

Samuel A J R Aparicio

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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	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
135	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. <i>Nature</i> , 2012 , 486, 346-52	50.4	3479
134	The GPR54 gene as a regulator of puberty. <i>New England Journal of Medicine</i> , 2003 , 349, 1614-27	59.2	1994
133	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012 , 486, 395-9	50.4	1417
132	Mutational processes molding the genomes of 21 breast cancers. <i>Cell</i> , 2012 , 149, 979-93	56.2	1279
131	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010 , 42, 181-5	36.3	1273
130	Whole-genome shotgun assembly and analysis of the genome of <i>Fugu rubripes</i> . <i>Science</i> , 2002 , 297, 1301-10	33.0	1272
129	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012 , 486, 400-4	50.4	1264
128	The life history of 21 breast cancers. <i>Cell</i> , 2012 , 149, 994-1007	56.2	979
127	Kisspeptin directly stimulates gonadotropin-releasing hormone release via G protein-coupled receptor 54. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1761-6	11.5	928
126	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009 , 461, 809-13	50.4	879
125	The somatic mutation profiles of 2,433 breast cancers refines their genomic and transcriptomic landscapes. <i>Nature Communications</i> , 2016 , 7, 11479	17.4	779
124	PyClone: statistical inference of clonal population structure in cancer. <i>Nature Methods</i> , 2014 , 11, 396-8	21.6	584
123	Eomesodermin is required for mouse trophoblast development and mesoderm formation. <i>Nature</i> , 2000 , 404, 95-9	50.4	494
122	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. <i>Blood</i> , 2011 , 117, 2451-9	2.2	458
121	Hypogonadotropic hypogonadism in mice lacking a functional Kiss1 gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 10714-9	11.5	453
120	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. <i>Nature</i> , 2015 , 518, 422-6	50.4	451

119	Fugu genome analysis provides evidence for a whole-genome duplication early during the evolution of ray-finned fishes. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1146-51	8.3	435
118	High-throughput microfluidic single-cell RT-qPCR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13999-4004	11.5	359
117	EMSY links the BRCA2 pathway to sporadic breast and ovarian cancer. <i>Cell</i> , 2003 , 115, 523-35	56.2	345
116	The implications of clonal genome evolution for cancer medicine. <i>New England Journal of Medicine</i> , 2013 , 368, 842-51	59.2	275
115	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020 , 21, 31	18.3	274
114	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. <i>Cell</i> , 2016 , 167, 260-274.e22	56.2	274
113	Transcriptome analysis of the normal human mammary cell commitment and differentiation process. <i>Cell Stem Cell</i> , 2008 , 3, 109-18	18	274
112	A method for quantifying normal human mammary epithelial stem cells with in vivo regenerative ability. <i>Nature Medicine</i> , 2008 , 14, 1384-9	50.5	262
111	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. <i>Nature Communications</i> , 2017 , 8, 14432	17.4	251
110	Distinct cis-essential modules direct the time-space pattern of the Pax6 gene activity. <i>Developmental Biology</i> , 1999 , 205, 79-97	3.1	247
109	Examining the utility of patient-derived xenograft mouse models. <i>Nature Reviews Cancer</i> , 2015 , 15, 311-6	51.3	246
108	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. <i>Genome Research</i> , 2014 , 24, 1881-93	9.7	218
107	A new genome-driven integrated classification of breast cancer and its implications. <i>EMBO Journal</i> , 2013 , 32, 617-28	13	212
106	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. <i>Nature Genetics</i> , 2016 , 48, 758-67	36.3	209
105	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. <i>Genome Research</i> , 2012 , 22, 1995-2007	9.7	181
104	TP53 mutation spectrum in breast cancer is subtype specific and has distinct prognostic relevance. <i>Clinical Cancer Research</i> , 2014 , 20, 3569-80	12.9	167
103	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018 , 173, 1755-1769.e22	57.2	159
102	Molecular evolution and domain structure of plasminogen-related growth factors (HGF/SF and HGF1/MSP). <i>Protein Science</i> , 1994 , 3, 2378-94	6.3	146

101	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , 2017 , 49, 856-865	36.3	141
100	Organization of the Fugu rubripes Hox clusters: evidence for continuing evolution of vertebrate Hox complexes. <i>Nature Genetics</i> , 1997 , 16, 79-83	36.3	138
99	Small is beautiful: comparative genomics with the pufferfish (Fugu rubripes). <i>Trends in Genetics</i> , 1996 , 12, 145-50	8.5	138
98	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 907-13	7.2	136
97	Patient-derived xenograft (PDX) models in basic and translational breast cancer research. <i>Cancer and Metastasis Reviews</i> , 2016 , 35, 547-573	9.6	133
96	p300 regulates p53-dependent apoptosis after DNA damage in colorectal cancer cells by modulation of PUMA/p21 levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 7386-91	11.5	125
95	Feature-based classifiers for somatic mutation detection in tumour-normal paired sequencing data. <i>Bioinformatics</i> , 2012 , 28, 167-75	7.2	114
94	Lapatinib or Trastuzumab Plus Taxane Therapy for Human Epidermal Growth Factor Receptor 2-Positive Advanced Breast Cancer: Final Results of NCIC CTG MA.31. <i>Journal of Clinical Oncology</i> , 2015 , 33, 1574-83	2.2	112
93	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. <i>Nature</i> , 2019 , 567, 399-404	50.4	108
92	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. <i>Nature Methods</i> , 2019 , 16, 1007-1015	21.6	107
91	Scalable whole-genome single-cell library preparation without preamplification. <i>Nature Methods</i> , 2017 , 14, 167-173	21.6	105
90	ZNF703 is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. <i>EMBO Molecular Medicine</i> , 2011 , 3, 167-80	12	97
89	Systematic analysis of challenge-driven improvements in molecular prognostic models for breast cancer. <i>Science Translational Medicine</i> , 2013 , 5, 181re1	17.5	94
88	MLL2, the second human homolog of the Drosophila trithorax gene, maps to 19q13.1 and is amplified in solid tumor cell lines. <i>Oncogene</i> , 1999 , 18, 7975-84	9.2	92
87	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer.. <i>Nature Cancer</i> , 2020 , 1, 163-175	15.4	90
86	Vertebrate evolution: recent perspectives from fish. <i>Trends in Genetics</i> , 2000 , 16, 54-6	8.5	86
85	Nucleic acid quantity and quality from paraffin blocks: defining optimal fixation, processing and DNA/RNA extraction techniques. <i>Experimental and Molecular Pathology</i> , 2012 , 92, 33-43	4.4	85
84	Insulin-like peptide 5 is an orexigenic gastrointestinal hormone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11133-8	11.5	84

83	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. <i>Genome Biology</i> , 2019 , 20, 210	18.3	77
82	CDK12 regulates alternative last exon mRNA splicing and promotes breast cancer cell invasion. <i>Nucleic Acids Research</i> , 2017 , 45, 6698-6716	20.1	75
81	Barcoding reveals complex clonal dynamics of de novo transformed human mammary cells. <i>Nature</i> , 2015 , 528, 267-71	50.4	75
80	Lessons learned from the application of whole-genome analysis to the treatment of patients with advanced cancers. <i>Journal of Physical Education and Sports Management</i> , 2015 , 1, a000570	2.8	75
79	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. <i>Genome Research</i> , 2006 , 16, 66-77	9.7	75
78	Clonal genotype and population structure inference from single-cell tumor sequencing. <i>Nature Methods</i> , 2016 , 13, 573-6	21.6	75
77	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019 , 179, 1207-1221.e22	56.2	73
76	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. <i>Cell Reports</i> , 2016 , 17, 2060-2074	10.6	72
75	Systematic analysis of somatic mutations impacting gene expression in 12 tumour types. <i>Nature Communications</i> , 2015 , 6, 8554	17.4	71
74	DNA barcoding reveals diverse growth kinetics of human breast tumour subclones in serially passaged xenografts. <i>Nature Communications</i> , 2014 , 5, 5871	17.4	66
73	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. <i>Nature Communications</i> , 2017 , 8, 7	17.4	64
72	The orphan adhesion-GPCR GPR126 is required for embryonic development in the mouse. <i>PLoS ONE</i> , 2010 , 5, e14047	3.7	62
71	Improving breast cancer survival analysis through competition-based multidimensional modeling. <i>PLoS Computational Biology</i> , 2013 , 9, e1003047	5	57
70	Inter-observer reproducibility of HER2 immunohistochemical assessment and concordance with fluorescent in situ hybridization (FISH): pathologist assessment compared to quantitative image analysis. <i>BMC Cancer</i> , 2009 , 9, 165	4.8	53
69	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , 2015 , 25, 814-24	9.7	52
68	P-cadherin expression as a prognostic biomarker in a 3992 case tissue microarray series of breast cancer. <i>Modern Pathology</i> , 2011 , 24, 64-81	9.8	50
67	High-Resolution Single-Cell DNA Methylation Measurements Reveal Epigenetically Distinct Hematopoietic Stem Cell Subpopulations. <i>Stem Cell Reports</i> , 2018 , 11, 578-592	8	47
66	Clonal analysis via barcoding reveals diverse growth and differentiation of transplanted mouse and human mammary stem cells. <i>Cell Stem Cell</i> , 2014 , 14, 253-63	18	46

65	Genomic structure and sequence of the Fugu rubripes glucose-6-phosphate dehydrogenase gene (G6PD). <i>Genomics</i> , 1995 , 26, 587-91	4.3	46
64	The omics of triple-negative breast cancers. <i>Clinical Chemistry</i> , 2014 , 60, 122-33	5.5	44
63	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. <i>Genome Biology</i> , 2019 , 20, 54	18.3	43
62	The breast cancer oncogene EMSY represses transcription of antimetastatic microRNA miR-31. <i>Molecular Cell</i> , 2014 , 53, 806-18	17.6	43
61	ddClone: joint statistical inference of clonal populations from single cell and bulk tumour sequencing data. <i>Genome Biology</i> , 2017 , 18, 44	18.3	40
60	Does massively parallel DNA resequencing signify the end of histopathology as we know it?. <i>Journal of Pathology</i> , 2010 , 220, 307-15	9.4	40
59	In vivo radioimaging of bradykinin receptor b1, a widely overexpressed molecule in human cancer. <i>Cancer Research</i> , 2015 , 75, 387-93	10.1	39
58	A novel SND1-BRAF fusion confers resistance to c-Met inhibitor PF-04217903 in GTL16 cells through [corrected] MAPK activation. <i>PLoS ONE</i> , 2012 , 7, e39653	3.7	38
57	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8484-9	11.5	37
56	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015 , 9, 115-27	7.9	35
55	Molecular alterations between the primary breast cancer and the subsequent locoregional/metastatic tumor. <i>Oncologist</i> , 2012 , 17, 172-8	5.7	35
54	MLL5 is required for normal spermatogenesis. <i>PLoS ONE</i> , 2011 , 6, e27127	3.7	35
53	Opening Pandora's Box--the new biology of driver mutations and clonal evolution in cancer as revealed by next generation sequencing. <i>Current Opinion in Genetics and Development</i> , 2012 , 22, 3-9	4.9	31
52	The RNA helicase DDX39B and its paralog DDX39A regulate androgen receptor splice variant AR-V7 generation. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 483, 271-276	3.4	30
51	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016 , 16, 2032-46.6	46.6	30
50	Isolation and characterization of a pufferfish MLL (mixed lineage leukemia)-like gene (fMLL) reveals evolutionary conservation in vertebrate genes related to <i>Drosophila trithorax</i> . <i>Oncogene</i> , 1998 , 16, 3233-41	9.2	29
49	TDP1 and PARP1 deficiency are cytotoxic to rhabdomyosarcoma cells. <i>Molecular Cancer Research</i> , 2013 , 11, 1179-92	6.6	26
48	Kisspeptins and GPR54--the new biology of the mammalian GnRH axis. <i>Cell Metabolism</i> , 2005 , 1, 293-6	24.6	26

47	Bimolecular complementation affinity purification (BiCAP) reveals dimer-specific protein interactions for ERBB2 dimers. <i>Science Signaling</i> , 2016 , 9, ra69	8.8	25
46	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23
45	Impact of MLL5 expression on decitabine efficacy and DNA methylation in acute myeloid leukemia. <i>Haematologica</i> , 2014 , 99, 1456-64	6.6	22
44	Discovery of Novel 1,4-Diacylpiperazines as Selective and Cell-Active eIF4A3 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 3335-3351	8.3	21
43	Solution NMR structure and histone binding of the PHD domain of human MLL5. <i>PLoS ONE</i> , 2013 , 8, e77020	9.7	21
42	Cell memory and cancer--the story of the trithorax and Polycomb group genes. <i>Cancer and Metastasis Reviews</i> , 1999 , 18, 313-29	9.6	21
41	A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. <i>Breast Cancer Research</i> , 2015 , 17, 4	8.3	20
40	Cooperative signaling between Wnt1 and integrin-linked kinase induces accelerated breast tumor development. <i>Breast Cancer Research</i> , 2010 , 12, R38	8.3	19
39	Discovery and Characterization of a Eukaryotic Initiation Factor 4A-3-Selective Inhibitor That Suppresses Nonsense-Mediated mRNA Decay. <i>ACS Chemical Biology</i> , 2017 , 12, 1760-1768	4.9	18
38	Up-regulation of the interferon-related genes in BRCA2 knockout epithelial cells. <i>Journal of Pathology</i> , 2014 , 234, 386-97	9.4	18
37	Discovery of selective ATP-competitive eIF4A3 inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2017 , 25, 2200-2209	3.4	17
36	Pharmacological systems analysis defines EIF4A3 functions in cell-cycle and RNA stress granule formation. <i>Communications Biology</i> , 2019 , 2, 165	6.7	17
35	Are columnar cell lesions the earliest histologically detectable non-obligate precursor of breast cancer?. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2008 , 452, 589-98	5.1	17
34	Columnar cell lesions, mammographic density and breast cancer risk. <i>Breast Cancer Research and Treatment</i> , 2009 , 115, 561-71	4.4	16
33	p53: a new kingpin in the stem cell arena. <i>Cell</i> , 2009 , 138, 1060-2	56.2	14
32	Intensity calibration and automated cell cycle gating for high-throughput image-based siRNA screens of mammalian cells. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008 , 73, 904-17	4.6	14
31	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. <i>Communications Biology</i> , 2020 , 3, 310	6.7	11
30	Homologous Recombination Deficiency in Breast Cancer: A Clinical Review.. <i>JCO Precision Oncology</i> , 2017 , 1, 1-13	3.6	11

29	The pufferfish SLP-1 gene, a new member of the SCL/TAL-1 family of transcription factors. <i>Genomics</i> , 1998 , 48, 52-62	4.3	11
28	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. <i>PLoS ONE</i> , 2016 , 11, e0150675	3.7	11
27	Impact of serum HER2, TIMP-1, and CAIX on outcome for HER2+ metastatic breast cancer patients: CCTG MA.31 (lapatinib vs. trastuzumab). <i>Breast Cancer Research and Treatment</i> , 2017 , 164, 571-580	4.4	10
26	Atrophia controls developmental signaling pathways via interactions with Trithorax-like. <i>ELife</i> , 2017 , 6,	8.9	10
25	Exploding vertebrate genomes. <i>Nature Genetics</i> , 1998 , 18, 301-3	36.3	10
24	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021 , 595, 585-590	5.4	10
23	Resource: Scalable whole genome sequencing of 40,000 single cells identifies stochastic aneuploidies, genome replication states and clonal repertoires		9
22	Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. <i>Breast Cancer Research</i> , 2016 , 18, 70	8.3	9
21	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. <i>PLoS Computational Biology</i> , 2020 , 16, e1008270	5	8
20	Age-correlated protein and transcript expression in breast cancer and normal breast tissues is dominated by host endocrine effects.. <i>Nature Cancer</i> , 2020 , 1, 518-532	15.4	7
19	Identification of a selective DDX3X inhibitor with newly developed quantitative high-throughput RNA helicase assays. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 523, 795-801	3.4	7
18	Probabilistic cell type assignment of single-cell transcriptomic data reveals spatiotemporal microenvironment dynamics in human cancers		7
17	Decoding Transcriptome Dynamics of Genome-Encoded Polyadenylation and Autoregulation with Small-Molecule Modulators of Alternative Polyadenylation. <i>Cell Chemical Biology</i> , 2018 , 25, 1470-1484.e5	8.2	6
16	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. <i>Nature Communications</i> , 2021 , 12, 5406	17.4	6
15	Evolution of plasminogen-related growth factors (HGF/SF and HGF1/MSP). <i>Novartis Foundation Symposium</i> , 1997 , 212, 24-35; discussion 35-41, 42-5		4
14	Cancer phylogenetic tree inference at scale from 1000s of single cell genomes		4
13	Engineered in-vitro cell line mixtures and robust evaluation of computational methods for clonal decomposition and longitudinal dynamics in cancer. <i>Scientific Reports</i> , 2017 , 7, 13467	4.9	3
12	Open-source work even more vital to genome project than to software. <i>Nature</i> , 2000 , 404, 809	50.4	3

11	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
10	Single cell fitness landscapes induced by genetic and pharmacologic perturbations in cancer		3
9	Ubiquitin-mediated DNA damage response is synthetic lethal with G-quadruplex stabilizer CX-5461. <i>Scientific Reports</i> , 2021 , 11, 9812	4-9	3
8	Evolutionary tracking of cancer haplotypes at single-cell resolution		3
7	Epiclomal: probabilistic clustering of sparse single-cell DNA methylation data		2
6	Dissociation of solid tumour tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses		2
5	The impact of mutational processes on structural genomic plasticity in cancer cells		2
4	The interface of malignant and immunologic clonal dynamics in high-grade serous ovarian cancer		1
3	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , 2021 , 12, 665888	4-5	1
2	Genetic approaches to unraveling G protein-coupled receptor biology. <i>Current Opinion in Drug Discovery & Development</i> , 2004 , 7, 658-64		1
1	Gene regulatory network analysis defines transcriptome landscape with alternative splicing of human umbilical vein endothelial cells during replicative senescence. <i>BMC Genomics</i> , 2021 , 22, 869	4-5	0