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	Anti-CAIX BBℓ CAR4/8 TÂcells exhibit superior efficacy in a ccRCC mouse model. Molecular Therapy - Oncolytics, 2022, 24, 385-399.	4.4	15
2	Pleiotropic Mechanisms Drive Endocrine Resistance in the Three-Dimensional Bone Microenvironment. Cancer Research, 2021, 81, 371-383.	0.9	10
3	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
4	An Embryonic Diapause-like Adaptation with Suppressed Myc Activity Enables Tumor Treatment Persistence. Cancer Cell, 2021, 39, 240-256.e11.	16.8	143
5	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. Nature Genetics, 2021, 53, 1196-1206.	21.4	47
6	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
7	Community-wide hackathons to identify central themes in single-cell multi-omics. Genome Biology, 2021, 22, 220.	8.8	9
8	Functional Genomic and Immune Response Characterization of PTEN Loss: Therapeutic Implications for Myeloma. Blood, 2021, 138, 1612-1612.	1.4	0
9	Functional Oncogenomic and Immune Response Landscape for Genes Recurrently Mutated in Myeloma. Blood, 2021, 138, 1589-1589.	1.4	0
10	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
11	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
12	Deep phenotyping of 34,128 adult patients hospitalised with COVID-19 in an international network study. Nature Communications, 2020, 11, 5009.	12.8	86
13	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
14	Impact of Data Preprocessing on Integrative Matrix Factorization of Single Cell Data. Frontiers in Oncology, 2020, 10, 973.	2.8	10
15	<i>POU2AF1</i> As a Master Regulator of Oncogenic Transcription Factor Networks in Myeloma. Blood, 2020, 136, 18-19.	1.4	4
16	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
17	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
18	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. Molecular and Cellular Proteomics, 2019, 18, S153-S168.	3.8	59

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19	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
20	CRISPR-based functional genomics landscape of genes recurrently mutated in MM. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e77-e78.	0.4	0
21	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
22	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
23	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
24	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
25	Enter the Matrix: Factorization Uncovers Knowledge from Omics. Trends in Genetics, 2018, 34, 790-805.	6.7	181
26	Functional Genomic Landscape of Genes with Recurrent Mutations in Multiple Myeloma. Blood, 2018, 132, 189-189.	1.4	2
27	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
28	Molecular Subtypes Improve Prognostic Value of International Metastatic Renal Cell Carcinoma Database Consortium Prognostic Model. Oncologist, 2017, 22, 286-292.	3.7	54
29	In Reply. Oncologist, 2017, 22, 1561-1561.	3.7	0
30	Software for the Integration of Multiomics Experiments in Bioconductor. Cancer Research, 2017, 77, e39-e42.	0.9	80
31	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
32	Abstract 5016: High-throughput patient-derived 3-dimensional organoid cultures as personalized models to assess drug response and post-treatment residual disease. , 2017, , .		0
33	Abstract LB-118: Characterization of lineage vs. context-dependent essential genes in multiple myeloma using CRISPR-Cas9 genome editing. , 2017, , .		0
34	Integrative Exploratory Analysis of Two or More Genomic Datasets. Methods in Molecular Biology, 2016, 1418, 19-38.	0.9	3
35	Dimension reduction techniques for the integrative analysis of multi-omics data. Briefings in Bioinformatics, 2016, 17, 628-641.	6.5	280
36	*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

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37	Public data and open source tools for multi-assay genomic investigation of disease. Briefings in Bioinformatics, 2016, 17, 603-615.	6.5	46
38	Abstract LB-162: BRCA2, and not BRCA1, dependent crosstalk between replication stress suppression and nucleotide excision repair - Clinical implications. , 2016, , .		0
39	Characterization of Lineage Vs. Context-Dependent Essential Genes in Multiple Myeloma Using Crispr/Cas9 Genome Editing. Blood, 2016, 128, 119-119.	1.4	0
40	RelA-Induced Interferon Response Negatively Regulates Proliferation. PLoS ONE, 2015, 10, e0140243.	2.5	16
41	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
42	Taxonomy of breast cancer based on normal cell phenotype predicts outcome. Journal of Clinical Investigation, 2014, 124, 859-870.	8.2	164
43	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
44	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	110
45	A multivariate approach to the integration of multi-omics datasets. BMC Bioinformatics, 2014, 15, 162.	2.6	238
46	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
47	Abstract 2355: Risk prediction for late-stage ovarian cancer by meta-analysis of 1,525 patient samples. , 2014, , .		1
48	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. Genome Medicine, 2013, 5, 2.	8.2	96
49	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
50	Significance Analysis of Prognostic Signatures. PLoS Computational Biology, 2013, 9, e1002875.	3.2	27
51	RamiGO: an R/Bioconductor package providing an AmiGO Visualize interface. Bioinformatics, 2013, 29, 666-668.	4.1	25
52	<i>Palb2</i> synergizes with <i>Trp53</i> 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
53	Stem Cell-Like Gene Expression in Ovarian Cancer Predicts Type II Subtype and Prognosis. PLoS ONE, 2013, 8, e57799.	2.5	30
54	Abstract B067: Taxonomy of breast cancer based on normal cell phenotype and ontology. , 2013, , .		0

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55	iBBiG: iterative binary bi-clustering of gene sets. Bioinformatics, 2012, 28, 2484-2492.	4.1	46
56	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
57	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
58	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. Journal of the National Cancer Institute, 2012, 104, 311-325.	6.3	272
59	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. Nucleic Acids Research, 2012, 40, D1060-D1066.	14.5	108
60	Profiles of Genomic Instability in High-Grade Serous Ovarian Cancer Predict Treatment Outcome. Clinical Cancer Research, 2012, 18, 5806-5815.	7.0	150
61	The cocaine- and amphetamine-regulated transcript mediates ligand-independent activation of ERÎ±, and is an independent prognostic factor in node-negative breast cancer. Oncogene, 2012, 31, 3483-3494.	5.9	10
62	Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer. PLoS ONE, 2012, 7, e30269.	2.5	107
63	Integrated Analysis of Multiple Microarray Datasets Identifies a Reproducible Survival Predictor in Ovarian Cancer. PLoS ONE, 2011, 6, e18202.	2.5	35
64	*survcomp*: an R/Bioconductor package for performance assessment and comparison of survival models. Bioinformatics, 2011, 27, 3206-3208.	4.1	384
65	Abstract LB-278: Transcriptomic profiling of castrate resistant prostate cancer cells: identification of transcription factors associated with androgen resistance. , 2011, , .		0
66	Proliferative genes dominate malignancy-risk gene signature in histologically-normal breast tissue. Breast Cancer Research and Treatment, 2010, 119, 335-346.	2.5	119
67	Therapeutic Implications of GIPC1 Silencing in Cancer. PLoS ONE, 2010, 5, e15581.	2.5	22
68	GeneSigDBâ€"a curated database of gene expression signatures. Nucleic Acids Research, 2010, 38, D716-D725.	14.5	91
69	Abstract 2135: Genetic relationships between ovarian and breast cancers. , 2010, , .		0
70	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
71	Confounding Effects in â€œA Six-Gene Signature Predicting Breast Cancer Lung Metastasisâ€. Cancer Research, 2009, 69, 7480-7485.	0.9	34
72	Identification of Novel Kinase Targets for the Treatment of Estrogen Receptorâ€"Negative Breast Cancer. Clinical Cancer Research, 2009, 15, 6327-6340.	7.0	89

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73	Repeatability of published microarray gene expression analyses. Nature Genetics, 2009, 41, 149-155.	21.4	477
74	AI Methods for Analyzing Microarray Data. , 2009, , 65-70.		0
75	Mechanisms Driving Local Breast Cancer Recurrence in a Model of Breast-Conserving Surgery. Annals of Surgical Oncology, 2008, 15, 2954-2964.	1.5	16
76	Functional classification analysis of somatically mutated genes in human breast and colorectal cancers. Genomics, 2008, 91, 508-511.	2.9	48
77	Epithelial Progeny of Estrogen-Exposed Breast Progenitor Cells Display a Cancer-like Methylome. Cancer Research, 2008, 68, 1786-1796.	0.9	127
78	Altered Cytoplasmic-to-Nuclear Ratio of Survivin Is a Prognostic Indicator in Breast Cancer. Clinical Cancer Research, 2008, 14, 2681-2689.	7.0	83
79	RAP80 Targets BRCA1 to Specific Ubiquitin Structures at DNA Damage Sites. Science, 2007, 316, 1198-1202.	12.6	599
80	Integrating transcription factor binding site information with gene expression datasets. Bioinformatics, 2007, 23, 298-305.	4.1	32
81	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
82	A multivariate analysis approach to the integration of proteomic and gene expression data. Proteomics, 2007, 7, 2162-2171.	2.2	70
83	Common Molecular Mechanisms of Mammary Gland Development and Breast Cancer. Cellular and Molecular Life Sciences, 2007, 64, 3185-3200.	5.4	11
84	Comparison and evaluation of methods for generating differentially expressed gene lists from microarray data. BMC Bioinformatics, 2006, 7, 359.	2.6	295
85	OPTIMIZATION OF BETWEEN GROUP ANALYSIS OF GENE EXPRESSION DISEASE CLASS PREDICTION. , 2006, , .		0
86	Optimized between-group classification: a new jackknife-based gene selection procedure for genome-wide expression data. BMC Bioinformatics, 2005, 6, 239.	2.6	8
87	MADE4: an R package for multivariate analysis of gene expression data. Bioinformatics, 2005, 21, 2789-2790.	4.1	364
88	Multiple markers for melanoma progression regulated by DNA methylation: insights from transcriptomic studies. Carcinogenesis, 2005, 26, 1856-1867.	2.8	108
89	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
90	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

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91	Oligonucleotide microarray analysis of gene expression in neuroblastoma displaying loss of chromosome 11q. Carcinogenesis, 2004, 25, 1599-1609.	2.8	61
92	Expression Profiler: next generation--an online platform for analysis of microarray data. Nucleic Acids Research, 2004, 32, W465-W470.	14.5	105
93	Cross-platform comparison and visualisation of gene expression data using co-inertia analysis. BMC Bioinformatics, 2003, 4, 59.	2.6	125
94	Between-group analysis of microarray data. Bioinformatics, 2002, 18, 1600-1608.	4.1	200
95	Detection of the interleukin 18 family in rat brain by RT-PCR. Molecular Brain Research, 2000, 77, 290-293.	2.3	54
96	Cloning of rat brain interleukin-18 cDNA. Molecular Psychiatry, 1998, 3, 362-366.	7.9	85
97	Apoptosis: Molecular Regulation of Cell Death. FEBS Journal, 1996, 236, 1-26.	0.2	563
98	AI Methods for Analyzing Microarray Data. , 0, , 877-884.		0