Sarah E Hunt

List of Publications by Year
in descending order

88 papers	67,638 citations	17405 63 h-index	49773 87 g-index
94 all docs	94 docs citations	94 times ranked	91768 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	The Ensembl Variant Effect Predictor. Genome Biology, 2016, 17, 122.	3.8	5,181
3	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
4	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710
5	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
6	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
7	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
8	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
9	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
10	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
11	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
12	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
13	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
14	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
15	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
16	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
17	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
18	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103

#	Article	IF	Citations
19	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
20	The DNA sequence of the human X chromosome. Nature, 2005, 434, 325-337.	13.7	985
21	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
22	The Fine-Scale Structure of Recombination Rate Variation in the Human Genome. Science, 2004, 304, 581-584.	6.0	941
23	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	9.4	918
24	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
25	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	9.4	871
26	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856
27	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	9.4	778
28	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
29	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	9.4	682
30	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
31	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
32	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	9.4	558
33	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
34	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
35	Genome-Wide Associations of Gene Expression Variation in Humans. PLoS Genetics, 2005, 1, e78.	1.5	467
36	DNA microarrays for comparative genomic hybridization based on DOP-PCR amplification of BAC and PAC clones. Genes Chromosomes and Cancer, 2003, 36, 361-374.	1.5	439

#	Article	IF	Citations
37	Ensembl Genomes 2020â€"enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	6.5	416
38	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
39	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. Nature Genetics, 2011, 43, 117-120.	9.4	390
40	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	377
41	A first-generation linkage disequilibrium map of human chromosome 22. Nature, 2002, 418, 544-548.	13.7	376
42	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	9.4	375
43	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	6.3	373
44	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	9.4	345
45	Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. Nature Genetics, 2013, 45, 664-669.	9.4	337
46	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. Genome Research, 2004, 14, 1176-1187.	2.4	260
47	Genetic Variation Near the Hepatocyte Nuclear Factor-4Â Gene Predicts Susceptibility to Type 2 Diabetes. Diabetes, 2004, 53, 1141-1149.	0.3	255
48	A High-Resolution Linkage-Disequilibrium Map of the Human Major Histocompatibility Complex and First Generation of Tag Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2005, 76, 634-646.	2.6	237
49	The Influence of Recombination on Human Genetic Diversity. PLoS Genetics, 2006, 2, e148.	1.5	231
50	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. Human Molecular Genetics, 2011, 20, 345-353.	1.4	202
51	Investigation of Crohn's Disease Risk Loci in Ulcerative Colitis Further Defines Their Molecular Relationship. Gastroenterology, 2009, 136, 523-529.e3.	0.6	198
52	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
53	The impact of SNP density on fine-scale patterns of linkage disequilibrium. Human Molecular Genetics, 2004, 13, 577-588.	1.4	184
54	Linkage Disequilibrium Mapping via Cladistic Analysis of Single-Nucleotide Polymorphism Haplotypes. American Journal of Human Genetics, 2004, 75, 35-43.	2.6	173

#	Article	IF	Citations
55	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	9.4	162
56	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. Human Molecular Genetics, 2013, 22, 1039-1049.	1.4	122
57	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
58	Common variants in the HLA-DRB1â€“HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	9.4	86
59	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. Nature Communications, 2019, 10, 2373.	5.8	86
60	The portability of tagSNPs across populations: A worldwide survey. Genome Research, 2006, 16, 323-330.	2.4	82
61	A Variant in LDLR Is Associated With Abdominal Aortic Aneurysm. Circulation: Cardiovascular Genetics, 2013, 6, 498-504.	5.1	78
62	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	5.8	72
63	A SNP Resource for Human Chromosome 22: Extracting Dense Clusters of SNPs From the Genomic Sequence. Genome Research, 2001, 11, 170-178.	2.4	69
64	A Genome-wide Survey of the Prevalence and Evolutionary Forces Acting on Human Nonsense SNPs. American Journal of Human Genetics, 2009, 84, 224-234.	2.6	69
65	A Whole-Genome Mouse BAC Microarray With 1-Mb Resolution for Analysis of DNA Copy Number Changes by Array Comparative Genomic Hybridization. Genome Research, 2003, 14, 188-196.	2.4	62
66	The GENCODE exome: sequencing the complete human exome. European Journal of Human Genetics, 2011, 19, 827-831.	1.4	58
67	Efficiency and consistency of haplotype tagging of dense SNP maps in multiple samples. Human Molecular Genetics, 2004, 13, 2557-2565.	1.4	54
68	Clustered Coding Variants in the Glutamate Receptor Complexes of Individuals with Schizophrenia and Bipolar Disorder. PLoS ONE, 2011, 6, e19011.	1.1	54
69	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. Bioinformatics, 2019, 35, 2315-2317.	1.8	52
70	The European Variation Archive: a FAIR resource of genomic variation for all species. Nucleic Acids Research, 2022, 50, D1216-D1220.	6.5	50
71	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	1.6	45
72	Impact of population structure, effective bottleneck time, and allele frequency on linkage disequilibrium maps. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 18075-18080.	3.3	44

#	Article	IF	Citations
73	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. Nature Genetics, 2012, 44, 3-5.	9.4	44
74	A Genome-wide Association Analysis of a Broad Psychosis Phenotype Identifies Three Loci for Further Investigation. Biological Psychiatry, 2014, 75, 386-397.	0.7	44
75	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	2.6	39
76	Variation Within the Gene Encoding the Upstream Stimulatory Factor 1 Does Not Influence Susceptibility to Type 2 Diabetes in Samples From Populations With Replicated Evidence of Linkage to Chromosome 1q. Diabetes, 2006, 55, 2541-2548.	0.3	37
77	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. Diabetes, 2008, 57, 3161-3165.	0.3	37
78	A comparison of tagging methods and their tagging space. Human Molecular Genetics, 2005, 14, 2757-2767.	1.4	36
79	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€”A tutorial. Human Mutation, 2022, 43, 986-997.	1.1	30
80	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. Human Molecular Genetics, 2013, 22, 4653-4660.	1.4	29
81	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. Genome Research, 2005, 15, 1503-1510.	2.4	26
82	Genetic Determinants of Major Blood Lipids in Pakistanis Compared With Europeans. Circulation: Cardiovascular Genetics, 2010, 3, 348-357.	5.1	25
83	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	3.0	18
84	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. Nucleic Acids Research, 2022, 50, D765-D770.	6.5	10
85	DECIPHER: Supporting the interpretation and sharing of rare disease phenotypeâ€linked variant data to advance diagnosis and research. Human Mutation, 2022, , .	1.1	10
86	Scripting Analyses of Genomes in Ensembl Plants. Methods in Molecular Biology, 2022, 2443, 27-55.	0.4	6
87	The value of primary transcripts to the clinical and nonâ€clinical genomics community: Survey results and roadmap for improvements. Molecular Genetics & Genomic Medicine, 2021, 9, e1786.	0.6	5
88	Annotation and curation of human genomic variations: an ELIXIR Implementation Study. F1000Research, 0, 9, 1207.	0.8	0