Nicola Crosetto

List of Publications by Year in descending order

44 papers	3,759 citations	377584 21 h-index	299063 42 g-index
55 all docs	55 docs citations	55 times ranked	7813 citing authors

#	Article	IF	Citations
1	RNA gradients: Shapers of 3D genome architecture. Current Opinion in Cell Biology, 2022, 74, 7-12.	2.6	11
2	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH. Scientific Data, 2022, 9, 47.	2.4	2
3	The era of 3D and spatial genomics. Trends in Genetics, 2022, 38, 1062-1075.	2.9	25
4	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. Scientific Data, 2022, 9, .	2.4	3
5	Abstract PS18-27: Integrated immuno-genomic analyses in early breast cancer: Results from the Scandinavian breast group 2004-1 (SBG-2004-1) randomized phase II trial. , 2021, , .		0
6	Cytokine Profiling of End Stage Cancer Patients Treated with Immunotherapy. Vaccines, 2021, 9, 235.	2.1	3
7	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. Nature Communications, 2021, 12, 3903.	5.8	14
8	Somatic Copy Number Alterations in Human Cancers: An Analysis of Publicly Available Data From The Cancer Genome Atlas. Frontiers in Oncology, 2021, 11, 700568.	1.3	33
9	Genome-Wide CRISPR Off-Target DNA Break Detection by the BLISS Method. Methods in Molecular Biology, 2021, 2162, 261-281.	0.4	4
10	Interplay between copy number alterations and immune profiles in the early breast cancer Scandinavian Breast Group 2004-1 randomized phase II trial: results from a feasibility study. Npj Breast Cancer, 2021, 7, 144.	2.3	3
11	Topoisomerase 1 activity during mitotic transcription favors the transition from mitosis to G1. Molecular Cell, 2021, 81, 5007-5024.e9.	4.5	16
12	A recurrent chromosomal inversion suffices for driving escape from oncogene-induced senescence via subTAD reorganization. Molecular Cell, 2021, 81, 4907-4923.e8.	4.5	28
13	The Role of Intratumor Heterogeneity in the Response of Metastatic Non-Small Cell Lung Cancer to Immune Checkpoint Inhibitors. Frontiers in Oncology, 2020, 10, 569202.	1.3	22
14	Treating patients with cancer amidst the COVID-19 pandemic: experience of a regional hospital in the Piedmont region in northern Italy. Tumori, 2020, 106, 427-431.	0.6	1
15	Exploratory analysis of circulating cytokines in patients with metastatic breast cancer treated with eribulin: the TRANSERI-GONO (Gruppo Oncologico del Nord Ovest) study. ESMO Open, 2020, 5, e000876.	2.0	12
16	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. Nature Protocols, 2020, 15, 3894-3941.	5.5	19
17	Colibactin DNA-damage signature indicates mutational impact in colorectal cancer. Nature Medicine, 2020, 26, 1063-1069.	15.2	149
18	Radial Organization in the Mammalian Nucleus. Frontiers in Genetics, 2020, 11, 33.	1.1	32

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19	GPSeq reveals the radial organization of chromatin in the cell nucleus. Nature Biotechnology, 2020, 38, 1184-1193.	9.4	49
20	Activation of Oncogenic Super-Enhancers Is Coupled with DNA Repair by RAD51. Cell Reports, 2019, 29, 560-572.e4.	2.9	39
21	CUTseq is a versatile method for preparing multiplexed DNA sequencing libraries from low-input samples. Nature Communications, 2019, 10, 4732.	5.8	12
22	Spatial Chromosome Folding and Active Transcription Drive DNA Fragility and Formation of Oncogenic MLL Translocations. Molecular Cell, 2019, 75, 267-283.e12.	4.5	104
23	Release of paused RNA polymerase II at specific loci favors DNA double-strand-break formation and promotes cancer translocations. Nature Genetics, 2019, 51, 1011-1023.	9.4	73
24	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. Nature Communications, 2019, 10, 1636.	5.8	41
25	Modeling double strand break susceptibility to interrogate structural variation in cancer. Genome Biology, 2019, 20, 28.	3.8	11
26	Chemoresistance Evolution in Triple-Negative Breast Cancer Delineated by Single-Cell Sequencing. Cell, 2018, 173, 879-893.e13.	13.5	777
27	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. Methods in Molecular Biology, 2018, 1766, 303-333.	0.4	8
28	Genome-Wide Profiling of DNA Double-Strand Breaks by the BLESS and BLISS Methods. Methods in Molecular Biology, 2018, 1672, 167-194.	0.4	15
29	RollFISH achieves robust quantification of single-molecule RNA biomarkers in paraffin-embedded tumor tissue samples. Communications Biology, 2018, 1, 209.	2.0	26
30	Endogenous DNA Double-Strand Breaks during DNA Transactions: Emerging Insights and Methods for Genome-Wide Profiling. Genes, 2018, 9, 632.	1.0	43
31	i-BLESS is an ultra-sensitive method for detection of DNA double-strand breaks. Communications Biology, 2018, 1, 181.	2.0	37
32	Ssb1 and Ssb2 cooperate to regulate mouse hematopoietic stem and progenitor cells by resolving replicative stress. Blood, 2017, 129, 2479-2492.	0.6	18
33	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. Nature Communications, 2017, 8, 15058.	5.8	298
34	A damaged genomeâ€™s transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. Nature Communications, 2017, 8, 15656.	5.8	89
35	Nanogrid single-nucleus RNA sequencing reveals phenotypic diversity in breast cancer. Nature Communications, 2017, 8, 228.	5.8	105
36	Synthetic lethality between androgen receptor signalling and the PARP pathway in prostate cancer. Nature Communications, 2017, 8, 374.	5.8	180

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37	Engineered Cpf1 variants with altered PAM specificities. Nature Biotechnology, 2017, 35, 789-792.	9.4	351
38	Quantification of HER2 and estrogen receptor heterogeneity in breast cancer by single-molecule RNA fluorescence in situ hybridization. Oncotarget, 2017, 8, 18680-18698.	0.8	24
39	Combined inhibition of DDR1 and Notch signaling is a therapeutic strategy for KRAS-driven lung adenocarcinoma. Nature Medicine, 2016, 22, 270-277.	15.2	150
40	Spatially resolved transcriptomics and beyond. Nature Reviews Genetics, 2015, 16, 57-66.	7.7	406
41	FuseFISH: Robust Detection of Transcribed Gene Fusions in Single Cells. Cell Reports, 2014, 6, 18-23.	2.9	39
42	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. Nature Methods, 2013, 10, 122-124.	9.0	66
43	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. Nature Methods, 2013, 10, 361-365.	9.0	409
44	iFISH:a publically available resource enabling versatile DNA FISH to study genome architecture. Protocol Exchange, 0, , .	0.3	3