

# Scott Wood

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9356885/publications.pdf>

Version: 2024-02-01

20  
papers

4,632  
citations

516710

16  
h-index

752698

20  
g-index

21  
all docs

21  
docs citations

21  
times ranked

10045  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
2	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
3	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	27.8	716
4	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	12.8	205
5	Hypermethylation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	1.3	174
6	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	12.8	102
7	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
8	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. <i>Nature Communications</i> , 2020, 11, 2408.	12.8	86
9	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. <i>Journal of Pathology</i> , 2019, 247, 214-227.	4.5	73
10	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	2.5	67
11	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
12	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
13	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
14	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. <i>Nature Immunology</i> , 2020, 21, 1597-1610.	14.5	43
15	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, 155.	4.4	26
16	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	1.5	19
17	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. <i>Npj Breast Cancer</i> , 2020, 6, 33.	5.2	19
18	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. <i>Scientific Reports</i> , 2020, 10, 17687.	3.3	14

#	ARTICLE	IF	CITATIONS
19	qmotif: determination of telomere content from whole-genome sequence data. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	5
20	Running Genomic Analyses in the Cloud. <i>Studies in Health Technology and Informatics</i> , 2019, 266, 149-155.	0.3	1