Similarities and differences in patterns of germline mut

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Citation Report

#	Article	IF	Citations
1	De Novo Mutations Reflect Development and Aging of the Human Germline. Trends in Genetics, 2019, 35, 828-839.	2.9	80
2	Overlooked roles of DNA damage and maternal age in generating human germline mutations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9491-9500.	3.3	155
3	Age-related accumulation of de novo mitochondrial mutations in mammalian oocytes and somatic tissues. PLoS Biology, 2020, 18, e3000745.	2.6	62
4	Changes in life history and population size can explain the relative neutral diversity levels on X and autosomes in extant human populations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20063-20069.	3.3	5
5	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. PLoS Biology, 2020, 18, e3000838.	2.6	64
6	Germline Mutation of PLCD1 Contributes to Human Multiple Pilomatricomas through Protein Kinase D/Extracellular Signalâ€“Regulated Kinase1/2 Cascade and TRPV6. Journal of Investigative Dermatology, 2021, 141, 533-544.	0.3	5
7	Inbred lab mice are not isogenic: genetic variation within inbred strains used to infer the mutation rate per nucleotide site. Heredity, 2021, 126, 107-116.	1.2	20
8	Meiosis and beyond â€“ understanding the mechanistic and evolutionary processes shaping the germline genome. Biological Reviews, 2021, 96, 822-841.	4.7	25
11	The germline mutational process in rhesus macaque and its implications for phylogenetic dating. GigaScience, 2021, 10, .	3.3	26
12	Stability across the Whole Nuclear Genome in the Presence and Absence of DNA Mismatch Repair. Cells, 2021, 10, 1224.	1.8	8
14	The rate and molecular spectrum of mutation are selectively maintained in yeast. Nature Communications, 2021, 12, 4044.	5.8	18
15	The challenge and promise of estimating the de novo mutation rate from wholeâ€genome comparisons among closely related individuals. Molecular Ecology, 2021, 30, 6087-6100.	2.0	26
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18	The origin of human mutation in light of genomic data. Nature Reviews Genetics, 2021, 22, 672-686.	7.7	26
19	Pedigree-based and phylogenetic methods support surprising patterns of mutation rate and spectrum in the gray mouse lemur. Heredity, 2021, 127, 233-244.	1.2	30
23	Genomic footprints of Quaternary colonization and population expansion in the Patagonianâ€Fuegian region rules out a separate southern refugium in Tierra del Fuego. Journal of Biogeography, 2021, 48, 2656-2670.	1.4	7
25	Pleiotropy or linkage? Their relative contributions to the genetic correlation of quantitative traits and detection by multitrait GWA studies. Genetics, 2021, 219, .	1.2	24
26	Whole Exome for the Identification of Mutations in CD8+ T-Cells. Methods in Molecular Biology, 2021, 2325, 155-182.	0.4	0

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27	Differences between germline genomes of monozygotic twins. Nature Genetics, 2021, 53, 27-34.	9.4	83
32	The Mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. ELife, 2022, 11, .	2.8	38
33	Distinct sequence features underlie microdeletions and gross deletions in the human genome. Human Mutation, 2022, 43, 328-346.	1.1	3
34	How Sequence Context-Dependent Mutability Drives Mutation Rate Variation in the Genome. Genome Biology and Evolution, 2022, 14, .	1.1	10
35	Parental folate deficiency induces birth defects in mice accompanied with increased de novo mutations. Cell Discovery, 2022, 8, 18.	3.1	3
37	Role of sperm DNA damage in creating de-novo mutations in human offspring: the â€˜post-meiotic oocyte collusionâ€™ hypothesis. Reproductive BioMedicine Online, 2022, 45, 109-124.	1.1	18
38	Advanced age increases frequencies of de novo mitochondrial mutations in macaque oocytes and somatic tissues. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2118740119.	3.3	14
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41	Cost-Efficient Sequence-Based Nonextensible Oligonucleotide in Real-Time PCR and High-Throughput Sequencing. ACS Sensors, 2022, 7, 1165-1174.	4.0	0
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43	A natural mutator allele shapes mutation spectrum variation in mice. Nature, 2022, 605, 497-502.	13.7	38
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50	Cancer Risk and Mutational Patterns Following Organ Transplantation. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	1
51	A paternal bias in germline mutation is widespread in amniotes and can arise independently of cell division numbers. ELife, 0, 11, .	2.8	20
53	De novo mutations, genetic mosaicism and human disease. Frontiers in Genetics, 0, 13, .	1.1	19
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63	Cytosine base editors induce off-target mutations and adverse phenotypic effects in transgenic mice. Nature Communications, 2023, 14, .	5.8	10
64	Evolution of the SARS-CoV-2 Mutational Spectrum. Molecular Biology and Evolution, 2023, 40, .	3.5	16
65	The origins and functional effects of postzygotic mutations throughout the human life span. Science, 2023, 380, .	6.0	6
66	Identification and characterisation of de novo germline structural variants in two commercial pig lines using trio-based whole genome sequencing. BMC Genomics, 2023, 24, .	1.2	0