

# Jason P Ross

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8745605/publications.pdf>

Version: 2024-02-01

22  
papers

1,036  
citations

623734

14  
h-index

677142

22  
g-index

23  
all docs

23  
docs citations

23  
times ranked

2190  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Methylation Cancer Biomarkers: Translation to the Clinic. <i>Frontiers in Genetics</i> , 2019, 10, 1150.	2.3	301
2	A panel of genes methylated with high frequency in colorectal cancer. <i>BMC Cancer</i> , 2014, 14, 54.	2.6	138
3	Hypomethylation of repeated DNA sequences in cancer. <i>Epigenomics</i> , 2010, 2, 245-269.	2.1	105
4	Cpipe: a shared variant detection pipeline designed for diagnostic settings. <i>Genome Medicine</i> , 2015, 7, 68.	8.2	78
5	Microbial biodiversity in a Malaysian oil field and a systematic comparison with oil reservoirs worldwide. <i>Archives of Microbiology</i> , 2012, 194, 513-523.	2.2	49
6	Risk-conscious correction of batch effects: maximising information extraction from high-throughput genomic datasets. <i>BMC Bioinformatics</i> , 2016, 17, 332.	2.6	49
7	Evaluation of Methylation Biomarkers for Detection of Circulating Tumor DNA and Application to Colorectal Cancer. <i>Genes</i> , 2016, 7, 125.	2.4	47
8	<i>CAHM</i> , a long non-coding RNA gene hypermethylated in colorectal neoplasia. <i>Epigenetics</i> , 2014, 9, 1071-1082.	2.7	41
9	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020, 12, 105.	8.2	41
10	STaRRRT: a table of short tandem repeats in regulatory regions of the human genome. <i>BMC Genomics</i> , 2013, 14, 795.	2.8	33
11	Mother's child transmission of epigenetic information by tunable polymorphic imprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11970-E11977.	7.1	33
12	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , 2019, 9, 9511.	3.3	24
13	Recombinant mammalian DNA methyltransferase activity on model transcriptional gene silencing short RNA-DNA heteroduplex substrates. <i>Biochemical Journal</i> , 2010, 432, 323-332.	3.7	20
14	Epigenetic aging in newborns: role of maternal diet. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 555-561.	4.7	20
15	The Varied Roles of Nuclear Argonaute-Small RNA Complexes and Avenues for Therapy. <i>Molecular Therapy - Nucleic Acids</i> , 2014, 3, e203.	5.1	14
16	Evidence of linkage to chromosomes 10p15.3-p15.1, 14q24.3-q31.1 and 9q33.3-q34.3 in non-syndromic colorectal cancer families. <i>European Journal of Human Genetics</i> , 2012, 20, 91-96.	2.8	11
17	COBRA-Seq: Sensitive and Quantitative Methylome Profiling. <i>Genes</i> , 2015, 6, 1140-1163.	2.4	10
18	Identification of differentially methylated regions using streptavidin bisulfite ligand methylation enrichment (SuBLiME), a new method to enrich for methylated DNA prior to deep bisulfite genomic sequencing. <i>Epigenetics</i> , 2013, 8, 113-127.	2.7	7

#	ARTICLE	IF	CITATIONS
19	Maternal dietary fatty acid composition and newborn epigenetic aging—a geometric framework approach. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 118-127.	4.7	7
20	An association between the PTGS2 rs5275 polymorphism and colorectal cancer risk in families with inherited non-syndromic predisposition. <i>European Journal of Human Genetics</i> , 2013, 21, 1389-1395.	2.8	6
21	Little evidence for association between the TGFBR1*6A variant and colorectal cancer: a family-based association study on non-syndromic family members from Australia and Spain. <i>BMC Cancer</i> , 2014, 14, 475.	2.6	1
22	Helper-Dependent Chain Reaction (HDCR) for Selective Amplification of Methylated DNA Sequences. <i>Methods in Molecular Biology</i> , 2018, 1708, 587-601.	0.9	1