Aedin C Culhane

List of Publications by Year
in descending order

98 papers	11,764 citations	53794 45 h-index	66911 78 g-index
110 all docs	110 docs citations	110 times ranked	20314 citing authors

#	Article	IF	Citations
1	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
2	RAP80 Targets BRCA1 to Specific Ubiquitin Structures at DNA Damage Sites. Science, 2007, 316, 1198-1202.	12.6	599
3	Apoptosis: Molecular Regulation of Cell Death. FEBS Journal, 1996, 236, 1-26.	0.2	563
4	Repeatability of published microarray gene expression analyses. Nature Genetics, 2009, 41, 149-155.	21.4	477
5	*survcomp*: an R/Bioconductor package for performance assessment and comparison of survival models. Bioinformatics, 2011, 27, 3206-3208.	4.1	384
6	MADE4: an R package for multivariate analysis of gene expression data. Bioinformatics, 2005, 21, 2789-2790.	4.1	364
7	Comparison and evaluation of methods for generating differentially expressed gene lists from microarray data. BMC Bioinformatics, 2006, 7, 359.	2.6	295
8	Dimension reduction techniques for the integrative analysis of multi-omics data. Briefings in Bioinformatics, 2016, 17, 628-641.	6.5	280
9	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. Journal of the National Cancer Institute, 2012, 104, 311-325.	6.3	272
10	A multivariate approach to the integration of multi-omics datasets. BMC Bioinformatics, 2014, 15, 162.	2.6	238
11	Between-group analysis of microarray data. Bioinformatics, 2002, 18, 1600-1608.	4.1	200
12	Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples. Journal of the National Cancer Institute, 2014, 106, .	6.3	184
13	Enter the Matrix: Factorization Uncovers Knowledge from Omics. Trends in Genetics, 2018, 34, 790-805.	6.7	181
14	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
15	Taxonomy of breast cancer based on normal cell phenotype predicts outcome. Journal of Clinical Investigation, 2014, 124, 859-870.	8.2	164
16	Profiles of Genomic Instability in High-Grade Serous Ovarian Cancer Predict Treatment Outcome. Clinical Cancer Research, 2012, 18, 5806-5815.	7.0	150
17	Gene Expression Atlas update--a value-added database of microarray and sequencing-based functional genomics experiments. Nucleic Acids Research, 2012, 40, D1077-D1081.	14.5	143
18	An Embryonic Diapause-like Adaptation with Suppressed Myc Activity Enables Tumor Treatment Persistence. Cancer Cell, 2021, 39, 240-256.e11.	16.8	143

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19	Epithelial Progeny of Estrogen-Exposed Breast Progenitor Cells Display a Cancer-like Methylome. Cancer Research, 2008, 68, 1786-1796.	0.9	127
20	Cross-platform comparison and visualisation of gene expression data using co-inertia analysis. BMC Bioinformatics, 2003, 4, 59.	2.6	125
21	Proliferative genes dominate malignancy-risk gene signature in histologically-normal breast tissue. Breast Cancer Research and Treatment, 2010, 119, 335-346.	2.5	119
22	Risk of hydroxychloroquine alone and in combination with azithromycin in the treatment of rheumatoid arthritis: a multinational, retrospective study. Lancet Rheumatology, The, 2020, 2, e698-e711.	3.9	117
23	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	110
24	Multiple markers for melanoma progression regulated by DNA methylation: insights from transcriptomic studies. Carcinogenesis, 2005, 26, 1856-1867.	2.8	108
25	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. Nucleic Acids Research, 2012, 40, D1060-D1066.	14.5	108
26	Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer. PLoS ONE, 2012, 7, e30269.	2.5	107
27	Expression Profiler: next generation--an online platform for analysis of microarray data. Nucleic Acids Research, 2004, 32, W465-W470.	14.5	105
28	CENP-F expression is associated with poor prognosis and chromosomal instability in patients with primary breast cancer. International Journal of Cancer, 2007, 120, 1434-1443.	5.1	98
29	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. Genome Medicine, 2013, 5, 2.	8.2	96
30	GeneSigDBâ€"a curated database of gene expression signatures. Nucleic Acids Research, 2010, 38, D716-D725.	14.5	91
31	Identification of Novel Kinase Targets for the Treatment of Estrogen Receptorâ€"Negative Breast Cancer. Clinical Cancer Research, 2009, 15, 6327-6340.	7.0	89
32	Deep phenotyping of 34,128 adult patients hospitalised with COVID-19 in an international network study. Nature Communications, 2020, 11, 5009.	12.8	86
33	Cloning of rat brain interleukin-18 cDNA. Molecular Psychiatry, 1998, 3, 362-366.	7.9	85
34	Altered Cytoplasmic-to-Nuclear Ratio of Survivin Is a Prognostic Indicator in Breast Cancer. Clinical Cancer Research, 2008, 14, 2681-2689.	7.0	83
35	Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42.	0.9	80
36	A multivariate analysis approach to the integration of proteomic and gene expression data. Proteomics, 2007, 7, 2162-2171.	2.2	70

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37	Oligonucleotide microarray analysis of gene expression in neuroblastoma displaying loss of chromosome 11q. Carcinogenesis, 2004, 25, 1599-1609.	2.8	61
38	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. Molecular and Cellular Proteomics, 2019, 18, S153-S168.	3.8	59
39	*MECP2* Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. Cancer Discovery, 2016, 6, 45-58.	9.4	57
40	Detection of the interleukin 18 family in rat brain by RT-PCR. Molecular Brain Research, 2000, 77, 290-293.	2.3	54
41	*Palb2* synergizes with *Trp53* to suppress mammary tumor formation in a model of inherited breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8632-8637.	7.1	54
42	Molecular Subtypes Improve Prognostic Value of International Metastatic Renal Cell Carcinoma Database Consortium Prognostic Model. Oncologist, 2017, 22, 286-292.	3.7	54
43	Functional Genomics Identify Distinct and Overlapping Genes Mediating Resistance to Different Classes of Heterobifunctional Degraders of Oncoproteins. Cell Reports, 2021, 34, 108532.	6.4	54
44	Functional classification analysis of somatically mutated genes in human breast and colorectal cancers. Genomics, 2008, 91, 508-511.	2.9	48
45	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. Nature Genetics, 2021, 53, 1196-1206.	21.4	47
46	Application of DNA microarray technology in determining breast cancer prognosis and therapeutic response. Expert Opinion on Biological Therapy, 2005, 5, 1069-1083.	3.1	46
47	iBBiG: iterative binary bi-clustering of gene sets. Bioinformatics, 2012, 28, 2484-2492.	4.1	46
48	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	6.5	46
49	Integrated Analysis of Multiple Microarray Datasets Identifies a Reproducible Survival Predictor in Ovarian Cancer. PLoS ONE, 2011, 6, e18202.	2.5	35
50	Confounding Effects in â€œA Six-Gene Signature Predicting Breast Cancer Lung Metastasisâ€• Cancer Research, 2009, 69, 7480-7485.	0.9	34
51	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 509-519.	2.5	34
52	Analysis of differential gene expression in colorectal cancer and stroma using fluorescence-activated cell sorting purification. British Journal of Cancer, 2009, 100, 1452-1464.	6.4	33
53	Integrating transcription factor binding site information with gene expression datasets. Bioinformatics, 2007, 23, 298-305.	4.1	32
54	Stem Cell-Like Gene Expression in Ovarian Cancer Predicts Type II Subtype and Prognosis. PLoS ONE, 2013, 8, e57799.	2.5	30

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55	The Stem Cell Discovery Engine: an integrated repository and analysis system for cancer stem cell comparisons. Nucleic Acids Research, 2012, 40, D984-D991.	14.5	29
56	Significance Analysis of Prognostic Signatures. PLoS Computational Biology, 2013, 9, e1002875.	3.2	27
57	RamiGO: an R/Bioconductor package providing an AmiGO Visualize interface. Bioinformatics, 2013, 29, 666-668.	4.1	25
58	Therapeutic Implications of GIPC1 Silencing in Cancer. PLoS ONE, 2010, 5, e15581.	2.5	22
59	BRCA1-IRIS promotes human tumor progression through PTEN blockade and HIF-1α activation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9600-E9609.	7.1	20
60	Identification of transcription factors associated with castration€resistance: Is the serum responsive factor a potential therapeutic target?. Prostate, 2013, 73, 743-753.	2.3	18
61	Mechanisms Driving Local Breast Cancer Recurrence in a Model of Breast-Conserving Surgery. Annals of Surgical Oncology, 2008, 15, 2954-2964.	1.5	16
62	RelA-Induced Interferon Response Negatively Regulates Proliferation. PLoS ONE, 2015, 10, e0140243.	2.5	16
63	Anti-CAIX BBζ CAR4/8 T cells exhibit superior efficacy in a ccRCC mouse model. Molecular Therapy - Oncolytics, 2022, 24, 385-399.	4.4	15
64	Common Molecular Mechanisms of Mammary Gland Development and Breast Cancer. Cellular and Molecular Life Sciences, 2007, 64, 3185-3200.	5.4	11
65	DNA Microarray-Based Gene Expression Profiling in Cancer: Aiding Cancer Diagnosis, Assessing Prognosis and Predicting Response to Therapy. Current Pharmacogenomics and Personalized Medicine: the International Journal for Expert Reviews in Pharmacogenomics, 2005, 3, 289-304.	0.3	10
66	The cocaine- and amphetamine-regulated transcript mediates ligand-independent activation of ERα, and is an independent prognostic factor in node-negative breast cancer. Oncogene, 2012, 31, 3483-3494.	5.9	10
67	Impact of Data Preprocessing on Integrative Matrix Factorization of Single Cell Data. Frontiers in Oncology, 2020, 10, 973.	2.8	10
68	Pleiotropic Mechanisms Drive Endocrine Resistance in the Three-Dimensional Bone Microenvironment. Cancer Research, 2021, 81, 371-383.	0.9	10
69	Community-wide hackathons to identify central themes in single-cell multi-omics. Genome Biology, 2021, 22, 220.	8.8	9
70	Optimized between-group classification: a new jackknife-based gene selection procedure for genome-wide expression data. BMC Bioinformatics, 2005, 6, 239.	2.6	8
71	Characteristics and Outcomes of Over 300,000 Patients with COVID-19 and History of Cancer in the United States and Spain. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1884-1894.	2.5	6
72	Systematic Characterization of Genes Representing Preferential Molecular Vulnerabilities for Myeloma Cells Compared to Other Neoplasias - Implications for the Biology and Therapeutic Targeting of Myeloma. Blood, 2019, 134, 4407-4407.	1.4	4

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73	*POU2AF1* As a Master Regulator of Oncogenic Transcription Factor Networks in Myeloma. Blood, 2020, 136, 18-19.	1.4	4
74	Integrative Exploratory Analysis of Two or More Genomic Datasets. Methods in Molecular Biology, 2016, 1418, 19-38.	0.9	3
75	Functional Genomic Landscape of Genes with Recurrent Mutations in Multiple Myeloma. Blood, 2018, 132, 189-189.	1.4	2
76	Use of Olfactory Receptor Genes As Controls for Genome-Scale CRISPR Functional Genomic Studies to Define Treatment Resistance Mechanisms. Blood, 2020, 136, 36-36.	1.4	2
77	Molecular markers of myeloma cell sensitivity vs. resistance to heterobifunctional degraders of oncoproteins: therapeutic implications.. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e134.	0.4	1
78	Abstract 2355: Risk prediction for late-stage ovarian cancer by meta-analysis of 1,525 patient samples. , 2014, , .		1
79	In Reply. Oncologist, 2017, 22, 1561-1561.	3.7	0
80	CRISPR studies identify genes preferentially essential for myeloma cells vs. other neoplasias: implications for future therapies selective against MM. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e48-e49.	0.4	0
81	CRISPR-based functional genomics landscape of genes recurrently mutated in MM. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e77-e78.	0.4	0
82	OPTIMIZATION OF BETWEEN GROUP ANALYSIS OF GENE EXPRESSION DISEASE CLASS PREDICTION. , 2006, , .		0
83	AI Methods for Analyzing Microarray Data. , 2009, , 65-70.		0
84	Abstract 2135: Genetic relationships between ovarian and breast cancers. , 2010, , .		0
85	Abstract LB-278: Transcriptomic profiling of castrate resistant prostate cancer cells: identification of transcription factors associated with androgen resistance. , 2011, , .		0
86	Abstract B067: Taxonomy of breast cancer based on normal cell phenotype and ontology. , 2013, , .		0
87	Meta-analysis of public microarray databases for prognostic and predictive gene signatures of late-stage ovarian cancer.. Journal of Clinical Oncology, 2014, 32, 5531-5531.	1.6	0
88	Prognostic value of genomic signatures in metastatic Clear Cell Renal Cell Carcinoma (mRCC) using The Cancer Genome Atlas (TCGA) data.. Journal of Clinical Oncology, 2015, 33, 4560-4560.	1.6	0
89	Abstract LB-162: BRCA2, and not BRCA1, dependent crosstalk between replication stress suppression and nucleotide excision repair - Clinical implications. , 2016, , .		0
90	Characterization of Lineage Vs. Context-Dependent Essential Genes in Multiple Myeloma Using Crispr/Cas9 Genome Editing. Blood, 2016, 128, 119-119.	1.4	0

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91	Topological Pathway Enrichment Analysis of Gene Expression in High Grade Serous Ovarian Cancer Reveals Tumor-Stoma Cross-Talk. Trends in Mathematics, 2017, , 59-63.	0.1	0
92	Abstract 5016: High-throughput patient-derived 3-dimensional organoid cultures as personalized models to assess drug response and post-treatment residual disease. , 2017, , .		0
93	Abstract LB-118: Characterization of lineage vs. context-dependent essential genes in multiple myeloma using CRISPR-Cas9 genome editing. , 2017, , .		0
94	CRISPR-Based Functional Genomics Studies Reveal Distinct and Overlapping Genes Mediating Resistance to Different Classes of Heterobifunctional Degraders of Oncoproteins: Implications for Novel Therapeutics across Diverse Neoplasias. Blood, 2018, 132, 1367-1367.	1.4	0
95	Functional Characterization of E3 Ligases and Their Regulators: Therapeutic Implications for Development of New Proteolysis-Targeting Chimeric Degraders of Oncoproteins. Blood, 2019, 134, 318-318.	1.4	0
96	Functional Genomic and Immune Response Characterization of PTEN Loss: Therapeutic Implications for Myeloma. Blood, 2021, 138, 1612-1612.	1.4	0
97	Functional Oncogenomic and Immune Response Landscape for Genes Recurrently Mutated in Myeloma. Blood, 2021, 138, 1589-1589.	1.4	0
98	AI Methods for Analyzing Microarray Data. , 0, , 877-884.		0