

# Jonathan Foox

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

2,151  
citations

394421

19  
h-index

302126

39  
g-index

45  
all docs

45  
docs citations

45  
times ranked

4183  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. <i>Genome Biology</i> , 2022, 23, 2.	8.8	18
2	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	6.5	24
3	Betacoronavirus-specific alternate splicing. <i>Genomics</i> , 2022, 114, 110270.	2.9	12
4	Genomic Characterization of the Titan-like Cell Producing <i>Naganishia tulchinskyi</i> , the First Novel Eukaryote Isolated from the International Space Station. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 165.	3.5	5
5	Transcriptional response modules characterize IL-1 $\beta$ and IL-6 activity in COVID-19. <i>iScience</i> , 2021, 24, 101896.	4.1	28
6	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. <i>Science Advances</i> , 2021, 7, .	10.3	79
7	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	5.5	39
8	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. <i>Nature Communications</i> , 2021, 12, 1660.	12.8	132
9	The spatial landscape of lung pathology during COVID-19 progression. <i>Nature</i> , 2021, 593, 564-569.	27.8	249
10	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
11	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	8.8	29
12	Investigation of product-derived lymphoma following infusion of <i>piggyBac</i> -modified CD19 chimeric antigen receptor T cells. <i>Blood</i> , 2021, 138, 1391-1405.	1.4	87
13	Haplotype diversity and sequence heterogeneity of human telomeres. <i>Genome Research</i> , 2021, 31, 1269-1279.	5.5	19
14	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109839.	6.4	52
15	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	17.5	39
16	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. <i>Nature Biotechnology</i> , 2021, 39, 1129-1140.	17.5	69
17	Epigenetic Forensics for Suspect Identification and Age Prediction. <i>Forensic Genomics</i> , 2021, 1, 83-86.	0.5	1
18	DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation. <i>Genome Biology</i> , 2021, 22, 295.	8.8	6

#	ARTICLE	IF	CITATIONS
19	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. <i>Scientific Data</i> , 2021, 8, 296.	5.3	15
20	PRMT5 Inhibition Modulates E2F1 and P53 to Restore Cell Cycle Regulation and Drive DNA Damage Response in Ibrutinib-Resistant Mantle Cell Lymphoma. <i>Blood</i> , 2021, 138, 787-787.	1.4	0
21	Molecular Characterization of Increased Amplicon Lengths in SARS-CoV-2 Reverse Transcription Loop-Mediated Isothermal Amplification Assays. <i>Journal of Biomolecular Techniques</i> , 2021, 32, 199-205.	1.5	2
22	The SEQC2 epigenomics quality control (EpiQC) study. <i>Genome Biology</i> , 2021, 22, 332.	8.8	20
23	Comparative Analysis of Single-Cell RNA Sequencing Platforms and Methods. <i>Journal of Biomolecular Techniques</i> , 2021, 32, 3fc1f5fe.3eccea01.	1.5	5
24	Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration. <i>Cell</i> , 2020, 183, 1162-1184.	28.9	185
25	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. <i>Cell</i> , 2020, 183, 1185-1201.e20.	28.9	161
26	Clonal Hematopoiesis Before, During, and After Human Spaceflight. <i>Cell Reports</i> , 2020, 33, 108458.	6.4	30
27	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. <i>IScience</i> , 2020, 23, 101844.	4.1	31
28	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. <i>Nature Medicine</i> , 2020, 26, 1609-1615.	30.7	255
29	Temporal Telomere and DNA Damage Responses in the Space Radiation Environment. <i>Cell Reports</i> , 2020, 33, 108435.	6.4	40
30	Illuminating Genetic Mysteries of the Dead Sea Scrolls. <i>Cell</i> , 2020, 181, 1218-1231.e27.	28.9	10
31	Identification of Radioresponsive Genes in Esophageal Cancer from Longitudinal and Single Cell Exome Sequencing. <i>International Journal of Radiation Oncology Biology Physics</i> , 2020, 108, 1103-1114.	0.8	11
32	Applying evolutionary genetics to developmental toxicology and risk assessment. <i>Reproductive Toxicology</i> , 2017, 69, 174-186.	2.9	15
33	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017, 18, 182.	8.8	260
34	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , 2017, 28, 31-39.	1.5	53
35	Data for constructing insect genome content matrices for phylogenetic analysis and functional annotation. <i>Data in Brief</i> , 2016, 6, 279-281.	1.0	2
36	Insect genome content phylogeny and functional annotation of core insect genomes. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 224-232.	2.7	11

#	ARTICLE	IF	CITATIONS
37	Multiplexed pyrosequencing of nine sea anemone (Cnidaria: Anthozoa: Hexacorallia: Actiniaria) mitochondrial genomes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2826-2832.	0.7	21