Dmitri A Papatsenko

List of Publications by Year
in descending order

57 papers	3,263 citations	172457 29 h-index	206112 48 g-index
57 all docs	57 docs citations	57 times ranked	4719 citing authors

#	Article	IF	Citations
1	A self-organizing system of repressor gradients establishes segmental complexity in Drosophila. Nature, 2003, 426, 849-853.	27.8	423
2	Induction of a Hemogenic Program in Mouse Fibroblasts. Cell Stem Cell, 2013, 13, 205-218.	11.1	195
3	Modeling Familial Cancer with Induced Pluripotent Stem Cells. Cell, 2015, 161, 240-254.	28.9	191
4	Restraining Lysosomal Activity Preserves Hematopoietic Stem Cell Quiescence and Potency. Cell Stem Cell, 2020, 26, 359-376.e7.	11.1	169
5	The role of binding site cluster strength in Bicoid-dependent patterning in Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4960-4965.	7.1	163
6	Computational Models for Neurogenic Gene Expression in the Drosophila Embryo. Current Biology, 2006, 16, 1358-1365.	3.9	156
7	Distinction between Color Photoreceptor Cell Fates Is Controlled by Prospero in Drosophila. Developmental Cell, 2003, 4, 853-864.	7.0	153
8	Homotypic Regulatory Clusters in Drosophila. Genome Research, 2003, 13, 579-588.	5.5	140
9	Otd/Crx, a Dual Regulator for the Specification of Ommatidia Subtypes in the Drosophila Retina. Developmental Cell, 2003, 5, 391-402.	7.0	130
10	How the Dorsal gradient works: Insights from postgenome technologies. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20072-20076.	7.1	116
11	Divisional History and Hematopoietic Stem Cell Function during Homeostasis. Stem Cell Reports, 2014, 2, 473-490.	4.8	106
12	Short fuzzy tandem repeats in genomic sequences, identification, and possible role in regulation of gene expression. Bioinformatics, 2006, 22, 676-684.	4.1	88
13	Tex10 Coordinates Epigenetic Control of Super-Enhancer Activity in Pluripotency and Reprogramming. Cell Stem Cell, 2015, 16, 653-668.	11.1	80
14	Dual regulation by the Hunchback gradient in the <i>Drosophila</i> embryo. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2901-2906.	7.1	77
15	Extraction of Functional Binding Sites from Unique Regulatory Regions: The <i>Drosophila</i> Early Developmental Enhancers. Genome Research, 2002, 12, 470-481.	5.5	75
16	Distance preferences in the arrangement of binding motifs and hierarchical levels in organization of transcription regulatory information. Nucleic Acids Research, 2003, 31, 6016-6026.	14.5	74
17	Quantitative analysis of binding motifs mediating diverse spatial readouts of the Dorsal gradient in the Drosophila embryo. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4966-4971.	7.1	74
18	FOXO3â€mTOR metabolic cooperation in the regulation of erythroid cell maturation and homeostasis. American Journal of Hematology, 2014, 89, 954-963.	4.1	73

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19	Direct reprogramming of fibroblasts into antigen-presenting dendritic cells. Science Immunology, 2018, 3, .	11.9	62
20	Evolution of the Ventral Midline in Insect Embryos. Developmental Cell, 2006, 11, 895-902.	7.0	58
21	A conserved regulatory element present in all Drosophila rhodopsin genes mediates Pax6 functions and participates in the fine-tuning of cell-specific expression. Mechanisms of Development, 2001, 101, 143-153.	1.7	57
22	A Systems Approach Identifies Essential FOXO3 Functions at Key Steps of Terminal Erythropoiesis. PLoS Genetics, 2015, 11, e1005526.	3.5	55
23	Tbx3 Controls Dppa3 Levels and Exit from Pluripotency toward Mesoderm. Stem Cell Reports, 2015, 5, 97-110.	4.8	52
24	Organization of developmental enhancers in the Drosophila embryo. Nucleic Acids Research, 2009, 37, 5665-5677.	14.5	51
25	The Drosophila Gap Gene Network Is Composed of Two Parallel Toggle Switches. PLoS ONE, 2011, 6, e21145.	2.5	43
26	Single-Cell Analyses of ESCs Reveal Alternative Pluripotent Cell States and Molecular Mechanisms that Control Self-Renewal. Stem Cell Reports, 2015, 5, 207-220.	4.8	40
27	Enhancer Responses to Similarly Distributed Antagonistic Gradients in Development. PLoS Computational Biology, 2007, 3, e84.	3.2	39
28	Hematopoietic Reprogramming InÂVitro Informs InÂVivo Identification of Hemogenic Precursors to Definitive Hematopoietic Stem Cells. Developmental Cell, 2016, 36, 525-539.	7.0	34
29	A rationale for the enhanceosome and other evolutionarily constrained enhancers. Current Biology, 2007, 17, R955-R957.	3.9	32
30	ClusterDraw web server: a tool to identify and visualize clusters of binding motifs for transcription factors. Bioinformatics, 2007, 23, 1032-1034.	4.1	27
31	Stripe formation in the early fly embryo: principles, models, and networks. BioEssays, 2009, 31, 1172-1180.	2.5	27
32	Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. Cell Reports, 2018, 25, 2821-2835.e7.	6.4	27
33	Feedback control of pluripotency in embryonic stem cells: Signaling, transcription and epigenetics. Stem Cell Research, 2018, 29, 180-188.	0.7	23
34	Statistical extraction of Drosophila cis-regulatory modules using exhaustive assessment of local word frequency. BMC Bioinformatics, 2003, 4, 65.	2.6	20
35	Computational identification of regulatory DNAs underlying animal development. Nature Methods, 2005, 2, 529-534.	19.0	19
36	Conservation patterns in different functional sequence categories of divergent Drosophila species. Genomics, 2006, 88, 431-442.	2.9	18

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37	Expression of Podocalyxin Separates the Hematopoietic and Vascular Potentials of Mouse Embryonic Stem Cell-Derived Mesoderm. Stem Cells, 2014, 32, 191-203.	3.2	14
38	Context-dependent transcriptional interpretation of mitogen activated protein kinase signaling in the <i>Drosophila</i> embryo. Chaos, 2013, 23, 025105.	2.5	13
39	Temporal waves of coherent gene expression during <i>Drosophila</i> embryogenesis. Bioinformatics, 2010, 26, 2731-2736.	4.1	11
40	Clusters of Temporal Discordances Reveal Distinct Embryonic Patterning Mechanisms in Drosophila and Anopheles. PLoS Biology, 2011, 9, e1000584.	5.6	11
41	Memory of Divisional History Directs the Continuous Process of Primitive Hematopoietic Lineage Commitment. Stem Cell Reports, 2020, 14, 561-574.	4.8	11
42	Time warping of evolutionary distant temporal gene expression data based on noise suppression. BMC Bioinformatics, 2009, 10, 353.	2.6	9
43	Loss Of p53 Rescues The Defective Function Of Foxo3-/- Hematopoietic Stem Cells But Enhances Their Predisposition To Malignancy. Blood, 2013, 122, 4199-4199.	1.4	9
44	A Systems Approach Identifies Essential FOXO3 Functions in Erythroblast Enucleation Process. Blood, 2014, 124, 445-445.	1.4	6
45	Emerging Modeling Concepts and Solutions in Stem Cell Research. Current Topics in Developmental Biology, 2016, 116, 709-721.	2.2	4
46	NetExplore: a web server for modeling small network motifs. Bioinformatics, 2015, 31, 1860-1862.	4.1	3
47	Quantitative Approaches to Model Pluripotency and Differentiation in Stem Cells. , 2013, , 59-74.		3
48	A Method to Synthesize Strand-Specific Probes. Analytical Biochemistry, 1996, 240, 152-154.	2.4	1
49	Distinct gene expression profile may be key in distinguishing normal HSC and leukemic stem cells. Experimental Hematology, 2014, 42, S46.	0.4	1
50	A Regulatory Network Controlling Drosophila Development. Lecture Notes in Computer Science, 2005, , 101-101.	1.3	0
51	Biological and Quantitative Models for Stem Cell Self-Renewal and Differentiation. , 2013, , 427-441.		0
52	Enhancer Responses to Similarly Distributed Antagonistic Gradients in Development. PLoS Computational Biology, 2005, preprint, e84.	3.2	0
53	Regulation of Primitive Erythroid Progenitor Development. Blood, 2012, 120, 1211-1211.	1.4	0
54	Abstract 5129: Model osteosarcoma by Li-Fraumeni syndrome patient-specific induced pluripotent stem cells. , 2015, , .		0

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55	Activated but Not Quiescent Hematopoietic Stem Cells Rely Readily on Glycolysis As Their Main Source of Energy. Blood, 2019, 134, 271-271.	1.4	0
56	Lysosomal Activation Is Required for Priming of Quiescent Hematopoietic Stem Cells. Blood, 2019, 134, 722-722.	1.4	0
57	Transcriptome analysis reveals high tumor heterogeneity with respect to re-activation of stemness and proliferation programs. PLoS ONE, 2022, 17, e0268626.	2.5	0