

France Gagnon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10950079/publications.pdf>

Version: 2024-02-01

22
papers

1,632
citations

687335

13
h-index

713444

21
g-index

22
all docs

22
docs citations

22
times ranked

4338
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
2	Statistical power in COVID-19 case-control host genomic study design. <i>Genome Medicine</i> , 2020, 12, 115.	8.2	7
3	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , 2018, 132, 1842-1850.	1.4	16
4	Genome-wide association study with additional genetic and post-transcriptional analyses reveals novel regulators of plasma factor XI levels. <i>Human Molecular Genetics</i> , 2017, 26, ddw401.	2.9	35
5	Leveraging cell type specific regulatory regions to detect SNPs associated with tissue factor pathway inhibitor plasma levels. <i>Genetic Epidemiology</i> , 2017, 41, 455-466.	1.3	1
6	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. <i>Epigenomics</i> , 2017, 9, 1403-1422.	2.1	6
7	Blood triglyceride levels are associated with DNA methylation at the serine metabolism gene PHGDH. <i>Scientific Reports</i> , 2017, 7, 11207.	3.3	32
8	Sex-specific effect of CPB2 Ala147Thr but not Thr325Ile variants on the risk of venous thrombosis: A comprehensive meta-analysis. <i>PLoS ONE</i> , 2017, 12, e0177768.	2.5	5
9	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	2.5	10
10	Association of the <i>APOE-ε4</i> allele with outcome of traumatic brain injury in children and youth: a meta-analysis and meta-regression. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2016, 87, 433-440.	1.9	44
11	Thrombin Generation Potential and Whole-Blood DNA methylation. <i>Thrombosis Research</i> , 2015, 135, 561-564.	1.7	7
12	Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. <i>Nature Communications</i> , 2015, 6, 6326.	12.8	115
13	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.	6.2	222
14	Robust validation of methylation levels association at CPT1A locus with lipid plasma levels. <i>Journal of Lipid Research</i> , 2014, 55, 1189-1191.	4.2	32
15	DNA methylation and body-mass index: a genome-wide analysis. <i>Lancet, The</i> , 2014, 383, 1990-1998.	13.7	686
16	Genome-Wide Investigation of DNA Methylation Marks Associated with FV Leiden Mutation. <i>PLoS ONE</i> , 2014, 9, e108087.	2.5	7
17	The Factor XII ϵ 4 Variant and Risk of Common Thrombotic Disorders: A HuGE Review and Meta-Analysis of Evidence From Observational Studies. <i>American Journal of Epidemiology</i> , 2011, 173, 136-144.	3.4	21
18	Factor XIII Val34Leu Variant Is Protective against Venous Thromboembolism: A HuGE Review and Meta-Analysis. <i>American Journal of Epidemiology</i> , 2006, 164, 101-109.	3.4	84

#	ARTICLE	IF	CITATIONS
19	Genome scan for quantitative trait loci influencing HDL levels: evidence for multilocus inheritance in familial combined hyperlipidemia. <i>Human Genetics</i> , 2005, 117, 494-505.	3.8	21
20	Factor XIII Val34Leu Polymorphism and the Risk of Myocardial Infarction: A Meta-Analysis.. <i>Blood</i> , 2005, 106, 1637-1637.	1.4	0
21	Low-Density Lipoprotein Particle Size Loci in Familial Combined Hyperlipidemia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004, 24, 1942-1950.	2.4	37
22	Evidence of linkage of HDL level variation to APOC3 in two samples with different ascertainment. <i>Human Genetics</i> , 2003, 113, 522-533.	3.8	26