

Olivier Gandrillon

List of Publications by Year in descending order

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43
papers

1,250
citations

471509

17
h-index

414414

32
g-index

58
all docs

58
docs citations

58
times ranked

1231
citing authors

#	ARTICLE	IF	CITATIONS
1	Hematopoietic differentiation is characterized by a transient peak of entropy at a single-cell level. BMC Biology, 2022, 20, 60.	3.8	12
2	Evidence for close molecular proximity between reverting and undifferentiated cells. BMC Biology, 2022, 20, .	3.8	3
3	Entropy as a measure of variability and stemness in single-cell transcriptomics. Current Opinion in Systems Biology, 2021, 27, 100348.	2.6	11
4	Practical identifiability in the frame of nonlinear mixed effects models: the example of the in vitro erythropoiesis. BMC Bioinformatics, 2021, 22, 478.	2.6	4
5	Reduction of a stochastic model of gene expression: Lagrangian dynamics gives access to basins of attraction as cell types and metastability. Journal of Mathematical Biology, 2021, 83, 59.	1.9	5
6	The quiescent fraction of chronic myeloid leukemic stem cells depends on BMPR1B, Stat3 and BMP4-niche signals to persist in patients in remission. Haematologica, 2020, 106, 111-122.	3.5	22
7	WASABI: a dynamic iterative framework for gene regulatory network inference. BMC Bioinformatics, 2019, 20, 220.	2.6	37
8	Calibration, Selection and Identifiability Analysis of a Mathematical Model of the in vitro Erythropoiesis in Normal and Perturbed Contexts. In Silico Biology, 2019, 13, 55-69.	0.9	6
9	Model-Based Assessment of the Role of Uneven Partitioning of Molecular Content on Heterogeneity and Regulation of Differentiation in CD8 T-Cell Immune Responses. Frontiers in Immunology, 2019, 10, 230.	4.8	9
10	Erythroid differentiation displays a peak of energy consumption concomitant with glycolytic metabolism rearrangements. PLoS ONE, 2019, 14, e0221472.	2.5	26
11	Drugs modulating stochastic gene expression affect the erythroid differentiation process. PLoS ONE, 2019, 14, e0225166.	2.5	22
12	SINCERITIES: inferring gene regulatory networks from time-stamped single cell transcriptional expression profiles. Bioinformatics, 2018, 34, 258-266.	4.1	141
13	Automated cell cycle and cell size measurements for single-cell gene expression studies. BMC Research Notes, 2018, 11, 92.	1.4	1
14	A Cloud-aware Autonomous Workflow Engine and Its Application to Gene Regulatory Networks Inference. , 2018, , .		2
15	Identification of Nascent Memory CD8 T Cells and Modeling of Their Ontogeny. Cell Systems, 2017, 4, 306-317.e4.	6.2	36
16	Inferring gene regulatory networks from single-cell data: a mechanistic approach. BMC Systems Biology, 2017, 11, 105.	3.0	48
17	Integrated time-lapse and single-cell transcription studies highlight the variable and dynamic nature of human hematopoietic cell fate commitment. PLoS Biology, 2017, 15, e2001867.	5.6	53
18	IL-2 sensitivity and exogenous IL-2 concentration gradient tune the productive contact duration of CD8+ T cell-APC: a multiscale modeling study. BMC Systems Biology, 2016, 10, 77.	3.0	20

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19	Single-Cell-Based Analysis Highlights a Surge in Cell-to-Cell Molecular Variability Preceding Irreversible Commitment in a Differentiation Process. <i>PLoS Biology</i> , 2016, 14, e1002585.	5.6	220
20	Temperature-induced variation in gene expression burst size in metazoan cells. <i>BMC Molecular Biology</i> , 2015, 16, 20.	3.0	12
21	Multiscale Modeling of the Early CD8 T-Cell Immune Response in Lymph Nodes: An Integrative Study. <i>Computation</i> , 2014, 2, 159-181.	2.0	29
22	Stochastic Fluctuations and Distributed Control of Gene Expression Impact Cellular Memory. <i>PLoS ONE</i> , 2014, 9, e115574.	2.5	37
23	Quantifying the contribution of chromatin dynamics to stochastic gene expression reveals long, locus-dependent periods between transcriptional bursts. <i>BMC Biology</i> , 2013, 11, 15.	3.8	51
24	Towards experimental manipulation of stochasticity in gene expression. <i>Progress in Biophysics and Molecular Biology</i> , 2012, 110, 44-53.	2.9	16
25	Chance at the heart of the cell. <i>Progress in Biophysics and Molecular Biology</i> , 2012, 110, 1-4.	2.9	14
26	Mathematical model of the primary CD8 T cell immune response: stability analysis of a nonlinear age-structured system. <i>Journal of Mathematical Biology</i> , 2012, 65, 263-291.	1.9	11
27	Identification of human, rat and chicken ribosomal proteins by a combination of two-dimensional polyacrylamide gel electrophoresis and mass spectrometry. <i>Journal of Proteomics</i> , 2011, 74, 167-185.	2.4	4
28	On the spontaneous stochastic dynamics of a single gene: complexity of the molecular interplay at the promoter. <i>BMC Systems Biology</i> , 2010, 4, 2.	3.0	67
29	Mathematical study of feedback control roles and relevance in stress erythropoiesis. <i>Journal of Theoretical Biology</i> , 2010, 263, 303-316.	1.7	28
30	Extracting Signature Motifs from Promoter Sets of Differentially Expressed Genes. <i>In Silico Biology</i> , 2009, 9, S17-S39.	0.9	1
31	A combination of transposable elements and magnetic cell sorting provides a very efficient transgenesis system for chicken primary erythroid progenitors. <i>BMC Biotechnology</i> , 2009, 9, 81.	3.3	7
32	Adding self-renewal in committed erythroid progenitors improves the biological relevance of a mathematical model of erythropoiesis. <i>Journal of Theoretical Biology</i> , 2008, 250, 322-338.	1.7	45
33	Large-scale analysis by SAGE reveals new mechanisms of v-erbA oncogene action. <i>BMC Genomics</i> , 2007, 8, 390.	2.8	15
34	Broadening of DNA replication origin usage during metazoan cell differentiation. <i>EMBO Reports</i> , 2006, 7, 806-811.	4.5	35
35	Global transcription analysis of immature avian erythrocytic progenitors: from self-renewal to differentiation. <i>Oncogene</i> , 2004, 23, 7628-7643.	5.9	15
36	Identitag, a relational database for SAGE tag identification and interspecies comparison of SAGE libraries. <i>BMC Bioinformatics</i> , 2004, 5, 143.	2.6	14

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37	The MEK-1/ERKs signalling pathway is differentially involved in the self-renewal of early and late avian erythroid progenitor cells. <i>Oncogene</i> , 2003, 22, 9205-9216.	5.9	26
38	The v-erbA Oncogene: Assessing Its Differentiation-Blocking Ability Using Normal. , 2002, 202, 91-107.		3
39	The v-erbA oncogene blocks expression of $\beta_2\beta_1$ integrin a normal inhibitor of erythroid progenitor proliferation. <i>Oncogene</i> , 2002, 21, 2864-2872.	5.9	8
40	The v-ErbA oncoprotein quenches the activity of an erythroid-specific enhancer. <i>Oncogene</i> , 2001, 20, 775-787.	5.9	4
41	TGF- β_2 cooperates with TGF- β_1 to induce the self-renewal of normal erythrocytic progenitors: evidence for an autocrine mechanism. <i>EMBO Journal</i> , 1999, 18, 2764-2781.	7.8	82
42	Role of the different RAR isoforms in controlling the erythrocytic differentiation sequence. Interference with the v-erbA and p135gag-myb-ets nuclear oncogenes. <i>Oncogene</i> , 1998, 16, 563-574.	5.9	22
43	Chapitre 3. Mécanismes moléculaires et fonction biologique de la variabilité de l'expression génique. L'unicité de la cellule unique: une approche systématique. <i>Sciences & Philosophie</i> , 0, , 82-111.	0.0	0