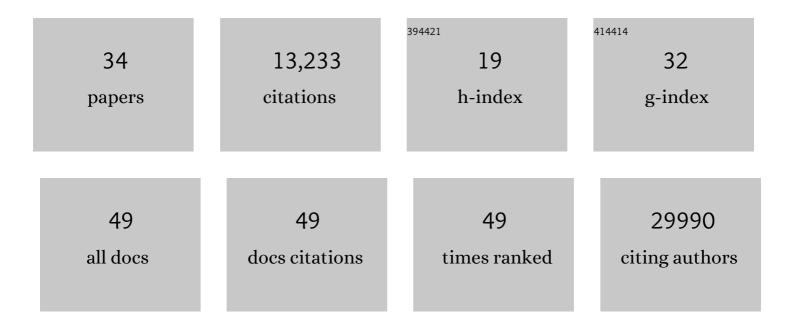
Erik Schultes

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	FAIR Digital Twins for Data-Intensive Research. Frontiers in Big Data, 2022, 5, .	2.9	8
2	An Academic Publishers' GO FAIR Implementation Network (APIN). Information Services and Use, 2021, 40, 333-341.	0.2	5
3	Design of a FAIR digital data health infrastructure in Africa for COVIDâ€19 reporting and research. Genetics & Genomics Next, 2021, 2, e10050.	1.5	27
4	FAIR Convergence Matrix: Optimizing the Reuse of Existing FAIR-Related Resources. Data Intelligence, 2020, 2, 158-170.	1.5	10
5	FAIR Principles: Interpretations and Implementation Considerations. Data Intelligence, 2020, 2, 10-29.	1.5	149
6	A Generic Workflow for the Data FAIRification Process. Data Intelligence, 2020, 2, 56-65.	1.5	59
7	The FAIR Principles: First Generation Implementation Choices and Challenges. Data Intelligence, 2020, 2, 1-9.	1.5	19
8	From FAIR Leading Practices to FAIR Implementation and Back: An Inclusive Approach to FAIR at Leiden University Libraries. Data Science Journal, 2020, 19, .	1.3	2
9	Reusable FAIR Implementation Profiles as Accelerators of FAIR Convergence. Lecture Notes in Computer Science, 2020, , 138-147.	1.3	15
10	Evaluating FAIR maturity through a scalable, automated, community-governed framework. Scientific Data, 2019, 6, 174.	5.3	82
11	FAIR Principles and Digital Objects: Accelerating Convergence on a Data Infrastructure. Communications in Computer and Information Science, 2019, , 3-16.	0.5	20
12	Community Detection in NK Landscapes - An Empirical Study of Complexity Transitions in Interactive Networks. Advances in Intelligent Systems and Computing, 2018, , 163-176.	0.6	0
13	A design framework and exemplar metrics for FAIRness. Scientific Data, 2018, 5, 180118.	5.3	145
14	Automated extraction of potential migraine biomarkers using a semantic graph. Journal of Biomedical Informatics, 2017, 71, 178-189.	4.3	24
15	The Implicitome: A Resource for Rationalizing Gene-Disease Associations. PLoS ONE, 2016, 11, e0149621.	2.5	22
16	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
17	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	21.4	313
18	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687

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#	Article	IF	CITATIONS
19	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
20	Preserving sequence annotations across reference sequences. Journal of Biomedical Semantics, 2014, 5, S6.	1.6	3
21	An autonomously selfâ€assembling dendritic DNA nanostructure for target DNA detection. Biotechnology Journal, 2013, 8, 221-227.	3.5	64
22	Generic Information Can Retrieve Known Biological Associations: Implications for Biomedical Knowledge Discovery. PLoS ONE, 2013, 8, e78665.	2.5	10
23	Theoretical and technological building blocks for an innovation accelerator. European Physical Journal: Special Topics, 2012, 214, 183-214.	2.6	12
24	Microattribution and nanopublication as means to incentivize the placement of human genome variation data into the public domain. Human Mutation, 2012, 33, 1503-1512.	2.5	59
25	Phage display screening without repetitious selection rounds. Analytical Biochemistry, 2012, 421, 622-631.	2.4	149
26	Protein Folding Absent Selection. Genes, 2011, 2, 608-626.	2.4	24
27	The value of data. Nature Genetics, 2011, 43, 281-283.	21.4	126
28	Compact and ordered collapse of randomly generated RNA sequences. Nature Structural and Molecular Biology, 2005, 12, 1130-1136.	8.2	72
29	One Sequence, Two Ribozymes: Implications for the Emergence of New Ribozyme Folds. Science, 2000, 289, 448-452.	12.6	340
30	Presidential Politics: Constrained by Complexity?. Science, 2000, 290, 933-933.	12.6	0
31	Estimating the Contributions of Selection and Self-Organization in RNA Secondary Structure. Journal of Molecular Evolution, 1999, 49, 76-83.	1.8	87
32	A parameterization of RNA sequence space. Complexity, 1999, 4, 61-71.	1.6	8
33	Interoperability and FAIRness through a novel combination of Web technologies. PeerJ Computer Science, 0, 3, e110.	4.5	58
34	A putative role for genome-wide epigenetic regulatory mechanisms in Huntington's disease: A computational assessment. F1000Research, 0, 6, 1888.	1.6	0