Kasper Lage

List of Publications by Year
in descending order

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	A human phenome-interactome network of protein complexes implicated in genetic disorders. Nature Biotechnology, 2007, 25, 309-316.	9.4	871
2	Pervasive Sharing of Genetic Effects in Autoimmune Disease. PLoS Genetics, 2011, 7, e1002254.	1.5	540
3	Sequencing Chromosomal Abnormalities Reveals Neurodevelopmental Loci that Confer Risk across Diagnostic Boundaries. Cell, 2012, 149, 525-537.	13.5	534
4	A scored human proteinâ€“protein interaction network to catalyze genomic interpretation. Nature Methods, 2017, 14, 61-64.	9.0	534
5	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. Cell Reports, 2012, 2, 419-431.	2.9	493
6	Proteins Encoded in Genomic Regions Associated with Immune-Mediated Disease Physically Interact and Suggest Underlying Biology. PLoS Genetics, 2011, 7, e1001273.	1.5	450
7	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
8	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. Nature Communications, 2012, 3, 876.	5.8	307
9	A large-scale analysis of tissue-specific pathology and gene expression of human disease genes and complexes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20870-20875.	3.3	288
10	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
11	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
12	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	9.0	213
13	Ataxia, Dementia, and Hypogonadotropism Caused by Disordered Ubiquitination. New England Journal of Medicine, 2013, 368, 1992-2003.	13.9	208
14	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
15	Autism genes converge on asynchronous development of shared neuron classes. Nature, 2022, 602, 268-273.	13.7	180
16	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. Cancer Discovery, 2016, 6, 714-726.	7.7	139
17	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
18	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113

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19	Proteinâ€“protein interactions and genetic diseases: The interactome. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1971-1980.	1.8	105
20	NetSig: network-based discovery from cancer genomes. Nature Methods, 2018, 15, 61-66.	9.0	95
21	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
22	Dissecting spatioâ€temporal protein networks driving human heart development and related disorders. Molecular Systems Biology, 2010, 6, 381.	3.2	80
23	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
24	Proteomics Analysis of Cytokine-induced Dysfunction and Death in Insulin-producing INS-1E Cells. Molecular and Cellular Proteomics, 2007, 6, 2180-2199.	2.5	73
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	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	1.5	70
27	GeNets: a unified web platform for network-based genomic analyses. Nature Methods, 2018, 15, 543-546.	9.0	62
28	A Wiring of the Human Nucleolus. Molecular Cell, 2006, 22, 285-295.	4.5	56
29	Huntingtin-interacting protein 14 is a type 1 diabetes candidate protein regulating insulin secretion and Î²-cell apoptosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E681-8.	3.3	55
30	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in Î²-Catenin-Active Cancers. Cell Systems, 2016, 3, 302-316.e4.	2.9	55
31	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. Nature Genetics, 2018, 50, 937-943.	9.4	55
32	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. Genome Biology, 2007, 8, R253.	13.9	52
33	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
34	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. Nature Communications, 2019, 10, 4064.	5.8	48
35	BraInMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. Cell Systems, 2020, 10, 333-350.e14.	2.9	48
36	Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. Nature Neuroscience, 2021, 24, 1313-1323.	7.1	44

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37	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
38	CD44 Splice Variant v8-10 as a Marker of Serous Ovarian Cancer Prognosis. PLoS ONE, 2016, 11, e0156595.	1.1	38
39	Single-cell sequencing of neonatal uterus reveals an Misr2+ endometrial progenitor indispensable for fertility. ELife, 2019, 8, .	2.8	36
40	Targeting acute myeloid leukemia dependency on VCP-mediated DNA repair through a selective second-generation small-molecule inhibitor. Science Translational Medicine, 2021, 13, .	5.8	29
41	Prediction of cancer driver genes through network-based moment propagation of mutation scores. Bioinformatics, 2020, 36, i508-i515.	1.8	19
42	Genoppi is an open-source software for robust and standardized integration of proteomic and genetic data. Nature Communications, 2021, 12, 2580.	5.8	15
43	Systematic auditing is essential to debiasing machine learning in biology. Communications Biology, 2021, 4, 183.	2.0	14
44	Translating polygenic risk scores for clinical use by estimating the confidence bounds of risk prediction. Nature Communications, 2021, 12, 5276.	5.8	12
45	TCF12 haploinsufficiency causes autosomal dominant Kallmann syndrome and reveals network-level interactions between causal loci. Human Molecular Genetics, 2020, 29, 2435-2450.	1.4	10
46	Endothelial ARHGEF26 is an angiogenic factor promoting VEGF signalling. Cardiovascular Research, 2022, 118, 2833-2846.	1.8	3