

# Kasper Lage

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

7,446  
citations

109264

35  
h-index

223716

46  
g-index

55  
all docs

55  
docs citations

55  
times ranked

16563  
citing authors

#	ARTICLE	IF	CITATIONS
1	Endothelial ARHGEF26 is an angiogenic factor promoting VEGF signalling. <i>Cardiovascular Research</i> , 2022, 118, 2833-2846.	1.8	3
2	Autism genes converge on asynchronous development of shared neuron classes. <i>Nature</i> , 2022, 602, 268-273.	13.7	180
3	Systematic auditing is essential to debiasing machine learning in biology. <i>Communications Biology</i> , 2021, 4, 183.	2.0	14
4	Targeting acute myeloid leukemia dependency on VCP-mediated DNA repair through a selective second-generation small-molecule inhibitor. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	29
5	Genoppi is an open-source software for robust and standardized integration of proteomic and genetic data. <i>Nature Communications</i> , 2021, 12, 2580.	5.8	15
6	Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. <i>Nature Neuroscience</i> , 2021, 24, 1313-1323.	7.1	44
7	Translating polygenic risk scores for clinical use by estimating the confidence bounds of risk prediction. <i>Nature Communications</i> , 2021, 12, 5276.	5.8	12
8	Prediction of cancer driver genes through network-based moment propagation of mutation scores. <i>Bioinformatics</i> , 2020, 36, i508-i515.	1.8	19
9	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	2.9	48
10	TCF12 haploinsufficiency causes autosomal dominant Kallmann syndrome and reveals network-level interactions between causal loci. <i>Human Molecular Genetics</i> , 2020, 29, 2435-2450.	1.4	10
11	Assessment of network module identification across complex diseases. <i>Nature Methods</i> , 2019, 16, 843-852.	9.0	213
12	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. <i>Nature Communications</i> , 2019, 10, 4064.	5.8	48
13	Single-cell sequencing of neonatal uterus reveals an Misr2+ endometrial progenitor indispensable for fertility. <i>ELife</i> , 2019, 8, .	2.8	36
14	NetSig: network-based discovery from cancer genomes. <i>Nature Methods</i> , 2018, 15, 61-66.	9.0	95
15	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018, 50, 937-943.	9.4	55
16	GeNets: a unified web platform for network-based genomic analyses. <i>Nature Methods</i> , 2018, 15, 543-546.	9.0	62
17	A scored human protein-protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , 2017, 14, 61-64.	9.0	534
18	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. <i>Genome Medicine</i> , 2017, 9, 114.	3.6	86

#	ARTICLE	IF	CITATIONS
19	CD44 Splice Variant v8-10 as a Marker of Serous Ovarian Cancer Prognosis. PLoS ONE, 2016, 11, e0156595.	1.1	38
20	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. Cancer Discovery, 2016, 6, 714-726.	7.7	139
21	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in $\beta$ -Catenin-Active Cancers. Cell Systems, 2016, 3, 302-316.e4.	2.9	55
22	52 Genetic Loci Influencing Myocardial Mass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
23	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	1.5	70
24	Comprehensive assessment of cancer missense mutation clustering in protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5486-95.	3.3	195
25	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	9.0	70
26	Molecular pathogenesis of congenital diaphragmatic hernia revealed by exome sequencing, developmental data, and bioinformatics. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12450-12455.	3.3	49
27	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
28	Protein-protein interactions and genetic diseases: The interactome. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1971-1980.	1.8	105
29	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
30	Mutations in FGF17, IL17RD, DUSP6, SPRY4, and FLRT3 Are Identified in Individuals with Congenital Hypogonadotropic Hypogonadism. American Journal of Human Genetics, 2013, 92, 725-743.	2.6	227
31	Ataxia, Dementia, and Hypogonadotropism Caused by Disordered Ubiquitination. New England Journal of Medicine, 2013, 368, 1992-2003.	13.9	208
32	Genetic and environmental risk factors in congenital heart disease functionally converge in protein networks driving heart development. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14035-14040.	3.3	117
33	Congenital diaphragmatic hernia candidate genes derived from embryonic transcriptomes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2978-2983.	3.3	78
34	Congenital diaphragmatic hernia interval on chromosome 8p23.1 characterized by genetics and protein interaction networks. American Journal of Medical Genetics, Part A, 2012, 158A, 3148-3158.	0.7	42
35	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. Cell Reports, 2012, 2, 419-431.	2.9	493
36	Sequencing Chromosomal Abnormalities Reveals Neurodevelopmental Loci that Confer Risk across Diagnostic Boundaries. Cell, 2012, 149, 525-537.	13.5	534

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37	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <i>Nature Communications</i> , 2012, 3, 876.	5.8	307
38	Huntingtin-interacting protein 14 is a type 1 diabetes candidate protein regulating insulin secretion and Î²-cell apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E681-8.	3.3	55
39	Pervasive Sharing of Genetic Effects in Autoimmune Disease. <i>PLoS Genetics</i> , 2011, 7, e1002254.	1.5	540
40	Proteins Encoded in Genomic Regions Associated with Immune-Mediated Disease Physically Interact and Suggest Underlying Biology. <i>PLoS Genetics</i> , 2011, 7, e1001273.	1.5	450
41	Dissecting spatio-temporal protein networks driving human heart development and related disorders. <i>Molecular Systems Biology</i> , 2010, 6, 381.	3.2	80
42	A large-scale analysis of tissue-specific pathology and gene expression of human disease genes and complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20870-20875.	3.3	288
43	Proteomics Analysis of Cytokine-induced Dysfunction and Death in Insulin-producing INS-1E Cells. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2180-2199.	2.5	73
44	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. <i>Genome Biology</i> , 2007, 8, R253.	13.9	52
45	A human phenome-interactome network of protein complexes implicated in genetic disorders. <i>Nature Biotechnology</i> , 2007, 25, 309-316.	9.4	871
46	A Wiring of the Human Nucleolus. <i>Molecular Cell</i> , 2006, 22, 285-295.	4.5	56