# Florian Markowetz

## List of Publications by Year in descending order



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|---|---|---|---|
| 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 | Computational pathology aids derivation of microRNA biomarker signals from Cytosponge samples. EBioMedicine, 2022, 76, 103814. | 6.1 | 0 |
| 2 | Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629. | 27.8 | 187 |
| 3 | Development of a miRNAâ€based classifier for detection of colorectal cancer molecular subtypes. Molecular Oncology, 2022, 16, 2693-2709. | 4.6 | 6 |
| 4 | The Genomic Landscape of Early-Stage Ovarian High-Grade Serous Carcinoma. Clinical Cancer Research, 2022, 28, 2911-2922. | 7.0 | 19 |
| 5 | A pan-cancer compendium of chromosomal instability. Nature, 2022, 606, 976-983. | 27.8 | 111 |
| 6 | 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 |
| 7 | Allele-specific multi-sample copy number segmentation in ASCAT. Bioinformatics, 2021, 37, 1909-1911. | 4.1 | 16 |
| 8 | 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 |
| 9 | 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 |
| 10 | Triage-driven diagnosis of Barrettâ€™s esophagus for early detection of esophageal adenocarcinoma using deep learning. Nature Medicine, 2021, 27, 833-841. | 30.7 | 65 |
| 11 | Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39. | 28.9 | 260 |
| 12 | Reproducibility standards for machine learning in the life sciences. Nature Methods, 2021, 18, 1132-1135. | 19.0 | 96 |
| 13 | 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 |
| 14 | 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 |
| 15 | Unraveling tumorâ€“immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593. | 21.4 | 136 |
| 16 | Inferring structural variant cancer cell fraction. Nature Communications, 2020, 11, 730. | 12.8 | 33 |
| 17 | The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128. | 27.8 | 690 |
| 18 | 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 |

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|---|---|---|---|
| 19 | Integrative radiogenomics for virtual biopsy and treatment monitoring in ovarian cancer. Insights Into Imaging, 2020, 11, 94. | 3.4 | 30 |
| 20 | The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10. | 6.4 | 95 |
| 21 | 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 |
| 22 | 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 |
| 23 | Decoding the Interdependence of Multiparametric Magnetic Resonance Imaging to Reveal Patient Subgroups Correlated with Survivals. Neoplasia, 2019, 21, 442-449. | 5.3 | 9 |
| 24 | Immunophenotypes of pancreatic ductal adenocarcinoma: Metaâ€analysis of transcriptional subtypes. International Journal of Cancer, 2019, 145, 1125-1137. | 5.1 | 30 |
| 25 | Parallel factor ChIP provides essential internal control for quantitative differential ChIP-seq. Nucleic Acids Research, 2018, 46, e75-e75. | 14.5 | 21 |
| 26 | Refining cellular pathway models using an ensemble of heterogeneous data sources. Annals of Applied Statistics, 2018, 12, . | 1.1 | 1 |
| 27 | Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633. | 21.4 | 59 |
| 28 | Copy number signatures and mutational processes in ovarian carcinoma. Nature Genetics, 2018, 50, 1262-1270. | 21.4 | 320 |
| 29 | KHS101 disrupts energy metabolism in human glioblastoma cells and reduces tumor growth in mice. Science Translational Medicine, 2018, 10, . | 12.4 | 54 |
| 30 | Intratumor heterogeneity defines treatmentâ€resistant <scp>HER</scp>2+ breast tumors. Molecular Oncology, 2018, 12, 1838-1855. | 4.6 | 74 |
| 31 | A quantitative mass spectrometry-based approach to monitor the dynamics of endogenous chromatin-associated protein complexes. Nature Communications, 2018, 9, 2311. | 12.8 | 104 |
| 32 | Genome-wide Estrogen Receptor-Î± activation is sustained, not cyclical. ELife, 2018, 7, . | 6.0 | 12 |
| 33 | BaalChIP: Bayesian analysis of allele-specific transcription factor binding in cancer genomes. Genome Biology, 2017, 18, 39. | 8.8 | 26 |
| 34 | How Subclonal Modeling Is Changing the Metastatic Paradigm. Clinical Cancer Research, 2017, 23, 630-635. | 7.0 | 34 |
| 35 | Practical and Robust Identification of Molecular Subtypes in Colorectal Cancer by Immunohistochemistry. Clinical Cancer Research, 2017, 23, 387-398. | 7.0 | 128 |
| 36 | Analysis of heterogeneity in T2-weighted MR images can differentiate pseudoprogression from progression in glioblastoma. PLoS ONE, 2017, 12, e0176528. | 2.5 | 34 |

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|---|---|---|---|
| 37 | All biology is computational biology. PLoS Biology, 2017, 15, e2002050. | 5.6 | 73 |
| 38 | Inferring modulators of genetic interactions with epistatic nested effects models. PLoS Computational Biology, 2017, 13, e1005496. | 3.2 | 13 |
| 39 | Master Regulators of Oncogenic KRAS Response in Pancreatic Cancer: An Integrative Network Biology Analysis. PLoS Medicine, 2017, 14, e1002223. | 8.4 | 39 |
| 40 | A phylogenetic latent feature model for clonal deconvolution. Annals of Applied Statistics, 2016, 10, . | 1.1 | 42 |
| 41 | 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 |
| 42 | A saltationist theory of cancer evolution. Nature Genetics, 2016, 48, 1102-1103. | 21.4 | 18 |
| 43 | OncoNEM: inferring tumor evolution from single-cell sequencing data. Genome Biology, 2016, 17, 69. | 8.8 | 199 |
| 44 | 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 |
| 45 | Regulators of genetic risk of breast cancer identified by integrative network analysis. Nature Genetics, 2016, 48, 12-21. | 21.4 | 163 |
| 46 | Five selfish reasons to work reproducibly. Genome Biology, 2015, 16, 274. | 8.8 | 63 |
| 47 | Spatial and Temporal Heterogeneity in High-Grade Serous Ovarian Cancer: A Phylogenetic Analysis. PLoS Medicine, 2015, 12, e1001789. | 8.4 | 314 |
| 48 | BitPhylogeny: a probabilistic framework for reconstructing intra-tumor phylogenies. Genome Biology, 2015, 16, 36. | 8.8 | 103 |
| 49 | Cancer Evolution: Mathematical Models and Computational Inference. Systematic Biology, 2015, 64, e1-e25. | 5.6 | 292 |
| 50 | You Are Not Working for Me; I Am Working with You. PLoS Computational Biology, 2015, 11, e1004387. | 3.2 | 3 |
| 51 | 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 |
| 52 | SANTA: Quantifying the Functional Content of Molecular Networks. PLoS Computational Biology, 2014, 10, e1003808. | 3.2 | 66 |
| 53 | Phylogenetic Quantification of Intra-tumour Heterogeneity. PLoS Computational Biology, 2014, 10, e1003535. | 3.2 | 126 |
| 54 | GoIFISH: a system for the quantification of single cell heterogeneity from IFISH images. Genome Biology, 2014, 15, 442. | 8.8 | 8 |

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|---|---|---|---|
| 55 | Reconstructing evolving signalling networks by hidden Markov nested effects models. Annals of Applied Statistics, 2014, 8, . | 1.1 | 16 |
| 56 | Dissecting cancer heterogeneity â€“ An unsupervised classification approach. International Journal of Biochemistry and Cell Biology, 2013, 45, 2574-2579. | 2.8 | 28 |
| 57 | 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 |
| 58 | Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 2013, 4, 2464. | 12.8 | 180 |
| 59 | Posterior Association Networks and Functional Modules Inferred from Rich Phenotypes of Gene Perturbations. PLoS Computational Biology, 2012, 8, e1002566. | 3.2 | 18 |
| 60 | Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143. | 12.4 | 356 |
| 61 | RedeR: R/Bioconductor package for representing modular structures, nested networks and multiple levels of hierarchical associations.. Genome Biology, 2012, 13, R29. | 9.6 | 91 |
| 62 | Diverse epigenetic strategies interact to control epidermal differentiation. Nature Cell Biology, 2012, 14, 753-763. | 10.3 | 139 |
| 63 | The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352. | 27.8 | 4,708 |
| 64 | Differential C3NET reveals disease networks of direct physical interactions. BMC Bioinformatics, 2011, 12, 296. | 2.6 | 35 |
| 65 | Deregulation upon DNA damage revealed by joint analysis of context-specific perturbation data. BMC Bioinformatics, 2011, 12, 249. | 2.6 | 1 |
| 66 | HTSanalyzeR: an R/Bioconductor package for integrated network analysis of high-throughput screens. Bioinformatics, 2011, 27, 879-880. | 4.1 | 131 |
| 67 | Patient-Specific Data Fusion Defines Prognostic Cancer Subtypes. PLoS Computational Biology, 2011, 7, e1002227. | 3.2 | 81 |
| 68 | How to Understand the Cell by Breaking It: Network Analysis of Gene Perturbation Screens. PLoS Computational Biology, 2010, 6, e1000655. | 3.2 | 51 |
| 69 | Mapping Dynamic Histone Acetylation Patterns to Gene Expression in Nanog-Depleted Murine Embryonic Stem Cells. PLoS Computational Biology, 2010, 6, e1001034. | 3.2 | 23 |
| 70 | A sparse regulatory network of copy-number driven expression reveals putative breast cancer oncogenes. , 2010, , . | | 2 |
| 71 | Evolutionary Distances in the Twilight Zoneâ€”A Rational Kernel Approach. PLoS ONE, 2010, 5, e15788. | 2.5 | 13 |
| 72 | Systems-level dynamic analyses of fate change in murine embryonic stem cells. Nature, 2009, 462, 358-362. | 27.8 | 277 |

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|---|---|---|---|
| 73 | Computational Diagnostics with Gene Expression Profiles. Methods in Molecular Biology, 2008, 453, 281-296. | 0.9 | 7 |
| 74 | Structure Learning in Nested Effects Models. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article9. | 0.6 | 42 |
| 75 | Nested effects models for high-dimensional phenotyping screens. Bioinformatics, 2007, 23, i305-i312. | 4.1 | 94 |
| 76 | Computational identification of cellular networks and pathways. Molecular BioSystems, 2007, 3, 478. | 2.9 | 20 |
| 77 | Inferring cellular networks â€“ a review. BMC Bioinformatics, 2007, 8, S5. | 2.6 | 311 |
| 78 | Non-transcriptional pathway features reconstructed from secondary effects of RNA interference. Bioinformatics, 2005, 21, 4026-4032. | 4.1 | 86 |
| 79 | Computational Diagnostics. , 2005, , 324-327. | | 0 |
| 80 | Support Vector Machines for Protein Fold Class Prediction. Biometrical Journal, 2003, 45, 377-389. | 1.0 | 36 |
| 81 | Acetylcysteine for prevention of contrast nephropathy: meta-analysis. Lancet, The, 2003, 362, 598-603. | 13.7 | 486 |
| 82 | 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 |
| 83 | An introduction to systems genetics. , 0, , 1-11. | | 2 |
| 84 | Genetic interactions and network reliability. , 0, , 51-64. | | 0 |
| 85 | Joining the dots: network analysis of gene perturbation data. , 0, , 83-107. | | 0 |
| 86 | 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 |