Samuel A J R Aparicio

List of Publications by Year
in descending order

132	43,039	13827	12910
papers	citations	67	131
		h-index	g-index

151	151	151	54330
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
2	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	13.7	4,708
3	TheGPR54Gene as a Regulator of Puberty. New England Journal of Medicine, 2003, 349, 1614-1627.	13.9	2,297
4	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	13.7	1,778
5	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	13.5	1,673
6	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	13.7	1,535
7	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	9.4	1,504
8	Whole-Genome Shotgun Assembly and Analysis of the Genome of Fugu rubripes. Science, 2002, 297, 1301-1310.	6.0	1,432
9	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	13.5	1,249
10	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	5.8	1,221
11	Kisspeptin directly stimulates gonadotropin-releasing hormone release via G protein-coupled receptor 54. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1761-1766.	3.3	1,047
12	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	13.7	984
13	PyClone: statistical inference of clonal population structure in cancer. Nature Methods, 2014, 11, 396-398.	9.0	817
14	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
15	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459.	0.6	556
16	Eomesodermin is required for mouse trophoblast development and mesoderm formation. Nature, 2000, 404, 95-99.	13.7	547
17	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	13.7	545
18	Hypogonadotropic hypogonadism in mice lacking a functional Kiss1 gene. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10714-10719.	3.3	522

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19	Fugu Genome Analysis Provides Evidence for a Whole-Genome Duplication Early During the Evolution of Ray-Finned Fishes. Molecular Biology and Evolution, 2004, 21, 1146-1151.	3.5	490
20	High-throughput microfluidic single-cell RT-qPCR. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13999-14004.	3.3	406
21	EMSY Links the BRCA2 Pathway to Sporadic Breast and Ovarian Cancer. Cell, 2003, 115, 523-535.	13.5	389
22	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. Nature Communications, 2017, 8, 14432.	5.8	379
23	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	13.5	376
24	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. Genome Research, 2014, 24, 1881-1893.	2.4	322
25	The Implications of Clonal Genome Evolution for Cancer Medicine. New England Journal of Medicine, 2013, 368, 842-851.	13.9	316
26	Transcriptome Analysis of the Normal Human Mammary Cell Commitment and Differentiation Process. Cell Stem Cell, 2008, 3, 109-118.	5.2	310
27	Examining the utility of patient-derived xenograft mouse models. Nature Reviews Cancer, 2015, 15, 311-316.	12.8	300
28	A method for quantifying normal human mammary epithelial stem cells with in vivo regenerative ability. Nature Medicine, 2008, 14, 1384-1389.	15.2	298
29	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. Nature Genetics, 2016, 48, 758-767.	9.4	287
30	Distinctcis-Essential Modules Direct the Time–Space Pattern of thePax6Gene Activity. Developmental Biology, 1999, 205, 79-97.	0.9	278
31	A new genome-driven integrated classification of breast cancer and its implications. EMBO Journal, 2013, 32, 617-628.	3.5	267
32	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	13.5	261
33	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nature Methods, 2019, 16, 1007-1015.	9.0	241
34	*TP53* Mutation Spectrum in Breast Cancer Is Subtype Specific and Has Distinct Prognostic Relevance. Clinical Cancer Research, 2014, 20, 3569-3580.	3.2	240
35	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	13.7	239
36	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome Research, 2012, 22, 1995-2007.	2.4	237

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37	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865.	9.4	220
38	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer. Nature Cancer, 2020, 1, 163-175.	5.7	209
39	Patient-derived xenograft (PDX) models in basic and translational breast cancer research. Cancer and Metastasis Reviews, 2016, 35, 547-573.	2.7	189
40	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. Genome Biology, 2019, 20, 210.	3.8	171
41	Molecular evolution and domain structure of plasminogen–related growth factors (HGF/SF and) Tj ETQq1 1 0.784314 rgBT /Overlock	3.1	166
42	Scalable whole-genome single-cell library preparation without preamplification. Nature Methods, 2017, 14, 167-173.	9.0	164
43	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	13.5	162
44	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. Bioinformatics, 2012, 28, 907-913.	1.8	159
45	Small is beautiful: comparative genomics with the pufferfish (Fugu rubripes). Trends in Genetics, 1996, 12, 145-150.	2.9	150
46	Organization of the Fugu rubripes Hox clusters: evidence for continuing evolution of vertebrate Hox complexes. Nature Genetics, 1997, 16, 79-83.	9.4	148
47	Lapatinib or Trastuzumab Plus Taxane Therapy for Human Epidermal Growth Factor Receptor 2–Positive Advanced Breast Cancer: Final Results of NCIC CTG MA.31. Journal of Clinical Oncology, 2015, 33, 1574-1583.	0.8	146
48	p300 regulates p53-dependent apoptosis after DNA damage in colorectal cancer cells by modulation of PUMA/p21 levels. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7386-7391.	3.3	133
49	Feature-based classifiers for somatic mutation detection in tumour–normal paired sequencing data. Bioinformatics, 2012, 28, 167-175.	1.8	130
50	Insulin-like peptide 5 is an orexigenic gastrointestinal hormone. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11133-11138.	3.3	120
51	<i>ZNF703</i> is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. EMBO Molecular Medicine, 2011, 3, 167-180.	3.3	119
52	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. Nucleic Acids Research, 2017, 45, 6698-6716.	6.5	114
53	Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. Science Translational Medicine, 2013, 5, 181re1.	5.8	108
54	Clonal genotype and population structure inference from single-cell tumor sequencing. Nature Methods, 2016, 13, 573-576.	9.0	108

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55	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. Nature Communications, 2017, 8, 7.	5.8	108
56	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. Nature Communications, 2015, 6, 8554.	5.8	102
57	Barcoding reveals complex clonal dynamics of de novo transformed human mammary cells. Nature, 2015, 528, 267-271.	13.7	101
58	MLL2, the second human homolog of the Drosophila trithorax gene, maps to 19q13.1 and is amplified in solid tumor cell lines. Oncogene, 1999, 18, 7975-7984.	2.6	100
59	Nucleic acid quantity and quality from paraffin blocks: Defining optimal fixation, processing and DNA/RNA extraction techniques. Experimental and Molecular Pathology, 2012, 92, 33-43.	0.9	100
60	Vertebrate evolution: recent perspectives from fish. Trends in Genetics, 2000, 16, 54-56.	2.9	92
61	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. Genome Research, 2005, 16, 66-77.	2.4	92
62	Lessons learned from the application of whole-genome analysis to the treatment of patients with advanced cancers. Journal of Physical Education and Sports Management, 2015, 1, a000570.	0.5	92
63	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. Genome Biology, 2019, 20, 54.	3.8	92
64	How to count… human genes. Nature Genetics, 2000, 25, 129-130.	9.4	91
65	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. Cell Reports, 2016, 17, 2060-2074.	2.9	90
66	Breast tumor microenvironment structures are associated with genomic features and clinical outcome. Nature Genetics, 2022, 54, 660-669.	9.4	88
67	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. Nature Communications, 2014, 5, 5871.	5.8	86
68	High-Resolution Single-Cell DNA Methylation Measurements Reveal Epigenetically Distinct Hematopoietic Stem Cell Subpopulations. Stem Cell Reports, 2018, 11, 578-592.	2.3	79
69	The Orphan Adhesion-GPCR GPR126 Is Required for Embryonic Development in the Mouse. PLoS ONE, 2010, 5, e14047.	1.1	78
70	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. PLoS Computational Biology, 2013, 9, e1003047.	1.5	76
71	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	13.7	71
72	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69

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73	Inter-observer reproducibility of HER2 immunohistochemical assessment and concordance with fluorescent in situhybridization (FISH): pathologist assessment compared to quantitative image analysis. BMC Cancer, 2009, 9, 165.	1.1	68
74	P-cadherin expression as a prognostic biomarker in a 3992 case tissue microarray series of breast cancer. Modern Pathology, 2011, 24, 64-81.	2.9	60
75	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	5.8	60
76	Clonal Analysis via Barcoding Reveals Diverse Growth and Differentiation of Transplanted Mouse and Human Mammary Stem Cells. Cell Stem Cell, 2014, 14, 253-263.	5.2	57
77	The Breast Cancer Oncogene EMSY Represses Transcription of Antimetastatic microRNA miR-31. Molecular Cell, 2014, 53, 806-818.	4.5	55
78	The RNA helicase DDX39B and its paralog DDX39A regulate androgen receptor splice variant AR-V7 generation. Biochemical and Biophysical Research Communications, 2017, 483, 271-276.	1.0	54
79	Genomic structure and sequence of the fugu rubripes glucose-6-phosphate dehydrogenase gene (G6PD). Genomics, 1995, 26, 587-591.	1.3	52
80	The Omics of Triple-Negative Breast Cancers. Clinical Chemistry, 2014, 60, 122-133.	1.5	52
81	ddClone: joint statistical inference of clonal populations from single cell and bulk tumour sequencing data. Genome Biology, 2017, 18, 44.	3.8	52
82	Bimolecular complementation affinity purification (BiCAP) reveals dimer-specific protein interactions for ERBB2 dimers. Science Signaling, 2016, 9, ra69.	1.6	51
83	Mll5 Is Required for Normal Spermatogenesis. PLoS ONE, 2011, 6, e27127.	1.1	50
84	Homologous Recombination Deficiency in Breast Cancer: A Clinical Review. JCO Precision Oncology, 2017, 1, 1-13.	1.5	50
85	Does massively parallel DNA resequencing signify the end of histopathology as we know it?. Journal of Pathology, 2010, 220, 307-315.	2.1	48
86	*In Vivo* Radioimaging of Bradykinin Receptor B1, a Widely Overexpressed Molecule in Human Cancer. Cancer Research, 2015, 75, 387-393.	0.4	48
87	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8484-8489.	3.3	45
88	A Novel SND1-BRAF Fusion Confers Resistance to c-Met Inhibitor PF-04217903 in GTL16 Cells though MAPK Activation. PLoS ONE, 2012, 7, e39653.	1.1	43
89	Results of the phase I CCTG IND.231 trial of CX-5461 in patients with advanced solid tumors enriched for DNA-repair deficiencies. Nature Communications, 2022, 13, .	5.8	43
90	Molecular Alterations Between the Primary Breast Cancer and the Subsequent Locoregional/Metastatic Tumor. Oncologist, 2012, 17, 172-178.	1.9	39

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91	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	2.1	38
92	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	2.9	36
93	Opening Pandora's Box—the new biology of driver mutations and clonal evolution in cancer as revealed by next generation sequencing. Current Opinion in Genetics and Development, 2012, 22, 3-9.	1.5	34
94	Isolation and characterization of a Pufferfish MLL (Mixed lineage leukemia)-like gene (fMll) reveals evolutionary conservation in vertebrate genes related to Drosophila trithorax. Oncogene, 1998, 16, 3233-3241.	2.6	31
95	Kisspeptins and GPR54—The new biology of the mammalian GnRH axis. Cell Metabolism, 2005, 1, 293-296.	7.2	31
96	TDP1 and PARP1 Deficiency Are Cytotoxic to Rhabdomyosarcoma Cells. Molecular Cancer Research, 2013, 11, 1179-1192.	1.5	31
97	Discovery of Novel 1,4-Diacylpiperazines as Selective and Cell-Active eIF4A3 Inhibitors. Journal of Medicinal Chemistry, 2017, 60, 3335-3351.	2.9	29
98	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. Communications Biology, 2019, 2, 165.	2.0	29
99	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. Nature Communications, 2021, 12, 5406.	5.8	29
100	Discovery and Characterization of a Eukaryotic Initiation Factor 4A-3-Selective Inhibitor That Suppresses Nonsense-Mediated mRNA Decay. ACS Chemical Biology, 2017, 12, 1760-1768.	1.6	28
101	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. Communications Biology, 2020, 3, 310.	2.0	28
102	Solution NMR Structure and Histone Binding of the PHD Domain of Human MLL5. PLoS ONE, 2013, 8, e77020.	1.1	26
103	Impact of MLL5 expression on decitabine efficacy and DNA methylation in acute myeloid leukemia. Haematologica, 2014, 99, 1456-1464.	1.7	26
104	Cell memory and cancer--the story of the trithorax and Polycomb group genes. , 1999, 18, 313-329.		25
105	Up-regulation of the interferon-related genes in BRCA2 knockout epithelial cells. Journal of Pathology, 2014, 234, 386-397.	2.1	25
106	A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. Breast Cancer Research, 2015, 17, 4.	2.2	24
107	Discovery of selective ATP-competitive eIF4A3 inhibitors. Bioorganic and Medicinal Chemistry, 2017, 25, 2200-2209.	1.4	23
108	Columnar cell lesions, mammographic density and breast cancer risk. Breast Cancer Research and Treatment, 2009, 115, 561-571.	1.1	22

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109	Cooperative signaling between Wnt1 and integrin-linked kinase induces accelerated breast tumor development. Breast Cancer Research, 2010, 12, R38.	2.2	21
110	Are columnar cell lesions the earliest histologically detectable non-obligate precursor of breast cancer?. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2008, 452, 589-598.	1.4	19
111	Decoding Transcriptome Dynamics of Genome-Encoded Polyadenylation and Autoregulation with Small-Molecule Modulators of Alternative Polyadenylation. Cell Chemical Biology, 2018, 25, 1470-1484.e5.	2.5	18
112	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. PLoS Computational Biology, 2020, 16, e1008270.	1.5	18
113	Intensity calibration and automated cell cycle gating for high-throughput image-based siRNA screens of mammalian cells. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 904-917.	1.1	17
114	Exploding vertebrate genomes. Nature Genetics, 1998, 18, 301-303.	9.4	16
115	p53: A New Kingpin in the Stem Cell Arena. Cell, 2009, 138, 1060-1062.	13.5	16
116	Atrophin controls developmental signaling pathways via interactions with Trithorax-like. ELife, 2017, 6, .	2.8	15
117	The PufferfishSLP-1Gene, a New Member of theSCL/TAL-1Family of Transcription Factors. Genomics, 1998, 48, 52-62.	1.3	14
118	Impact of serum HER2, TIMP-1, and CAIX on outcome for HER2+Âmetastatic breast cancer patients: CCTG MA.31 (lapatinib vs. trastuzumab). Breast Cancer Research and Treatment, 2017, 164, 571-580.	1.1	13
119	Exploding vertebrate genomes. Nature Genetics, 1998, 18, 301-303.	9.4	13
120	Combined Use of Gene Expression Modeling and siRNA Screening Identifies Genes and Pathways Which Enhance the Activity of Cisplatin When Added at No Effect Levels to Non-Small Cell Lung Cancer Cells In Vitro. PLoS ONE, 2016, 11, e0150675.	1.1	12
121	Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. Breast Cancer Research, 2016, 18, 70.	2.2	11
122	Age-correlated protein and transcript expression in breast cancer and normal breast tissues is dominated by host endocrine effects. Nature Cancer, 2020, 1, 518-532.	5.7	11
123	Identification of a selective DDX3X inhibitor with newly developed quantitative high-throughput RNA helicase assays. Biochemical and Biophysical Research Communications, 2020, 523, 795-801.	1.0	9
124	Ubiquitin-mediated DNA damage response is synthetic lethal with G-quadruplex stabilizer CX-5461. Scientific Reports, 2021, 11, 9812.	1.6	9
125	Evolution of Plasminogen-Related Growth Factors (HGF/SF and HGF1/MSP). Novartis Foundation Symposium, 1997, 212, 24-45.	1.2	8
126	Open-source work even more vital to genome project than to software. Nature, 2000, 404, 809-809.	13.7	4

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127	Engineered in-vitro cell line mixtures and robust evaluation of computational methods for clonal decomposition and longitudinal dynamics in cancer. Scientific Reports, 2017, 7, 13467.	1.6	4
128	Abstract PD4-02: Canadian cancer trials group trial IND.231: A phase 1 trial evaluating CX-5461, a novel first-in-class G-quadruplex stabilizer in patients with advanced solid tumors enriched for DNA-repair deficiencies. , 2020, , .		4
129	Gene regulatory network analysis defines transcriptome landscape with alternative splicing of human umbilical vein endothelial cells during replicative senescence. BMC Genomics, 2021, 22, 869.	1.2	4
130	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics, 2021, 12, 665888.	1.1	2
131	Genetic approaches to unraveling G protein-coupled receptor biology. Current Opinion in Drug Discovery & Development, 2004, 7, 658-64.	1.9	1
132	Genome archaeology. , 2005, , .		0