

# 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	Observation bias correction with an ensemble Kalman filter. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2022, 61, 210.	0.8	46
2	The use of machine learning to discover regulatory networks controlling biological systems. <i>Molecular Cell</i> , 2022, 82, 260-273.	4.5	11
3	A tumor-derived type III collagen-rich ECM niche regulates tumor cell dormancy. <i>Nature Cancer</i> , 2022, 3, 90-107.	5.7	110
4	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
5	Ten quick tips for deep learning in biology. <i>PLoS Computational Biology</i> , 2022, 18, e1009803.	1.5	14
6	Antitumor T-cell Immunity Contributes to Pancreatic Cancer Immune Resistance. <i>Cancer Immunology Research</i> , 2021, 9, 386-400.	1.6	9
7	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
8	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
9	Abstract 2372: Mechanisms of microRNA-21 dysregulation in pancreatic ductal adenocarcinoma (PDAC). , 2021, , .		0
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	From bench to bedside: Single-cell analysis for cancer immunotherapy. <i>Cancer Cell</i> , 2021, 39, 1062-1080.	7.7	67
12	Evaluating the impact of age on immune checkpoint therapy biomarkers. <i>Cell Reports</i> , 2021, 36, 109599.	2.9	27
13	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
14	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
15	Forecasting cancer: from precision to predictive medicine. <i>Med</i> , 2021, 2, 1004-1010.	2.2	8
16	Systemic inhibition of PTPN22 augments anticancer immunity. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	24
17	Spatial correlation statistics enable transcriptome-wide characterization of RNA structure binding. <i>Cell Reports Methods</i> , 2021, 1, 100088.	1.4	2
18	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

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19	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
20	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	2.6	6
21	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
22	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
23	Integrated immunological analysis of a successful conversion of locally advanced hepatocellular carcinoma to resectability with neoadjuvant therapy. , 2020, 8, e000932.		16
24	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
25	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
26	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. <i>Oncogene</i> , 2020, 39, 6327-6339.	2.6	48
27	A Mentee™s Baby Registry: Supporting New Academic Parents in 2020. <i>Cell Systems</i> , 2020, 11, 331-335.	2.9	2
28	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
29	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
30	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
31	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
32	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
33	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
34	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
35	projectR: an R/Bioconductor package for transfer learning via PCA, NMF, correlation and clustering. <i>Bioinformatics</i> , 2020, 36, 3592-3593.	1.8	45
36	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

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37	Variation of Human Neural Stem Cells Generating Organizer States In Vitro before Committing to Cortical Excitatory or Inhibitory Neuronal Fates. <i>Cell Reports</i> , 2020, 31, 107599.	2.9	20
38	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
39	Viral status, immune microenvironment and immunological response to checkpoint inhibitors in hepatocellular carcinoma. , 2020, 8, e000394.		39
40	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
41	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
42	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
43	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
44	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
45	Differentially Methylated Super-Enhancers Regulate Target Gene Expression in Human Cancer. <i>Scientific Reports</i> , 2019, 9, 15034.	1.6	9
46	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
47	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
48	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
49	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
50	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
51	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
52	A Mechanism of Resistance to Antibody-Targeted Immune Attack. <i>Cancer Immunology Research</i> , 2019, 7, 230-243.	1.6	39
53	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
54	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

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55	Epigenetic regulation of gene expression in cancer: techniques, resources and analysis. Briefings in Functional Genomics, 2018, 17, 49-63.	1.3	111
56	Integrated time course omics analysis distinguishes immediate therapeutic response from acquired resistance. Genome Medicine, 2018, 10, 37.	3.6	25
57	Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. Translational Research, 2018, 202, 109-119.	2.2	15
58	Molecular Portrait of Hypoxia in Breast Cancer: A Prognostic Signature and Novel HIF-Regulated Genes. Molecular Cancer Research, 2018, 16, 1889-1901.	1.5	68
59	Enter the Matrix: Factorization Uncovers Knowledge from Omics. Trends in Genetics, 2018, 34, 790-805.	2.9	181
60	The Genome-Wide Molecular Landscape of HPV-Driven and HPV-Negative Head and Neck Squamous Cell Carcinoma. Current Cancer Research, 2018, , 293-325.	0.2	4
61	Role of the NOTCH Signaling Pathway in Head and Neck Cancer. Current Cancer Research, 2018, , 229-248.	0.2	4
62	Comparative mutational landscape analysis of patient-derived tumour xenografts. British Journal of Cancer, 2017, 116, 515-523.	2.9	11
63	PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF. Bioinformatics, 2017, 33, 1892-1894.	1.8	39
64	SMAD4 Loss Is Associated with Cetuximab Resistance and Induction of MAPK/JNK Activation in Head and Neck Cancer Cells. Clinical Cancer Research, 2017, 23, 5162-5175.	3.2	64
65	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. Cancer Research, 2017, 77, 6538-6550.	0.4	50
66	A Novel Functional Splice Variant of <i>AKT3</i> Defined by Analysis of Alternative Splice Expression in HPV-Positive Oropharyngeal Cancers. Cancer Research, 2017, 77, 5248-5258.	0.4	41
67	An unbiased in vivo functional genomics screening approach in mice identifies novel tumor cell-based regulators of immune rejection. Cancer Immunology, Immunotherapy, 2017, 66, 1529-1544.	2.0	12
68	DNA methylation regulates TMEM16A/ANO1 expression through multiple CpG islands in head and neck squamous cell carcinoma. Scientific Reports, 2017, 7, 15173.	1.6	20
69	StereoGene: rapid estimation of genome-wide correlation of continuous or interval feature data. Bioinformatics, 2017, 33, 3158-3165.	1.8	22
70	A Software Application for Mining and Presenting Relevant Cancer Clinical Trials per Cancer Mutation. Cancer Informatics, 2017, 16, 117693511771194.	0.9	4
71	Integrative computational analysis of transcriptional and epigenetic alterations implicates <i>DTX1</i> as a putative tumor suppressor gene in HNSCC. Oncotarget, 2017, 8, 15349-15363.	0.8	16
72	Synthesizer: Expediting synthesis studies from context-free data with information retrieval techniques. PLoS ONE, 2017, 12, e0175860.	1.1	0

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73	Abstract 633: Induction of ADCC resistance profoundly alters tumor cell phenotype and stress response. , 2017, , .		0
74	CoGAPS matrix factorization algorithm identifies transcriptional changes in AP-2alpha target genes in feedback from therapeutic inhibition of the EGFR network. Oncotarget, 2016, 7, 73845-73864.	0.8	16
75	Identification of methylated genes in salivary gland adenoid cystic carcinoma xenografts using global demethylation and methylation microarray screening. International Journal of Oncology, 2016, 49, 225-234.	1.4	5
76	Characterization of functionally active gene fusions in human papillomavirus related oropharyngeal squamous cell carcinoma. International Journal of Cancer, 2016, 139, 373-382.	2.3	44
77	Systems Approaches to Cancer Biology. Cancer Research, 2016, 76, 6774-6777.	0.4	26
78	Toward Signaling-Driven Biomarkers Immune to Normal Tissue Contamination. Cancer Informatics, 2016, 15, CIN.S32468.	0.9	7
79	Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. Cancer Prevention Research, 2016, 9, 265-274.	0.7	80
80	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	9.0	209
81	Abstract 777: The CoGAPS matrix factorization algorithm infers feedback mechanisms from therapeutic inhibition of EGFR that increases expression of growth factor receptors. , 2016, , .		1
82	Epigenetic screening of salivary gland mucoepidermoid carcinoma identifies hypomethylation of CLIC3 as a common alteration. Oral Oncology, 2015, 51, 1120-1125.	0.8	15
83	The estimation of dimensionality in gene expression data using Nonnegative Matrix Factorization. , 2015, , .		1
84	Structure-Function Studies of the bHLH Phosphorylation Domain of TWIST1 in Prostate Cancer Cells. Neoplasia, 2015, 17, 16-31.	2.3	21
85	Analysis of gene expression of secreted factors associated with breast cancer metastases in breast cancer subtypes. Scientific Reports, 2015, 5, 12133.	1.6	36
86	Decreased SMAD4 expression is associated with induction of epithelial-to-mesenchymal transition and cetuximab resistance in head and neck squamous cell carcinoma. Cancer Biology and Therapy, 2015, 16, 1252-1258.	1.5	36
87	NF-κB and stat3 transcription factor signatures differentiate HPV-positive and HPV-negative head and neck squamous cell carcinoma. International Journal of Cancer, 2015, 137, 1879-1889.	2.3	51
88	switchBox: an R package for “Top Scoring Pairs classifier development. Bioinformatics, 2015, 31, 273-274.	1.8	40
89	Expression Microarray Analysis Reveals Alternative Splicing of LAMA3 and DST Genes in Head and Neck Squamous Cell Carcinoma. PLoS ONE, 2014, 9, e91263.	1.1	35
90	Functional normalization of 450k methylation array data improves replication in large cancer studies. Genome Biology, 2014, 15, 503.	3.8	665

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91	Learning Dysregulated Pathways in Cancers from Differential Variability Analysis. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14066.	0.9	37
92	Key tumor suppressor genes inactivated by CpG greater promoter methylation and somatic mutations in head and neck cancer. <i>Epigenetics</i> , 2014, 9, 1031-1046.	1.3	122
93	Activation of the NOTCH Pathway in Head and Neck Cancer. <i>Cancer Research</i> , 2014, 74, 1091-1104.	0.4	181
94	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
95	Preserving biological heterogeneity with a permuted surrogate variable analysis for genomics batch correction. <i>Bioinformatics</i> , 2014, 30, 2757-2763.	1.8	102
96	Breast cancer cells condition lymphatic endothelial cells within pre-metastatic niches to promote metastasis. <i>Nature Communications</i> , 2014, 5, 4715.	5.8	154
97	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
98	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
99	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
100	Abstract LB-317: Interactive pipeline for reproducible genomics analyses. , 2014, , .		0
101	Abstract 2474: Smad4 loss induces cetuximab resistance and increased metastatic potential in head and neck squamous cell carcinoma. , 2014, , .		0
102	Dynamics in hybrid complex systems of switches and oscillators. <i>Chaos</i> , 2013, 23, 033142.	1.0	0
103	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
104	The Twist Box Domain Is Required for Twist1-induced Prostate Cancer Metastasis. <i>Molecular Cancer Research</i> , 2013, 11, 1387-1400.	1.5	79
105	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
106	Abstract 3100: MicroRNA profiling reveals miR-205 upregulation is associated with head and neck squamous cell carcinoma and modulates E2F1 signaling.. , 2013, , .		1
107	Abstract 2901: An integrated matrix factorization algorithm for DNA methylation and gene expression identifies HNSCC clinical subtypes and GLI1 signaling specific to HPV-negative HNSCC.. , 2013, , .		0
108	Matrix factorization for transcriptional regulatory network inference. , 2012, 2012, 387-396.		24

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109	Inhibition of TGF- $\beta$ 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
110	Identifying context-specific transcription factor targets from prior knowledge and gene expression data. , 2012, , .		2
111	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
112	Quantifying the Dynamics of Coupled Networks of Switches and Oscillators. <i>PLoS ONE</i> , 2012, 7, e29497.	1.1	3
113	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
114	Quantifying the Dynamics of Coupled Networks of Switches and Oscillators. <i>Lecture Notes in Computer Science</i> , 2012, , 60-61.	1.0	0
115	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
116	<i>Cancer Systems Biology</i> . , 2011, , 533-565.		1
117	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
118	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
119	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
120	Observation bias correction with an ensemble Kalman filter. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2009, , .	0.8	0
121	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
122	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
123	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, , .	0.8	1
124	Assimilating non-local observations with a local ensemble Kalman filter. <i>Tellus, Series A: Dynamic Meteorology and Oceanography</i> , 2007, , .	0.8	0