Erika M Kvikstad

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3702908/publications.pdf

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15	1,160	623734 14	996975 15
papers	citations	h-index	g-index

18	18	18	2827
all docs	docs citations	times ranked	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.	21.4	234
2	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	5.5	206
3	The complete costs of genome sequencing: a microcosting study in cancer and rare diseases from a single center in the United Kingdom. Genetics in Medicine, 2020, 22, 85-94.	2.4	133
4	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	6.2	72
5	Identification of a new VHL exon and complex splicing alterations in familial erythrocytosis or von Hippel-Lindau disease. Blood, 2018, 132, 469-483.	1.4	70
6	A Whole-Genome Shotgun Optical Map of Yersinia pestis Strain KIM. Applied and Environmental Microbiology, 2002, 68, 6321-6331.	3.1	65
7	Single-Molecule Approach to Bacterial Genomic Comparisons via Optical Mapping. Journal of Bacteriology, 2004, 186, 7773-7782.	2.2	63
8	A Macaque's-Eye View of Human Insertions and Deletions: Differences in Mechanisms. PLoS Computational Biology, 2007, 3, e176.	3.2	55
9	Whole-Genome Shotgun Optical Mapping of Rhodobacter sphaeroides strain 2.4.1 and Its Use for Whole-Genome Shotgun Sequence Assembly. Genome Research, 2003, 13, 2142-2151.	5.5	49
10	The (r)evolution of SINE versus LINE distributions in primate genomes: Sex chromosomes are important. Genome Research, 2010, 20, 600-613.	5.5	48
11	Shotgun optical mapping of the entire Leishmania major Friedlin genome. Molecular and Biochemical Parasitology, 2004, 138, 97-106.	1.1	41
12	Ride the wavelet: A multiscale analysis of genomic contexts flanking small insertions and deletions. Genome Research, 2009, 19, 1153-1164.	5.5	27
13	Clinically actionable mutation profiles in patients with cancer identified by whole-genome sequencing. Journal of Physical Education and Sports Management, 2018, 4, a002279.	1.2	21
14	Strong Heterogeneity in Mutation Rate Causes Misleading Hallmarks of Natural Selection on Indel Mutations in the Human Genome. Molecular Biology and Evolution, 2014, 31, 23-36.	8.9	16
15	A high throughput screen for active human transposable elements. BMC Genomics, 2018, 19, 115.	2.8	14