

Kathleen M Fisch

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

1,831
citations

279798

23
h-index

315739

38
g-index

67
all docs

67
docs citations

67
times ranked

3937
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-coding Transcription Instructs Chromatin Folding and Compartmentalization to Dictate Enhancer-Promoter Communication and T Cell Fate. <i>Cell</i> , 2017, 171, 103-119.e18.	28.9	251
2	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. <i>Cancer Discovery</i> , 2017, 7, 410-423.	9.4	121
3	A Multiscale Map of the Stem Cell State in Pancreatic Adenocarcinoma. <i>Cell</i> , 2019, 177, 572-586.e22.	28.9	107
4	Integrating Gene and Protein Expression Reveals Perturbed Functional Networks in Alzheimer's Disease. <i>Cell Reports</i> , 2019, 28, 1103-1116.e4.	6.4	67
5	Variations in HPV function are associated with survival in squamous cell carcinoma. <i>JCI Insight</i> , 2019, 4, .	5.0	67
6	Omics Pipe: a community-based framework for reproducible multi-omics data analysis. <i>Bioinformatics</i> , 2015, 31, 1724-1728.	4.1	66
7	Aquaculture Methods for a Genetically Managed Population of Endangered Delta Smelt. <i>North American Journal of Aquaculture</i> , 2013, 75, 186-196.	1.4	63
8	Increased DNA Methylation and Reduced Expression of Transcription Factors in Human Osteoarthritis Cartilage. <i>Arthritis and Rheumatology</i> , 2016, 68, 1876-1886.	5.6	61
9	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. <i>Nature Communications</i> , 2019, 10, 2188.	12.8	61
10	Oxidative Stress Diverts tRNA Synthetase to Nucleus for Protection against DNA Damage. <i>Molecular Cell</i> , 2014, 56, 323-332.	9.7	60
11	Selective Whole-Genome Amplification Is a Robust Method That Enables Scalable Whole-Genome Sequencing of <i>Plasmodium vivax</i> from Unprocessed Clinical Samples. <i>MBio</i> , 2017, 8, .	4.1	59
12	DNA methylation changes associated with Parkinson's disease progression: outcomes from the first longitudinal genome-wide methylation analysis in blood. <i>Epigenetics</i> , 2019, 14, 365-382.	2.7	58
13	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. <i>Oncogene</i> , 2020, 39, 6327-6339.	5.9	48
14	Transient genomic instability drives tumorigenesis through accelerated clonal evolution. <i>Genes and Development</i> , 2021, 35, 1093-1108.	5.9	48
15	Activation of NF- κ B and p300/CBP potentiates cancer chemoimmunotherapy through induction of MHC-I antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	47
16	Fish Hatchery Genetic Management Techniques: Integrating Theory with Implementation. <i>North American Journal of Aquaculture</i> , 2015, 77, 343-357.	1.4	39
17	Evaluating the Performance of Captive Breeding Techniques for Conservation Hatcheries: A Case Study of the Delta Smelt Captive Breeding Program. <i>Journal of Heredity</i> , 2013, 104, 92-104.	2.4	37
18	Characterization of Alternative Splicing Events in HPV-Negative Head and Neck Squamous Cell Carcinoma Identifies an Oncogenic DOCK5 Variant. <i>Clinical Cancer Research</i> , 2018, 24, 5123-5132.	7.0	36

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19	Proteasome activity regulates CD8+ T lymphocyte metabolism and fate specification. <i>Journal of Clinical Investigation</i> , 2017, 127, 3609-3623.	8.2	35
20	Map of synthetic rescue interactions for the Fanconi anemia DNA repair pathway identifies USP48. <i>Nature Communications</i> , 2018, 9, 2280.	12.8	34
21	Downregulation of 26S proteasome catalytic activity promotes epithelial-mesenchymal transition. <i>Oncotarget</i> , 2016, 7, 21527-21541.	1.8	32
22	A New Era for Space Life Science: International Standards for Space Omics Processing. <i>Patterns</i> , 2020, 1, 100148.	5.9	28
23	Id3 Orchestrates Germinal Center B Cell Development. <i>Molecular and Cellular Biology</i> , 2016, 36, 2543-2552.	2.3	26
24	Mutation of chromatin regulators and focal hotspot alterations characterize human papillomavirus-positive oropharyngeal squamous cell carcinoma. <i>Cancer</i> , 2019, 125, 2423-2434.	4.1	22
25	Increased Fibrogenic Gene Expression in Multifidus Muscles of Patients With Chronic Versus Acute Lumbar Spine Pathology. <i>Spine</i> , 2020, 45, E189-E195.	2.0	22
26	Single-Cell Transcriptomes Reveal a Complex Cellular Landscape in the Middle Ear and Differential Capacities for Acute Response to Infection. <i>Frontiers in Genetics</i> , 2020, 11, 358.	2.3	22
27	Inflammation-driven deaminase deregulation fuels human pre-leukemia stem cell evolution. <i>Cell Reports</i> , 2021, 34, 108670.	6.4	22
28	A Conservation Hatchery Population of Delta Smelt Shows Evidence of Genetic Adaptation to Captivity After 9 Generations. <i>Journal of Heredity</i> , 2018, 109, 689-699.	2.4	20
29	NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. <i>IScience</i> , 2021, 24, 102361.	4.1	20
30	Extrachromosomal DNA in HPV-Mediated Oropharyngeal Cancer Drives Diverse Oncogene Transcription. <i>Clinical Cancer Research</i> , 2021, 27, 6772-6786.	7.0	20
31	A convergent molecular network underlying autism and congenital heart disease. <i>Cell Systems</i> , 2021, 12, 1094-1107.e6.	6.2	19
32	Machine learning approach to predicting persistent opioid use following lower extremity joint arthroplasty. <i>Regional Anesthesia and Pain Medicine</i> , 2022, 47, 313-319.	2.3	17
33	Interactive network visualization in Jupyter notebooks: visJS2jupyter. <i>Bioinformatics</i> , 2018, 34, 126-128.	4.1	14
34	Aberrant expression of CPSF1 promotes head and neck squamous cell carcinoma via regulating alternative splicing. <i>PLoS ONE</i> , 2020, 15, e0233380.	2.5	13
35	OncoRep: an n-of-1 reporting tool to support genome-guided treatment for breast cancer patients using RNA-sequencing. <i>BMC Medical Genomics</i> , 2015, 8, 24.	1.5	12
36	Extremes of age are associated with differences in the expression of selected pattern recognition receptor genes and ACE2, the receptor for SARS-CoV-2: implications for the epidemiology of COVID-19 disease. <i>BMC Medical Genomics</i> , 2021, 14, 138.	1.5	12

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37	The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction. <i>Scientific Reports</i> , 2022, 12, 5077.	3.3	12
38	Spawning Behavior of Cultured Delta Smelt in a Conservation Hatchery. <i>North American Journal of Aquaculture</i> , 2015, 77, 255-266.	1.4	11
39	Mechanisms of vascular permeability and remodeling associated with hemarthrosis in factor VIII-deficient mice. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 1815-1826.	3.8	11
40	Characterization of 24 microsatellite loci in delta smelt, <i>Hypomesus transpacificus</i> , and their cross-species amplification in two other smelt species of the Osmeridae family. <i>Molecular Ecology Resources</i> , 2009, 9, 405-408.	4.8	10
41	On entropy and information in gene interaction networks. <i>Bioinformatics</i> , 2019, 35, 815-822.	4.1	10
42	Strategies to Identify Mesenchymal Stromal Cells in Minimally Manipulated Human Bone Marrow Aspirate Concentrate Lack Consensus. <i>American Journal of Sports Medicine</i> , 2021, 49, 1313-1322.	4.2	10
43	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 35-53.	4.5	10
44	Metabolomic profiles associated with a mouse model of antipsychotic-induced food intake and weight gain. <i>Scientific Reports</i> , 2020, 10, 18581.	3.3	9
45	Heterogeneous muscle gene expression patterns in patients with massive rotator cuff tears. <i>PLoS ONE</i> , 2018, 13, e0190439.	2.5	8
46	Nonalcoholic fatty liver disease risk and histologic severity are associated with genetic polymorphisms in children. <i>Hepatology</i> , 2023, 77, 197-212.	7.3	8
47	Hybridization between delta smelt and two other species within the family Osmeridae in the San Francisco Bay-Delta. <i>Conservation Genetics</i> , 2014, 15, 489-494.	1.5	6
48	The Lung Microenvironment Instructs Gene Transcription in Neonatal and Adult Alveolar Macrophages. <i>Journal of Immunology</i> , 2022, 208, 1947-1959.	0.8	6
49	Differential expression of nuclear genes encoding mitochondrial proteins from urban and rural populations in Morocco. <i>Cell Stress and Chaperones</i> , 2020, 25, 847-856.	2.9	5
50	Transcriptional Time Course After Rotator Cuff Tear. <i>Frontiers in Physiology</i> , 2021, 12, 707116.	2.8	5
51	Imetelstat Inhibits Telomerase and Prevents Propagation of ADAR1-Activated Myeloproliferative Neoplasm and Leukemia Stem Cells. <i>Blood</i> , 2020, 136, 18-18.	1.4	3
52	Population genetics and conservation implications for the endangered delta smelt in the San Francisco Bay-Delta. <i>Conservation Genetics</i> , 2011, 12, 1421-1434.	1.5	2
53	Rational genomic optimization of DNA detection for human papillomavirus type 16 in head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2020, 42, 688-697.	2.0	2
54	Efficient population-scale variant analysis and prioritization with VAPr. <i>Bioinformatics</i> , 2018, 34, 2843-2845.	4.1	1

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55	Biological Interpretation of Complex Genomic Data. <i>Methods in Molecular Biology</i> , 2019, 1908, 61-71.	0.9	1
56	Mechanisms of Iron Clearance from the Joint in FVIII-Deficient Mice after Induced Hemarthrosis. <i>Blood</i> , 2019, 134, 157-157.	1.4	1
57	Selective Targeting of Alternative Splicing Deregulation in Pediatric Acute Myeloid Stem and Progenitor Cells. <i>Blood</i> , 2020, 136, 8-8.	1.4	1
58	Systemic Transcriptional Responses to Hemarthrosis and FVIII Replacement in FVIII-Deficient Mice. <i>Blood</i> , 2018, 132, 381-381.	1.4	0
59	Effects of Hemostasis Correction on Vascular Remodeling and Synovial Gene Expression Changes in Mice after Induced Hemarthrosis. <i>Blood</i> , 2018, 132, 1188-1188.	1.4	0
60	Lymphatic Remodeling Associated with Hemophilic Joint Bleeding in FVIII-Deficient Mice. <i>Blood</i> , 2020, 136, 20-20.	1.4	0