

Franziska Michor

List of Publications by Citations

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137
papers

10,565
citations

53
h-index

102
g-index

144
ext. papers

12,884
ext. citations

13
avg, IF

6.32
L-index

#	Paper	IF	Citations
137	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. <i>Nature</i> , 2014 , 512, 155-60	50.4	730
136	Dynamics of chronic myeloid leukaemia. <i>Nature</i> , 2005 , 435, 1267-70	50.4	667
135	Non-cell-autonomous driving of tumour growth supports sub-clonal heterogeneity. <i>Nature</i> , 2014 , 514, 54-8	50.4	397
134	Optimization of dosing for EGFR-mutant non-small cell lung cancer with evolutionary cancer modeling. <i>Science Translational Medicine</i> , 2011 , 3, 90ra59	17.5	383
133	The mathematics of cancer: integrating quantitative models. <i>Nature Reviews Cancer</i> , 2015 , 15, 730-45	31.3	357
132	Dynamics of cancer progression. <i>Nature Reviews Cancer</i> , 2004 , 4, 197-205	31.3	311
131	Computational modeling of pancreatic cancer reveals kinetics of metastasis suggesting optimum treatment strategies. <i>Cell</i> , 2012 , 148, 362-75	56.2	292
130	Punctuated copy number evolution and clonal stasis in triple-negative breast cancer. <i>Nature Genetics</i> , 2016 , 48, 1119-30	36.3	290
129	Studying clonal dynamics in response to cancer therapy using high-complexity barcoding. <i>Nature Medicine</i> , 2015 , 21, 440-8	50.5	273
128	Most human non-GCIMP glioblastoma subtypes evolve from a common proneural-like precursor glioma. <i>Cancer Cell</i> , 2014 , 26, 288-300	24.3	261
127	Polyploidy can drive rapid adaptation in yeast. <i>Nature</i> , 2015 , 519, 349-52	50.4	258
126	Cellular and genetic diversity in the progression of in situ human breast carcinomas to an invasive phenotype. <i>Journal of Clinical Investigation</i> , 2010 , 120, 636-44	15.9	258
125	Clonal Hematopoiesis Associated With Adverse Outcomes After Autologous Stem-Cell Transplantation for Lymphoma. <i>Journal of Clinical Oncology</i> , 2017 , 35, 1598-1605	2.2	208
124	Inference of tumor evolution during chemotherapy by computational modeling and in situ analysis of genetic and phenotypic cellular diversity. <i>Cell Reports</i> , 2014 , 6, 514-27	10.6	194
123	JAK-STAT pathway activation in malignant and nonmalignant cells contributes to MPN pathogenesis and therapeutic response. <i>Cancer Discovery</i> , 2015 , 5, 316-31	24.4	188
122	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. <i>Nature Communications</i> , 2018 , 9, 3588	17.4	187
121	Mathematical modeling of PDGF-driven glioblastoma reveals optimized radiation dosing schedules. <i>Cell</i> , 2014 , 156, 603-616	56.2	184

120	Stochastic tunnels in evolutionary dynamics. <i>Genetics</i> , 2004 , 166, 1571-9	4	176
119	DNA secondary structures and epigenetic determinants of cancer genome evolution. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 950-5	17.6	169
118	Evolution of resistance during clonal expansion. <i>Genetics</i> , 2006 , 172, 2557-66	4	168
117	Evolution of acquired resistance to anti-cancer therapy. <i>Journal of Theoretical Biology</i> , 2014 , 355, 10-20	2.3	167
116	Can chromosomal instability initiate tumorigenesis?. <i>Seminars in Cancer Biology</i> , 2005 , 15, 43-9	12.7	150
115	The linear process of somatic evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 14966-9	11.5	149
114	What does physics have to do with cancer?. <i>Nature Reviews Cancer</i> , 2011 , 11, 657-70	31.3	143
113	The origins and implications of intratumor heterogeneity. <i>Cancer Prevention Research</i> , 2010 , 3, 1361-4	3.2	141
112	Genetic and phenotypic diversity in breast tumor metastases. <i>Cancer Research</i> , 2014 , 74, 1338-48	10.1	137
111	DNA replication timing and long-range DNA interactions predict mutational landscapes of cancer genomes. <i>Nature Biotechnology</i> , 2011 , 29, 1103-8	44.5	129
110	Risk prediction for late-stage ovarian cancer by meta-analysis of 1525 patient samples. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	123
109	In situ single-cell analysis identifies heterogeneity for PIK3CA mutation and HER2 amplification in HER2-positive breast cancer. <i>Nature Genetics</i> , 2015 , 47, 1212-9	36.3	117
108	Immune Escape in Breast Cancer During to Invasive Carcinoma Transition. <i>Cancer Discovery</i> , 2017 , 7, 1098-1115	11.15	113
107	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	110
106	DNA methyltransferase 1 and DNA methylation patterning contribute to germinal center B-cell differentiation. <i>Blood</i> , 2011 , 118, 3559-69	2.2	107
105	A mathematical framework to determine the temporal sequence of somatic genetic events in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17604-9	11.5	99
104	CXCR4 Regulates Extra-Medullary Myeloma through Epithelial-Mesenchymal-Transition-like Transcriptional Activation. <i>Cell Reports</i> , 2015 , 12, 622-35	10.6	94
103	Dynamics of colorectal cancer. <i>Seminars in Cancer Biology</i> , 2005 , 15, 484-93	12.7	93

102	KDM5 Histone Demethylase Activity Links Cellular Transcriptomic Heterogeneity to Therapeutic Resistance. <i>Cancer Cell</i> , 2018 , 34, 939-953.e9	24.3	93
101	Aberration in DNA methylation in B-cell lymphomas has a complex origin and increases with disease severity. <i>PLoS Genetics</i> , 2013 , 9, e1003137	6	91
100	Intratumor heterogeneity in evolutionary models of tumor progression. <i>Genetics</i> , 2011 , 188, 461-77	4	86
99	Evolution of resistance to targeted anti-cancer therapies during continuous and pulsed administration strategies. <i>PLoS Computational Biology</i> , 2009 , 5, e1000557	5	85
98	DNA replication timing and higher-order nuclear organization determine single-nucleotide substitution patterns in cancer genomes. <i>Nature Communications</i> , 2013 , 4, 1502	17.4	82
97	Evolutionary dynamics of tumor suppressor gene inactivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 10635-8	11.5	81
96	Ascl2-Dependent Cell Dedifferentiation Drives Regeneration of Ablated Intestinal Stem Cells. <i>Cell Stem Cell</i> , 2020 , 26, 377-390.e6	18	77
95	Analysis of somatic microsatellite indels identifies driver events in human tumors. <i>Nature Biotechnology</i> , 2017 , 35, 951-959	44.5	72
94	Improving Cancer Treatment via Mathematical Modeling: Surmounting the Challenges Is Worth the Effort. <i>Cell</i> , 2015 , 163, 1059-1063	56.2	71
93	Subclonal cooperation drives metastasis by modulating local and systemic immune microenvironments. <i>Nature Cell Biology</i> , 2019 , 21, 879-888	23.4	69
92	Evolutionary dynamics of escape from biomedical intervention. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003 , 270, 2573-8	4.4	69
91	Evolution of resistance to cancer therapy. <i>Current Pharmaceutical Design</i> , 2006 , 12, 261-71	3.3	68
90	The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. <i>Cell Reports</i> , 2017 , 19, 218-224.e6	16.6	67
89	The age incidence of chronic myeloid leukemia can be explained by a one-mutation model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 14931-4	11.5	65
88	Evolution of resistance to anti-cancer therapy during general dosing schedules. <i>Journal of Theoretical Biology</i> , 2010 , 263, 179-88	2.3	62
87	mTOR and HDAC Inhibitors Converge on the TXNIP/Thioredoxin Pathway to Cause Catastrophic Oxidative Stress and Regression of RAS-Driven Tumors. <i>Cancer Discovery</i> , 2017 , 7, 1450-1463	24.4	59
86	Phase II study of ruxolitinib, a selective JAK1/2 inhibitor, in patients with metastatic triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2018 , 4, 10	7.8	58
85	Effects of pharmacokinetic processes and varied dosing schedules on the dynamics of acquired resistance to erlotinib in EGFR-mutant lung cancer. <i>Journal of Thoracic Oncology</i> , 2012 , 7, 1583-93	8.9	58

84	Dynamics of chronic myeloid leukemia response to long-term targeted therapy reveal treatment effects on leukemic stem cells. <i>Blood</i> , 2011 , 118, 1622-31	2.2	52
83	Stochastic dynamics of metastasis formation. <i>Journal of Theoretical Biology</i> , 2006 , 240, 521-30	2.3	52
82	The Impact of Microenvironmental Heterogeneity on the Evolution of Drug Resistance in Cancer Cells. <i>Cancer Informatics</i> , 2015 , 14, 19-31	2.4	48
81	Somatic selection for and against cancer. <i>Journal of Theoretical Biology</i> , 2003 , 225, 377-82	2.3	48
80	The evolution of two mutations during clonal expansion. <i>Genetics</i> , 2007 , 177, 2209-21	4	47
79	A mathematical methodology for determining the temporal order of pathway alterations arising during gliomagenesis. <i>PLoS Computational Biology</i> , 2012 , 8, e1002337	5	46
78	Fitness conferred by BCR-ABL kinase domain mutations determines the risk of pre-existing resistance in chronic myeloid leukemia. <i>PLoS ONE</i> , 2011 , 6, e27682	3.7	44
77	Evolutionary dynamics of intratumor heterogeneity. <i>PLoS ONE</i> , 2011 , 6, e17866	3.7	44
76	The therapeutic implications of plasticity of the cancer stem cell phenotype. <i>PLoS ONE</i> , 2010 , 5, e14366	3.7	43
75	Reconstructing the Lineage Histories and Differentiation Trajectories of Individual Cancer Cells in Myeloproliferative Neoplasms. <i>Cell Stem Cell</i> , 2021 , 28, 514-523.e9	18	42
74	Evolutionary modeling of combination treatment strategies to overcome resistance to tyrosine kinase inhibitors in non-small cell lung cancer. <i>Molecular Pharmaceutics</i> , 2011 , 8, 2069-79	5.6	40
73	Integrative analysis of 1q23.3 copy-number gain in metastatic urothelial carcinoma. <i>Clinical Cancer Research</i> , 2014 , 20, 1873-83	12.9	38
72	Stochastic elimination of cancer cells. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003 , 270, 2017-24	4.4	38
71	Pharmacokinetics and Drug Interactions Determine Optimum Combination Strategies in Computational Models of Cancer Evolution. <i>Cancer Research</i> , 2017 , 77, 3908-3921	10.1	36
70	ABCG2 regulates self-renewal and stem cell marker expression but not tumorigenicity or radiation resistance of glioma cells. <i>Scientific Reports</i> , 2016 , 6, 25956	4.9	36
69	Linear model of colon cancer initiation. <i>Cell Cycle</i> , 2004 , 3, 358-62	4.7	36
68	Synthetic Lethal and Resistance Interactions with BET Bromodomain Inhibitors in Triple-Negative Breast Cancer. <i>Molecular Cell</i> , 2020 , 78, 1096-1113.e8	17.6	35
67	Local regulation of homeostasis favors chromosomal instability. <i>Current Biology</i> , 2003 , 13, 581-4	6.3	34

66	Breast tumours maintain a reservoir of subclonal diversity during expansion. <i>Nature</i> , 2021 , 592, 302-308	50.4	33
65	A computational strategy to adjust for copy number in tumor Hi-C data. <i>Bioinformatics</i> , 2016 , 32, 3695-3701	21	31
64	A differentiation-based phylogeny of cancer subtypes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000777	5	30
63	Drug Sensitivity and Allele Specificity of First-Line Osimertinib Resistance Mutations. <i>Cancer Research</i> , 2020 , 80, 2017-2030	10.1	27
62	The probable cell of origin of NF1- and PDGF-driven glioblastomas. <i>PLoS ONE</i> , 2011 , 6, e24454	3.7	26
61	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. <i>Nucleic Acids Research</i> , 2017 , 45, e77	20.1	24
60	Nuclear topology modulates the mutational landscapes of cancer genomes. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 1000-1006	17.6	22
59	Mathematical modeling of erythrocyte chimerism informs genetic intervention strategies for sickle cell disease. <i>American Journal of Hematology</i> , 2016 , 91, 931-7	7.1	22
58	Hidden heterogeneity and circadian-controlled cell fate inferred from single cell lineages. <i>Nature Communications</i> , 2018 , 9, 5372	17.4	22
57	Increased expression provides a selective advantage for gain of whole chromosome 7 in IDH wild-type glioblastoma. <i>Genes and Development</i> , 2018 , 32, 512-523	12.6	21
56	Mathematical modeling identifies optimum lapatinib dosing schedules for the treatment of glioblastoma patients. <i>PLoS Computational Biology</i> , 2018 , 14, e1005924	5	21
55	An Evolutionary Approach for Identifying Driver Mutations in Colorectal Cancer. <i>PLoS Computational Biology</i> , 2015 , 11, e1004350	5	21
54	DNA copy number analysis of metastatic urothelial carcinoma with comparison to primary tumors. <i>BMC Cancer</i> , 2015 , 15, 242	4.8	20
53	Understanding tissue context influences on intratumour heterogeneity. <i>Nature Cell Biology</i> , 2014 , 16, 301-2	23.4	20
52	Patterns of proliferative activity in the colonic crypt determine crypt stability and rates of somatic evolution. <i>PLoS Computational Biology</i> , 2013 , 9, e1003082	5	19
51	Myeloma Cell Dynamics in Response to Treatment Supports a Model of Hierarchical Differentiation and Clonal Evolution. <i>Clinical Cancer Research</i> , 2016 , 22, 4206-4214	12.9	18
50	On the validity of using increases in 5-year survival rates to measure success in the fight against cancer. <i>PLoS ONE</i> , 2014 , 9, e83100	3.7	18
49	Histone modifications are associated with transcript isoform diversity in normal and cancer cells. <i>PLoS Computational Biology</i> , 2014 , 10, e1003611	5	18

48	Chromosomal instability and human cancer. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005 , 360, 631-5	5.8	18
47	A PDGFR β -driven mouse model of glioblastoma reveals a stathmin1-mediated mechanism of sensitivity to vinblastine. <i>Nature Communications</i> , 2018 , 9, 3116	17.4	17
46	Currently available bulk sequencing data do not necessarily support a model of neutral tumor evolution. <i>Nature Genetics</i> , 2018 , 50, 1620-1623	36.3	17
45	Acquired resistance to combined BET and CDK4/6 inhibition in triple-negative breast cancer. <i>Nature Communications</i> , 2020 , 11, 2350	17.4	15
44	Dose-Dependent Mutation Rates Determine Optimum Erlotinib Dosing Strategies for EGFR Mutant Non-Small Cell Lung Cancer Patients. <i>PLoS ONE</i> , 2015 , 10, e0141665	3.7	15
43	Dynamics of chronic myeloid leukemia response to dasatinib, nilotinib, and high-dose imatinib. <i>Haematologica</i> , 2014 , 99, 1701-9	6.6	12
42	Epigenetic diversity in hematopoietic neoplasms. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2014 , 1846, 477-84	11.2	10
41	Mutational Profile and Prognostic Relevance of Circulating Tumor Cells in Multiple Myeloma. <i>Blood</i> , 2015 , 126, 23-23	2.2	10
40	Probabilistic Modeling of Reprogramming to Induced Pluripotent Stem Cells. <i>Cell Reports</i> , 2016 , 17, 3395-3406	10.4	10
39	Stochastic tunneling and metastable states during the somatic evolution of cancer. <i>Genetics</i> , 2015 , 199, 1213-28	4	9
38	A race between tumor immunoescape and genome maintenance selects for optimum levels of (epi)genetic instability. <i>PLoS Computational Biology</i> , 2012 , 8, e1002370	5	9
37	Progression signature underlies clonal evolution and dissemination of multiple myeloma. <i>Blood</i> , 2021 , 137, 2360-2372	2.2	9
36	Computational Model of Progression to Multiple Myeloma Identifies Optimum Screening Strategies. <i>JCO Clinical Cancer Informatics</i> , 2018 , 2, 1-12	5.2	8
35	Distance in cancer gene expression from stem cells predicts patient survival. <i>PLoS ONE</i> , 2017 , 12, e0173589	3.7	7
34	Stochastic Tunneling of Two Mutations in a Population of Cancer Cells. <i>PLoS ONE</i> , 2013 , 8, e65724	3.7	7
33	Circadian clock effects on cellular proliferation: Insights from theory and experiments. <i>Current Opinion in Cell Biology</i> , 2020 , 67, 17-26	9	7
32	SIApopr: a computational method to simulate evolutionary branching trees for analysis of tumor clonal evolution. <i>Bioinformatics</i> , 2017 , 33, 2221-2223	7.2	5
31	Mathematical Modeling Links Pregnancy-Associated Changes and Breast Cancer Risk. <i>Cancer Research</i> , 2017 , 77, 2800-2809	10.1	5

30	Identification of optimal dosing schedules of dacomitinib and osimertinib for a phase I/II trial in advanced EGFR-mutant non-small cell lung cancer. <i>Nature Communications</i> , 2021 , 12, 3697	17.4	5
29	Imaging dynamic mTORC1 pathway activity in vivo reveals marked shifts that support time-specific inhibitor therapy in AML. <i>Nature Communications</i> , 2021 , 12, 245	17.4	5
28	Computational modeling of pancreatic cancer patients receiving FOLFIRINOX and gemcitabine-based therapies identifies optimum intervention strategies. <i>PLoS ONE</i> , 2019 , 14, e0215409	3.7	4
27	Pharmacokinetic Profiles Determine Optimal Combination Treatment Schedules in Computational Models of Drug Resistance. <i>Cancer Research</i> , 2020 , 80, 3372-3382	10.1	4
26	Reply to Parsons: Many tumor types follow the monoclonal model of tumor initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E16-E16	11.5	4
25	Reconstructing the Lineage Histories and Differentiation Trajectories of Individual Hematopoietic Stem Cells in JAK2-Mutant Myeloproliferative Neoplasms. <i>Blood</i> , 2020 , 136, 7-8	2.2	4
24	Computational modelling of perivascular-niche dynamics for the optimization of treatment schedules for glioblastoma. <i>Nature Biomedical Engineering</i> , 2021 , 5, 346-359	19	4
23	Response to comment on "Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2". <i>Science Translational Medicine</i> , 2021 , 13, eabj3222	17.5	3
22	The impact of tumor epithelial and microenvironmental heterogeneity on treatment responses in HER2+ breast cancer. <i>JCI Insight</i> , 2021 , 6,	9.9	3
21	A Quantitative Paradigm for Decision-Making in Precision Oncology. <i>Trends in Cancer</i> , 2021 , 7, 293-300	12.5	2
20	Fitness variation in isogenic populations leads to a novel evolutionary mechanism for crossing fitness valleys. <i>Communications Biology</i> , 2018 , 1, 151	6.7	2
19	Topological isolation of developmental regulators in mammalian genomes. <i>Nature Communications</i> , 2021 , 12, 4897	17.4	2
18	DIFFpop: a stochastic computational approach to simulate differentiation hierarchies with single cell barcoding. <i>Bioinformatics</i> , 2019 , 35, 3849-3851	7.2	1
17	Estimating mono- and bi-phasic regression parameters using a mixture piecewise linear Bayesian hierarchical model. <i>PLoS ONE</i> , 2017 , 12, e0180756	3.7	1
16	Clonal Hematopoiesis Associated with Adverse Outcomes Following Autologous Stem Cell Transplantation for Non-Hodgkin Lymphoma. <i>Blood</i> , 2016 , 128, 986-986	2.2	1
15	FGFR3 protein expression and gene mutation in primary and metastatic urothelial carcinoma (UC) tumors.. <i>Journal of Clinical Oncology</i> , 2012 , 30, 4577-4577	2.2	1
14	Reconstructing the lineage histories and differentiation trajectories of individual cancer cells in JAK2-mutant myeloproliferative neoplasms		1
13	Epigenetic Dereglulation In Relapsed Acute Myeloid Leukemia. <i>Blood</i> , 2013 , 122, 2499-2499	2.2	1

12	Systematic tissue collection during clinical breast biopsy is feasible, safe and enables high-content translational analyses. <i>Npj Precision Oncology</i> , 2021 , 5, 85	9.8	1
11	Analyzing the association of SCNA boundaries with replication timing. <i>Nature Biotechnology</i> , 2012 , 30, 1045-1046	44.5	
10	Deciphering Clonal Evolution and Dissemination of Multiple Myeloma Cells In Vivo. <i>Blood</i> , 2018 , 132, 55-55	2.2	
9	Drug Sensitivity and Allele-specificity of First-line Osimertinib Resistance EGFR Mutations. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	
8	Meta-analysis of public microarray databases for prognostic and predictive gene signatures of late-stage ovarian cancer.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 5531-5531	2.2	
7	In Vivo Analysis of Clonal Evolution of Multiple Myeloma. <i>Blood</i> , 2016 , 128, 799-799	2.2	
6	Epigenetic Profiling of Primary DLBCLs Reveals Novel DNA Methylation-Based Clusters and New Underlying Mechanisms of Lymphomagenesis. <i>Blood</i> , 2011 , 118, 556-556	2.2	
5	External validation of somatic copy number alteration (SCNA) at chromosome 1q23.3 in advanced urothelial carcinoma (UC).. <i>Journal of Clinical Oncology</i> , 2012 , 30, 4585-4585	2.2	
4	Genomic characterization of metastatic urothelial carcinoma.. <i>Journal of Clinical Oncology</i> , 2013 , 31, 247-247	2.2	
3	Peroxisome proliferator-activated receptor gamma (PPARG) gene amplifications in urothelial carcinoma (UC).. <i>Journal of Clinical Oncology</i> , 2013 , 31, 279-279	2.2	
2	Mathematical modeling reveals alternative JAK inhibitor treatment in myeloproliferative neoplasms. <i>Haematologica</i> , 2020 , 105, e91-e94	6.6	
1	Designing optimal allocations for cancer screening using queuing network models. <i>PLoS Computational Biology</i> , 2022 , 18, e1010179	5	