

# Erik K Flemington

## List of Publications by Year in descending order

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117  
papers

6,161  
citations

71102

41  
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76900

74  
g-index

127  
all docs

127  
docs citations

127  
times ranked

8932  
citing authors

#	ARTICLE	IF	CITATIONS
1	Salt-Inducible Kinase 1 is a potential therapeutic target in Desmoplastic Small Round Cell Tumor. <i>Oncogenesis</i> , 2022, 11, 18.	4.9	7
2	Circulating Exosomal Proteins are linked to Neuropathogenesis in SIV-infected Rhesus Macaque: A Proteomic Approach. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
3	A Polymorphism in the Epstein-Barr Virus EBER2 Noncoding RNA Drives <i>In Vivo</i> Expansion of Latently Infected B Cells. <i>MBio</i> , 2022, 13, .	4.1	2
4	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.	4.6	5
5	Transcriptional signatures of Zika virus infection in astrocytes. <i>Journal of NeuroVirology</i> , 2021, 27, 116-125.	2.1	3
6	Data of relative mRNA and protein abundances of androgen receptor splice variants in castration-resistant prostate cancer. <i>Data in Brief</i> , 2021, 34, 106774.	1.0	2
7	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.	4.3	56
8	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.	7.2	17
9	EBV miRNAs are potent effectors of tumor cell transcriptome remodeling in promoting immune escape. <i>PLoS Pathogens</i> , 2021, 17, e1009217.	4.7	19
10	Multiomics Uncover Sexual Disparities in the Expression of Genes and Proteins in Rat Cerebral Microvessels. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
11	SON drives oncogenic RNA splicing in glioblastoma by regulating PTBP1/PTBP2 switching and RBFOX2 activity. <i>Nature Communications</i> , 2021, 12, 5551.	12.8	17
12	Screen technical noise in single cell RNA sequencing data. <i>Genomics</i> , 2020, 112, 346-355.	2.9	5
13	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.	3.3	8
14	Somatic mutations in the DNA repairome in prostate cancers in African Americans and Caucasians. <i>Oncogene</i> , 2020, 39, 4299-4311.	5.9	30
15	Assessment of viral RNA in idiopathic pulmonary fibrosis using RNA-seq. <i>BMC Pulmonary Medicine</i> , 2020, 20, 81.	2.0	12
16	Circular RNAs add diversity to androgen receptor isoform repertoire in castration-resistant prostate cancer. <i>Oncogene</i> , 2019, 38, 7060-7072.	5.9	31
17	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, .	2.9	13
18	Genome-wide Transcript Structure Resolution Reveals Abundant Alternate Isoform Usage from Murine Gammaherpesvirus 68. <i>Cell Reports</i> , 2019, 27, 3988-4002.e5.	6.4	32

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19	Detection of Epstein-Barr Virus Infection in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2019, 11, 759.	3.7	36
20	Defining the dynamic chromatin landscape of mouse nephron progenitors. <i>Biology Open</i> , 2019, 8, .	1.2	21
21	SpliceV: analysis and publication quality printing of linear and circular RNA splicing, expression and regulation. <i>BMC Bioinformatics</i> , 2019, 20, 231.	2.6	10
22	Gammaherpesvirus RNAs Come Full Circle. <i>MBio</i> , 2019, 10, .	4.1	23
23	A positive role of c-Myc in regulating androgen receptor and its splice variants in prostate cancer. <i>Oncogene</i> , 2019, 38, 4977-4989.	5.9	80
24	Comparative Analysis of Gammaherpesvirus Circular RNA Repertoires: Conserved and Unique Viral Circular RNAs. <i>Journal of Virology</i> , 2019, 93, .	3.4	58
25	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, 6.	2.6	18
26	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.	2.5	5
27	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. <i>Blood</i> , 2019, 134, 1288-1288.	1.4	0
28	Connivance, Complicity, or Collusion? The Role of Noncoding RNAs in Promoting Gammaherpesvirus Tumorigenesis. <i>Trends in Cancer</i> , 2018, 4, 729-740.	7.4	8
29	Driver gene mutations based clustering of tumors: methods and applications. <i>Bioinformatics</i> , 2018, 34, i404-i411.	4.1	6
30	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.	2.8	11
31	The Epstein Barr virus circRNAome. <i>PLoS Pathogens</i> , 2018, 14, e1007206.	4.7	112
32	Transactivation of human endogenous retrovirus K (HERV-K) by KSHV promotes Kaposi's sarcoma development. <i>Oncogene</i> , 2018, 37, 4534-4545.	5.9	43
33	Reduced mitochondrial activity in colonocytes facilitates AMPK-dependent inflammation. <i>FASEB Journal</i> , 2017, 31, 2013-2025.	0.5	24
34	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.	1.3	7
35	Significant Prognostic Features and Patterns of Somatic TP53 Mutations in Human Cancers. <i>Cancer Informatics</i> , 2017, 16, 117693511769126.	1.9	16
36	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.	3.3	37

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37	MALT1 Inhibition Is Efficacious in Both Naïve and Ibrutinib-Resistant Chronic Lymphocytic Leukemia. <i>Cancer Research</i> , 2017, 77, 7038-7048.	0.9	41
38	Lipids, lipid metabolism and Kaposi's sarcoma-associated herpesvirus pathogenesis. <i>Virologica Sinica</i> , 2017, 32, 369-375.	3.0	6
39	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.	4.6	29
40	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.	2.8	34
41	Arsenic trioxide inhibits EBV reactivation and promotes cell death in EBV-positive lymphoma cells. <i>Virology Journal</i> , 2017, 14, 121.	3.4	8
42	Interplay between Cytoplasmic and Nuclear Androgen Receptor Splice Variants Mediates Castration Resistance. <i>Molecular Cancer Research</i> , 2017, 15, 59-68.	3.4	57
43	Analysis of EBV Transcription Using High-Throughput RNA Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1532, 105-121.	0.9	2
44	A comprehensive approach to expression of L1 loci. <i>Nucleic Acids Research</i> , 2017, 45, e31-e31.	14.5	86
45	Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. <i>Oncotarget</i> , 2017, 8, 38399-38412.	1.8	11
46	In colonic $\rho^0$ cells reduced mitochondrial function mediates transcriptomic alterations associated with cancer. <i>Oncoscience</i> , 2017, 4, 189-198.	2.2	11
47	Gene network analysis reveals a novel 22-gene signature of carbon metabolism in hepatocellular carcinoma. <i>Oncotarget</i> , 2016, 7, 49232-49245.	1.8	17
48	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.	5.2	57
49	TFIIIS.h, a new target of p53, regulates transcription efficiency of pro-apoptotic bax gene. <i>Scientific Reports</i> , 2016, 6, 23542.	3.3	13
50	Methylation status and AP1 elements are involved in EBV-mediated miR-155 expression in EBV positive lymphoma cells. <i>Virology</i> , 2016, 494, 158-167.	2.4	20
51	Global transcript structure resolution of high gene density genomes through multi-platform data integration. <i>Nucleic Acids Research</i> , 2016, 44, e145-e145.	14.5	96
52	Mutant TP53 disrupts age-related accumulation patterns of somatic mutations in multiple cancer types. <i>Cancer Genetics</i> , 2016, 209, 376-380.	0.4	10
53	Secreted Oral Epithelial Cell Membrane Vesicles Induce Epstein-Barr Virus Reactivation in Latently Infected B Cells. <i>Journal of Virology</i> , 2016, 90, 3469-3479.	3.4	32
54	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.	2.2	16

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55	SON and Its Alternatively Spliced Isoforms Control MLL Complex-Mediated H3K4me3 and Transcription of Leukemia-Associated Genes. <i>Molecular Cell</i> , 2016, 61, 859-873.	9.7	41
56	RNA-sequencing study of peripheral blood monocytes in chronic periodontitis. <i>Gene</i> , 2016, 581, 152-160.	2.2	21
57	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.	2.3	3
58	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.	1.8	18
59	Nerve growth factor receptor negates the tumor suppressor p53 as a feedback regulator. <i>ELife</i> , 2016, 5, .	6.0	62
60	Targeting MALT1 with the Small Molecule Inhibitor MI2 Induces a Caspase-Dependent Apoptosis and Inhibits the NF- $\kappa$ B Pathway in Chronic Lymphocytic Leukemia Primary Cells. <i>Blood</i> , 2016, 128, 1597-1597.	1.4	0
61	Androgen Receptor Splice Variants Dimerize to Transactivate Target Genes. <i>Cancer Research</i> , 2015, 75, 3663-3671.	0.9	158
62	Effects of the Endocrine-Disrupting Chemical DDT on Self-Renewal and Differentiation of Human Mesenchymal Stem Cells. <i>Environmental Health Perspectives</i> , 2015, 123, 42-48.	6.0	59
63	Latent Expression of the Epstein-Barr Virus (EBV)-Encoded Major Histocompatibility Complex Class I TAP Inhibitor, <i>BNLF2a</i> , in EBV-Positive Gastric Carcinomas. <i>Journal of Virology</i> , 2015, 89, 10110-10114.	3.4	30
64	New Noncoding Lytic Transcripts Derived from the Epstein-Barr Virus Latency Origin of Replication, <i>oriP</i> , Are Hyperedited, Bind the Paraspeckle Protein, NONO/p54nrb, and Support Viral Lytic Transcription. <i>Journal of Virology</i> , 2015, 89, 7120-7132.	3.4	46
65	Elevated expression of long intergenic non-coding RNA HOTAIR in a basal-like variant of MCF7 breast cancer cells. <i>Molecular Carcinogenesis</i> , 2015, 54, 1656-1667.	2.7	35
66	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, 713-729.	3.4	61
67	Somatic Mutations Favorable to Patient Survival Are Predominant in Ovarian Carcinomas. <i>PLoS ONE</i> , 2014, 9, e112561.	2.5	3
68	GE-33 * A 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.	1.2	0
69	Microbial Contamination in Next Generation Sequencing: Implications for Sequence-Based Analysis of Clinical Samples. <i>PLoS Pathogens</i> , 2014, 10, e1004437.	4.7	159
70	Expanding the Conversation on High-Throughput Virome Sequencing Standards To Include Consideration of Microbial Contamination Sources. <i>MBio</i> , 2014, 5, e01989.	4.1	2
71	Global Bidirectional Transcription of the Epstein-Barr Virus Genome during Reactivation. <i>Journal of Virology</i> , 2014, 88, 1604-1616.	3.4	57
72	RNA CoMPASS: A Dual Approach for Pathogen and Host Transcriptome Analysis of RNA-Seq Datasets. <i>PLoS ONE</i> , 2014, 9, e89445.	2.5	38

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73	Targeting Sphingosine Kinase Induces Apoptosis and Tumor Regression for KSHV-Associated Primary Effusion Lymphoma. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 154-164.	4.1	52
74	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.	2.7	45
75	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, 353-364.	1.9	16
76	S100P/RAGE signaling regulates microRNA-155 expression via AP-1 activation in colon cancer. <i>Experimental Cell Research</i> , 2013, 319, 2081-2090.	2.6	48
77	Whole-Genome Sequencing of the Akata and Mutu Epstein-Barr Virus Strains. <i>Journal of Virology</i> , 2013, 87, 1172-1182.	3.4	98
78	OncomiR Addiction Is Generated by a miR-155 Feedback Loop in Theileria-Transformed Leukocytes. <i>PLoS Pathogens</i> , 2013, 9, e1003222.	4.7	54
79	Differences in Gastric Carcinoma Microenvironment Stratify According to EBV Infection Intensity: Implications for Possible Immune Adjuvant Therapy. <i>PLoS Pathogens</i> , 2013, 9, e1003341.	4.7	140
80	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, 13059-13062.	3.4	35
81	The Sequence Structures of Human MicroRNA Molecules and Their Implications. <i>PLoS ONE</i> , 2013, 8, e54215.	2.5	56
82	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.	2.5	4
83	Targeting Sphingosine Kinase Induces Apoptosis and Regression Of Virus-Associated Lymphoma In Vivo. <i>Blood</i> , 2013, 122, 4414-4414.	1.4	0
84	Differential regulation of microRNA-146a and microRNA-146b-5p in human retinal pigment epithelial cells by interleukin-1 $\beta$ , tumor necrosis factor- $\alpha$ , and interferon- $\beta$ . <i>Molecular Vision</i> , 2013, 19, 737-50.	1.1	73
85	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, 2970-2977.	3.4	27
86	Identification of New Viral Genes and Transcript Isoforms during Epstein-Barr Virus Reactivation using RNA-Seq. <i>Journal of Virology</i> , 2012, 86, 1458-1467.	3.4	54
87	The microRNA expression associated with morphogenesis of breast cancer cells in three-dimensional organotypic culture. <i>Oncology Reports</i> , 2012, 28, 117-126.	2.6	16
88	Comparative profiling of miRNA expression of lung adenocarcinoma cells in two-dimensional and three-dimensional cultures. <i>Gene</i> , 2012, 511, 143-150.	2.2	18
89	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.	2.5	38
90	miRNA-Mediated Relationships between Cis-SNP Genotypes and Transcript Intensities in Lymphocyte Cell Lines. <i>PLoS ONE</i> , 2012, 7, e31429.	2.5	15

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91	miRNAs in the pathogenesis of oncogenic human viruses. <i>Cancer Letters</i> , 2011, 305, 186-199.	7.2	55
92	SAMMate: a GUI tool for processing short read alignments in SAM/BAM format. <i>Source Code for Biology and Medicine</i> , 2011, 6, 2.	1.7	54
93	Post-transcriptional up-regulation of miR-21 by type I collagen. <i>Molecular Carcinogenesis</i> , 2011, 50, 563-570.	2.7	28
94	The Epstein-Barr Virus Latent Membrane Protein 1 and Transforming Growth Factor- $\beta$ 1 Synergistically Induce Epithelial-Mesenchymal Transition in Lung Epithelial Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2011, 44, 852-862.	2.9	56
95	Isoform-level microRNA-155 target prediction using RNA-seq. <i>Nucleic Acids Research</i> , 2011, 39, e61-e61.	14.5	27
96	Transcriptome and targetome analysis in MIR155 expressing cells using RNA-seq. <i>Rna</i> , 2010, 16, 1610-1622.	3.5	53
97	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, 13053-13058.	3.4	43
98	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, 7892-7897.	3.4	44
99	MicroRNA miR-155 Inhibits Bone Morphogenetic Protein (BMP) Signaling and BMP-Mediated Epstein-Barr Virus Reactivation. <i>Journal of Virology</i> , 2010, 84, 6318-6327.	3.4	89
100	<i>E2F1</i> Expression Is Deregulated and Plays an Oncogenic Role in Sporadic Burkitt's Lymphoma. <i>Cancer Research</i> , 2009, 69, 4052-4058.	0.9	39
101	A novel factor distinct from E2F mediates C-MYC promoter activation through its E2F element during exit from quiescence. <i>Carcinogenesis</i> , 2009, 30, 440-448.	2.8	13
102	Epstein-Barr virus growth/latency III program alters cellular microRNA expression. <i>Virology</i> , 2008, 382, 257-266.	2.4	140
103	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, 5295-5306.	3.4	233
104	B-cell Receptor Activation Induces BIC/miR-155 Expression through a Conserved AP-1 Element. <i>Journal of Biological Chemistry</i> , 2008, 283, 2654-2662.	3.4	200
105	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, 1946-1958.	3.4	273
106	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, 18372-18377.	7.1	171
107	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, 511-519.	5.0	39
108	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, 11962-11971.	3.4	17

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109	Histone deacetylase inhibitors prevent oxidative neuronal death independent of expanded polyglutamine repeats via an Sp1-dependent pathway. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4281-4286.	7.1	241
110	Cell Cycle Analysis of Epstein-Barr Virus-Infected Cells following Treatment with Lytic Cycle-Inducing Agents. Journal of Virology, 2001, 75, 4482-4489.	3.4	47
111	Herpesvirus Lytic Replication and the Cell Cycle: Arresting New Developments. Journal of Virology, 2001, 75, 4475-4481.	3.4	156
112	Transfection-Mediated Cell-Cycle Signaling: Considerations for Transient Transfection-Based Cell-Cycle Studies. Analytical Biochemistry, 1999, 272, 171-181.	2.4	30
113	Distinct Cellular Factors Regulate the c- <i>myb</i> Promoter through Its E2F Element. Molecular and Cellular Biology, 1999, 19, 8442-8450.	2.3	41
114	Genetic Dissection of Cell Growth Arrest Functions Mediated by the Epstein-Barr Virus Lytic Gene Product, Zta. Journal of Virology, 1999, 73, 9029-9038.	3.4	53
115	G0/G1 Growth Arrest Mediated by a Region Encompassing the Basic Leucine Zipper (bZIP) Domain of the Epstein-Barr Virus Transactivator Zta. Journal of Biological Chemistry, 1996, 271, 31799-31802.	3.4	64
116	Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F-like properties. Cell, 1992, 70, 351-364.	28.9	916
117	Sequence, structure and promoter characterization of the human thymidine kinase gene. Gene, 1987, 52, 267-277.	2.2	133