Lili Hao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5922360/publications.pdf

Version: 2024-02-01

		1306789	1281420	
11	119	7	11	
papers	citations	h-index	g-index	
11	11	11	199	
all docs	docs citations	times ranked	citing authors	

#	Article	IF	Citations
1	Expression Profiles of Exosomal MicroRNAs Derived from Cerebrospinal Fluid in Patients with Congenital Hydrocephalus Determined by MicroRNA Sequencing. Disease Markers, 2022, 2022, 1-16.	0.6	3
2	<i>WDR62</i> variants contribute to congenital heart disease by inhibiting cardiomyocyte proliferation. Clinical and Translational Medicine, 2022, 12, .	1.7	3
3	Long non-coding RNA SAP30-2:1 is downregulated in congenital heart disease and regulates cell proliferation by targeting HAND2. Frontiers of Medicine, 2021, 15, 91-100.	1.5	7
4	Hypermethylationâ€mediated downâ€regulation of lncRNA TBX5â€AS1:2 in Tetralogy of Fallot inhibits cell proliferation by reducingTBX5expression. Journal of Cellular and Molecular Medicine, 2020, 24, 6472-6484.	1.6	16
5	Early onset developmental delay and epilepsy in pediatric patients with WDR45 variants. European Journal of Medical Genetics, 2019, 62, 149-160.	0.7	16
6	Two novel <i>ANK1</i> lossâ€ofâ€function mutations in Chinese families with hereditary spherocytosis. Journal of Cellular and Molecular Medicine, 2019, 23, 4454-4463.	1.6	10
7	The Novel Pathogenic Mutation c.849dupT in <i>BRCA2</i> Contributes to the Nonsense-Mediated mRNA Decay of <i>BRCA2</i> in Familial Breast Cancer. Journal of Breast Cancer, 2018, 21, 330.	0.8	1
8	The roles of SMYD4 in epigenetic regulation of cardiac development in zebrafish. PLoS Genetics, 2018, 14, e1007578.	1.5	17
9	Multiple gene variations contributed to congenital heart disease via GATA family transcriptional regulation. Journal of Translational Medicine, 2017, 15, 69.	1.8	22
10	Hypomethylation and decreased expression of <i>BRG1</i> in the myocardium of patients with congenital heart disease. Birth Defects Research, 2017, 109, 1183-1195.	0.8	14
11	Exome sequencing identifies a mutation in TMC1 as a novel cause of autosomal recessive nonsyndromic hearing loss. Journal of Translational Medicine, 2016, 14, 29.	1.8	10