Henrik Bengtsson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10838080/publications.pdf

Version: 2024-02-01

27 papers	4,260 citations	430874 18 h-index	580821 25 g-index
27 all docs	27 docs citations	27 times ranked	9331 citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple Tissue Biomarkers Independently and Additively Predict Prostate Cancer Pathology Outcomes. European Urology, 2021, 79, 141-149.	1.9	4
2	Human pediatric B-cell acute lymphoblastic leukemias can be classified as B-1 or B-2-like based on a minimal transcriptional signature. Experimental Hematology, 2020, 90, 65-71.e1.	0.4	7
3	GENE-47. A 3D ATLAS TO EVALUATE THE SPATIAL PATTERNING OF GENETIC ALTERATIONS AND TUMOR CELL STATES IN GLIOMA. Neuro-Oncology, 2019, 21, vi107-vi108.	1.2	0
4	Genomic analysis of the origins and evolution of multicentric diffuse lower-grade gliomas. Neuro-Oncology, 2018, 20, 632-641.	1.2	33
5	Validation of GEMCaP as a DNA Based Biomarker to Predict Prostate Cancer Recurrence after Radical Prostatectomy. Journal of Urology, 2018, 199, 719-725.	0.4	4
6	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant <i>IDH1</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10743-10748.	7.1	109
7	Discovering hotspots in functional genomic data superposed on 3D chromatin configuration reconstructions. Nucleic Acids Research, 2016, 44, 2028-2035.	14.5	21
8	Cytomegalovirus Immediate-Early Proteins Promote Stemness Properties in Glioblastoma. Cancer Research, 2015, 75, 3065-3076.	0.9	74
9	Validating the Use of Google Trends to Enhance Pertussis Surveillance in California. PLOS Currents, 2015, 7, .	1.4	20
10	DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Genome Research, 2014, 24, 2022-2032.	5.5	362
11	illuminaio: An open source IDAT parsing tool for Illumina microarrays. F1000Research, 2013, 2, 264.	1.6	65
12	CalMaTe: a method and software to improve allele-specific copy number of SNP arrays for downstream segmentation. Bioinformatics, 2012, 28, 1793-1794.	4.1	16
13	Subtype and pathway specific responses to anticancer compounds in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2724-2729.	7.1	417
14	Parent-specific copy number in paired tumorâ€“normal studies using circular binary segmentation. Bioinformatics, 2011, 27, 2038-2046.	4.1	100
15	Two Distinct Routes to Oral Cancer Differing in Genome Instability and Risk for Cervical Node Metastasis. Clinical Cancer Research, 2011, 17, 7024-7034.	7.0	60
16	Statistical Analysis of Single Nucleotide Polymorphism Microarrays in Cancer Studies. , 2011, , 225-255.		4
17	Identification of SOX3 as an XX male sex reversal gene in mice and humans. Journal of Clinical Investigation, 2011, 121, 328-341.	8.2	234
18	Copy Number Variation in Patients with Disorders of Sex Development Due to 46,XY Gonadal Dysgenesis. PLoS ONE, 2011, 6, e17793.	2.5	116

#	ARTICLE	IF	CITATIONS
19	TumorBoost: Normalization of allele-specific tumor copy numbers from a single pair of tumor-normal genotyping microarrays. BMC Bioinformatics, 2010, 11, 245.	2.6	49
20	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	16.8	2,078
21	A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays including GenomeWideSNP 5 & 6. Bioinformatics, 2009, 25, 2149-2156.	4.1	144
22	A single-sample method for normalizing and combining full-resolution copy numbers from multiple platforms, labs and analysis methods. Bioinformatics, 2009, 25, 861-867.	4.1	37
23	Exploration, normalization, and genotype calls of high-density oligonucleotide SNP array data. Biostatistics, 2007, 8, 485-499.	1.5	214
24	Methodological study of affine transformations of gene expression data with proposed robust non-parametric multi-dimensional normalization method. BMC Bioinformatics, 2006, 7, 100.	2.6	22
25	Microarray image analysis: background estimation using quantile and morphological filters. BMC Bioinformatics, 2006, 7, 96.	2.6	25
26	Calibration and assessment of channel-specific biases in microarray data with extended dynamical range. BMC Bioinformatics, 2004, 5, 177.	2.6	37
27	Identifying Differentially Expressed Genes in cDNA Microarray Experiments Authors. Science of Aging Knowledge Environment: SAGE KE, 2001, 2001, 8vp-8.	0.8	8