

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