# 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 | 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 Alzheimerâ€™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 |

| # | 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 |