Frederick Klauschen

List of Publications by Year
in descending order

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	On Pixel-Wise Explanations for Non-Linear Classifier Decisions by Layer-Wise Relevance Propagation. PLoS ONE, 2015, 10, e0130140.	2.5	2,319
2	Tumour-infiltrating lymphocytes and prognosis in different subtypes of breast cancer: a pooled analysis of 3771 patients treated with neoadjuvant therapy. Lancet Oncology, The, 2018, 19, 40-50.	10.7	1,327
3	Robust Anti-viral Immunity Requires Multiple Distinct T Cell-Dendritic Cell Interactions. Cell, 2015, 162, 1322-1337.	28.9	299
4	CD8+ T Cells Orchestrate pDC-XCR1+ Dendritic Cell Spatial and Functional Cooperativity to Optimize Priming. Immunity, 2017, 46, 205-219.	14.3	278
5	Standardized evaluation of tumor-infiltrating lymphocytes in breast cancer: results of the ring studies of the international immuno-oncology biomarker working group. Modern Pathology, 2016, 29, 1155-1164.	5.5	230
6	T-Cell-Receptor-Dependent Signal Intensity Dominantly Controls CD4+ T Cell Polarization InÂVivo. Immunity, 2014, 41, 63-74.	14.3	214
7	The landscape of metastatic progression patterns across major human cancers. Oncotarget, 2015, 6, 570-583.	1.8	208
8	Fate mapping reveals origin and dynamics of lymph node follicular dendritic cells. Journal of Experimental Medicine, 2014, 211, 1109-1122.	8.5	152
9	Strategies for developing Ki67 as a useful biomarker in breast cancer. Breast, 2015, 24, S67-S72.	2.2	130
10	T Cell Zone Resident Macrophages Silently Dispose of Apoptotic Cells in the Lymph Node. Immunity, 2017, 47, 349-362.e5.	14.3	107
11	Machine learning analysis of DNA methylation profiles distinguishes primary lung squamous cell carcinomas from head and neck metastases. Science Translational Medicine, 2019, 11, .	12.4	100
12	Resolving challenges in deep learning-based analyses of histopathological images using explanation methods. Scientific Reports, 2020, 10, 6423.	3.3	97
13	BRAF V600E-specific immunohistochemistry reveals low mutation rates in biliary tract cancer and restriction to intrahepatic cholangiocarcinoma. Modern Pathology, 2014, 27, 1028-1034.	5.5	96
14	Classical pathology and mutational load of breast cancer â€" integration of two worlds. Journal of Pathology: Clinical Research, 2015, 1, 225-238.	3.0	91
15	Standardized Ki67 Diagnostics Using Automated Scoringâ€"Clinical Validation in the GeparTrio Breast Cancer Study. Clinical Cancer Research, 2015, 21, 3651-3657.	7.0	85
16	DNA copy number changes define spatial patterns of heterogeneity in colorectal cancer. Nature Communications, 2017, 8, 14093.	12.8	85
17	Targeted ultra-deep sequencing reveals recurrent and mutually exclusive mutations of cancer genes in blastic plasmacytoid dendritic cell neoplasm. Oncotarget, 2014, 5, 6404-6413.	1.8	82
18	Panâ€cancer analysis of copy number changes in programmed deathâ€ligand 1 (PDâ€Ł1, CD274) â€" associations with gene expression, mutational load, and survival. Genes Chromosomes and Cancer, 2016, 55, 626-639.	2.8	80

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19	Epidermal $\gamma\delta$ T cells originate from yolk sac hematopoiesis and clonally self-renew in the adult. Journal of Experimental Medicine, 2018, 215, 2994-3005.	8.5	80
20	Subgroup-specific immune and stromal microenvironment in medulloblastoma. OncoImmunology, 2018, 7, e1462430.	4.6	77
21	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76
22	Morphological and molecular breast cancer profiling through explainable machine learning. Nature Machine Intelligence, 2021, 3, 355-366.	16.0	72
23	Single-cell RNA sequencing reveals distinct tumor microenvironmental patterns in lung adenocarcinoma. Oncogene, 2021, 40, 6748-6758.	5.9	70
24	Deep Learning for the Classification of Small-Cell and Non-Small-Cell Lung Cancer. Cancers, 2020, 12, 1604.	3.7	63
25	Distribution of <i>MED12</i> mutations in fibroadenomas and phyllodes tumors of the breastâ€"implications for tumor biology and pathological diagnosis. Genes Chromosomes and Cancer, 2015, 54, 444-452.	2.8	55
26	PD-L1 (CD274) copy number gain, expression, and immune cell infiltration as candidate predictors for response to immune checkpoint inhibitors in soft-tissue sarcoma. OncoImmunology, 2017, 6, e1279777.	4.6	50
27	Clonal Proliferation and Stochastic Pruning Orchestrate Lymph Node Vasculature Remodeling. Immunity, 2016, 45, 877-888.	14.3	48
28	The combinatorial complexity of cancer precision medicine. Oncoscience, 2014, 1, 504-509.	2.2	48
29	Copy number changes of clinically actionable genes in melanoma, nonâ€small cell lung cancer and colorectal cancerâ€"A survey across 822 routine diagnostic cases. Genes Chromosomes and Cancer, 2016, 55, 821-833.	2.8	43
30	Highâ€protein diet more effectively reduces hepatic fat than lowâ€protein diet despite lower autophagy and FGF21 levels. Liver International, 2020, 40, 2982-2997.	3.9	42
31	Artificial intelligence and pathology: From principles to practice and future applications in histomorphology and molecular profiling. Seminars in Cancer Biology, 2022, 84, 129-143.	9.6	41
32	Type 1 conventional dendritic cells maintain and guide the differentiation of precursors of exhausted T cells in distinct cellular niches. Immunity, 2022, 55, 656-670.e8.	14.3	41
33	Comprehensive micro-scaled proteome and phosphoproteome characterization of archived retrospective cancer repositories. Nature Communications, 2021, 12, 3576.	12.8	39
34	ALK-FISH borderline cases in non-small cell lung cancer: Implications for diagnostics and clinical decision making. Lung Cancer, 2015, 90, 465-471.	2.0	36
35	DNA methylation profiling reliably distinguishes pulmonary enteric adenocarcinoma from metastatic colorectal cancer. Modern Pathology, 2019, 32, 855-865.	5.5	36
36	Hidden Variables in Deep Learning Digital Pathology and Their Potential to Cause Batch Effects: Prediction Model Study. Journal of Medical Internet Research, 2021, 23, e23436.	4.3	36

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37	Mutation patterns in genes encoding interferon signaling and antigen presentation: A pan‑cancer survey with implications for the use of immune checkpoint inhibitors. Genes Chromosomes and Cancer, 2017, 56, 651-659.	2.8	35
38	Immunologic Profiling of Mutational and Transcriptional Subgroups in Pediatric and Adult High-Grade Gliomas. Cancer Immunology Research, 2019, 7, 1401-1411.	3.4	35
39	Mutational Diversity and Therapy Response in Breast Cancer: A Sequencing Analysis in the Neoadjuvant GeparSepto Trial. Clinical Cancer Research, 2019, 25, 3986-3995.	7.0	32
40	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. Clinical Lung Cancer, 2020, 21, e607-e621.	2.6	32
41	Mutations in genes encoding PI3K‑AKT and MAPK signaling define anogenital papillary hidradenoma. Genes Chromosomes and Cancer, 2016, 55, 113-119.	2.8	29
42	TP53 Mutations Predict Sensitivity to Adjuvant Gemcitabine in Patients with Pancreatic Ductal Adenocarcinoma: Next-Generation Sequencing Results from the CONKO-001 Trial. Clinical Cancer Research, 2020, 26, 3732-3739.	7.0	28
43	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. Oncotarget, 2016, 7, 75379-75393.	1.8	27
44	Support of a molecular tumour board by an evidence-based decision management system for precision oncology. European Journal of Cancer, 2020, 127, 41-51.	2.8	25
45	Next generation sequencing of lung adenocarcinoma subtypes with intestinal differentiation reveals distinct molecular signatures associated with histomorphology and therapeutic options. Lung Cancer, 2019, 138, 43-51.	2.0	24
46	Artificial Intelligence in Pathology. Deutsches Ärzteblatt International, 2021, 118, 194-204.	0.9	23
47	Ioncopy: a novel method for calling copy number alterations in amplicon sequencing data including significance assessment. Oncotarget, 2016, 7, 13236-13247.	1.8	23
48	Human leucocyte antigen class I in hormone receptor-positive, HER2-negative breast cancer: association with response and survival after neoadjuvant chemotherapy. Breast Cancer Research, 2019, 21, 142.	5.0	21
49	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. JCO Precision Oncology, 2018, 2, 1-13.	3.0	20
50	Targeted deep sequencing of effusion cytology samples is feasible, informs spatiotemporal tumor evolution, and has clinical and diagnostic utility. Genes Chromosomes and Cancer, 2018, 57, 70-79.	2.8	19
51	Machine learning models predict the primary sites of head and neck squamous cell carcinoma metastases based on DNA methylation. Journal of Pathology, 2022, 256, 378-387.	4.5	19
52	Sphingosine Kinase 1 Regulates Inflammation and Contributes to Acute Lung Injury in Pneumococcal Pneumonia via the Sphingosine-1-Phosphate Receptor 2. Critical Care Medicine, 2018, 46, e258-e267.	0.9	16
53	Basket Trials: Just the End of the First Quarter. Journal of Clinical Oncology, 2015, 33, 2823-2824.	1.6	15
54	Comprehensive analysis of clinico-pathological data reveals heterogeneous relations between atherosclerosis and cancer. Journal of Clinical Pathology, 2014, 67, 482-490.	2.0	13

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55	Immunohistochemical analysis of Bclâ€2, nuclear S100A4, MITF and Ki67 for risk stratification of earlyâ€stage melanoma â€" A combined IHC score for melanoma risk stratification. JDDG - Journal of the German Society of Dermatology, 2019, 17, 800-808.	0.8	12
56	Mucosal melanomas of different anatomic sites share a common global <scp>DNA</scp> methylation profile with cutaneous melanoma but show locationâ€dependent patterns of genetic and epigenetic alterations. Journal of Pathology, 2022, 256, 61-70.	4.5	12
57	Patient-level proteomic network prediction by explainable artificial intelligence. Npj Precision Oncology, 2022, 6, .	5.4	11
58	Histological tumor typing in the age of molecular profiling. Pathology Research and Practice, 2015, 211, 897-900.	2.3	10
59	Clinical and analytical validation of Ki-67 in 9069 patients from IBCSG VIIIâ€‰+â€‰IX, BIG1-98 and GeparTrio trial: systematic modulation of interobserver variance in a comprehensive in silico ring trial. Breast Cancer Research and Treatment, 2019, 176, 557-568.	2.5	10
60	Clinical Impact of Rare and Compound Mutations of Epidermal Growth Factor Receptor in Patients With Nonâ€"Small-Cell Lung Cancer. Clinical Lung Cancer, 2019, 20, 350-362.e4.	2.6	10
61	Computational analysis reveals histotype-dependent molecular profile and actionable mutation effects across cancers. Genome Medicine, 2018, 10, 83.	8.2	8
62	Proteogenomic systems analysis identifies targeted therapy resistance mechanisms in EGFRâ€mutated lung cancer. International Journal of Cancer, 2019, 144, 545-557.	5.1	8
63	The DNA index as a prognostic tool in hilar cholangiocarcinoma. Journal of Surgical Oncology, 2015, 112, 214-218.	1.7	7
64	Fibrosis in low-grade follicular lymphoma â€" a link to the TH2 immune reaction. Leukemia and Lymphoma, 2017, 58, 1190-1196.	1.3	7
65	Hepatic Wnt1 Inducible Signaling Pathway Protein 1 (WISP-1/CCN4) Associates with Markers of Liver Fibrosis in Severe Obesity. Cells, 2021, 10, 1048.	4.1	7
66	The singleâ€cell transcriptional landscape of lung carcinoid tumors. International Journal of Cancer, 2022, 150, 2058-2071.	5.1	7
67	Intratumoral morphological heterogeneity can be an indicator of genetic heterogeneity in colorectal cancer. Experimental and Molecular Pathology, 2018, 104, 76-81.	2.1	6
68	Peptide Signatures for Prognostic Markers of Pancreatic Cancer by MALDI Mass Spectrometry Imaging. Biology, 2021, 10, 1033.	2.8	6
69	Semiconductor sequencing: how many flows do you need?. Bioinformatics, 2015, 31, 1199-1203.	4.1	5
70	Expression patterns of CD168 correlate with the stage and grade of squamous cell carcinoma of head and neck. Molecular and Clinical Oncology, 2017, 6, 597-602.	1.0	5
71	Interpretable Deep Neural Network to Predict Estrogen Receptor Status from Haematoxylin-Eosin Images. Lecture Notes in Computer Science, 2020, , 16-37.	1.3	5
72	Biomarker-driven therapies for metastatic uveal melanoma: A prospective precision oncology feasibility study. European Journal of Cancer, 2022, 169, 146-155.	2.8	4

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73	Influence of mucinous and necrotic tissue in colorectal cancer samples on KRAS mutation analysis. Pathology Research and Practice, 2017, 213, 606-611.	2.3	3
74	Somatic genome alterations in relation to age in lung squamous cell carcinoma. Oncotarget, 2018, 9, 32161-32172.	1.8	3
75	p130Cas Is Correlated with EREG Expression and a Prognostic Factor Depending on Colorectal Cancer Stage and Localization Reducing FOLFIRI Efficacy. International Journal of Molecular Sciences, 2021, 22, 12364.	4.1	3
76	AURKA is a prognostic biomarker for good overall survival in stage II colorectal cancer patients. Pathology Research and Practice, 2022, 235, 153936.	2.3	3
77	DNA methylation-based machine learning classification distinguishes pleural mesothelioma from chronic pleuritis, pleural carcinosis, and pleomorphic lung carcinomas. Lung Cancer, 2022, 170, 105-113.	2.0	3
78	Multiclass cancer classification in fresh frozen and formalin-fixed paraffin-embedded tissue by DigiWest multiplex protein analysis. Laboratory Investigation, 2020, 100, 1288-1299.	3.7	2
79	Association of an APOBEC mutational signature, mutational load, and BRCAness with inflammation and PD-L1 expression in HNSCC.. Journal of Clinical Oncology, 2017, 35, e14613-e14613.	1.6	2
80	DNA methylation profiling identifies two distinct subgroups in breast cancers with low hormone receptor expression, mainly associated with HER2 amplification status. Clinical Epigenetics, 2021, 13, 184.	4.1	2
81	Systems proteogenomics for precision oncology. Oncotarget, 2019, 10, 692-693.	1.8	2
82	VISTA in Soft Tissue Sarcomas: A Perspective for Immunotherapy?. Cancers, 2022, 14, 1006.	3.7	2
83	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.. Journal of Clinical Oncology, 2022, 40, 3576-3576.	1.6	2
84	Somatic genome alterations in relation to age in lung adenocarcinoma. International Journal of Cancer, 2019, 145, 2091-2099.	5.1	1
85	Clinicopathologic Features and Risk Factors of Proteinuria in Transplant Glomerulopathy. Frontiers in Medicine, 2021, 8, 666319.	2.6	1
86	Efficacy of a structured workflow for the interpretation of comprehensive genomic analysis data in clinical routine.. Journal of Clinical Oncology, 2018, 36, e24164-e24164.	1.6	1
87	Association of a STK11/KEAP1-mutation gene expression signature in lung adenocarcinoma with immune desertion in squamous cell carcinomas and mediation by NFE2L2 deregulation.. Journal of Clinical Oncology, 2020, 38, 3082-3082.	1.6	1
88	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. Pathology Research and Practice, 2022, 229, 153689.	2.3	1
89	Association of methylation of homologous repair genes with expression of immune checkpoints in squamous cell carcinoma of head and neck, lung and cervix.. Journal of Clinical Oncology, 2016, 34, 11543-11543.	1.6	0
90	Collecting wisdom: Creating an evidence framework for personalized cancer therapy.. Journal of Clinical Oncology, 2016, 34, e23141-e23141.	1.6	0

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91	Treatment of metastatic uveal melanoma (mUM) directed by a comprehensive molecular tumour analysis program (CMTA).. Journal of Clinical Oncology, 2018, 36, 9566-9566.	1.6	0
92	Clinical impact of comprehensive versus targeted genomic analysis for precision oncology.. Journal of Clinical Oncology, 2019, 37, e13033-e13033.	1.6	0
93	Precision oncology for the treatment of salivary gland tumors.. Journal of Clinical Oncology, 2019, 37, e17577-e17577.	1.6	0