Erik Larsson Lekholm

List of Publications by Year
in descending order

77 papers	29,395 citations	117453 34 h-index	82410 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. Scientific Reports, 2022, 12, .	1.6	2
2	Mitochondrial DNA variants in inclusion body myositis characterized by deep sequencing. Brain Pathology, 2021, 31, e12931.	2.1	17
3	Non-coding driver mutations in human cancer. Nature Reviews Cancer, 2021, 21, 500-509.	12.8	59
4	Independent somatic evolution underlies clustered neuroendocrine tumors in the human small intestine. Nature Communications, 2021, 12, 6367.	5.8	11
5	DamID transcriptional profiling identifies the Snail/Scratch transcription factor Kahuli as an Alk target in the Drosophila visceral mesoderm. Development (Cambridge), 2021, 148, .	1.2	2
6	Patient-derived scaffolds uncover breast cancer promoting properties of the microenvironment. Biomaterials, 2020, 235, 119705.	5.7	41
7	MicroRNA-708 is a novel regulator of the Hoxa9 program in myeloid cells. Leukemia, 2020, 34, 1253-1265.	3.3	12
8	Systematic investigation of promoter substitutions resulting from somatic intrachromosomal structural alterations in diverse human cancers. Scientific Reports, 2020, 10, 18176.	1.6	0
9	Characterization of cell-free breast cancer patient-derived scaffolds using liquid chromatography-mass spectrometry/mass spectrometry data and RNA sequencing data. Data in Brief, 2020, 31, 105860.	0.5	5
10	Molecular profiling of driver events in metastatic uveal melanoma. Nature Communications, 2020, 11, 1894.	5.8	108
11	Deep sequencing of mitochondrial DNA and characterization of a novel POLG mutation in a patient with arPEO. Neurology: Genetics, 2020, 6, e391.	0.9	8
12	Accurate mapping of mitochondrial DNA deletions and duplications using deep sequencing. PLoS Genetics, 2020, 16, e1009242.	1.5	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. Scientific Reports, 2019, 9, 14667.	1.6	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. Frontiers in Genetics, 2019, 10, 500.	1.1	26

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19	Targeting Filamin A Reduces Macrophage Activity and Atherosclerosis. Circulation, 2019, 140, 67-79.	1.6	38
20	Copy-choice recombination during mitochondrial L-strand synthesis causes DNA deletions. Nature Communications, 2019, 10, 759.	5.8	34
21	Intragenomic variability and extended sequence patterns in the mutational signature of ultraviolet light. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20411-20417.	3.3	22
22	Lack of detectable neoantigen depletion signals in the untreated cancer genome. Nature Genetics, 2019, 51, 1741-1748.	9.4	59
23	DNA polymerase Î· contributes to genome-wide lagging strand synthesis. Nucleic Acids Research, 2019, 47, 2425-2435.	6.5	17
24	A Catalogue of Putative cis-Regulatory Interactions Between Long Non-coding RNAs and Proximal Coding Genes Based on Correlative Analysis Across Diverse Human Tumors. G3: Genes, Genomes, Genetics, 2018, 8, 2019-2025.	0.8	3
25	Topoisomerase 3Î± Is Required for Decatenation and Segregation of Human mtDNA. Molecular Cell, 2018, 69, 9-23.e6.	4.5	102
26	Mutational Signature and Transcriptomic Classification Analyses as the Decisive Diagnostic Tools for a Cancer of Unknown Primary. JCO Precision Oncology, 2018, 2, 1-25.	1.5	10
27	Phosphoproteome and gene expression profiling of ALK inhibition in neuroblastoma cell lines reveals conserved oncogenic pathways. Science Signaling, 2018, 11, .	1.6	36
28	Elevated pyrimidine dimer formation at distinct genomic bases underlies promoter mutation hotspots in UV-exposed cancers. PLoS Genetics, 2018, 14, e1007849.	1.5	60
29	An antisense RNA capable of modulating the expression of the tumor suppressor microRNA-34a. Cell Death and Disease, 2018, 9, 736.	2.7	7
30	Clinical response of the novel activating ALK-I1171T mutation in neuroblastoma to the ALK inhibitor ceritinib. Journal of Physical Education and Sports Management, 2018, 4, a002550.	0.5	47
31	Transcriptomic Characterization of the Human Cell Cycle in Individual Unsynchronized Cells. Journal of Molecular Biology, 2017, 429, 3909-3924.	2.0	11
32	Tumour virology in the era of high-throughput genomics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160265.	1.8	26
33	Mutational Signatures Are Critical for Proper Estimation of Purifying Selection Pressures in Cancer Somatic Mutation Data When Using the dN/dS Metric. Frontiers in Genetics, 2017, 8, 74.	1.1	33
34	Recurrent promoter mutations in melanoma are defined by an extended context-specific mutational signature. PLoS Genetics, 2017, 13, e1006773.	1.5	67
35	Transcriptional profiling of the rat nucleus accumbens after modest or high alcohol exposure. PLoS ONE, 2017, 12, e0181084.	1.1	7
36	Global analysis of somatic structural genomic alterations and their impact on gene expression in diverse human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13768-13773.	3.3	50

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37	Pan-cancer transcriptomic analysis associates long non-coding RNAs with key mutational driver events. Nature Communications, 2016, 7, 13197.	5.8	54
38	FocalScan: Scanning for altered genes in cancer based on coordinated DNA and RNA change. Nucleic Acids Research, 2016, 44, gkw674.	6.5	3
39	Searching the Evolutionary Origin of Epithelial Mucus Protein Componentsâ€"Mucins and FCGBP. Molecular Biology and Evolution, 2016, 33, 1921-1936.	3.5	104
40	Somatic Mutation Patterns in Hemizygous Genomic Regions Unveil Purifying Selection during Tumor Evolution. PLoS Genetics, 2016, 12, e1006506.	1.5	24
41	Absence of cytomegalovirus in highâ€coverage DNA sequencing of human glioblastoma multiforme. International Journal of Cancer, 2015, 136, 977-981.	2.3	35
42	The gut microbiota modulates host amino acid and glutathione metabolism in mice. Molecular Systems Biology, 2015, 11, 834.	3.2	291
43	Simultaneous DNA and RNA Mapping of Somatic Mitochondrial Mutations across Diverse Human Cancers. PLoS Genetics, 2015, 11, e1005333.	1.5	102
44	Deficiency of filamin A in endothelial cells impairs left ventricular remodelling after myocardial infarction. Cardiovascular Research, 2015, 105, 151-159.	1.8	12
45	The Cell Cycle Regulator CCDC6 Is a Key Target of RNA-Binding Protein EWS. PLoS ONE, 2015, 10, e0119066.	1.1	9
46	Temporal separation of replication and transcription during S-phase progression. Cell Cycle, 2014, 13, 3241-3248.	1.3	39
47	LCâ€"MS/MS characterization of combined glycogenin-1 and glycogenin-2 enzymatic activities reveals their self-glucosylation preferences. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 398-405.	1.1	11
48	Identification of the RNA recognition element of the RBPMS family of RNA-binding proteins and their transcriptome-wide mRNA targets. Rna, 2014, 20, 1090-1102.	1.6	64
49	Antioxidants Accelerate Lung Cancer Progression in Mice. Science Translational Medicine, 2014, 6, 221ra15.	5.8	663
50	Systematic analysis of noncoding somatic mutations and gene expression alterations across 14 tumor types. Nature Genetics, 2014, 46, 1258-1263.	9.4	269
51	The Risk-Associated Long Noncoding RNA NBAT-1 Controls Neuroblastoma Progression by Regulating Cell Proliferation and Neuronal Differentiation. Cancer Cell, 2014, 26, 722-737.	7.7	287
52	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. Science Signaling, 2013, 6, pl1.	1.6	11,344
53	The landscape of viral expression and host gene fusion and adaptation in human cancer. Nature Communications, 2013, 4, 2513.	5.8	274
54	MicroRNA-24 Suppression of N-Deacetylase/N-Sulfotransferase-1 (NDST1) Reduces Endothelial Cell Responsiveness to Vascular Endothelial Growth Factor A (VEGFA). Journal of Biological Chemistry, 2013, 288, 25956-25963.	1.6	28

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55	Hypertension and Genetic Variation in Endothelial-Specific Genes. PLoS ONE, 2013, 8, e62035.	1.1	9
56	Zinc Finger Protein 148 Is Dispensable for Primitive and Definitive Hematopoiesis in Mice. PLoS ONE, 2013, 8, e70022.	1.1	5
57	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. PLoS ONE, 2013, 8, e80306.	1.1	90
58	Zfp148 Deficiency Causes Lung Maturation Defects and Lethality in Newborn Mice That Are Rescued by Deletion of p53 or Antioxidant Treatment. PLoS ONE, 2013, 8, e55720.	1.1	16
59	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.	7.7	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. Gut, 2012, 61, 1124-1131.	6.1	321
61	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. PLoS ONE, 2012, 7, e34546.	1.1	104
62	The Non-Coding Oncogene: A Case of Missing DNA Evidence?. Frontiers in Genetics, 2012, 3, 170.	1.1	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. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16375-16380.	3.3	124
64	Vascular endothelial growth factor B controls endothelial fatty acid uptake. Nature, 2010, 464, 917-921.	13.7	423
65	Hypoxic regulation of secreted proteoglycans in macrophages. Glycobiology, 2010, 20, 33-40.	1.3	48
66	Cyclosporine Does Not Reduce Myocardial Infarct Size in a Porcine Ischemia-Reperfusion Model. Journal of Cardiovascular Pharmacology and Therapeutics, 2010, 15, 182-189.	1.0	52
67	mRNA turnover rate limits siRNA and microRNA efficacy. Molecular Systems Biology, 2010, 6, 433.	3.2	94
68	Target mRNA abundance dilutes microRNA and siRNA activity. Molecular Systems Biology, 2010, 6, 363.	3.2	299
69	Endothelial cells are activated during hypoxia via endoglin/ALK-1/SMAD1/5 signaling in vivo and in vitro. Biochemical and Biophysical Research Communications, 2010, 392, 283-288.	1.0	44
70	Transcriptional profiling reveals a critical role for tyrosine phosphatase VEâ€PTP in regulation of VEGFR2 activity and endothelial cell morphogenesis. FASEB Journal, 2009, 23, 1490-1502.	0.2	98
71	Discovery of microvascular miRNAs using public gene expression data: miR-145 is expressed in pericytes and is a regulator of Fli1. Genome Medicine, 2009, 1, 108.	3.6	82
72	Do two mutually exclusive gene modules define the phenotypic diversity of mammalian smooth muscle?. Molecular Genetics and Genomics, 2008, 280, 127-37.	1.0	15

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73	Identification of a Core Set of 58 Gene Transcripts With Broad and Specific Expression in the Microvasculature. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1469-1476.	1.1	95
74	Smooth Muscle Expression of Lipoma Preferred Partner Is Mediated by an Alternative Intronic Promoter That Is Regulated by Serum Response Factor/Myocardin. Circulation Research, 2008, 103, 61-69.	2.0	17
75	RhoA-Dependent Vascular Smooth Muscle Cellâ€“Specific Transcription. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 448-449.	1.1	2
76	HeliCis: a DNA motif discovery tool for colocalized motif pairs with periodic spacing. BMC Bioinformatics, 2007, 8, 418.	1.2	9
77	New Insights to Vascular Smooth Muscle Cell and Pericyte Differentiation of Mouse Embryonic Stem Cells In Vitro. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 1457-1464.	1.1	26