Erin N Smith

List of Publications by Year
in descending order

25 papers	1,916 citations	489802 18 h-index	651938 25 g-index
31 all docs	31 docs citations	31 times ranked	5447 citing authors

#	Article	IF	Citations
1	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. Nature Genetics, 2021, 53, 942-948.	9.4	234
2	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. Nature Communications, 2020, 11, 2928.	5.8	22
3	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. Nature Communications, 2020, 11, 2927.	5.8	67
4	Fibrinogen gamma gene rs2066865 and risk of cancer-related venous thromboembolism. Haematologica, 2020, 105, 1963-1968.	1.7	10
5	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
6	Association of Human iPSC Gene Signatures and X Chromosome Dosage with Two Distinct Cardiac Differentiation Trajectories. Stem Cell Reports, 2019, 13, 924-938.	2.3	44
7	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
8	Human iPSC-Derived Retinal Pigment Epithelium: A Model System for Prioritizing and Functionally Characterizing Causal Variants at AMD Risk Loci. Stem Cell Reports, 2019, 12, 1342-1353.	2.3	32
9	Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. Nature Communications, 2019, 10, 1054.	5.8	100
10	Activation of hedgehog signaling associates with early disease progression in chronic lymphocytic leukemia. Blood, 2019, 133, 2651-2663.	0.6	15
11	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. Nature Genetics, 2019, 51, 1506-1517.	9.4	35
12	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.3	7
13	Identification of Common and Rare Genetic Variation Associated With Plasma Protein Levels Using Whole-Exome Sequencing and Mass Spectrometry. Circulation Genomic and Precision Medicine, 2018, 11, e002170.	1.6	26
14	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
15	Insights into the Mutational Burden of Human Induced Pluripotent Stem Cells from an Integrative Multi-Omics Approach. Cell Reports, 2018, 24, 883-894.	2.9	85
16	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. Human Genetics, 2017, 136, 897-902.	1.8	46
17	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 533-546.e7.	5.2	157
18	iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. Stem Cell Reports, 2017, 8, 1086-1100.	2.3	147

#	Article	IF	Citations
19	Aberrant DNA Methylation in Human iPSCs Associates with MYC-Binding Motifs in a Clone-Specific Manner Independent of Genetics. Cell Stem Cell, 2017, 20, 505-517.e6.	5.2	33
20	Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. BMC Bioinformatics, 2017, 18, 207.	1.2	35
21	Joint effects of cancer and variants in the factor 5 gene on the risk of venous thromboembolism. Haematologica, 2016, 101, 1046-1053.	1.7	28
22	Fine-mapping, novel loci identification, and SNP association transferability in a genome-wide association study of QRS duration in African Americans. Human Molecular Genetics, 2016, 25, 4350-4368.	1.4	37
23	Associations Between Common and Rare Exonic Genetic Variants and Serum Levels of 20 Cardiovascular-Related Proteins. Circulation: Cardiovascular Genetics, 2016, 9, 375-383.	5.1	18
24	Consanguinity and rare mutations outside of MCCC genes underlie nonspecific phenotypes of MCCD. Genetics in Medicine, 2015, 17, 660-667.	1.1	9
25	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158