

# Fritz Lekschas

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1644642/publications.pdf>

Version: 2024-02-01

18  
papers

1,608  
citations

840776

11  
h-index

940533

16  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1772  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gosling: A Grammar-based Toolkit for Scalable and Interactive Genomics Data Visualization. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 140-150.	4.4	24
2	The Pattern is in the Details: An Evaluation of Interaction Techniques for Locating, Searching, and Contextualizing Details in Multivariate Matrix Visualizations. , 2022, , .		4
3	A Generic Framework and Library for Exploration of Small Multiples through Interactive Piling. IEEE Transactions on Visualization and Computer Graphics, 2021, 27, 358-368.	4.4	10
4	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	27.8	332
5	P<scp>eax</scp>: Interactive Visual Pattern Search in Sequential Data Using Unsupervised Deep Representation Learning. Computer Graphics Forum, 2020, 39, 167-179.	3.0	20
6	Pattern-Driven Navigation in 2D Multiscale Visualizations with Scalable Insets. IEEE Transactions on Visualization and Computer Graphics, 2019, 26, 1-1.	4.4	11
7	HiPiler: Visual Exploration of Large Genome Interaction Matrices with Interactive Small Multiples. IEEE Transactions on Visualization and Computer Graphics, 2018, 24, 522-531.	4.4	37
8	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem Cell Reports, 2018, 10, 1-6.	4.8	53
9	Visual Pattern-Driven Exploration of Big Data. , 2018, 2018, .		2
10	SATORI: a system for ontology-guided visual exploration of biomedical data repositories. Bioinformatics, 2018, 34, 1200-1207.	4.1	10
11	HiGlass: web-based visual exploration and analysis of genome interaction maps. Genome Biology, 2018, 19, 125.	8.8	950
12	Compresso: Efficient Compression of Segmentation Data for Connectomics. Lecture Notes in Computer Science, 2017, , 781-788.	1.3	9
13	hPSCregâ€”the human pluripotent stem cell registry. Nucleic Acids Research, 2016, 44, D757-D763.	14.5	46
14	MGMF: a novel tool for detection of tissue and cell specific marker genes from microarray gene expression data. BMC Genomics, 2015, 16, 645.	2.8	10
15	Semantic Body Browser: graphical exploration of an organism and spatially resolved expression data visualization. Bioinformatics, 2015, 31, 794-796.	4.1	4
16	CellFinder: a cell data repository. Nucleic Acids Research, 2014, 42, D950-D958.	14.5	26
17	CELDA â€” an ontology for the comprehensive representation of cells in complex systems. BMC Bioinformatics, 2013, 14, 228.	2.6	15
18	Preliminary evaluation of the CellFinder literature curation pipeline for gene expression in kidney cells and anatomical parts. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat020.	3.0	13