

J Lynn Fink

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

63
papers

10,649
citations

34
h-index

67
g-index

67
ext. papers

13,976
ext. citations

16.3
avg, IF

7.12
L-index

#	Paper	IF	Citations
63	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. <i>Gastroenterology</i> , 2021 , 160, 362-377.e13	13.3	32
62	Subtype-Specific Analyses Reveal Infiltrative Basal Cell Carcinomas Are Highly Interactive with their Environment. <i>Journal of Investigative Dermatology</i> , 2021 , 141, 2380-2390	4.3	5
61	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. <i>Cell Reports</i> , 2020 , 31, 107625	10.6	34
60	Chromosome arm aneuploidies shape tumour evolution and drug response. <i>Nature Communications</i> , 2020 , 11, 449	17.4	30
59	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020 , 11, 733	17.4	40
58	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. <i>Nature Communications</i> , 2020 , 11, 736	17.4	32
57	Combined burden and functional impact tests for cancer driver discovery using DriverPower. <i>Nature Communications</i> , 2020 , 11, 734	17.4	16
56	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020 , 11, 735	17.4	53
55	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
54	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020 , 578, 112-121	50.4	232
53	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
52	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
51	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
50	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020 , 52, 294-305	36.3	81
49	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
48	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020 , 3, 56	6.7	77
47	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008480	4.8	4

46	Progression of Disease Within 24 Months in Follicular Lymphoma Is Associated With Reduced Intratumoral Immune Infiltration. <i>Journal of Clinical Oncology</i> , 2019 , 37, 3300-3309	2.2	43
45	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019 , 10, 470	17.4	84
44	Subclonal evolution in disease progression from MGUS/SMM to multiple myeloma is characterised by clonal stability. <i>Leukemia</i> , 2019 , 33, 457-468	10.7	51
43	deletion drives acute myeloid leukemia resistance to MEK inhibitors. <i>Oncotarget</i> , 2019 , 10, 5755-5767	3.3	5
42	Translocation Breakpoints Preferentially Occur in Euchromatin and Acrocentric Chromosomes. <i>Cancers</i> , 2018 , 10,	6.6	12
41	Targeted Next-Generation Sequencing for Detecting Gene Fusions in Leukemia. <i>Molecular Cancer Research</i> , 2018 , 16, 279-285	6.6	20
40	Single-cell RNA-seq reveals dynamic transcriptome profiling in human early neural differentiation. <i>GigaScience</i> , 2018 , 7,	7.6	11
39	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017 , 543, 65-71	50.4	482
38	Cutting edge genomics reveal new insights into tumour development, disease progression and therapeutic impacts in multiple myeloma. <i>British Journal of Haematology</i> , 2017 , 178, 196-208	4.5	13
37	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017 , 152, 68-74.e2	13.3	130
36	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016 , 531, 47-52	50.4	1785
35	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015 , 518, 495-501	50.4	1579
34	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015 , 237, 363-78	9.4	72
33	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015 , 521, 489-94	50.4	890
32	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014 , 5, 5224	17.4	176
31	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. <i>BioTechniques</i> , 2014 , 57, 31-8	2.5	
30	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. <i>International Journal of Cancer</i> , 2014 , 135, 1110-8	7.5	149
29	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013 , 10, 723-9	21.6	129

28	Somatic point mutation calling in low cellularity tumors. <i>PLoS ONE</i> , 2013 , 8, e74380	3.7	49
27	RON is not a prognostic marker for resectable pancreatic cancer. <i>BMC Cancer</i> , 2012 , 12, 395	4.8	16
26	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012 , 491, 399-405	30.4	1427
25	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , 2012 , 486, 266-70	50.4	253
24	Sleeping Beauty mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 5934-41	11.5	179
23	qpure: A tool to estimate tumor cellularity from genome-wide single-nucleotide polymorphism profiles. <i>PLoS ONE</i> , 2012 , 7, e45835	3.7	80
22	Word add-in for ontology recognition: semantic enrichment of scientific literature. <i>BMC Bioinformatics</i> , 2010 , 11, 103	3.6	10
21	Integration of open access literature into the RCSB Protein Data Bank using BioLit. <i>BMC Bioinformatics</i> , 2010 , 11, 220	3.6	7
20	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
19	Literature Databases 2009 , 331-345		
18	Towards defining the nuclear proteome. <i>Genome Biology</i> , 2008 , 9, R15	18.3	27
17	Computational biology resources lack persistence and usability. <i>PLoS Computational Biology</i> , 2008 , 4, e1000136	5	23
16	BioLit: integrating biological literature with databases. <i>Nucleic Acids Research</i> , 2008 , 36, W385-9	20.1	26
15	I am not a scientist, I am a number. <i>PLoS Computational Biology</i> , 2008 , 4, e1000247	5	8
14	LOCATE: a mammalian protein subcellular localization database. <i>Nucleic Acids Research</i> , 2008 , 36, D230-3	30.1	108
13	INTRINSIC EVALUATION OF TEXT MINING TOOLS MAY NOT PREDICT PERFORMANCE ON REALISTIC TASKS 2007 ,		4
12	DomainDraw: a macromolecular feature drawing program. <i>In Silico Biology</i> , 2007 , 7, 145-50	2	12
11	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , 2006 , 7, 82	3.6	16

10	Evaluation and comparison of mammalian subcellular localization prediction methods. <i>BMC Bioinformatics</i> , 2006 , 7 Suppl 5, S3	3.6	46
9	LOCATE: a mouse protein subcellular localization database. <i>Nucleic Acids Research</i> , 2006 , 34, D213-7	20.1	65
8	Differential use of signal peptides and membrane domains is a common occurrence in the protein output of transcriptional units. <i>PLoS Genetics</i> , 2006 , 2, e46	6	25
7	Subcellular localization of mammalian type II membrane proteins. <i>Traffic</i> , 2006 , 7, 613-25	5.7	17
6	IL-2- and STAT5-regulated cytokine gene expression in cells expressing the Tax protein of HTLV-1. <i>Oncogene</i> , 2005 , 24, 4624-33	9.2	31
5	2HAPI: a microarray data analysis system. <i>Bioinformatics</i> , 2003 , 19, 1443-5	7.2	7
4	The PlantsP and PlantsT Functional Genomics Databases. <i>Nucleic Acids Research</i> , 2003 , 31, 342-4	20.1	49
3	Rival penalized competitive learning (RPCL): a topology-determining algorithm for analyzing gene expression data. <i>Computational Biology and Chemistry</i> , 2003 , 27, 565-74	3.6	12
2	Use of keyword hierarchies to interpret gene expression patterns. <i>Bioinformatics</i> , 2001 , 17, 319-26	7.2	101
1	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity		5