

# Nicolas Servant

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Human papilloma virus integration sites and genomic signatures in head and neck squamous cell carcinoma. <i>Molecular Oncology</i> , 2022, 16, 3001-3016.	4.6	7
2	Inversion of a topological domain leads to restricted changes in its gene expression and affects interdomain communication. <i>Development (Cambridge)</i> , 2022, 149, .	2.5	10
3	Human papilloma virus (HPV) integration signature in Cervical Cancer: identification of MACROD2 gene as HPV hot spot integration site. <i>British Journal of Cancer</i> , 2021, 124, 777-785.	6.4	44
4	A computational method for prioritizing targeted therapies in precision oncology: performance analysis in the SHIVA01 trial. <i>Npj Precision Oncology</i> , 2021, 5, 59.	5.4	16
5	Bioinformatic Analysis of Single-Cell Hi-C Data from Early Mouse Embryo. <i>Methods in Molecular Biology</i> , 2021, 2214, 295-316.	0.9	0
6	A Conserved Noncoding Locus Regulates Random Monoallelic Xist Expression across a Topological Boundary. <i>Molecular Cell</i> , 2020, 77, 352-367.e8.	9.7	48
7	Interactive analysis of single-cell epigenomic landscapes with ChromScape. <i>Nature Communications</i> , 2020, 11, 5702.	12.8	17
8	CD44 regulates epigenetic plasticity by mediating iron endocytosis. <i>Nature Chemistry</i> , 2020, 12, 929-938.	13.6	132
9	Parental-to-embryo switch of chromosome organization in early embryogenesis. <i>Nature</i> , 2020, 580, 142-146.	27.8	116
10	Clonally Expanded T Cells Reveal Immunogenicity of Rhabdoid Tumors. <i>Cancer Cell</i> , 2019, 36, 597-612.e8.	16.8	100
11	Improving breast cancer sensitivity to paclitaxel by increasing aneuploidy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23691-23697.	7.1	32
12	EZH1P constrains Polycomb Repressive Complex 2 activity in germ cells. <i>Nature Communications</i> , 2019, 10, 3858.	12.8	76
13	BAP1 complex promotes transcription by opposing PRC1-mediated H2A ubiquitylation. <i>Nature Communications</i> , 2019, 10, 348.	12.8	105
14	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. <i>Nature Genetics</i> , 2019, 51, 1024-1034.	21.4	60
15	EZH1/2 function mostly within canonical PRC2 and exhibit proliferation-dependent redundancy that shapes mutational signatures in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6075-6080.	7.1	42
16	Clinical and genetic landscape of treatment naive cervical cancer: Alterations in PIK3CA and in epigenetic modulators associated with sub-optimal outcome. <i>EBioMedicine</i> , 2019, 43, 253-260.	6.1	37
17	Mechanistic Signatures of Human Papillomavirus Insertions in Anal Squamous Cell Carcinomas. <i>Cancers</i> , 2019, 11, 1846.	3.7	19
18	Familial breast cancer and DNA repair genes: Insights into known and novel susceptibility genes from the GENESIS study, and implications for multigene panel testing. <i>International Journal of Cancer</i> , 2019, 144, 1962-1974.	5.1	50

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19	iced: fast and memory efficient normalization of contact maps. Journal of Open Source Software, 2019, 4, 1286.	4.6	2
20	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
21	Effective normalization for copy number variation in Hi-C data. BMC Bioinformatics, 2018, 19, 313.	2.6	27
22	Transcriptome Profiling of Single Mouse Oocytes. Methods in Molecular Biology, 2018, 1818, 51-65.	0.9	2
23	Exome sequencing reveals aberrant signalling pathways as hallmark of treatment-naive anal squamous cell carcinoma. Oncotarget, 2018, 9, 464-476.	1.8	23
24	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
25	<scp>PRC</scp>2 is dispensable for <i><scp>HOTAIR</scp></i>-mediated transcriptional repression. EMBO Journal, 2017, 36, 981-994.	7.8	146
26	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
27	Contribution of epigenetic landscapes and transcription factors to X-chromosome reactivation in the inner cell mass. Nature Communications, 2017, 8, 1297.	12.8	52
28	Maternal LSD1/KDM1A is an essential regulator of chromatin and transcription landscapes during zygotic genome activation. ELife, 2016, 5, .	6.0	107
29	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
30	Impaired PRC2 activity promotes transcriptional instability and favors breast tumorigenesis. Genes and Development, 2015, 29, 2547-2562.	5.9	77
31	Jarid2 Methylation via the PRC2 Complex Regulates H3K27me3 Deposition during Cell Differentiation. Molecular Cell, 2015, 57, 769-783.	9.7	229
32	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. Genome Biology, 2015, 16, 259.	8.8	1,632
33	DNA methylation restrains transposons from adopting a chromatin signature permissive for meiotic recombination. Genes and Development, 2015, 29, 1256-1270.	5.9	146
34	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
35	Mechanical induction of the tumorigenic $\beta$ -catenin pathway by tumour growth pressure. Nature, 2015, 523, 92-95.	27.8	288
36	Bioinformatics for Precision Medicine in Oncology. , 2015, , 69-99.		0

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37	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. <i>Lancet Oncology</i> , The, 2015, 16, 1324-1334.	10.7	897
38	Pros and cons of HaloPlex enrichment in cancer predisposition genetic diagnosis. <i>AIMS Genetics</i> , 2015, 02, 263-280.	1.9	7
39	Design and statistical principles of the SHIVA trial. <i>Chinese Clinical Oncology</i> , 2015, 4, 32.	1.2	1
40	Epigenomic Alterations in Breast Carcinoma from Primary Tumor to Locoregional Recurrences. <i>PLoS ONE</i> , 2014, 9, e103986.	2.5	12
41	Challenges for the implementation of high-throughput testing and liquid biopsies in personalized medicine cancer trials. <i>Personalized Medicine</i> , 2014, 11, 545-558.	1.5	8
42	Bioinformatics for precision medicine in oncology: principles and application to the SHIVA clinical trial. <i>Frontiers in Genetics</i> , 2014, 5, 152.	2.3	72
43	Multi-factor data normalization enables the detection of copy number aberrations in amplicon sequencing data. <i>Bioinformatics</i> , 2014, 30, 3443-3450.	4.1	109
44	Developmental Dynamics and Disease Potential of Random Monoallelic Gene Expression. <i>Developmental Cell</i> , 2014, 28, 366-380.	7.0	118
45	Combinatorial flexibility of cytokine function during human T helper cell differentiation. <i>Nature Communications</i> , 2014, 5, 3987.	12.8	38
46	The spectrum of clinical trials aiming at personalizing medicine. <i>Chinese Clinical Oncology</i> , 2014, 3, 13.	1.2	15
47	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	6.5	1,064
48	Changes in the organization of the genome during the mammalian cell cycle. <i>Genome Biology</i> , 2013, 14, 142.	9.6	8
49	RNAi-Dependent and Independent Control of LINE1 Accumulation and Mobility in Mouse Embryonic Stem Cells. <i>PLoS Genetics</i> , 2013, 9, e1003791.	3.5	37
50	Telomere crisis in kidney epithelial cells promotes the acquisition of a microRNA signature retrieved in aggressive renal cell carcinomas. <i>Carcinogenesis</i> , 2013, 34, 1173-1180.	2.8	19
51	ncPRO-seq: a tool for annotation and profiling of ncRNAs in sRNA-seq data. <i>Bioinformatics</i> , 2012, 28, 3147-3149.	4.1	91
52	Independent transcriptional reprogramming and apoptosis induction by cisplatin. <i>Cell Cycle</i> , 2012, 11, 3472-3480.	2.6	32
53	Search for a Gene Expression Signature of Breast Cancer Local Recurrence in Young Women. <i>Clinical Cancer Research</i> , 2012, 18, 1704-1715.	7.0	67
54	HiTC: exploration of high-throughput "C&E"™ experiments. <i>Bioinformatics</i> , 2012, 28, 2843-2844.	4.1	165

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55	Designs and challenges for personalized medicine studies in oncology: focus on the SHIVA trial. Targeted Oncology, 2012, 7, 253-265.	3.6	57
56	Prognostic Impact of Vitamin B6 Metabolism in Lung Cancer. Cell Reports, 2012, 2, 257-269.	6.4	122
57	Deep-Sequencing Protocols Influence the Results Obtained in Small-RNA Sequencing. PLoS ONE, 2012, 7, e32724.	2.5	31
58	Spatial partitioning of the regulatory landscape of the X-inactivation centre. Nature, 2012, 485, 381-385.	27.8	2,595
59	EMA - A R package for Easy Microarray data analysis. BMC Research Notes, 2010, 3, 277.	1.4	44
60	miR-181a and miR-630 Regulate Cisplatin-Induced Cancer Cell Death. Cancer Research, 2010, 70, 1793-1803.	0.9	262
61	LINE-1 Activity in Facultative Heterochromatin Formation during X Chromosome Inactivation. Cell, 2010, 141, 956-969.	28.9	296
62	Highly Dynamic and Sex-Specific Expression of microRNAs During Early ES Cell Differentiation. PLoS Genetics, 2009, 5, e1000620.	3.5	73
63	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
64	A critical function for transforming growth factor- $\beta$ 2, interleukin 23 and proinflammatory cytokines in driving and modulating human TH-17 responses. Nature Immunology, 2008, 9, 650-657.	14.5	844
65	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
66	VAMP: Visualization and analysis of array-CGH, transcriptome and other molecular profiles. Bioinformatics, 2006, 22, 2066-2073.	4.1	106
67	P23: CAP: a Web-based platform for aCGH-array management and analysis. European Journal of Medical Genetics, 2005, 48, 471-472.	1.3	0