Sarah J Lindsay

List of Publications by Year
in descending order

15 papers	16,540 citations	687363 13 h-index	888059 17 g-index
20 all docs	20 docs citations	20 times ranked	34745 citing authors

#	Article	IF	Citations
1	Similarities and differences in patterns of germline mutation between mice and humans. Nature Communications, 2019, 10, 4053.	12.8	79
2	Paternal exposure to benzo(a)pyrene induces genome-wide mutations in mouse offspring. Communications Biology, 2019, 2, 228.	4.4	25
3	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	28.9	66
4	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	21.4	502
5	The genome-wide effects of ionizing radiation on mutation induction in the mammalian germline. Nature Communications, 2015, 6, 6684.	12.8	112
6	Absence of Heterozygosity Due to Template Switching during Replicative Rearrangements. American Journal of Human Genetics, 2015, 96, 555-564.	6.2	45
7	The Rate of Nonallelic Homologous Recombination in Males Is Highly Variable, Correlated between Monozygotic Twins and Independent of Age. PLoS Genetics, 2014, 10, e1004195.	3.5	17
8	Rare Variants in NR2F2 Cause Congenital Heart Defects in Humans. American Journal of Human Genetics, 2014, 94, 574-585.	6.2	146
9	Genome-wide SNP and CNV analysis identifies common and low-frequency variants associated with severe early-onset obesity. Nature Genetics, 2013, 45, 513-517.	21.4	278
10	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
11	Variation in genome-wide mutation rates within and between human families. Nature Genetics, 2011, 43, 712-714.	21.4	525
12	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
13	Mutation spectrum revealed by breakpoint sequencing of human germline CNVs. Nature Genetics, 2010, 42, 385-391.	21.4	211
14	A Chromosomal Rearrangement Hotspot Can Be Identified from Population Genetic Variation and Is Coincident with a Hotspot for Allelic Recombination. American Journal of Human Genetics, 2006, 79, 890-902.	6.2	92
15	Shotgun haplotyping: a novel method for surveying allelic sequence variation. Nucleic Acids Research, 2005, 33, e152-e152.	14.5	7