

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	Plasma tumor DNA is associated with increased risk of venous thromboembolism in metastatic castration-resistant cancer patients. <i>International Journal of Cancer</i> , 2022, 150, 1166-1173.	5.1	4
2	PolymPact: exploring functional relations among common human genetic variants. <i>Nucleic Acids Research</i> , 2022, 50, 1335-1350.	14.5	3
3	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
4	Intraepithelial noncanonical Activin A signaling safeguards prostate progenitor quiescence. <i>EMBO Reports</i> , 2022, 23, e54049.	4.5	8
5	ETS-related gene (ERG) undermines genome stability in mouse prostate progenitors via Gsk3 β dependent Nrx3.1 degradation. <i>Cancer Letters</i> , 2022, 534, 215612.	7.2	6
6	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
7	One-shot analysis of translated mammalian lncRNAs with AHARIBO. <i>ELife</i> , 2021, 10, .	6.0	15
8	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
9	ABEMUS: platform-specific and data-informed detection of somatic SNVs in cfDNA. <i>Bioinformatics</i> , 2020, 36, 2665-2674.	4.1	7
10	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
11	Exploring functionally annotated transcriptional consensus regulatory elements with CONREL. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	2
12	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
13	Inherited variant in NF κ B 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
14	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	16.8	151
15	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
16	Integrative Molecular Analysis of Patients With Advanced and Metastatic Cancer. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	3.0	24
17	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
18	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

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19	PaCBAM: fast and scalable processing of whole exome and targeted sequencing data. BMC Genomics, 2019, 20, 1018.	2.8	9
20	A Phase II Trial of the Aurora Kinase A Inhibitor Alisertib for Patients with Castration-resistant and Neuroendocrine Prostate Cancer: Efficacy and Biomarkers. Clinical Cancer Research, 2019, 25, 43-51.	7.0	177
21	Allele-Specific Expression Analysis in Cancer Using Next-Generation Sequencing Data. Methods in Molecular Biology, 2019, 1878, 125-137.	0.9	4
22	RB1 Heterogeneity in Advanced Metastatic Castration-Resistant Prostate Cancer. Clinical Cancer Research, 2019, 25, 687-697.	7.0	43
23	Circulating tumor DNA fraction (ctDNA) as a surrogate predictive biomarker in metastatic castration-resistant prostate cancer (mCRPC).. Journal of Clinical Oncology, 2019, 37, 5039-5039.	1.6	1
24	A highly specific SpCas9 variant is identified by in vivo screening in yeast. Nature Biotechnology, 2018, 36, 265-271.	17.5	377
25	EthSEQ: ethnicity annotation from whole exome sequencing data. Bioinformatics, 2017, 33, 2402-2404.	4.1	31
26	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. Cancer Discovery, 2017, 7, 973-983.	9.4	94
27	Hit and go CAS9 delivered through a lentiviral based self-limiting circuit. Nature Communications, 2017, 8, 15334.	12.8	75
28	Inherited determinants of early recurrent somatic mutations in prostate cancer. Nature Communications, 2017, 8, 48.	12.8	23
29	Development and validation of a whole-exome sequencing test for simultaneous detection of point mutations, indels and copy-number alterations for precision cancer care. Npj Genomic Medicine, 2016, 1, .	3.8	68
30	Whole-Exome Sequencing of Metastatic Cancer and Biomarkers of Treatment Response. JAMA Oncology, 2015, 1, 466.	7.1	264
31	On the impact of discreteness and abstractions on modelling noise in gene regulatory networks. Computational Biology and Chemistry, 2015, 56, 98-108.	2.3	4
32	ASEQ: fast allele-specific studies from next-generation sequencing data. BMC Medical Genomics, 2015, 8, 9.	1.5	51
33	Plasma <i>AR</i> and abiraterone-resistant prostate cancer. Science Translational Medicine, 2015, 7, 312re10.	12.4	366
34	<i>In silico</i> identification and functional validation of allele-dependent AR enhancers. Oncotarget, 2015, 6, 4816-4828.	1.8	6
35	Unraveling the clonal hierarchy of somatic genomic aberrations. Genome Biology, 2014, 15, 439.	8.8	80
36	Tumor clone dynamics in lethal prostate cancer. Science Translational Medicine, 2014, 6, 254ra125.	12.4	298

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37	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	28.9	1,107
38	Transcriptional Regulation Is a Major Controller of Cell Cycle Transition Dynamics. <i>PLoS ONE</i> , 2012, 7, e29716.	2.5	15
39	On the computational power of BlenX. <i>Theoretical Computer Science</i> , 2010, 411, 542-565.	0.9	1
40	Estimating the divisibility of complex biological networks by sparseness indices. <i>Briefings in Bioinformatics</i> , 2010, 11, 364-374.	6.5	14
41	Modelling Self-assembly in BlenX. <i>Lecture Notes in Computer Science</i> , 2010, , 163-198.	1.3	1
42	BlenX Static and Dynamic Semantics. <i>Lecture Notes in Computer Science</i> , 2009, , 37-52.	1.3	7
43	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
44	The BlenX Language: A Tutorial. <i>Lecture Notes in Computer Science</i> , 2008, , 313-365.	1.3	43
45	The Decidability of the Structural Congruence for Beta-binders. <i>Electronic Notes in Theoretical Computer Science</i> , 2007, 171, 155-170.	0.9	4
46	Modeling Static Biological Compartments with Beta-binders. <i>Lecture Notes in Computer Science</i> , 2007, , 247-261.	1.3	8