Nicolas Servant

List of Publications by Year
in descending order

67 papers	11,337 citations	87888 38 h-index	106344 65 g-index
74 all docs	74 docs citations	74 times ranked	20343 citing authors

#	Article	IF	Citations
1	Spatial partitioning of the regulatory landscape of the X-inactivation centre. Nature, 2012, 485, 381-385.	27.8	2,595
2	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. Genome Biology, 2015, 16, 259.	8.8	1,632
3	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. Briefings in Bioinformatics, 2013, 14, 671-683.	6.5	1,064
4	Molecularly targeted therapy based on tumour molecular profiling versus conventional therapy for advanced cancer (SHIVA): a multicentre, open-label, proof-of-concept, randomised, controlled phase 2 trial. Lancet Oncology, The, 2015, 16, 1324-1334.	10.7	897
5	A critical function for transforming growth factor-Î², interleukin 23 and proinflammatory cytokines in driving and modulating human TH-17 responses. Nature Immunology, 2008, 9, 650-657.	14.5	844
6	LINE-1 Activity in Facultative Heterochromatin Formation during X Chromosome Inactivation. Cell, 2010, 141, 956-969.	28.9	296
7	Mechanical induction of the tumorigenic Î²-catenin pathway by tumour growth pressure. Nature, 2015, 523, 92-95.	27.8	288
8	miR-181a and miR-630 Regulate Cisplatin-Induced Cancer Cell Death. Cancer Research, 2010, 70, 1793-1803.	0.9	262
9	Jarid2 Methylation via the PRC2 Complex Regulates H3K27me3 Deposition during Cell Differentiation. Molecular Cell, 2015, 57, 769-783.	9.7	229
10	HiTC: exploration of high-throughput â€˜Câ€™ experiments. Bioinformatics, 2012, 28, 2843-2844.	4.1	165
11	DNA methylation restrains transposons from adopting a chromatin signature permissive for meiotic recombination. Genes and Development, 2015, 29, 1256-1270.	5.9	146
12	<scp>PRC</scp>2 is dispensable for <i><scp>HOTAIR</scp></i>â€mediated transcriptional repression. EMBO Journal, 2017, 36, 981-994.	7.8	146
13	CD44 regulates epigenetic plasticity by mediating iron endocytosis. Nature Chemistry, 2020, 12, 929-938.	13.6	132
14	Prognostic Impact of Vitamin B6 Metabolism in Lung Cancer. Cell Reports, 2012, 2, 257-269.	6.4	122
15	Xist-dependent imprinted X inactivation and the early developmental consequences of its failure. Nature Structural and Molecular Biology, 2017, 24, 226-233.	8.2	122
16	Developmental Dynamics and Disease Potential of Random Monoallelic Gene Expression. Developmental Cell, 2014, 28, 366-380.	7.0	118
17	Parental-to-embryo switch of chromosome organization in early embryogenesis. Nature, 2020, 580, 142-146.	27.8	116
18	Multi-factor data normalization enables the detection of copy number aberrations in amplicon sequencing data. Bioinformatics, 2014, 30, 3443-3450.	4.1	109

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19	Maternal LSD1/KDM1A is an essential regulator of chromatin and transcription landscapes during zygotic genome activation. ELife, 2016, 5, .	6.0	107
20	VAMP: Visualization and analysis of array-CGH, transcriptome and other molecular profiles. Bioinformatics, 2006, 22, 2066-2073.	4.1	106
21	BAP1 complex promotes transcription by opposing PRC1-mediated H2A ubiquitylation. Nature Communications, 2019, 10, 348.	12.8	105
22	Integration of a Radiosensitivity Molecular Signature Into the Assessment of Local Recurrence Risk in Breast Cancer. International Journal of Radiation Oncology Biology Physics, 2015, 93, 631-638.	0.8	102
23	Clonally Expanded T Cells Reveal Immunogenicity of Rhabdoid Tumors. Cancer Cell, 2019, 36, 597-612.e8.	16.8	100
24	Multiparametric analysis of cytokine-driven human Th17 differentiation reveals a differential regulation of IL-17 and IL-22 production. Blood, 2009, 114, 3610-3614.	1.4	91
25	ncPRO-seq: a tool for annotation and profiling of ncRNAs in sRNA-seq data. Bioinformatics, 2012, 28, 3147-3149.	4.1	91
26	Impaired PRC2 activity promotes transcriptional instability and favors breast tumorigenesis. Genes and Development, 2015, 29, 2547-2562.	5.9	77
27	EZHIP constrains Polycomb Repressive Complex 2 activity in germ cells. Nature Communications, 2019, 10, 3858.	12.8	76
28	Highly Dynamic and Sex-Specific Expression of microRNAs During Early ES Cell Differentiation. PLoS Genetics, 2009, 5, e1000620.	3.5	73
29	Bioinformatics for precision medicine in oncology: principles and application to the SHIVA clinical trial. Frontiers in Genetics, 2014, 5, 152.	2.3	72
30	Treatment Algorithms Based on Tumor Molecular Profiling: The Essence of Precision Medicine Trials. Journal of the National Cancer Institute, 2016, 108, djv362.	6.3	71
31	Search for a Gene Expression Signature of Breast Cancer Local Recurrence in Young Women. Clinical Cancer Research, 2012, 18, 1704-1715.	7.0	67
32	High-Resolution Mapping of DNA Breakpoints to Define True Recurrences Among Ipsilateral Breast Cancers. Journal of the National Cancer Institute, 2008, 100, 48-58.	6.3	61
33	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. Nature Genetics, 2019, 51, 1024-1034.	21.4	60
34	Designs and challenges for personalized medicine studies in oncology: focus on the SHIVA trial. Targeted Oncology, 2012, 7, 253-265.	3.6	57
35	Contribution of epigenetic landscapes and transcription factors to X-chromosome reactivation in the inner cell mass. Nature Communications, 2017, 8, 1297.	12.8	52
36	Genetic and epigenetic features direct differential efficiency of Xist-mediated silencing at X-chromosomal and autosomal locations. Nature Communications, 2017, 8, 690.	12.8	50

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37	Familial breast cancer and DNA repair genes: Insights into known and novel susceptibility genes from the GENESIS study, and implications for multigene panel testing. International Journal of Cancer, 2019, 144, 1962-1974.	5.1	50
38	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. Molecular Cell, 2020, 77, 352-367.e8.	9.7	48
39	EMA - A R package for Easy Microarray data analysis. BMC Research Notes, 2010, 3, 277.	1.4	44
40	Human papilloma virus (HPV) integration signature in Cervical Cancer: identification of MACROD2 gene as HPV hot spot integration site. British Journal of Cancer, 2021, 124, 777-785.	6.4	44
41	EZH1/2 function mostly within canonical PRC2 and exhibit proliferation-dependent redundancy that shapes mutational signatures in cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6075-6080.	7.1	42
42	Combinatorial flexibility of cytokine function during human T helper cell differentiation. Nature Communications, 2014, 5, 3987.	12.8	38
43	RNAi-Dependent and Independent Control of LINE1 Accumulation and Mobility in Mouse Embryonic Stem Cells. PLoS Genetics, 2013, 9, e1003791.	3.5	37
44	Clinical and genetic landscape of treatment naive cervical cancer: Alterations in PIK3CA and in epigenetic modulators associated with sub-optimal outcome. EBioMedicine, 2019, 43, 253-260.	6.1	37
45	Independent transcriptional reprogramming and apoptosis induction by cisplatin. Cell Cycle, 2012, 11, 3472-3480.	2.6	32
46	Improving breast cancer sensitivity to paclitaxel by increasing aneuploidy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23691-23697.	7.1	32
47	Deep-Sequencing Protocols Influence the Results Obtained in Small-RNA Sequencing. PLoS ONE, 2012, 7, e32724.	2.5	31
48	Effective normalization for copy number variation in Hi-C data. BMC Bioinformatics, 2018, 19, 313.	2.6	27
49	Exome sequencing reveals aberrant signalling pathways as hallmark of treatment-naive anal squamous cell carcinoma. Oncotarget, 2018, 9, 464-476.	1.8	23
50	Telomere crisis in kidney epithelial cells promotes the acquisition of a microRNA signature retrieved in aggressive renal cell carcinomas. Carcinogenesis, 2013, 34, 1173-1180.	2.8	19
51	Mechanistic Signatures of Human Papillomavirus Insertions in Anal Squamous Cell Carcinomas. Cancers, 2019, 11, 1846.	3.7	19
52	Interactive analysis of single-cell epigenomic landscapes with ChromSCape. Nature Communications, 2020, 11, 5702.	12.8	17
53	A computational method for prioritizing targeted therapies in precision oncology: performance analysis in the SHIVA01 trial. Npj Precision Oncology, 2021, 5, 59.	5.4	16
54	The spectrum of clinical trials aiming at personalizing medicine. Chinese Clinical Oncology, 2014, 3, 13.	1.2	15

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55	Epigenomic Alterations in Breast Carcinoma from Primary Tumor to Locoregional Recurrences. PLoS ONE, 2014, 9, e103986.	2.5	12
56	Inversion of a topological domain leads to restricted changes in its gene expression and affects interdomain communication. Development (Cambridge), 2022, 149, .	2.5	10
57	Changes in the organization of the genome during the mammalian cell cycle. Genome Biology, 2013, 14, 142.	9.6	8
58	Challenges for the implementation of high-throughput testing and liquid biopsies in personalized medicine cancer trials. Personalized Medicine, 2014, 11, 545-558.	1.5	8
59	Pros and cons of HaloPlex enrichment in cancer predisposition genetic diagnosis. AIMS Genetics, 2015, 02, 263-280.	1.9	7
60	Human papilloma virus integration sites and genomic signatures in head and neck squamous cell carcinoma. Molecular Oncology, 2022, 16, 3001-3016.	4.6	7
61	Revisited analysis of a SHIVA 01 trial cohort using functional mutational analyses successfully predicted treatment outcome. Molecular Oncology, 2018, 12, 594-601.	4.6	3
62	Transcriptome Profiling of Single Mouse Oocytes. Methods in Molecular Biology, 2018, 1818, 51-65.	0.9	2
63	iced: fast and memory efficient normalization of contact maps. Journal of Open Source Software, 2019, 4, 1286.	4.6	2
64	Design and statistical principles of the SHIVA trial. Chinese Clinical Oncology, 2015, 4, 32.	1.2	1
65	P23: CAP: aÂWeb-based platform forÂCGH-array management andÂanalysis. European Journal of Medical Genetics, 2005, 48, 471-472.	1.3	0
66	Bioinformatics for Precision Medicine in Oncology. , 2015, , 69-99.		0
67	Bioinformatic Analysis of Single-Cell Hi-C Data from Early Mouse Embryo. Methods in Molecular Biology, 2021, 2214, 295-316.	0.9	0