Samuel A J R Aparicio

List of Publications by Year in Descending Order

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136 papers	32,839 citations	64 h-index	151 g-index
151 ext. papers	39,149 ext. citations	18.3 avg, IF	6.18 L-index

#	Paper	IF	Citations
136	Gene regulatory network analysis defines transcriptome landscape with alternative splicing of human umbilical vein endothelial cells during replicative senescence. *BMC Genomics*, **2021**, 22, 869	4.5	0
135	Ubiquitin-mediated DNA damage response is synthetic lethal with G-quadruplex stabilizer CX-5461. *Scientific Reports*, **2021**, 11, 9812	4.9	3
134	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. *Frontiers in Genetics*, **2021**, 12, 665888	4.5	1
133	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. *Nature*, **2021**, 595, 585-590	50.4	10
132	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. *Nature Communications*, **2021**, 12, 5406	17.4	6
131	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	15.4	7
130	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. *Communications Biology*, **2020**, 3, 310	6.7	11
129	Eleven grand challenges in single-cell data science. *Genome Biology*, **2020**, 21, 31	18.3	274
128	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer.. *Nature Cancer*, **2020**, 1, 163-175	15.4	90
127	Identification of a selective DDX3X inhibitor with newly developed quantitative high-throughput RNA helicase assays. *Biochemical and Biophysical Research Communications*, **2020**, 523, 795-801	3.4	7
126	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**,		3
125	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. *PLoS Computational Biology*, **2020**, 16, e1008270	5	8
124	Sex differences in oncogenic mutational processes. *Nature Communications*, **2020**, 11, 4330	17.4	23
123	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. *Nature Methods*, **2019**, 16, 1007-1015	21.6	107
122	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. *Communications Biology*, **2019**, 2, 165	6.7	17
121	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. *Genome Biology*, **2019**, 20, 54	18.3	43
120	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. *Nature*, **2019**, 567, 399-404	50.4	108

119	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	18.3	77
118	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. *Cell*, **2019**, 179, 1207-1221.e22	56.2	73
117	High-Resolution Single-Cell DNA Methylation Measurements Reveal Epigenetically Distinct Hematopoietic Stem Cell Subpopulations. *Stem Cell Reports*, **2018**, 11, 578-592	8	47
116	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. *Cell*, **2018**, 173, 1755-1769.e22	56.2	159
115	Decoding Transcriptome Dynamics of Genome-Encoded Polyadenylation and Autoregulation with Small-Molecule Modulators of Alternative Polyadenylation. *Cell Chemical Biology*, **2018**, 25, 1470-1484.e5	8.2	6
114	Scalable whole-genome single-cell library preparation without preamplification. *Nature Methods*, **2017**, 14, 167-173	21.6	105
113	Discovery of selective ATP-competitive eIF4A3 inhibitors. *Bioorganic and Medicinal Chemistry*, **2017**, 25, 2200-2209	3.4	17
112	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. *Nature Communications*, **2017**, 8, 14432	17.4	251
111	ddClone: joint statistical inference of clonal populations from single cell and bulk tumour sequencing data. *Genome Biology*, **2017**, 18, 44	18.3	40
110	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. *Nature Genetics*, **2017**, 49, 856-865	36.3	141
109	Impact of serum HER2, TIMP-1, and CAIX on outcome for HER2+ metastatic breast cancer patients: CCTG MA.31 (lapatinib vs. trastuzumab). *Breast Cancer Research and Treatment*, **2017**, 164, 571-580	4.4	10
108	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	4.9	18
107	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. *Nucleic Acids Research*, **2017**, 45, 6698-6716	20.1	75
106	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. *Nature Communications*, **2017**, 8, 7	17.4	64
105	Discovery of Novel 1,4-Diacylpiperazines as Selective and Cell-Active eIF4A3 Inhibitors. *Journal of Medicinal Chemistry*, **2017**, 60, 3335-3351	8.3	21
104	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	3.4	30
103	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	4.9	3
102	Homologous Recombination Deficiency in Breast Cancer: A Clinical Review.. *JCO Precision Oncology*, **2017**, 1, 1-13	3.6	11

101	Atrophin controls developmental signaling pathways via interactions with Trithorax-like. *ELife*, **2017**, 6,	8.9	10
100	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. *Cell*, **2016**, 167, 260-274.e22	56.2	274
99	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, 8484-9	11.5	37
98	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. *Cell Reports*, **2016**, 17, 2060-2074	10.6	72
97	Bimolecular complementation affinity purification (BiCAP) reveals dimer-specific protein interactions for ERBB2 dimers. *Science Signaling*, **2016**, 9, ra69	8.8	25
96	The somatic mutation profiles of 2,433 breast cancers refines their genomic and transcriptomic landscapes. *Nature Communications*, **2016**, 7, 11479	17.4	779
95	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	3.7	11
94	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	8.3	9
93	Patient-derived xenograft (PDX) models in basic and translational breast cancer research. *Cancer and Metastasis Reviews*, **2016**, 35, 547-573	9.6	133
92	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. *Nature Genetics*, **2016**, 48, 758-67	36.3	209
91	Clonal genotype and population structure inference from single-cell tumor sequencing. *Nature Methods*, **2016**, 13, 573-6	21.6	75
90	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-46	16.6	30
89	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. *Molecular Oncology*, **2015**, 9, 115-27	7.9	35
88	Examining the utility of patient-derived xenograft mouse models. *Nature Reviews Cancer*, **2015**, 15, 311-6	31.3	246
87	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, 1574-83	2.2	112
86	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. *Genome Research*, **2015**, 25, 814-24	9.7	52
85	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. *Nature Communications*, **2015**, 6, 8554	17.4	71
84	Barcoding reveals complex clonal dynamics of de novo transformed human mammary cells. *Nature*, **2015**, 528, 267-71	50.4	75

83	In vivo radioimaging of bradykinin receptor b1, a widely overexpressed molecule in human cancer. *Cancer Research*, **2015**, 75, 387-93	10.1	39
82	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. *Nature*, **2015**, 518, 422-6	50.4	451
81	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	8.3	20
80	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	2.8	75
79	The breast cancer oncogene EMSY represses transcription of antimetastatic microRNA miR-31. *Molecular Cell*, **2014**, 53, 806-18	17.6	43
78	Clonal analysis via barcoding reveals diverse growth and differentiation of transplanted mouse and human mammary stem cells. *Cell Stem Cell*, **2014**, 14, 253-63	18	46
77	Insulin-like peptide 5 is an orexigenic gastrointestinal hormone. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 11133-8	11.5	84
76	Up-regulation of the interferon-related genes in BRCA2 knockout epithelial cells. *Journal of Pathology*, **2014**, 234, 386-97	9.4	18
75	Impact of MLL5 expression on decitabine efficacy and DNA methylation in acute myeloid leukemia. *Haematologica*, **2014**, 99, 1456-64	6.6	22
74	PyClone: statistical inference of clonal population structure in cancer. *Nature Methods*, **2014**, 11, 396-8	21.6	584
73	The omics of triple-negative breast cancers. *Clinical Chemistry*, **2014**, 60, 122-33	5.5	44
72	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. *Genome Research*, **2014**, 24, 1881-93	9.7	218
71	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. *Nature Communications*, **2014**, 5, 5871	17.4	66
70	TP53 mutation spectrum in breast cancer is subtype specific and has distinct prognostic relevance. *Clinical Cancer Research*, **2014**, 20, 3569-80	12.9	167
69	A new genome-driven integrated classification of breast cancer and its implications. *EMBO Journal*, **2013**, 32, 617-28	13	212
68	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
67	The implications of clonal genome evolution for cancer medicine. *New England Journal of Medicine*, **2013**, 368, 842-51	59.2	275
66	TDP1 and PARP1 deficiency are cytotoxic to rhabdomyosarcoma cells. *Molecular Cancer Research*, **2013**, 11, 1179-92	6.6	26

65	Improving breast cancer survival analysis through competition-based multidimensional modeling. *PLoS Computational Biology*, **2013**, 9, e1003047	5	57
64	Systematic analysis of challenge-driven improvements in molecular prognostic models for breast cancer. *Science Translational Medicine*, **2013**, 5, 181re1	17.5	94
63	Solution NMR structure and histone binding of the PHD domain of human MLL5. *PLoS ONE*, **2013**, 8, e77020	3.7	21
62	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	4.4	85
61	Molecular alterations between the primary breast cancer and the subsequent locoregional/metastatic tumor. *Oncologist*, **2012**, 17, 172-8	5.7	35
60	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	4.9	31
59	A novel SND1-BRAF fusion confers resistance to c-Met inhibitor PF-04217903 in GTL16 cells through [corrected] MAPK activation. *PLoS ONE*, **2012**, 7, e39653	3.7	38
58	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
57	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
56	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
55	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. *Nature*, **2012**, 486, 346-52	50.4	3479
54	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. *Nature*, **2012**, 486, 395-9	50.4	1417
53	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	9.7	181
52	Feature-based classifiers for somatic mutation detection in tumour-normal paired sequencing data. *Bioinformatics*, **2012**, 28, 167-75	7.2	114
51	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. *Bioinformatics*, **2012**, 28, 907-13	7.2	136
50	High-throughput microfluidic single-cell RT-qPCR. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 13999-4004	11.5	359
49	Mll5 is required for normal spermatogenesis. *PLoS ONE*, **2011**, 6, e27127	3.7	35
48	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. *Blood*, **2011**, 117, 2451-9	2.2	458

47	ZNF703 is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. *EMBO Molecular Medicine*, **2011**, 3, 167-80	12	97
46	P-cadherin expression as a prognostic biomarker in a 3992 case tissue microarray series of breast cancer. *Modern Pathology*, **2011**, 24, 64-81	9.8	50
45	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. *Nature Genetics*, **2010**, 42, 181-5	36.3	1273
44	The orphan adhesion-GPCR GPR126 is required for embryonic development in the mouse. *PLoS ONE*, **2010**, 5, e14047	3.7	62
43	Cooperative signaling between Wnt1 and integrin-linked kinase induces accelerated breast tumor development. *Breast Cancer Research*, **2010**, 12, R38	8.3	19
42	Does massively parallel DNA resequencing signify the end of histopathology as we know it?. *Journal of Pathology*, **2010**, 220, 307-15	9.4	40
41	Inter-observer reproducibility of HER2 immunohistochemical assessment and concordance with fluorescent in situ hybridization (FISH): pathologist assessment compared to quantitative image analysis. *BMC Cancer*, **2009**, 9, 165	4.8	53
40	Columnar cell lesions, mammographic density and breast cancer risk. *Breast Cancer Research and Treatment*, **2009**, 115, 561-71	4.4	16
39	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature*, **2009**, 461, 809-13	50.4	879
38	p53: a new kingpin in the stem cell arena. *Cell*, **2009**, 138, 1060-2	56.2	14
37	A method for quantifying normal human mammary epithelial stem cells with in vivo regenerative ability. *Nature Medicine*, **2008**, 14, 1384-9	50.5	262
36	Transcriptome analysis of the normal human mammary cell commitment and differentiation process. *Cell Stem Cell*, **2008**, 3, 109-18	18	274
35	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, 589-98	5.1	17
34	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**, 73, 904-17	4.6	14
33	Hypogonadotropic hypogonadism in mice lacking a functional Kiss1 gene. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 10714-9	11.5	453
32	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. *Genome Research*, **2006**, 16, 66-77	9.7	75
31	Kisspeptins and GPR54--the new biology of the mammalian GnRH axis. *Cell Metabolism*, **2005**, 1, 293-6	24.6	26
30	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, 1761-6	11.5	928

29	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, 7386-91	11.5	125
28	Fugu genome analysis provides evidence for a whole-genome duplication early during the evolution of ray-finned fishes. *Molecular Biology and Evolution*, **2004**, 21, 1146-51	8.3	435
27	Genetic approaches to unraveling G protein-coupled receptor biology. *Current Opinion in Drug Discovery & Development*, **2004**, 7, 658-64		1
26	The GPR54 gene as a regulator of puberty. *New England Journal of Medicine*, **2003**, 349, 1614-27	59.2	1994
25	EMSY links the BRCA2 pathway to sporadic breast and ovarian cancer. *Cell*, **2003**, 115, 523-35	56.2	345
24	Whole-genome shotgun assembly and analysis of the genome of Fugu rubripes. *Science*, **2002**, 297, 1301-10	33.5	1272
23	Eomesodermin is required for mouse trophoblast development and mesoderm formation. *Nature*, **2000**, 404, 95-9	50.4	494
22	Open-source work even more vital to genome project than to software. *Nature*, **2000**, 404, 809	50.4	3
21	Vertebrate evolution: recent perspectives from fish. *Trends in Genetics*, **2000**, 16, 54-6	8.5	86
20	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, 7975-84	9.2	92
19	Cell memory and cancer--the story of the trithorax and Polycomb group genes. *Cancer and Metastasis Reviews*, **1999**, 18, 313-29	9.6	21
18	Distinct cis-essential modules direct the time-space pattern of the Pax6 gene activity. *Developmental Biology*, **1999**, 205, 79-97	3.1	247
17	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, 3233-41	9.2	29
16	The pufferfish SLP-1 gene, a new member of the SCL/TAL-1 family of transcription factors. *Genomics*, **1998**, 48, 52-62	4.3	11
15	Exploding vertebrate genomes. *Nature Genetics*, **1998**, 18, 301-3	36.3	10
14	Organization of the Fugu rubripes Hox clusters: evidence for continuing evolution of vertebrate Hox complexes. *Nature Genetics*, **1997**, 16, 79-83	36.3	138
13	Evolution of plasminogen-related growth factors (HGF/SF and HGF1/MSP). *Novartis Foundation Symposium*, **1997**, 212, 24-35; discussion 35-41, 42-5		4
12	Small is beautiful: comparative genomics with the pufferfish (Fugu rubripes). *Trends in Genetics*, **1996**, 12, 145-50	8.5	138

11	Genomic structure and sequence of the Fugu rubripes glucose-6-phosphate dehydrogenase gene (G6PD). *Genomics*, **1995**, 26, 587-91	4.3	46
10	Molecular evolution and domain structure of plasminogen-related growth factors (HGF/SF and HGF1/MSP). *Protein Science*, **1994**, 3, 2378-94	6.3	146
9	Cancer phylogenetic tree inference at scale from 1000s of single cell genomes		4
8	Single cell fitness landscapes induced by genetic and pharmacologic perturbations in cancer		3
7	Resource: Scalable whole genome sequencing of 40,000 single cells identifies stochastic aneuploidies, genome replication states and clonal repertoires		9
6	Epiclomal: probabilistic clustering of sparse single-cell DNA methylation data		2
5	Probabilistic cell type assignment of single-cell transcriptomic data reveals spatiotemporal microenvironment dynamics in human cancers		7
4	Dissociation of solid tumour tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses		2
3	The interface of malignant and immunologic clonal dynamics in high-grade serous ovarian cancer		1
2	Evolutionary tracking of cancer haplotypes at single-cell resolution		3
1	The impact of mutational processes on structural genomic plasticity in cancer cells		2