

# Frederick Klauschen

## List of Publications by Year in descending order

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Version: 2024-02-01

93  
papers

7,543  
citations

117625

34  
h-index

56724

83  
g-index

97  
all docs

97  
docs citations

97  
times ranked

11999  
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence and pathology: From principles to practice and future applications in histomorphology and molecular profiling. <i>Seminars in Cancer Biology</i> , 2022, 84, 129-143.	9.6	41
2	Mucosal melanomas of different anatomic sites share a common global <sc>DNA</sc> methylation profile with cutaneous melanoma but show locationâ€dependent patterns of genetic and epigenetic alterations. <i>Journal of Pathology</i> , 2022, 256, 61-70.	4.5	12
3	Comparative investigation of cell cycle and immunomodulatory genes in mucosal and cutaneous melanomas: Preliminary data suggest a potential promising clinical role for p16 and the PD-1/PD-L1 axis. <i>Pathology Research and Practice</i> , 2022, 229, 153689.	2.3	1
4	Machine learning models predict the primary sites of head and neck squamous cell carcinoma metastases based on <sc>DNA</sc> methylation. <i>Journal of Pathology</i> , 2022, 256, 378-387.	4.5	19
5	VISTA in Soft Tissue Sarcomas: A Perspective for Immunotherapy?. <i>Cancers</i> , 2022, 14, 1006.	3.7	2
6	The singleâ€cell transcriptional landscape of lung carcinoid tumors. <i>International Journal of Cancer</i> , 2022, 150, 2058-2071.	5.1	7
7	Type 1 conventional dendritic cells maintain and guide the differentiation of precursors of exhausted Tâ€cells in distinct cellular niches. <i>Immunity</i> , 2022, 55, 656-670.e8.	14.3	41
8	AURKA is a prognostic biomarker for good overall survival in stage II colorectal cancer patients. <i>Pathology Research and Practice</i> , 2022, 235, 153936.	2.3	3
9	Biomarker-driven therapies for metastatic uveal melanoma: A prospective precision oncology feasibility study. <i>European Journal of Cancer</i> , 2022, 169, 146-155.	2.8	4
10	Patient-level proteomic network prediction by explainable artificial intelligence. <i>Npj Precision Oncology</i> , 2022, 6, .	5.4	11
11	BRAF-mutant metastatic colorectal cancer: Prognostic and predictive value of primary tumor locationâ€A pooled analysis of the AIO studies FIRE-1, CIOX, XELAVIRI, FIRE-3, and VOLFI.. <i>Journal of Clinical Oncology</i> , 2022, 40, 3576-3576.	1.6	2
12	DNA methylation-based machine learning classification distinguishes pleural mesothelioma from chronic pleuritis, pleural carcinosis, and pleomorphic lung carcinomas. <i>Lung Cancer</i> , 2022, 170, 105-113.	2.0	3
13	Hidden Variables in Deep Learning Digital Pathology and Their Potential to Cause Batch Effects: Prediction Model Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e23436.	4.3	36
14	Morphological and molecular breast cancer profiling through explainable machine learning. <i>Nature Machine Intelligence</i> , 2021, 3, 355-366.	16.0	72
15	Artificial Intelligence in Pathology. <i>Deutsches A&amp;#x0308;rzteblatt International</i> , 2021, 118, 194-204.	0.9	23
16	Hepatic Wnt1 Inducible Signaling Pathway Protein 1 (WISP-1/CCN4) Associates with Markers of Liver Fibrosis in Severe Obesity. <i>Cells</i> , 2021, 10, 1048.	4.1	7
17	Comprehensive micro-scaled proteome and phosphoproteome characterization of archived retrospective cancer repositories. <i>Nature Communications</i> , 2021, 12, 3576.	12.8	39
18	Clinicopathologic Features and Risk Factors of Proteinuria in Transplant Glomerulopathy. <i>Frontiers in Medicine</i> , 2021, 8, 666319.	2.6	1

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19	Peptide Signatures for Prognostic Markers of Pancreatic Cancer by MALDI Mass Spectrometry Imaging. <i>Biology</i> , 2021, 10, 1033.	2.8	6
20	DNA methylation profiling identifies two distinct subgroups in breast cancers with low hormone receptor expression, mainly associated with HER2 amplification status. <i>Clinical Epigenetics</i> , 2021, 13, 184.	4.1	2
21	Single-cell RNA sequencing reveals distinct tumor microenvironmental patterns in lung adenocarcinoma. <i>Oncogene</i> , 2021, 40, 6748-6758.	5.9	70
22	p130Cas Is Correlated with EREG Expression and a Prognostic Factor Depending on Colorectal Cancer Stage and Localization Reducing FOLFIRI Efficacy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12364.	4.1	3
23	High-protein diet more effectively reduces hepatic fat than low-protein diet despite lower autophagy and FGF21 levels. <i>Liver International</i> , 2020, 40, 2982-2997.	3.9	42
24	Multiclass cancer classification in fresh frozen and formalin-fixed paraffin-embedded tissue by DigiWest multiplex protein analysis. <i>Laboratory Investigation</i> , 2020, 100, 1288-1299.	3.7	2
25	Resolving challenges in deep learning-based analyses of histopathological images using explanation methods. <i>Scientific Reports</i> , 2020, 10, 6423.	3.3	97
26	Pemetrexed-Based Chemotherapy Is Inferior to Pemetrexed-Free Regimens in Thyroid Transcription Factor 1 (TTF-1)-Negative, EGFR/ALK-Negative Lung Adenocarcinoma: A Propensity Score Matched Pairs Analysis. <i>Clinical Lung Cancer</i> , 2020, 21, e607-e621.	2.6	32
27	Deep Learning for the Classification of Small-Cell and Non-Small-Cell Lung Cancer. <i>Cancers</i> , 2020, 12, 1604.	3.7	63
28	Support of a molecular tumour board by an evidence-based decision management system for precision oncology. <i>European Journal of Cancer</i> , 2020, 127, 41-51.	2.8	25
29	TP53 Mutations Predict Sensitivity to Adjuvant Gemcitabine in Patients with Pancreatic Ductal Adenocarcinoma: Next-Generation Sequencing Results from the CONKO-001 Trial. <i>Clinical Cancer Research</i> , 2020, 26, 3732-3739.	7.0	28
30	Interpretable Deep Neural Network to Predict Estrogen Receptor Status from Haematoxylin-Eosin Images. <i>Lecture Notes in Computer Science</i> , 2020, , 16-37.	1.3	5
31	Association of a STK11/KEAP1-mutation gene expression signature in lung adenocarcinoma with immune desertion in squamous cell carcinomas and mediation by NFE2L2 deregulation.. <i>Journal of Clinical Oncology</i> , 2020, 38, 3082-3082.	1.6	1
32	Immunohistochemical analysis of Bcl-2, nuclear S100A4, MITF and Ki67 for risk stratification of early-stage melanoma – A combined IHC score for melanoma risk stratification. <i>JDDG - Journal of the German Society of Dermatology</i> , 2019, 17, 800-808.	0.8	12
33	Immunologic Profiling of Mutational and Transcriptional Subgroups in Pediatric and Adult High-Grade Gliomas. <i>Cancer Immunology Research</i> , 2019, 7, 1401-1411.	3.4	35
34	Next generation sequencing of lung adenocarcinoma subtypes with intestinal differentiation reveals distinct molecular signatures associated with histomorphology and therapeutic options. <i>Lung Cancer</i> , 2019, 138, 43-51.	2.0	24
35	Machine learning analysis of DNA methylation profiles distinguishes primary lung squamous cell carcinomas from head and neck metastases. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	100
36	DNA methylation profiling reliably distinguishes pulmonary enteric adenocarcinoma from metastatic colorectal cancer. <i>Modern Pathology</i> , 2019, 32, 855-865.	5.5	36

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37	Clinical and analytical validation of Ki-67 in 9069 patients from IBCSG VIII and IX, BIG1-98 and GeparTrio trial: systematic modulation of interobserver variance in a comprehensive in silico ring trial. <i>Breast Cancer Research and Treatment</i> , 2019, 176, 557-568.	2.5	10
38	Clinical Impact of Rare and Compound Mutations of Epidermal Growth Factor Receptor in Patients With Non-Small-Cell Lung Cancer. <i>Clinical Lung Cancer</i> , 2019, 20, 350-362.e4.	2.6	10
39	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010.	5.1	76
40	Somatic genome alterations in relation to age in lung adenocarcinoma. <i>International Journal of Cancer</i> , 2019, 145, 2091-2099.	5.1	1
41	Mutational Diversity and Therapy Response in Breast Cancer: A Sequencing Analysis in the Neoadjuvant GeparSepto Trial. <i>Clinical Cancer Research</i> , 2019, 25, 3986-3995.	7.0	32
42	Human leucocyte antigen class I in hormone receptor-positive, HER2-negative breast cancer: association with response and survival after neoadjuvant chemotherapy. <i>Breast Cancer Research</i> , 2019, 21, 142.	5.0	21
43	Proteogenomic systems analysis identifies targeted therapy resistance mechanisms in EGFR-mutated lung cancer. <i>International Journal of Cancer</i> , 2019, 144, 545-557.	5.1	8
44	Systems proteogenomics for precision oncology. <i>Oncotarget</i> , 2019, 10, 692-693.	1.8	2
45	Clinical impact of comprehensive versus targeted genomic analysis for precision oncology.. <i>Journal of Clinical Oncology</i> , 2019, 37, e13033-e13033.	1.6	0
46	Precision oncology for the treatment of salivary gland tumors.. <i>Journal of Clinical Oncology</i> , 2019, 37, e17577-e17577.	1.6	0
47	Intratumoral morphological heterogeneity can be an indicator of genetic heterogeneity in colorectal cancer. <i>Experimental and Molecular Pathology</i> , 2018, 104, 76-81.	2.1	6
48	Sphingosine Kinase 1 Regulates Inflammation and Contributes to Acute Lung Injury in Pneumococcal Pneumonia via the Sphingosine-1-Phosphate Receptor 2. <i>Critical Care Medicine</i> , 2018, 46, e258-e267.	0.9	16
49	Targeted deep sequencing of effusion cytology samples is feasible, informs spatiotemporal tumor evolution, and has clinical and diagnostic utility. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 70-79.	2.8	19
50	Tumour-infiltrating lymphocytes and prognosis in different subtypes of breast cancer: a pooled analysis of 3771 patients treated with neoadjuvant therapy. <i>Lancet Oncology</i> , The, 2018, 19, 40-50.	10.7	1,327
51	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. <i>JCO Precision Oncology</i> , 2018, 2, 1-13.	3.0	20
52	Computational analysis reveals histotype-dependent molecular profile and actionable mutation effects across cancers. <i>Genome Medicine</i> , 2018, 10, 83.	8.2	8
53	Epidermal $\gamma$ T cells originate from yolk sac hematopoiesis and clonally self-renew in the adult. <i>Journal of Experimental Medicine</i> , 2018, 215, 2994-3005.	8.5	80
54	Somatic genome alterations in relation to age in lung squamous cell carcinoma. <i>Oncotarget</i> , 2018, 9, 32161-32172.	1.8	3

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55	Subgroup-specific immune and stromal microenvironment in medulloblastoma. <i>Oncolmmunology</i> , 2018, 7, e1462430.	4.6	77
56	Efficacy of a structured workflow for the interpretation of comprehensive genomic analysis data in clinical routine.. <i>Journal of Clinical Oncology</i> , 2018, 36, e24164-e24164.	1.6	1
57	Treatment of metastatic uveal melanoma (mUM) directed by a comprehensive molecular tumour analysis program (CMTA).. <i>Journal of Clinical Oncology</i> , 2018, 36, 9566-9566.	1.6	0
58	PD-L1 (CD274) copy number gain, expression, and immune cell infiltration as candidate predictors for response to immune checkpoint inhibitors in soft-tissue sarcoma. <i>Oncolmmunology</i> , 2017, 6, e1279777.	4.6	50
59	DNA copy number changes define spatial patterns of heterogeneity in colorectal cancer. <i>Nature Communications</i> , 2017, 8, 14093.	12.8	85
60	CD8+ T Cells Orchestrate pDC-XCR1+ Dendritic Cell Spatial and Functional Cooperativity to Optimize Priming. <i>Immunity</i> , 2017, 46, 205-219.	14.3	278
61	Mutation patterns in genes encoding interferon signaling and antigen presentation: A panâ€cancer survey with implications for the use of immune checkpoint inhibitors. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 651-659.	2.8	35
62	Expression patterns of CD168 correlate with the stage and grade of squamous cell carcinoma of head and neck. <i>Molecular and Clinical Oncology</i> , 2017, 6, 597-602.	1.0	5
63	Influence of mucinous and necrotic tissue in colorectal cancer samples on KRAS mutation analysis. <i>Pathology Research and Practice</i> , 2017, 213, 606-611.	2.3	3
64	T Cell Zone Resident Macrophages Silently Dispose of Apoptotic Cells in the Lymph Node. <i>Immunity</i> , 2017, 47, 349-362.e5.	14.3	107
65	Fibrosis in low-grade follicular lymphoma â€ a link to the TH2 immune reaction. <i>Leukemia and Lymphoma</i> , 2017, 58, 1190-1196.	1.3	7
66	Association of an APOBEC mutational signature, mutational load, and BRCAness with inflammation and PD-L1 expression in HNSCC.. <i>Journal of Clinical Oncology</i> , 2017, 35, e14613-e14613.	1.6	2
67	Methylation of RAD51B, XRCC3 and other homologous recombination genes is associated with expression of immune checkpoints and an inflammatory signature in squamous cell carcinoma of the head and neck, lung and cervix. <i>Oncotarget</i> , 2016, 7, 75379-75393.	1.8	27
68	Mutations in genes encoding <scp>PI3Kâ€AKT</scp> and <scp>MAPK</scp> signaling define anogenital papillary hidradenoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 113-119.	2.8	29
69	Standardized evaluation of tumor-infiltrating lymphocytes in breast cancer: results of the ring studies of the international immuno-oncology biomarker working group. <i>Modern Pathology</i> , 2016, 29, 1155-1164.	5.5	230
70	Panâ€cancer analysis of copy number changes in programmed deathâ€ligand 1 (PDâ€L1, CD274) â€ associations with gene expression, mutational load, and survival. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 626-639.	2.8	80
71	Clonal Proliferation and Stochastic Pruning Orchestrate Lymph Node Vasculature Remodeling. <i>Immunity</i> , 2016, 45, 877-888.	14.3	48
72	Copy number changes of clinically actionable genes in melanoma, nonâ€small cell lung cancer and colorectal cancerâ€ A survey across 822 routine diagnostic cases. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 821-833.	2.8	43

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73	loncopy: a novel method for calling copy number alterations in amplicon sequencing data including significance assessment. <i>Oncotarget</i> , 2016, 7, 13236-13247.	1.8	23
74	Association of methylation of homologous repair genes with expression of immune checkpoints in squamous cell carcinoma of head and neck, lung and cervix.. <i>Journal of Clinical Oncology</i> , 2016, 34, 11543-11543.	1.6	0
75	Collecting wisdom: Creating an evidence framework for personalized cancer therapy.. <i>Journal of Clinical Oncology</i> , 2016, 34, e23141-e23141.	1.6	0
76	Basket Trials: Just the End of the First Quarter. <i>Journal of Clinical Oncology</i> , 2015, 33, 2823-2824.	1.6	15
77	Distribution of <i>MED12</i> mutations in fibroadenomas and phyllodes tumors of the breast—implications for tumor biology and pathological diagnosis. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 444-452.	2.8	55
78	The DNA index as a prognostic tool in hilar cholangiocarcinoma. <i>Journal of Surgical Oncology</i> , 2015, 112, 214-218.	1.7	7
79	On Pixel-Wise Explanations for Non-Linear Classifier Decisions by Layer-Wise Relevance Propagation. <i>PLoS ONE</i> , 2015, 10, e0130140.	2.5	2,319
80	The landscape of metastatic progression patterns across major human cancers. <i>Oncotarget</i> , 2015, 6, 570-583.	1.8	208
81	Classical pathology and mutational load of breast cancer — integration of two worlds. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 225-238.	3.0	91
82	Robust Anti-viral Immunity Requires Multiple Distinct T Cell-Dendritic Cell Interactions. <i>Cell</i> , 2015, 162, 1322-1337.	28.9	299
83	Strategies for developing Ki67 as a useful biomarker in breast cancer. <i>Breast</i> , 2015, 24, S67-S72.	2.2	130
84	Histological tumor typing in the age of molecular profiling. <i>Pathology Research and Practice</i> , 2015, 211, 897-900.	2.3	10
85	ALK-FISH borderline cases in non-small cell lung cancer: Implications for diagnostics and clinical decision making. <i>Lung Cancer</i> , 2015, 90, 465-471.	2.0	36
86	Standardized Ki67 Diagnostics Using Automated Scoring—Clinical Validation in the GeparTrio Breast Cancer Study. <i>Clinical Cancer Research</i> , 2015, 21, 3651-3657.	7.0	85
87	Semiconductor sequencing: how many flows do you need?. <i>Bioinformatics</i> , 2015, 31, 1199-1203.	4.1	5
88	BRAF V600E-specific immunohistochemistry reveals low mutation rates in biliary tract cancer and restriction to intrahepatic cholangiocarcinoma. <i>Modern Pathology</i> , 2014, 27, 1028-1034.	5.5	96
89	Comprehensive analysis of clinico-pathological data reveals heterogeneous relations between atherosclerosis and cancer. <i>Journal of Clinical Pathology</i> , 2014, 67, 482-490.	2.0	13
90	T-Cell-Receptor-Dependent Signal Intensity Dominantly Controls CD4+ T Cell Polarization In Vivo. <i>Immunity</i> , 2014, 41, 63-74.	14.3	214

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91	Fate mapping reveals origin and dynamics of lymph node follicular dendritic cells. <i>Journal of Experimental Medicine</i> , 2014, 211, 1109-1122.	8.5	152
92	The combinatorial complexity of cancer precision medicine. <i>Oncoscience</i> , 2014, 1, 504-509.	2.2	48
93	Targeted ultra-deep sequencing reveals recurrent and mutually exclusive mutations of cancer genes in blastic plasmacytoid dendritic cell neoplasm. <i>Oncotarget</i> , 2014, 5, 6404-6413.	1.8	82