Carl A Anderson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8004130/publications.pdf

Version: 2024-02-01

56	25,837	76326	138484
papers	citations	40 h-index	58 g-index

66	66	66	35655
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	27.8	4,038
2	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature Genetics, 2008, 40, 955-962.	21.4	2,422
3	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
4	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	21.4	2,284
5	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	21.4	1,965
6	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	21.4	1,213
7	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	21.4	1,201
8	Sequence variants in the autophagy gene IRGM and multiple other replicating loci contribute to Crohn's disease susceptibility. Nature Genetics, 2007, 39, 830-832.	21.4	1,063
9	Data quality control in genetic case-control association studies. Nature Protocols, 2010, 5, 1564-1573.	12.0	1,030
10	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261.	21.4	943
11	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	21.4	581
12	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. Nature Genetics, 2009, 41, 1330-1334.	21.4	483
13	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	27.8	473
14	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	21.4	459
15	Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2011, 43, 329-332.	21.4	441
16	Basic statistical analysis in genetic case-control studies. Nature Protocols, 2011, 6, 121-133.	12.0	426
17	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. Nature Genetics, 2008, 40, 710-712.	21.4	403
18	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	21.4	339

#	Article	IF	Citations
19	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	21.4	261
20	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	21.4	257
21	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141.	21.4	251
22	Genome-wide association study identifies distinct genetic contributions to prognosis and susceptibility in Crohn's disease. Nature Genetics, 2017, 49, 262-268.	21.4	250
23	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. Nature Communications, 2015, 6, 8019.	12.8	245
24	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.	21.4	230
25	Human SNP Links Differential Outcomes in Inflammatory and Infectious Disease to a FOXO3-Regulated Pathway. Cell, 2013, 155, 57-69.	28.9	200
26	Investigation of Crohn's Disease Risk Loci in Ulcerative Colitis Further Defines Their Molecular Relationship. Gastroenterology, 2009, 136, 523-529.e3.	1.3	198
27	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. Nature Genetics, 2017, 49, 186-192.	21.4	153
28	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	28.9	122
29	Synthetic Associations Are Unlikely to Account for Many Common Disease Genome-Wide Association Signals. PLoS Biology, 2011, 9, e1000580.	5.6	102
30	Confirmation of the role of ATG16l1 as a CrohnÊ¼s disease susceptibility gene. Inflammatory Bowel Diseases, 2007, 13, 941-946.	1.9	98
31	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. Science Immunology, 2019, 4, .	11.9	98
32	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.	21.4	96
33	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.	6.2	93
34	Genetic studies of Crohn's disease: Past, present and future. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2014, 28, 373-386.	2.4	87
35	Comprehensive Screening of Eight Known Causative Genes in Congenital Hypothyroidism With Gland-in-Situ. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4521-4531.	3.6	82
36	Estimation of Variance Components for Age at Menarche in Twin Families. Behavior Genetics, 2007, 37, 668-677.	2.1	69

#	Article	IF	Citations
37	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
38	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329.	3.5	66
39	Genomewide Study of Multiple Sclerosis. New England Journal of Medicine, 2007, 357, 2199-2201.	27.0	54
40	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. Nature Communications, 2016, 7, 12342.	12.8	50
41	Homozygous loss-of-function mutations in SLC26A7 cause goitrous congenital hypothyroidism. JCI Insight, 2018, 3, .	5.0	44
42	Marker selection for genetic caseâ€“control association studies. Nature Protocols, 2009, 4, 743-752.	12.0	43
43	Common and Rare Variant Prediction and Penetrance of IBD in a Large, Multi-ethnic, Health System-based Biobank Cohort. Gastroenterology, 2021, 160, 1546-1557.	1.3	43
44	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. Gut, 2018, 67, 1517-1524.	12.1	42
45	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.	3.6	40
46	Somatic mosaicism and common genetic variation contribute to the risk of very-early-onset inflammatory bowel disease. Nature Communications, 2020, 11, 995.	12.8	37
47	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	1.3	37
48	Somatic mutations provide important and unique insights into the biology of complex diseases. Trends in Genetics, 2021, 37, 872-881.	6.7	32
49	Generation of primary human intestinal T cell transcriptomes reveals differential expression at genetic risk loci for immune-mediated disease. Gut, 2015, 64, 250-259.	12.1	30
50	Genetics in PSC: What Do the â€œRisk Genesâ€•Teach Us?. Clinical Reviews in Allergy and Immunology, 2015, 48, 154-164.	6.5	27
51	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	21.4	23
52	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.	4.8	22
53	Genome-wide rare copy number variation screening in ulcerative colitis identifies potential susceptibility loci. BMC Medical Genetics, 2016, 17, 26.	2.1	14
54	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.	3.5	10

#	Article	IF	Citations
55	A Simple Linear Regression Method for Quantitative Trait Loci Linkage Analysis With Censored Observations. Genetics, 2006, 173, 1735-1745.	2.9	4
56	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.	1.7	0