Raheleh Rahbari

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3276412/publications.pdf

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23 papers	2,712 citations	394421 19 h-index	642732 23 g-index
35 all docs	35 docs citations	35 times ranked	4734 citing authors

#	Article	IF	Citations
1	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	21.4	502
2	The mutational landscape of normal human endometrial epithelium. Nature, 2020, 580, 640-646.	27.8	338
3	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	27.8	254
4	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
5	Histone Lysine Methylases and Demethylases in the Landscape of Human Developmental Disorders. American Journal of Human Genetics, 2018, 102, 175-187.	6.2	204
6	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	27.8	180
7	Inherent mosaicism and extensive mutation of human placentas. Nature, 2021, 592, 80-85.	27.8	126
8	A novel L1 retrotransposon marker for HeLa cell line identification. BioTechniques, 2009, 46, 277-284.	1.8	115
9	Extensive phylogenies of human development inferred from somatic mutations. Nature, 2021, 597, 387-392.	27.8	87
10	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	27.8	87
11	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	21.4	85
12	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. Nature Communications, 2017, 8, 303.	12.8	81
13	Similarities and differences in patterns of germline mutation between mice and humans. Nature Communications, 2019, 10, 4053.	12.8	79
14	Bi-allelic Loss-of-Function CACNA1B Mutations in Progressive Epilepsy-Dyskinesia. American Journal of Human Genetics, 2019, 104, 948-956.	6.2	45
15	Detection of structural mosaicism from targeted and whole-genome sequencing data. Genome Research, 2017, 27, 1704-1714.	5.5	44
16	Genetic and chemotherapeutic influences on germline hypermutation. Nature, 2022, 605, 503-508.	27.8	43
17	Transduction-Specific ATLAS Reveals a Cohort of Highly Active L1 Retrotransposons in Human Populations. Human Mutation, 2013, 34, 974-985.	2.5	38
18	Common clonal origin of conventional T cells and induced regulatory T cells in breast cancer patients. Nature Communications, 2021, 12, 1119.	12.8	26

#	Article	IF	Citations
19	Meiosis and beyond â€“ understanding the mechanistic and evolutionary processes shaping the germline genome. Biological Reviews, 2021, 96, 822-841.	10.4	25
20	Understanding the Genomic Structure of Copy-Number Variation of the Low-Affinity Fcî³ Receptor Region Allows Confirmation of the Association ofFCGR3BDeletion with Rheumatoid Arthritis. Human Mutation, 2017, 38, 390-399.	2.5	21
21	Somatic Mutations Detected in Parkinson Disease Could Affect Genes With a Role in Synaptic and Neuronal Processes. Frontiers in Aging, 2022, 3, .	2.6	7
22	Combining Amplification Typing of L1 Active Subfamilies (ATLAS) with High-Throughput Sequencing. Methods in Molecular Biology, 2016, 1400, 95-106.	0.9	6
23	IAP Display: A Simple Method to Identify Mouse Strain Specific IAP Insertions. Molecular Biotechnology, 2011, 47, 243-252.	2.4	4