

Dylan AÃssi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5199979/publications.pdf>

Version: 2024-02-01

18
papers

1,496
citations

933447

10
h-index

888059

17
g-index

23
all docs

23
docs citations

23
times ranked

4141
citing authors

#	ARTICLE	IF	CITATIONS
1	Common and Rare 5â€™UTR Variants Altering Upstream Open Reading Frames in Cardiovascular Genomics. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 841032.	2.4	9
2	CRIP1 expression in monocytes related to hypertension. <i>Clinical Science</i> , 2021, 135, 911-924.	4.3	5
3	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
4	Epigenome-wide association study identifies DNA methylation markers for asthma remission in whole blood and nasal epithelium. <i>Clinical and Translational Allergy</i> , 2020, 10, 60.	3.2	12
5	bioSyntax: syntax highlighting for computational biology. <i>BMC Bioinformatics</i> , 2018, 19, 303.	2.6	2
6	DNA methylation and serum total immunoglobulin E (IgE) levels: a methylome-wide association study in adults with asthma. , 2018, , .		0
7	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	8.8	71
8	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. <i>Epigenomics</i> , 2017, 9, 1403-1422.	2.1	6
9	Blood triglyceride levels are associated with DNA methylation at the serine metabolism gene PHGDH. <i>Scientific Reports</i> , 2017, 7, 11207.	3.3	32
10	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
11	DNA methylation and lung function: an epigenome-wide association study. , 2017, , .		0
12	Single nucleotide polymorphisms in an intergenic chromosome 2q region associated with tissue factor pathway inhibitor plasma levels and venous thromboembolism. <i>Journal of Thrombosis and Haemostasis</i> , 2016, 14, 1960-1970.	3.8	3
13	Thrombin Generation Potential and Whole-Blood DNA methylation. <i>Thrombosis Research</i> , 2015, 135, 561-564.	1.7	7
14	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
15	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
16	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
17	DNA methylation and body-mass index: a genome-wide analysis. <i>Lancet, The</i> , 2014, 383, 1990-1998.	13.7	686
18	Genome-Wide Investigation of DNA Methylation Marks Associated with FV Leiden Mutation. <i>PLoS ONE</i> , 2014, 9, e108087.	2.5	7