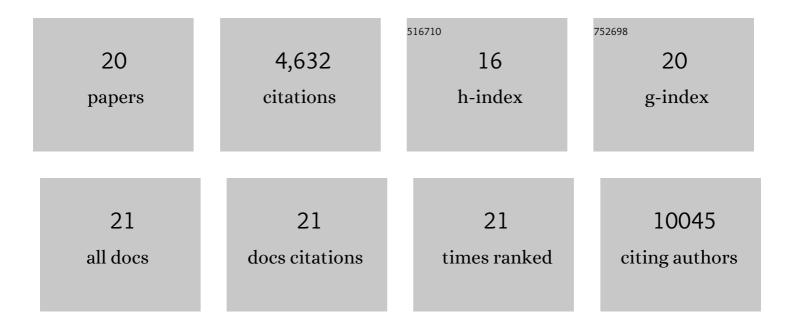
## Scott Wood

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9356885/publications.pdf Version: 2024-02-01



SCOTT WOOD

#	Article	IF	CITATIONS
1	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
2	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
3	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	27.8	716
4	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
5	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	1.3	174
6	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
7	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	4.5	98
8	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	12.8	86
9	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	4.5	73
10	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	2.5	67
11	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	16.8	64
12	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 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. International Journal of Cancer, 2019, 144, 1049-1060.	5.1	54
14	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. Nature Immunology, 2020, 21, 1597-1610.	14.5	43
15	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	4.4	26
16	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	1.5	19
17	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	5.2	19
18	Pathogenic germline variants are associated with poor survival in stage III/IV melanoma patients. Scientific Reports, 2020, 10, 17687.	3.3	14

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