Luke Jostins

List of Publications by Year
in descending order

36 papers	15,353 citations	249298 26 h-index	388640 36 g-index
42 all docs	42 docs citations	42 times ranked	27799 citing authors

#	Article	IF	Citations
1	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	0.6	37
2	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. Nature Genetics, 2021, 53, 1543-1552.	9.4	96
3	Defactinib inhibits PYK2 phosphorylation of IRF5 and reduces intestinal inflammation. Nature Communications, 2021, 12, 6702.	5.8	13
4	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. Cell Genomics, 2021, 1, 100069.	3.0	15
5	Genomic profiling of T-cell activation suggests increased sensitivity of memory T cells to CD28 costimulation. Genes and Immunity, 2020, 21, 390-408.	2.2	17
6	Loss of IL-10 signaling in macrophages limits bacterial killing driven by prostaglandin E2. Journal of Experimental Medicine, 2020, 217, .	4.2	51
7	Comparison of LABORAS with static incapacitance testing for assessing spontaneous pain behaviour in surgically-induced murine osteoarthritis. Osteoarthritis and Cartilage Open, 2020, 2, 100101.	0.9	2
8	Bayesian metaâ€analysis across genomeâ€wide association studies of diverse phenotypes. Genetic Epidemiology, 2019, 43, 532-547.	0.6	27
9	Active immunisation targeting nerve growth factor attenuates chronic pain behaviour in murine osteoarthritis. Annals of the Rheumatic Diseases, 2019, 78, 672-675.	0.5	37
10	Graphical Model Selection for Gaussian Conditional Random Fields in the Presence of Latent Variables. Journal of the American Statistical Association, 2019, 114, 723-734.	1.8	6
11	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	1.5	66
12	Genome-wide association study identifies distinct genetic contributions to prognosis and susceptibility in Crohn's disease. Nature Genetics, 2017, 49, 262-268.	9.4	250
13	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261.	9.4	943
14	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. Nature Genetics, 2017, 49, 186-192.	9.4	153
15	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. Nature Genetics, 2017, 49, 269-273.	9.4	230
16	Bayesian analysis of genetic association across tree-structured routine healthcare data in the UK Biobank. Nature Genetics, 2017, 49, 1311-1318.	9.4	56
17	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	13.7	473
18	Genetic Complexity of Crohnâ€™s Disease in Two Large Ashkenazi Jewish Families. Gastroenterology, 2016, 151, 698-709.	0.6	54

#	Article	IF	Citations
19	Resolving TYK2 locus genotype-to-phenotype differences in autoimmunity. Science Translational Medicine, 2016, 8, 363ra149.	5.8	186
20	Trinculo: Bayesian and frequentist multinomial logistic regression for genome-wide association studies of multi-category phenotypes. Bioinformatics, 2016, 32, 1898-1900.	1.8	26
21	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
22	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet, The, 2016, 387, 156-167.	6.3	607
23	High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. Nature Genetics, 2015, 47, 172-179.	9.4	280
24	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	9.4	1,965
25	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312
26	Innate Immune Activity Conditions the Effect of Regulatory Variants upon Monocyte Gene Expression. Science, 2014, 343, 1246949.	6.0	706
27	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. Nature, 2013, 498, 232-235.	13.7	184
28	Using Genetic Prediction from Known Complex Disease Loci to Guide the Design of Next-Generation Sequencing Experiments. PLoS ONE, 2013, 8, e76328.	1.1	13
29	Misuse of hierarchical linear models overstates the significance of a reported association between OXTR and prosociality. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1048.	3.3	6
30	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141.	9.4	251
31	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
32	Defective tumor necrosis factor release from CrohnÊ¼s disease macrophages in response to toll-like receptor activation: Relationship to phenotype and genome-wide association susceptibility loci. Inflammatory Bowel Diseases, 2012, 18, 2120-2127.	0.9	28
33	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
34	Genetic risk prediction in complex disease. Human Molecular Genetics, 2011, 20, R182-R188.	1.4	154
35	Imputation of low-frequency variants using the HapMap3 benefits from large, diverse reference sets. European Journal of Human Genetics, 2011, 19, 662-666.	1.4	40
36	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	9.4	2,284