

Nils Gehlenborg

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89 papers	22,643 citations	38 h-index	124 g-index
124 ext. papers	30,935 ext. citations	18.6 avg, IF	5.86 L-index

#	Paper	IF	Citations
89	MITI minimum information guidelines for highly multiplexed tissue images.. <i>Nature Methods</i> , 2022 , 19, 262-267	21.6	2
88	Effective Communication of Personalized Risks and Patient Preferences During Surgical Informed Consent Using Data Visualization: Qualitative Semistructured Interview Study With Patients After Surgery.. <i>JMIR Human Factors</i> , 2022 , 9, e29118	2.5	0
87	Viv: multiscale visualization of high-resolution multiplexed bioimaging data on the web.. <i>Nature Methods</i> , 2022 , 19, 515-516	21.6	1
86	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data.. <i>Nature Communications</i> , 2022 , 13, 2365	17.4	3
85	User-Centric Process of Designing a Molecular & Cellular Query Interface for Biomedical Research. <i>Proceedings of the Design Society</i> , 2022 , 2, 221-230		
84	Gosling: A Grammar-based Toolkit for Scalable and Interactive Genomics Data Visualization. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2021 , PP,	4	4
83	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. <i>Scientific Reports</i> , 2021 , 11, 20238	4.9	3
82	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. <i>Journal of Medical Internet Research</i> , 2021 , 23, e22219	7.6	13
81	International Changes in COVID-19 Clinical Trajectories Across 315 Hospitals and 6 Countries: Retrospective Cohort Study. <i>Journal of Medical Internet Research</i> , 2021 , 23, e31400	7.6	2
80	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. <i>JAMA Network Open</i> , 2021 , 4, e2112596	10.4	12
79	OncoThreads: visualization of large-scale longitudinal cancer molecular data. <i>Bioinformatics</i> , 2021 , 37, i59-i66	7.2	1
78	Pattern-Driven Navigation in 2D Multiscale Visualizations with Scalable Insets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2020 , 26, 611-621	4	4
77	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020 , 38, 1384-1386	44.5	9
76	Peax: Interactive Visual Pattern Search in Sequential Data Using Unsupervised Deep Representation Learning. <i>Computer Graphics Forum</i> , 2020 , 39, 167-179	2.4	8
75	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. <i>Npj Digital Medicine</i> , 2020 , 3, 109	15.7	61
74	Tasks, Techniques, and Tools for Genomic Data Visualization. <i>Computer Graphics Forum</i> , 2019 , 38, 781-805	5.4	19
73	Lineage: Visualizing Multivariate Clinical Data in Genealogy Graphs. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2019 , 25, 1543-1558	4	13

72	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	21
71	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
70	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
69	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
68	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
67	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
66	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
65	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
64	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
63	HiGlass: web-based visual exploration and analysis of genome interaction maps. <i>Genome Biology</i> , 2018 , 19, 125	18.3	242
62	SATORI: a system for ontology-guided visual exploration of biomedical data repositories. <i>Bioinformatics</i> , 2018 , 34, 1200-1207	7.2	6
61	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
60	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
59	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247
58	Interactive visual exploration and refinement of cluster assignments. <i>BMC Bioinformatics</i> , 2017 , 18, 406	3.6	8
57	UpSetR: an R package for the visualization of intersecting sets and their properties. <i>Bioinformatics</i> , 2017 , 33, 2938-2940	7.2	920
56	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
55	AVOCADO: Visualization of Workflow-Derived Data Provenance for Reproducible Biomedical Research. <i>Computer Graphics Forum</i> , 2016 , 35, 481-490	2.4	18

54	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
53	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016 , 21, 180-182	1.3	5
52	From Visual Exploration to Storytelling and Back Again. <i>Computer Graphics Forum</i> , 2016 , 35, 491-500	2.4	31
51	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
50	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
49	Response to "Plotting intersections" by Lentini. <i>Nature Methods</i> , 2015 , 12, 281	21.6	
48	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
47	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
46	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15544-9	11.5	229
45	Guided visual exploration of genomic stratifications in cancer. <i>Nature Methods</i> , 2014 , 11, 884-885	21.6	17
44	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014 , 512, 449-52	50.4	265
43	Bar charts and box plots. <i>Nature Methods</i> , 2014 , 11, 117	21.6	47
42	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
41	Ontologies in biological data visualization. <i>IEEE Computer Graphics and Applications</i> , 2014 , 34, 8-15	1.7	15
40	Domino: Extracting, Comparing, and Manipulating Subsets Across Multiple Tabular Datasets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014 , 20, 2023-32	4	34
39	UpSet: Visualization of Intersecting Sets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014 , 20, 1983-92	4	752
38	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
37	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900

36	Nozzle: a report generation toolkit for data analysis pipelines. <i>Bioinformatics</i> , 2013 , 29, 1089-91	7.2	15
35	LineUp: visual analysis of multi-attribute rankings. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2013 , 19, 2277-86	4	154
34	Diverse mechanisms of somatic structural variations in human cancer genomes. <i>Cell</i> , 2013 , 153, 919-29	56.2	238
33	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. <i>PLoS Computational Biology</i> , 2013 , 9, e1002834	5	2
32	StratomeX: Visual Analysis of Large-Scale Heterogeneous Genomics Data for Cancer Subtype Characterization. <i>Computer Graphics Forum</i> , 2012 , 31, 1175-1184	2.4	59
31	Points of View: Heat maps. <i>Nature Methods</i> , 2012 , 9, 213	21.6	45
30	Points of view: Networks. <i>Nature Methods</i> , 2012 , 9, 115	21.6	8
29	Power of the plane. <i>Nature Methods</i> , 2012 , 9, 935	21.6	5
28	Points of view: Integrating data. <i>Nature Methods</i> , 2012 , 9, 315	21.6	5
27	Into the third dimension. <i>Nature Methods</i> , 2012 , 9, 851	21.6	11
26	Points of view: Mapping quantitative data to color. <i>Nature Methods</i> , 2012 , 9, 769	21.6	16
25	Data-driven information retrieval in heterogeneous collections of transcriptomics data links SIM2s to malignant pleural mesothelioma. <i>Bioinformatics</i> , 2012 , 28, 246-53	7.2	13
24	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010 , 7, S56-68	21.6	459
23	Visualizing biological data-now and in the future. <i>Nature Methods</i> , 2010 , 7, S2-4	21.6	85
22	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap011	5	16
21	A systems approach to prion disease. <i>Molecular Systems Biology</i> , 2009 , 5, 252	12.2	195
20	Prequips--an extensible software platform for integration, visualization and analysis of LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2009 , 25, 682-3	7.2	11
19	Probabilistic retrieval and visualization of biologically relevant microarray experiments. <i>Bioinformatics</i> , 2009 , 25, i145-53	7.2	37

18	Visualization of large microarray experiments with space maps. <i>BMC Bioinformatics</i> , 2009 , 10,	3.6	5
17	Probabilistic retrieval and visualization of biologically relevant microarray experiments. <i>BMC Bioinformatics</i> , 2009 , 10,	3.6	5
16	An integrated, directed mass spectrometric approach for in-depth characterization of complex peptide mixtures. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2138-50	7.6	119
15	Ten simple rules for organizing a scientific meeting. <i>PLoS Computational Biology</i> , 2008 , 4, e1000080	5	7
14	Highlights from the Third International Society for Computational Biology Student Council Symposium at the Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology. <i>BMC Bioinformatics</i> , 2007 , 8, 11	3.6	4
13	Mayday--a microarray data analysis workbench. <i>Bioinformatics</i> , 2006 , 22, 1010-2	7.2	43
12	A Framework for Visualization of Microarray Data and Integrated Meta Information. <i>Information Visualization</i> , 2005 , 4, 164-175	2.4	16
11	Viv: Multiscale Visualization of High-Resolution Multiplexed Bioimaging Data on the Web		4
10	The 4D Nucleome Data Portal: a resource for searching and visualizing curated nucleomics data		3
9	Halyos: A patient-facing visual EHR interface for longitudinal risk awareness		1
8	SATORI: A System for Ontology-Guided Visual Exploration of Biomedical Data Repositories		1
7	From Visual Exploration to Storytelling and Back Again		3
6	UpSetR: An R Package for the Visualization of Intersecting Sets and their Properties		11
5	HiGlass: Web-based Visual Exploration and Analysis of Genome Interaction Maps		11
4	International Electronic Health Record-Derived COVID-19 Clinical Course Profiles: The 4CE Consortium		9
3	Pattern-Driven Navigation in 2D Multiscale Visualizations with Scalable Insets		1
2	Peax Interactive Visual Pattern Search in Sequential Data Using Unsupervised Deep Representation Learning		1
1	HiPiler: Visual Exploration of Large Genome Interaction Matrices with Interactive Small Multiples		1

