J Lynn Fink

List of Publications by Year
in descending order

64 papers	16,212 citations	94269 37 h-index	114278 63 g-index
67 all docs	67 docs citations	67 times ranked	25048 citing authors

#	Article	IF	Citations
1	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
2	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
3	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
4	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
5	Whole–genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
6	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
7	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
8	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
9	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
10	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
11	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. Nature, 2012, 486, 266-270.	13.7	297
12	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
13	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
14	*Sleeping Beauty* mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5934-5941.	3.3	201
15	Genome–wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT–ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	2.3	192
16	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. Nature Genetics, 2020, 52, 294-305.	9.4	180
17	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
18	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161

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19	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. Nature Communications, 2019, 10, 470.	5.8	156
20	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. Communications Biology, 2020, 3, 56.	2.0	140
21	Integrative pathway enrichment analysis of multivariate omics data. Nature Communications, 2020, 11, 735.	5.8	125
22	LOCATE: a mammalian protein subcellular localization database. Nucleic Acids Research, 2007, 36, D230-D233.	6.5	124
23	Use of keyword hierarchies to interpret gene expression patterns. Bioinformatics, 2001, 17, 319-326.	1.8	118
24	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
25	Subclonal evolution in disease progression from MGUS/SMM to multiple myeloma is characterised by clonal stability. Leukemia, 2019, 33, 457-468.	3.3	96
26	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	1.1	92
27	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	0.6	90
28	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	5.8	87
29	Progression of Disease Within 24 Months in Follicular Lymphoma Is Associated With Reduced Intratumoral Immune Infiltration. Journal of Clinical Oncology, 2019, 37, 3300-3309.	0.8	83
30	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	2.9	78
31	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
32	LOCATE: a mouse protein subcellular localization database. Nucleic Acids Research, 2006, 34, D213-D217.	6.5	72
33	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
34	Chromosome arm aneuploidies shape tumour evolution and drug response. Nature Communications, 2020, 11, 449.	5.8	65
35	The PlantsP and PlantsT Functional Genomics Databases. Nucleic Acids Research, 2003, 31, 342-344.	6.5	54
36	Evaluation and comparison of mammalian subcellular localization prediction methods. BMC Bioinformatics, 2006, 7, S3.	1.2	52

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37	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. Nature Communications, 2020, 11, 736.	5.8	50
38	Combined burden and functional impact tests for cancer driver discovery using DriverPower. Nature Communications, 2020, 11, 734.	5.8	39
39	Differential Use of Signal Peptides and Membrane Domains Is a Common Occurrence in the Protein Output of Transcriptional Units. PLoS Genetics, 2006, 2, e46.	1.5	34
40	IL-2- and STAT5-regulated cytokine gene expression in cells expressing the Tax protein of HTLV-1. Oncogene, 2005, 24, 4624-4633.	2.6	31
41	BioLit: integrating biological literature with databases. Nucleic Acids Research, 2008, 36, W385-W389.	6.5	30
42	Towards defining the nuclear proteome. Genome Biology, 2008, 9, R15.	13.9	29
43	Targeted Next-Generation Sequencing for Detecting *MLL* Gene Fusions in Leukemia. Molecular Cancer Research, 2018, 16, 279-285.	1.5	27
44	Computational Biology Resources Lack Persistence and Usability. PLoS Computational Biology, 2008, 4, e1000136.	1.5	26
45	Rival penalized competitive learning (RPCL): a topology-determining algorithm for analyzing gene expression data. Computational Biology and Chemistry, 2003, 27, 565-574.	1.1	20
46	Subcellular Localization of Mammalian Type II Membrane Proteins. Traffic, 2006, 7, 613-625.	1.3	19
47	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. BMC Bioinformatics, 2006, 7, 82.	1.2	18
48	Single-cell RNA-seq reveals dynamic transcriptome profiling in human early neural differentiation. GigaScience, 2018, 7, .	3.3	18
49	RON is not a prognostic marker for resectable pancreatic cancer. BMC Cancer, 2012, 12, 395.	1.1	17
50	Cutting edge genomics reveal new insights into tumour development, disease progression and therapeutic impacts in multiple myeloma. British Journal of Haematology, 2017, 178, 196-208.	1.2	17
51	Open Access: Taking Full Advantage of the Content. PLoS Computational Biology, 2008, 4, e1000037.	1.5	16
52	Translocation Breakpoints Preferentially Occur in Euchromatin and Acrocentric Chromosomes. Cancers, 2018, 10, 13.	1.7	16
53	Word add-in for ontology recognition: semantic enrichment of scientific literature. BMC Bioinformatics, 2010, 11, 103.	1.2	13
54	Subtype-Specific Analyses Reveal Infiltrative Basal Cell Carcinomas Are Highly Interactive with their Environment. Journal of Investigative Dermatology, 2021, 141, 2380-2390.	0.3	13

#	ARTICLE	IF	CITATIONS
55	DomainDraw: a macromolecular feature drawing program. In Silico Biology, 2007, 7, 145-50.	0.4	13
56	INTRINSIC EVALUATION OF TEXT MINING TOOLS MAY NOT PREDICT PERFORMANCE ON REALISTIC TASKS. , 2007, , .		12
57	I Am Not a Scientist, I Am a Number. PLoS Computational Biology, 2008, 4, e1000247.	1.5	9
58	*PTEN* deletion drives acute myeloid leukemia resistance to MEK inhibitors. Oncotarget, 2019, 10, 5755-5767.	0.8	9
59	2HAPI: a microarray data analysis system. Bioinformatics, 2003, 19, 1443-1445.	1.8	7
60	Integration of open access literature into the RCSB Protein Data Bank using BioLit. BMC Bioinformatics, 2010, 11, 220.	1.2	7
61	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke Clonorchis sinensis. PLoS Neglected Tropical Diseases, 2020, 14, e0008480.	1.3	6
62	Using genomics to better define high-risk MGUS/SMM patients. Oncotarget, 2018, 9, 36549-36550.	0.8	2
63	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
64	Literature Databases. , 2009, , 331-345.		0