

Elana J Fertig

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

5,823
citations

109137

35
h-index

102304

66
g-index

160
all docs

160
docs citations

160
times ranked

10554
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional normalization of 450k methylation array data improves replication in large cancer studies. <i>Genome Biology</i> , 2014, 15, 503.	3.8	665
2	Single-Cell RNA-Seq Analysis of Retinal Development Identifies NFI Factors as Regulating Mitotic Exit and Late-Born Cell Specification. <i>Neuron</i> , 2019, 102, 1111-1126.e5.	3.8	343
3	p16 Protein Expression and Human Papillomavirus Status As Prognostic Biomarkers of Nonoropharyngeal Head and Neck Squamous Cell Carcinoma. <i>Journal of Clinical Oncology</i> , 2014, 32, 3930-3938.	0.8	313
4	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016, 13, 310-318.	9.0	209
5	Activation of the <i>NOTCH</i> Pathway in Head and Neck Cancer. <i>Cancer Research</i> , 2014, 74, 1091-1104.	0.4	181
6	Enter the Matrix: Factorization Uncovers Knowledge from Omics. <i>Trends in Genetics</i> , 2018, 34, 790-805.	2.9	181
7	Programmed Cell Death Ligand-1 (PD-L1) and CD8 Expression Profiling Identify an Immunologic Subtype of Pancreatic Ductal Adenocarcinomas with Favorable Survival. <i>Cancer Immunology Research</i> , 2019, 7, 886-895.	1.6	171
8	Single-Cell Analysis of Human Retina Identifies Evolutionarily Conserved and Species-Specific Mechanisms Controlling Development. <i>Developmental Cell</i> , 2020, 53, 473-491.e9.	3.1	170
9	Breast cancer cells condition lymphatic endothelial cells within pre-metastatic niches to promote metastasis. <i>Nature Communications</i> , 2014, 5, 4715.	5.8	154
10	Neoadjuvant cabozantinib and nivolumab convert locally advanced hepatocellular carcinoma into resectable disease with enhanced antitumor immunity. <i>Nature Cancer</i> , 2021, 2, 891-903.	5.7	147
11	Key tumor suppressor genes inactivated by <i>greater promoter</i> methylation and somatic mutations in head and neck cancer. <i>Epigenetics</i> , 2014, 9, 1031-1046.	1.3	122
12	Decomposing Cell Identity for Transfer Learning across Cellular Measurements, Platforms, Tissues, and Species. <i>Cell Systems</i> , 2019, 8, 395-411.e8.	2.9	121
13	Epigenetic regulation of gene expression in cancer: techniques, resources and analysis. <i>Briefings in Functional Genomics</i> , 2018, 17, 49-63.	1.3	111
14	A tumor-derived type III collagen-rich ECM niche regulates tumor cell dormancy. <i>Nature Cancer</i> , 2022, 3, 90-107.	5.7	110
15	Preserving biological heterogeneity with a permuted surrogate variable analysis for genomics batch correction. <i>Bioinformatics</i> , 2014, 30, 2757-2763.	1.8	102
16	A comparative study of 4D-VAR and a 4D Ensemble Kalman Filter: perfect model simulations with Lorenz-96. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2007, 59, 96-100.	0.8	90
17	CoGAPS: an R/C++ package to identify patterns and biological process activity in transcriptomic data. <i>Bioinformatics</i> , 2010, 26, 2792-2793.	1.8	84
18	Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. <i>Cancer Prevention Research</i> , 2016, 9, 265-274.	0.7	80

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19	The Twist Box Domain Is Required for Twist1-induced Prostate Cancer Metastasis. <i>Molecular Cancer Research</i> , 2013, 11, 1387-1400.	1.5	79
20	Evaluation of Cyclophosphamide/GVAX Pancreas Followed by Listeria-Mesothelin (CRS-207) with or without Nivolumab in Patients with Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 3578-3588.	3.2	76
21	Molecular Portrait of Hypoxia in Breast Cancer: A Prognostic Signature and Novel HIF-Regulated Genes. <i>Molecular Cancer Research</i> , 2018, 16, 1889-1901.	1.5	68
22	A Phase II Study of Allogeneic GM-CSF-Transfected Pancreatic Tumor Vaccine (GVAX) with Ipilimumab as Maintenance Treatment for Metastatic Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 5129-5139.	3.2	67
23	From bench to bedside: Single-cell analysis for cancer immunotherapy. <i>Cancer Cell</i> , 2021, 39, 1062-1080.	7.7	67
24	Inhibition of TGF- β 2 Enhances the <i>In Vivo</i> Antitumor Efficacy of EGF Receptor-Targeted Therapy. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 2429-2439.	1.9	66
25	SMAD4 Loss Is Associated with Cetuximab Resistance and Induction of MAPK/JNK Activation in Head and Neck Cancer Cells. <i>Clinical Cancer Research</i> , 2017, 23, 5162-5175.	3.2	64
26	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. <i>Nature Communications</i> , 2019, 10, 2188.	5.8	61
27	NF- κ B and stat3 transcription factor signatures differentiate HPV-positive and HPV-negative head and neck squamous cell carcinoma. <i>International Journal of Cancer</i> , 2015, 137, 1879-1889.	2.3	51
28	Integrated Analysis of Whole-Genome CHIP-Seq and RNA-Seq Data of Primary Head and Neck Tumor Samples Associates HPV Integration Sites with Open Chromatin Marks. <i>Cancer Research</i> , 2017, 77, 6538-6550.	0.4	50
29	Assimilating non-local observations with a local ensemble Kalman filter. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2007, 59, 719-730.	0.8	49
30	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. <i>Oncogene</i> , 2020, 39, 6327-6339.	2.6	48
31	Asporin Restricts Mesenchymal Stromal Cell Differentiation, Alters the Tumor Microenvironment, and Drives Metastatic Progression. <i>Cancer Research</i> , 2019, 79, 3636-3650.	0.4	47
32	Observation bias correction with an ensemble Kalman filter. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2022, 61, 210.	0.8	46
33	projectR: an R/Bioconductor package for transfer learning via PCA, NMF, correlation and clustering. <i>Bioinformatics</i> , 2020, 36, 3592-3593.	1.8	45
34	Characterization of functionally active gene fusions in human papillomavirus related oropharyngeal squamous cell carcinoma. <i>International Journal of Cancer</i> , 2016, 139, 373-382.	2.3	44
35	Digital Pathology Analysis Quantifies Spatial Heterogeneity of CD3, CD4, CD8, CD20, and FoxP3 Immune Markers in Triple-Negative Breast Cancer. <i>Frontiers in Physiology</i> , 2020, 11, 583333.	1.3	42
36	A Novel Functional Splice Variant of AKT3 Defined by Analysis of Alternative Splice Expression in HPV-Positive Oropharyngeal Cancers. <i>Cancer Research</i> , 2017, 77, 5248-5258.	0.4	41

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37	switchBox: an R package for "Top Scoring Pairs classifier development. <i>Bioinformatics</i> , 2015, 31, 273-274.	1.8	40
38	Computational reconstruction of the signalling networks surrounding implanted biomaterials from single-cell transcriptomics. <i>Nature Biomedical Engineering</i> , 2021, 5, 1228-1238.	11.6	40
39	Preferential Activation of the Hedgehog Pathway by Epigenetic Modulations in HPV Negative HNSCC Identified with Meta-Pathway Analysis. <i>PLoS ONE</i> , 2013, 8, e78127.	1.1	39
40	PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF. <i>Bioinformatics</i> , 2017, 33, 1892-1894.	1.8	39
41	A Mechanism of Resistance to Antibody-Targeted Immune Attack. <i>Cancer Immunology Research</i> , 2019, 7, 230-243.	1.6	39
42	Viral status, immune microenvironment and immunological response to checkpoint inhibitors in hepatocellular carcinoma. , 2020, 8, e000394.		39
43	Integrated single-cell and bulk gene expression and ATAC-seq reveals heterogeneity and early changes in pathways associated with resistance to cetuximab in HNSCC-sensitive cell lines. <i>British Journal of Cancer</i> , 2020, 123, 101-113.	2.9	38
44	Learning Dysregulated Pathways in Cancers from Differential Variability Analysis. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14066.	0.9	37
45	A 3' UTR KRAS-variant is associated with cisplatin resistance in patients with recurrent and/or metastatic head and neck squamous cell carcinoma. <i>Annals of Oncology</i> , 2014, 25, 2230-2236.	0.6	36
46	Analysis of gene expression of secreted factors associated with breast cancer metastases in breast cancer subtypes. <i>Scientific Reports</i> , 2015, 5, 12133.	1.6	36
47	Decreased SMAD4 expression is associated with induction of epithelial-to-mesenchymal transition and cetuximab resistance in head and neck squamous cell carcinoma. <i>Cancer Biology and Therapy</i> , 2015, 16, 1252-1258.	1.5	36
48	Expression Microarray Analysis Reveals Alternative Splicing of LAMA3 and DST Genes in Head and Neck Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2014, 9, e91263.	1.1	35
49	Multi-omic profiling of lung and liver tumor microenvironments of metastatic pancreatic cancer reveals site-specific immune regulatory pathways. <i>Genome Biology</i> , 2021, 22, 154.	3.8	30
50	Eastern oyster (<i>Crassostrea virginica</i>) $\delta^{15}N$ as a bioindicator of nitrogen sources: Observations and modeling. <i>Marine Pollution Bulletin</i> , 2010, 60, 1288-1298.	2.3	29
51	Gene expression signatures modulated by epidermal growth factor receptor activation and their relationship to cetuximab resistance in head and neck squamous cell carcinoma. <i>BMC Genomics</i> , 2012, 13, 160.	1.2	29
52	Evaluating the impact of age on immune checkpoint therapy biomarkers. <i>Cell Reports</i> , 2021, 36, 109599.	2.9	27
53	Loss of Trop2 causes ErbB3 activation through a neuregulin-1-dependent mechanism in the mesenchymal subtype of HNSCC. <i>Oncotarget</i> , 2014, 5, 9281-9294.	0.8	27
54	Evaluation of a Strategy for the Assimilation of Satellite Radiance Observations with the Local Ensemble Transform Kalman Filter. <i>Monthly Weather Review</i> , 2011, 139, 1932-1951.	0.5	26

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55	Systems Approaches to Cancer Biology. <i>Cancer Research</i> , 2016, 76, 6774-6777.	0.4	26
56	Entinostat Decreases Immune Suppression to Promote Antitumor Responses in a HER2+ Breast Tumor Microenvironment. <i>Cancer Immunology Research</i> , 2022, 10, 656-669.	1.6	26
57	Integrated time course omics analysis distinguishes immediate therapeutic response from acquired resistance. <i>Genome Medicine</i> , 2018, 10, 37.	3.6	25
58	Matrix factorization for transcriptional regulatory network inference. , 2012, 2012, 387-396.		24
59	Systemic inhibition of PTPN22 augments anticancer immunity. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	24
60	Digitizing omics profiles by divergence from a baseline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4545-4552.	3.3	23
61	Differential Variation Analysis Enables Detection of Tumor Heterogeneity Using Single-Cell RNA-Sequencing Data. <i>Cancer Research</i> , 2019, 79, 5102-5112.	0.4	23
62	DPP inhibition alters the CXCR3 axis and enhances NK and CD8+ T cell infiltration to improve anti-PD1 efficacy in murine models of pancreatic ductal adenocarcinoma. , 2021, 9, e002837.		23
63	StereoGene: rapid estimation of genome-wide correlation of continuous or interval feature data. <i>Bioinformatics</i> , 2017, 33, 3158-3165.	1.8	22
64	CoGAPS 3: Bayesian non-negative matrix factorization for single-cell analysis with asynchronous updates and sparse data structures. <i>BMC Bioinformatics</i> , 2020, 21, 453.	1.2	22
65	Structure-Function Studies of the bHLH Phosphorylation Domain of TWIST1 in Prostate Cancer Cells. <i>Neoplasia</i> , 2015, 17, 16-31.	2.3	21
66	DNA methylation regulates TMEM16A/ANO1 expression through multiple CpG islands in head and neck squamous cell carcinoma. <i>Scientific Reports</i> , 2017, 7, 15173.	1.6	20
67	Variation of Human Neural Stem Cells Generating Organizer States InÂVitro before Committing to Cortical Excitatory or Inhibitory Neuronal Fates. <i>Cell Reports</i> , 2020, 31, 107599.	2.9	20
68	Extracellular Vesicles Released by Tumor Endothelial Cells Spread Immunosuppressive and Transforming Signals Through Various Recipient Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 698.	1.8	18
69	Integrating single cell sequencing with a spatial quantitative systems pharmacology model spQSP for personalized prediction of triple-negative breast cancer immunotherapy response. <i>Immunoinformatics</i> , 2021, 1-2, 100002.	1.2	18
70	Mechanistically detailed systems biology modeling of the HGF/Met pathway in hepatocellular carcinoma. <i>Npj Systems Biology and Applications</i> , 2019, 5, 29.	1.4	17
71	Cytokines secreted by stromal cells in TNBC microenvironment as potential targets for cancer therapy. <i>Cancer Biology and Therapy</i> , 2020, 21, 560-569.	1.5	17
72	Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. <i>Epigenetics</i> , 2020, 15, 959-971.	1.3	17

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73	Transfer learning between preclinical models and human tumors identifies a conserved NK cell activation signature in anti-CTLA-4 responsive tumors. <i>Genome Medicine</i> , 2021, 13, 129.	3.6	17
74	Multipanel mass cytometry reveals anti-“PD-1 therapy” mediated B and T cell compartment remodeling in tumor-draining lymph nodes. <i>JCI Insight</i> , 2020, 5, .	2.3	17
75	CoGAPS matrix factorization algorithm identifies transcriptional changes in AP-2alpha target genes in feedback from therapeutic inhibition of the EGFR network. <i>Oncotarget</i> , 2016, 7, 73845-73864.	0.8	16
76	Integrated immunological analysis of a successful conversion of locally advanced hepatocellular carcinoma to resectability with neoadjuvant therapy. , 2020, 8, e000932.		16
77	Integrative computational analysis of transcriptional and epigenetic alterations implicates <i>DTX1</i> as a putative tumor suppressor gene in HNSCC. <i>Oncotarget</i> , 2017, 8, 15349-15363.	0.8	16
78	Epigenetic screening of salivary gland mucoepidermoid carcinoma identifies hypomethylation of CLIC3 as a common alteration. <i>Oral Oncology</i> , 2015, 51, 1120-1125.	0.8	15
79	Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. <i>Translational Research</i> , 2018, 202, 109-119.	2.2	15
80	Inhibition of miR-21 Regulates Mutant KRAS Effector Pathways and Intercepts Pancreatic Ductal Adenocarcinoma Development. <i>Cancer Prevention Research</i> , 2020, 13, 569-582.	0.7	14
81	Ten quick tips for deep learning in biology. <i>PLoS Computational Biology</i> , 2022, 18, e1009803.	1.5	14
82	Aberrant expression of CPSF1 promotes head and neck squamous cell carcinoma via regulating alternative splicing. <i>PLoS ONE</i> , 2020, 15, e0233380.	1.1	13
83	An unbiased in vivo functional genomics screening approach in mice identifies novel tumor cell-based regulators of immune rejection. <i>Cancer Immunology, Immunotherapy</i> , 2017, 66, 1529-1544.	2.0	12
84	Identifying Context-Specific Transcription Factor Targets From Prior Knowledge and Gene Expression Data. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 142-149.	2.2	11
85	Comparative mutational landscape analysis of patient-derived tumour xenografts. <i>British Journal of Cancer</i> , 2017, 116, 515-523.	2.9	11
86	Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer. <i>Bioinformatics</i> , 2018, 34, 1859-1867.	1.8	11
87	Application of Genomic and Proteomic Technologies in Biomarker Discovery. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2012, , 377-382.	1.8	11
88	The use of machine learning to discover regulatory networks controlling biological systems. <i>Molecular Cell</i> , 2022, 82, 260-273.	4.5	11
89	Forecasting cellular states: from descriptive to predictive biology via single-cell multiomics. <i>Current Opinion in Systems Biology</i> , 2021, 26, 24-32.	1.3	10
90	Newly Identified Members of FGFR1 Splice Variants Engage in Cross-talk with AXL/AKT Axis in Salivary Adenoid Cystic Carcinoma. <i>Cancer Research</i> , 2021, 81, 1001-1013.	0.4	10

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91	Differentially Methylated Super-Enhancers Regulate Target Gene Expression in Human Cancer. <i>Scientific Reports</i> , 2019, 9, 15034.	1.6	9
92	Antitumor T-cell Immunity Contributes to Pancreatic Cancer Immune Resistance. <i>Cancer Immunology Research</i> , 2021, 9, 386-400.	1.6	9
93	Pattern Identification in Time-Course Gene Expression Data with the CoGAPS Matrix Factorization. <i>Methods in Molecular Biology</i> , 2014, 1101, 87-112.	0.4	9
94	Hybrid Modeling of Cell Signaling and Transcriptional Reprogramming and Its Application in <i>C. elegans</i> Development. <i>Frontiers in Genetics</i> , 2011, 2, 77.	1.1	8
95	Matrix factorization and transfer learning uncover regulatory biology across multiple single-cell ATAC-seq data sets. <i>Nucleic Acids Research</i> , 2020, 48, e68-e68.	6.5	8
96	Forecasting cancer: from precision to predictive medicine. <i>Med</i> , 2021, 2, 1004-1010.	2.2	8
97	Toward Signaling-Driven Biomarkers Immune to Normal Tissue Contamination. <i>Cancer Informatics</i> , 2016, 15, CIN.S32468.	0.9	7
98	A preliminary analysis of interleukin-1 ligands as potential predictive biomarkers of response to cetuximab. <i>Biomarker Research</i> , 2019, 7, 14.	2.8	6
99	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	2.6	6
100	Identification of methylated genes in salivary gland adenoid cystic carcinoma xenografts using global demethylation and methylation microarray screening. <i>International Journal of Oncology</i> , 2016, 49, 225-234.	1.4	5
101	A Software Application for Mining and Presenting Relevant Cancer Clinical Trials per Cancer Mutation. <i>Cancer Informatics</i> , 2017, 16, 117693511771194.	0.9	4
102	The Genome-Wide Molecular Landscape of HPV-Driven and HPV-Negative Head and Neck Squamous Cell Carcinoma. <i>Current Cancer Research</i> , 2018, , 293-325.	0.2	4
103	Role of the NOTCH Signaling Pathway in Head and Neck Cancer. <i>Current Cancer Research</i> , 2018, , 229-248.	0.2	4
104	Quantifying the Dynamics of Coupled Networks of Switches and Oscillators. <i>PLoS ONE</i> , 2012, 7, e29497.	1.1	3
105	CancerInSilico: An R/Bioconductor package for combining mathematical and statistical modeling to simulate time course bulk and single cell gene expression data in cancer. <i>PLoS Computational Biology</i> , 2019, 14, e1006935.	1.5	3
106	Identifying context-specific transcription factor targets from prior knowledge and gene expression data. , 2012, , .		2
107	A Mentee's Baby Registry: Supporting New Academic Parents in 2020. <i>Cell Systems</i> , 2020, 11, 331-335.	2.9	2
108	Spatial correlation statistics enable transcriptome-wide characterization of RNA structure binding. <i>Cell Reports Methods</i> , 2021, 1, 100088.	1.4	2

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109	Cancer Systems Biology. , 2011, , 533-565.		1
110	The estimation of dimensionality in gene expression data using Nonnegative Matrix Factorization. , 2015, , .		1
111	A comparative study of 4D-VAR and a 4D Ensemble Kalman Filter: perfect model simulations with Lorenz-96. Tellus, Series A: Dynamic Meteorology and Oceanography, 2007, , .	0.8	1
112	Abstract 3100: MicroRNA profiling reveals miR-205 upregulation is associated with head and neck squamous cell carcinoma and modulates E2F1 signaling.. , 2013, , .		1
113	Abstract 777: The CoGAPS matrix factorization algorithm infers feedback mechanisms from therapeutic inhibition of EGFR that increases expression of growth factor receptors. , 2016, , .		1
114	Dynamics in hybrid complex systems of switches and oscillators. Chaos, 2013, 23, 033142.	1.0	0
115	Abstract 2372: Mechanisms of microRNA-21 dysregulation in pancreatic ductal adenocarcinoma (PDAC). , 2021, , .		0
116	Assimilating non-local observations with a local ensemble Kalman filter. Tellus, Series A: Dynamic Meteorology and Oceanography, 2007, , .	0.8	0
117	Observation bias correction with an ensemble Kalman filter. Tellus, Series A: Dynamic Meteorology and Oceanography, 2009, , .	0.8	0
118	Quantifying the Dynamics of Coupled Networks of Switches and Oscillators. Lecture Notes in Computer Science, 2012, , 60-61.	1.0	0
119	Abstract 2901: An integrated matrix factorization algorithm for DNA methylation and gene expression identifies HNSCC clinical subtypes and G11 signaling specific to HPV-negative HNSCC.. , 2013, , .		0
120	Abstract LB-317: Interactive pipeline for reproducible genomics analyses. , 2014, , .		0
121	Abstract 2474: Smad4 loss induces cetuximab resistance and increased metastatic potential in head and neck squamous cell carcinoma. , 2014, , .		0
122	Synthesizer: Expediting synthesis studies from context-free data with information retrieval techniques. PLoS ONE, 2017, 12, e0175860.	1.1	0
123	Abstract 633: Induction of ADCC resistance profoundly alters tumor cell phenotype and stress response. , 2017, , .		0
124	Abstract PO-111: A human single-cell RNA sequencing atlas of pancreatic ductal adenocarcinoma enables harmonized cell type calling and comprehensive analyses of potential intercellular signaling. , 2021, , .		0