Klaus Schughart

List of Publications by Year
in descending order

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		94433	102487
116	5,140	37	66
papers	citations	h-index	g-index

129	129	129	7485
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide, large-scale production of mutant mice by ENU mutagenesis. Nature Genetics, 2000, 25, 444-447.	21.4	658
2	The Expression of the MouseZic1, Zic2,andZic3Gene Suggests an Essential Role forZicGenes in Body Pattern Formation. Developmental Biology, 1997, 182, 299-313.	2.0	307
3	Mouse Hox-2.2 specifies thoracic segmental identity in Drosophila embryos and larvae. Cell, 1990, 63, 961-967.	28.9	200
4	Host Genetic Background Strongly Influences the Response to Influenza A Virus Infections. PLoS ONE, 2009, 4, e4857.	2.5	186
5	TMPRSS2 and TMPRSS4 Facilitate Trypsin-Independent Spread of Influenza Virus in Caco-2 Cells. Journal of Virology, 2010, 84, 10016-10025.	3.4	180
6	Tmprss2 Is Essential for Influenza H1N1 Virus Pathogenesis in Mice. PLoS Pathogens, 2013, 9, e1003774.	4.7	163
7	Long-Term Neuroinflammation Induced by Influenza A Virus Infection and the Impact on Hippocampal Neuron Morphology and Function. Journal of Neuroscience, 2018, 38, 3060-3080.	3.6	143
8	Early Evolutionary Origin of Major Homeodomain Sequence Classes. Genomics, 1993, 18, 54-70.	2.9	137
9	Lim1 Activity Is Required for Intermediate Mesoderm Differentiation in the Mouse Embryo. Developmental Biology, 2000, 223, 77-90.	2.0	126
10	Neutrophils-related host factors associated with severe disease and fatality in patients with influenza infection. Nature Communications, 2019, 10, 3422.	12.8	114
11	Directed mutagenesis of DNA cloned in filamentous phage: influence of hemimethylated GATC sites on marker recovery from restriction fragments. Nucleic Acids Research, 1982, 10, 6475-6485.	14.5	101
12	A novel immune biomarker IFI27 discriminates between influenza and bacteria in patients with suspected respiratory infection. European Respiratory Journal, 2017, 49, 1602098.	6.7	100
13	Retinoic Acid Receptor Î± Function in Vertebrate Limb Skeletogenesis: a Modulator of Chondrogenesis. Journal of Cell Biology, 1997, 136, 445-457.	5.2	93
14	Global Transcriptome Analysis in Influenza-Infected Mouse Lungs Reveals the Kinetics of Innate and Adaptive Host Immune Responses. PLoS ONE, 2012, 7, e41169.	2.5	93
15	Computer-based three-dimensional visualization of developmental gene expression. Nature Genetics, 2000, 25, 147-152.	21.4	81
16	Characterization and Expression Pattern of thefrizzledGeneFzd9,the Mouse Homolog ofFZD9Which Is Deleted in Williamsâ€“Beuren Syndrome. Genomics, 1999, 57, 235-248.	2.9	79
17	Pathogenicity of different PR8 influenza A virus variants in mice is determined by both viral and host factors. Virology, 2011, 412, 36-45.	2.4	75
18	Equivalence of Self- and Staff-Collected Nasal Swabs for the Detection of Viral Respiratory Pathogens. PLoS ONE, 2012, 7, e48508.	2.5	64

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19	Tumor cell-targeting by phage-displayed peptides. Cancer Gene Therapy, 2002, 9, 606-612.	4.6	62
20	A New Mouse Model Reveals a Critical Role for Host Innate Immunity in Resistance to Rift Valley Fever. Journal of Immunology, 2010, 185, 6146-6156.	0.8	59
21	Data-driven assessment of eQTL mapping methods. BMC Genomics, 2010, 11, 502.	2.8	55
22	PLAU inferred from a correlation network is critical for suppressor function of regulatory T cells. Molecular Systems Biology, 2012, 8, 624.	7.2	54
23	Deletion of <i>Irf3</i> and <i>Irf7</i> Genes in Mice Results in Altered Interferon Pathway Activation and Granulocyte-Dominated Inflammatory Responses to Influenza A Infection. Journal of Innate Immunity, 2017, 9, 145-161.	3.8	54
24	Gene expression changes in the host response between resistant and susceptible inbred mouse strains after influenza A infection. Microbes and Infection, 2010, 12, 309-318.	1.9	52
25	Sustaining the Data and Bioresource Commons. Science, 2010, 330, 592-593.	12.6	52
26	Isolation and Embryonic Expression of the Novel Mouse Gene Hic1, the Homologue of HIC1, a Candidate Gene for the Miller-Dieker Syndrome. Human Molecular Genetics, 1999, 8, 697-710.	2.9	50
27	Distinct gene loci control the host response to influenza H1N1 virus infection in a time-dependent manner. BMC Genomics, 2012, 13, 411.	2.8	50
28	IFIT2 Is an Effector Protein of Type I IFNâ€“Mediated Amplification of Lipopolysaccharide (LPS)-Induced TNF-Î± Secretion and LPS-Induced Endotoxin Shock. Journal of Immunology, 2013, 191, 3913-3921.	0.8	48
29	Influenza H3N2 infection of the collaborative cross founder strains reveals highly divergent host responses and identifies a unique phenotype in CAST/EiJ mice. BMC Genomics, 2016, 17, 143.	2.8	48
30	Novel Human Gene Transfer Vectors: Evaluation of Wild-Type and Recombinant Animal Adenoviruses in Human-Derived Cells. Human Gene Therapy, 1999, 10, 2587-2599.	2.7	47
31	ATR-FTIR spectroscopy reveals genomic loci regulating the tissue response in high fat diet fed BXD recombinant inbred mouse strains. BMC Genomics, 2013, 14, 386.	2.8	47
32	Protection from Severe Influenza Virus Infections in Mice Carrying theMx1Influenza Virus Resistance Gene Strongly Depends on Genetic Background. Journal of Virology, 2015, 89, 9998-10009.	3.4	47
33	TMPRSS11A activates the influenza A virus hemagglutinin and the MERS coronavirus spike protein and is insensitive against blockade by HAI-1. Journal of Biological Chemistry, 2018, 293, 13863-13873.	3.4	47
34	RNAseq expression analysis of resistant and susceptible mice after influenza A virus infection identifies novel genes associated with virus replication and important for host resistance to infection. BMC Genomics, 2015, 16, 655.	2.8	46
35	Inhibition of lung serine proteases in mice: a potentially new approach to control influenza infection. Virology Journal, 2011, 8, 27.	3.4	41
36	The Proteolytic Activation of (H3N2) Influenza A Virus Hemagglutinin Is Facilitated by Different Type II Transmembrane Serine Proteases. Journal of Virology, 2016, 90, 4298-4307.	3.4	40

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37	QTLminer: identifying genes regulating quantitative traits. BMC Bioinformatics, 2010, 11, 516.	2.6	39
38	Screening for dysmorphological abnormalitiesâ€"a powerful tool to isolate new mouse mutants. Mammalian Genome, 2000, 11, 528-530.	2.2	38
39	Generation and characterization of pilocarpine-sensitive C57BL/6 mice as a model of temporal lobe epilepsy. Behavioural Brain Research, 2012, 230, 182-191.	2.2	38
40	Paradox segmentation along inter- and intrasomitic borderlines is followed by dysmorphology of the axial skeleton in theopen brain (opb) mouse mutant. , 1998, 22, 359-373.		36
41	Itaconate and derivatives reduce interferon responses and inflammation in influenza A virus infection. PLoS Pathogens, 2022, 18, e1010219.	4.7	35
42	Isolation and regional localization of the murine homeobox-containing gene Hox-3.3 to mouse chromosome region 15E. Genomics, 1989, 5, 76-83.	2.9	32
43	Infection- and procedure-dependent effects on pulmonary gene expression in the early phase of influenza A virus infection in mice. BMC Microbiology, 2013, 13, 293.	3.3	32
44	Complex Genetic Architecture Underlies Regulation of Influenza-A-Virus-Specific Antibody Responses in the Collaborative Cross. Cell Reports, 2020, 31, 107587.	6.4	31
45	Transcriptome profiling and protease inhibition experiments identify proteases that activate H3N2 influenza A and influenza B viruses in murine airways. Journal of Biological Chemistry, 2020, 295, 11388-11407.	3.4	31
46	Antiviral potential of human IFN-Î± subtypes against influenza A H3N2 infection in human lung explants reveals subtype-specific activities. Emerging Microbes and Infections, 2019, 8, 1763-1776.	6.5	30
47	E-mail-based symptomatic surveillance combined with self-collection of nasal swabs: a new tool for acute respiratory infection epidemiology. International Journal of Infectious Diseases, 2011, 15, e799-e803.	3.3	29
48	Controlling complexity: the clinical relevance of mouse complex genetics. European Journal of Human Genetics, 2013, 21, 1191-1196.	2.8	29
49	Analysis of LacZ reporter genes in transgenic embryos suggests the presence of several cis-acting regulatory elements in the murine Hoxb-6 gene. Developmental Dynamics, 1993, 196, 205-216.	1.8	28
50	Models for financial sustainability of biological databases and resources. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap017-bap017.	3.0	27
51	Long-Term Consequence of Non-neurotropic H3N2 Influenza A Virus Infection for the Progression of Alzheimerâ€™s Disease Symptoms. Frontiers in Cellular Neuroscience, 2021, 15, 643650.	3.7	27
52	System to identify individual somites and their derivatives in the developing mouse embryo. , 1997, 210, 216-226.		26
53	Tmprss2 knock-out mice are resistant to H10 influenza A virus pathogenesis. Journal of General Virology, 2019, 100, 1073-1078.	2.9	26
54	OP7, a novel influenza A virus defective interfering particle: production, purification, and animal experiments demonstrating antiviral potential. Applied Microbiology and Biotechnology, 2021, 105, 129-146.	3.6	25

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55	Conserved regulatory element involved in the early onset ofHoxb6 gene expression. Developmental Dynamics, 1996, 205, 73-81.	1.8	24
56	Respiratory Mucosal Proteome Quantification in Human Influenza Infections. PLoS ONE, 2016, 11, e0153674.	2.5	24
57	Considerations on Genetic and Environmental Factors That Contribute to Resistance or Sensitivity of Mammals Including Humans to Toxicity of 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) and Related Compounds. Ecotoxicology and Environmental Safety, 1997, 36, 213-230.	6.0	23
58	Genome-wide analysis of the mouse lung transcriptome reveals novel molecular gene interaction networks and cell-specific expression signatures. Respiratory Research, 2011, 12, 61.	3.6	23
59	Cellular Changes in Blood Indicate Severe Respiratory Disease during Influenza Infections in Mice. PLoS ONE, 2014, 9, e103149.	2.5	23
60	The Interferon-Induced Gene Ifi27l2a is Active in Lung Macrophages and Lymphocytes After Influenza A Infection but Deletion of Ifi27l2a in Mice Does Not Increase Susceptibility to Infection. PLoS ONE, 2014, 9, e106392.	2.5	23
61	Genetically diverse CC-founder mouse strains replicate the human influenza gene expression signature. Scientific Reports, 2016, 6, 26437.	3.3	23
62	A comprehensive and comparative phenotypic analysis of the collaborative founder strains identifies new and known phenotypes. Mammalian Genome, 2020, 31, 30-48.	2.2	22
63	Sustained viral load and late death in Rag2-/- mice after influenza A virus infection. Virology Journal, 2010, 7, 172.	3.4	21
64	Endosomal Toll-Like Receptors 7 and 9 Cooperate in Detection of Murine Gammaherpesvirus 68 Infection. Journal of Virology, 2019, 93, .	3.4	21
65	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. Genome Biology, 2010, 11, R27.	9.6	20
66	Host Genetic Background Strongly Affects Pulmonary microRNA Expression before and during Influenza A Virus Infection. Frontiers in Immunology, 2017, 8, 246.	4.8	20
67	Systems Genetics of Liver Fibrosis: Identification of Fibrogenic and Expression Quantitative Trait Loci in the BXD Murine Reference Population. PLoS ONE, 2014, 9, e89279.	2.5	20
68	Influence of internalin a murinisation on host resistance to orally acquired listeriosis in mice. BMC Microbiology, 2013, 13, 90.	3.3	19
69	Microarray gene expression analysis reveals major differences between Toxocara canis and Toxocara cati neurotoxocarosis and involvement of T. canis in lipid biosynthetic processes. International Journal for Parasitology, 2015, 45, 495-503.	3.1	19
70	Absence of regulator of G-protein signaling 4 does not protect against dopamine neuron dysfunction and injury in the mouse 6-hydroxydopamine lesion model of Parkinson's disease. Neurobiology of Aging, 2017, 58, 30-33.	3.1	19
71	Of mice and men: the host response to influenza virus infection. Mammalian Genome, 2018, 29, 446-470.	2.2	19
72	Translational Neuroscience of Schizophrenia: Seeking a Meeting of Minds Between Mouse and Man. Science Translational Medicine, 2011, 3, 102mr3.	12.4	18

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73	The Mouse as Model System to Study Hostâ€Pathogen Interactions in Influenza A Infections. Current Protocols in Mouse Biology, 2012, 2, 177-205.	1.2	18
74	Systems biology and systems geneticsâ€"novel innovative approaches to study hostâ€"pathogen interactions during influenza infection. Current Opinion in Virology, 2014, 6, 47-54.	5.4	18
75	Cell culture-based production and in vivo characterization of purely clonal defective interfering influenza virus particles. BMC Biology, 2021, 19, 91.	3.8	18
76	Identification of specific residues in avian influenza A virus NS1 that enhance viral replication and pathogenicity in mammalian systems. Journal of General Virology, 2016, 97, 2135-2148.	2.9	17
77	Neural tube morphogenesis. Current Opinion in Genetics and Development, 1997, 7, 507-512.	3.3	16
78	Dynamic gene network reconstruction from gene expression data in mice after influenza A (H1N1) infection. Journal of Clinical Bioinformatics, 2011, 1, 27.	1.2	14
79	Pathway mapping of leukocyte transcriptome in influenza patients reveals distinct pathogenic mechanisms associated with progression to severe infection. BMC Medical Genomics, 2020, 13, 28.	1.5	14
80	Genetic Dissection of the Regulatory Mechanisms of Ace2 in the Infected Mouse Lung. Frontiers in Immunology, 2020, 11, 607314.	4.8	14
81	Prospective validation study of prognostic biomarkers to predict adverse outcomes in patients with COVID-19: a study protocol. BMJ Open, 2021, 11, e044497.	1.9	14
82	Strength to strength for mouse models. Nature, 2012, 492, 41-41.	27.8	13
83	H2 influenza A virus is not pathogenic in Tmprss2 knock-out mice. Virology Journal, 2020, 17, 56.	3.4	13
84	The Host Response to Viral Infections Reveals Common and Virus-Specific Signatures in the Peripheral Blood. Frontiers in Immunology, 2021, 12, 741837.	4.8	13
85	Influenza A Immunomics and Public Health Omics: The Dynamic Pathway Interplay in Host Response to H1N1 Infection. OMICS A Journal of Integrative Biology, 2014, 18, 167-183.	2.0	12
86	Blood transcriptome analysis of patients with uncomplicated bacterial infection and sepsis. BMC Research Notes, 2021, 14, 76.	1.4	12
87	Exchange of amino acids in the H1-haemagglutinin to H3 residues is required for efficient influenza A virus replication and pathology in Tmprss2 knock-out mice. Journal of General Virology, 2018, 99, 1187-1198.	2.9	12
88	Organization and Expression of Homeobox Genes in Mouse and Man. Annals of the New York Academy of Sciences, 1989, 567, 243-252.	3.8	11
89	Bioinformatics tools and database resources for systems genetics analysis in mice--a short review and an evaluation of future needs. Briefings in Bioinformatics, 2012, 13, 135-142.	6.5	11
90	TLR8 regulation of LILRA3 in monocytes is abrogated in human immunodeficiency virus infection and correlates to CD4 counts and virus loads. Retrovirology, 2016, 13, 15.	2.0	10

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91	Expression QTL mapping in regulatory and helper T cells from the BXD family of strains reveals novel cell-specific genes, gene-gene interactions and candidate genes for auto-immune disease. BMC Genomics, 2011, 12, 610.	2.8	9
92	The limb/LPM enhancer of the murine Hoxb6 gene: reporter gene analysis in transgenic embryos and studies of DNA-protein interactions. Pharmaceutica Acta Helvetiae, 1996, 71, 29-35.	1.2	8
93	The bioluminescent Listeria monocytogenes strain Xen32 is defective in flagella expression and highly attenuated in orally infected BALB/cJ mice. Gut Pathogens, 2013, 5, 19.	3.4	8
94	Structure and expression of adenovirus type 12 E1B 58K protein in infected and transformed cells: Studies using antibodies directed against a synthetic peptide. Virus Research, 1985, 3, 41-56.	2.2	7
95	The open brain (opb) mutation maps to mouse chromosome 1. Mammalian Genome, 1997, 8, 583-585.	2.2	7
96	CASIMIR: Coordination and Sustainability of International Mouse Informatics Resources. , 2008, , .		7
97	Immunization with live virus vaccine protects highly susceptible DBA/2J mice from lethal influenza A H1N1 infection. Virology Journal, 2012, 9, 212.	3.4	7
98	Segregation of a Spontaneous Klrd1 (CD94) Mutation in DBA/2 Mouse Substrains. G3: Genes, Genomes, Genetics, 2015, 5, 235-239.	1.8	7
99	Multiplex profiling of inflammation-related bioactive lipid mediators in Toxocara canis- and Toxocara cati-induced neurotoxocarosis. PLoS Neglected Tropical Diseases, 2019, 13, e0007706.	3.0	7
100	Analysis of the lung transcriptome in Mycobacterium tuberculosis-infected mice reveals major differences in immune response pathways between TB-susceptible and resistant hosts. Tuberculosis, 2013, 93, 263-269.	1.9	6
101	Hematological parameters in the early phase of influenza A virus infection in differentially susceptible inbred mouse strains. BMC Research Notes, 2015, 8, 225.	1.4	6
102	Impaired beta-oxidation increases vulnerability to influenza A infection. Journal of Biological Chemistry, 2021, 297, 101298.	3.4	6
103	Toxocara canis- and Toxocara cati-Induced Neurotoxocarosis Is Associated with Comprehensive Brain Transcriptomic Alterations. Microorganisms, 2022, 10, 177.	3.6	6
104	Lst1 deficiency has a minor impact on course and outcome of the host response to influenza A H1N1 infections in mice. Virology Journal, 2016, 13, 17.	3.4	5
105	QTL Mapping and Identification of Candidate Genes in DO Mice: A Use Case Model Derived from a Benzene Toxicity Experiment. Methods in Molecular Biology, 2017, 1488, 265-281.	0.9	5
106	Expression of adenovirus type 12 Elb 58-kDa protein in Escherichia coli and production of antibodies raised against a 58-kDa::Î²-galactosidase fusion protein. Gene, 1987, 53, 173-180.	2.2	4
107	Solvoplex Synthetic Vector for Intrapulmonary Gene Delivery: Preparation and Use. , 2002, 69, 083-094.		4
108	Increased virulence of a PB2/HA mutant of an avian H9N2 influenza strain after three passages in porcine differentiated airway epithelial cells. Veterinary Microbiology, 2017, 211, 129-134.	1.9	4

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109	Pituitary Tumor Transforming Gene 1 Orchestrates Gene Regulatory Variation in Mouse Ventral Midbrain During Aging. Frontiers in Genetics, 2020, 11, 566734.	2.3	4
110	Exogenous and Endogenous Triggers Differentially Stimulate Pigr Expression and Antibacterial Secretory Immunity in the Murine Respiratory Tract. Lung, 2022, 200, 119-128.	3.3	4
111	Towards the integration of mouse databases - definition and implementation of solutions to two use-cases in mouse functional genomics. BMC Research Notes, 2010, 3, 16.	1.4	3
112	Mouse Resource Browser--a database of mouse databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq010-baq010.	3.0	3
113	Highly dampened blood transcriptome response in HIV patients after respiratory infection. Scientific Reports, 2021, 11, 4465.	3.3	2
114	Quantitative trait locus mapping identifies a locus linked toÂstriatal dopamine and points to collagen <scp>IV</scp> alphaâ€6 chain asÂa novel regulator of striatal axonal branching in mice. Genes, Brain and Behavior, 2021, 20, e12769.	2.2	2
115	Towards dynamic database infrastructures for mouse genetics. , 2008, , .		1
116	Transcriptome profiling and protease inhibition experiments identify proteases that activate H3N2 influenza A and influenza B viruses in murine airways. FASEB Journal, 2021, 35, .	0.5	1