Olivier Gandrillon

List of Publications by Year
in descending order

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	Single-Cell-Based Analysis Highlights a Surge in Cell-to-Cell Molecular Variability Preceding Irreversible Commitment in a Differentiation Process. PLoS Biology, 2016, 14, e1002585.	5.6	220
2	SINCERITIES: inferring gene regulatory networks from time-stamped single cell transcriptional expression profiles. Bioinformatics, 2018, 34, 258-266.	4.1	141
3	TGF-β cooperates with TGF-α to induce the self–renewal of normal erythrocytic progenitors: evidence for an autocrine mechanism. EMBO Journal, 1999, 18, 2764-2781.	7.8	82
4	On the spontaneous stochastic dynamics of a single gene: complexity of the molecular interplay at the promoter. BMC Systems Biology, 2010, 4, 2.	3.0	67
5	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
6	Quantifying the contribution of chromatin dynamics to stochastic gene expression reveals long, locus-dependent periods between transcriptional bursts. BMC Biology, 2013, 11, 15.	3.8	51
7	Inferring gene regulatory networks from single-cell data: a mechanistic approach. BMC Systems Biology, 2017, 11, 105.	3.0	48
8	Adding self-renewal in committed erythroid progenitors improves the biological relevance of a mathematical model of erythropoiesis. Journal of Theoretical Biology, 2008, 250, 322-338.	1.7	45
9	WASABI: a dynamic iterative framework for gene regulatory network inference. BMC Bioinformatics, 2019, 20, 220.	2.6	37
10	Stochastic Fluctuations and Distributed Control of Gene Expression Impact Cellular Memory. PLoS ONE, 2014, 9, e115574.	2.5	37
11	Identification of Nascent Memory CD8 T Cells and Modeling of Their Ontogeny. Cell Systems, 2017, 4, 306-317.e4.	6.2	36
12	Broadening of DNA replication origin usage during metazoan cell differentiation. EMBO Reports, 2006, 7, 806-811.	4.5	35
13	Multiscale Modeling of the Early CD8 T-Cell Immune Response in Lymph Nodes: An Integrative Study. Computation, 2014, 2, 159-181.	2.0	29
14	Mathematical study of feedback control roles and relevance in stress erythropoiesis. Journal of Theoretical Biology, 2010, 263, 303-316.	1.7	28
15	The MEK-1/ERKs signalling pathway is differentially involved in the self-renewal of early and late avian erythroid progenitor cells. Oncogene, 2003, 22, 9205-9216.	5.9	26
16	Erythroid differentiation displays a peak of energy consumption concomitant with glycolytic metabolism rearrangements. PLoS ONE, 2019, 14, e0221472.	2.5	26
17	Role of the different RAR isoforms in controlling the erythrocytic differentiation sequence. Interference with the v-erbA and p135gag-myb-ets nuclear oncogenes. Oncogene, 1998, 16, 563-574.	5.9	22
18	Drugs modulating stochastic gene expression affect the erythroid differentiation process. PLoS ONE, 2019, 14, e0225166.	2.5	22

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19	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
20	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
21	Towards experimental manipulation of stochasticity in gene expression. Progress in Biophysics and Molecular Biology, 2012, 110, 44-53.	2.9	16
22	Global transcription analysis of immature avian erythrocytic progenitors: from self-renewal to differentiation. Oncogene, 2004, 23, 7628-7643.	5.9	15
23	Large-scale analysis by SAGE reveals new mechanisms of v-erbA oncogene action. BMC Genomics, 2007, 8, 390.	2.8	15
24	Identitag, a relational database for SAGE tag identification and interspecies comparison of SAGE libraries. BMC Bioinformatics, 2004, 5, 143.	2.6	14
25	Chance at the heart of the cell. Progress in Biophysics and Molecular Biology, 2012, 110, 1-4.	2.9	14
26	Temperature-induced variation in gene expression burst size in metazoan cells. BMC Molecular Biology, 2015, 16, 20.	3.0	12
27	Hematopoietic differentiation is characterized by a transient peak of entropy at a single-cell level. BMC Biology, 2022, 20, 60.	3.8	12
28	Mathematical model of the primary CD8 T cell immune response: stability analysis of a nonlinear age-structured system. Journal of Mathematical Biology, 2012, 65, 263-291.	1.9	11
29	Entropy as a measure of variability and stemness in single-cell transcriptomics. Current Opinion in Systems Biology, 2021, 27, 100348.	2.6	11
30	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
31	The v-erbA oncogene blocks expression of α2β1 integrin a normal inhibitor of erythroid progenitor proliferation. Oncogene, 2002, 21, 2864-2872.	5.9	8
32	A combination of transposable elements and magnetic cell sorting provides a very efficient transgenesis system for chicken primary erythroid progenitors. BMC Biotechnology, 2009, 9, 81.	3.3	7
33	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
34	Reduction of a stochastic model of gene expression: Lagrangian dynamics gives access to basins of attraction as cell types and metastabilty. Journal of Mathematical Biology, 2021, 83, 59.	1.9	5
35	The v-ErbA oncoprotein quenches the activity of an erythroid-specific enhancer. Oncogene, 2001, 20, 775-787.	5.9	4
36	Identification of human, rat and chicken ribosomal proteins by a combination of two-dimensional polyacrylamide gel electrophoresis and mass spectrometry. Journal of Proteomics, 2011, 74, 167-185.	2.4	4

#	Article	IF	Citations
37	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
38	The v-erbA Oncogene: Assessing Its Differentiation-Blocking Ability Using Normal. , 2002, 202, 91-107.		3
39	Evidence for close molecular proximity between reverting and undifferentiated cells. BMC Biology, 2022, 20, .	3.8	3
40	A Cloud-aware Autonomous Workflow Engine and Its Application to Gene Regulatory Networks Inference. , 2018, , .		2
41	Extracting Signature Motifs from Promoter Sets of Differentially Expressed Genes. In Silico Biology, 2009, 9, S17-S39.	0.9	1
42	Automated cell cycle and cell size measurements for single-cell gene expression studies. BMC Research Notes, 2018, 11, 92.	1.4	1
43	Chapitre 3. Mécanismes moléculaires et fonction biologique de la variabilité de l'expression génique à l'échelle de la cellule unique: une approche systémique. Sciences & Philosophie, 0, , 82-111.	0.0	0