

# Conrad Leonard

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

11,487  
citations

257357

24  
h-index

377752

34  
g-index

35  
all docs

35  
docs citations

35  
times ranked

18677  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. <i>Gastroenterology</i> , 2022, 162, 320-324.e4.	0.6	26
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.	7.7	64
3	qmotif: determination of telomere content from whole-genome sequence data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	5
4	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. <i>Genome Medicine</i> , 2022, 14, .	3.6	24
5	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. <i>Gastroenterology</i> , 2021, 160, 362-377.e13.	0.6	90
6	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, 155.	2.0	26
7	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. <i>Human Mutation</i> , 2021, 42, 530-536.	1.1	8
8	ROR1 and ROR2 expression in pancreatic cancer. <i>BMC Cancer</i> , 2021, 21, 1199.	1.1	4
9	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	5.8	102
10	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. <i>Npj Breast Cancer</i> , 2020, 6, 33.	2.3	19
11	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. <i>Nature Communications</i> , 2020, 11, 2408.	5.8	86
12	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020, 31, 107625.	2.9	78
13	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	5.8	205
14	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. <i>Annals of Oncology</i> , 2019, 30, 1071-1079.	0.6	64
15	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	0.7	19
16	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.	2.3	54
17	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. <i>Journal of Pathology</i> , 2019, 247, 214-227.	2.1	73
18	Running Genomic Analyses in the Cloud. <i>Studies in Health Technology and Informatics</i> , 2019, 266, 149-155.	0.2	1

#	ARTICLE	IF	CITATIONS
19	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	1.1	57
20	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
21	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
22	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	3.6	27
23	Hypermethylation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
24	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
25	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
26	Whole-genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
27	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
28	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
29	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	2.3	192
30	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
31	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
32	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
33	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	1.1	92