

Tobias L Lenz

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5842802/publications.pdf>

Version: 2024-02-01

57
papers

5,481
citations

126708

33
h-index

138251

58
g-index

65
all docs

65
docs citations

65
times ranked

11231
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. <i>New England Journal of Medicine</i> , 2020, 383, 1522-1534.	13.9	1,548
2	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. <i>Nature Genetics</i> , 2015, 47, 898-905.	9.4	235
3	Rapid and adaptive evolution of MHC genes under parasite selection in experimental vertebrate populations. <i>Nature Communications</i> , 2012, 3, 621.	5.8	231
4	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013, 4, 2212.	5.8	213
5	Evolutionary divergence of HLA class I genotype impacts efficacy of cancer immunotherapy. <i>Nature Medicine</i> , 2019, 25, 1715-1720.	15.2	194
6	Advances in the Evolutionary Understanding of MHC Polymorphism. <i>Trends in Genetics</i> , 2020, 36, 298-311.	2.9	188
7	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. <i>Nature Genetics</i> , 2015, 47, 1085-1090.	9.4	164
8	Simple approach to reduce PCR artefact formation leads to reliable genotyping of MHC and other highly polymorphic loci – Implications for evolutionary analysis. <i>Gene</i> , 2008, 427, 117-123.	1.0	155
9	MHC-based mate choice combines good genes and maintenance of MHC polymorphism. <i>Molecular Ecology</i> , 2009, 18, 3316-3329.	2.0	154
10	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14658-14663.	3.3	154
11	Genomics of Divergence along a Continuum of Parapatric Population Differentiation. <i>PLoS Genetics</i> , 2015, 11, e1004966.	1.5	135
12	Divergent selection on locally adapted major histocompatibility complex immune genes experimentally proven in the field. <i>Ecology Letters</i> , 2012, 15, 723-731.	3.0	134
13	Divergent Allele Advantage at Human MHC Genes: Signatures of Past and Ongoing Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 2145-2158.	3.5	128
14	Human leukocyte antigen variation is associated with adverse events of checkpoint inhibitors. <i>European Journal of Cancer</i> , 2019, 107, 8-14.	1.3	127
15	Parasite diversity, patterns of MHC II variation and olfactory based mate choice in diverging three-spined stickleback ecotypes. <i>Evolutionary Ecology</i> , 2011, 25, 605-622.	0.5	110
16	Improved prediction of immune checkpoint blockade efficacy across multiple cancer types. <i>Nature Biotechnology</i> , 2022, 40, 499-506.	9.4	110
17	Major histocompatibility complex polymorphism: dynamics and consequences of parasite-mediated local adaptation in fishes. <i>Journal of Fish Biology</i> , 2010, 77, 2023-2047.	0.7	96
18	Speciation accelerated and stabilized by pleiotropic major histocompatibility complex immunogenes. <i>Ecology Letters</i> , 2009, 12, 5-12.	3.0	90

#	ARTICLE	IF	CITATIONS
19	Genes with monoallelic expression contribute disproportionately to genetic diversity in humans. <i>Nature Genetics</i> , 2016, 48, 231-237.	9.4	83
20	Exploring local immunological adaptation of two stickleback ecotypes by experimental infection and transcriptome-wide digital gene expression analysis. <i>Molecular Ecology</i> , 2013, 22, 774-786.	2.0	79
21	COMPUTATIONAL PREDICTION OF MHC II-ANTIGEN BINDING SUPPORTS DIVERGENT ALLELE ADVANTAGE AND EXPLAINS TRANS-SPECIES POLYMORPHISM. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 2380-2390.	1.1	78
22	Genome-wide patterns of standing genetic variation in a marine population of three-spined sticklebacks. <i>Molecular Ecology</i> , 2013, 22, 635-649.	2.0	78
23	Extensive Copy-Number Variation of Young Genes across Stickleback Populations. <i>PLoS Genetics</i> , 2014, 10, e1004830.	1.5	70
24	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. <i>Nature Communications</i> , 2018, 9, 1569.	5.8	67
25	HLA Heterozygote Advantage against HIV-1 Is Driven by Quantitative and Qualitative Differences in HLA Allele-Specific Peptide Presentation. <i>Molecular Biology and Evolution</i> , 2020, 37, 639-650.	3.5	60
26	Pathogen diversity drives the evolution of generalist MHC-II alleles in human populations. <i>PLoS Biology</i> , 2019, 17, e3000131.	2.6	56
27	Excess of Deleterious Mutations around HLA Genes Reveals Evolutionary Cost of Balancing Selection. <i>Molecular Biology and Evolution</i> , 2016, 33, 2555-2564.	3.5	55
28	Diverse MHC IIB allele repertoire increases parasite resistance and body condition in the Long-tailed giant rat (<i>Leopoldamys sabanus</i>). <i>BMC Evolutionary Biology</i> , 2009, 9, 269.	3.2	54
29	Divergent allele advantage at MHC-DRB through direct and maternal genotypic effects and its consequences for allele pool composition and mating. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130714.	1.2	54
30	Transcriptome profiling of immune tissues reveals habitat-specific gene expression between lake and river sticklebacks. <i>Molecular Ecology</i> , 2016, 25, 943-958.	2.0	49
31	Construction and benchmarking of a multi-ethnic reference panel for the imputation of HLA class I and II alleles. <i>Human Molecular Genetics</i> , 2019, 28, 2078-2092.	1.4	48
32	EVALUATING PATTERNS OF CONVERGENT EVOLUTION AND TRANS-SPECIES POLYMORPHISM AT MHC IMMUNOGENES IN TWO SYMPATRIC STICKLEBACK SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2400-2412.	1.1	43
33	RSCA genotyping of MHC for high-throughput evolutionary studies in the model organism three-spined stickleback <i>Gasterosteus aculeatus</i> . <i>BMC Evolutionary Biology</i> , 2009, 9, 57.	3.2	39
34	Experimental parasite infection reveals costs and benefits of paternal effects. <i>Ecology Letters</i> , 2014, 17, 1409-1417.	3.0	29
35	Manipulating sex ratio to increase population growth: the example of the Lesser Kestrel. <i>Animal Conservation</i> , 2007, 10, 236-244.	1.5	28
36	Disentangling the role of MHC-dependent 'good genes' and 'compatible genes' in mate-choice decisions of three-spined sticklebacks <i>Gasterosteus aculeatus</i> under semi-natural conditions. <i>Journal of Fish Biology</i> , 2009, 75, 2122-2142.	0.7	28

#	ARTICLE	IF	CITATIONS
37	The similarity of class II HLA genotypes defines patterns of autoreactivity in idiopathic bone marrow failure disorders. <i>Blood</i> , 2021, 138, 2781-2798.	0.6	27
38	Cryptic haplotype-specific gamete selection yields offspring with optimal MHC immune genes. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 2478-2490.	1.1	26
39	HIV peptidome-wide association study reveals patient-specific epitope repertoires associated with HIV control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 944-949.	3.3	26
40	Sperm velocity in an Alpine whitefish: effects of age, size, condition, fluctuating asymmetry and gonad abnormalities. <i>Journal of Fish Biology</i> , 2007, 71, 672-683.	0.7	25
41	Adaptive value of novel MHC immune gene variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1414-1416.	3.3	22
42	Common Denominators in the Immunobiology of IgG4 Autoimmune Diseases: What Do Glomerulonephritis, Pemphigus Vulgaris, Myasthenia Gravis, Thrombotic Thrombocytopenic Purpura and Autoimmune Encephalitis Have in Common?. <i>Frontiers in Immunology</i> , 2020, 11, 605214.	2.2	21
43	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. <i>Communications Biology</i> , 2021, 4, 113.	2.0	20
44	A field reciprocal transplant experiment reveals asymmetric costs of migration between lake and river ecotypes of three-spined sticklebacks (<i>Gasterosteus aculeatus</i>). <i>Journal of Evolutionary Biology</i> , 2017, 30, 938-950.	0.8	19
45	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. <i>Human Molecular Genetics</i> , 2021, 30, 356-369.	1.4	19
46	Genome-Wide Genotype-Expression Relationships Reveal Both Copy Number and Single Nucleotide Differentiation Contribute to Differential Gene Expression between Stickleback Ecotypes. <i>Genome Biology and Evolution</i> , 2019, 11, 2344-2359.	1.1	16
47	Experimental Parasite Infection Causes Genome-Wide Changes in DNA Methylation. <i>Molecular Biology and Evolution</i> , 2020, 37, 2287-2299.	3.5	16
48	Induction of diploid gynogenesis in an evolutionary model organism, the three-spined stickleback (<i>Gasterosteus aculeatus</i>). <i>BMC Developmental Biology</i> , 2011, 11, 55.	2.1	12
49	The contribution of post-copulatory mechanisms to incipient ecological speciation in sticklebacks. <i>Biology Letters</i> , 2015, 11, 20140933.	1.0	9
50	Transcription in space – environmental vs. genetic effects on differential immune gene expression. <i>Molecular Ecology</i> , 2015, 24, 4583-4585.	2.0	8
51	Unique Pathogen Peptidomes Facilitate Pathogen-Specific Selection and Specialization of MHC Alleles. <i>Molecular Biology and Evolution</i> , 2021, 38, 4376-4387.	3.5	7
52	Targeted analysis of polymorphic loci from low-coverage shotgun sequence data allows accurate genotyping of HLA genes in historical human populations. <i>Scientific Reports</i> , 2020, 10, 7339.	1.6	6
53	Presence of autoantibodies in serum does not impact the occurrence of immune checkpoint inhibitor-induced hepatitis in a prospective cohort of cancer patients. <i>Journal of Cancer Research and Clinical Oncology</i> , 2022, 148, 647-656.	1.2	6
54	Ancient DNA Study in Medieval Europeans Shows an Association Between HLA-DRB1*03 and Paratyphoid Fever. <i>Frontiers in Immunology</i> , 2021, 12, 691475.	2.2	3

#	ARTICLE	IF	CITATIONS
55	Immunopeptidomics toolkit library (IPTK): a python-based modular toolbox for analyzing immunopeptidomics data. BMC Bioinformatics, 2021, 22, 405.	1.2	3
56	Uterine selection for immunocompetent offspring. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E253-E253.	3.3	1
57	The One Past Health workshop: connecting ancient DNA and zoonosis research. BioEssays, 2017, 39, 1700075.	1.2	1