Sarah E Hunt

List of Publications by Year in Descending Order

88 papers	48,962 citations	58 h-index	94 g-index
94 ext. papers	60,879 ext. citations	21.1 avg, IF	5.91 L-index

#	Paper	IF	Citations
88	Scripting Analyses of Genomes in Ensembl Plants.. *Methods in Molecular Biology*, **2022**, 2443, 27-55	1.4	0
87	DECIPHER: Supporting the interpretation and sharing of rare disease phenotype-linked variant data to advance diagnosis and research.. *Human Mutation*, **2022**,	4.7	2
86	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
85	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification.. *Cell Genomics*, **2021**, 1, 100027-100027		4
84	The European Variation Archive: a FAIR resource of genomic variation for all species. *Nucleic Acids Research*, **2021**,	20.1	10
83	Ensembl 2022. *Nucleic Acids Research*, **2021**,	20.1	72
82	Ensembl 2021. *Nucleic Acids Research*, **2021**, 49, D884-D891	20.1	324
81	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. *Nucleic Acids Research*, **2021**,	20.1	3
80	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. *Molecular Genetics & Genomic Medicine*, **2021**, e1786	2.3	2
79	Ensembl 2020. *Nucleic Acids Research*, **2020**, 48, D682-D688	20.1	645
78	Ensembl Genomes 2020-enabling non-vertebrate genomic research. *Nucleic Acids Research*, **2020**, 48, D689-D695	20.1	214
77	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. *Nature Communications*, **2019**, 10, 2373	17.4	22
76	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. *Bioinformatics*, **2019**, 35, 2315-2317	7.2	19
75	Ensembl 2019. *Nucleic Acids Research*, **2019**, 47, D745-D751	20.1	554
74	Ensembl 2018. *Nucleic Acids Research*, **2018**, 46, D754-D761	20.1	1822
73	Ensembl variation resources. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	230
72	Ensembl 2017. *Nucleic Acids Research*, **2017**, 45, D635-D642	20.1	404

71	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal of the American Heart Association*, **2016**, 5,	6	34
70	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. *American Journal of Human Genetics*, **2016**, 98, 1092-1100	11	30
69	Ensembl 2016. *Nucleic Acids Research*, **2016**, 44, D710-6	20.1	1094
68	The Ensembl Variant Effect Predictor. *Genome Biology*, **2016**, 17, 122	18.3	2595
67	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
66	Ensembl 2015. *Nucleic Acids Research*, **2015**, 43, D662-9	20.1	1013
65	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. *Nature Communications*, **2014**, 5, 4204	17.4	54
64	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
63	A genome-wide association analysis of a broad psychosis phenotype identifies three loci for further investigation. *Biological Psychiatry*, **2014**, 75, 386-97	7.9	36
62	Ensembl 2014. *Nucleic Acids Research*, **2014**, 42, D749-55	20.1	1087
61	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
60	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
59	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
58	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. *Nature Genetics*, **2013**, 45, 208-13	36.3	76
57	Ensembl 2013. *Nucleic Acids Research*, **2013**, 41, D48-55	20.1	797
56	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
55	Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. *Nature Genetics*, **2013**, 45, 664-9	36.3	256
54	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. *Human Molecular Genetics*, **2013**, 22, 4653-60	5.6	24

53	A variant in LDLR is associated with abdominal aortic aneurysm. *Circulation: Cardiovascular Genetics*, **2013**, 6, 498-504		58
52	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson\'s disease. *Human Molecular Genetics*, **2013**, 22, 1039-49	5.6	96
51	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 1336-40	36.3	436
50	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. *Lancet, The*, **2012**, 380, 815-23	40	275
49	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. *Nature Genetics*, **2012**, 44, 328-33	36.3	314
48	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
47	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett\'s esophagus. *Nature Genetics*, **2012**, 44, 1131-6	36.3	139
46	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. *Nature Genetics*, **2011**, 43, 117-20	36.3	319
45	The GENCODE exome: sequencing the complete human exome. *European Journal of Human Genetics*, **2011**, 19, 827-31	5.3	50
44	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, 761-7	36.3	646
43	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. *American Journal of Human Genetics*, **2011**, 89, 619-27	11	145
42	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
41	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. *Nature Genetics*, **2011**, 43, 1193-201	36.3	535
40	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, 345-53	5.6	178
39	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. *Nature Genetics*, **2011**, 44, 3-5	36.3	39
38	Clustered coding variants in the glutamate receptor complexes of individuals with schizophrenia and bipolar disorder. *PLoS ONE*, **2011**, 6, e19011	3.7	48
37	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
36	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135

35	Multiple common variants for celiac disease influencing immune gene expression. *Nature Genetics*, **2010**, 42, 295-302	36.3	727
34	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. *Nature Genetics*, **2010**, 42, 985-90	36.3	773
33	Genetic determinants of major blood lipids in Pakistanis compared with Europeans. *Circulation: Cardiovascular Genetics*, **2010**, 3, 348-57		20
32	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
31	Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nature Genetics*, **2009**, 41, 657-65	36.3	297
30	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. *Nature Genetics*, **2009**, 41, 1330-4	36.3	411
29	A genome-wide survey of the prevalence and evolutionary forces acting on human nonsense SNPs. *American Journal of Human Genetics*, **2009**, 84, 224-34	11	58
28	Investigation of Crohn\'s disease risk loci in ulcerative colitis further defines their molecular relationship. *Gastroenterology*, **2009**, 136, 523-9.e3	13.3	152
27	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
26	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn\'s disease. *Nature Genetics*, **2008**, 40, 710-2	36.3	353
25	Population-specific risk of type 2 diabetes conferred by HNF4A P2 promoter variants: a lesson for replication studies. *Diabetes*, **2008**, 57, 3161-5	0.9	33
24	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
23	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
22	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
21	The influence of recombination on human genetic diversity. *PLoS Genetics*, **2006**, 2, e148	6	185
20	The portability of tagSNPs across populations: a worldwide survey. *Genome Research*, **2006**, 16, 323-30	9.7	72
19	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, 2541-8	0.9	33
18	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, 634-46	11	209

17	The DNA sequence of the human X chromosome. *Nature*, **2005**, 434, 325-37	50.4	822
16	Genome-wide associations of gene expression variation in humans. *PLoS Genetics*, **2005**, 1, e78	6	431
15	A comparison of tagging methods and their tagging space. *Human Molecular Genetics*, **2005**, 14, 2757-67	5.6	33
14	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. *Genome Research*, **2005**, 15, 1503-10	9.7	22
13	The impact of SNP density on fine-scale patterns of linkage disequilibrium. *Human Molecular Genetics*, **2004**, 13, 577-88	5.6	171
12	Efficiency and consistency of haplotype tagging of dense SNP maps in multiple samples. *Human Molecular Genetics*, **2004**, 13, 2557-65	5.6	50
11	Complete MHC haplotype sequencing for common disease gene mapping. *Genome Research*, **2004**, 14, 1176-87	9.7	235
10	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, 18075-80	11.5	33
9	A whole-genome mouse BAC microarray with 1-Mb resolution for analysis of DNA copy number changes by array comparative genomic hybridization. *Genome Research*, **2004**, 14, 188-96	9.7	55
8	The fine-scale structure of recombination rate variation in the human genome. *Science*, **2004**, 304, 581-4	33.3	796
7	Genetic variation near the hepatocyte nuclear factor-4 alpha gene predicts susceptibility to type 2 diabetes. *Diabetes*, **2004**, 53, 1141-9	0.9	229
6	Linkage disequilibrium mapping via cladistic analysis of single-nucleotide polymorphism haplotypes. *American Journal of Human Genetics*, **2004**, 75, 35-43	11	168
5	DNA microarrays for comparative genomic hybridization based on DOP-PCR amplification of BAC and PAC clones. *Genes Chromosomes and Cancer*, **2003**, 36, 361-74	5	416
4	A first-generation linkage disequilibrium map of human chromosome 22. *Nature*, **2002**, 418, 544-8	50.4	342
3	A SNP resource for human chromosome 22: extracting dense clusters of SNPs from the genomic sequence. *Genome Research*, **2001**, 11, 170-8	9.7	53
2	Annotation and curation of human genomic variations: an ELIXIR Implementation Study. *F1000Research*,9, 1207	3.6	
1	The GA4GH Variation Representation Specification (VRS): a Computational Framework for the Precise Representation and Federated Identification of Molecular Variation		3