

Jaime I Davila

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

3,005
citations

186265

28
h-index

168389

53
g-index

68
all docs

68
docs citations

68
times ranked

5850
citing authors

#	ARTICLE	IF	CITATIONS
1	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. <i>Journal of Clinical Oncology</i> , 2015, 33, 304-311.	1.6	521
2	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. <i>BMC Bioinformatics</i> , 2014, 15, 224.	2.6	284
3	Double-strand break repair processes drive evolution of the mitochondrial genome in Arabidopsis. <i>BMC Biology</i> , 2011, 9, 64.	3.8	209
4	Diversity of the Arabidopsis Mitochondrial Genome Occurs via Nuclear-Controlled Recombination Activity. <i>Genetics</i> , 2009, 183, 1261-1268.	2.9	161
5	MutS HOMOLOG1 Is a Nucleoid Protein That Alters Mitochondrial and Plastid Properties and Plant Response to High Light Å. <i>Plant Cell</i> , 2011, 23, 3428-3441.	6.6	125
6	IL-6 facilitates oncogene-induced cholangiocarcinoma in mice by an interleukin-6 sensitive mechanism. <i>Hepatology</i> , 2015, 61, 1627-1642.	7.3	115
7	Integrated mate-pair and RNA sequencing identifies novel, targetable gene fusions in peripheral T-cell lymphoma. <i>Blood</i> , 2016, 128, 1234-1245.	1.4	105
8	RNA Toxicity and Missplicing in the Common Eye Disease Fuchs Endothelial Corneal Dystrophy. <i>Journal of Biological Chemistry</i> , 2015, 290, 5979-5990.	3.4	104
9	Gastroblastoma harbors a recurrent somatic MALAT1-GLI1 fusion gene. <i>Modern Pathology</i> , 2017, 30, 1443-1452.	5.5	93
10	Fast and Practical Algorithms for Planted (l, d) Motif Search. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 544-552.	3.0	92
11	Extensive Rearrangement of the Arabidopsis Mitochondrial Genome Elicits Cellular Conditions for Thermotolerance. <i>Plant Physiology</i> , 2010, 152, 1960-1970.	4.8	77
12	Recurrent STAT3-JAK2 fusions in indolent T-cell lymphoproliferative disorder of the gastrointestinal tract. <i>Blood</i> , 2018, 131, 2262-2266.	1.4	77
13	Contraction of T cell richness in lung cancer brain metastases. <i>Scientific Reports</i> , 2018, 8, 2171.	3.3	74
14	Development and characterization of human-induced pluripotent stem cell-derived cholangiocytes. <i>Laboratory Investigation</i> , 2015, 95, 684-696.	3.7	66
15	Spindle cell rhabdomyosarcoma of bone with <i>FUS</i> - <i>TFCP2L1</i> fusion: confirmation of a very recently described rhabdomyosarcoma subtype. <i>Histopathology</i> , 2018, 73, 514-520.	2.9	63
16	Cytoplasmic Male Sterility-Associated Chimeric Open Reading Frames Identified by Mitochondrial Genome Sequencing of Four <i>Cajanus</i> Genotypes. <i>DNA Research</i> , 2013, 20, 485-495.	3.4	58
17	ST3GAL1 is a target of the SOX2-GLI1 transcriptional complex and promotes melanoma metastasis through AXL. <i>Nature Communications</i> , 2020, 11, 5865.	12.8	54
18	Novel <i>TRAF1-ALK</i> fusion identified by deep RNA sequencing of anaplastic large cell lymphoma. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 1097-1102.	2.8	51

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19	Proteomic Detection of Immunoglobulin Light Chain Variable Region Peptides from Amyloidosis Patient Biopsies. <i>Journal of Proteome Research</i> , 2015, 14, 1957-1967.	3.7	50
20	<i>TP53</i> mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. <i>Nucleic Acids Research</i> , 2015, 43, 6945-6958.	14.5	46
21	Uterine inflammatory myofibroblastic tumors in pregnant women with and without involvement of the placenta: a study of 6 cases with identification of a novel TIMP3-RET fusion. <i>Human Pathology</i> , 2020, 97, 29-39.	2.0	43
22	Composite hemangioendothelioma with neuroendocrine marker expression: an aggressive variant. <i>Modern Pathology</i> , 2017, 30, 1589-1602.	5.5	38
23	qPMS7: A Fast Algorithm for Finding (a, “, d)-Motifs in DNA and Protein Sequences. <i>PLoS ONE</i> , 2012, 7, e41425.	2.5	38
24	Bioinformatics and DNA-extraction strategies to reliably detect genetic variants from FFPE breast tissue samples. <i>BMC Genomics</i> , 2019, 20, 689.	2.8	37
25	Murine Leukemia Virus Uses NXF1 for Nuclear Export of Spliced and Unspliced Viral Transcripts. <i>Journal of Virology</i> , 2014, 88, 4069-4082.	3.4	36
26	Development and Verification of an RNA Sequencing (RNA-Seq) Assay for the Detection of Gene Fusions in Tumors. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 495-511.	2.8	36
27	RVboost: RNA-seq variants prioritization using a boosting method. <i>Bioinformatics</i> , 2014, 30, 3414-3416.	4.1	34
28	Impact of RNA degradation on fusion detection by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 814.	2.8	34
29	Gene expression differences between matched pairs of ovarian cancer patient tumors and patient-derived xenografts. <i>Scientific Reports</i> , 2019, 9, 6314.	3.3	33
30	RNA sequencing identifies a novel <i>USP9A</i> – <i>USP6</i> promoter swap gene fusion in a primary aneurysmal bone cyst. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 589-594.	2.8	27
31	Space and Time Efficient Algorithms for Planted Motif Search. <i>Lecture Notes in Computer Science</i> , 2006, , 822-829.	1.3	25
32	Desmoplastic Infantile Ganglioglioma: A MAPK Pathway-Driven and Microglia/Macrophage-Rich Neuroepithelial Tumor. <i>Journal of Neuropathology and Experimental Neurology</i> , 2019, 78, 1011-1021.	1.7	21
33	RNA-Seq Reveals Differences in Expressed Tumor Mutation Burden in Colorectal and Endometrial Cancers with and without Defective DNA-Mismatch Repair. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 555-564.	2.8	16
34	Molecular and Immunohistochemical Analysis of Mucinous Cystic Neoplasm of the Liver. <i>American Journal of Clinical Pathology</i> , 2020, 154, 837-847.	0.7	14
35	Xanthogranulomatous epithelial tumor: report of 6 cases of a novel, potentially deceptive lesion with a predilection for young women. <i>Modern Pathology</i> , 2020, 33, 1889-1895.	5.5	13
36	Polymorphous Low-Grade Neuroepithelial Tumor of the Young (PLNTY): Molecular Profiling Confirms Frequent MAPK Pathway Activation. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021, 80, 821-829.	1.7	13

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37	Leiomyoma with KAT6B-KANSL1 fusion: case report of a rapidly enlarging uterine mass in a postmenopausal woman. <i>Diagnostic Pathology</i> , 2019, 14, 32.	2.0	11
38	Identification and Development of a Lung Adenocarcinoma PDX Model With STRN-ALK Fusion. <i>Clinical Lung Cancer</i> , 2019, 20, e142-e147.	2.6	11
39	Frequent POLE-driven hypermutation in ovarian endometrioid cancer revealed by mutational signatures in RNA sequencing. <i>BMC Medical Genomics</i> , 2021, 14, 165.	1.5	10
40	Transcriptomic and Proteomic Analysis of Steatohepatic Hepatocellular Carcinoma Reveals Novel Distinct Biologic Features. <i>American Journal of Clinical Pathology</i> , 2021, 155, 87-96.	0.7	9
41	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. <i>Rare Tumors</i> , 2017, 9, 50-53.	0.6	8
42	Malignant Peritoneal Mesothelioma Arising in Young Adults With Long-standing Indwelling Intra-abdominal Shunt Catheters. <i>American Journal of Surgical Pathology</i> , 2021, 45, 255-262.	3.7	6
43	Molecular Genetic Landscape of Sclerosing Pneumocytomas. <i>American Journal of Clinical Pathology</i> , 2021, 155, 397-404.	0.7	5
44	Determining mutational burden and signature using RNA-seq from tumor-only samples. <i>BMC Medical Genomics</i> , 2021, 14, 65.	1.5	5
45	Semi-Supervised Topological Analysis for Elucidating Hidden Structures in High-Dimensional Transcriptome Datasets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1620-1631.	3.0	4
46	Gene Expression Profiling Identifies Distinct Signatures for Dysplastic and Proliferative Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2016, 128, 110-110.	1.4	4
47	Novel Phenotypic and Genetic Analysis of T-Cell Prolymphocytic Leukemia (T-PLL). <i>Blood</i> , 2014, 124, 1682-1682.	1.4	3
48	Stage-Specific Non-Coding RNA Expression Patterns during In Vitro Human B Cell Differentiation into Antibody Secreting Plasma Cells. <i>Non-coding RNA</i> , 2022, 8, 15.	2.6	3
49	RANDOMIZED SORTING ON THE POPS NETWORK. <i>International Journal of Foundations of Computer Science</i> , 2005, 16, 105-116.	1.1	2
50	Multiple isodicentric Y chromosomes in myeloid malignancies: a unique cytogenetic entity and potential therapeutic target. <i>Leukemia and Lymphoma</i> , 2019, 60, 821-824.	1.3	2
51	Network-directed cis-mediator analysis of normal prostate tissue expression profiles reveals downstream regulatory associations of prostate cancer susceptibility loci. <i>Oncotarget</i> , 2017, 8, 85896-85908.	1.8	2
52	Packet routing and selection on the POPS network. <i>Journal of Parallel and Distributed Computing</i> , 2005, 65, 927-933.	4.1	1
53	Extending Pattern Branching to Handle Challenging Instances. , 2006, , .		1
54	Sorting- and FFT-Based Techniques in the Discovery of Biopatterns. , 2007, , 93-115.		1

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55	Fast Algorithms for Selecting Specific siRNA in Complete mRNA Data. Lecture Notes in Computer Science, 2007, , 302-309.	1.3	1
56	CLL Mesenchymal Stromal Cells Have Decreased Replicative Potential and Senescent Phenotype: Clinical and Biologic Implications. Blood, 2014, 124, 3282-3282.	1.4	1
57	Developing a FHIR-based Framework for Phenome Wide Association Studies: A Case Study with A Pan-Cancer Cohort. AMIA Summits on Translational Science Proceedings, 2020, 2020, 750-759.	0.4	1
58	Data-driven Sublanguage Analysis for Cancer Genomics Knowledge Modeling: Applications in Mining Oncological Genetics Information from Patients' Genetic Reports. AMIA Summits on Translational Science Proceedings, 2020, 2020, 720-729.	0.4	1
59	Challenges of using RNA-seq in the clinical setting. , 2017, , .		0
60	Randomized Packet Routing, Selection, and Sorting on the POPS Network. Chapman & Hall/CRC Computer and Information Science Series, 2007, , 13-1-13-14.	0.4	0
61	A tool to predict post-transcriptional instability related to the dysregulation of the SETD2 histone methyltransferase in renal cell carcinoma (RCC).. Journal of Clinical Oncology, 2014, 32, 11072-11072.	1.6	0
62	Abstract 1894: Extensive genomic profiling of a rare extranodal-follicular dendritic cell sarcoma: Implications for future individualized therapy. , 2014, , .		0
63	Abstract 3462: Comparative RNA-Seq analysis of MIS signaling: Potential relevance as therapeutic strategy in ovarian cancer treatment. , 2014, , .		0
64	Abstract 5585: Integrated DNA/RNA sequencing for discovery and orthogonal validation of expressed fusion genes in peripheral T-cell lymphomas. , 2014, , .		0
65	RNA-Seq Based Immunoglobulin Repertoire Analysis of Normal Plasma Cells Generated in an in Vitro B Cell Differentiation System. Blood, 2019, 134, 1051-1051.	1.4	0