

Axel KÃ¼nstner

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

3,678
citations

236925

25
h-index

175258

52
g-index

63
all docs

63
docs citations

63
times ranked

6180
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative genomic and transcriptomic analysis in plasmablastic lymphoma identifies disruption of key regulatory pathways. <i>Blood Advances</i> , 2022, 6, 637-651.	5.2	15
2	Gain-of-function mutations in RPA1 cause a syndrome with short telomeres and somatic genetic rescue. <i>Blood</i> , 2022, 139, 1039-1051.	1.4	29
3	Mutational landscape of high-grade B-cell lymphoma with <i>MYC</i>, <i>BCL2</i> and/or <i>BCL6</i> rearrangements characterized by whole-exome sequencing. <i>Haematologica</i> , 2022, 107, 1850-1863.	3.5	17
4	Changes of Gut Microbiota by Natural mtDNA Variant Differences Augment Susceptibility to Metabolic Disease and Ageing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1056.	4.1	3
5	Predominance of Staphylococcus Correlates with Wound Burden and Disease Activity in Dystrophic Epidermolysis Bullosa: A Prospective Case-Control Study. <i>Journal of Investigative Dermatology</i> , 2022, 142, 2117-2127.e8.	0.7	10
6	Palatinose™ (Isomaltulose) and Prebiotic Inulin-Type Fructans Have Beneficial Effects on Glycemic Response and Gut Microbiota Composition in Healthy Volunteers—A Real-Life, Retrospective Study of a Cohort That Participated in a Digital Nutrition Program. <i>Frontiers in Nutrition</i> , 2022, 9, 829933.	3.7	2
7	Longitudinal Characterization of the Fungal Skin Microbiota in Healthy Subjects Over the Period of One Year. <i>Journal of Investigative Dermatology</i> , 2022, , .	0.7	1
8	Data on draft genomes and transcriptomes from females and males of the flour moth, <i>Ephestia kuehniella</i> . <i>Data in Brief</i> , 2022, 42, 108140.	1.0	0
9	Therapy-Related Transcriptional Subtypes in Matched Primary and Recurrent Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 1038-1052.	7.0	13
10	Biodiversity of mycobial communities in health and onychomycosis. <i>Scientific Reports</i> , 2022, 12, .	3.3	3
11	Integrative molecular profiling identifies two molecularly and clinically distinct subtypes of blastic plasmacytoid dendritic cell neoplasm. <i>Blood Cancer Journal</i> , 2022, 12, .	6.2	5
12	Host plant diet affects growth and induces altered gene expression and microbiome composition in the wood white (<i>Leptidea sinapis</i>) butterfly. <i>Molecular Ecology</i> , 2021, 30, 499-516.	3.9	17
13	Diagnostic Value and Practicability of Serration Pattern Analysis by Direct Immunofluorescence Microscopy in Pemphigoid Diseases. <i>Acta Dermato-Venereologica</i> , 2021, 101, adv00410.	1.3	9
14	A Mitochondrial Polymorphism Alters Immune Cell Metabolism and Protects Mice from Skin Inflammation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1006.	4.1	17
15	Performance of international prognostic indices in plasmablastic lymphoma: a comparative evaluation. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 3043-3050.	2.5	6
16	Effect of Differences in the Microbiome of Cyp17a1-Deficient Mice on Atherosclerotic Background. <i>Cells</i> , 2021, 10, 1292.	4.1	3
17	Genomic insights into the pathogenesis of Epstein–Barr virus-associated diffuse large B-cell lymphoma by whole-genome and targeted amplicon sequencing. <i>Blood Cancer Journal</i> , 2021, 11, 102.	6.2	28
18	Systems Immunology Analysis Reveals the Contribution of Pulmonary and Extrapulmonary Tissues to the Immunopathogenesis of Severe COVID-19 Patients. <i>Frontiers in Immunology</i> , 2021, 12, 595150.	4.8	18

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19	Telmisartan induces a specific gut microbiota signature which may mediate its antiobesity effect. <i>Pharmacological Research</i> , 2021, 170, 105724.	7.1	6
20	Hyperoxia/Hypoxia Exposure Primes a Sustained Pro-Inflammatory Profile of Preterm Infant Macrophages Upon LPS Stimulation. <i>Frontiers in Immunology</i> , 2021, 12, 762789.	4.8	12
21	Interactions between host genetics and gut microbiota determine susceptibility to CNS autoimmunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27516-27527.	7.1	58
22	An integrated personal and population-based Egyptian genome reference. <i>Nature Communications</i> , 2020, 11, 4719.	12.8	20
23	Linking Complement C3 and B Cells in Nasal Polyposis. <i>Journal of Immunology Research</i> , 2020, 2020, 1-12.	2.2	3
24	A Comprehensive Molecular Characterization of the Pancreatic Neuroendocrine Tumor Cell Lines BON-1 and QGP-1. <i>Cancers</i> , 2020, 12, 691.	3.7	29
25	Saccharin Supplementation Inhibits Bacterial Growth and Reduces Experimental Colitis in Mice. <i>Nutrients</i> , 2020, 12, 1122.	4.1	18
26	Short-term high-fat diet feeding protects from the development of experimental allergic asthma in mice. <i>Clinical and Experimental Allergy</i> , 2019, 49, 1245-1257.	2.9	10
27	A Natural mtDNA Polymorphism in Complex III Is a Modifier of Healthspan in Mice. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2359.	4.1	12
28	Combined culture and metagenomic analyses reveal significant shifts in the composition of the cutaneous microbiome in psoriasis. <i>British Journal of Dermatology</i> , 2019, 181, 1254-1264.	1.5	57
29	Genetics and Omics Analysis of Autoimmune Skin Blistering Diseases. <i>Frontiers in Immunology</i> , 2019, 10, 2327.	4.8	24
30	IL-17A is functionally relevant and a potential therapeutic target in bullous pemphigoid. <i>Journal of Autoimmunity</i> , 2019, 96, 104-112.	6.5	85
31	Dietary ursolic acid improves health span and life span in male <i>Drosophila melanogaster</i> . <i>BioFactors</i> , 2019, 45, 169-186.	5.4	39
32	Low-level mitochondrial heteroplasmy modulates DNA replication, glucose metabolism and lifespan in mice. <i>Scientific Reports</i> , 2018, 8, 5872.	3.3	26
33	Analytic Methods in Microbiome Studies. , 2018, , 29-42.		0
34	A distinct cutaneous microbiota profile in autoimmune bullous disease patients. <i>Experimental Dermatology</i> , 2017, 26, 1221-1227.	2.9	28
35	Gut microbiota in Parkinson disease in a northern German cohort. <i>Brain Research</i> , 2017, 1667, 41-45.	2.2	264
36	Mitochondrial gene polymorphism is associated with gut microbial communities in mice. <i>Scientific Reports</i> , 2017, 7, 15293.	3.3	49

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37	Circadian rhythm disruption impairs tissue homeostasis and exacerbates chronic inflammation in the intestine. <i>FASEB Journal</i> , 2017, 31, 4707-4719.	0.5	59
38	The Genome of the Trinidadian Guppy, <i>Poecilia reticulata</i> , and Variation in the Guanapo Population. <i>PLoS ONE</i> , 2016, 11, e0169087.	2.5	79
39	Divergence in gene expression within and between two closely related flycatcher species. <i>Molecular Ecology</i> , 2016, 25, 2015-2028.	3.9	57
40	Mitochondrial gene polymorphisms alter hepatic cellular energy metabolism and aggravate diet-induced non-alcoholic steatohepatitis. <i>Molecular Metabolism</i> , 2016, 5, 283-295.	6.5	45
41	<i>Adenylate cyclase 5</i> is required for melanophore and male pattern development in the guppy (<i>Poecilia reticulata</i>). <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 545-558.	3.3	13
42	Pheomelanin in fish?. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 355-356.	3.3	32
43	Population genomics of natural and experimental populations of guppies (<i>Poecilia reticulata</i>). <i>Molecular Ecology</i> , 2015, 24, 389-408.	3.9	79
44	Transcriptome assemblies for studying sex-biased gene expression in the guppy, <i>Poecilia reticulata</i> . <i>BMC Genomics</i> , 2014, 15, 400.	2.8	82
45	Challenges and strategies in transcriptome assembly and differential gene expression quantification. A comprehensive <i>in silico</i> assessment of <i>RNA-seq</i> experiments. <i>Molecular Ecology</i> , 2013, 22, 620-634.	3.9	210
46	Transcriptome Sequencing Reveals the Character of Incomplete Dosage Compensation across Multiple Tissues in Flycatchers. <i>Genome Biology and Evolution</i> , 2013, 5, 1555-1566.	2.5	59
47	The genomic landscape of species divergence in <i>Ficedula</i> flycatchers. <i>Nature</i> , 2012, 491, 756-760.	27.8	589
48	Significant Selective Constraint at 4-Fold Degenerate Sites in the Avian Genome and Its Consequence for Detection of Positive Selection. <i>Genome Biology and Evolution</i> , 2011, 3, 1381-1389.	2.5	31
49	Dynamic Evolution of Base Composition: Causes and Consequences in Avian Phylogenomics. <i>Molecular Biology and Evolution</i> , 2011, 28, 2197-2210.	8.9	84
50	Evolutionary Constraint in Flanking Regions of Avian Genes. <i>Molecular Biology and Evolution</i> , 2011, 28, 2481-2489.	8.9	5
51	ConDeTri - A Content Dependent Read Trimmer for Illumina Data. <i>PLoS ONE</i> , 2011, 6, e26314.	2.5	216
52	Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. <i>Molecular Ecology</i> , 2010, 19, 266-276.	3.9	105
53	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	27.8	770
54	Molecular evolution of genes in avian genomes. <i>Genome Biology</i> , 2010, 11, R68.	9.6	125

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55	Nonlinear Dynamics of Nonsynonymous (dN) and Synonymous (dS) Substitution Rates Affects Inference of Selection. <i>Genome Biology and Evolution</i> , 2009, 1, 308-319.	2.5	95