

Nicolai J Birkbak

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

10,618
citations

430442

18
h-index

676716

22
g-index

25
all docs

25
docs citations

25
times ranked

17704
citing authors

#	ARTICLE	IF	CITATIONS
1	Clonal neoantigens elicit T cell immunoreactivity and sensitivity to immune checkpoint blockade. <i>Science</i> , 2016, 351, 1463-1469.	6.0	2,445
2	Tracking the Evolution of Non-Small-Cell Lung Cancer. <i>New England Journal of Medicine</i> , 2017, 376, 2109-2121.	13.9	1,786
3	Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. <i>Nature</i> , 2017, 545, 446-451.	13.7	1,287
4	Chromosomal instability drives metastasis through a cytosolic DNA response. <i>Nature</i> , 2018, 553, 467-472.	13.7	1,002
5	Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution. <i>Cell</i> , 2017, 171, 1259-1271.e11.	13.5	968
6	Neoantigen-directed immune escape in lung cancer evolution. <i>Nature</i> , 2019, 567, 479-485.	13.7	639
7	Deterministic Evolutionary Trajectories Influence Primary Tumor Growth: TRACERx Renal. <i>Cell</i> , 2018, 173, 595-610.e11.	13.5	472
8	Evolution and clinical impact of co-occurring genetic alterations in advanced-stage EGFR-mutant lung cancers. <i>Nature Genetics</i> , 2017, 49, 1693-1704.	9.4	423
9	Early stage NSCLC challenges to implementing ctDNA-based screening and MRD detection. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 577-586.	12.5	281
10	Jetset: selecting the optimal microarray probe set to represent a gene. <i>BMC Bioinformatics</i> , 2011, 12, 474.	1.2	277
11	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , 2020, 587, 126-132.	13.7	221
12	Interplay between whole-genome doubling and the accumulation of deleterious alterations in cancer evolution. <i>Nature Genetics</i> , 2020, 52, 283-293.	9.4	168
13	An integrated multi-omics analysis identifies prognostic molecular subtypes of non-muscle-invasive bladder cancer. <i>Nature Communications</i> , 2021, 12, 2301.	5.8	159
14	Spatial heterogeneity of the T cell receptor repertoire reflects the mutational landscape in lung cancer. <i>Nature Medicine</i> , 2019, 25, 1549-1559.	15.2	147
15	Cancer Genome Evolutionary Trajectories in Metastasis. <i>Cancer Cell</i> , 2020, 37, 8-19.	7.7	140
16	A clonal expression biomarker associates with lung cancer mortality. <i>Nature Medicine</i> , 2019, 25, 1540-1548.	15.2	75
17	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. <i>Cell Reports</i> , 2020, 31, 107550.	2.9	51
18	Using DNA sequencing data to quantify T cell fraction and therapy response. <i>Nature</i> , 2021, 597, 555-560.	13.7	36

#	ARTICLE	IF	CITATIONS
19	E3 ligase RFW3 is a novel modulator of stalled fork stability in BRCA2-deficient cells. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	13
20	Treatment Represents a Key Driver of Metastatic Cancer Evolution. <i>Cancer Research</i> , 2022, 82, 2918-2927.	0.4	11
21	Increased Soluble PD-1 Predicts Response to Nivolumab plus Ipilimumab in Melanoma. <i>Cancers</i> , 2022, 14, 3342.	1.7	9
22	Classifying cGAS-STING Activity Links Chromosomal Instability with Immunotherapy Response in Metastatic Bladder Cancer. <i>Cancer Research Communications</i> , 2022, 2, 762-771.	0.7	6
23	Abstract 6091: Evolutionary characterisation of lung adenocarcinoma pathological subtypes in TRACERx. <i>Cancer Research</i> , 2022, 82, 6091-6091.	0.4	0