Florian Markowetz

List of Publications by Year
in descending order

86 papers	13,083 citations	71102 41 h-index	64796 79 g-index
110 all docs	110 docs citations	110 times ranked	22456 citing authors

#	Article	IF	Citations
1	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
2	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	27.8	690
3	Poor-prognosis colon cancer is defined by a molecularly distinct subtype and develops from serrated precursor lesions. Nature Medicine, 2013, 19, 614-618.	30.7	656
4	Acetylcysteine for prevention of contrast nephropathy: meta-analysis. Lancet, The, 2003, 362, 598-603.	13.7	486
5	Patterns of Immune Infiltration in Breast Cancer and Their Clinical Implications: A Gene-Expression-Based Retrospective Study. PLoS Medicine, 2016, 13, e1002194.	8.4	473
6	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143.	12.4	356
7	Copy number signatures and mutational processes in ovarian carcinoma. Nature Genetics, 2018, 50, 1262-1270.	21.4	320
8	Spatial and Temporal Heterogeneity in High-Grade Serous Ovarian Cancer: A Phylogenetic Analysis. PLoS Medicine, 2015, 12, e1001789.	8.4	314
9	Inferring cellular networks â€" a review. BMC Bioinformatics, 2007, 8, S5.	2.6	311
10	Cancer Evolution: Mathematical Models and Computational Inference. Systematic Biology, 2015, 64, e1-e25.	5.6	292
11	Systems-level dynamic analyses of fate change in murine embryonic stem cells. Nature, 2009, 462, 358-362.	27.8	277
12	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
13	OncoNEM: inferring tumor evolution from single-cell sequencing data. Genome Biology, 2016, 17, 69.	8.8	199
14	Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629.	27.8	187
15	Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 2013, 4, 2464.	12.8	180
16	Regulators of genetic risk of breast cancer identified by integrative network analysis. Nature Genetics, 2016, 48, 12-21.	21.4	163
17	Cytosponge-trefoil factor 3 versus usual care to identify Barrett's oesophagus in a primary care setting: a multicentre, pragmatic, randomised controlled trial. Lancet, The, 2020, 396, 333-344.	13.7	143
18	Diverse epigenetic strategies interact to control epidermal differentiation. Nature Cell Biology, 2012, 14, 753-763.	10.3	139

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19	Unraveling tumor–immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593.	21.4	136
20	HTSanalyzeR: an R/Bioconductor package for integrated network analysis of high-throughput screens. Bioinformatics, 2011, 27, 879-880.	4.1	131
21	Practical and Robust Identification of Molecular Subtypes in Colorectal Cancer by Immunohistochemistry. Clinical Cancer Research, 2017, 23, 387-398.	7.0	128
22	Phylogenetic Quantification of Intra-tumour Heterogeneity. PLoS Computational Biology, 2014, 10, e1003535.	3.2	126
23	A pan-cancer compendium of chromosomal instability. Nature, 2022, 606, 976-983.	27.8	111
24	A quantitative mass spectrometry-based approach to monitor the dynamics of endogenous chromatin-associated protein complexes. Nature Communications, 2018, 9, 2311.	12.8	104
25	BitPhylogeny: a probabilistic framework for reconstructing intra-tumor phylogenies. Genome Biology, 2015, 16, 36.	8.8	103
26	Reproducibility standards for machine learning in the life sciences. Nature Methods, 2021, 18, 1132-1135.	19.0	96
27	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.	6.4	95
28	Nested effects models for high-dimensional phenotyping screens. Bioinformatics, 2007, 23, i305-i312.	4.1	94
29	Combined image and genomic analysis of high-grade serous ovarian cancer reveals PTEN loss as a common driver event and prognostic classifier. Genome Biology, 2014, 15, 526.	8.8	93
30	RedeR: R/Bioconductor package for representing modular structures, nested networks and multiple levels of hierarchical associations.. Genome Biology, 2012, 13, R29.	9.6	91
31	Non-transcriptional pathway features reconstructed from secondary effects of RNA interference. Bioinformatics, 2005, 21, 4026-4032.	4.1	86
32	Patient-Specific Data Fusion Defines Prognostic Cancer Subtypes. PLoS Computational Biology, 2011, 7, e1002227.	3.2	81
33	Accumulated Metabolites of Hydroxybutyric Acid Serve as Diagnostic and Prognostic Biomarkers of Ovarian High-Grade Serous Carcinomas. Cancer Research, 2016, 76, 796-804.	0.9	74
34	Intratumor heterogeneity defines treatment–resistant <scp>HER</scp>2+ breast tumors. Molecular Oncology, 2018, 12, 1838-1855.	4.6	74
35	All biology is computational biology. PLoS Biology, 2017, 15, e2002050.	5.6	73
36	SANTA: Quantifying the Functional Content of Molecular Networks. PLoS Computational Biology, 2014, 10, e1003808.	3.2	66

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37	Triage-driven diagnosis of Barrett's esophagus for early detection of esophageal adenocarcinoma using deep learning. Nature Medicine, 2021, 27, 833-841.	30.7	65
38	Five selfish reasons to work reproducibly. Genome Biology, 2015, 16, 274.	8.8	63
39	Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633.	21.4	59
40	KHS101 disrupts energy metabolism in human glioblastoma cells and reduces tumor growth in mice. Science Translational Medicine, 2018, 10, .	12.4	54
41	How to Understand the Cell by Breaking It: Network Analysis of Gene Perturbation Screens. PLoS Computational Biology, 2010, 6, e1000655.	3.2	51
42	Structure Learning in Nested Effects Models. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article9.	0.6	42
43	A phylogenetic latent feature model for clonal deconvolution. Annals of Applied Statistics, 2016, 10, .	1.1	42
44	Master Regulators of Oncogenic KRAS Response in Pancreatic Cancer: An Integrative Network Biology Analysis. PLoS Medicine, 2017, 14, e1002223.	8.4	39
45	Support Vector Machines for Protein Fold Class Prediction. Biometrical Journal, 2003, 45, 377-389.	1.0	36
46	Differential C3NET reveals disease networks of direct physical interactions. BMC Bioinformatics, 2011, 12, 296.	2.6	35
47	How Subclonal Modeling Is Changing the Metastatic Paradigm. Clinical Cancer Research, 2017, 23, 630-635.	7.0	34
48	Analysis of heterogeneity in T2-weighted MR images can differentiate pseudoprogression from progression in glioblastoma. PLoS ONE, 2017, 12, e0176528.	2.5	34
49	Inferring structural variant cancer cell fraction. Nature Communications, 2020, 11, 730.	12.8	33
50	Immunophenotypes of pancreatic ductal adenocarcinoma: Meta-analysis of transcriptional subtypes. International Journal of Cancer, 2019, 145, 1125-1137.	5.1	30
51	Integrative radiogenomics for virtual biopsy and treatment monitoring in ovarian cancer. Insights Into Imaging, 2020, 11, 94.	3.4	30
52	Dissecting cancer heterogeneity – An unsupervised classification approach. International Journal of Biochemistry and Cell Biology, 2013, 45, 2574-2579.	2.8	28
53	Tissue-specific and interpretable sub-segmentation of whole tumour burden on CT images by unsupervised fuzzy clustering. Computers in Biology and Medicine, 2020, 120, 103751.	7.0	27
54	BaalChIP: Bayesian analysis of allele-specific transcription factor binding in cancer genomes. Genome Biology, 2017, 18, 39.	8.8	26

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55	VULCAN integrates ChIP-seq with patient-derived co-expression networks to identify GRHL2 as a key co-regulator of ERa at enhancers in breast cancer. Genome Biology, 2019, 20, 91.	8.8	24
56	Mapping Dynamic Histone Acetylation Patterns to Gene Expression in Nanog-Depleted Murine Embryonic Stem Cells. PLoS Computational Biology, 2010, 6, e1001034.	3.2	23
57	Parallel factor ChIP provides essential internal control for quantitative differential ChIP-seq. Nucleic Acids Research, 2018, 46, e75-e75.	14.5	21
58	Computational identification of cellular networks and pathways. Molecular BioSystems, 2007, 3, 478.	2.9	20
59	Ultrasound-guided targeted biopsies of CT-based radiomic tumour habitats: technical development and initial experience in metastatic ovarian cancer. European Radiology, 2021, 31, 3765-3772.	4.5	20
60	The Genomic Landscape of Early-Stage Ovarian High-Grade Serous Carcinoma. Clinical Cancer Research, 2022, 28, 2911-2922.	7.0	19
61	Posterior Association Networks and Functional Modules Inferred from Rich Phenotypes of Gene Perturbations. PLoS Computational Biology, 2012, 8, e1002566.	3.2	18
62	A saltationist theory of cancer evolution. Nature Genetics, 2016, 48, 1102-1103.	21.4	18
63	Reconstructing evolving signalling networks by hidden Markov nested effects models. Annals of Applied Statistics, 2014, 8, .	1.1	16
64	Allele-specific multi-sample copy number segmentation in ASCAT. Bioinformatics, 2021, 37, 1909-1911.	4.1	16
65	Low perfusion compartments in glioblastoma quantified by advanced magnetic resonance imaging and correlated with patient survival. Radiotherapy and Oncology, 2019, 134, 17-24.	0.6	15
66	Inferring modulators of genetic interactions with epistatic nested effects models. PLoS Computational Biology, 2017, 13, e1005496.	3.2	13
67	Evolutionary Distances in the Twilight Zoneâ€"A Rational Kernel Approach. PLoS ONE, 2010, 5, e15788.	2.5	13
68	Genome-wide Estrogen Receptor-Î± activation is sustained, not cyclical. ELife, 2018, 7, .	6.0	12
69	Clinically Interpretable Radiomics-Based Prediction of Histopathologic Response to Neoadjuvant Chemotherapy in High-Grade Serous Ovarian Carcinoma. Frontiers in Oncology, 0, 12, .	2.8	12
70	Decoding the Interdependence of Multiparametric Magnetic Resonance Imaging to Reveal Patient Subgroups Correlated with Survivals. Neoplasia, 2019, 21, 442-449.	5.3	9
71	GoIFISH: a system for the quantification of single cell heterogeneity from IFISH images. Genome Biology, 2014, 15, 442.	8.8	8
72	Computational Diagnostics with Gene Expression Profiles. Methods in Molecular Biology, 2008, 453, 281-296.	0.9	7

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73	Development of a miRNAâ€based classifier for detection of colorectal cancer molecular subtypes. Molecular Oncology, 2022, 16, 2693-2709.	4.6	6
74	Data generation and network reconstruction strategies for single cell transcriptomic profiles of CRISPR-mediated gene perturbations. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194441.	1.9	4
75	You Are Not Working for Me; I Am Working with You. PLoS Computational Biology, 2015, 11, e1004387.	3.2	3
76	A sparse regulatory network of copy-number driven expression reveals putative breast cancer oncogenes. , 2010, , .		2
77	An introduction to systems genetics. , 0, , 1-11.		2
78	FrenchFISH: Poisson Models for Quantifying DNA Copy Number From Fluorescence In Situ Hybridization of Tissue Sections. JCO Clinical Cancer Informatics, 2021, 5, 176-186.	2.1	2
79	Class Discovery in Gene Expression Data: Characterizing Splits by Support Vector Machines. Studies in Classification, Data Analysis, and Knowledge Organization, 2003, , 662-669.	0.2	2
80	Quantification of TFF3 expression from a non-endoscopic device predicts clinically relevant Barrett's oesophagus by machine learning. EBioMedicine, 2022, 82, 104160.	6.1	2
81	Deregulation upon DNA damage revealed by joint analysis of context-specific perturbation data. BMC Bioinformatics, 2011, 12, 249.	2.6	1
82	Refining cellular pathway models using an ensemble of heterogeneous data sources. Annals of Applied Statistics, 2018, 12, .	1.1	1
83	Genetic interactions and network reliability. , 0, , 51-64.		0
84	Joining the dots: network analysis of gene perturbation data. , 0, , 83-107.		0
85	Computational pathology aids derivation of microRNA biomarker signals from Cytosponge samples. EBioMedicine, 2022, 76, 103814.	6.1	0
86	Computational Diagnostics. , 2005, , 324-327.		0