Klaus Lehnert

List of Publications by Year
in descending order

55	1,755	304743	302126
papers	citations	22 h-index	39 g-index

60	60	60	3198
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Capra hircus chromosome 19 locus linked to milk production influences mammary conformation. Journal of Animal Science and Biotechnology, 2022, 13, 4.	5.3	3
2	The (apparent) antibody paradox in COVID-19. Expert Review of Clinical Immunology, 2022, 18, 335-345.	3.0	9
3	Screening for phenotypic outliers identifies an unusually low concentration of a Î²-lactoglobulin B protein isoform in bovine milk caused by a synonymous SNP. Genetics Selection Evolution, 2022, 54, 22.	3.0	4
4	Severe COVID-19 is a T cell immune dysregulatory disorder triggered by SARS-CoV-2. Expert Review of Clinical Immunology, 2022, 18, 557-565.	3.0	10
5	Under-ascertainment of breast cancer susceptibility gene carriers in a cohort of New Zealand female breast cancer patients. Breast Cancer Research and Treatment, 2021, 185, 583-590.	2.5	0
6	Perspective: diagnostic laboratories should urgently develop T cell assays for SARS-CoV-2 infection. Expert Review of Clinical Immunology, 2021, 17, 421-430.	3.0	24
7	Perspective: Application of the American College of Medical Genetics Variant Interpretation Criteria to Common Variable Immunodeficiency Disorders. Clinical Reviews in Allergy and Immunology, 2021, 61, 226-235.	6.5	15
8	Perspective: the nose and the stomach play a critical role in the NZACE2-PÄtari* (modified ACE2) drug treatment project of SARS-CoV-2 infection. Expert Review of Clinical Immunology, 2021, 17, 553-560.	3.0	10
9	Common Variable Immunodeficiency Disorders, T-Cell Responses to SARS-CoV-2 Vaccines, and the Risk of Chronic COVID-19. Journal of Allergy and Clinical Immunology: in Practice, 2021, 9, 3575-3583.	3.8	41
10	Novel PRMT7 mutation in a rare case of dysmorphism and intellectual disability. Journal of Human Genetics, 2021, , .	2.3	6
11	Are All Primary Immunodeficiency Disorders Inborn Errors of Immunity?. Frontiers in Immunology, 2021, 12, 706796.	4.8	6
12	Response to letter to the editor: the clinical utility of diagnostic T cell assays for COVID-19. Expert Review of Clinical Immunology, 2021, 17, 1159-1161.	3.0	5
13	Advantage of including Genomic Information to Predict Breeding Values for Lactation Yields of Milk, Fat, and Protein or Somatic Cell Score in a New Zealand Dairy Goat Herd. Animals, 2021, 11, 24.	2.3	6
14	Common Variable Immunodeficiency Disorders as a Model for Assessing COVID-19 Vaccine Responses in Immunocompromised Patients. Frontiers in Immunology, 2021, 12, 798389.	4.8	6
15	Genetic parameters for total lactation yields of milk, fat, protein, and somatic cell score in New Zealand dairy goats. Animal Science Journal, 2020, 91, e13310.	1.4	14
16	Genome-wide association studies of lactation yields of milk, fat, protein and somatic cell score in New Zealand dairy goats. Journal of Animal Science and Biotechnology, 2020, 11, 55.	5.3	25
17	Inhaled modified angiotensin converting enzyme 2 (ACE2) as a decoy to mitigate SARS-CoV-2 infection. New Zealand Medical Journal, 2020, 133, 112-118.	0.5	7
18	RBV: Read balance validator, a tool for prioritising copy number variations in germline conditions. Scientific Reports, 2019, 9, 16934.	3.3	0

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19	Evaluation of the performance of copy number variant prediction tools for the detection of deletions from whole genome sequencing data. Journal of Biomedical Informatics, 2019, 94, 103174.	4.3	20
20	All Patients With Common Variable Immunodeficiency Disorders (CVID) Should Be Routinely Offered Diagnostic Genetic Testing. Frontiers in Immunology, 2019, 10, 2678.	4.8	15
21	Penetrance and expressivity of the R858H CACNA1C variant in a fiveâ€generation pedigree segregating an arrhythmogenic channelopathy. Molecular Genetics & Genomic Medicine, 2019, 7, e00476.	1.2	11
22	Review: Diagnosing Common Variable Immunodeficiency Disorder in the Era of Genome Sequencing. Clinical Reviews in Allergy and Immunology, 2018, 54, 261-268.	6.5	69
23	Modelling brain dopamine-serotonin vesicular transport disease in Caenorhabditis elegans. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	8
24	De Novo Pathogenic Variants in CACNA1E Cause Developmental and Epileptic Encephalopathy with Contractures, Macrocephaly, and Dyskinesias. American Journal of Human Genetics, 2018, 103, 666-678.	6.2	87
25	Copy number variants implicate cardiac function and development pathways in earthquake-induced stress cardiomyopathy. Scientific Reports, 2018, 8, 7548.	3.3	8
26	Keeping it in the family: the case for considering late-onset combined immunodeficiency a subset of common variable immunodeficiency disorders. Expert Review of Clinical Immunology, 2018, 14, 549-556.	3.0	27
27	The New Zealand minds for minds autism spectrum disorder self-reported cohort. Research in Autism Spectrum Disorders, 2017, 36, 1-7.	1.5	4
28	Compound heterozygous SLC19A3 mutations further refine the critical promoter region for biotin-thiamine-responsive basal ganglia disease. Journal of Physical Education and Sports Management, 2017, 3, a001909.	1.2	20
29	Compound Heterozygous Inheritance of Mutations in Coenzyme Q8A Results in Autosomal Recessive Cerebellar Ataxia and Coenzyme Q10 Deficiency in a Female Sib-Pair. JIMD Reports, 2017, 42, 31-36.	1.5	21
30	Epistatic interactions between mutations of TACI (TNFRSF13B) and TCF3 result in a severe primary immunodeficiency disorder and systemic lupus erythematosus. Clinical and Translational Immunology, 2017, 6, e159.	3.8	54
31	Clinical Implications of Digenic Inheritance and Epistasis in Primary Immunodeficiency Disorders. Frontiers in Immunology, 2017, 8, 1965.	4.8	44
32	Cross-Comparison of Exome Analysis, Next-Generation Sequencing of Amplicons, and the iPLEXÂ® ADME PGx Panel for Pharmacogenomic Profiling. Frontiers in Pharmacology, 2016, 7, 1.	3.5	231
33	Sequence-based Association Analysis Reveals an MGST1 eQTL with Pleiotropic Effects on Bovine Milk Composition. Scientific Reports, 2016, 6, 25376.	3.3	103
34	Brain dopamineâ€serotonin vesicular transport disease presenting as a severe infantile hypotonic parkinsonian disorder. Journal of Inherited Metabolic Disease, 2016, 39, 305-308.	3.6	41
35	Whole Exome Sequencing Reveals Compound Heterozygosity for Ethnically Distinct PEX7 Mutations Responsible for Rhizomelic Chondrodysplasia Punctata, Type 1. Case Reports in Genetics, 2015, 2015, 1-4.	0.2	3
36	Phenotypic population screen identifies a new mutation in bovine DGAT1 responsible for unsaturated milk fat. Scientific Reports, 2015, 5, 8484.	3.3	14

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37	Haploinsufficiency of the NF-Î¹B1 Subunit p50 in Common Variable Immunodeficiency. American Journal of Human Genetics, 2015, 97, 389-403.	6.2	232
38	Expression Variants of the Lipogenic AGPAT6 Gene Affect Diverse Milk Composition Phenotypes in Bos taurus. PLoS ONE, 2014, 9, e85757.	2.5	58
39	Estimation of genetic and crossbreeding parameters of fatty acid concentrations in milk fat predicted by mid-infrared spectroscopy in New Zealand dairy cattle. Journal of Dairy Research, 2014, 81, 340-349.	1.4	25
40	An Immunological Approach to Increase the Brainâ€™s Resilience to Insults. ISRN Neuroscience, 2014, 2014, 1-10.	1.5	13
41	Rapid, quantitative analysis of 3â€²- and 6â€²-sialyllactose in milk by flow-injection analysisâ€“mass spectrometry: Screening of milks for naturally elevated sialyllactose concentration. Journal of Dairy Science, 2013, 96, 7684-7691.	3.4	21
42	A Triad of Highly Divergent Polymeric Immunoglobulin Receptor (PIGR) Haplotypes with Major Effect on IgA Concentration in Bovine Milk. PLoS ONE, 2013, 8, e57219.	2.5	9
43	Metabolic proteomics of the liver and mammary gland during lactation. Journal of Proteomics, 2012, 75, 4429-4435.	2.4	39
44	Modulation of the maternal immune system by the pre-implantation embryo. BMC Genomics, 2010, 11, 474.	2.8	112
45	Profiling the metabolic proteome of bovine mammary tissue. Proteomics, 2008, 8, 1502-1515.	2.2	32
46	Proteomic Analysis of Microsomes from Lactating Bovine Mammary Gland. Journal of Proteome Research, 2008, 7, 1427-1432.	3.7	29
47	Angiostatin enhances B7.1-mediated cancer immunotherapy independently of effects on vascular endothelial growth factor expression. Cancer Gene Therapy, 2001, 8, 719-727.	4.6	30
48	Induction of systemic antitumor immunity by gene transfer of mammalian heat shock protein 70.1 into tumors in situ. Cancer Gene Therapy, 2001, 8, 974-981.	4.6	12
49	Mouse M290 is the functional homologue of the human mucosal lymphocyte integrin HML-1: Antagonism between the integrin ligands E-cadherin and RGD tripeptide. Immunology and Cell Biology, 1999, 77, 337-344.	2.3	9
50	Cloning, Sequence Analysis, and Chromosomal Localization of the Novel Human Integrin Î±11 Subunit (ITGA11). Genomics, 1999, 60, 179-187.	2.9	29
51	LPAM-1 (integrin Î±4Î²7)-ligand binding: overlapping binding sites recognizing VCAM-1, MAdCAM-1 and CS-1 are blocked by fibrinogen, a fibronectin-like polymer and RGD-like cyclic peptides. European Journal of Immunology, 1998, 28, 995-1004.	2.9	23
52	MAdCAM-1 costimulates T cell proliferation exclusively through integrin Î±4Î²7, whereas VCAM-1 and CS-1 peptide use Î±4Î²1: evidence for â€œremoteâ€•costimulation and induction of hyperresponsiveness to B7 molecules. European Journal of Immunology, 1998, 28, 3605-3615.	2.9	45
53	MAdCAM-1 costimulates T cell proliferation exclusively through integrin Î±4Î²7, whereas VCAM-1 and CS-1 peptide use Î±4Î²1: evidence for "remote" costimulation and induction of hyperresponsiveness to B7 molecules. European Journal of Immunology, 1998, 28, 3605-3615.	2.9	1
54	Interaction of monocytoid cells with the mucosal addressin MAdCAM-1 via the integrins VLA-4 and LPAM-1. Immunology and Cell Biology, 1996, 74, 383-393.	2.3	18

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55	Glycoprotein biosynthesis inSaccharomyces cerevisiae: ngd29, anN-glycosylation mutant allelic tooch1having a defect in the initiation of outer chain formation. FEBS Letters, 1995, 370, 41-45.	2.8	42