

Lutz Krause

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

9,963
citations

53794

45
h-index

53230

85
g-index

87
all docs

87
docs citations

87
times ranked

16339
citing authors

#	ARTICLE	IF	CITATIONS
1	Administration of Hookworm Excretory/Secretory Proteins Improves Glucose Tolerance in a Mouse Model of Type 2 Diabetes. <i>Biomolecules</i> , 2022, 12, 637.	4.0	6
2	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 643682.	3.5	25
3	Infection with the sheep gastrointestinal nematode <i>Teladorsagia circumcincta</i> increases luminal pathobionts. <i>Microbiome</i> , 2020, 8, 60.	11.1	40
4	Chronic High-Fat Diet Induces Early Barrett's Esophagus in Mice through Lipidome Remodeling. <i>Biomolecules</i> , 2020, 10, 776.	4.0	10
5	Immune Signature Against <i>Plasmodium falciparum</i> Antigens Predicts Clinical Immunity in Distinct Malaria Endemic Communities. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 101-113.	3.8	16
6	The Association between the Comprehensive Epstein-Barr Virus Serologic Profile and Endemic Burkitt Lymphoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 57-62.	2.5	23
7	Helminths, polyparasitism, and the gut microbiome in the Philippines. <i>International Journal for Parasitology</i> , 2020, 50, 217-225.	3.1	20
8	Chromosome arm aneuploidies shape tumour evolution and drug response. <i>Nature Communications</i> , 2020, 11, 449.	12.8	65
9	Gastrointestinal Helminth Infection Improves Insulin Sensitivity, Decreases Systemic Inflammation, and Alters the Composition of Gut Microbiota in Distinct Mouse Models of Type 2 Diabetes. <i>Frontiers in Endocrinology</i> , 2020, 11, 606530.	3.5	17
10	The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers. <i>Nutrients</i> , 2019, 11, 261.	4.1	62
11	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	4.7	49
12	Whole-genome sequencing of human malignant mesothelioma tumours and cell lines. <i>Carcinogenesis</i> , 2019, 40, 724-734.	2.8	24
13	Analysis of the Effects of Dietary Pattern on the Oral Microbiome of Elite Endurance Athletes. <i>Nutrients</i> , 2019, 11, 614.	4.1	54
14	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	1.5	19
15	Increased susceptibility of airway epithelial cells from ataxia-telangiectasia to <i>S. pneumoniae</i> infection due to oxidative damage and impaired innate immunity. <i>Scientific Reports</i> , 2019, 9, 2627.	3.3	21
16	Potential clinical utility of multiple target quantitative polymerase chain reaction (qPCR) array to detect microbial pathogens in patients with chronic obstructive pulmonary disease (COPD). <i>Journal of Thoracic Disease</i> , 2019, 11, S2254-S2265.	1.4	4
17	Microbiota and Body Composition During the Period of Complementary Feeding. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019, 69, 726-732.	1.8	6
18	Vitamin D and the gut microbiome: a systematic review of in vivo studies. <i>European Journal of Nutrition</i> , 2019, 58, 2895-2910.	3.9	117

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19	Whole-genome sequence of the oriental lung fluke <i>Paragonimus westermani</i> . GigaScience, 2019, 8, .	6.4	29
20	Patterns of Interindividual Variability in the Antibody Repertoire Targeting Proteins Across the Epstein-Barr Virus Proteome. Journal of Infectious Diseases, 2018, 217, 1923-1931.	4.0	13
21	Growth and protein-rich food intake in infancy is associated with fat-free mass index at 2-3 years of age. Journal of Paediatrics and Child Health, 2018, 54, 770-775.	0.8	4
22	Mapping the virome in wild-caught Aedes aegypti from Cairns and Bangkok. Scientific Reports, 2018, 8, 4690.	3.3	84
23	Identification of a Novel, EBV-Based Antibody Risk Stratification Signature for Early Detection of Nasopharyngeal Carcinoma in Taiwan. Clinical Cancer Research, 2018, 24, 1305-1314.	7.0	52
24	Male-specific Association Between Fat-Free Mass Index and Fecal Microbiota in 2- to 3-Year-Old Australian Children. Journal of Pediatric Gastroenterology and Nutrition, 2018, 66, 147-151.	1.8	11
25	A comprehensive analysis of the faecal microbiome and metabolome of Strongyloides stercoralis infected volunteers from a non-endemic area. Scientific Reports, 2018, 8, 15651.	3.3	51
26	Calypso: a user-friendly web-server for mining and visualizing microbiome-environment interactions. Bioinformatics, 2017, 33, 782-783.	4.1	627
27	Long-term Health-related Quality of Life Following Esophagectomy. Annals of Surgery, 2017, 265, 1158-1165.	4.2	38
28	Associations between micronutrient intakes and gut microbiota in a group of adults with cystic fibrosis. Clinical Nutrition, 2017, 36, 1097-1104.	5.0	46
29	Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. PLoS ONE, 2017, 12, e0184719.	2.5	100
30	Microbiota of little penguins and short-tailed shearwaters during development. PLoS ONE, 2017, 12, e0183117.	2.5	23
31	Mothers Secretor Status Affects Development of Childrens Microbiota Composition and Function: A Pilot Study. PLoS ONE, 2016, 11, e0161211.	2.5	63
32	Mining, visualizing and comparing multidimensional biomolecular data using the Genomics Data Miner (GMine) Web-Server. Scientific Reports, 2016, 6, 38178.	3.3	22
33	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. Scientific Reports, 2016, 6, 36797.	3.3	59
34	High fat diet drives obesity regardless the composition of gut microbiota in mice. Scientific Reports, 2016, 6, 32484.	3.3	97
35	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. Carcinogenesis, 2016, 37, 356-365.	2.8	46
36	Neonatal environment exerts a sustained influence on the development of the intestinal microbiota and metabolic phenotype. ISME Journal, 2016, 10, 145-157.	9.8	44

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37	Obesity-induced sperm DNA methylation changes at satellite repeats are reprogrammed in rat offspring. Asian Journal of Andrology, 2016, 18, 930.	1.6	26
38	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. Scientific Reports, 2015, 5, 13797.	3.3	86
39	Suppression of inflammation by helminths: a role for the gut microbiota?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140296.	4.0	78
40	The coral core microbiome identifies rare bacterial taxa as ubiquitous endosymbionts. ISME Journal, 2015, 9, 2261-2274.	9.8	548
41	Meta-analysis of the global gene expression profile of triple-negative breast cancer identifies genes for the prognostication and treatment of aggressive breast cancer. Oncogenesis, 2014, 3, e100-e100.	4.9	70
42	Scabies Mites Alter the Skin Microbiome and Promote Growth of Opportunistic Pathogens in a Porcine Model. PLoS Neglected Tropical Diseases, 2014, 8, e2897.	3.0	67
43	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. Genome Biology, 2014, 15, R56.	9.6	87
44	Molecular investigation of bacterial communities on intravascular catheters: no longer just Staphylococcus. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 1189-1198.	2.9	26
45	Genome-wide analysis of esophageal adenocarcinoma yields specific copy number aberrations that correlate with prognosis. Genes Chromosomes and Cancer, 2014, 53, 324-338.	2.8	38
46	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. Journal of Infectious Diseases, 2014, 210, 1431-1434.	4.0	153
47	Common variants in the CYP2C19 gene are associated with susceptibility to endometriosis. Fertility and Sterility, 2014, 102, 496-502.e5.	1.0	15
48	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	12.8	236
49	Pyrosequencing reveals transient cystic fibrosis lung microbiome changes with intravenous antibiotics. European Respiratory Journal, 2014, 44, 922-930.	6.7	71
50	BRAF mutation status is an independent prognostic factor for resected stage IIIB and IIIC melanoma: Implications for melanoma staging and adjuvant therapy. European Journal of Cancer, 2014, 50, 2668-2676.	2.8	67
51	Interspecific variations in the faecal microbiota of <i>Procellariiform</i> seabirds. FEMS Microbiology Ecology, 2014, 89, 47-55.	2.7	44
52	Influence of Fasting during Moulting on the Faecal Microbiota of Penguins. PLoS ONE, 2014, 9, e99996.	2.5	41
53	Smchd1 regulates a subset of autosomal genes subject to monoallelic expression in addition to being critical for X inactivation. Epigenetics and Chromatin, 2013, 6, 19.	3.9	88
54	Infection with the carcinogenic liver fluke <i>Opisthorchis viverrini</i> modifies intestinal and biliary microbiome. FASEB Journal, 2013, 27, 4572-4584.	0.5	116

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55	Safety analysis of a Russian phage cocktail: From MetaGenomic analysis to oral application in healthy human subjects. <i>Virology</i> , 2013, 443, 187-196.	2.4	211
56	Impact of Dietary Dairy Polar Lipids on Lipid Metabolism of Mice Fed a High-Fat Diet. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 2729-2738.	5.2	22
57	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. <i>Translational Psychiatry</i> , 2013, 3, e269-e269.	4.8	89
58	Germline copy number variants are not associated with globally acquired copy number changes in familial breast tumours. <i>Breast Cancer Research and Treatment</i> , 2012, 134, 1005-1011.	2.5	7
59	Oral T4-like phage cocktail application to healthy adult volunteers from Bangladesh. <i>Virology</i> , 2012, 434, 222-232.	2.4	201
60	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e14519.	2.5	208
61	Colonization-Induced Host-Gut Microbial Metabolic Interaction. <i>MBio</i> , 2011, 2, e00271-10.	4.1	342
62	Nutrigenomics: where are we with genetic and epigenetic markers for disposition and susceptibility?. <i>Nutrition Reviews</i> , 2010, 68, S38-S47.	5.8	42
63	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0
64	TACOA “ Taxonomic classification of environmental genomic fragments using a kernelized nearest neighbor approach. <i>BMC Bioinformatics</i> , 2009, 10, 56.	2.6	160
65	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , 2009, 11, 1038-1055.	3.8	100
66	Phylogenetic characterization of a biogas plant microbial community integrating clone library 16S-rDNA sequences and metagenome sequence data obtained by 454-pyrosequencing. <i>Journal of Biotechnology</i> , 2009, 142, 38-49.	3.8	248
67	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. <i>Journal of Biotechnology</i> , 2008, 136, 65-76.	3.8	87
68	Insight into the plasmid metagenome of wastewater treatment plant bacteria showing reduced susceptibility to antimicrobial drugs analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 54-64.	3.8	74
69	The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 77-90.	3.8	329
70	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	3.8	202
71	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	3.8	238
72	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	14.5	246

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73	The Genome Sequence of the Tomato-Pathogenic Actinomycete <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB382 Reveals a Large Island Involved in Pathogenicity. Journal of Bacteriology, 2008, 190, 2138-2149.	2.2	153
74	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. PLoS ONE, 2008, 3, e1584.	2.5	383
75	Genomic sequence of chorioallantois vaccinia virus Ankara, the ancestor of modified vaccinia virus Ankara. Journal of General Virology, 2007, 88, 3249-3259.	2.9	71
76	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . Nature Biotechnology, 2007, 25, 1281-1289.	17.5	354
77	REGANOR. Applied Bioinformatics, 2006, 5, 193-198.	1.6	44
78	GISMO—gene identification using a support vector machine for ORF classification. Nucleic Acids Research, 2006, 35, 540-549.	14.5	47
79	Complete genome of the mutualistic, N ₂ -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. Nature Biotechnology, 2006, 24, 1384-1390.	17.5	237
80	Finding novel genes in bacterial communities isolated from the environment. Bioinformatics, 2006, 22, e281-e289.	4.1	68
81	BRIGEP—the BRIDGE-based genome-transcriptome-proteome browser. Nucleic Acids Research, 2005, 33, W710-W716.	14.5	20
82	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. Nucleic Acids Research, 2005, 33, 5691-5702.	14.5	1,806
83	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. Journal of Biotechnology, 2003, 106, 157-167.	3.8	22
84	EMMA: a platform for consistent storage and efficient analysis of microarray data. Journal of Biotechnology, 2003, 106, 135-146.	3.8	100