

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	Human endogenous retroviruses form a reservoir of T cell targets in hematological cancers. <i>Nature Communications</i> , 2020, 11, 5660.	5.8	55
2	Tumor-Infiltrating T Cells From Clear Cell Renal Cell Carcinoma Patients Recognize Neopeptides Derived From Point and Frameshift Mutations. <i>Frontiers in Immunology</i> , 2020, 11, 373.	2.2	27
3	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
4	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
5	MuPeXI: prediction of neo-epitopes from tumor sequencing data. <i>Cancer Immunology, Immunotherapy</i> , 2017, 66, 1123-1130.	2.0	177
6	An Analysis of Natural T Cell Responses to Predicted Tumor Neopeptides. <i>Frontiers in Immunology</i> , 2017, 8, 1566.	2.2	103
7	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
8	A robust prognostic gene expression signature for early stage lung adenocarcinoma. <i>Biomarker Research</i> , 2016, 4, 4.	2.8	22
9	<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
10	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
11	Clioblastoma 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
12	Relationship of postoperative thrombocytosis and survival of patients with colorectal cancer. <i>International Journal of Surgery</i> , 2015, 18, 1-6.	1.1	49
13	Exposure to perfluorononanoic acid combined with a low-dose mixture of 14 human-relevant compounds disturbs energy/lipid homeostasis in rats. <i>Metabolomics</i> , 2015, 11, 1451-1464.	1.4	4
14	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
15	Sequenza: allele-specific copy number and mutation profiles from tumor sequencing data. <i>Annals of Oncology</i> , 2015, 26, 64-70.	0.6	591
16	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
17	Biasogram: Visualization of Confounding Technical Bias in Gene Expression Data. <i>PLoS ONE</i> , 2013, 8, e61872.	1.1	7
18	The CIN4 Chromosomal Instability qPCR Classifier Defines Tumor Aneuploidy and Stratifies Outcome in Grade 2 Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e56707.	1.1	28

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19	Tumor Mutation Burden Forecasts Outcome in Ovarian Cancer with BRCA1 or BRCA2 Mutations. <i>PLoS ONE</i> , 2013, 8, e80023.	1.1	131
20	Telomeric Allelic Imbalance Indicates Defective DNA Repair and Sensitivity to DNA-Damaging Agents. <i>Cancer Discovery</i> , 2012, 2, 366-375.	7.7	464
21	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. <i>New England Journal of Medicine</i> , 2012, 366, 883-892.	13.9	6,769
22	Prediction of drug efficacy for cancer treatment based on comparative analysis of chemosensitivity and gene expression data. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 167-176.	1.4	4
23	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. <i>BMC Bioinformatics</i> , 2011, 12, 310.	1.2	4
24	Jetset: selecting the optimal microarray probe set to represent a gene. <i>BMC Bioinformatics</i> , 2011, 12, 474.	1.2	277
25	Paradoxical Relationship between Chromosomal Instability and Survival Outcome in Cancer. <i>Cancer Research</i> , 2011, 71, 3447-3452.	0.4	296
26	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
27	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
28	Optimization of the BLASTN substitution matrix for prediction of non-specific DNA microarray hybridization. <i>Nucleic Acids Research</i> , 2010, 38, e27-e27.	6.5	12
29	Efficacy of Neoadjuvant Cisplatin in Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 1145-1153.	0.8	860
30	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
31	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> , 2010, 11, 358-365.	5.1	116
32	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010, 2, 53.	3.6	43
33	Minimising Immunohistochemical False Negative ER Classification Using a Complementary 23 Gene Expression Signature of ER Status. <i>PLoS ONE</i> , 2010, 5, e15031.	1.1	26
34	Evaluation of Microarray Preprocessing Algorithms Based on Concordance with RT-PCR in Clinical Samples. <i>PLoS ONE</i> , 2009, 4, e5645.	1.1	80
35	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
36	MicroRNA profile analysis of human prostate cancers. <i>Cancer Gene Therapy</i> , 2009, 16, 206-216.	2.2	251

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37	Correction of technical bias in clinical microarray data improves concordance with known biological information. <i>Genome Biology</i> , 2008, 9, R26.	13.9	63
38	Concordance of exon array and real-time PCR assessment of gene expression following cancer cell cytotoxic drug exposure. <i>Cell Cycle</i> , 2008, 7, 3947-3948.	1.3	3
39	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
40	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
41	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
42	Replacing cRNA targets with cDNA reduces microarray cross-hybridization. <i>Nature Biotechnology</i> , 2006, 24, 1071-1073.	9.4	65
43	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
44	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
45	Reliability and reproducibility issues in DNA microarray measurements. <i>Trends in Genetics</i> , 2006, 22, 101-109.	2.9	516
46	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
47	Spatiotemporal patterns of gene expression during fetal monkey brain development. <i>Developmental Brain Research</i> , 2003, 146, 99-106.	2.1	18