

# Lutz Krause

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9003106/publications.pdf>

Version: 2024-02-01

84  
papers

9,963  
citations

53660

45  
h-index

53109

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.	1.8	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.	1.5	25
3	Infection with the sheep gastrointestinal nematode <i>Teladorsagia circumcincta</i> increases luminal pathobionts. <i>Microbiome</i> , 2020, 8, 60.	4.9	40
4	Chronic High-Fat Diet Induces Early Barrett's Esophagus in Mice through Lipidome Remodeling. <i>Biomolecules</i> , 2020, 10, 776.	1.8	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.	2.5	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.	1.1	23
7	Helminths, polyparasitism, and the gut microbiome in the Philippines. <i>International Journal for Parasitology</i> , 2020, 50, 217-225.	1.3	20
8	Chromosome arm aneuploidies shape tumour evolution and drug response. <i>Nature Communications</i> , 2020, 11, 449.	5.8	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.	1.5	17
10	The Effects of Dietary Pattern during Intensified Training on Stool Microbiota of Elite Race Walkers. <i>Nutrients</i> , 2019, 11, 261.	1.7	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.	2.1	49
12	Whole-genome sequencing of human malignant mesothelioma tumours and cell lines. <i>Carcinogenesis</i> , 2019, 40, 724-734.	1.3	24
13	Analysis of the Effects of Dietary Pattern on the Oral Microbiome of Elite Endurance Athletes. <i>Nutrients</i> , 2019, 11, 614.	1.7	54
14	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	0.7	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.	1.6	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.	0.6	4
17	Microbiota and Body Composition During the Period of Complementary Feeding. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2019, 69, 726-732.	0.9	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.	1.8	117

#	ARTICLE	IF	CITATIONS
19	Whole-genome sequence of the oriental lung fluke <i>Paragonimus westermani</i> . <i>GigaScience</i> , 2019, 8, .	3.3	29
20	Patterns of Interindividual Variability in the Antibody Repertoire Targeting Proteins Across the Epstein-Barr Virus Proteome. <i>Journal of Infectious Diseases</i> , 2018, 217, 1923-1931.	1.9	13
21	Growth and protein-rich food intake in infancy is associated with fat-free mass index at 2-3 years of age. <i>Journal of Paediatrics and Child Health</i> , 2018, 54, 770-775.	0.4	4
22	Mapping the virome in wild-caught <i>Aedes aegypti</i> from Cairns and Bangkok. <i>Scientific Reports</i> , 2018, 8, 4690.	1.6	84
23	Identification of a Novel, EBV-Based Antibody Risk Stratification Signature for Early Detection of Nasopharyngeal Carcinoma in Taiwan. <i>Clinical Cancer Research</i> , 2018, 24, 1305-1314.	3.2	52
24	Male-specific Association Between Fat-Free Mass Index and Fecal Microbiota in 2- to 3-Year-Old Australian Children. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2018, 66, 147-151.	0.9	11
25	A comprehensive analysis of the faecal microbiome and metabolome of <i>Strongyloides stercoralis</i> infected volunteers from a non-endemic area. <i>Scientific Reports</i> , 2018, 8, 15651.	1.6	51
26	Calypso: a user-friendly web-server for mining and visualizing microbiome-environment interactions. <i>Bioinformatics</i> , 2017, 33, 782-783.	1.8	627
27	Long-term Health-related Quality of Life Following Esophagectomy. <i>Annals of Surgery</i> , 2017, 265, 1158-1165.	2.1	38
28	Associations between micronutrient intakes and gut microbiota in a group of adults with cystic fibrosis. <i>Clinical Nutrition</i> , 2017, 36, 1097-1104.	2.3	46
29	Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. <i>PLoS ONE</i> , 2017, 12, e0184719.	1.1	100
30	Microbiota of little penguins and short-tailed shearwaters during development. <i>PLoS ONE</i> , 2017, 12, e0183117.	1.1	23
31	Mothers Secretor Status Affects Development of Childrens Microbiota Composition and Function: A Pilot Study. <i>PLoS ONE</i> , 2016, 11, e0161211.	1.1	63
32	Mining, visualizing and comparing multidimensional biomolecular data using the Genomics Data Miner (GMine) Web-Server. <i>Scientific Reports</i> , 2016, 6, 38178.	1.6	22
33	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. <i>Scientific Reports</i> , 2016, 6, 36797.	1.6	59
34	High fat diet drives obesity regardless the composition of gut microbiota in mice. <i>Scientific Reports</i> , 2016, 6, 32484.	1.6	97
35	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. <i>Carcinogenesis</i> , 2016, 37, 356-365.	1.3	46
36	Neonatal environment exerts a sustained influence on the development of the intestinal microbiota and metabolic phenotype. <i>ISME Journal</i> , 2016, 10, 145-157.	4.4	44

#	ARTICLE	IF	CITATIONS
37	Obesity-induced sperm DNA methylation changes at satellite repeats are reprogrammed in rat offspring. <i>Asian Journal of Andrology</i> , 2016, 18, 930.	0.8	26
38	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. <i>Scientific Reports</i> , 2015, 5, 13797.	1.6	86
39	Suppression of inflammation by helminths: a role for the gut microbiota?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140296.	1.8	78
40	The coral core microbiome identifies rare bacterial taxa as ubiquitous endosymbionts. <i>ISME Journal</i> , 2015, 9, 2261-2274.	4.4	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. <i>Oncogenesis</i> , 2014, 3, e100-e100.	2.1	70
42	Scabies Mites Alter the Skin Microbiome and Promote Growth of Opportunistic Pathogens in a Porcine Model. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2897.	1.3	67
43	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014, 15, R56.	13.9	87
44	Molecular investigation of bacterial communities on intravascular catheters: no longer just <i>Staphylococcus</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2014, 33, 1189-1198.	1.3	26
45	Genome-wide analysis of esophageal adenocarcinoma yields specific copy number aberrations that correlate with prognosis. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 324-338.	1.5	38
46	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. <i>Journal of Infectious Diseases</i> , 2014, 210, 1431-1434.	1.9	153
47	Common variants in the CYP2C19 gene are associated with susceptibility to endometriosis. <i>Fertility and Sterility</i> , 2014, 102, 496-502.e5.	0.5	15
48	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	5.8	236
49	Pyrosequencing reveals transient cystic fibrosis lung microbiome changes with intravenous antibiotics. <i>European Respiratory Journal</i> , 2014, 44, 922-930.	3.1	71
50	BRAF mutation status is an independent prognostic factor for resected stage IIIB and IIIC melanoma: Implications for melanoma staging and adjuvant therapy. <i>European Journal of Cancer</i> , 2014, 50, 2668-2676.	1.3	67
51	Interspecific variations in the faecal microbiota of <i>Procellariiform</i> seabirds. <i>FEMS Microbiology Ecology</i> , 2014, 89, 47-55.	1.3	44
52	Influence of Fasting during Moulting on the Faecal Microbiota of Penguins. <i>PLoS ONE</i> , 2014, 9, e99996.	1.1	41
53	<i>Smchd1</i> regulates a subset of autosomal genes subject to monoallelic expression in addition to being critical for X inactivation. <i>Epigenetics and Chromatin</i> , 2013, 6, 19.	1.8	88
54	Infection with the carcinogenic liver fluke <i>Opisthorchis viverrini</i> modifies intestinal and biliary microbiome. <i>FASEB Journal</i> , 2013, 27, 4572-4584.	0.2	116

#	ARTICLE	IF	CITATIONS
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.	1.1	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.	2.4	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.	2.4	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.	1.1	7
59	Oral T4-like phage cocktail application to healthy adult volunteers from Bangladesh. <i>Virology</i> , 2012, 434, 222-232.	1.1	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.	1.1	208
61	Colonization-Induced Host-Gut Microbial Metabolic Interaction. <i>MBio</i> , 2011, 2, e00271-10.	1.8	342
62	Nutrigenomics: where are we with genetic and epigenetic markers for disposition and susceptibility?. <i>Nutrition Reviews</i> , 2010, 68, S38-S47.	2.6	42
63	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0
64	TACO A " Taxonomic classification of environmental genomic fragments using a kernelized nearest neighbor approach. <i>BMC Bioinformatics</i> , 2009, 10, 56.	1.2	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.	1.8	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.	1.9	248
67	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. <i>Journal of Biotechnology</i> , 2008, 136, 65-76.	1.9	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.	1.9	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.	1.9	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.	1.9	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.	1.9	238
72	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	6.5	246

#	ARTICLE	IF	CITATIONS
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. <i>Journal of Bacteriology</i> , 2008, 190, 2138-2149.	1.0	153
74	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. <i>PLoS ONE</i> , 2008, 3, e1584.	1.1	383
75	Genomic sequence of chorioallantois vaccinia virus Ankara, the ancestor of modified vaccinia virus Ankara. <i>Journal of General Virology</i> , 2007, 88, 3249-3259.	1.3	71
76	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	9.4	354
77	REGANOR. <i>Applied Bioinformatics</i> , 2006, 5, 193-198.	1.7	44
78	GISMO—gene identification using a support vector machine for ORF classification. <i>Nucleic Acids Research</i> , 2006, 35, 540-549.	6.5	47
79	Complete genome of the mutualistic, N <sub>2</sub> -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. <i>Nature Biotechnology</i> , 2006, 24, 1384-1390.	9.4	237
80	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , 2006, 22, e281-e289.	1.8	68
81	BRIGEP—the BRIDGE-based genome-transcriptome-proteome browser. <i>Nucleic Acids Research</i> , 2005, 33, W710-W716.	6.5	20
82	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5691-5702.	6.5	1,806
83	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , 2003, 106, 157-167.	1.9	22
84	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , 2003, 106, 135-146.	1.9	100