Serena Nik-Zainal

List of Publications by Year
in descending order

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86 papers	32,325 citations	24978 57 h-index	51492 86 g-index
94 all docs	94 docs citations	94 times ranked	40262 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
2	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. Cell, 2011, 144, 27-40.	13.5	2,020
3	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
4	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	13.5	1,673
5	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	13.7	1,535
6	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	13.5	1,249
7	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	2.9	1,087
8	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	13.7	972
9	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	6.0	842
10	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	9.4	837
11	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	15.2	769
12	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	5.8	741
13	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	15.2	711
14	Mechanisms underlying mutational signatures in human cancers. Nature Reviews Genetics, 2014, 15, 585-598.	7.7	703
15	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. Nature Genetics, 2013, 45, 1479-1482.	9.4	667
16	A Compendium of Mutational Signatures of Environmental Agents. Cell, 2019, 177, 821-836.e16.	13.5	437
17	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	9.4	380
18	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348

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19	Use of CRISPR-modified human stem cell organoids to study the origin of mutational signatures in cancer. Science, 2017, 358, 234-238.	6.0	337
20	DNA deaminases induce break-associated mutation showers with implication of APOBEC3B and 3A in breast cancer kataegis. ELife, 2013, 2, e00534.	2.8	322
21	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318
22	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	13.7	315
23	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 116-125.	9.4	313
24	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	13.5	298
25	Alcohol and endogenous aldehydes damage chromosomes and mutate stem cells. Nature, 2018, 553, 171-177.	13.7	284
26	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. Nature Genetics, 2014, 46, 487-491.	9.4	254
27	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. Nature Genetics, 2019, 51, 1450-1458.	9.4	250
28	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	5.8	235
29	Whole exome sequencing of adenoid cystic carcinoma. Journal of Clinical Investigation, 2013, 123, 2965-2968.	3.9	233
30	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
31	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	15.2	218
32	Mutational signatures of ionizing radiation in second malignancies. Nature Communications, 2016, 7, 12605.	5.8	214
33	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. Nature Genetics, 2013, 45, 923-926.	9.4	180
34	The genome as a record of environmental exposure. Mutagenesis, 2015, 30, gev073.	1.0	174
35	Ductal carcinoma in situ: to treat or not to treat, that is the question. British Journal of Cancer, 2019, 121, 285-292.	2.9	168
36	A practical framework and online tool for mutational signature analyses show intertissue variation and driver dependencies. Nature Cancer, 2020, 1, 249-263.	5.7	166

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37	Homologous recombination DNA repair deficiency and PARP inhibition activity in primary triple negative breast cancer. Nature Communications, 2020, 11, 2662.	5.8	157
38	cgpCaVEManWrapper: Simple Execution of CaVEMan in Order to Detect Somatic Single Nucleotide Variants in NGS Data. Current Protocols in Bioinformatics, 2016, 56, 15.10.1-15.10.18.	25.8	155
39	A mutational signature in gastric cancer suggests therapeutic strategies. Nature Communications, 2015, 6, 8683.	5.8	146
40	A practical guide for mutational signature analysis in hematological malignancies. Nature Communications, 2019, 10, 2969.	5.8	145
41	Validating the concept of mutational signatures with isogenic cell models. Nature Communications, 2018, 9, 1744.	5.8	128
42	Mutational signatures: emerging concepts, caveats and clinical applications. Nature Reviews Cancer, 2021, 21, 619-637.	12.8	128
43	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	5.8	119
44	A whole-genome sequence and transcriptome perspective on HER2-positive breast cancers. Nature Communications, 2016, 7, 12222.	5.8	113
45	Estimation of rearrangement phylogeny for cancer genomes. Genome Research, 2012, 22, 346-361.	2.4	108
46	cgpPindel: Identifying Somatically Acquired Insertion and Deletion Events from Paired End Sequencing. Current Protocols in Bioinformatics, 2015, 52, 15.7.1-15.7.12.	25.8	104
47	Substitution mutational signatures in whole-genomeâ€“sequenced cancers in the UK population. Science, 2022, 376, .	6.0	104
48	Mutational Signatures in Breast Cancer: The Problem at the DNA Level. Clinical Cancer Research, 2017, 23, 2617-2629.	3.2	102
49	Mutational History of a Human Cell Lineage from Somatic to Induced Pluripotent Stem Cells. PLoS Genetics, 2016, 12, e1005932.	1.5	96
50	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.	2.9	95
51	A systematic CRISPR screen defines mutational mechanisms underpinning signatures caused by replication errors and endogenous DNA damage. Nature Cancer, 2021, 2, 643-657.	5.7	94
52	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	5.8	86
53	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	2.4	85
54	Whole-Genome Sequencing Reveals Breast Cancers with Mismatch Repair Deficiency. Cancer Research, 2017, 77, 4755-4762.	0.4	81

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55	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	9.4	75
56	Uncovering the genomic heterogeneity of multifocal breast cancer. Journal of Pathology, 2015, 236, 457-466.	2.1	72
57	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69
58	Low rates of mutation in clinical grade human pluripotent stem cells under different culture conditions. Nature Communications, 2020, 11, 1528.	5.8	67
59	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	0.6	64
60	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	5.8	60
61	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	5.8	53
62	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. Genome Biology, 2013, 14, R113.	13.9	40
63	Preclinical In Vivo Validation of the RAD51 Test for Identification of Homologous Recombination-Deficient Tumors and Patient Stratification. Cancer Research, 2022, 82, 1646-1657.	0.4	40
64	APOBEC3A/B deletion polymorphism and cancer risk. Carcinogenesis, 2018, 39, 118-124.	1.3	39
65	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	2.9	36
66	Dramatic response of metastatic cutaneous angiosarcoma to an immune checkpoint inhibitor in a patient with xeroderma pigmentosum: whole-genome sequencing aids treatment decision in end-stage disease. Journal of Physical Education and Sports Management, 2019, 5, a004408.	0.5	34
67	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. Nature Genetics, 2022, 54, 850-860.	9.4	34
68	Spectrum of mutational signatures in T-cell lymphoma reveals a key role for UV radiation in cutaneous T-cell lymphoma. Scientific Reports, 2021, 11, 3962.	1.6	33
69	Familial Adrenocortical Carcinoma in Association With Lynch Syndrome. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 2269-2272.	1.8	27
70	Mutational signatures: experimental design and analytical framework. Genome Biology, 2020, 21, 37.	3.8	27
71	Short inverted repeats contribute to localized mutability in human somatic cells. Nucleic Acids Research, 2017, 45, 11213-11221.	6.5	26
72	Mutational mechanisms of amplifications revealed by analysis of clustered rearrangements in breast cancers. Annals of Oncology, 2018, 29, 2223-2231.	0.6	26

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73	Epigenetic modifiers DNMT3A and BCOR are recurrently mutated in CYLD cutaneous syndrome. Nature Communications, 2019, 10, 4717.	5.8	20
74	Transcription-coupled repair and mismatch repair contribute towards preserving genome integrity at mononucleotide repeat tracts. Nature Communications, 2020, 11, 1980.	5.8	19
75	Whole-Genome Sequencing of Retinoblastoma Reveals the Diversity of Rearrangements Disrupting RB1 and Uncovers a Treatment-Related Mutational Signature. Cancers, 2021, 13, 754.	1.7	16
76	Adrenal-permissive HSD3B1 genetic inheritance and risk of estrogen-driven postmenopausal breast cancer. JCI Insight, 2021, 6, .	2.3	13
77	Cellular survival over genomic perfection. Science, 2019, 366, 802-803.	6.0	12
78	FANCD2-Associated Nuclease 1 Partially Compensates for the Lack of Exonuclease 1 in Mismatch Repair. Molecular and Cellular Biology, 2021, 41, e0030321.	1.1	11
79	Functional RECAP (REpair CAPacity) assay identifies homologous recombination deficiency undetected by DNA-based BRCAness tests. Oncogene, 2022, 41, 3498-3506.	2.6	9
80	From genome integrity to cancer. Genome Medicine, 2019, 11, 4.	3.6	8
81	Holistic cancer genome profiling for every patient. Swiss Medical Weekly, 2020, 150, w20158.	0.8	5
82	Keipert syndrome: two further cases and review of the literature. Clinical Dysmorphology, 2008, 17, 169-175.	0.1	3
83	Insights into cancer biology through next-generation sequencing. Clinical Medicine, 2014, 14, s71-s77.	0.8	3
84	A path inspired by people. Nature Medicine, 2019, 25, 1329-1329.	15.2	1
85	The duty to speak up. Nature Cell Biology, 2018, 20, 1006-1006.	4.6	0
86	Abstract P1-22-05: Identifying predictors of invasive recurrence based on molecular profiles of DCIS lesions. Cancer Research, 2022, 82, P1-22-05-P1-22-05.	0.4	0