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List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10009933/publications.pdf

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29 papers	4,268 citations	394421 19 h-index	477307 29 g-index
30 all docs	30 docs citations	30 times ranked	5609 citing authors

#	Article	IF	Citations
1	Emergence and patterning dynamics of mouse-definitive endoderm. IScience, 2022, 25, 103556.	4.1	9
2	NaÃ¯ve-like pluripotency to pave the way for saving the northern white rhinoceros from extinction. Scientific Reports, 2022, 12, 3100.	3.3	6
3	Polycomb-mediated genome architecture enables long-range spreading of H3K27 methylation. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
4	Non-coding deletions identify Maenli lncRNA as a limb-specific En1 regulator. Nature, 2021, 592, 93-98.	27.8	53
5	Dnmt1 has de novo activity targeted to transposable elements. Nature Structural and Molecular Biology, 2021, 28, 594-603.	8.2	83
6	A CRISPR-Cas9â€“engineered mouse model for GPI-anchor deficiency mirrors human phenotypes and exhibits hippocampal synaptic dysfunctions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
7	A 37â€…kb region upstream of brachyury comprising a notochord enhancer is essential for notochord and tail development. Development (Cambridge), 2021, 148, .	2.5	9
8	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. Science, 2020, 370, 208-214.	12.6	41
9	SLC20A1 Is Involved in Urinary Tract and Urorectal Development. Frontiers in Cell and Developmental Biology, 2020, 8, 567.	3.7	22
10	Epigenetic regulator function through mouse gastrulation. Nature, 2020, 584, 102-108.	27.8	89
11	Mouse embryonic stem cells self-organize into trunk-like structures with neural tube and somites. Science, 2020, 370, .	12.6	193
12	Functional dissection of the Sox9â€“Kcnj2 locus identifies nonessential and instructive roles of TAD architecture. Nature Genetics, 2019, 51, 1263-1271.	21.4	223
13	Preformed chromatin topology assists transcriptional robustness of Shh during limb development. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12390-12399.	7.1	131
14	Serial genomic inversions induce tissue-specific architectural stripes, gene misexpression and congenital malformations. Nature Cell Biology, 2019, 21, 305-310.	10.3	107
15	Polymer physics predicts the effects of structural variants on chromatin architecture. Nature Genetics, 2018, 50, 662-667.	21.4	179
16	Noncoding copy-number variations are associated with congenital limb malformation. Genetics in Medicine, 2018, 20, 599-607.	2.4	42
17	BRACHYURY directs histone acetylation to target loci during mesoderm development. EMBO Reports, 2018, 19, 118-134.	4.5	23
18	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. Nature Genetics, 2018, 50, 1463-1473.	21.4	147

#	Article	IF	Citations
19	Patterning and gastrulation defects caused by thetw18lethal are due to loss ofPpp2r1a. Biology Open, 2017, 6, 752-764.	1.2	14
20	Antagonistic Activities of Sox2 and Brachyury Control the Fate Choice of Neuro-Mesodermal Progenitors. Developmental Cell, 2017, 42, 514-526.e7.	7.0	139
21	Composition and dosage of a multipartite enhancer cluster control developmental expression of Ihh (Indian hedgehog). Nature Genetics, 2017, 49, 1539-1545.	21.4	107
22	Formation of new chromatin domains determines pathogenicity of genomic duplications. Nature, 2016, 538, 265-269.	27.8	582
23	Different Concentrations of FGF Ligands, FGF2 or FGF8 Determine Distinct States of WNT-Induced Presomitic Mesoderm. Stem Cells, 2016, 34, 1790-1800.	3.2	23
24	Analysis of the Fam181 gene family during mouse development reveals distinct strain-specific expression patterns, suggesting a role in nervous system development and function. Gene, 2016, 575, 438-451.	2.2	13
25	Exome sequencing and CRISPR/Cas genome editing identify mutations of ZAK as a cause of limb defects in humans and mice. Genome Research, 2016, 26, 183-191.	5.5	52
26	Deletions, Inversions, Duplications: Engineering of Structural Variants using CRISPR/Cas in Mice. Cell Reports, 2015, 10, 833-839.	6.4	181
27	Disruptions of Topological Chromatin Domains Cause Pathogenic Rewiring of Gene-Enhancer Interactions. Cell, 2015, 161, 1012-1025.	28.9	1,725
28	Genome-wide association study and mouse expression data identify a highly conserved 32 kb intergenic region between WNT3 and WNT9b as possible susceptibility locus for isolated classic exstrophy of the bladder. Human Molecular Genetics, 2014, 23, 5536-5544.	2.9	19
29	SRF is essential for mesodermal cell migration during elongation of the embryonic body axis. Mechanisms of Development, 2014, 133, 23-35.	1.7	14