Andrea Pauli

List of Publications by Year in descending order

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ΔΝΠΦΕΛ ΡΛΙΙΙΙ

#	Article	IF	CITATIONS
1	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. Genome Research, 2012, 22, 577-591.	2.4	809
2	Efficient Mutagenesis by Cas9 Protein-Mediated Oligonucleotide Insertion and Large-Scale Assessment of Single-Guide RNAs. PLoS ONE, 2014, 9, e98186.	1.1	794
3	Non-coding RNAs as regulators of embryogenesis. Nature Reviews Genetics, 2011, 12, 136-149.	7.7	558
4	Toddler: An Embryonic Signal That Promotes Cell Movement via Apelin Receptors. Science, 2014, 343, 1248636.	6.0	498
5	Cell-Type-Specific TEV Protease Cleavage Reveals Cohesin Functions in Drosophila Neurons. Developmental Cell, 2008, 14, 239-251.	3.1	251
6	Ribosome profiling reveals resemblance between long non-coding RNAs and 5′ leaders of coding RNAs. Development (Cambridge), 2013, 140, 2828-2834.	1.2	237
7	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. Cell, 2014, 159, 1698-1710.	13.5	196
8	Conservation of uORF repressiveness and sequence features in mouse, human and zebrafish. Nature Communications, 2016, 7, 11663.	5.8	158
9	Cohesin cleavage and Cdk inhibition trigger formation of daughter nuclei. Nature Cell Biology, 2010, 12, 185-192.	4.6	155
10	Identifying (nonâ€)coding RNAs and small peptides: Challenges and opportunities. BioEssays, 2015, 37, 103-112.	1.2	96
11	Selective Roles of Vertebrate PCF11 in Premature and Full-Length Transcript Termination. Molecular Cell, 2019, 74, 158-172.e9.	4.5	95
12	Polycomb purification by in vivo biotinylation tagging reveals cohesin and Trithorax group proteins as interaction partners. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5572-5577.	3.3	92
13	Formation and Nuclear Export of Preribosomes Are Functionally Linked to the Small-Ubiquitin-Related Modifier Pathway. Traffic, 2006, 7, 1311-1321.	1.3	87
14	Canonical nucleosome organization at promoters forms during genome activation. Genome Research, 2014, 24, 260-266.	2.4	87
15	The Ly6/uPAR protein Bouncer is necessary and sufficient for species-specific fertilization. Science, 2018, 361, 1029-1033.	6.0	81
16	A Direct Role for Cohesin in Gene Regulation and Ecdysone Response in Drosophila Salivary Glands. Current Biology, 2010, 20, 1787-1798.	1.8	57
17	Decoding sORF translation – from small proteins to gene regulation. RNA Biology, 2016, 13, 1051-1059.	1.5	54
18	Loss of Apela Peptide in Mice Causes Low Penetrance Embryonic Lethality and Defects in Early Mesodermal Derivatives. Cell Reports, 2017, 20, 2116-2130.	2.9	53

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19	Nodal patterning without Lefty inhibitory feedback is functional but fragile. ELife, 2017, 6, .	2.8	52
20	Antisense Oligonucleotide-Mediated Transcript Knockdown in Zebrafish. PLoS ONE, 2015, 10, e0139504.	1.1	35
21	The conserved fertility factor SPACA4/Bouncer has divergent modes of action in vertebrate fertilization. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	27
22	The Fertilization Enigma: How Sperm and Egg Fuse. Annual Review of Cell and Developmental Biology, 2021, 37, 391-414.	4.0	26
23	Toddler signaling regulates mesodermal cell migration downstream of Nodal signaling. ELife, 2017, 6, .	2.8	24
24	Self-organized cell migration across scales – from single cell movement to tissue formation. Development (Cambridge), 2021, 148, .	1.2	22
25	Sperm membrane proteins DCST1 and DCST2 are required for sperm-egg interaction in mice and fish. Communications Biology, 2022, 5, 332.	2.0	21
26	NMD is required for timely cell fate transitions by fine-tuning gene expression and regulating translation. Genes and Development, 2022, 36, 348-367.	2.7	17
27	Zebrafish Ski7 tunes RNA levels during the oocyte-to-embryo transition. PLoS Genetics, 2021, 17, e1009390.	1.5	15
28	The Sperm Protein Spaca6 is Essential for Fertilization in Zebrafish. Frontiers in Cell and Developmental Biology, 2021, 9, 806982.	1.8	13
29	Species-specific mechanisms during fertilization. Current Topics in Developmental Biology, 2020, 140, 121-144.	1.0	7
30	Systematic refinement of gene annotations by parsing mRNA 3′ end sequencing datasets. Methods in Enzymology, 2021, 655, 205-223.	0.4	2