

Sarah E Hunt

List of Publications by Year in descending order

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Version: 2024-02-01

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	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770.	6.5	10
2	The European Variation Archive: a FAIR resource of genomic variation for all species. <i>Nucleic Acids Research</i> , 2022, 50, D1216-D1220.	6.5	50
3	Ensembl 2022. <i>Nucleic Acids Research</i> , 2022, 50, D988-D995.	6.5	1,103
4	Scripting Analyses of Genomes in Ensembl Plants. <i>Methods in Molecular Biology</i> , 2022, 2443, 27-55.	0.4	6
5	DECIPHER: Supporting the interpretation and sharing of rare disease phenotype-linked variant data to advance diagnosis and research. <i>Human Mutation</i> , 2022, , .	1.1	10
6	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictor—a tutorial. <i>Human Mutation</i> , 2022, 43, 986-997.	1.1	30
7	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021, 49, D884-D891.	6.5	1,231
8	The value of primary transcripts to the clinical and non-clinical genomics community: Survey results and roadmap for improvements. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1786.	0.6	5
9	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
10	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. <i>Cell Genomics</i> , 2021, 1, 100027.	3.0	18
11	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
12	Ensembl Genomes 2020—enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	6.5	416
13	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. <i>Nature Communications</i> , 2019, 10, 2373.	5.8	86
14	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. <i>Bioinformatics</i> , 2019, 35, 2315-2317.	1.8	52
15	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019, 47, D745-D751.	6.5	879
16	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018, 46, D754-D761.	6.5	2,710
17	Ensembl variation resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	377
18	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017, 45, D635-D642.	6.5	535

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19	The Ensembl Variant Effect Predictor. <i>Genome Biology</i> , 2016, 17, 122.	3.8	5,181
20	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. <i>Journal of the American Heart Association</i> , 2016, 5, .	1.6	45
21	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016, 98, 1092-1100.	2.6	39
22	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016, 44, D710-D716.	6.5	1,372
23	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
24	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015, 43, D662-D669.	6.5	1,145
25	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014, 42, D749-D755.	6.5	1,211
26	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014, 5, 4204.	5.8	72
27	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	9.4	959
28	A Genome-wide Association Analysis of a Broad Psychosis Phenotype Identifies Three Loci for Further Investigation. <i>Biological Psychiatry</i> , 2014, 75, 386-397.	0.7	44
29	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	9.4	1,395
30	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	9.4	1,213
31	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 25-33.	9.4	1,439
32	Common variants in the HLA-DRB1 and HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013, 45, 208-213.	9.4	86
33	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
34	Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. <i>Nature Genetics</i> , 2013, 45, 664-669.	9.4	337
35	Genome-wide association study of intraocular pressure identifies the GLCC1/ICA1 region as a glaucoma susceptibility locus. <i>Human Molecular Genetics</i> , 2013, 22, 4653-4660.	1.4	29
36	A Variant in <i>LDLR</i> Is Associated With Abdominal Aortic Aneurysm. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 498-504.	5.1	78

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37	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. <i>Human Molecular Genetics</i> , 2013, 22, 1039-1049.	1.4	122
38	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. <i>Nature Genetics</i> , 2012, 44, 3-5.	9.4	44
39	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. <i>Nature Genetics</i> , 2012, 44, 1131-1136.	9.4	162
40	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 1336-1340.	9.4	558
41	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. <i>Lancet</i> , The, 2012, 380, 815-823.	6.3	373
42	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , 2012, 44, 328-333.	9.4	375
43	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	9.4	1,748
44	Ensembl 2013. <i>Nucleic Acids Research</i> , 2012, 41, D48-D55.	6.5	856
45	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	13.7	2,400
46	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. <i>Nature Genetics</i> , 2011, 43, 1193-1201.	9.4	682
47	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. <i>Nature Genetics</i> , 2011, 43, 117-120.	9.4	390
48	The GENCODE exome: sequencing the complete human exome. <i>European Journal of Human Genetics</i> , 2011, 19, 827-831.	1.4	58
49	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. <i>Nature Genetics</i> , 2011, 43, 761-767.	9.4	778
50	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. <i>American Journal of Human Genetics</i> , 2011, 89, 619-627.	2.6	185
51	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. <i>Human Molecular Genetics</i> , 2011, 20, 345-353.	1.4	202
52	Clustered Coding Variants in the Glutamate Receptor Complexes of Individuals with Schizophrenia and Bipolar Disorder. <i>PLoS ONE</i> , 2011, 6, e19011.	1.1	54
53	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	13.7	737
54	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	13.7	2,625

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55	Multiple common variants for celiac disease influencing immune gene expression. <i>Nature Genetics</i> , 2010, 42, 295-302.	9.4	871
56	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010, 42, 985-990.	9.4	918
57	Genetic Determinants of Major Blood Lipids in Pakistanis Compared With Europeans. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 348-357.	5.1	25
58	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	9.4	662
59	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
60	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. <i>Nature Genetics</i> , 2009, 41, 1330-1334.	9.4	483
61	A Genome-wide Survey of the Prevalence and Evolutionary Forces Acting on Human Nonsense SNPs. <i>American Journal of Human Genetics</i> , 2009, 84, 224-234.	2.6	69
62	Investigation of Crohn's Disease Risk Loci in Ulcerative Colitis Further Defines Their Molecular Relationship. <i>Gastroenterology</i> , 2009, 136, 523-529.e3.	0.6	198
63	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	9.4	1,179
64	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 710-712.	9.4	403
65	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. <i>Diabetes</i> , 2008, 57, 3161-3165.	0.3	37
66	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. <i>Nature Genetics</i> , 2007, 39, 1329-1337.	9.4	1,298
67	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
68	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
69	The Influence of Recombination on Human Genetic Diversity. <i>PLoS Genetics</i> , 2006, 2, e148.	1.5	231
70	The portability of tagSNPs across populations: A worldwide survey. <i>Genome Research</i> , 2006, 16, 323-330.	2.4	82
71	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. <i>Diabetes</i> , 2006, 55, 2541-2548.	0.3	37
72	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	13.7	985

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73	Genome-Wide Associations of Gene Expression Variation in Humans. <i>PLoS Genetics</i> , 2005, 1, e78.	1.5	467
74	A comparison of tagging methods and their tagging space. <i>Human Molecular Genetics</i> , 2005, 14, 2757-2767.	1.4	36
75	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. <i>Genome Research</i> , 2005, 15, 1503-1510.	2.4	26
76	A High-Resolution Linkage-Disequilibrium Map of the Human Major Histocompatibility Complex and First Generation of Tag Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2005, 76, 634-646.	2.6	237
77	The impact of SNP density on fine-scale patterns of linkage disequilibrium. <i>Human Molecular Genetics</i> , 2004, 13, 577-588.	1.4	184
78	Efficiency and consistency of haplotype tagging of dense SNP maps in multiple samples. <i>Human Molecular Genetics</i> , 2004, 13, 2557-2565.	1.4	54
79	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. <i>Genome Research</i> , 2004, 14, 1176-1187.	2.4	260
80	Impact of population structure, effective bottleneck time, and allele frequency on linkage disequilibrium maps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 18075-18080.	3.3	44
81	The Fine-Scale Structure of Recombination Rate Variation in the Human Genome. <i>Science</i> , 2004, 304, 581-584.	6.0	941
82	Genetic Variation Near the Hepatocyte Nuclear Factor-4 Gene Predicts Susceptibility to Type 2 Diabetes. <i>Diabetes</i> , 2004, 53, 1141-1149.	0.3	255
83	Linkage Disequilibrium Mapping via Cladistic Analysis of Single-Nucleotide Polymorphism Haplotypes. <i>American Journal of Human Genetics</i> , 2004, 75, 35-43.	2.6	173
84	DNA microarrays for comparative genomic hybridization based on DOP-PCR amplification of BAC and PAC clones. <i>Genes Chromosomes and Cancer</i> , 2003, 36, 361-374.	1.5	439
85	A Whole-Genome Mouse BAC Microarray With 1-Mb Resolution for Analysis of DNA Copy Number Changes by Array Comparative Genomic Hybridization. <i>Genome Research</i> , 2003, 14, 188-196.	2.4	62
86	A first-generation linkage disequilibrium map of human chromosome 22. <i>Nature</i> , 2002, 418, 544-548.	13.7	376
87	A SNP Resource for Human Chromosome 22: Extracting Dense Clusters of SNPs From the Genomic Sequence. <i>Genome Research</i> , 2001, 11, 170-178.	2.4	69
88	Annotation and curation of human genomic variations: an ELIXIR Implementation Study. <i>F1000Research</i> , 0, 9, 1207.	0.8	0