

# 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

706676

14  
h-index

759306

22  
g-index

23  
all docs

23  
docs citations

23  
times ranked

2351  
citing authors

#	ARTICLE	IF	CITATIONS
1	Maternal dietary fatty acid composition and newborn epigenetic aging—a geometric framework approach. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 118-127.	2.2	7
2	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020, 12, 105.	3.6	41
3	Epigenetic aging in newborns: role of maternal diet. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 555-561.	2.2	20
4	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , 2019, 9, 9511.	1.6	24
5	DNA Methylation Cancer Biomarkers: Translation to the Clinic. <i>Frontiers in Genetics</i> , 2019, 10, 1150.	1.1	301
6	Helper-Dependent Chain Reaction (HDCR) for Selective Amplification of Methylated DNA Sequences. <i>Methods in Molecular Biology</i> , 2018, 1708, 587-601.	0.4	1
7	Mother-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.	3.3	33
8	Evaluation of Methylation Biomarkers for Detection of Circulating Tumor DNA and Application to Colorectal Cancer. <i>Genes</i> , 2016, 7, 125.	1.0	47
9	Risk-conscious correction of batch effects: maximising information extraction from high-throughput genomic datasets. <i>BMC Bioinformatics</i> , 2016, 17, 332.	1.2	49
10	Cpipe: a shared variant detection pipeline designed for diagnostic settings. <i>Genome Medicine</i> , 2015, 7, 68.	3.6	78
11	COBRA-Seq: Sensitive and Quantitative Methylome Profiling. <i>Genes</i> , 2015, 6, 1140-1163.	1.0	10
12	<i>CAHM</i> , a long non-coding RNA gene hypermethylated in colorectal neoplasia. <i>Epigenetics</i> , 2014, 9, 1071-1082.	1.3	41
13	A panel of genes methylated with high frequency in colorectal cancer. <i>BMC Cancer</i> , 2014, 14, 54.	1.1	138
14	The Varied Roles of Nuclear Argonaute-Small RNA Complexes and Avenues for Therapy. <i>Molecular Therapy - Nucleic Acids</i> , 2014, 3, e203.	2.3	14
15	Little evidence for association between the <i>TGFB1</i> *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.	1.1	1
16	An association between the <i>PTGS2</i> rs5275 polymorphism and colorectal cancer risk in families with inherited non-syndromic predisposition. <i>European Journal of Human Genetics</i> , 2013, 21, 1389-1395.	1.4	6
17	STARRRT: a table of short tandem repeats in regulatory regions of the human genome. <i>BMC Genomics</i> , 2013, 14, 795.	1.2	33
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.	1.3	7

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19	Evidence of linkage to chromosomes 10p15.3â€“p15.1, 14q24.3â€“q31.1 and 9q33.3â€“q34.3 in non-syndromic colorectal cancer families. <i>European Journal of Human Genetics</i> , 2012, 20, 91-96.	1.4	11
20	Microbial biodiversity in a Malaysian oil field and a systematic comparison with oil reservoirs worldwide. <i>Archives of Microbiology</i> , 2012, 194, 513-523.	1.0	49
21	Recombinant mammalian DNA methyltransferase activity on model transcriptional gene silencing short RNAâ€“DNA heteroduplex substrates. <i>Biochemical Journal</i> , 2010, 432, 323-332.	1.7	20
22	Hypomethylation of repeated DNA sequences in cancer. <i>Epigenomics</i> , 2010, 2, 245-269.	1.0	105