

# Na Zhu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11607071/publications.pdf>

Version: 2024-02-01

13  
papers

806  
citations

840776

11  
h-index

1125743

13  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1516  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayesian Inference Associates Rare <i>KDR</i> Variants With Specific Phenotypes in Pulmonary Arterial Hypertension. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, .	3.6	29
2	Rare variant analysis of 4241 pulmonary arterial hypertension cases from an international consortium implicates <i>FBLN2</i> , <i>PDGFD</i> , and rare de novo variants in PAH. <i>Genome Medicine</i> , 2021, 13, 80.	8.2	43
3	Novel Mutations and Decreased Expression of the Epigenetic Regulator <i>TET2</i> in Pulmonary Arterial Hypertension. <i>Circulation</i> , 2020, 141, 1986-2000.	1.6	75
4	PEDIA: prioritization of exome data by image analysis. <i>Genetics in Medicine</i> , 2019, 21, 2807-2814.	2.4	58
5	Novel risk genes and mechanisms implicated by exome sequencing of 2572 individuals with pulmonary arterial hypertension. <i>Genome Medicine</i> , 2019, 11, 69.	8.2	86
6	Exome Sequencing in Children With Pulmonary Arterial Hypertension Demonstrates Differences Compared With Adults. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001887.	3.6	104
7	De novo variants in congenital diaphragmatic hernia identify <i>MYRF</i> as a new syndrome and reveal genetic overlaps with other developmental disorders. <i>PLoS Genetics</i> , 2018, 14, e1007822.	3.5	79
8	Loss-of-Function <i>ABCC8</i> Mutations in Pulmonary Arterial Hypertension. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002087.	3.6	62
9	Rare variants in <i>SOX17</i> are associated with pulmonary arterial hypertension with congenital heart disease. <i>Genome Medicine</i> , 2018, 10, 56.	8.2	112
10	The Genomic Birthday Paradox: How Much Is Enough?. <i>Human Mutation</i> , 2015, 36, 989-997.	2.5	13
11	Strategies to improve the performance of rare variant association studies by optimizing the selection of controls. <i>Bioinformatics</i> , 2015, 31, btv457.	4.1	0
12	Homozygous and Compound-Heterozygous Mutations in <i>TGDS</i> Cause Catel-Manzke Syndrome. <i>American Journal of Human Genetics</i> , 2014, 95, 763-770.	6.2	37
13	<i>PGAP2</i> Mutations, Affecting the GPI-Anchor-Synthesis Pathway, Cause Hyperphosphatasia with Mental Retardation Syndrome. <i>American Journal of Human Genetics</i> , 2013, 92, 584-589.	6.2	98