David Porubsky

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1636202/publications.pdf

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26	4,887	331670	526287
papers	citations	21 h-index	27 g-index

41	41	41	4608
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	6.2	32
2	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
3	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
4	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
5	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	17.5	127
6	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	27.8	221
7	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
8	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. Nature Communications, 2021, 12, 1935.	12.8	64
9	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
10	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. Bioinformatics, 2020, 36, 1260-1261.	4.1	32
11	Improved assembly and variant detection of a haploid human genome using singleâ€molecule, highâ€fidelity long reads. Annals of Human Genetics, 2020, 84, 125-140.	0.8	100
12	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59
13	Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. Genome Research, 2020, 30, 1680-1693.	5.5	16
14	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
15	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
16	Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. Science, 2019, 366, .	12.6	65
17	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
18	Human-specific tandem repeat expansion and differential gene expression during primate evolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23243-23253.	7.1	82

#	Article	IF	Citations
19	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	4.1	24
20	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
21	Genome-wide mapping of sister chromatid exchange events in single yeast cells using Strand-seq. ELife, 2017, 6, .	6.0	30
22	Single-cell whole genome sequencing reveals no evidence for common aneuploidy in normal and Alzheimerâ€™s disease neurons. Genome Biology, 2016, 17, 116.	8.8	118
23	Characterizing polymorphic inversions in human genomes by single-cell sequencing. Genome Research, 2016, 26, 1575-1587.	5.5	67
24	Direct chromosome-length haplotyping by single-cell sequencing. Genome Research, 2016, 26, 1565-1574.	5.5	52
25	Single-cell sequencing reveals karyotype heterogeneity in murine and human malignancies. Genome Biology, 2016, 17, 115.	8.8	178
26	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. Cell Stem Cell, 2014, 15, 295-309.	11.1	137