

# 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

932766

10  
h-index

887659

17  
g-index

23  
all docs

23  
docs citations

23  
times ranked

4141  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation and body-mass index: a genome-wide analysis. <i>Lancet</i> , The, 2014, 383, 1990-1998.	6.3	686
2	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.	2.6	222
3	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
4	Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. <i>Nature Communications</i> , 2015, 6, 6326.	5.8	115
5	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.	3.8	71
6	Robust validation of methylation levels association at CPT1A locus with lipid plasma levels. <i>Journal of Lipid Research</i> , 2014, 55, 1189-1191.	2.0	32
7	Blood triglyceride levels are associated with DNA methylation at the serine metabolism gene PHGDH. <i>Scientific Reports</i> , 2017, 7, 11207.	1.6	32
8	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.	1.4	12
9	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	1.1	10
10	Common and Rare 5â€™UTR Variants Altering Upstream Open Reading Frames in Cardiovascular Genomics. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 841032.	1.1	9
11	Thrombin Generation Potential and Whole-Blood DNA methylation. <i>Thrombosis Research</i> , 2015, 135, 561-564.	0.8	7
12	Genome-Wide Investigation of DNA Methylation Marks Associated with FV Leiden Mutation. <i>PLoS ONE</i> , 2014, 9, e108087.	1.1	7
13	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. <i>Epigenomics</i> , 2017, 9, 1403-1422.	1.0	6
14	CRIP1 expression in monocytes related to hypertension. <i>Clinical Science</i> , 2021, 135, 911-924.	1.8	5
15	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.	1.9	3
16	bioSyntax: syntax highlighting for computational biology. <i>BMC Bioinformatics</i> , 2018, 19, 303.	1.2	2
17	DNA methylation and lung function: an epigenome-wide association study. , 2017, , .		0
18	DNA methylation and serum total immunoglobulin E (IgE) levels: a methylome-wide association study in adults with asthma. , 2018, , .		0