

Dmitri A Papatsenko

List of Publications by Year in descending order

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57
papers

3,263
citations

172457

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all docs

57
docs citations

57
times ranked

4719
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome analysis reveals high tumor heterogeneity with respect to re-activation of stemness and proliferation programs. PLoS ONE, 2022, 17, e0268626.	2.5	0
2	Memory of Divisional History Directs the Continuous Process of Primitive Hematopoietic Lineage Commitment. Stem Cell Reports, 2020, 14, 561-574.	4.8	11
3	Restraining Lysosomal Activity Preserves Hematopoietic Stem Cell Quiescence and Potency. Cell Stem Cell, 2020, 26, 359-376.e7.	11.1	169
4	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
5	Lysosomal Activation Is Required for Priming of Quiescent Hematopoietic Stem Cells. Blood, 2019, 134, 722-722.	1.4	0
6	Feedback control of pluripotency in embryonic stem cells: Signaling, transcription and epigenetics. Stem Cell Research, 2018, 29, 180-188.	0.7	23
7	Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. Cell Reports, 2018, 25, 2821-2835.e7.	6.4	27
8	Direct reprogramming of fibroblasts into antigen-presenting dendritic cells. Science Immunology, 2018, 3, .	11.9	62
9	Emerging Modeling Concepts and Solutions in Stem Cell Research. Current Topics in Developmental Biology, 2016, 116, 709-721.	2.2	4
10	Hematopoietic Reprogramming InÂVitro Informs InÂVivo Identification of Hemogenic Precursors to Definitive Hematopoietic Stem Cells. Developmental Cell, 2016, 36, 525-539.	7.0	34
11	Tbx3 Controls Dppa3 Levels and Exit from Pluripotency toward Mesoderm. Stem Cell Reports, 2015, 5, 97-110.	4.8	52
12	NetExplore: a web server for modeling small network motifs. Bioinformatics, 2015, 31, 1860-1862.	4.1	3
13	Tex10 Coordinates Epigenetic Control of Super-Enhancer Activity in Pluripotency and Reprogramming. Cell Stem Cell, 2015, 16, 653-668.	11.1	80
14	Modeling Familial Cancer with Induced Pluripotent Stem Cells. Cell, 2015, 161, 240-254.	28.9	191
15	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
16	A Systems Approach Identifies Essential FOXO3 Functions at Key Steps of Terminal Erythropoiesis. PLoS Genetics, 2015, 11, e1005526.	3.5	55
17	Abstract 5129: Model osteosarcoma by Li-Fraumeni syndrome patient-specific induced pluripotent stem cells. , 2015, , .		0
18	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

#	ARTICLE	IF	CITATIONS
19	Divisional History and Hematopoietic Stem Cell Function during Homeostasis. <i>Stem Cell Reports</i> , 2014, 2, 473-490.	4.8	106
20	FOXO3–mTOR metabolic cooperation in the regulation of erythroid cell maturation and homeostasis. <i>American Journal of Hematology</i> , 2014, 89, 954-963.	4.1	73
21	Distinct gene expression profile may be key in distinguishing normal HSC and leukemic stem cells. <i>Experimental Hematology</i> , 2014, 42, S46.	0.4	1
22	A Systems Approach Identifies Essential FOXO3 Functions in Erythroblast Enucleation Process. <i>Blood</i> , 2014, 124, 445-445.	1.4	6
23	Biological and Quantitative Models for Stem Cell Self-Renewal and Differentiation. , 2013, , 427-441.		0
24	Induction of a Hemogenic Program in Mouse Fibroblasts. <i>Cell Stem Cell</i> , 2013, 13, 205-218.	11.1	195
25	Context-dependent transcriptional interpretation of mitogen activated protein kinase signaling in the <i>Drosophila</i> embryo. <i>Chaos</i> , 2013, 23, 025105.	2.5	13
26	Quantitative Approaches to Model Pluripotency and Differentiation in Stem Cells. , 2013, , 59-74.		3
27	Loss Of p53 Rescues The Defective Function Of Foxo3-/- Hematopoietic Stem Cells But Enhances Their Predisposition To Malignancy. <i>Blood</i> , 2013, 122, 4199-4199.	1.4	9
28	Regulation of Primitive Erythroid Progenitor Development. <i>Blood</i> , 2012, 120, 1211-1211.	1.4	0
29	Clusters of Temporal Discordances Reveal Distinct Embryonic Patterning Mechanisms in <i>Drosophila</i> and <i>Anopheles</i> . <i>PLoS Biology</i> , 2011, 9, e1000584.	5.6	11
30	The <i>Drosophila</i> Gap Gene Network Is Composed of Two Parallel Toggle Switches. <i>PLoS ONE</i> , 2011, 6, e21145.	2.5	43
31	Temporal waves of coherent gene expression during <i>Drosophila</i> embryogenesis. <i>Bioinformatics</i> , 2010, 26, 2731-2736.	4.1	11
32	Organization of developmental enhancers in the <i>Drosophila</i> embryo. <i>Nucleic Acids Research</i> , 2009, 37, 5665-5677.	14.5	51
33	Time warping of evolutionary distant temporal gene expression data based on noise suppression. <i>BMC Bioinformatics</i> , 2009, 10, 353.	2.6	9
34	Stripe formation in the early fly embryo: principles, models, and networks. <i>BioEssays</i> , 2009, 31, 1172-1180.	2.5	27
35	Dual regulation by the Hunchback gradient in the <i>Drosophila</i> embryo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2901-2906.	7.1	77
36	How the Dorsal gradient works: Insights from postgenome technologies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20072-20076.	7.1	116

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37	Enhancer Responses to Similarly Distributed Antagonistic Gradients in Development. PLoS Computational Biology, 2007, 3, e84.	3.2	39
38	ClusterDraw web server: a tool to identify and visualize clusters of binding motifs for transcription factors. Bioinformatics, 2007, 23, 1032-1034.	4.1	27
39	A rationale for the enhanceosome and other evolutionarily constrained enhancers. Current Biology, 2007, 17, R955-R957.	3.9	32
40	Evolution of the Ventral Midline in Insect Embryos. Developmental Cell, 2006, 11, 895-902.	7.0	58
41	Conservation patterns in different functional sequence categories of divergent Drosophila species. Genomics, 2006, 88, 431-442.	2.9	18
42	Computational Models for Neurogenic Gene Expression in the Drosophila Embryo. Current Biology, 2006, 16, 1358-1365.	3.9	156
43	Short fuzzy tandem repeats in genomic sequences, identification, and possible role in regulation of gene expression. Bioinformatics, 2006, 22, 676-684.	4.1	88
44	Computational identification of regulatory DNAs underlying animal development. Nature Methods, 2005, 2, 529-534.	19.0	19
45	A Regulatory Network Controlling Drosophila Development. Lecture Notes in Computer Science, 2005, , 101-101.	1.3	0
46	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
47	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
48	Enhancer Responses to Similarly Distributed Antagonistic Gradients in Development. PLoS Computational Biology, 2005, preprint, e84.	3.2	0
49	Statistical extraction of Drosophila cis-regulatory modules using exhaustive assessment of local word frequency. BMC Bioinformatics, 2003, 4, 65.	2.6	20
50	A self-organizing system of repressor gradients establishes segmental complexity in Drosophila. Nature, 2003, 426, 849-853.	27.8	423
51	Distinction between Color Photoreceptor Cell Fates Is Controlled by Prospero in Drosophila. Developmental Cell, 2003, 4, 853-864.	7.0	153
52	Otd/Crx, a Dual Regulator for the Specification of Ommatidia Subtypes in the Drosophila Retina. Developmental Cell, 2003, 5, 391-402.	7.0	130
53	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
54	Homotypic Regulatory Clusters in Drosophila. Genome Research, 2003, 13, 579-588.	5.5	140

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55	Extraction of Functional Binding Sites from Unique Regulatory Regions: The <i>Drosophila</i> Early Developmental Enhancers. <i>Genome Research</i> , 2002, 12, 470-481.	5.5	75
56	A conserved regulatory element present in all <i>Drosophila</i> rhodopsin genes mediates Pax6 functions and participates in the fine-tuning of cell-specific expression. <i>Mechanisms of Development</i> , 2001, 101, 143-153.	1.7	57
57	A Method to Synthesize Strand-Specific Probes. <i>Analytical Biochemistry</i> , 1996, 240, 152-154.	2.4	1