

# Erik Larsson Lekholm

## List of Publications by Year in descending order

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Version: 2024-02-01

77  
papers

29,395  
citations

117625

34  
h-index

82547

72  
g-index

81  
all docs

81  
docs citations

81  
times ranked

43274  
citing authors

#	ARTICLE	IF	CITATIONS
1	A clinically annotated post-mortem approach to study multi-organ somatic mutational clonality in normal tissues. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
2	Mitochondrial DNA variants in inclusion body myositis characterized by deep sequencing. <i>Brain Pathology</i> , 2021, 31, e12931.	4.1	17
3	Non-coding driver mutations in human cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 500-509.	28.4	59
4	Independent somatic evolution underlies clustered neuroendocrine tumors in the human small intestine. <i>Nature Communications</i> , 2021, 12, 6367.	12.8	11
5	DamID transcriptional profiling identifies the Snail/Scratch transcription factor Kahuli as an Alk target in the <i>Drosophila</i> visceral mesoderm. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	2
6	Patient-derived scaffolds uncover breast cancer promoting properties of the microenvironment. <i>Biomaterials</i> , 2020, 235, 119705.	11.4	41
7	MicroRNA-708 is a novel regulator of the Hoxa9 program in myeloid cells. <i>Leukemia</i> , 2020, 34, 1253-1265.	7.2	12
8	Systematic investigation of promoter substitutions resulting from somatic intrachromosomal structural alterations in diverse human cancers. <i>Scientific Reports</i> , 2020, 10, 18176.	3.3	0
9	Characterization of cell-free breast cancer patient-derived scaffolds using liquid chromatography-mass spectrometry/mass spectrometry data and RNA sequencing data. <i>Data in Brief</i> , 2020, 31, 105860.	1.0	5
10	Molecular profiling of driver events in metastatic uveal melanoma. <i>Nature Communications</i> , 2020, 11, 1894.	12.8	108
11	Deep sequencing of mitochondrial DNA and characterization of a novel POLG mutation in a patient with arPEO. <i>Neurology: Genetics</i> , 2020, 6, e391.	1.9	8
12	Accurate mapping of mitochondrial DNA deletions and duplications using deep sequencing. <i>PLoS Genetics</i> , 2020, 16, e1009242.	3.5	41
13	Accurate mapping of mitochondrial DNA deletions and duplications using deep sequencing. , 2020, 16, e1009242.		0
14	Accurate mapping of mitochondrial DNA deletions and duplications using deep sequencing. , 2020, 16, e1009242.		0
15	Accurate mapping of mitochondrial DNA deletions and duplications using deep sequencing. , 2020, 16, e1009242.		0
16	Accurate mapping of mitochondrial DNA deletions and duplications using deep sequencing. , 2020, 16, e1009242.		0
17	The MTH1 inhibitor TH588 is a microtubule-modulating agent that eliminates cancer cells by activating the mitotic surveillance pathway. <i>Scientific Reports</i> , 2019, 9, 14667.	3.3	19
18	Identification of Breast Cancer Stem Cell Related Genes Using Functional Cellular Assays Combined With Single-Cell RNA Sequencing in MDA-MB-231 Cells. <i>Frontiers in Genetics</i> , 2019, 10, 500.	2.3	26

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19	Targeting Filamin A Reduces Macrophage Activity and Atherosclerosis. <i>Circulation</i> , 2019, 140, 67-79.	1.6	38
20	Copy-choice recombination during mitochondrial L-strand synthesis causes DNA deletions. <i>Nature Communications</i> , 2019, 10, 759.	12.8	34
21	Intragenomic variability and extended sequence patterns in the mutational signature of ultraviolet light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20411-20417.	7.1	22
22	Lack of detectable neoantigen depletion signals in the untreated cancer genome. <i>Nature Genetics</i> , 2019, 51, 1741-1748.	21.4	59
23	DNA polymerase $\delta$ contributes to genome-wide lagging strand synthesis. <i>Nucleic Acids Research</i> , 2019, 47, 2425-2435.	14.5	17
24	A Catalogue of Putative <i>cis</i> -Regulatory Interactions Between Long Non-coding RNAs and Proximal Coding Genes Based on Correlative Analysis Across Diverse Human Tumors. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2019-2025.	1.8	3
25	Topoisomerase 3 $\beta$ Is Required for Decatenation and Segregation of Human mtDNA. <i>Molecular Cell</i> , 2018, 69, 9-23.e6.	9.7	102
26	Mutational Signature and Transcriptomic Classification Analyses as the Decisive Diagnostic Tools for a Cancer of Unknown Primary. <i>JCO Precision Oncology</i> , 2018, 2, 1-25.	3.0	10
27	Phosphoproteome and gene expression profiling of ALK inhibition in neuroblastoma cell lines reveals conserved oncogenic pathways. <i>Science Signaling</i> , 2018, 11, .	3.6	36
28	Elevated pyrimidine dimer formation at distinct genomic bases underlies promoter mutation hotspots in UV-exposed cancers. <i>PLoS Genetics</i> , 2018, 14, e1007849.	3.5	60
29	An antisense RNA capable of modulating the expression of the tumor suppressor microRNA-34a. <i>Cell Death and Disease</i> , 2018, 9, 736.	6.3	7
30	Clinical response of the novel activating ALK-I1171T mutation in neuroblastoma to the ALK inhibitor ceritinib. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002550.	1.2	47
31	Transcriptomic Characterization of the Human Cell Cycle in Individual Unsynchronized Cells. <i>Journal of Molecular Biology</i> , 2017, 429, 3909-3924.	4.2	11
32	Tumour virology in the era of high-throughput genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160265.	4.0	26
33	Mutational Signatures Are Critical for Proper Estimation of Purifying Selection Pressures in Cancer Somatic Mutation Data When Using the dN/dS Metric. <i>Frontiers in Genetics</i> , 2017, 8, 74.	2.3	33
34	Recurrent promoter mutations in melanoma are defined by an extended context-specific mutational signature. <i>PLoS Genetics</i> , 2017, 13, e1006773.	3.5	67
35	Transcriptional profiling of the rat nucleus accumbens after modest or high alcohol exposure. <i>PLoS ONE</i> , 2017, 12, e0181084.	2.5	7
36	Global analysis of somatic structural genomic alterations and their impact on gene expression in diverse human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13768-13773.	7.1	50

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37	Pan-cancer transcriptomic analysis associates long non-coding RNAs with key mutational driver events. <i>Nature Communications</i> , 2016, 7, 13197.	12.8	54
38	FocalScan: Scanning for altered genes in cancer based on coordinated DNA and RNA change. <i>Nucleic Acids Research</i> , 2016, 44, gkw674.	14.5	3
39	Searching the Evolutionary Origin of Epithelial Mucus Protein Componentsâ€”Mucins and FCGBP. <i>Molecular Biology and Evolution</i> , 2016, 33, 1921-1936.	8.9	104
40	Somatic Mutation Patterns in Hemizygous Genomic Regions Unveil Purifying Selection during Tumor Evolution. <i>PLoS Genetics</i> , 2016, 12, e1006506.	3.5	24
41	Absence of cytomegalovirus in highâ€œcoverage DNA sequencing of human glioblastoma multiforme. <i>International Journal of Cancer</i> , 2015, 136, 977-981.	5.1	35
42	The gut microbiota modulates host amino acid and glutathione metabolism in mice. <i>Molecular Systems Biology</i> , 2015, 11, 834.	7.2	291
43	Simultaneous DNA and RNA Mapping of Somatic Mitochondrial Mutations across Diverse Human Cancers. <i>PLoS Genetics</i> , 2015, 11, e1005333.	3.5	102
44	Deficiency of filamin A in endothelial cells impairs left ventricular remodelling after myocardial infarction. <i>Cardiovascular Research</i> , 2015, 105, 151-159.	3.8	12
45	The Cell Cycle Regulator CCDC6 Is a Key Target of RNA-Binding Protein EWS. <i>PLoS ONE</i> , 2015, 10, e0119066.	2.5	9
46	Temporal separation of replication and transcription during S-phase progression. <i>Cell Cycle</i> , 2014, 13, 3241-3248.	2.6	39
47	LCâ€œMS/MS characterization of combined glycogenin-1 and glycogenin-2 enzymatic activities reveals their self-glucosylation preferences. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 398-405.	2.3	11
48	Identification of the RNA recognition element of the RBPMS family of RNA-binding proteins and their transcriptome-wide mRNA targets. <i>Rna</i> , 2014, 20, 1090-1102.	3.5	64
49	Antioxidants Accelerate Lung Cancer Progression in Mice. <i>Science Translational Medicine</i> , 2014, 6, 221ra15.	12.4	663
50	Systematic analysis of noncoding somatic mutations and gene expression alterations across 14 tumor types. <i>Nature Genetics</i> , 2014, 46, 1258-1263.	21.4	269
51	The Risk-Associated Long Noncoding RNA NBAT-1 Controls Neuroblastoma Progression by Regulating Cell Proliferation and Neuronal Differentiation. <i>Cancer Cell</i> , 2014, 26, 722-737.	16.8	287
52	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, pl1.	3.6	11,344
53	The landscape of viral expression and host gene fusion and adaptation in human cancer. <i>Nature Communications</i> , 2013, 4, 2513.	12.8	274
54	MicroRNA-24 Suppression of N-Deacetylase/N-Sulfotransferase-1 (NDST1) Reduces Endothelial Cell Responsiveness to Vascular Endothelial Growth Factor A (VEGFA). <i>Journal of Biological Chemistry</i> , 2013, 288, 25956-25963.	3.4	28

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55	Hypertension and Genetic Variation in Endothelial-Specific Genes. <i>PLoS ONE</i> , 2013, 8, e62035.	2.5	9
56	Zinc Finger Protein 148 Is Dispensable for Primitive and Definitive Hematopoiesis in Mice. <i>PLoS ONE</i> , 2013, 8, e70022.	2.5	5
57	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. <i>PLoS ONE</i> , 2013, 8, e80306.	2.5	90
58	Zfp148 Deficiency Causes Lung Maturation Defects and Lethality in Newborn Mice That Are Rescued by Deletion of p53 or Antioxidant Treatment. <i>PLoS ONE</i> , 2013, 8, e55720.	2.5	16
59	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	9.4	12,801
60	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. <i>Gut</i> , 2012, 61, 1124-1131.	12.1	321
61	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	2.5	104
62	The Non-Coding Oncogene: A Case of Missing DNA Evidence?. <i>Frontiers in Genetics</i> , 2012, 3, 170.	2.3	26
63	Superoxide dismutase 1 (SOD1) is a target for a small molecule identified in a screen for inhibitors of the growth of lung adenocarcinoma cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16375-16380.	7.1	124
64	Vascular endothelial growth factor B controls endothelial fatty acid uptake. <i>Nature</i> , 2010, 464, 917-921.	27.8	423
65	Hypoxic regulation of secreted proteoglycans in macrophages. <i>Glycobiology</i> , 2010, 20, 33-40.	2.5	48
66	Cyclosporine Does Not Reduce Myocardial Infarct Size in a Porcine Ischemia-Reperfusion Model. <i>Journal of Cardiovascular Pharmacology and Therapeutics</i> , 2010, 15, 182-189.	2.0	52
67	mRNA turnover rate limits siRNA and microRNA efficacy. <i>Molecular Systems Biology</i> , 2010, 6, 433.	7.2	94
68	Target mRNA abundance dilutes microRNA and siRNA activity. <i>Molecular Systems Biology</i> , 2010, 6, 363.	7.2	299
69	Endothelial cells are activated during hypoxia via endoglin/ALK-1/SMAD1/5 signaling in vivo and in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2010, 392, 283-288.	2.1	44
70	Transcriptional profiling reveals a critical role for tyrosine phosphatase VEâ€PTP in regulation of VEGFR2 activity and endothelial cell morphogenesis. <i>FASEB Journal</i> , 2009, 23, 1490-1502.	0.5	98
71	Discovery of microvascular miRNAs using public gene expression data: miR-145 is expressed in pericytes and is a regulator of Fli1. <i>Genome Medicine</i> , 2009, 1, 108.	8.2	82
72	Do two mutually exclusive gene modules define the phenotypic diversity of mammalian smooth muscle?. <i>Molecular Genetics and Genomics</i> , 2008, 280, 127-37.	2.1	15

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73	Identification of a Core Set of 58 Gene Transcripts With Broad and Specific Expression in the Microvasculature. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2008, 28, 1469-1476.	2.4	95
74	Smooth Muscle Expression of Lipoma Preferred Partner Is Mediated by an Alternative Intronic Promoter That Is Regulated by Serum Response Factor/Myocardin. <i>Circulation Research</i> , 2008, 103, 61-69.	4.5	17
75	RhoA-Dependent Vascular Smooth Muscle Cell-Specific Transcription. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2007, 27, 448-449.	2.4	2
76	HeliCis: a DNA motif discovery tool for colocalized motif pairs with periodic spacing. <i>BMC Bioinformatics</i> , 2007, 8, 418.	2.6	9
77	New Insights to Vascular Smooth Muscle Cell and Pericyte Differentiation of Mouse Embryonic Stem Cells In Vitro. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2006, 26, 1457-1464.	2.4	26