reports*, **2019**, 9, 6281	4.9	16
47	Meeting on data sharing for Duchenne 21-22 March 2019 Amsterdam, the Netherlands. *Neuromuscular Disorders*, **2019**, 29, 800-810	2.9	3

46	The RD-Connect Registry & Biobank Finder: a tool for sharing aggregated data and metadata among rare disease researchers. *European Journal of Human Genetics*, **2018**, 26, 631-643	5.3	27
45	MECP2 variation in Rett syndrome-An overview of current coverage of genetic and phenotype data within existing databases. *Human Mutation*, **2018**, 39, 914-924	4.7	12
44	Recommendations for Improving the Quality of Rare Disease Registries. *International Journal of Environmental Research and Public Health*, **2018**, 15,	4.6	56
43	Meeting Patients' Right to the Correct Diagnosis: Ongoing International Initiatives on Undiagnosed Rare Diseases and Ethical and Social Issues. *International Journal of Environmental Research and Public Health*, **2018**, 15,	4.6	22
42	Meta-analysis of polycystic kidney disease expression profiles defines strong involvement of injury repair processes. *American Journal of Physiology - Renal Physiology*, **2017**, 312, F806-F817	4.3	19
41	Linked Registries: Connecting Rare Diseases Patient Registries through a Semantic Web Layer. *BioMed Research International*, **2017**, 2017, 8327980	3	13
40	Preparing Data at the Source to Foster Interoperability across Rare Disease Resources. *Advances in Experimental Medicine and Biology*, **2017**, 1031, 165-179	3.6	8
39	Consent Codes: Upholding Standard Data Use Conditions. *PLoS Genetics*, **2016**, 12, e1005772	6	51
38	The Implicitome: A Resource for Rationalizing Gene-Disease Associations. *PLoS ONE*, **2016**, 11, e0149621	3.7	18
37	Common disease signatures from gene expression analysis in Huntington's disease human blood and brain. *Orphanet Journal of Rare Diseases*, **2016**, 11, 97	4.2	24
36	The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data*, **2016**, 3, 160018	8.2	4154
35	Nanopublications for exposing experimental data in the life-sciences: a Huntington's Disease case study. *Journal of Biomedical Semantics*, **2015**, 6, 5	2.2	10
34	Multidisciplinary Collaboration to Facilitate Hypotheses Generation in Huntington's Disease **2015**,		2
33	From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. *PLoS ONE*, **2015**, 10, e0127612	3.7	18
32	Preserving sequence annotations across reference sequences. *Journal of Biomedical Semantics*, **2014**, 5, S6	2.2	3
31	Structuring research methods and data with the research object model: genomics workflows as a case study. *Journal of Biomedical Semantics*, **2014**, 5, 41	2.2	21
30	A Nanopublishing Architecture for Biomedical Data. *Advances in Intelligent Systems and Computing*, **2014**, 277-284	0.4	4
29	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. *BMC Genomics*, **2013**, 14, 865	4.5	13

28	Workflow forever **2012**,		3
27	Microattribution and nanopublication as means to incentivize the placement of human genome variation data into the public domain. *Human Mutation*, **2012**, 33, 1503-12	4.7	54
26	Why workflows break Understanding and combating decay in Taverna workflows **2012**,		34
25	In silico discovery and experimental validation of new protein-protein interactions. *Proteomics*, **2011**, 11, 843-53	4.8	18
24	myExperiment: a repository and social network for the sharing of bioinformatics workflows. *Nucleic Acids Research*, **2010**, 38, W677-82	20.1	201
23	BioCatalogue: a universal catalogue of web services for the life sciences. *Nucleic Acids Research*, **2010**, 38, W689-94	20.1	160
22	The Evolution of myExperiment **2010**,		5
21	A Linked Data Approach to Sharing Workflows and Workflow Results. *Lecture Notes in Computer Science*, **2010**, 340-354	0.9	2
20	Semantic Disclosure in an e-Science Environment. *Annals of Information Systems*, **2010**, 29-65		
19	The construction of genome-based transcriptional units. *OMICS A Journal of Integrative Biology*, **2009**, 13, 105-14	3.8	
18	Structuring and extracting knowledge for the support of hypothesis generation in molecular biology. *BMC Bioinformatics*, **2009**, 10 Suppl 10, S9	3.6	11
17	SigWin-detector: a Grid-enabled workflow for discovering enriched windows of genomic features related to DNA sequences. *BMC Research Notes*, **2008**, 1, 63	2.3	4
16	VLAM-G: Interactive Data Driven Workflow Engine for Grid-Enabled Resources. *Scientific Programming*, **2007**, 15, 173-188	1.4	14
15	Taking the example of computer systems engineering for the analysis of biological cell systems. *BioSystems*, **2007**, 90, 623-35	1.9	2
14	A semantic web approach applied to integrative bioinformatics experimentation: a biological use case with genomics data. *Bioinformatics*, **2007**, 23, 3080-7	7.2	32
13	The promise of a virtual lab in drug discovery. *Drug Discovery Today*, **2006**, 11, 228-36	8.8	36
12	Interactive Workflows in a Virtual Laboratory for e-Bioscience: The SigWin-Detector Tool for Gene Expression Analysis **2006**,		2
11	Using Semantic Web Tools to Integrate Experimental Measurement Data on Our Own Terms. *Lecture Notes in Computer Science*, **2006**, 679-688	0.9	4

List of Publications

10	The human transcriptome map reveals extremes in gene density, intron length, GC content, and repeat pattern for domains of highly and weakly expressed genes. *Genome Research*, **2003**, 13, 1998-2004	9.7	262
9	Models on stickiness of replicated Escherichia coli oriC. *Microbiology (United Kingdom)*, **2002**, 148, 3327-3338	2.9	6
8	The replicated ftsQAZ and minB chromosomal regions of Escherichia coli segregate on average in line with nucleoid movement. *Molecular Microbiology*, **2001**, 39, 633-40	4.1	27
7	Experiments on movement of DNA regions in Escherichia coli evaluated by computer simulation. *Biochimie*, **2001**, 83, 67-74	4.6	5
6	Cellular localization of oriC during the cell cycle of Escherichia coli as analyzed by fluorescent in situ hybridization. *Biochimie*, **1999**, 81, 797-802	4.6	33
5	Explain your data by Concept Profile Analysis Web Services. *F1000Research*,3, 173	3.6	4
4	The de novo FAIRification process of a registry for vascular anomalies		4
3	A putative role for genome-wide epigenetic regulatory mechanisms in Huntington's disease: A computational assessment. *F1000Research*,6, 1888	3.6	
2	De-novo FAIRification via an Electronic Data Capture system by automated transformation of filled electronic Case Report Forms into machine-readable data		4
1	Semantic modelling of Common Data Elements for Rare Disease registries, and a prototype workflow for their deployment over registry data		1