

# Alessandro Romanel

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

3,701  
citations

361413  
20  
h-index

214800  
47  
g-index

53  
all docs

53  
docs citations

53  
times ranked

7109  
citing authors

#	ARTICLE	IF	CITATIONS
1	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	28.9	1,107
2	A highly specific SpCas9 variant is identified by in vivo screening in yeast. <i>Nature Biotechnology</i> , 2018, 36, 265-271.	17.5	377
3	Plasma <i>AR</i> and abiraterone-resistant prostate cancer. <i>Science Translational Medicine</i> , 2015, 7, 312re10.	12.4	366
4	Tumor clone dynamics in lethal prostate cancer. <i>Science Translational Medicine</i> , 2014, 6, 254ra125.	12.4	298
5	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. <i>JAMA Oncology</i> , 2015, 1, 466.	7.1	264
6	A Phase II Trial of the Aurora Kinase A Inhibitor Alisertib for Patients with Castration-resistant and Neuroendocrine Prostate Cancer: Efficacy and Biomarkers. <i>Clinical Cancer Research</i> , 2019, 25, 43-51.	7.0	177
7	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	16.8	151
8	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 1653-1668.	8.2	122
9	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. <i>Cancer Discovery</i> , 2017, 7, 973-983.	9.4	94
10	Unraveling the clonal hierarchy of somatic genomic aberrations. <i>Genome Biology</i> , 2014, 15, 439.	8.8	80
11	Hit and go CAS9 delivered through a lentiviral based self-limiting circuit. <i>Nature Communications</i> , 2017, 8, 15334.	12.8	75
12	The Beta Workbench: a computational tool to study the dynamics of biological systems. <i>Briefings in Bioinformatics</i> , 2008, 9, 437-449.	6.5	68
13	Development and validation of a whole-exome sequencing test for simultaneous detection of point mutations, indels and copy-number alterations for precision cancer care. <i>Npj Genomic Medicine</i> , 2016, 1, .	3.8	68
14	ASEQ: fast allele-specific studies from next-generation sequencing data. <i>BMC Medical Genomics</i> , 2015, 8, 9.	1.5	51
15	Third generation EGFR inhibitor osimertinib combined with pemetrexed or cisplatin exerts long-lasting anti-tumor effect in EGFR-mutated pre-clinical models of NSCLC. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 222.	8.6	45
16	RB1 Heterogeneity in Advanced Metastatic Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 687-697.	7.0	43
17	The BlenX Language: A Tutorial. <i>Lecture Notes in Computer Science</i> , 2008, , 313-365.	1.3	43
18	EthSEQ: ethnicity annotation from whole exome sequencing data. <i>Bioinformatics</i> , 2017, 33, 2402-2404.	4.1	31

#	ARTICLE	IF	CITATIONS
19	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	3.0	24
20	Inherited determinants of early recurrent somatic mutations in prostate cancer. <i>Nature Communications</i> , 2017, 8, 48.	12.8	23
21	Plasma tumour DNA as an early indicator of treatment response in metastatic castration-resistant prostate cancer. <i>British Journal of Cancer</i> , 2020, 123, 982-987.	6.4	22
22	Calcium cytotoxicity sensitizes prostate cancer cells to standard-of-care treatments for locally advanced tumors. <i>Cell Death and Disease</i> , 2020, 11, 1039.	6.3	20
23	Transcriptional Regulation Is a Major Controller of Cell Cycle Transition Dynamics. <i>PLoS ONE</i> , 2012, 7, e29716.	2.5	15
24	One-shot analysis of translated mammalian lncRNAs with AHARIBO. <i>ELife</i> , 2021, 10, .	6.0	15
25	Estimating the divisibility of complex biological networks by sparseness indices. <i>Briefings in Bioinformatics</i> , 2010, 11, 364-374.	6.5	14
26	PaCBAM: fast and scalable processing of whole exome and targeted sequencing data. <i>BMC Genomics</i> , 2019, 20, 1018.	2.8	9
27	Modeling Static Biological Compartments with Beta-binders. <i>Lecture Notes in Computer Science</i> , 2007, , 247-261.	1.3	8
28	Intraepithelial noncanonical Activin A signaling safeguards prostate progenitor quiescence. <i>EMBO Reports</i> , 2022, 23, e54049.	4.5	8
29	Core Biopsies from Prostate Cancer Patients in Active Surveillance Protocols Harbor PTEN and MYC Alterations. <i>European Urology Oncology</i> , 2019, 2, 277-285.	5.4	7
30	ABEMUS: platform-specific and data-informed detection of somatic SNVs in cfDNA. <i>Bioinformatics</i> , 2020, 36, 2665-2674.	4.1	7
31	BlenX Static and Dynamic Semantics. <i>Lecture Notes in Computer Science</i> , 2009, , 37-52.	1.3	7
32	<i>In silico</i> identification and functional validation of allele-dependent AR enhancers. <i>Oncotarget</i> , 2015, 6, 4816-4828.	1.8	6
33	ETS-related gene (ERG) undermines genome stability in mouse prostate progenitors via Gsk3 <sup>β</sup> dependent Nrx3.1 degradation. <i>Cancer Letters</i> , 2022, 534, 215612.	7.2	6
34	Inherited variant in NF1 promoter is associated with increased risk of IBD in an Algerian population and modulates SOX9 binding. <i>Cancer Reports</i> , 2020, 3, e1240.	1.4	5
35	The Decidability of the Structural Congruence for Beta-binders. <i>Electronic Notes in Theoretical Computer Science</i> , 2007, 171, 155-170.	0.9	4
36	On the impact of discreteness and abstractions on modelling noise in gene regulatory networks. <i>Computational Biology and Chemistry</i> , 2015, 56, 98-108.	2.3	4

#	ARTICLE	IF	CITATIONS
37	Allele-Specific Expression Analysis in Cancer Using Next-Generation Sequencing Data. <i>Methods in Molecular Biology</i> , 2019, 1878, 125-137.	0.9	4
38	Plasma tumor <scp>DNA</scp> is associated with increased risk of venous thromboembolism in metastatic castrationâ€resistant cancer patients. <i>International Journal of Cancer</i> , 2022, 150, 1166-1173.	5.1	4
39	Allele-informed copy number evaluation of plasma DNA samples from metastatic prostate cancer patients: the PCF_SELECT consortium assay. <i>NAR Cancer</i> , 2022, 4, .	3.1	4
40	Polypact: exploring functional relations among common human genetic variants. <i>Nucleic Acids Research</i> , 2022, 50, 1335-1350.	14.5	3
41	YES1 and MYC Amplifications as Synergistic Resistance Mechanisms to Different Generation ALK Tyrosine Kinase Inhibitors in Advanced NSCLC: Brief Report of Clinical and Preclinical Proofs. <i>JTO Clinical and Research Reports</i> , 2022, 3, 100278.	1.1	3
42	Exploring functionally annotated transcriptional consensus regulatory elements with CONREL. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	2
43	TranSNPs: A class of functional SNPs affecting mRNA translation potential revealed by fraction-based allelic imbalance. <i>IScience</i> , 2021, 24, 103531.	4.1	2
44	On the computational power of BlenX. <i>Theoretical Computer Science</i> , 2010, 411, 542-565.	0.9	1
45	Modelling Self-assembly in BlenX. <i>Lecture Notes in Computer Science</i> , 2010, , 163-198.	1.3	1
46	Circulating tumor DNA fraction (ctDNA) as a surrogate predictive biomarker in metastatic castration-resistant prostate cancer (mCRPC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 5039-5039.	1.6	1