Carl A Anderson

List of Publications by Year
in descending order

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56	25,837	87401 40	156644 58
papers	citations	h-index	g-index

66	66	66	39089
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	0.6	37
2	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	9.4	23
3	Common and Rare Variant Prediction and Penetrance of IBD in a Large, Multi-ethnic, Health System-based Biobank Cohort. Gastroenterology, 2021, 160, 1546-1557.	0.6	43
4	Somatic mutations provide important and unique insights into the biology of complex diseases. Trends in Genetics, 2021, 37, 872-881.	2.9	32
5	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
6	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	13.5	122
7	Somatic mosaicism and common genetic variation contribute to the risk of very-early-onset inflammatory bowel disease. Nature Communications, 2020, 11, 995.	5.8	37
8	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. Science Immunology, 2019, 4, .	5.6	98
9	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. Gut, 2018, 67, 1517-1524.	6.1	42
10	Amino acid residues in five separate HLA genes can explain most of the known associations between the MHC and primary biliary cholangitis. PLoS Genetics, 2018, 14, e1007833.	1.5	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. Frontiers in Immunology, 2018, 9, 1784.	2.2	22
12	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	1.5	66
13	Homozygous loss-of-function mutations in SLC26A7 cause goitrous congenital hypothyroidism. JCI Insight, 2018, 3, .	2.3	44
14	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
15	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261.	9.4	943
16	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
17	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
18	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	13.7	473

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19	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
20	Comprehensive Screening of Eight Known Causative Genes in Congenital Hypothyroidism With Gland-in-Situ. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4521-4531.	1.8	82
21	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. Nature Communications, 2016, 7, 12342.	5.8	50
22	Genome-wide rare copy number variation screening in ulcerative colitis identifies potential susceptibility loci. BMC Medical Genetics, 2016, 17, 26.	2.1	14
23	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
24	Generation of primary human intestinal T cell transcriptomes reveals differential expression at genetic risk loci for immune-mediated disease. Gut, 2015, 64, 250-259.	6.1	30
25	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. Nature Communications, 2015, 6, 8019.	5.8	245
26	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
27	Genetics in PSC: What Do the â€œRisk Genesâ€•Teach Us?. Clinical Reviews in Allergy and Immunology, 2015, 48, 154-164.	2.9	27
28	Genetic studies of Crohn's disease: Past, present and future. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2014, 28, 373-386.	1.0	87
29	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
30	Human SNP Links Differential Outcomes in Inflammatory and Infectious Disease to a FOXO3-Regulated Pathway. Cell, 2013, 155, 57-69.	13.5	200
31	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	9.4	339
32	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	9.4	257
33	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141.	9.4	251
34	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
35	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261
36	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201

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37	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2011, 43, 329-332.	9.4	441
38	Basic statistical analysis in genetic case-control studies. Nature Protocols, 2011, 6, 121-133.	5.5	426
39	Synthetic Associations Are Unlikely to Account for Many Common Disease Genome-Wide Association Signals. PLoS Biology, 2011, 9, e1000580.	2.6	102
40	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	9.4	581
41	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
42	Data quality control in genetic case-control association studies. Nature Protocols, 2010, 5, 1564-1573.	5.5	1,030
43	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. Nature Genetics, 2009, 41, 1330-1334.	9.4	483
44	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	9.4	459
45	Marker selection for genetic caseâ€“control association studies. Nature Protocols, 2009, 4, 743-752.	5.5	43
46	Investigation of Crohn's Disease Risk Loci in Ulcerative Colitis Further Defines Their Molecular Relationship. Gastroenterology, 2009, 136, 523-529.e3.	0.6	198
47	A genomeâ€wide linkage study in families with major depression and coâ€morbid unexplained swelling. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 356-362.	1.1	0
48	Evaluating the Effects of Imputation on the Power, Coverage, and Cost Efficiency of Genome-wide SNP Platforms. American Journal of Human Genetics, 2008, 83, 112-119.	2.6	93
49	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. Nature Genetics, 2008, 40, 710-712.	9.4	403
50	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature Genetics, 2008, 40, 955-962.	9.4	2,422
51	A Genome-Wide Linkage Scan for Age at Menarche in Three Populations of European Descent. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 3965-3970.	1.8	40
52	Genomewide Study of Multiple Sclerosis. New England Journal of Medicine, 2007, 357, 2199-2201.	13.9	54
53	Confirmation of the role of ATG16l1 as a CrohnÊ¼s disease susceptibility gene. Inflammatory Bowel Diseases, 2007, 13, 941-946.	0.9	98
54	Sequence variants in the autophagy gene IRGM and multiple other replicating loci contribute to Crohn's disease susceptibility. Nature Genetics, 2007, 39, 830-832.	9.4	1,063

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55	Estimation of Variance Components for Age at Menarche in Twin Families. Behavior Genetics, 2007, 37, 668-677.	1.4	69
56	A Simple Linear Regression Method for Quantitative Trait Loci Linkage Analysis With Censored Observations. Genetics, 2006, 173, 1735-1745.	1.2	4