

# Stephen H Kazakoff

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/747409/publications.pdf>

Version: 2024-02-01

39  
papers

9,660  
citations

236925

25  
h-index

302126

39  
g-index

41  
all docs

41  
docs citations

41  
times ranked

17310  
citing authors

#	ARTICLE	IF	CITATIONS
1	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. <i>Genome Medicine</i> , 2022, 14, 3.	8.2	16
2	Multioomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. <i>Cancer Cell</i> , 2022, 40, 88-102.e7.	16.8	64
3	Combined Inhibition of G9a and EZH2 Suppresses Tumor Growth via Synergistic Induction of IL24-Mediated Apoptosis. <i>Cancer Research</i> , 2022, 82, 1208-1221.	0.9	8
4	Injection site vaccinology of a recombinant vaccinia-based vector reveals diverse innate immune signatures. <i>PLoS Pathogens</i> , 2021, 17, e1009215.	4.7	13
5	IFN- $\gamma$ therapy prevents severe gastrointestinal graft-versus-host disease. <i>Blood</i> , 2021, 138, 722-737.	1.4	21
6	Chromatin interactome mapping at 139 independent breast cancer risk signals. <i>Genome Biology</i> , 2020, 21, 8.	8.8	27
7	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	12.8	102
8	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. <i>Npj Breast Cancer</i> , 2020, 6, 33.	5.2	19
9	APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. <i>Cancers</i> , 2020, 12, 1171.	3.7	28
10	Alterations in signaling pathways that accompany spontaneous transition to malignancy in a mouse model of BRAF mutant microsatellite stable colorectal cancer. <i>Neoplasia</i> , 2020, 22, 120-128.	5.3	14
11	Non-coding RNAs underlie genetic predisposition to breast cancer. <i>Genome Biology</i> , 2020, 21, 7.	8.8	21
12	Neoantigens Are Typically Associated with Intact HLA Class I Presentation in Early-Stage Follicular Lymphoma. <i>Blood</i> , 2020, 136, 37-38.	1.4	1
13	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	12.8	205
14	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 8, 269-290.	4.5	42
15	Molecular Genomic Profiling of Melanocytic Nevus. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1762-1768.	0.7	55
16	Diff-Quik Cytology Smears from Endobronchial Ultrasound Transbronchial Needle Aspiration Lymph Node Specimens as a Source of DNA for Next-Generation Sequencing Instead of Cell Blocks. <i>Respiration</i> , 2019, 97, 525-539.	2.6	25
17	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	1.5	19
18	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. <i>Cancers</i> , 2019, 11, 190.	3.7	39

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19	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. <i>International Journal of Cancer</i> , 2019, 144, 1049-1060.	5.1	54
20	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. <i>Bioinformatics</i> , 2019, 35, 2315-2317.	4.1	52
21	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. <i>Journal of Pathology</i> , 2019, 247, 214-227.	4.5	73
22	Characterization of a novel breast cancer cell line derived from a metastatic bone lesion of a breast cancer patient. <i>Breast Cancer Research and Treatment</i> , 2018, 170, 179-188.	2.5	5
23	Mixed ductal&lobular carcinomas: evidence for progression from ductal to lobular morphology. <i>Journal of Pathology</i> , 2018, 244, 460-468.	4.5	31
24	Jak2V617F and Dnmt3a loss cooperate to induce myelofibrosis through activated enhancer-driven inflammation. <i>Blood</i> , 2018, 132, 2707-2721.	1.4	56
25	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. <i>PLoS ONE</i> , 2018, 13, e0190264.	2.5	57
26	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	27.8	716
27	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
28	Interleukin-12 from CD103+ Batf3-Dependent Dendritic Cells Required for NK-Cell Suppression of Metastasis. <i>Cancer Immunology Research</i> , 2017, 5, 1098-1108.	3.4	98
29	Next-Generation Sequencing of Endobronchial Ultrasound Transbronchial Needle Aspiration Specimens in Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 388-391.	5.6	14
30	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. <i>American Journal of Human Genetics</i> , 2017, 101, 255-266.	6.2	77
31	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. <i>BMC Cancer</i> , 2017, 17, 396.	2.6	30
32	Hypermethylation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	1.3	174
33	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. <i>American Journal of Human Genetics</i> , 2016, 98, 1159-1169.	6.2	32
34	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	27.8	2,700
35	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015, 237, 363-378.	4.5	98
36	Whole&quot;genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	27.8	1,206

#	ARTICLE	IF	CITATIONS
37	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	27.8	2,132
38	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. <i>International Journal of Cancer</i> , 2014, 135, 1110-1118.	5.1	192
39	Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree <i>Pongamia pinnata</i> . <i>PLoS ONE</i> , 2012, 7, e51687.	2.5	73