Angela H Depace

List of Publications by Year
in descending order

25 papers	1,251 citations	471509 17 h-index	610901 24 g-index
37 all docs	37 docs citations	37 times ranked	1256 citing authors

#	Article	IF	Citations
1	A Quantitative Spatiotemporal Atlas of Gene Expression in the Drosophila Blastoderm. Cell, 2008, 133, 364-374.	28.9	263
2	Information Integration and Energy Expenditure in Gene Regulation. Cell, 2016, 166, 234-244.	28.9	127
3	Three-dimensional morphology and gene expression in the Drosophila blastoderm at cellular resolution I: data acquisition pipeline. Genome Biology, 2006, 7, R123.	9.6	121
4	Depleting Gene Activities in Early Drosophila Embryos with the â€œMaternal-Gal4â€“shRNAâ€•System. Genetics, 2013, 193, 51-61.	2.9	98
5	Combinatorial Gene Regulation through Kinetic Control of the Transcription Cycle. Cell Systems, 2017, 4, 97-108.e9.	6.2	63
6	KrÃ¼ppel Expression Levels Are Maintained through Compensatory Evolution of Shadow Enhancers. Cell Reports, 2015, 12, 1740-1747.	6.4	55
7	A Conserved Developmental Patterning Network Produces Quantitatively Different Output in Multiple Species of Drosophila. PLoS Genetics, 2011, 7, e1002346.	3.5	51
8	Dissecting the sharp response of a canonical developmental enhancer reveals multiple sources of cooperativity. ELife, 2019, 8, .	6.0	47
9	Cellular resolution models for even skipped regulation in the entire Drosophila embryo. ELife, 2013, 2, e00522.	6.0	45
10	Shadow enhancers enable Hunchback bifunctionality in the Drosophila embryo. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 785-790.	7.1	44
11	The appeasement of Doug: a synthetic approach to enhancer biology. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Overlock	1.3	42
12	Transcriptional precision and accuracy in development: from measurements to models and mechanisms. Development (Cambridge), 2017, 144, 3855-3866.	2.5	34
13	Signal Integration by Shadow Enhancers and Enhancer Duplications Varies across the Drosophila Embryo. Cell Reports, 2019, 26, 2407-2418.e5.	6.4	34
14	A gene expression atlas of a bicoid-depleted Drosophila embryo reveals early canalization of cell fate. Development (Cambridge), 2015, 142, 587-596.	2.5	31
15	Modeling transcriptional networks in Drosophila development at multiple scales. Current Opinion in Genetics and Development, 2011, 21, 711-718.	3.3	28
16	Dissecting sources of quantitative gene expression pattern divergence between Drosophila species. Molecular Systems Biology, 2012, 8, 604.	7.2	27
17	Hunchback is counter-repressed to regulate even-skipped stripe 2 expression in Drosophila embryos. PLoS Genetics, 2018, 14, e1007644.	3.5	25
18	Yearly Planning Meetings: Individualized Development Plans Arenâ€™t Just More Paperwork. Molecular Cell, 2015, 58, 718-721.	9.7	21

#	Article	IF	Citations
19	Comparing mRNA levels using in situ hybridization of a target gene and co-stain. Methods, 2014, 68, 233-241.	3.8	16
20	SiteOut: An Online Tool to Design Binding Site-Free DNA Sequences. PLoS ONE, 2016, 11, e0151740.	2.5	15
21	Analysis of Genetic Variation Indicates DNA Shape Involvement in Purifying Selection. Molecular Biology and Evolution, 2018, 35, 1958-1967.	8.9	14
22	A Mutation in theDrosophila melanogaster eveStripe 2 Minimal Enhancer Is Buffered by Flanking Sequences. G3: Genes, Genomes, Genetics, 2020, 10, 4473-4482.	1.8	13
23	Quantitative Measurement and Thermodynamic Modeling of Fused Enhancers Support a Two-Tiered Mechanism for Interpreting Regulatory DNA. Cell Reports, 2017, 21, 236-245.	6.4	11
24	Quantitative Comparison of the Anterior-Posterior Patterning System in the Embryos of FiveDrosophilaSpecies. G3: Genes, Genomes, Genetics, 2019, 9, 2171-2182.	1.8	9
25	Defining Kinetic Roles of Transcriptional Activators in the Early Drosophila Embryo. SSRN Electronic Journal, 0, , .	0.4	0