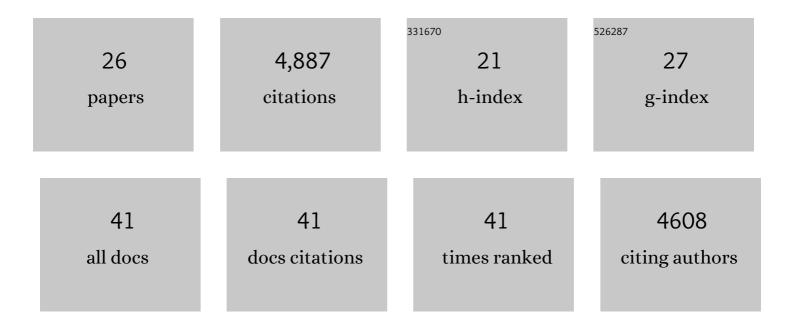
David Porubsky

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1636202/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
3	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
4	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
5	The structure, function and evolution of a complete human chromosome 8. Nature, 2021, 593, 101-107.	27.8	221
6	Single-cell sequencing reveals karyotype heterogeneity in murine and human malignancies. Genome Biology, 2016, 17, 115.	8.8	178
7	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. Cell Stem Cell, 2014, 15, 295-309.	11.1	137
8	Segmental duplications and their variation in a complete human genome. Science, 2022, 376, eabj6965.	12.6	130
9	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
10	Single-cell whole genome sequencing reveals no evidence for common aneuploidy in normal and Alzheimer's disease neurons. Genome Biology, 2016, 17, 116.	8.8	118
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	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
13	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
14	Characterizing polymorphic inversions in human genomes by single-cell sequencing. Genome Research, 2016, 26, 1575-1587.	5.5	67
15	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
16	Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. Science, 2019, 366, .	12.6	65
17	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. Nature Communications, 2021, 12, 1935.	12.8	64
18	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59

DAVID PORUBSKY

#	Article	IF	CITATIONS
19	Direct chromosome-length haplotyping by single-cell sequencing. Genome Research, 2016, 26, 1565-1574.	5.5	52
20	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
21	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
22	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. Bioinformatics, 2020, 36, 1260-1261.	4.1	32
23	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	6.2	32
24	Genome-wide mapping of sister chromatid exchange events in single yeast cells using Strand-seq. ELife, 2017, 6, .	6.0	30
25	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	4.1	24
26	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

reuse during primate evolution. Genome Research, 2020, 30, 1680-1693. 26