AmÃ©lie C Pinard

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8082504/publications.pdf

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18	890	840776 11	888059 17
papers	citations	h-index	g-index

20	20	20	2042
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Preventing Acute Aortic Dissections: The Power of Familial Screening and Risk Assessment. Journal of the American Heart Association, 2022, 11, e025441.	3.7	1
2	Association of De Novo RNF213 Variants With Childhood Onset Moyamoya Disease and Diffuse Occlusive Vasculopathy. Neurology, 2021, 96, e1783-e1791.	1.1	21
3	Update on the genetic risk for thoracic aortic aneurysms and acute aortic dissections: implications for clinical care. Journal of Cardiovascular Surgery, 2021, 62, 203-210.	0.6	11
4	DIAPH1 Variants in Nonâ€“East Asian Patients With Sporadic Moyamoya Disease. JAMA Neurology, 2021, 78, 993.	9.0	33
5	The pleiotropy associated with de novo variants in CHD4, CNOT3, and SETD5 extends to moyamoya angiopathy. Genetics in Medicine, 2020, 22, 427-431.	2.4	34
6	Rare deleterious variants of NOTCH1, GATA4, SMAD6, and ROBO4 are enriched in BAV with early onset complications but not in BAV with heritable thoracic aortic disease. Molecular Genetics & Genomic Medicine, 2020, 8, e1406.	1.2	17
7	Piezo1 is required for outflow tract and aortic valve development.. Journal of Molecular and Cellular Cardiology, 2020, 143, 51-62.	1.9	44
8	Genetics of Thoracic and Abdominal Aortic Diseases. Circulation Research, 2019, 124, 588-606.	4.5	253
9	A genome-wide search for new imprinted genes in the human placenta identifies DSCAM as the first imprinted gene on chromosome 21. European Journal of Human Genetics, 2019, 27, 49-60.	2.8	8
10	LTBP3 Pathogenic Variants Predispose Individuals to Thoracic Aortic Aneurysms and Dissections. American Journal of Human Genetics, 2018, 102, 706-712.	6.2	51
11	Analysis of HOXB1 gene in a cohort of patients with sporadic ventricular septal defect. Molecular Biology Reports, 2018, 45, 1507-1513.	2.3	0
12	UMDâ€Predictor: A Highâ€Throughput Sequencing Compliant System for Pathogenicity Prediction of any Human cDNA Substitution. Human Mutation, 2016, 37, 439-446.	2.5	104
13	Actionable Genes, Core Databases, and Locus-Specific Databases. Human Mutation, 2016, 37, 1299-1307.	2.5	6
14	WES/WGS Reporting of Mutations from Cardiovascular â€œActionableâ€•Genes in Clinical Practice: A Key Role for UMD Knowledgebases in the Era of Big Databases. Human Mutation, 2016, 37, 1308-1317.	2.5	5
15	An uncommon cause of tricuspid regurgitation: three-dimensional echocardiographic incremental value, surgical and genetic insights. European Journal of Cardio-thoracic Surgery, 2016, 50, 180-182.	1.4	1
16	The revised ghent nosology; reclassifying isolated ectopia lentis. Clinical Genetics, 2015, 87, 284-287.	2.0	41
17	Comparative genomics of emerging pathogens in the Candida glabrata clade. BMC Genomics, 2013, 14, 623.	2.8	174
18	A genome-wide approach reveals novel imprinted genes expressed in the human placenta. Epigenetics, 2012, 7, 1079-1090.	2.7	81