Andrea Sottoriva

List of Publications by Year
in descending order

59 papers	8,545 citations	136950 32 h-index	133252 59 g-index
86 all docs	86 docs citations	86 times ranked	14588 citing authors

#	Article	IF	Citations
1	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4009-4014.	7.1	1,471
2	Patient-derived organoids model treatment response of metastatic gastrointestinal cancers. Science, 2018, 359, 920-926.	12.6	1,199
3	A Big Bang model of human colorectal tumor growth. Nature Genetics, 2015, 47, 209-216.	21.4	867
4	Identification of neutral tumor evolution across cancer types. Nature Genetics, 2016, 48, 238-244.	21.4	525
5	Resolving genetic heterogeneity in cancer. Nature Reviews Genetics, 2019, 20, 404-416.	16.3	443
6	The shaping and functional consequences of the microRNA landscape in breast cancer. Nature, 2013, 497, 378-382.	27.8	370
7	Defining Stem Cell Dynamics in Models of Intestinal Tumor Initiation. Science, 2013, 342, 995-998.	12.6	355
8	Classifying the evolutionary and ecological features of neoplasms. Nature Reviews Cancer, 2017, 17, 605-619.	28.4	303
9	Cancer Evolution and the Limits of Predictability in Precision Cancer Medicine. Trends in Cancer, 2016, 2, 49-63.	7.4	222
10	Quantification of subclonal selection in cancer from bulk sequencing data. Nature Genetics, 2018, 50, 895-903.	21.4	222
11	Longitudinal Liquid Biopsy and Mathematical Modeling of Clonal Evolution Forecast Time to Treatment Failure in the PROSPECT-C Phase II Colorectal Cancer Clinical Trial. Cancer Discovery, 2018, 8, 1270-1285.	9.4	187
12	Cancer Stem Cell Tumor Model Reveals Invasive Morphology and Increased Phenotypical Heterogeneity. Cancer Research, 2010, 70, 46-56.	0.9	180
13	A multiphysics and multiscale software environment for modeling astrophysical systems. New Astronomy, 2009, 14, 369-378.	1.8	146
14	Between-region genetic divergence reflects the mode and tempo of tumor evolution. Nature Genetics, 2017, 49, 1015-1024.	21.4	144
15	Detecting repeated cancer evolution from multi-region tumor sequencing data. Nature Methods, 2018, 15, 707-714.	19.0	124
16	The evolutionary landscape of colorectal tumorigenesis. Nature Ecology and Evolution, 2018, 2, 1661-1672.	7.8	99
17	Measuring cancer evolution from the genome. Journal of Pathology, 2017, 241, 183-191.	4.5	93
18	Exploiting evolutionary steering to induce collateral drug sensitivity in cancer. Nature Communications, 2020, 11, 1923.	12.8	79

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19	EGFRvIII mutations can emerge as late and heterogenous events in glioblastoma development and promote angiogenesis through Src activation. Neuro-Oncology, 2016, 18, 1644-1655.	1.2	78
20	Current Challenges in Glioblastoma: Intratumour Heterogeneity, Residual Disease, and Models to Predict Disease Recurrence. Frontiers in Oncology, 2015, 5, 251.	2.8	77
21	Subclonal reconstruction of tumors by using machine learning and population genetics. Nature Genetics, 2020, 52, 898-907.	21.4	77
22	Prediction of Benefit from Checkpoint Inhibitors in Mismatch Repair Deficient Metastatic Colorectal Cancer: Role of Tumor Infiltrating Lymphocytes. Oncologist, 2020, 25, 481-487.	3.7	77
23	Single-Molecule Genomic Data Delineate Patient-Specific Tumor Profiles and Cancer Stem Cell Organization. Cancer Research, 2013, 73, 41-49.	0.9	68
24	Evolutionary dynamics of neoantigens in growing tumors. Nature Genetics, 2020, 52, 1057-1066.	21.4	68
25	The Cancer Stem Cell Fraction in Hierarchically Organized Tumors Can Be Estimated Using Mathematical Modeling and Patient-Specific Treatment Trajectories. Cancer Research, 2016, 76, 1705-1713.	0.9	65
26	Spatially constrained tumour growth affects the patterns of clonal selection and neutral drift in cancer genomic data. PLoS Computational Biology, 2019, 15, e1007243.	3.2	59
27	Robust RNA-based in situ mutation detection delineates colorectal cancer subclonal evolution. Nature Communications, 2017, 8, 1998.	12.8	57
28	Modeling Evolutionary Dynamics of Epigenetic Mutations in Hierarchically Organized Tumors. PLoS Computational Biology, 2011, 7, e1001132.	3.2	53
29	Measuring Clonal Evolution in Cancer with Genomics. Annual Review of Genomics and Human Genetics, 2019, 20, 309-329.	6.2	52
30	Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. Cancer Research, 2015, 75, 194-202.	0.9	48
31	Evolutionary dynamics of residual disease in human glioblastoma. Annals of Oncology, 2019, 30, 456-463.	1.2	47
32	Measuring single cell divisions in human tissues from multi-region sequencing data. Nature Communications, 2020, 11, 1035.	12.8	41
33	Colorectal cancer residual disease at maximal response to EGFR blockade displays a druggable Paneth cellâ€"like phenotype. Science Translational Medicine, 2020, 12, .	12.4	40
34	Epigenetic Profile of Human Adventitial Progenitor Cells Correlates With Therapeutic Outcomes in a Mouse Model of Limb Ischemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 675-688.	2.4	38
35	Reconstructing single-cell karyotype alterations in colorectal cancer identifies punctuated and gradual diversification patterns. Nature Genetics, 2021, 53, 1187-1195.	21.4	37
36	Microenvironmental niche divergence shapes BRCA1-dysregulated ovarian cancer morphological plasticity. Nature Communications, 2018, 9, 3917.	12.8	33

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37	Exploring cancer stem cell niche directed tumor growth. Cell Cycle, 2010, 9, 1472-1479.	2.6	32
38	Measuring the distribution of fitness effects in somatic evolution by combining clonal dynamics with dN/dS ratios. ELife, 2020, 9, .	6.0	32
39	Many private mutations originate from the first few divisions of a human colorectal adenoma. Journal of Pathology, 2015, 237, 355-362.	4.5	30
40	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. Clinical Cancer Research, 2018, 24, 4763-4770.	7.0	30
41	Mapping the breast cancer metastatic cascade onto ctDNA using genetic and epigenetic clonal tracking. Nature Communications, 2020, 11, 1446.	12.8	28
42	Reply to 'Neutral tumor evolution?'. Nature Genetics, 2018, 50, 1633-1637.	21.4	27
43	Variation of mutational burden in healthy human tissues suggests non-random strand segregation and allows measuring somatic mutation rates. PLoS Computational Biology, 2018, 14, e1006233.	3.2	26
44	Carbon dating cancer: defining the chronology of metastatic progression in colorectal cancer. Annals of Oncology, 2017, 28, 1243-1249.	1.2	25
45	Detecting truly clonal alterations from multi-region profiling of tumours. Scientific Reports, 2017, 7, 44991.	3.3	24
46	EGFR amplification and outcome in a randomised phase III trial of chemotherapy alone or chemotherapy plus panitumumab for advanced gastro-oesophageal cancers. Gut, 2021, 70, 1632-1641.	12.1	24
47	Catch my drift? Making sense of genomic intra-tumour heterogeneity. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 95-100.	7.4	23
48	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. American Journal of Human Genetics, 2022, 109, 953-960.	6.2	23
49	Immunosuppressive niche engineering at the onset of human colorectal cancer. Nature Communications, 2022, 13, 1798.	12.8	19
50	The MOBSTER R package for tumour subclonal deconvolution from bulk DNA whole-genome sequencing data. BMC Bioinformatics, 2020, 21, 531.	2.6	18
51	Circulating tumour DNA sequencing to determine therapeutic response and identify tumour heterogeneity in patients with paediatric solid tumours. European Journal of Cancer, 2022, 162, 209-220.	2.8	12
52	Reply to 'Currently available bulk sequencing data do not necessarily support a model of neutral tumor evolution'. Nature Genetics, 2018, 50, 1624-1626.	21.4	11
53	Analysis of tumour ecological balance reveals resource-dependent adaptive strategies of ovarian cancer. EBioMedicine, 2019, 48, 224-235.	6.1	8
54	Reply: Uncertainties in tumor allele frequencies limit power to infer evolutionary pressures. Nature Genetics, 2017, 49, 1289-1291.	21.4	7

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55	The role of sub-ventricular zone in gliomagenesis. Aging, 2015, 7, 738-739.	3.1	6
56	Functional versus non-functional intratumor heterogeneity in cancer. Molecular and Cellular Oncology, 2016, 3, e1162897.	0.7	5
57	Reply to â€˜Revisiting signatures of neutral tumor evolution in the light of complexity of cancer genomic dataâ€™. Nature Genetics, 2018, 50, 1628-1630.	21.4	5
58	Reply: Is the evolution of tumors Darwinian or non-Darwinian?. National Science Review, 2018, 5, 17-19.	9.5	3
59	Reply: Neutral tumor evolution?. , 0, , .		1