# Jeffrey C Barrett

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2946629/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 95 papers | 51,831 citations | 14653 66 h-index | 40976 93 g-index |
| 117 all docs | 117 docs citations | 117 times ranked | 65751 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 | A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 2007, 316, 889-894. | 12.6 | 3,884 |
| 3 | The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503. | 27.8 | 3,708 |
| 4 | Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature Genetics, 2008, 40, 955-962. | 21.4 | 2,422 |
| 5 | A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283. | 21.4 | 2,421 |
| 6 | 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 |
| 7 | Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215. | 27.8 | 2,254 |
| 8 | Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341. | 12.6 | 2,040 |
| 9 | 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 |
| 10 | Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. Nature Genetics, 2009, 41, 703-707. | 21.4 | 1,513 |
| 11 | Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337. | 21.4 | 1,298 |
| 12 | Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360. | 21.4 | 1,213 |
| 13 | 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 |
| 14 | A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828. | 12.6 | 1,095 |
| 15 | 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 |
| 16 | The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90. | 27.8 | 1,014 |
| 17 | Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593, 266-269. | 27.8 | 1,001 |
| 18 | Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261. | 21.4 | 943 |

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|---|---|---|---|
| 19 | Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302. | 21.4 | 871 |
| 20 | Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720. | 27.8 | 737 |
| 21 | Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201. | 21.4 | 682 |
| 22 | Genetic diagnosis of developmental disorders in the DDD study: a scalable analysis of genome-wide research data. Lancet, The, 2015, 385, 1305-1314. | 13.7 | 651 |
| 23 | Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518. | 21.4 | 617 |
| 24 | Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet, The, 2016, 387, 156-167. | 13.7 | 607 |
| 25 | Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature Genetics, 2015, 47, 381-386. | 21.4 | 589 |
| 26 | Phosphoinositide 3-Kinase Î´ Gene Mutation Predisposes to Respiratory Infection and Airway Damage. Science, 2013, 342, 866-871. | 12.6 | 541 |
| 27 | Pervasive Sharing of Genetic Effects in Autoimmune Disease. PLoS Genetics, 2011, 7, e1002254. | 3.5 | 540 |
| 28 | Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178. | 27.8 | 473 |
| 29 | Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340. | 21.4 | 459 |
| 30 | 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 |
| 31 | Evaluating coverage of genome-wide association studies. Nature Genetics, 2006, 38, 659-662. | 21.4 | 389 |
| 32 | Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577. | 14.8 | 388 |
| 33 | Open Targets Platform: new developments and updates two years on. Nucleic Acids Research, 2019, 47, D1056-D1065. | 14.5 | 364 |
| 34 | Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994. | 14.5 | 355 |
| 35 | Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494. | 3.5 | 351 |
| 36 | Distinct genetic architectures for syndromic and nonsyndromic congenital heart defects identified by exome sequencing. Nature Genetics, 2016, 48, 1060-1065. | 21.4 | 351 |

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|---|---|---|---|
| 37 | Evidence for 28 genetic disorders discovered by combining healthcare and research data. Nature, 2020, 586, 757-762. | 27.8 | 343 |
| 38 | Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583. | 2.5 | 339 |
| 39 | Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113. | 21.4 | 312 |
| 40 | Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. Nucleic Acids Research, 2021, 49, D1311-D1320. | 14.5 | 295 |
| 41 | Haploview: Visualization and Analysis of SNP Genotype Data. Cold Spring Harbor Protocols, 2009, 2009, pdb.ip71. | 0.3 | 290 |
| 42 | 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. | 21.4 | 280 |
| 43 | Making new genetic diagnoses with old data: iterative reanalysis and reporting from genome-wide data in 1,133 families with developmental disorders. Genetics in Medicine, 2018, 20, 1216-1223. | 2.4 | 255 |
| 44 | Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. Nature Genetics, 2012, 44, 1137-1141. | 21.4 | 251 |
| 45 | HLA-DQA1*05 Carriage Associated With Development of Anti-Drug Antibodies to Infliximab and Adalimumab in Patients With Crohnâ€™s Disease. Gastroenterology, 2020, 158, 189-199. | 1.3 | 249 |
| 46 | Common genetic variants contribute to risk of rare severe neurodevelopmental disorders. Nature, 2018, 562, 268-271. | 27.8 | 246 |
| 47 | De novo mutations in regulatory elements in neurodevelopmental disorders. Nature, 2018, 555, 611-616. | 27.8 | 232 |
| 48 | An open approach to systematically prioritize causal variants and genes at all published human GWAS trait-associated loci. Nature Genetics, 2021, 53, 1527-1533. | 21.4 | 208 |
| 49 | Human SNP Links Differential Outcomes in Inflammatory and Infectious Disease to a FOXO3-Regulated Pathway. Cell, 2013, 155, 57-69. | 28.9 | 200 |
| 50 | The contribution of rare variants to risk of schizophrenia in individuals with and without intellectual disability. Nature Genetics, 2017, 49, 1167-1173. | 21.4 | 200 |
| 51 | Investigation of Crohn's Disease Risk Loci in Ulcerative Colitis Further Defines Their Molecular Relationship. Gastroenterology, 2009, 136, 523-529.e3. | 1.3 | 198 |
| 52 | Strategies for fine-mapping complex traits. Human Molecular Genetics, 2015, 24, R111-R119. | 2.9 | 191 |
| 53 | Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. Nature, 2013, 498, 232-235. | 27.8 | 184 |
| 54 | Quantifying the contribution of recessive coding variation to developmental disorders. Science, 2018, 362, 1161-1164. | 12.6 | 158 |

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|---|---|---|---|
| 55 | Susceptibility to tuberculosis is associated with variants in the ASAP1 gene encoding a regulator of dendritic cell migration. Nature Genetics, 2015, 47, 523-527. | 21.4 | 156 |
| 56 | Genetic risk prediction in complex disease. Human Molecular Genetics, 2011, 20, R182-R188. | 2.9 | 154 |
| 57 | 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 |
| 58 | Understanding inflammatory bowel disease via immunogenetics. Journal of Autoimmunity, 2015, 64, 91-100. | 6.5 | 144 |
| 59 | Discovery of four recessive developmental disorders using probabilistic genotype and phenotype matching among 4,125 families. Nature Genetics, 2015, 47, 1363-1369. | 21.4 | 133 |
| 60 | HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322. | 21.4 | 123 |
| 61 | Worldwide population differentiation at disease-associated SNPs. BMC Medical Genomics, 2008, 1, 22. | 1.5 | 114 |
| 62 | Synthetic Associations Are Unlikely to Account for Many Common Disease Genome-Wide Association Signals. PLoS Biology, 2011, 9, e1000580. | 5.6 | 102 |
| 63 | Confirmation of the role of ATG16l1 as a CrohnÊ¼s disease susceptibility gene. Inflammatory Bowel Diseases, 2007, 13, 941-946. | 1.9 | 98 |
| 64 | Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. PLoS Genetics, 2013, 9, e1003509. | 3.5 | 95 |
| 65 | 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 |
| 66 | Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. Nature Communications, 2019, 10, 2176. | 12.8 | 83 |
| 67 | Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511. | 27.8 | 80 |
| 68 | Genome Wide Association Study of Fetal Hemoglobin in Sickle Cell Anemia in Tanzania. PLoS ONE, 2014, 9, e111464. | 2.5 | 78 |
| 69 | The intermediate filament protein, vimentin, is a regulator of NOD2 activity. Gut, 2013, 62, 695-707. | 12.1 | 71 |
| 70 | How next-generation sequencing is transforming complex disease genetics. Trends in Genetics, 2013, 29, 23-30. | 6.7 | 70 |
| 71 | Pathogenicity and selective constraint on variation near splice sites. Genome Research, 2019, 29, 159-170. | 5.5 | 70 |
| 72 | Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. PLoS Genetics, 2018, 14, e1007329. | 3.5 | 66 |

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|---|---|---|---|
| 73 | Pooled Sequencing of 531 Genes in Inflammatory Bowel Disease Identifies an Associated Rare Variant in BTNL2 and Implicates Other Immune Related Genes. PLoS Genetics, 2015, 11, e1004955. | 3.5 | 59 |
| 74 | Genetic Complexity of Crohnâ€™s Disease in Two Large Ashkenazi Jewish Families. Gastroenterology, 2016, 151, 698-709. | 1.3 | 54 |
| 75 | Synthetic associations in the context of genome-wide association scan signals. Human Molecular Genetics, 2010, 19, R137-R144. | 2.9 | 53 |
| 76 | Marker selection for genetic caseâ€“control association studies. Nature Protocols, 2009, 4, 743-752. | 12.0 | 43 |
| 77 | Imputation of low-frequency variants using the HapMap3 benefits from large, diverse reference sets. European Journal of Human Genetics, 2011, 19, 662-666. | 2.8 | 40 |
| 78 | COVID-19 due to the B.1.617.2 (Delta) variant compared to B.1.1.7 (Alpha) variant of SARS-CoV-2: a prospective observational cohort study. Scientific Reports, 2022, 12, . | 3.3 | 39 |
| 79 | Evoker: a visualization tool for genotype intensity data. Bioinformatics, 2010, 26, 1786-1787. | 4.1 | 37 |
| 80 | 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 |
| 81 | Using human genetics to make new medicines. Nature Reviews Genetics, 2015, 16, 561-562. | 16.3 | 25 |
| 82 | Genetic association of fetal-hemoglobin levels in individuals with sickle cell disease in Tanzania maps to conserved regulatory elements within the MYB core enhancer. BMC Medical Genetics, 2015, 16, 4. | 2.1 | 24 |
| 83 | Multiomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. Gastroenterology, 2018, 155, e1-e4. | 1.3 | 24 |
| 84 | Returning genome sequences to research participants: Policy and practice. Wellcome Open Research, 2017, 2, 15. | 1.8 | 24 |
| 85 | Variation at Spike position 142 in SARS-CoV-2 Delta genomes is a technical artifact caused by dropout of a sequencing amplicon. Wellcome Open Research, 0, 6, 305. | 1.8 | 24 |
| 86 | To what extent do scans of non-synonymous SNPs complement denser genome-wide association studies?. European Journal of Human Genetics, 2008, 16, 718-723. | 2.8 | 23 |
| 87 | Characterization of Expression Quantitative Trait Loci in the Human Colon. Inflammatory Bowel Diseases, 2015, 21, 251-256. | 1.9 | 22 |
| 88 | High-throughput and quantitative genome-wide messenger RNA sequencing for molecular phenotyping. BMC Genomics, 2015, 16, 578. | 2.8 | 19 |
| 89 | Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934. | 3.2 | 17 |
| 90 | Exome Sequencing and Genotyping Identify a Rare Variant inNLRP7Gene Associated With Ulcerative Colitis. Journal of Crohn's and Colitis, 2018, 12, 321-326. | 1.3 | 14 |

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|---|---|---|---|
| 91 | Using Genetic Prediction from Known Complex Disease Loci to Guide the Design of Next-Generation Sequencing Experiments. PLoS ONE, 2013, 8, e76328. | 2.5 | 13 |
| 92 | Olorin: combining gene flow with exome sequencing in large family studies of complex disease. Bioinformatics, 2012, 28, 3320-3321. | 4.1 | 10 |
| 93 | 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. | 7.1 | 6 |
| 94 | Complex Disease Genes and Their Discovery. , 2013, , 87-97. | | 0 |
| 95 | Complex Disease Genes and Their Discovery. , 2019, , 79-89. | | 0 |