Raili Ermel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3700918/publications.pdf

Version: 2024-02-01

16 papers	1,773 citations	1040056 9 h-index	1058476 14 g-index
20 all docs	20 docs citations	20 times ranked	4686 citing authors

#	Article	IF	Citations
1	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
2	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. Basic Research in Cardiology, 2022, 117, 6.	5.9	22
3	Integrative Prioritization of Causal Genes for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003365.	3.6	11
4	The HDAC9-associated risk locus promotes coronary artery disease by governing TWIST1. PLoS Genetics, 2022, 18, e1010261.	3.5	2
5	<scp>European Society of Cardiology Working Group</scp> on Adult Congenital Heart Disease and <scp>Study Group for Adult Congenital Heart Care in Central and South Eastern European Countries</scp> consensus paper: current status, provision gaps and investment required. European Journal of Heart Failure, 2021, 23, 445-453.	7.1	9
6	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
7	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. Journal of Human Genetics, 2021, 66, 625-636.	2.3	40
8	Multiple independent mechanisms link gene polymorphisms in the region of ZEB2 with risk of coronary artery disease. Atherosclerosis, 2020, 311, 20-29.	0.8	9
9	OR09-04 Common Genetic Variants Associated with SERPINA6 Expression in Liver Influence Cortisol-Responsive Transcriptional Networks in Human Adipose Tissue. Journal of the Endocrine Society, 2020, 4, .	0.2	0
10	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. BMC Medical Genomics, 2019, 12, 108.	1.5	8
11	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	21.4	592
12	Global analysis of A-to-I RNA editing reveals association with common disease variants. PeerJ, 2018, 6, e4466.	2.0	21
13	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
14	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	12.6	241
15	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. Cell Systems, 2016, 2, 196-208.	6.2	120
16	Expression Quantitative Trait Loci Acting Across Multiple Tissues Are Enriched in Inherited Risk for Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2015, 8, 305-315.	5.1	39