

Michal Mokry

List of Publications by Year in descending order

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Version: 2024-02-01

106
papers

6,830
citations

81900

39
h-index

69250

77
g-index

119
all docs

119
docs citations

119
times ranked

14404
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced single-cell RNA-seq workflow reveals coronary artery disease cellular cross-talk and candidate drug targets. <i>Atherosclerosis</i> , 2022, 340, 12-22.	0.8	35
2	Dynamic changes in chromatin accessibility are associated with the atherogenic transitioning of vascular smooth muscle cells. <i>Cardiovascular Research</i> , 2022, 118, 2792-2804.	3.8	17
3	Chromatin Immunoprecipitation Sequencing (ChIP-seq) Protocol for Small Amounts of Frozen Biobanked Cardiac. <i>Methods in Molecular Biology</i> , 2022, 2458, 97-111.	0.9	1
4	The Applications of Single-Cell RNA Sequencing in Atherosclerotic Disease. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 826103.	2.4	14
5	Intersecting single-cell transcriptomics and genome-wide association studies identifies crucial cell populations and candidate genes for atherosclerosis. <i>European Heart Journal Open</i> , 2022, 2, oeab043.	2.3	34
6	Proteomic and Functional Studies Reveal Detyrosinated Tubulin as Treatment Target in Sarcomere Mutation-Induced Hypertrophic Cardiomyopathy. <i>Circulation: Heart Failure</i> , 2021, 14, e007022.	3.9	58
7	Sex-Stratified Gene Regulatory Networks Reveal Female Key Driver Genes of Atherosclerosis Involved in Smooth Muscle Cell Phenotype Switching. <i>Circulation</i> , 2021, 143, 713-726.	1.6	61
8	A Unique Monocyte Transcriptome Discriminates Sickle Cell Disease From Other Hereditary Hemolytic Anemias and Shows the Particular Importance of Lipid and Interferon Signaling. <i>HemaSphere</i> , 2021, 5, e531.	2.7	2
9	Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. <i>European Heart Journal</i> , 2021, 42, 2000-2011.	2.2	49
10	Conserved human effector Treg cell transcriptomic and epigenetic signature in arthritic joint inflammation. <i>Nature Communications</i> , 2021, 12, 2710.	12.8	46
11	Activin-A Induces Early Differential Gene Expression Exclusively in Periodontal Ligament Fibroblasts from Fibrodysplasia Ossificans Progressiva Patients. <i>Biomedicines</i> , 2021, 9, 629.	3.2	8
12	Sex-dependent gene co-expression in the human body. <i>Scientific Reports</i> , 2021, 11, 18758.	3.3	11
13	Regulation of a progenitor gene program by SOX4 is essential for mammary tumor proliferation. <i>Oncogene</i> , 2021, 40, 6343-6353.	5.9	9
14	The changing landscape of the vulnerable plaque: a call for fine-tuning of preclinical models. <i>Vascular Pharmacology</i> , 2021, 141, 106924.	2.1	4
15	Very Early Onset Inflammatory Bowel Disease: A Clinical Approach With a Focus on the Role of Genetics and Underlying Immune Deficiencies. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 820-842.	1.9	100
16	Microanatomy of the Human Atherosclerotic Plaque by Single-Cell Transcriptomics. <i>Circulation Research</i> , 2020, 127, 1437-1455.	4.5	283
17	Prime editing for functional repair in patient-derived disease models. <i>Nature Communications</i> , 2020, 11, 5352.	12.8	134
18	H3K27ac acetylome signatures reveal the epigenomic reorganization in remodeled non-failing human hearts. <i>Clinical Epigenetics</i> , 2020, 12, 106.	4.1	20

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19	Stem Cell Pluripotency Genes Klf4 and Oct4 Regulate Complex SMC Phenotypic Changes Critical in Late-Stage Atherosclerotic Lesion Pathogenesis. <i>Circulation</i> , 2020, 142, 2045-2059.	1.6	221
20	Functional investigation of the coronary artery disease gene SVEP1. <i>Basic Research in Cardiology</i> , 2020, 115, 67.	5.9	25
21	Developmental programming in human umbilical cord vein endothelial cells following fetal growth restriction. <i>Clinical Epigenetics</i> , 2020, 12, 185.	4.1	8
22	Intrinsic transcriptomic sex differences in human endothelial cells at birth and in adults are associated with coronary artery disease targets. <i>Scientific Reports</i> , 2020, 10, 12367.	3.3	39
23	Transcriptome of airway neutrophils reveals an interferon response in life-threatening respiratory syncytial virus infection. <i>Clinical Immunology</i> , 2020, 220, 108593.	3.2	21
24	Proteomic profiling of a large cohort of HCM patients: Genotype-specific protein changes. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 140, 7.	1.9	0
25	Microinjection induces changes in the transcriptome of bovine oocytes. <i>Scientific Reports</i> , 2020, 10, 11211.	3.3	3
26	Chemotherapy and Inflammation Induced Damage of Intestinal Epithelium Is Associated with Increased T Cell Chemotaxis. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, S166-S167.	2.0	0
27	Human Tregs at the materno-fetal interface show site-specific adaptation reminiscent of tumor Tregs. <i>JCI Insight</i> , 2020, 5, .	5.0	21
28	Dissociation between hypertrophy and fibrosis in the left ventricle early after experimental kidney transplantation. <i>Journal of Hypertension</i> , 2020, 38, 489-503.	0.5	0
29	Indoxyl Sulfate Stimulates Angiogenesis by Regulating Reactive Oxygen Species Production via CYP1B1. <i>Toxins</i> , 2019, 11, 454.	3.4	11
30	Limited synergy of obesity and hypertension, prevalent risk factors in onset and progression of heart failure with preserved ejection fraction. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 6666-6678.	3.6	19
31	Transcriptome analysis reveals microvascular endothelial cell-dependent pericyte differentiation. <i>Scientific Reports</i> , 2019, 9, 15586.	3.3	22
32	Platelet RNA modules point to coronary calcification in asymptomatic women with former preeclampsia. <i>Atherosclerosis</i> , 2019, 291, 114-121.	0.8	5
33	The Atherosclerosis Risk Variant rs2107595 Mediates Allele-Specific Transcriptional Regulation of <i>HDAC9</i> via E2F3 and Rb1. <i>Stroke</i> , 2019, 50, 2651-2660.	2.0	38
34	Non-coding DNA in IBD: from sequence variation in DNA regulatory elements to novel therapeutic potential. <i>Gut</i> , 2019, 68, 928-941.	12.1	22
35	Integrative Functional Annotation of 52 Genetic Loci Influencing Myocardial Mass Identifies Candidate Regulatory Variants and Target Genes. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002328.	3.6	7
36	Cord-Blood-Stem-Cell-Derived Conventional Dendritic Cells Specifically Originate from CD115-Expressing Precursors. <i>Cancers</i> , 2019, 11, 181.	3.7	16

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37	Characterization of Endothelial and Smooth Muscle Cells From Different Canine Vessels. <i>Frontiers in Physiology</i> , 2019, 10, 101.	2.8	20
38	Histone modifications underlie monocyte dysregulation in patients with systemic sclerosis, underlining the treatment potential of epigenetic targeting. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 529-538.	0.9	40
39	Human Fetal TNF- α -Cytokine-Producing CD4+ Effector Memory T Cells Promote Intestinal Development and Mediate Inflammation Early in Life. <i>Immunity</i> , 2019, 50, 462-476.e8.	14.3	146
40	Single Cell Rna-Sequencing Identifies Numerous Cell Sub-Types And Suggests Lineage Plasticity In Human Atherosclerotic Plaques. <i>Atherosclerosis</i> , 2019, 287, e96-e97.	0.8	0
41	Transcriptomic and Epigenomic Profiling of Histone Deacetylase Inhibitor Treatment Reveals Distinct Gene Regulation Profiles Leading to Impaired Neutrophil Development. <i>HemaSphere</i> , 2019, 3, e270.	2.7	3
42	Transcriptional and epigenetic profiling of nutrient-deprived cells to identify novel regulators of autophagy. <i>Autophagy</i> , 2019, 15, 98-112.	9.1	34
43	Aerobic glycolysis is essential to remodel the epigenetic landscape and initiate transcription during T cell activation. <i>FASEB Journal</i> , 2019, 33, 802.18.	0.5	0
44	Epigenetic modification of the oxytocin and glucocorticoid receptor genes is linked to attachment avoidance in young adults. <i>Attachment and Human Development</i> , 2018, 20, 439-454.	2.1	42
45	Reversal of Sepsis-Like Features of Neutrophils by Interleukin-1 Blockade in Patients With Systemic Onset Juvenile Idiopathic Arthritis. <i>Arthritis and Rheumatology</i> , 2018, 70, 943-956.	5.6	39
46	Intracranial Aneurysm-Associated Single-Nucleotide Polymorphisms Alter Regulatory DNA in the Human Circle of Willis. <i>Stroke</i> , 2018, 49, 447-453.	2.0	16
47	Chromatin Conformation Links Distal Target Genes to CKD Loci. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 462-476.	6.1	21
48	An oviduct-on-a-chip provides an enhanced in vitro environment for zygote genome reprogramming. <i>Nature Communications</i> , 2018, 9, 4934.	12.8	93
49	Genetic Susceptibility Loci for Cardiovascular Disease and Their Impact on Atherosclerotic Plaques. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002115.	3.6	20
50	P094 PROINFLAMMATORY RESPONSES OF THE INTESTINAL EPITHELIUM ARE PREDOMINANTLY FACILITATED BY STEM CELLS. <i>Gastroenterology</i> , 2018, 154, S48-S49.	1.3	0
51	Smoking is Associated to DNA Methylation in Atherosclerotic Carotid Lesions. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002030.	3.6	23
52	Suppression of T cells by mesenchymal and cardiac progenitor cells is partly mediated via extracellular vesicles. <i>Heliyon</i> , 2018, 4, e00642.	3.2	39
53	H3K27 acetylation and gene expression analysis reveals differences in placental chromatin activity in fetal growth restriction. <i>Clinical Epigenetics</i> , 2018, 10, 85.	4.1	39
54	Megakaryocyte lineage development is controlled by modulation of protein acetylation. <i>PLoS ONE</i> , 2018, 13, e0196400.	2.5	3

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55	PD-1+CD8+ T cells are clonally expanding effectors in human chronic inflammation. <i>Journal of Clinical Investigation</i> , 2018, 128, 4669-4681.	8.2	98
56	Global transcriptional analysis identifies a novel role for SOX4 in tumor-induced angiogenesis. <i>ELife</i> , 2018, 7, .	6.0	32
57	Additional Candidate Genes for Human Atherosclerotic Disease Identified Through Annotation Based on Chromatin Organization. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	17
58	Epidermal Growth Factor Receptor Expression Licenses Type-2 Helper T Cells to Function in a T Cell Receptor-Independent Fashion. <i>Immunity</i> , 2017, 47, 710-722.e6.	14.3	82
59	Identification of differential co-expressed gene networks in early rheumatoid arthritis achieving sustained drug-free remission after treatment with a tocilizumab-based or methotrexate-based strategy. <i>Arthritis Research and Therapy</i> , 2017, 19, 170.	3.5	16
60	Enhancers reside in a unique epigenetic environment during early zebrafish development. <i>Genome Biology</i> , 2016, 17, 146.	8.8	41
61	Systematic analysis of chromatin interactions at disease associated loci links novel candidate genes to inflammatory bowel disease. <i>Genome Biology</i> , 2016, 17, 247.	8.8	39
62	Autoimmune disease-associated gene expression is reduced by BET-inhibition. <i>Genomics Data</i> , 2016, 7, 14-17.	1.3	6
63	Tissue-specific mutation accumulation in human adult stem cells during life. <i>Nature</i> , 2016, 538, 260-264.	27.8	759
64	An siRNA screen for ATG protein depletion reveals the extent of the unconventional functions of the autophagy proteome in virus replication. <i>Journal of Cell Biology</i> , 2016, 214, 619-635.	5.2	52
65	Genome-wide analysis reveals <i>NRP1</i> as a direct HIF1 α -E2F7 target in the regulation of motorneuron guidance <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2016, 44, 3549-3566.	14.5	29
66	Gene expression profiling in human precision cut liver slices in response to the FXR agonist obeticholic acid. <i>Journal of Hepatology</i> , 2016, 64, 1158-1166.	3.7	76
67	FOXP3 can modulate TAL1 transcriptional activity through interaction with LMO2. <i>Oncogene</i> , 2016, 35, 4141-4148.	5.9	9
68	Neonatal thymectomy reveals differentiation and plasticity within human naive T cells. <i>Journal of Clinical Investigation</i> , 2016, 126, 1126-1136.	8.2	76
69	E2f8 mediates tumor suppression in postnatal liver development. <i>Journal of Clinical Investigation</i> , 2016, 126, 2955-2969.	8.2	72
70	Extensive Association of Common Disease Variants with Regulatory Sequence. <i>PLoS ONE</i> , 2016, 11, e0165893.	2.5	7
71	The forkhead transcription factor FOXP1 represses human plasma cell differentiation. <i>Blood</i> , 2015, 126, 2098-2109.	1.4	42
72	A systematic analysis of genetic dilated cardiomyopathy reveals numerous ubiquitously expressed and muscle-specific genes. <i>European Journal of Heart Failure</i> , 2015, 17, 484-493.	7.1	58

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73	Interleukin-22 promotes intestinal-stem-cell-mediated epithelial regeneration. <i>Nature</i> , 2015, 528, 560-564.	27.8	818
74	Ascl2 Acts as an R-spondin/Wnt-Responsive Switch to Control Stemness in Intestinal Crypts. <i>Cell Stem Cell</i> , 2015, 16, 158-170.	11.1	217
75	Inhibition of Super-Enhancer Activity in Autoinflammatory Site-Derived T Cells Reduces Disease-Associated Gene Expression. <i>Cell Reports</i> , 2015, 12, 1986-1996.	6.4	98
76	Adult Stem Cells in the Small Intestine Are Intrinsically Programmed with Their Location-Specific Function. <i>Stem Cells</i> , 2014, 32, 1083-1091.	3.2	255
77	Wnt-induced transcriptional activation is exclusively mediated by TCF/LEF. <i>EMBO Journal</i> , 2014, 33, 146-156.	7.8	157
78	Many Inflammatory Bowel Disease Risk Loci Include Regions That Regulate Gene Expression in Immune Cells and the Intestinal Epithelium. <i>Gastroenterology</i> , 2014, 146, 1040-1047.	1.3	92
79	FOXP1 directly represses transcription of proapoptotic genes and cooperates with NF- κ B to promote survival of human B cells. <i>Blood</i> , 2014, 124, 3431-3440.	1.4	86
80	Major and Minor Group Rhinoviruses Elicit Differential Signaling and Cytokine Responses as a Function of Receptor-Mediated Signal Transduction. <i>PLoS ONE</i> , 2014, 9, e93897.	2.5	26
81	Systematic biases in DNA copy number originate from isolation procedures. <i>Genome Biology</i> , 2013, 14, R33.	9.6	39
82	Canonical Wnt Signaling Negatively Modulates Regulatory T Cell Function. <i>Immunity</i> , 2013, 39, 298-310.	14.3	183
83	FOXO3 Selectively Amplifies Enhancer Activity to Establish Target Gene Regulation. <i>Cell Reports</i> , 2013, 5, 1664-1678.	6.4	60
84	Genome-wide analysis of FOXO3 mediated transcription regulation through RNA polymerase II profiling. <i>Molecular Systems Biology</i> , 2013, 9, 638.	7.2	104
85	FOXP1 acts through a negative feedback loop to suppress FOXO-induced apoptosis. <i>Cell Death and Differentiation</i> , 2013, 20, 1219-1229.	11.2	51
86	E2F7 represses a network of oscillating cell cycle genes to control S-phase progression. <i>Nucleic Acids Research</i> , 2012, 40, 3511-3523.	14.5	91
87	Primary Colorectal Cancers and Their Subsequent Hepatic Metastases Are Genetically Different: Implications for Selection of Patients for Targeted Treatment. <i>Clinical Cancer Research</i> , 2012, 18, 688-699.	7.0	136
88	Integrated genome-wide analysis of transcription factor occupancy, RNA polymerase II binding and steady-state RNA levels identify differentially regulated functional gene classes. <i>Nucleic Acids Research</i> , 2012, 40, 148-158.	14.5	65
89	Diabetes Risk Gene and Wnt Effector Tcf7l2/TCF4 Controls Hepatic Response to Perinatal and Adult Metabolic Demand. <i>Cell</i> , 2012, 151, 1595-1607.	28.9	202
90	Multiplexed array-based and in-solution genomic enrichment for flexible and cost-effective targeted next-generation sequencing. <i>Nature Protocols</i> , 2011, 6, 1870-1886.	12.0	65

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91	Genomic DNA Pooling Strategy for Next-Generation Sequencing-Based Rare Variant Discovery in Abdominal Aortic Aneurysm Regions of Interest—Challenges and Limitations. <i>Journal of Cardiovascular Translational Research</i> , 2011, 4, 271-280.	2.4	20
92	Identification of factors required for meristem function in <i>Arabidopsis</i> using a novel next generation sequencing fast forward genetics approach. <i>BMC Genomics</i> , 2011, 12, 256.	2.8	45
93	Mutation discovery by targeted genomic enrichment of multiplexed barcoded samples. <i>Nature Methods</i> , 2010, 7, 913-915.	19.0	64
94	Accurate SNP and mutation detection by targeted custom microarray-based genomic enrichment of short-fragment sequencing libraries. <i>Nucleic Acids Research</i> , 2010, 38, e116-e116.	14.5	79
95	Comparing genome-wide chromatin profiles using ChIP-chip or ChIP-seq. <i>Bioinformatics</i> , 2010, 26, 1000-1006.	4.1	28
96	Efficient Double Fragmentation ChIP-seq Provides Nucleotide Resolution Protein-DNA Binding Profiles. <i>PLoS ONE</i> , 2010, 5, e15092.	2.5	39
97	Effect of equal daily doses achieved by different power densities of low-level laser therapy at 635Ånm on open skin wound healing in normal and corticosteroid-treated rats. <i>Lasers in Medical Science</i> , 2009, 24, 539-547.	2.1	64
98	Chemokines as Possible Targets in Modulation of the Secondary Damage After Acute Spinal Cord Injury: A Review. <i>Cellular and Molecular Neurobiology</i> , 2009, 29, 1025-1035.	3.3	30
99	Postsurgical Administration of Estradiol Benzoate Decreases Tensile Strength of Healing Skin Wounds in Ovariectomized Rats. <i>Journal of Surgical Research</i> , 2008, 147, 117-122.	1.6	10
100	The <i>Atp1a1</i> Gene From Inbred Dahl Salt Sensitive Rats Does Not Contain the A1079T Missense Transversion. <i>Hypertension</i> , 2008, 51, 922-927.	2.7	9
101	Simple method of open skin wound healing model in corticosteroid-treated and diabetic rats: standardization of semi-quantitative and quantitative histological assessments. <i>Veterinarni Medicina</i> , 2008, 53, 652-659.	0.6	77
102	Experimental Study on Predicting Skin Flap Necrosis by Fluorescence in the FAD and NADH Bands During Surgery. <i>Photochemistry and Photobiology</i> , 2007, 83, 1193-1196.	2.5	16
103	Histological Assessment of the Effect of Laser Irradiation on Skin Wound Healing in Rats. <i>Photomedicine and Laser Surgery</i> , 2006, 24, 480-488.	2.0	100
104	In Vivo Monitoring the Changes of Interstitial pH and FAD/NADH Ratio by Fluorescence Spectroscopy in Healing Skin Wounds. <i>Photochemistry and Photobiology</i> , 2006, 82, 793.	2.5	23
105	Stem Cells are the Principal Intestinal Epithelial Responders to Bacterial Antigens. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
106	Bipotent Liver Progenitors Depend on Glycolysis and Mitochondrial Pyruvate Oxidation for Stem Cell Functions. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0