

James C Lee

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

19,064
citations

76326

40
h-index

91884

69
g-index

85
all docs

85
docs citations

85
times ranked

31397
citing authors

#	ARTICLE	IF	CITATIONS
1	How Do We Predict a Patient's Disease Course and Whether They Will Respond to Specific Treatments?. <i>Gastroenterology</i> , 2022, 162, 1383-1395.	1.3	31
2	A purine metabolic checkpoint that prevents autoimmunity and autoinflammation. <i>Cell Metabolism</i> , 2022, 34, 106-124.e10.	16.2	23
3	miR-374a-5p regulates inflammatory genes and monocyte function in patients with inflammatory bowel disease. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	7
4	P110's...Cost-effectiveness of a 17-gene classifier to guide treatment choice in Crohn's disease in the UK. , 2021, , .		0
5	Analytical Mistakes Confound Attempted Validation: A Response to "Transcription and DNA Methylation Patterns of Blood-Derived CD8+ T Cells Are Associated With Age and Inflammatory Bowel Disease But Do Not Predict Prognosis". <i>Gastroenterology</i> , 2021, 160, 2210-2211.	1.3	4
6	Impaired HA-specific T follicular helper cell and antibody responses to influenza vaccination are linked to inflammation in humans. <i>ELife</i> , 2021, 10, .	6.0	26
7	Personalised medicine in Crohn's disease. <i>The Lancet Gastroenterology and Hepatology</i> , 2020, 5, 80-92.	8.1	55
8	Genetic feature engineering enables characterisation of shared risk factors in immune-mediated diseases. <i>Genome Medicine</i> , 2020, 12, 106.	8.2	12
9	Structure of a nascent membrane protein as it folds on the BAM complex. <i>Nature</i> , 2020, 583, 473-478.	27.8	101
10	FAMIN Is a Multifunctional Purine Enzyme Enabling the Purine Nucleotide Cycle. <i>Cell</i> , 2020, 180, 278-295.e23.	28.9	42
11	Resolving mechanisms of immune-mediated disease in primary <sc>CD</sc> 4 T cells. <i>EMBO Molecular Medicine</i> , 2020, 12, e12112.	6.9	30
12	Identifying the immune interactions underlying HLA class I disease associations. <i>ELife</i> , 2020, 9, .	6.0	17
13	Comparative performances of machine learning methods for classifying Crohn Disease patients using genome-wide genotyping data. <i>Scientific Reports</i> , 2019, 9, 10351.	3.3	75
14	The Firre locus produces a trans-acting RNA molecule that functions in hematopoiesis. <i>Nature Communications</i> , 2019, 10, 5137.	12.8	60
15	High-throughput functional analysis of lncRNA core promoters elucidates rules governing tissue specificity. <i>Genome Research</i> , 2019, 29, 344-355.	5.5	100
16	Genetic and Genomic Markers for Prognostication. , 2019, , 323-331.		0
17	A blood-based prognostic biomarker in IBD. <i>Gut</i> , 2019, 68, 1386-1395.	12.1	132
18	Adjustment for index event bias in genome-wide association studies of subsequent events. <i>Nature Communications</i> , 2019, 10, 1561.	12.8	87

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19	EROS/CYBC1 mutations: Decreased NADPH oxidase function and chronic granulomatous disease. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 782-785.e1.	2.9	59
20	Formation of a β -barrel membrane protein is catalyzed by the interior surface of the assembly machine protein BamA. <i>ELife</i> , 2019, 8, .	6.0	45
21	Acetarsol Suppositories: Effective Treatment for Refractory Proctitis in a Cohort of Patients with Inflammatory Bowel Disease. <i>Digestive Diseases and Sciences</i> , 2018, 63, 1011-1015.	2.3	8
22	Genome-wide association studies in Crohn's disease: Past, present and future. <i>Clinical and Translational Immunology</i> , 2018, 7, e1001.	3.8	80
23	PWE-042...Profile biomarker: effect of steroid treatment on a prognostic gene expression signature. , 2018, , .		0
24	PRedicting Outcomes For Crohn's disease using a moLecular biomarkEr (PROFILE): protocol for a multicentre, randomised, biomarker-stratified trial. <i>BMJ Open</i> , 2018, 8, e026767.	1.9	55
25	Reduced monocyte and macrophage TNFSF15/TL1A expression is associated with susceptibility to inflammatory bowel disease. <i>PLoS Genetics</i> , 2018, 14, e1007458.	3.5	30
26	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. <i>Nature Communications</i> , 2018, 9, 2427.	12.8	159
27	Genome-wide association study identifies distinct genetic contributions to prognosis and susceptibility in Crohn's disease. <i>Nature Genetics</i> , 2017, 49, 262-268.	21.4	250
28	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 256-261.	21.4	943
29	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. <i>Nature Genetics</i> , 2017, 49, 186-192.	21.4	153
30	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. <i>Science Immunology</i> , 2017, 2, .	11.9	54
31	Eros is a novel transmembrane protein that controls the phagocyte respiratory burst and is essential for innate immunity. <i>Journal of Experimental Medicine</i> , 2017, 214, 1111-1128.	8.5	50
32	Beyond disease susceptibility...Leveraging genome-wide association studies for new insights into complex disease biology. <i>Hla</i> , 2017, 90, 329-334.	0.6	4
33	Targeted genomic analysis reveals widespread autoimmune disease association with regulatory variants in the TNF superfamily cytokine signalling network. <i>Genome Medicine</i> , 2016, 8, 76.	8.2	17
34	Role of Eros, a novel transmembrane protein, in regulation of host defence. <i>Lancet, The</i> , 2016, 387, S12.	13.7	0
35	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	6.2	21
36	Association Between Genetic Variation in <i>FOXO3</i> and Reductions in Inflammation and Disease Activity in Inflammatory Polyarthritis. <i>Arthritis and Rheumatology</i> , 2016, 68, 2629-2636.	5.6	32

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37	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
38	In Vivo Characterization of Linc-p21 Reveals Functional cis-Regulatory DNA Elements. <i>Cell Reports</i> , 2016, 16, 2178-2186.	6.4	94
39	Characterization of a stalled complex on the β -barrel assembly machine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8717-8722.	7.1	77
40	Leucocyte subset-specific type 1 interferon signatures in SLE and other immune-mediated diseases. <i>RMD Open</i> , 2016, 2, e000183.	3.8	24
41	Predicting Outcomes to Optimize Disease Management in Inflammatory Bowel Diseases. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 1385-1394.	1.3	115
42	The cellular composition of the human immune system is shaped by age and cohabitation. <i>Nature Immunology</i> , 2016, 17, 461-468.	14.5	258
43	MT-HESS: an efficient Bayesian approach for simultaneous association detection in OMICS datasets, with application to eQTL mapping in multiple tissues. <i>Bioinformatics</i> , 2016, 32, 523-532.	4.1	25
44	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. <i>Lancet, The</i> , 2016, 387, 156-167.	13.7	607
45	Insight into Genotype-Phenotype Associations through eQTL Mapping in Multiple Cell Types in Health and Immune-Mediated Disease. <i>PLoS Genetics</i> , 2016, 12, e1005908.	3.5	80
46	Low Serum Levels of MicroRNA-19 Are Associated with a Restricting Crohn's Disease Phenotype. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1926-1934.	1.9	49
47	Pooled Sequencing of 531 Genes in Inflammatory Bowel Disease Identifies an Associated Rare Variant in <i>BTNL2</i> and Implicates Other Immune Related Genes. <i>PLoS Genetics</i> , 2015, 11, e1004955.	3.5	59
48	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. <i>Nature Genetics</i> , 2015, 47, 979-986.	21.4	1,965
49	T-cell exhaustion, co-stimulation and clinical outcome in autoimmunity and infection. <i>Nature</i> , 2015, 523, 612-616.	27.8	535
50	Prognosis in autoimmune and infectious disease: new insights from genetics. <i>Clinical and Translational Immunology</i> , 2014, 3, e15.	3.8	12
51	Safety of the colonoscope magnetic imaging device (ScopeGuide) in patients with implantable cardiac devices. <i>Endoscopy</i> , 2014, 46, 135-138.	1.8	5
52	HLA-DQA1 and HLA-DRB1 variants confer susceptibility to pancreatitis induced by thiopurine immunosuppressants. <i>Nature Genetics</i> , 2014, 46, 1131-1134.	21.4	165
53	Comparison of gene expression microarray data with count-based RNA measurements informs microarray interpretation. <i>BMC Genomics</i> , 2014, 15, 649.	2.8	28
54	Making treatment personal: measurement of exhaustion to target treatment in autoimmunity, infection, and vaccination. <i>Lancet, The</i> , 2014, 383, S12.	13.7	1

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55	Novel developments in Crohn's disease. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2014, 28, 361.	2.4	0
56	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. <i>Gastroenterology</i> , 2013, 145, 339-347.	1.3	149
57	Signatures of CD4 T-cell help and CD8 exhaustion predict clinical outcome in autoimmunity, infection, and vaccination. <i>Lancet, The</i> , 2013, 381, S74.	13.7	2
58	Human SNP Links Differential Outcomes in Inflammatory and Infectious Disease to a FOXO3-Regulated Pathway. <i>Cell</i> , 2013, 155, 57-69.	28.9	200
59	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. <i>Nature</i> , 2013, 498, 232-235.	27.8	184
60	Comparison of Pentax HiLine and Olympus Lucera systems at screening colonoscopy. <i>World Journal of Gastrointestinal Endoscopy</i> , 2013, 5, 62.	1.2	7
61	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. <i>Nature Genetics</i> , 2012, 44, 3-5.	21.4	44
62	Predicting the Course of IBD: Light at the End of the Tunnel?. <i>Digestive Diseases</i> , 2012, 30, 95-99.	1.9	14
63	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012, 491, 119-124.	27.8	4,038
64	Genome-wide association studies and Crohn's disease. <i>Briefings in Functional Genomics</i> , 2011, 10, 71-76.	2.7	41
65	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. <i>Nature Genetics</i> , 2011, 43, 246-252.	21.4	1,201
66	Genetic association between NLRP3 variants and Crohn's disease does not replicate in a large UK panel. <i>Inflammatory Bowel Diseases</i> , 2011, 17, 1387-1391.	1.9	56
67	Gene expression profiling of CD8+ T cells predicts prognosis in patients with Crohn disease and ulcerative colitis. <i>Journal of Clinical Investigation</i> , 2011, 121, 4170-4179.	8.2	268
68	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	27.8	737
69	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 1118-1125.	21.4	2,284
70	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. <i>Nature Genetics</i> , 2009, 41, 1330-1334.	21.4	483
71	<i>Pneumocystis jirovecii</i> pneumonia and pneumomediastinum in an anti-TNF- α naive patient with ulcerative colitis. <i>World Journal of Gastroenterology</i> , 2009, 15, 1897.	3.3	18
72	Renal failure complicating myeloma in pregnancy. <i>Nephrology Dialysis Transplantation</i> , 2007, 22, 3652-3655.	0.7	24

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73	The Endoscopic Healing Index in Crohn's Disease: A Serum Proteomic Biomarker for Monitoring Disease Activity. Inflammatory Bowel Diseases, 0, , .	1.9	1