

Ernest Fraenkel

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

12,039
citations

87723

38
h-index

76769

74
g-index

88
all docs

88
docs citations

88
times ranked

16916
citing authors

#	ARTICLE	IF	CITATIONS
1	Answer ALS, a large-scale resource for sporadic and familial ALS combining clinical and multi-omics data from induced pluripotent cell lines. <i>Nature Neuroscience</i> , 2022, 25, 226-237.	7.1	66
2	Self-supervised learning of cell type specificity from immunohistochemical images. <i>Bioinformatics</i> , 2022, 38, i395-i403.	1.8	5
3	Phenotyping Neurodegeneration in Human iPSCs. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 83-100.	2.8	3
4	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. <i>Nature Genetics</i> , 2021, 53, 1196-1206.	9.4	47
5	Immortalized striatal precursor neurons from Huntington's disease patient-derived iPSC cells as a platform for target identification and screening for experimental therapeutics. <i>Human Molecular Genetics</i> , 2021, 30, 2469-2487.	1.4	7
6	An integrated multi-omic analysis of iPSC-derived motor neurons from C9ORF72 ALS patients. <i>IScience</i> , 2021, 24, 103221.	1.9	27
7	Bioenergetic deficits in Huntington's disease iPSC-derived neural cells and rescue with glycolytic metabolites. <i>Human Molecular Genetics</i> , 2020, 29, 1757-1771.	1.4	34
8	Comparative proteomic analysis highlights metabolic dysfunction in α -synucleinopathy. <i>Npj Parkinson's Disease</i> , 2020, 6, 40.	2.5	16
9	APOE4 is Associated with Differential Regional Vulnerability to Bioenergetic Deficits in Aged APOE Mice. <i>Scientific Reports</i> , 2020, 10, 4277.	1.6	34
10	Aberrant Development Corrected in Adult-Onset Huntington's Disease iPSC-Derived Neuronal Cultures via WNT Signaling Modulation. <i>Stem Cell Reports</i> , 2020, 14, 406-419.	2.3	45
11	A Multi-Omics Interpretable Machine Learning Model Reveals Modes of Action of Small Molecules. <i>Scientific Reports</i> , 2020, 10, 954.	1.6	27
12	Zfp281 (ZBP-99) plays a functionally redundant role with Zfp148 (ZBP-89) during erythroid development. <i>Blood Advances</i> , 2019, 3, 2499-2511.	2.5	7
13	Early epigenomic and transcriptional changes reveal Elk-1 transcription factor as a therapeutic target in Huntington's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24840-24851.	3.3	38
14	Characteristics of myeloproliferative neoplasms in patients exposed to ionizing radiation following the Chernobyl nuclear accident. <i>American Journal of Hematology</i> , 2019, 94, 62-73.	2.0	9
15	Shallow Sparsely-Connected Autoencoders for Gene Set Projection. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 374-385.	0.7	5
16	Discovering Altered Regulation and Signaling Through Network-based Integration of Transcriptomic, Epigenomic, and Proteomic Tumor Data. <i>Methods in Molecular Biology</i> , 2018, 1711, 13-26.	0.4	11
17	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	2.9	327
18	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. <i>Neuron</i> , 2018, 97, 1268-1283.e6.	3.8	517

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19	Functional Genomics Approach Identifies Novel Signaling Regulators of TGF β Ectodomain Shedding. <i>Molecular Cancer Research</i> , 2018, 16, 147-161.	1.5	3
20	Synthesizing Signaling Pathways from Temporal Phosphoproteomic Data. <i>Cell Reports</i> , 2018, 24, 3607-3618.	2.9	30
21	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2018, 34, 396-410.e8.	7.7	146
22	Tissue and cellular rigidity and mechanosensitive signaling activation in Alexander disease. <i>Nature Communications</i> , 2018, 9, 1899.	5.8	43
23	Turning omics data into therapeutic insights. <i>Current Opinion in Pharmacology</i> , 2018, 42, 95-101.	1.7	9
24	Shallow Sparsely-Connected Autoencoders for Gene Set Projection. , 2018, , .		4
25	Genome-Scale Networks Link Neurodegenerative Disease Genes to β -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017, 4, 157-170.e14.	2.9	102
26	Hyper- and hypo- nutrition studies of the hepatic transcriptome and epigenome suggest that PPAR α regulates anaerobic glycolysis. <i>Scientific Reports</i> , 2017, 7, 174.	1.6	12
27	Huntington's Disease iPSC-Derived Brain Microvascular Endothelial Cells Reveal WNT-Mediated Angiogenic and Blood-Brain Barrier Deficits. <i>Cell Reports</i> , 2017, 19, 1365-1377.	2.9	199
28	Identifying therapeutic targets by combining transcriptional data with ordinal clinical measurements. <i>Nature Communications</i> , 2017, 8, 623.	5.8	26
29	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
30	Hepatic Dysfunction Caused by Consumption of a High-Fat Diet. <i>Cell Reports</i> , 2017, 21, 3317-3328.	2.9	68
31	PCSF: An R-package for network-based interpretation of high-throughput data. <i>PLoS Computational Biology</i> , 2017, 13, e1005694.	1.5	35
32	A Fast Prize-Collecting Steiner Forest Algorithm for Functional Analyses in Biological Networks. <i>Lecture Notes in Computer Science</i> , 2017, , 263-276.	1.0	7
33	Network modeling of kinase inhibitor polypharmacology reveals pathways targeted in chemical screens. <i>PLoS ONE</i> , 2017, 12, e0185650.	1.1	3
34	DiSCoVeRiNg Innovative Therapies for Rare Tumors: Combining Genetically Accurate Disease Models with <i>In Silico</i> Analysis to Identify Novel Therapeutic Targets. <i>Clinical Cancer Research</i> , 2016, 22, 3903-3914.	3.2	54
35	Revealing disease-associated pathways by network integration of untargeted metabolomics. <i>Nature Methods</i> , 2016, 13, 770-776.	9.0	145
36	Chromatin Landscape and Epigenetic Signatures in Neurological Disorders. , 2016, , 519-537.		1

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37	Network Modeling Identifies Patient-specific Pathways in Glioblastoma. <i>Scientific Reports</i> , 2016, 6, 28668.	1.6	25
38	Cell freezing protocol suitable for ATAC-Seq on motor neurons derived from human induced pluripotent stem cells. <i>Scientific Reports</i> , 2016, 6, 25474.	1.6	49
39	MB-103DiSCoVERing INNOVATIVE THERAPIES: COMBINING GENETICALLY ACCURATE DISEASE MODELS OF MEDULLOBLASTOMA WITH ADVANCED IN SILICO ANALYSIS TO IDENTIFY NOVEL THERAPEUTIC TARGETS. <i>Neuro-Oncology</i> , 2016, 18, iii120.3-iii120.	0.6	0
40	Pathway-based network modeling finds hidden genes in shRNA screen for regulators of acute lymphoblastic leukemia. <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 761-774.	0.6	5
41	Elucidating MicroRNA Regulatory Networks Using Transcriptional, Post-transcriptional, and Histone Modification Measurements. <i>Cell Reports</i> , 2016, 14, 310-319.	2.9	86
42	Multiplexed barcoded CRISPR-Cas9 screening enabled by CombiGEM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2544-2549.	3.3	210
43	GATA Factor Switching during Erythroid Differentiation Is Facilitated By FBW7 Mediated Clearance of GATA2. <i>Blood</i> , 2016, 128, 1479-1479.	0.6	1
44	Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. <i>PLoS Computational Biology</i> , 2016, 12, e1004879.	1.5	123
45	SAMNetWeb: identifying condition-specific networks linking signaling and transcription. <i>Bioinformatics</i> , 2015, 31, 1124-1126.	1.8	14
46	Sharing information to reconstruct patient-specific pathways in heterogeneous diseases. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014, , 39-50.	0.7	4
47	Integrated network analyses for functional genomic studies in cancer. <i>Seminars in Cancer Biology</i> , 2013, 23, 213-218.	4.3	14
48	Analysis of In Vitro Insulin-Resistance Models and Their Physiological Relevance to In Vivo Diet-Induced Adipose Insulin Resistance. <i>Cell Reports</i> , 2013, 5, 259-270.	2.9	88
49	Linking Proteomic and Transcriptional Data through the Interactome and Epigenome Reveals a Map of Oncogene-induced Signaling. <i>PLoS Computational Biology</i> , 2013, 9, e1002887.	1.5	48
50	Targeting H3K4 trimethylation in Huntington disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3027-36.	3.3	151
51	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. <i>Journal of Computational Biology</i> , 2013, 20, 124-136.	0.8	108
52	Extensive changes in DNA methylation are associated with expression of mutant huntingtin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2354-2359.	3.3	152
53	SHARING INFORMATION TO RECONSTRUCT PATIENT-SPECIFIC PATHWAYS IN HETEROGENEOUS DISEASES. , 2013, , .		6
54	The Small Molecule Genistein Increases Hepcidin Expression by Activating Stat3 and Bone Morphogenic Protein Signaling. <i>FASEB Journal</i> , 2013, 27, 223.6.	0.2	0

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55	SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. <i>Nucleic Acids Research</i> , 2012, 40, W505-W509.	6.5	58
56	Swimming Upstream: Identifying Proteomic Signals that Drive Transcriptional Changes using the Interactome and Multiple Omics Datasets. <i>Methods in Cell Biology</i> , 2012, 110, 57-80.	0.5	3
57	HSF1 Drives a Transcriptional Program Distinct from Heat Shock to Support Highly Malignant Human Cancers. <i>Cell</i> , 2012, 150, 549-562.	13.5	602
58	SAMNet: a network-based approach to integrate multi-dimensional high throughput datasets. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 1415.	0.6	20
59	Direct Recruitment of Polycomb Repressive Complex 1 to Chromatin by Core Binding Transcription Factors. <i>Molecular Cell</i> , 2012, 45, 330-343.	4.5	188
60	Polyglutamine Expanded Huntingtin Dramatically Alters the Genome-Wide Binding of HSF1. <i>Journal of Huntington's Disease</i> , 2012, 1, 33-45.	0.9	40
61	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. <i>Lecture Notes in Computer Science</i> , 2012, , 287-301.	1.0	7
62	Poly-glutamine expanded huntingtin dramatically alters the genome wide binding of HSF1. <i>Journal of Huntington's Disease</i> , 2012, 1, 33-45.	0.9	25
63	ResponseNet: revealing signaling and regulatory networks linking genetic and transcriptomic screening data. <i>Nucleic Acids Research</i> , 2011, 39, W424-W429.	6.5	76
64	Genome-Wide Profiling of H3K56 Acetylation and Transcription Factor Binding Sites in Human Adipocytes. <i>PLoS ONE</i> , 2011, 6, e19778.	1.1	49
65	Unbiased, Genome-Wide <i>In Vivo</i> Mapping of Transcriptional Regulatory Elements Reveals Sex Differences in Chromatin Structure Associated with Sex-Specific Liver Gene Expression. <i>Molecular and Cellular Biology</i> , 2010, 30, 5531-5544.	1.1	98
66	A Quantitative Model of Transcriptional Regulation Reveals the Influence of Binding Location on Expression. <i>PLoS Computational Biology</i> , 2010, 6, e1000773.	1.5	67
67	Sequence Analysis of Chromatin Immunoprecipitation Data for Transcription Factors. <i>Methods in Molecular Biology</i> , 2010, 674, 179-193.	0.4	6
68	Role of Polycomb Repressive Complex 1 (PRC1) In Runx1 Mediated Gene Regulation. <i>Blood</i> , 2010, 116, 3863-3863.	0.6	0
69	Bridging high-throughput genetic and transcriptional data reveals cellular responses to alpha-synuclein toxicity. <i>Nature Genetics</i> , 2009, 41, 316-323.	9.4	266
70	Integrating Proteomic, Transcriptional, and Interactome Data Reveals Hidden Components of Signaling and Regulatory Networks. <i>Science Signaling</i> , 2009, 2, ra40.	1.6	161
71	WebMOTIFS: automated discovery, filtering and scoring of DNA sequence motifs using multiple programs and Bayesian approaches. <i>Nucleic Acids Research</i> , 2007, 35, W217-W220.	6.5	41
72	Tissue-specific transcriptional regulation has diverged significantly between human and mouse. <i>Nature Genetics</i> , 2007, 39, 730-732.	9.4	491

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73	High-resolution computational models of genome binding events. <i>Nature Biotechnology</i> , 2006, 24, 963-970.	9.4	82
74	An improved map of conserved regulatory sites for <i>Saccharomyces cerevisiae</i> . <i>BMC Bioinformatics</i> , 2006, 7, 113.	1.2	617
75	Practical Strategies for Discovering Regulatory DNA Sequence Motifs. <i>PLoS Computational Biology</i> , 2006, 2, e36.	1.5	137
76	A hypothesis-based approach for identifying the binding specificity of regulatory proteins from chromatin immunoprecipitation data. <i>Bioinformatics</i> , 2006, 22, 423-429.	1.8	73
77	Core transcriptional regulatory circuitry in human hepatocytes. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0017.	3.2	179
78	TAMO: a flexible, object-oriented framework for analyzing transcriptional regulation using DNA-sequence motifs. <i>Bioinformatics</i> , 2005, 21, 3164-3165.	1.8	81
79	Transcriptional regulatory code of a eukaryotic genome. <i>Nature</i> , 2004, 431, 99-104.	13.7	1,969
80	Transcriptional Regulatory Networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 298, 799-804.	6.0	2,706
81	Hepatic Dysfunction Caused by Consumption of a High-Fat Diet. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0