

Carl A Anderson

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

25,837
citations

76326
40
h-index

138484
58
g-index

66
all docs

66
docs citations

66
times ranked

35655
citing authors

#	ARTICLE	IF	CITATIONS
1	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2022, 162, 859-876.	1.3	37
2	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. <i>Nature Genetics</i> , 2022, 54, 251-262.	21.4	23
3	Common and Rare Variant Prediction and Penetrance of IBD in a Large, Multi-ethnic, Health System-based Biobank Cohort. <i>Gastroenterology</i> , 2021, 160, 1546-1557.	1.3	43
4	Somatic mutations provide important and unique insights into the biology of complex diseases. <i>Trends in Genetics</i> , 2021, 37, 872-881.	6.7	32
5	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. <i>Nature Genetics</i> , 2021, 53, 1543-1552.	21.4	96
6	Somatic Evolution in Non-neoplastic IBD-Affected Colon. <i>Cell</i> , 2020, 182, 672-684.e11.	28.9	122
7	Somatic mosaicism and common genetic variation contribute to the risk of very-early-onset inflammatory bowel disease. <i>Nature Communications</i> , 2020, 11, 995.	12.8	37
8	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. <i>Science Immunology</i> , 2019, 4, .	11.9	98
9	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. <i>Gut</i> , 2018, 67, 1517-1524.	12.1	42
10	Amino acid residues in five separate HLA genes can explain most of the known associations between the MHC and primary biliary cholangitis. <i>PLoS Genetics</i> , 2018, 14, e1007833.	3.5	10
11	Combined Influence of B-Cell Receptor Rearrangement and Somatic Hypermutation on B-Cell Class-Switch Fate in Health and in Chronic Lymphocytic Leukemia. <i>Frontiers in Immunology</i> , 2018, 9, 1784.	4.8	22
12	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. <i>PLoS Genetics</i> , 2018, 14, e1007329.	3.5	66
13	Homozygous loss-of-function mutations in SLC26A7 cause goitrous congenital hypothyroidism. <i>JCI Insight</i> , 2018, 3, .	5.0	44
14	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
15	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
16	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
17	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 269-273.	21.4	230
18	Fine-mapping inflammatory bowel disease loci to single-variant resolution. <i>Nature</i> , 2017, 547, 173-178.	27.8	473

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19	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
20	Comprehensive Screening of Eight Known Causative Genes in Congenital Hypothyroidism With Gland-in-Situ. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 4521-4531.	3.6	82
21	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. <i>Nature Communications</i> , 2016, 7, 12342.	12.8	50
22	Genome-wide rare copy number variation screening in ulcerative colitis identifies potential susceptibility loci. <i>BMC Medical Genetics</i> , 2016, 17, 26.	2.1	14
23	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
24	Generation of primary human intestinal T cell transcriptomes reveals differential expression at genetic risk loci for immune-mediated disease. <i>Gut</i> , 2015, 64, 250-259.	12.1	30
25	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. <i>Nature Communications</i> , 2015, 6, 8019.	12.8	245
26	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	2.9	68
27	Genetics in PSC: What Do the “Risk Genes” Teach Us?. <i>Clinical Reviews in Allergy and Immunology</i> , 2015, 48, 154-164.	6.5	27
28	Genetic studies of Crohn's disease: Past, present and future. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2014, 28, 373-386.	2.4	87
29	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	21.4	1,213
30	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
31	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. <i>Nature Genetics</i> , 2013, 45, 670-675.	21.4	339
32	Genome-wide association meta-analysis identifies new endometriosis risk loci. <i>Nature Genetics</i> , 2012, 44, 1355-1359.	21.4	257
33	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. <i>Nature Genetics</i> , 2012, 44, 1137-1141.	21.4	251
34	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012, 491, 119-124.	27.8	4,038
35	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. <i>Nature Genetics</i> , 2011, 43, 51-54.	21.4	261
36	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

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37	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. <i>Nature Genetics</i> , 2011, 43, 329-332.	21.4	441
38	Basic statistical analysis in genetic case-control studies. <i>Nature Protocols</i> , 2011, 6, 121-133.	12.0	426
39	Synthetic Associations Are Unlikely to Account for Many Common Disease Genome-Wide Association Signals. <i>PLoS Biology</i> , 2011, 9, e1000580.	5.6	102
40	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	21.4	581
41	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
42	Data quality control in genetic case-control association studies. <i>Nature Protocols</i> , 2010, 5, 1564-1573.	12.0	1,030
43	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
44	Common variants at five new loci associated with early-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2009, 41, 1335-1340.	21.4	459
45	Marker selection for genetic case-control association studies. <i>Nature Protocols</i> , 2009, 4, 743-752.	12.0	43
46	Investigation of Crohn's Disease Risk Loci in Ulcerative Colitis Further Defines Their Molecular Relationship. <i>Gastroenterology</i> , 2009, 136, 523-529.e3.	1.3	198
47	A genome-wide linkage study in families with major depression and co-morbid unexplained swelling. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008, 147B, 356-362.	1.7	0
48	Evaluating the Effects of Imputation on the Power, Coverage, and Cost Efficiency of Genome-wide SNP Platforms. <i>American Journal of Human Genetics</i> , 2008, 83, 112-119.	6.2	93
49	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 710-712.	21.4	403
50	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 955-962.	21.4	2,422
51	A Genome-Wide Linkage Scan for Age at Menarche in Three Populations of European Descent. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2008, 93, 3965-3970.	3.6	40
52	Genomewide Study of Multiple Sclerosis. <i>New England Journal of Medicine</i> , 2007, 357, 2199-2201.	27.0	54
53	Confirmation of the role of ATG16L1 as a Crohn's disease susceptibility gene. <i>Inflammatory Bowel Diseases</i> , 2007, 13, 941-946.	1.9	98
54	Sequence variants in the autophagy gene IRGM and multiple other replicating loci contribute to Crohn's disease susceptibility. <i>Nature Genetics</i> , 2007, 39, 830-832.	21.4	1,063

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55	Estimation of Variance Components for Age at Menarche in Twin Families. Behavior Genetics, 2007, 37, 668-677.	2.1	69
56	A Simple Linear Regression Method for Quantitative Trait Loci Linkage Analysis With Censored Observations. Genetics, 2006, 173, 1735-1745.	2.9	4