Nils Gehlenborg

List of Publications by Year
in descending order

86 papers	36,701 citations	66343 42 h-index	53230 85 g-index
124 all docs	124 docs citations	124 times ranked	54946 citing authors

#	Article	IF	Citations
1	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
2	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
3	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
4	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
5	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
6	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
7	UpSetR: an R package for the visualization of intersecting sets and their properties. Bioinformatics, 2017, 33, 2938-2940.	4.1	2,255
8	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
9	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
10	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
11	UpSet: Visualization of Intersecting Sets. IEEE Transactions on Visualization and Computer Graphics, 2014, 20, 1983-1992.	4.4	1,549
12	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
13	HiGlass: web-based visual exploration and analysis of genome interaction maps. Genome Biology, 2018, 19, 125.	8.8	950
14	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
15	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
16	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
17	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
18	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605

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19	Visualization of omics data for systems biology. Nature Methods, 2010, 7, S56-S68.	19.0	548
20	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
21	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
22	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	27.8	363
23	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
24	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
25	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
26	Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. Cell, 2013, 153, 919-929.	28.9	308
27	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
28	A systems approach to prion disease. Molecular Systems Biology, 2009, 5, 252.	7.2	230
29	LineUp: Visual Analysis of Multi-Attribute Rankings. IEEE Transactions on Visualization and Computer Graphics, 2013, 19, 2277-2286.	4.4	221
30	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. Npj Digital Medicine, 2020, 3, 109.	10.9	128
31	An Integrated, Directed Mass Spectrometric Approach for In-depth Characterization of Complex Peptide Mixtures. Molecular and Cellular Proteomics, 2008, 7, 2138-2150.	3.8	127
32	Visualizing biological data—now and in the future. Nature Methods, 2010, 7, S2-S4.	19.0	115
33	Heat maps. Nature Methods, 2012, 9, 213-213.	19.0	84
34	Sets and intersections. Nature Methods, 2014, 11, 779-779.	19.0	80
35	StratomeX: Visual Analysis of Large-Scale Heterogeneous Genomics Data for Cancer Subtype Characterization. Computer Graphics Forum, 2012, 31, 1175-1184.	3.0	74
36	Bar charts and box plots. Nature Methods, 2014, 11, 117-117.	19.0	68

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37	Tasks, Techniques, and Tools for Genomic Data Visualization. Computer Graphics Forum, 2019, 38, 781-805.	3.0	61
38	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. Journal of Medical Internet Research, 2021, 23, e22219.	4.3	61
39	Domino: Extracting, Comparing, and Manipulating Subsets Across Multiple Tabular Datasets. IEEE Transactions on Visualization and Computer Graphics, 2014, 20, 2023-2032.	4.4	53
40	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. Nature Communications, 2022, 13, 2365.	12.8	49
41	Mayday-a microarray data analysis workbench. Bioinformatics, 2006, 22, 1010-1012.	4.1	47
42	From Visual Exploration to Storytelling and Back Again. Computer Graphics Forum, 2016, 35, 491-500.	3.0	47
43	Probabilistic retrieval and visualization of biologically relevant microarray experiments. Bioinformatics, 2009, 25, i145-i153.	4.1	41
44	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
45	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
46	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. JAMA Network Open, 2021, 4, e2112596.	5.9	33
47	AVOCADO: Visualization of Workflow–Derived Data Provenance for Reproducible Biomedical Research. Computer Graphics Forum, 2016, 35, 481-490.	3.0	32
48	Guidelines for reporting single-cell RNA-seq experiments. Nature Biotechnology, 2020, 38, 1384-1386.	17.5	27
49	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
50	Ten Simple Rules for Organizing a Scientific Meeting. PLoS Computational Biology, 2008, 4, e1000080.	3.2	23
51	Lineage: Visualizing Multivariate Clinical Data in Genealogy Graphs. IEEE Transactions on Visualization and Computer Graphics, 2019, 25, 1543-1558.	4.4	23
52	Viv: multiscale visualization of high-resolution multiplexed bioimaging data on the web. Nature Methods, 2022, 19, 515-516.	19.0	21
53	Guided visual exploration of genomic stratifications in cancer. Nature Methods, 2014, 11, 884-885.	19.0	20
54	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

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55	A Framework for Visualization of Microarray Data and Integrated Meta Information. Information Visualization, 2005, 4, 164-175.	1.9	19
56	Mapping quantitative data to color. Nature Methods, 2012, 9, 769-769.	19.0	19
57	Nozzle: a report generation toolkit for data analysis pipelines. Bioinformatics, 2013, 29, 1089-1091.	4.1	19
58	Ontologies in Biological Data Visualization. IEEE Computer Graphics and Applications, 2014, 34, 8-15.	1.2	19
59	International Changes in COVID-19 Clinical Trajectories Across 315 Hospitals and 6 Countries: Retrospective Cohort Study. Journal of Medical Internet Research, 2021, 23, e31400.	4.3	19
60	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap011.	3.0	18
61	Interactive visual exploration and refinement of cluster assignments. BMC Bioinformatics, 2017, 18, 406.	2.6	17
62	International electronic health record-derived post-acute sequelae profiles of COVID-19 patients. Npj Digital Medicine, 2022, 5, .	10.9	17
63	Data-driven information retrieval in heterogeneous collections of transcriptomics data links SIM2s to malignant pleural mesothelioma. Bioinformatics, 2012, 28, 246-253.	4.1	13
64	Prequips—an extensible software platform for integration, visualization and analysis of LC-MS/MS proteomics data. Bioinformatics, 2009, 25, 682-683.	4.1	12
65	Into the third dimension. Nature Methods, 2012, 9, 851-851.	19.0	11
66	Pattern-Driven Navigation in 2D Multiscale Visualizations with Scalable Insets. IEEE Transactions on Visualization and Computer Graphics, 2019, 26, 1-1.	4.4	11
67	Networks. Nature Methods, 2012, 9, 115-115.	19.0	10
68	SATORI: a system for ontology-guided visual exploration of biomedical data repositories. Bioinformatics, 2018, 34, 1200-1207.	4.1	10
69	ThreadStates: State-based Visual Analysis of Disease Progression. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 238-247.	4.4	10
70	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. Scientific Reports, 2021, 11, 20238.	3.3	10
71	Probabilistic retrieval and visualization of biologically relevant microarray experiments. BMC Bioinformatics, 2009, 10, .	2.6	9
72	Highlights from the Third International Society for Computational Biology Student Council Symposium at the Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology. BMC Bioinformatics, 2007, 8, .	2.6	7

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73	Power of the plane. Nature Methods, 2012, 9, 935-935.	19.0	6
74	Integrating data. Nature Methods, 2012, 9, 315-315.	19.0	6
75	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 180-182.	0.7	6
76	Effective Communication of Personalized Risks and Patient Preferences During Surgical Informed Consent Using Data Visualization: Qualitative Semistructured Interview Study With Patients After Surgery. JMIR Human Factors, 2022, 9, e29118.	2.0	6
77	Visualization of large microarray experiments with space maps. BMC Bioinformatics, 2009, 10, .	2.6	5
78	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. PLoS Computational Biology, 2013, 9, e1002834.	3.2	3
79	Temporal data. Nature Methods, 2015, 12, 97-97.	19.0	3
80	Visual Pattern-Driven Exploration of Big Data. , 2018, 2018, .		2
81	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. , 2016, , .		2
82	An information retrieval perspective on visualization of gene expression data with ontological annotation. , 2010, , .		1
83	Response to "Plotting intersections" by Lentini. Nature Methods, 2015, 12, 281-281.	19.0	1
84	OUP accepted manuscript. Bioinformatics, 2021, 37, i59-i66.	4.1	1
85	Making Tools that People Will Use: User-Centered Design in Computational Biology Research. , 2020, , .		0
86	User-Centric Process of Designing a Molecular & Cellular Query Interface for Biomedical Research. Proceedings of the Design Society, 2022, 2, 221-230.	0.8	0