

Erik K Flemington

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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.

116 papers	5,122 citations	39 h-index	69 g-index
127 ext. papers	5,801 ext. citations	6.5 avg, IF	5.28 L-index

#	Paper	IF	Citations
116	Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F-like properties. <i>Cell</i> , 1992 , 70, 351-64	56.2	857
115	Epstein-Barr virus latent membrane protein 1 induces cellular MicroRNA miR-146a, a modulator of lymphocyte signaling pathways. <i>Journal of Virology</i> , 2008 , 82, 1946-58	6.6	251
114	Histone deacetylase inhibitors prevent oxidative neuronal death independent of expanded polyglutamine repeats via an Sp1-dependent pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4281-6	11.5	221
113	MicroRNA-155 is an Epstein-Barr virus-induced gene that modulates Epstein-Barr virus-regulated gene expression pathways. <i>Journal of Virology</i> , 2008 , 82, 5295-306	6.6	211
112	B-cell receptor activation induces BIC/miR-155 expression through a conserved AP-1 element. <i>Journal of Biological Chemistry</i> , 2008 , 283, 2654-62	5.4	177
111	Human multipotent stromal cells from bone marrow and microRNA: regulation of differentiation and leukemia inhibitory factor expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18372-7	11.5	155
110	Herpesvirus lytic replication and the cell cycle: arresting new developments. <i>Journal of Virology</i> , 2001 , 75, 4475-81	6.6	142
109	Sequence, structure and promoter characterization of the human thymidine kinase gene. <i>Gene</i> , 1987 , 52, 267-77	3.8	124
108	Androgen Receptor Splice Variants Dimerize to Transactivate Target Genes. <i>Cancer Research</i> , 2015 , 75, 3663-71	10.1	122
107	Epstein-Barr virus growth/latency III program alters cellular microRNA expression. <i>Virology</i> , 2008 , 382, 257-66	3.6	121
106	Microbial contamination in next generation sequencing: implications for sequence-based analysis of clinical samples. <i>PLoS Pathogens</i> , 2014 , 10, e1004437	7.6	118
105	Differences in gastric carcinoma microenvironment stratify according to EBV infection intensity: implications for possible immune adjuvant therapy. <i>PLoS Pathogens</i> , 2013 , 9, e1003341	7.6	108
104	Whole-genome sequencing of the Akata and Mutu Epstein-Barr virus strains. <i>Journal of Virology</i> , 2013 , 87, 1172-82	6.6	84
103	The Epstein Barr virus circRNAome. <i>PLoS Pathogens</i> , 2018 , 14, e1007206	7.6	79
102	GE-33A COMPREHENSIVE ASSESSMENT OF VIRAL TRANSCRIPTS IN DNA- AND RNA-SEQ DATASETS FROM HIGH-GRADE GLIOMAS REVEALS NO ASSOCIATION. <i>Neuro-Oncology</i> , 2014 , 16, v103-v103	1	78
101	MicroRNA miR-155 inhibits bone morphogenetic protein (BMP) signaling and BMP-mediated Epstein-Barr virus reactivation. <i>Journal of Virology</i> , 2010 , 84, 6318-27	6.6	78
100	Differential regulation of microRNA-146a and microRNA-146b-5p in human retinal pigment epithelial cells by interleukin-1 β tumor necrosis factor- β and interferon- γ <i>Molecular Vision</i> , 2013 , 19, 737-50	2.3	70

99	Global transcript structure resolution of high gene density genomes through multi-platform data integration. <i>Nucleic Acids Research</i> , 2016 , 44, e145	20.1	59
98	High-throughput RNA sequencing-based virome analysis of 50 lymphoma cell lines from the Cancer Cell Line Encyclopedia project. <i>Journal of Virology</i> , 2015 , 89, 713-29	6.6	56
97	G0/G1 growth arrest mediated by a region encompassing the basic leucine zipper (bZIP) domain of the Epstein-Barr virus transactivator Zta. <i>Journal of Biological Chemistry</i> , 1996 , 271, 31799-802	5.4	54
96	Identification of new viral genes and transcript isoforms during Epstein-Barr virus reactivation using RNA-Seq. <i>Journal of Virology</i> , 2012 , 86, 1458-67	6.6	52
95	A comprehensive approach to expression of L1 loci. <i>Nucleic Acids Research</i> , 2017 , 45, e31	20.1	51
94	SAMMate: a GUI tool for processing short read alignments in SAM/BAM format. <i>Source Code for Biology and Medicine</i> , 2011 , 6, 2	1.9	50
93	Global bidirectional transcription of the Epstein-Barr virus genome during reactivation. <i>Journal of Virology</i> , 2014 , 88, 1604-16	6.6	49
92	Effects of the endocrine-disrupting chemical DDT on self-renewal and differentiation of human mesenchymal stem cells. <i>Environmental Health Perspectives</i> , 2015 , 123, 42-8	8.4	48
91	Genetic dissection of cell growth arrest functions mediated by the Epstein-Barr virus lytic gene product, Zta. <i>Journal of Virology</i> , 1999 , 73, 9029-38	6.6	48
90	miRNAs in the pathogenesis of oncogenic human viruses. <i>Cancer Letters</i> , 2011 , 305, 186-99	9.9	46
89	Transcriptome and targetome analysis in MIR155 expressing cells using RNA-seq. <i>Rna</i> , 2010 , 16, 1610-22	5.8	46
88	The Epstein-Barr virus latent membrane protein 1 and transforming growth factor- β synergistically induce epithelial-mesenchymal transition in lung epithelial cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2011 , 44, 852-62	5.7	46
87	A positive role of c-Myc in regulating androgen receptor and its splice variants in prostate cancer. <i>Oncogene</i> , 2019 , 38, 4977-4989	9.2	46
86	S100P/RAGE signaling regulates microRNA-155 expression via AP-1 activation in colon cancer. <i>Experimental Cell Research</i> , 2013 , 319, 2081-2090	4.2	45
85	A comprehensive next generation sequencing-based virome assessment in brain tissue suggests no major virus - tumor association. <i>Acta Neuropathologica Communications</i> , 2016 , 4, 71	7.3	44
84	Targeting sphingosine kinase induces apoptosis and tumor regression for KSHV-associated primary effusion lymphoma. <i>Molecular Cancer Therapeutics</i> , 2014 , 13, 154-64	6.1	43
83	Cell cycle analysis of Epstein-Barr virus-infected cells following treatment with lytic cycle-inducing agents. <i>Journal of Virology</i> , 2001 , 75, 4482-9	6.6	43
82	The sequence structures of human microRNA molecules and their implications. <i>PLoS ONE</i> , 2013 , 8, e54215	3.7	42

81	Quantitative and qualitative RNA-Seq-based evaluation of Epstein-Barr virus transcription in type I latency Burkitt's lymphoma cells. <i>Journal of Virology</i> , 2010 , 84, 13053-8	6.6	42
80	Interplay between Cytoplasmic and Nuclear Androgen Receptor Splice Variants Mediates Castration Resistance. <i>Molecular Cancer Research</i> , 2017 , 15, 59-68	6.6	41
79	Preferential star strand biogenesis of pre-miR-24-2 targets PKC-alpha and suppresses cell survival in MCF-7 breast cancer cells. <i>Molecular Carcinogenesis</i> , 2014 , 53, 38-48	5	40
78	Nerve growth factor receptor negates the tumor suppressor p53 as a feedback regulator. <i>ELife</i> , 2016 , 5,	8.9	40
77	New Noncoding Lytic Transcripts Derived from the Epstein-Barr Virus Latency Origin of Replication, oriP, Are Hyperedited, Bind the Paraspeckle Protein, NONO/p54nrb, and Support Viral Lytic Transcription. <i>Journal of Virology</i> , 2015 , 89, 7120-32	6.6	39
76	OncomiR addiction is generated by a miR-155 feedback loop in Theileria-transformed leukocytes. <i>PLoS Pathogens</i> , 2013 , 9, e1003222	7.6	39
75	Differential expression of the miR-200 family microRNAs in epithelial and B cells and regulation of Epstein-Barr virus reactivation by the miR-200 family member miR-429. <i>Journal of Virology</i> , 2010 , 84, 7892-7	6.6	39
74	Comparative Analysis of Gammaherpesvirus Circular RNA Repertoires: Conserved and Unique Viral Circular RNAs. <i>Journal of Virology</i> , 2019 , 93,	6.6	37
73	miRNA-mRNA correlation-network modules in human prostate cancer and the differences between primary and metastatic tumor subtypes. <i>PLoS ONE</i> , 2012 , 7, e40130	3.7	36
72	Small interfering RNA effectively inhibits protein expression and negative strand RNA synthesis from a full-length hepatitis C virus clone. <i>Journal of Medical Virology</i> , 2005 , 76, 511-9	19.7	35
71	Distinct cellular factors regulate the c-myc promoter through its E2F element. <i>Molecular and Cellular Biology</i> , 1999 , 19, 8442-50	4.8	34
70	MALT1 Inhibition Is Efficacious in Both Naïve and Ibrutinib-Resistant Chronic Lymphocytic Leukemia. <i>Cancer Research</i> , 2017 , 77, 7038-7048	10.1	33
69	E2F1 expression is deregulated and plays an oncogenic role in sporadic Burkitt's lymphoma. <i>Cancer Research</i> , 2009 , 69, 4052-8	10.1	32
68	RNA CoMPASS: a dual approach for pathogen and host transcriptome analysis of RNA-seq datasets. <i>PLoS ONE</i> , 2014 , 9, e89445	3.7	31
67	SON and Its Alternatively Spliced Isoforms Control MLL Complex-Mediated H3K4me3 and Transcription of Leukemia-Associated Genes. <i>Molecular Cell</i> , 2016 , 61, 859-73	17.6	30
66	Epstein-Barr virus and human herpesvirus 6 detection in a non-Hodgkin's diffuse large B-cell lymphoma cohort by using RNA sequencing. <i>Journal of Virology</i> , 2013 , 87, 13059-62	6.6	30
65	Elevated expression of long intergenic non-coding RNA HOTAIR in a basal-like variant of MCF-7 breast cancer cells. <i>Molecular Carcinogenesis</i> , 2015 , 54, 1656-67	5	28
64	Transfection-mediated cell-cycle signaling: considerations for transient transfection-based cell-cycle studies. <i>Analytical Biochemistry</i> , 1999 , 272, 171-81	3.1	28

63	Post-transcriptional up-regulation of miR-21 by type I collagen. <i>Molecular Carcinogenesis</i> , 2011 , 50, 563-70	20.1	27
62	Isoform-level microRNA-155 target prediction using RNA-seq. <i>Nucleic Acids Research</i> , 2011 , 39, e61	20.1	26
61	Detection of murine leukemia virus in the Epstein-Barr virus-positive human B-cell line JY, using a computational RNA-Seq-based exogenous agent detection pipeline, PARSES. <i>Journal of Virology</i> , 2012 , 86, 2970-7	6.6	26
60	Racial disparities in patient survival and tumor mutation burden, and the association between tumor mutation burden and cancer incidence rate. <i>Scientific Reports</i> , 2017 , 7, 13639	4.9	25
59	High-fat diet induced leptin and Wnt expression: RNA-sequencing and pathway analysis of mouse colonic tissue and tumors. <i>Carcinogenesis</i> , 2017 , 38, 302-311	4.6	24
58	Latent Expression of the Epstein-Barr Virus (EBV)-Encoded Major Histocompatibility Complex Class I TAP Inhibitor, BNLF2a, in EBV-Positive Gastric Carcinomas. <i>Journal of Virology</i> , 2015 , 89, 10110-4	6.6	23
57	Induction of a novel isoform of the lncRNA HOTAIR in Claudin-low breast cancer cells attached to extracellular matrix. <i>Molecular Oncology</i> , 2017 , 11, 1698-1710	7.9	23
56	Secreted Oral Epithelial Cell Membrane Vesicles Induce Epstein-Barr Virus Reactivation in Latently Infected B Cells. <i>Journal of Virology</i> , 2016 , 90, 3469-79	6.6	22
55	Detection of Epstein-Barr Virus Infection in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2019 , 11,	6.6	19
54	Transactivation of human endogenous retrovirus K (HERV-K) by KSHV promotes Kaposi's sarcoma development. <i>Oncogene</i> , 2018 , 37, 4534-4545	9.2	19
53	Circular RNAs add diversity to androgen receptor isoform repertoire in castration-resistant prostate cancer. <i>Oncogene</i> , 2019 , 38, 7060-7072	9.2	18
52	Identification of a negative regulatory element in the Epstein-Barr virus Zta transactivation domain that is regulated by the cell cycle control factors c-Myc and E2F1. <i>Journal of Virology</i> , 2004 , 78, 11962-71	6.6	16
51	Gammaherpesvirus RNAs Come Full Circle. <i>MBio</i> , 2019 , 10,	7.8	15
50	Comparative profiling of miRNA expression of lung adenocarcinoma cells in two-dimensional and three-dimensional cultures. <i>Gene</i> , 2012 , 511, 143-50	3.8	15
49	The microRNA expression associated with morphogenesis of breast cancer cells in three-dimensional organotypic culture. <i>Oncology Reports</i> , 2012 , 28, 117-126	3.5	15
48	Methylation status and AP1 elements are involved in EBV-mediated miR-155 expression in EBV positive lymphoma cells. <i>Virology</i> , 2016 , 494, 158-67	3.6	15
47	Significant Prognostic Features and Patterns of Somatic Mutations in Human Cancers. <i>Cancer Informatics</i> , 2017 , 16, 1176935117691267	2.4	14
46	Genome-wide Transcript Structure Resolution Reveals Abundant Alternate Isoform Usage from Murine Gammaherpesvirus 68. <i>Cell Reports</i> , 2019 , 27, 3988-4002.e5	10.6	14

45	The impact of oil spill to lung health--Insights from an RNA-seq study of human airway epithelial cells. <i>Gene</i> , 2016 , 578, 38-51	3.8	14
44	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. <i>Gene</i> , 2016 , 581, 152-60	3.8	14
43	miR-155 induced transcriptome changes in the MCF-7 breast cancer cell line leads to enhanced mitogen activated protein kinase signaling. <i>Genes and Cancer</i> , 2014 , 5, 353-64	2.9	14
42	miRNA-mediated relationships between Cis-SNP genotypes and transcript intensities in lymphocyte cell lines. <i>PLoS ONE</i> , 2012 , 7, e31429	3.7	13
41	Gene network analysis reveals a novel 22-gene signature of carbon metabolism in hepatocellular carcinoma. <i>Oncotarget</i> , 2016 , 7, 49232-49245	3.3	13
40	Somatic mutations in the DNA repairome in prostate cancers in African Americans and Caucasians. <i>Oncogene</i> , 2020 , 39, 4299-4311	9.2	13
39	Reduced mitochondrial activity in colonocytes facilitates AMPK α -dependent inflammation. <i>FASEB Journal</i> , 2017 , 31, 2013-2025	0.9	12
38	Defining the dynamic chromatin landscape of mouse nephron progenitors. <i>Biology Open</i> , 2019 , 8,	2.2	12
37	Transcriptomic analysis of KSHV-infected primary oral fibroblasts: The role of interferon-induced genes in the latency of oncogenic virus. <i>Oncotarget</i> , 2016 , 7, 47052-47060	3.3	12
36	A novel factor distinct from E2F mediates C-MYC promoter activation through its E2F element during exit from quiescence. <i>Carcinogenesis</i> , 2009 , 30, 440-8	4.6	11
35	TFIIIS.h, a new target of p53, regulates transcription efficiency of pro-apoptotic bax gene. <i>Scientific Reports</i> , 2016 , 6, 23542	4.9	10
34	Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. <i>Oncotarget</i> , 2017 , 8, 38399-38412	3.3	8
33	Mutant TP53 disrupts age-related accumulation patterns of somatic mutations in multiple cancer types. <i>Cancer Genetics</i> , 2016 , 209, 376-380	2.3	8
32	Connivance, Complicity, or Collusion? The Role of Noncoding RNAs in Promoting Gammaherpesvirus Tumorigenesis. <i>Trends in Cancer</i> , 2018 , 4, 729-740	12.5	8
31	Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on M. tuberculosis. <i>BMC Genomics</i> , 2018 , 19, 505	4.5	7
30	EBV miRNAs are potent effectors of tumor cell transcriptome remodeling in promoting immune escape. <i>PLoS Pathogens</i> , 2021 , 17, e1009217	7.6	7
29	Gammaherpesvirus Readthrough Transcription Generates a Long Non-Coding RNA That Is Regulated by Antisense miRNAs and Correlates with Enhanced Lytic Replication In Vivo. <i>Non-coding RNA</i> , 2019 , 5,	7.1	7
28	Assessment of viral RNA in idiopathic pulmonary fibrosis using RNA-seq. <i>BMC Pulmonary Medicine</i> , 2020 , 20, 81	3.5	7

27	SpliceV: analysis and publication quality printing of linear and circular RNA splicing, expression and regulation. <i>BMC Bioinformatics</i> , 2019 , 20, 231	3.6	6
26	SEER and Gene Expression Data Analysis Deciphers Racial Disparity Patterns in Prostate Cancer Mortality and the Public Health Implication. <i>Scientific Reports</i> , 2020 , 10, 6820	4.9	6
25	High-Throughput Sequence Analysis of Peripheral T-Cell Lymphomas Indicates Subtype-Specific Viral Gene Expression Patterns and Immune Cell Microenvironments. <i>MSphere</i> , 2019 , 4,	5	6
24	Arsenic trioxide inhibits EBV reactivation and promotes cell death in EBV-positive lymphoma cells. <i>Virology Journal</i> , 2017 , 14, 121	6.1	6
23	In colonic L(rho0) cells reduced mitochondrial function mediates transcriptomic alterations associated with cancer. <i>Oncoscience</i> , 2017 , 4, 189-198	0.8	6
22	Transcriptome analysis reveals sexual disparities in gene expression in rat brain microvessels. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2021 , 41, 2311-2328	7.3	6
21	Increased transcription and high translation efficiency lead to accumulation of androgen receptor splice variant after androgen deprivation therapy. <i>Cancer Letters</i> , 2021 , 504, 37-48	9.9	5
20	Lipids, lipid metabolism and Kaposi's sarcoma-associated herpesvirus pathogenesis. <i>Virologica Sinica</i> , 2017 , 32, 369-375	6.4	4
19	Inferring polymorphism-induced regulatory gene networks active in human lymphocyte cell lines by weighted linear mixed model analysis of multiple RNA-Seq datasets. <i>PLoS ONE</i> , 2013 , 8, e78868	3.7	4
18	A computational framework for distinguishing direct versus indirect interactions in human functional protein-protein interaction networks. <i>Integrative Biology (United Kingdom)</i> , 2017 , 9, 595-606	3.7	3
17	The modularity and dynamicity of miRNA-mRNA interactions in high-grade serous ovarian carcinomas and the prognostic implication. <i>Computational Biology and Chemistry</i> , 2016 , 63, 3-14	3.6	3
16	Somatic mutations favorable to patient survival are predominant in ovarian carcinomas. <i>PLoS ONE</i> , 2014 , 9, e112561	3.7	3
15	Epigenetically Silenced Candidate Tumor Suppressor Genes in Prostate Cancer: Identified by Modeling Methylation Stratification and Applied to Progression Prediction. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 198-207	4	3
14	Screen technical noise in single cell RNA sequencing data. <i>Genomics</i> , 2020 , 112, 346-355	4.3	3
13	Expanding the conversation on high-throughput virome sequencing standards to include consideration of microbial contamination sources. <i>MBio</i> , 2014 , 5, e01989	7.8	2
12	EBV miRNAs are potent effectors of tumor cell transcriptome remodeling in promoting immune escape		2
11	SON inhibits megakaryocytic differentiation via repressing RUNX1 and the megakaryocytic gene expression program in acute megakaryoblastic leukemia. <i>Cancer Gene Therapy</i> , 2021 , 28, 1000-1015	5.4	2
10	Transcriptional signatures of Zika virus infection in astrocytes. <i>Journal of NeuroVirology</i> , 2021 , 27, 116-125		2

- 9 Driver gene mutations based clustering of tumors: methods and applications. *Bioinformatics*, **2018**, 34, i404-i411 7.2 2
- 8 Analysis of EBV Transcription Using High-Throughput RNA Sequencing. *Methods in Molecular Biology*, **2017**, 1532, 105-121 1.4 1
- 7 SpliceV: Analysis and publication quality printing of linear and circular RNA splicing, expression and regulation 1
- 6 Data of relative mRNA and protein abundances of androgen receptor splice variants in castration-resistant prostate cancer. *Data in Brief*, **2021**, 34, 106774 1.2 1
- 5 SON drives oncogenic RNA splicing in glioblastoma by regulating PTBP1/PTBP2 switching and RBFOX2 activity. *Nature Communications*, **2021**, 12, 5551 17.4 0
- 4 Salt-Inducible Kinase 1 is a potential therapeutic target in Desmoplastic Small Round Cell Tumor.. *Oncogenesis*, **2022**, 11, 18 6.6 0
- 3 The Paracaspase MALT1 Acts Independently of Pre-B-Cell Receptor Signaling As a Key Factor in Leukemic Cell Survival in Precursor B-Cell Acute Lymphoblastic Leukemia. *Blood*, **2019**, 134, 1288-1288 2.2
- 2 Targeting MALT1 with the Small Molecule Inhibitor MI2 Induces a Caspase-Dependent Apoptosis and Inhibits the NF- κ B Pathway in Chronic Lymphocytic Leukemia Primary Cells. *Blood*, **2016**, 128, 1597-1597 2.2
- 1 Targeting Sphingosine Kinase Induces Apoptosis and Regression Of Virus-Associated Lymphoma In Vivo. *Blood*, **2013**, 122, 4414-4414 2.2