

Aron Charles Eklund

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

19,589
citations

109264

35
h-index

206029

48
g-index

52
all docs

52
docs citations

52
times ranked

34464
citing authors

#	ARTICLE	IF	CITATIONS
1	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. <i>New England Journal of Medicine</i> , 2012, 366, 883-892.	13.9	6,769
2	An online survival analysis tool to rapidly assess the effect of 22,277 genes on breast cancer prognosis using microarray data of 1,809 patients. <i>Breast Cancer Research and Treatment</i> , 2010, 123, 725-731.	1.1	2,480
3	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. <i>Nature Biotechnology</i> , 2006, 24, 1151-1161.	9.4	1,927
4	A signature of chromosomal instability inferred from gene expression profiles predicts clinical outcome in multiple human cancers. <i>Nature Genetics</i> , 2006, 38, 1043-1048.	9.4	1,002
5	Efficacy of Neoadjuvant Cisplatin in Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 1145-1153.	0.8	860
6	PGC-1 β , A Potential Therapeutic Target for Early Intervention in Parkinson's Disease. <i>Science Translational Medicine</i> , 2010, 2, 52ra73.	5.8	691
7	Sequenza: allele-specific copy number and mutation profiles from tumor sequencing data. <i>Annals of Oncology</i> , 2015, 26, 64-70.	0.6	591
8	Reliability and reproducibility issues in DNA microarray measurements. <i>Trends in Genetics</i> , 2006, 22, 101-109.	2.9	516
9	Telomeric Allelic Imbalance Indicates Defective DNA Repair and Sensitivity to DNA-Damaging Agents. <i>Cancer Discovery</i> , 2012, 2, 366-375.	7.7	464
10	Molecular markers of early Parkinson's disease based on gene expression in blood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 955-960.	3.3	462
11	Paradoxical Relationship between Chromosomal Instability and Survival Outcome in Cancer. <i>Cancer Research</i> , 2011, 71, 3447-3452.	0.4	296
12	A large-scale analysis of tissue-specific pathology and gene expression of human disease genes and complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20870-20875.	3.3	288
13	Large-scale detection of antigen-specific T cells using peptide-MHC-I multimers labeled with DNA barcodes. <i>Nature Biotechnology</i> , 2016, 34, 1037-1045.	9.4	279
14	Jetset: selecting the optimal microarray probe set to represent a gene. <i>BMC Bioinformatics</i> , 2011, 12, 474.	1.2	277
15	GATA transcription factors directly regulate the Parkinson's disease-linked gene α -synuclein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10907-10912.	3.3	251
16	MicroRNA profile analysis of human prostate cancers. <i>Cancer Gene Therapy</i> , 2009, 16, 206-216.	2.2	251
17	Chromosomal instability determines taxane response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8671-8676.	3.3	244
18	Pan-cancer analysis of genomic scar signatures associated with homologous recombination deficiency suggests novel indications for existing cancer drugs. <i>Biomarker Research</i> , 2015, 3, 9.	2.8	214

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19	MuPeXI: prediction of neo-epitopes from tumor sequencing data. <i>Cancer Immunology, Immunotherapy</i> , 2017, 66, 1123-1130.	2.0	177
20	Migrating the SNP array-based homologous recombination deficiency measures to next generation sequencing data of breast cancer. <i>Npj Breast Cancer</i> , 2018, 4, 16.	2.3	163
21	Relationship of Extreme Chromosomal Instability with Long-term Survival in a Retrospective Analysis of Primary Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2183-2194.	1.1	141
22	Tumor Mutation Burden Forecasts Outcome in Ovarian Cancer with BRCA1 or BRCA2 Mutations. <i>PLoS ONE</i> , 2013, 8, e80023.	1.1	131
23	Assessment of an RNA interference screen-derived mitotic and ceramide pathway metagene as a predictor of response to neoadjuvant paclitaxel for primary triple-negative breast cancer: a retrospective analysis of five clinical trials. <i>Lancet Oncology</i> , The, 2010, 11, 358-365.	5.1	116
24	Redefinition of Affymetrix probe sets by sequence overlap with cDNA microarray probes reduces cross-platform inconsistencies in cancer-associated gene expression measurements. <i>BMC Bioinformatics</i> , 2005, 6, 107.	1.2	113
25	An Analysis of Natural T Cell Responses to Predicted Tumor Neoepitopes. <i>Frontiers in Immunology</i> , 2017, 8, 1566.	2.2	103
26	Evaluation of Microarray Preprocessing Algorithms Based on Concordance with RT-PCR in Clinical Samples. <i>PLoS ONE</i> , 2009, 4, e5645.	1.1	80
27	Replacing cRNA targets with cDNA reduces microarray cross-hybridization. <i>Nature Biotechnology</i> , 2006, 24, 1071-1073.	9.4	65
28	Correction of technical bias in clinical microarray data improves concordance with known biological information. <i>Genome Biology</i> , 2008, 9, R26.	13.9	63
29	Breast cancer brain metastases show increased levels of genomic aberration-based homologous recombination deficiency scores relative to their corresponding primary tumors. <i>Annals of Oncology</i> , 2018, 29, 1948-1954.	0.6	60
30	<i>MECP2</i> Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. <i>Cancer Discovery</i> , 2016, 6, 45-58.	7.7	57
31	Human endogenous retroviruses form a reservoir of T cell targets in hematological cancers. <i>Nature Communications</i> , 2020, 11, 5660.	5.8	55
32	The comparison of thrombocytosis and platelet-lymphocyte ratio as potential prognostic markers in colorectal cancer. <i>Thrombosis and Haemostasis</i> , 2014, 112, 483-490.	1.8	52
33	TumorTracer: a method to identify the tissue of origin from the somatic mutations of a tumor specimen. <i>BMC Medical Genomics</i> , 2015, 8, 58.	0.7	49
34	Relationship of postoperative thrombocytosis and survival of patients with colorectal cancer. <i>International Journal of Surgery</i> , 2015, 18, 1-6.	1.1	49
35	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010, 2, 53.	3.6	43
36	Glioblastoma adaptation traced through decline of an IDH1 clonal driver and macro-evolution of a double-minute chromosome. <i>Annals of Oncology</i> , 2015, 26, 880-887.	0.6	37

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37	The CIN4 Chromosomal Instability qPCR Classifier Defines Tumor Aneuploidy and Stratifies Outcome in Grade 2 Breast Cancer. PLoS ONE, 2013, 8, e56707.	1.1	28
38	Tumor-Infiltrating T Cells From Clear Cell Renal Cell Carcinoma Patients Recognize Neoepitopes Derived From Point and Frameshift Mutations. Frontiers in Immunology, 2020, 11, 373.	2.2	27
39	Minimising Immunohistochemical False Negative ER Classification Using a Complementary 23 Gene Expression Signature of ER Status. PLoS ONE, 2010, 5, e15031.	1.1	26
40	A robust prognostic gene expression signature for early stage lung adenocarcinoma. Biomarker Research, 2016, 4, 4.	2.8	22
41	Spatiotemporal patterns of gene expression during fetal monkey brain development. Developmental Brain Research, 2003, 146, 99-106.	2.1	18
42	Optimization of the BLASTN substitution matrix for prediction of non-specific DNA microarray hybridization. Nucleic Acids Research, 2010, 38, e27-e27.	6.5	12
43	Biasogram: Visualization of Confounding Technical Bias in Gene Expression Data. PLoS ONE, 2013, 8, e61872.	1.1	7
44	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. BMC Bioinformatics, 2011, 12, 310.	1.2	4
45	Prediction of drug efficacy for cancer treatment based on comparative analysis of chemosensitivity and gene expression data. Bioorganic and Medicinal Chemistry, 2012, 20, 167-176.	1.4	4
46	Exposure to perfluorononanoic acid combined with a low-dose mixture of 14 human-relevant compounds disturbs energy/lipid homeostasis in rats. Metabolomics, 2015, 11, 1451-1464.	1.4	4
47	Concordance of exon array and real-time PCR assessment of gene expression following cancer cell cytotoxic drug exposure. Cell Cycle, 2008, 7, 3947-3948.	1.3	3