

# Nicola Crosetto

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

3,759  
citations

331670

21  
h-index

265206

42  
g-index

55  
all docs

55  
docs citations

55  
times ranked

7086  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemoresistance Evolution in Triple-Negative Breast Cancer Delineated by Single-Cell Sequencing. <i>Cell</i> , 2018, 173, 879-893.e13.	28.9	777
2	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. <i>Nature Methods</i> , 2013, 10, 361-365.	19.0	409
3	Spatially resolved transcriptomics and beyond. <i>Nature Reviews Genetics</i> , 2015, 16, 57-66.	16.3	406
4	Engineered Cpf1 variants with altered PAM specificities. <i>Nature Biotechnology</i> , 2017, 35, 789-792.	17.5	351
5	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. <i>Nature Communications</i> , 2017, 8, 15058.	12.8	298
6	Synthetic lethality between androgen receptor signalling and the PARP pathway in prostate cancer. <i>Nature Communications</i> , 2017, 8, 374.	12.8	180
7	Combined inhibition of DDR1 and Notch signaling is a therapeutic strategy for KRAS-driven lung adenocarcinoma. <i>Nature Medicine</i> , 2016, 22, 270-277.	30.7	150
8	Colibactin DNA-damage signature indicates mutational impact in colorectal cancer. <i>Nature Medicine</i> , 2020, 26, 1063-1069.	30.7	149
9	Nanogrid single-nucleus RNA sequencing reveals phenotypic diversity in breast cancer. <i>Nature Communications</i> , 2017, 8, 228.	12.8	105
10	Spatial Chromosome Folding and Active Transcription Drive DNA Fragility and Formation of Oncogenic MLL Translocations. <i>Molecular Cell</i> , 2019, 75, 267-283.e12.	9.7	104
11	A damaged genome's transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. <i>Nature Communications</i> , 2017, 8, 15656.	12.8	89
12	Release of paused RNA polymerase II at specific loci favors DNA double-strand-break formation and promotes cancer translocations. <i>Nature Genetics</i> , 2019, 51, 1011-1023.	21.4	73
13	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. <i>Nature Methods</i> , 2013, 10, 122-124.	19.0	66
14	GPSeq reveals the radial organization of chromatin in the cell nucleus. <i>Nature Biotechnology</i> , 2020, 38, 1184-1193.	17.5	49
15	Endogenous DNA Double-Strand Breaks during DNA Transactions: Emerging Insights and Methods for Genome-Wide Profiling. <i>Genes</i> , 2018, 9, 632.	2.4	43
16	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Nature Communications</i> , 2019, 10, 1636.	12.8	41
17	FuseFISH: Robust Detection of Transcribed Gene Fusions in Single Cells. <i>Cell Reports</i> , 2014, 6, 18-23.	6.4	39
18	Activation of Oncogenic Super-Enhancers Is Coupled with DNA Repair by RAD51. <i>Cell Reports</i> , 2019, 29, 560-572.e4.	6.4	39

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19	i-BLESS is an ultra-sensitive method for detection of DNA double-strand breaks. <i>Communications Biology</i> , 2018, 1, 181.	4.4	37
20	Somatic Copy Number Alterations in Human Cancers: An Analysis of Publicly Available Data From The Cancer Genome Atlas. <i>Frontiers in Oncology</i> , 2021, 11, 700568.	2.8	33
21	Radial Organization in the Mammalian Nucleus. <i>Frontiers in Genetics</i> , 2020, 11, 33.	2.3	32
22	A recurrent chromosomal inversion suffices for driving escape from oncogene-induced senescence via subTAD reorganization. <i>Molecular Cell</i> , 2021, 81, 4907-4923.e8.	9.7	28
23	RollFISH achieves robust quantification of single-molecule RNA biomarkers in paraffin-embedded tumor tissue samples. <i>Communications Biology</i> , 2018, 1, 209.	4.4	26
24	The era of 3D and spatial genomics. <i>Trends in Genetics</i> , 2022, 38, 1062-1075.	6.7	25
25	Quantification of HER2 and estrogen receptor heterogeneity in breast cancer by single-molecule RNA fluorescence in situ hybridization. <i>Oncotarget</i> , 2017, 8, 18680-18698.	1.8	24
26	The Role of Intratumor Heterogeneity in the Response of Metastatic Non-Small Cell Lung Cancer to Immune Checkpoint Inhibitors. <i>Frontiers in Oncology</i> , 2020, 10, 569202.	2.8	22
27	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. <i>Nature Protocols</i> , 2020, 15, 3894-3941.	12.0	19
28	Ssb1 and Ssb2 cooperate to regulate mouse hematopoietic stem and progenitor cells by resolving replicative stress. <i>Blood</i> , 2017, 129, 2479-2492.	1.4	18
29	Topoisomerase 1 activity during mitotic transcription favors the transition from mitosis to G1. <i>Molecular Cell</i> , 2021, 81, 5007-5024.e9.	9.7	16
30	Genome-Wide Profiling of DNA Double-Strand Breaks by the BLESS and BLISS Methods. <i>Methods in Molecular Biology</i> , 2018, 1672, 167-194.	0.9	15
31	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. <i>Nature Communications</i> , 2021, 12, 3903.	12.8	14
32	CUTseq is a versatile method for preparing multiplexed DNA sequencing libraries from low-input samples. <i>Nature Communications</i> , 2019, 10, 4732.	12.8	12
33	Exploratory analysis of circulating cytokines in patients with metastatic breast cancer treated with eribulin: the TRANSERI-GONO (Gruppo Oncologico del Nord Ovest) study. <i>ESMO Open</i> , 2020, 5, e000876.	4.5	12
34	Modeling double strand break susceptibility to interrogate structural variation in cancer. <i>Genome Biology</i> , 2019, 20, 28.	8.8	11
35	RNA gradients: Shapers of 3D genome architecture. <i>Current Opinion in Cell Biology</i> , 2022, 74, 7-12.	5.4	11
36	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. <i>Methods in Molecular Biology</i> , 2018, 1766, 303-333.	0.9	8

#	ARTICLE	IF	CITATIONS
37	Genome-Wide CRISPR Off-Target DNA Break Detection by the BLISS Method. <i>Methods in Molecular Biology</i> , 2021, 2162, 261-281.	0.9	4
38	Cytokine Profiling of End Stage Cancer Patients Treated with Immunotherapy. <i>Vaccines</i> , 2021, 9, 235.	4.4	3
39	iFISH:a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Protocol Exchange</i> , 0, , .	0.3	3
40	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. <i>Npj Breast Cancer</i> , 2021, 7, 144.	5.2	3
41	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. <i>Scientific Data</i> , 2022, 9, .	5.3	3
42	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH. <i>Scientific Data</i> , 2022, 9, 47.	5.3	2
43	Treating patients with cancer amidst the COVID-19 pandemic: experience of a regional hospital in the Piedmont region in northern Italy. <i>Tumori</i> , 2020, 106, 427-431.	1.1	1
44	Abstract PS18-27: Integrated immuno-genomic analyses in early breast cancer: Results from the Scandinavian breast group 2004-1 (SBC-2004-1) randomized phase II trial. , 2021, , .		0