Marco Roos

List of Publications by Year
in descending order

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64 papers	10,922 citations	279487 23 h-index	149479 56 g-index
76 all docs	76 docs citations	76 times ranked	22605 citing authors

#	Article	IF	Citations
1	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	2.4	8,670
2	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.	2.4	306
3	myExperiment: a repository and social network for the sharing of bioinformatics workflows. Nucleic Acids Research, 2010, 38, W677-W682.	6.5	246
4	BioCatalogue: a universal catalogue of web services for the life sciences. Nucleic Acids Research, 2010, 38, W689-W694.	6.5	185
5	FAIR Principles: Interpretations and Implementation Considerations. Data Intelligence, 2020, 2, 10-29.	0.8	149
6	The value of data. Nature Genetics, 2011, 43, 281-283.	9.4	126
7	Recommendations for Improving the Quality of Rare Disease Registries. International Journal of Environmental Research and Public Health, 2018, 15, 1644.	1.2	116
8	Consent Codes: Upholding Standard Data Use Conditions. PLoS Genetics, 2016, 12, e1005772.	1.5	65
9	Microattribution and nanopublication as means to incentivize the placement of human genome variation data into the public domain. Human Mutation, 2012, 33, 1503-1512.	1.1	59
10	A Generic Workflow for the Data FAIRification Process. Data Intelligence, 2020, 2, 56-65.	0.8	59
11	Why workflows break — Understanding and combating decay in Taverna workflows. , 2012, , .		48
12	The promise of a virtual lab in drug discovery. Drug Discovery Today, 2006, 11, 228-236.	3.2	45
13	A semantic web approach applied to integrative bioinformatics experimentation: a biological use case with genomics data. Bioinformatics, 2007, 23, 3080-3087.	1.8	41
14	Meeting Patientsâ€™ 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, 2072.	1.2	40
15	Cellular localization of oriC during the cell cycle of Escherichia coli as analyzed by fluorescent in situ hybridization. Biochimie, 1999, 81, 797-802.	1.3	33
16	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.	1.4	33
17	Drug prioritization using the semantic properties of a knowledge graph. Scientific Reports, 2019, 9, 6281.	1.6	33
18	The case for open science: rare diseases. JAMIA Open, 2020, 3, 472-486.	1.0	33

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19	Common disease signatures from gene expression analysis in Huntingtonâ€™s disease human blood and brain. Orphanet Journal of Rare Diseases, 2016, 11, 97.	1.2	32
20	The replicated ftsQAZ and minB chromosomal regions of Escherichia coli segregate on average in line with nucleoid movement. Molecular Microbiology, 2001, 39, 633-640.	1.2	29
21	The â€œAâ€•of FAIR â€“ As Open as Possible, as Closed as Necessary. Data Intelligence, 2020, 2, 47-55.	0.8	29
22	Linked Registries: Connecting Rare Diseases Patient Registries through a Semantic Web Layer. BioMed Research International, 2017, 2017, 1-13.	0.9	28
23	From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. PLoS ONE, 2015, 10, e0127612.	1.1	27
24	Structuring research methods and data with the research object model: genomics workflows as a case study. Journal of Biomedical Semantics, 2014, 5, 41.	0.9	26
25	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.	1.3	26
26	The Implicitome: A Resource for Rationalizing Gene-Disease Associations. PLoS ONE, 2016, 11, e0149621.	1.1	22
27	Making FAIR Easy with FAIR Tools: From Creolization to Convergence. Data Intelligence, 2020, 2, 87-95.	0.8	21
28	Applying the FAIR principles to data in a hospital: challenges and opportunities in a pandemic. Journal of Biomedical Semantics, 2022, 13, 12.	0.9	21
29	In silico discovery and experimental validation of new proteinâ€“protein interactions. Proteomics, 2011, 11, 843-853.	1.3	20
30	ELIXIRâ€EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	3.5	18
31	VLAM-G: Interactive Data Driven Workflow Engine for Grid-Enabled Resources. Scientific Programming, 2007, 15, 173-188.	0.5	16
32	MECP2 variation in Rett syndrome-An overview of current coverage of genetic and phenotype data within existing databases. Human Mutation, 2018, 39, 914-924.	1.1	15
33	Structuring and extracting knowledge for the support of hypothesis generation in molecular biology. BMC Bioinformatics, 2009, 10, S9.	1.2	14
34	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. BMC Genomics, 2013, 14, 865.	1.2	14
35	Nanopublications for exposing experimental data in the life-sciences: a Huntington's Disease case study. Journal of Biomedical Semantics, 2015, 6, 5.	0.9	12
36	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.	2.5	12

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37	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. Scientific Data, 2021, 8, 10.	2.4	12
38	The Evolution of myExperiment. , 2010, , .		11
39	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.	0.9	11
40	Preparing Data at the Source to Foster Interoperability across Rare Disease Resources. Advances in Experimental Medicine and Biology, 2017, 1031, 165-179.	0.8	9
41	Using Personal Genomic Data within Primary Care: A Bioinformatics Approach to Pharmacogenomics. Genes, 2020, 11, 1443.	1.0	8
42	The de novo FAIRification process of a registry for vascular anomalies. Orphanet Journal of Rare Diseases, 2021, 16, 376.	1.2	8
43	FAIR Digital Twins for Data-Intensive Research. Frontiers in Big Data, 2022, 5, .	1.8	8
44	Workflow forever. , 2011, , .		6
45	Using Semantic Web Tools to Integrate Experimental Measurement Data on Our Own Terms. Lecture Notes in Computer Science, 2006, , 679-688.	1.0	6
46	Models on stickiness of replicated Escherichia coli oriC. Microbiology (United Kingdom), 2002, 148, 3327-3328.	0.7	6
47	Experiments on movement of DNA regions in Escherichia colievaluated by computer simulation. Biochimie, 2001, 83, 67-74.	1.3	5
48	SigWin-detector: a Grid-enabled workflow for discovering enriched windows of genomic features related to DNA sequences. BMC Research Notes, 2008, 1, 63.	0.6	5
49	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.	1.1	5
50	A Nanopublishing Architecture for Biomedical Data. Advances in Intelligent Systems and Computing, 2014, , 277-284.	0.5	5
51	Explain your data by Concept Profile Analysis Web Services. F1000Research, 0, 3, 173.	0.8	5
52	Applying the FAIR Data Principles to the Registry of Vascular Anomalies (VASCA). Studies in Health Technology and Informatics, 2020, 271, 115-116.	0.2	4
53	Taking the example of computer systems engineering for the analysis of biological cell systems. BioSystems, 2007, 90, 623-635.	0.9	3
54	Preserving sequence annotations across reference sequences. Journal of Biomedical Semantics, 2014, 5, S6.	0.9	3

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55	Multidisciplinary Collaboration to Facilitate Hypotheses Generation in Huntington's Disease. , 2015, , .		3
56	Meeting on data sharing for Duchenne 21â€“22 March 2019 Amsterdam, the Netherlands. Neuromuscular Disorders, 2019, 29, 800-810.	0.3	3
57	Interactive Workflows in a Virtual Laboratory for e-Bioscience: The SigWin-Detector Tool for Gene Expression Analysis. , 2006, , .		2
58	A Linked Data Approach to Sharing Workflows and Workflow Results. Lecture Notes in Computer Science, 2010, , 340-354.	1.0	2
59	Speeding up research with the Semantic Web. Orphanet Journal of Rare Diseases, 2012, 7, A11.	1.2	1
60	Enabling FAIR Discovery of Rare Disease Digital Resources. Studies in Health Technology and Informatics, 2021, 279, 144-146.	0.2	1
61	Huntington Disease Gene Expression Signatures in Blood Compared to Brain of YAC128 Mice as Candidates for Monitoring of Pathology. Molecular Neurobiology, 2022, 59, 2532-2551.	1.9	1
62	The Construction of Genome-Based Transcriptional Units. OMICS A Journal of Integrative Biology, 2009, 13, 105-114.	1.0	0
63	A putative role for genome-wide epigenetic regulatory mechanisms in Huntingtonâ€™s disease: A computational assessment. F1000Research, 0, 6, 1888.	0.8	0
64	A07â€…A comparative study on blood and brain hd signatures: comparing mouse and human hd gene expression data. , 2018, , .		0