Gavin Chapman

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4077891/publications.pdf

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41	2,413	236833	289141
papers	citations	25 h-index	40 g-index

43	43	43	3918
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Functional Notch signaling is required for BMP4-induced inhibition of myogenic differentiation. Development (Cambridge), 2003, 130, 6089-6099.	1.2	230
2	Mutation of the LUNATIC FRINGE Gene in Humans Causes Spondylocostal Dysostosis with a Severe Vertebral Phenotype. American Journal of Human Genetics, 2006, 78, 28-37.	2.6	223
3	Notch signaling in development and disease. Seminars in Cancer Biology, 2004, 14, 320-328.	4.3	206
4	A Mechanism for Gene-Environment Interaction in the Etiology of Congenital Scoliosis. Cell, 2012, 149, 295-306.	13.5	188
5	NAD Deficiency, Congenital Malformations, and Niacin Supplementation. New England Journal of Medicine, 2017, 377, 544-552.	13.9	177
6	Notch inhibition by the ligand Delta-Like 3 defines the mechanism of abnormal vertebral segmentation in spondylocostal dysostosis. Human Molecular Genetics, 2011, 20, 905-916.	1.4	159
7	Divergent functions and distinct localization of the Notch ligands DLL1 and DLL3 in vivo. Journal of Cell Biology, 2007, 178, 465-476.	2.3	134
8	A CADASIL-mutated Notch 3 receptor exhibits impaired intracellular trafficking and maturation but normal ligand-induced signaling. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 17119-17124.	3.3	102
9	High levels of Notch signaling down-regulate Numb and Numblike. Journal of Cell Biology, 2006, 175, 535-540.	2.3	76
10	A Screening Approach to Identify Clinically Actionable Variants Causing Congenital Heart Disease in Exome Data. Circulation Genomic and Precision Medicine, 2018, 11, e001978.	1.6	65
11	Loss of Cited2 causes congenital heart disease by perturbing leftâ€“right patterning of the body axis. Human Molecular Genetics, 2011, 20, 1097-1110.	1.4	54
12	Identification of clinically actionable variants from genome sequencing of families with congenital heart disease. Genetics in Medicine, 2019, 21, 1111-1120.	1.1	54
13	NKX2-5 mutations causative for congenital heart disease retain functionality and are directed to hundreds of targets. ELife, 2015, 4, .	2.8	54
14	Cited2 is required in trophoblasts for correct placental capillary patterning. Developmental Biology, 2014, 392, 62-79.	0.9	48
15	Differential, dominant activation and inhibition of Notch signalling and APP cleavage by truncations of PSEN1 in human disease. Human Molecular Genetics, 2014, 23, 602-617.	1.4	48
16	Gestational stress induces the unfolded protein response, resulting in heart defects. Development (Cambridge), 2016, 143, 2561-2572.	1.2	45
17	Notch4 reveals a novel mechanism regulating Notch signal transduction. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1272-1284.	1.9	44
18	The Mouse Homeobox Gene,Gbx2:Genomic Organization and Expression in Pluripotent Cellsin Vitroandin Vivo. Genomics, 1997, 46, 223-233.	1.3	43

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19	Gene-environment interaction impacts on heart development and embryo survival. Development (Cambridge), 2019, 146, .	1.2	43
20	Recording Notch Signaling in Real Time. Developmental Neuroscience, 2006, 28, 118-127.	1.0	42
21	De novo, deleterious sequence variants that alter the transcriptional activity of the homeoprotein PBX1 are associated with intellectual disability and pleiotropic developmental defects. Human Molecular Genetics, 2017, 26, 4849-4860.	1.4	42
22	CRTR-1, a Developmentally Regulated Transcriptional Repressor Related to the CP2 Family of Transcription Factors. Journal of Biological Chemistry, 2001, 276, 3324-3332.	1.6	37
23	Functional genomics and gene-environment interaction highlight the complexity of congenital heart disease caused by Notch pathway variants. Human Molecular Genetics, 2020, 29, 566-579.	1.4	32
24	The mouse notches up another success: understanding the causes of human vertebral malformation. Mammalian Genome, 2011, 22, 362-376.	1.0	28
25	Bi-allelic Mutations in NADSYN1 Cause Multiple Organ Defects and Expand the Genotypic Spectrum of Congenital NAD Deficiency Disorders. American Journal of Human Genetics, 2020, 106, 129-136.	2.6	27
26	Sequence and evolutionary conservation of the murine Gbx-2 homeobox gene. FEBS Letters, 1995, 364, 289-292.	1.3	26
27	Functional characterization of a novel PBX1 de novo missense variant identified in a patient with syndromic congenital heart disease. Human Molecular Genetics, 2020, 29, 1068-1082.	1.4	26
28	Notch1 endocytosis is induced by ligand and is required for signal transduction. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 166-177.	1.9	24
29	Disruption of the somitic molecular clock causes abnormal vertebral segmentation. Birth Defects Research Part C: Embryo Today Reviews, 2007, 81, 93-110.	3.6	23
30	A cell autonomous role for the Notch ligand Deltaâ€like 3 in Î±Î² Tâ€cell development. Immunology and Cell Biology, 2011, 89, 696-705.	1.0	23
31	New cases that expand the genotypic and phenotypic spectrum of Congenital NAD Deficiency Disorder. Human Mutation, 2021, 42, 862-876.	1.1	16
32	<scp>KIAA1217</scp>: A novel candidate gene associated with isolated and syndromic vertebral malformations. American Journal of Medical Genetics, Part A, 2020, 182, 1664-1672.	0.7	15
33	Heterozygous loss of WBP11 function causes multiple congenital defects in humans and mice. Human Molecular Genetics, 2021, 29, 3662-3678.	1.4	14
34	Geneâ€“environment interaction demonstrates the vulnerability of the embryonic heart. Developmental Biology, 2014, 391, 99-110.	0.9	13
35	The promises and challenges of exome sequencing in familial, non-syndromic congenital heart disease. International Journal of Cardiology, 2017, 230, 155-163.	0.8	10
36	VPOT: A Customizable Variant Prioritization Ordering Tool for Annotated Variants. Genomics, Proteomics and Bioinformatics, 2019, 17, 540-545.	3.0	10

#	Article	IF	Citations
37	An image analysis protocol using CellProfiler for automated quantification of post-ischemic cardiac parameters. STAR Protocols, 2022, 3, 101097.	0.5	5
38	Role of Delta-Like-3 in Mammalian Somitogenesis and Vertebral Column Formation. Advances in Experimental Medicine and Biology, 2008, 638, 95-112.	0.8	3
39	Cooperation between somatic Ikaros and Notch1 mutations at the inception of T-ALL. Leukemia Research, 2011, 35, 1512-1519.	0.4	2
40	Quantitative 3D analysis and visualization of cardiac fibrosis by microcomputed tomography. STAR Protocols, 2022, 3, 101055.	0.5	2
41	Divergent functions and distinct localization of the Notch ligands DLL1 and DLL3 in vivo. Journal of Experimental Medicine, 2007, 204, i20-i20.	4.2	0