Rajiv C Mccoy

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7475380/publications.pdf

Version: 2024-02-01

37 papers 4,536 citations

331259 21 h-index 35 g-index

48 all docs

48 docs citations

48 times ranked 5282 citing authors

| # | Article | IF | Citations |
|----|--|-----|-----------|
| 1 | Maternal selection of human embryos in early gestation: Insights from recurrent miscarriage. Seminars in Cell and Developmental Biology, 2022, 131, 14-24. | 2.3 | 30 |
| 2 | A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533. | 6.0 | 144 |
| 3 | The complete sequence of a human genome. Science, 2022, 376, 44-53. | 6.0 | 1,222 |
| 4 | Origins and mechanisms leading to aneuploidy in human eggs. Prenatal Diagnosis, 2021, 41, 620-630. | 1.1 | 33 |
| 5 | Chromosomal mosaicism: Origins and clinical implications in preimplantation and prenatal diagnosis. Prenatal Diagnosis, 2021, 41, 631-641. | 1.1 | 27 |
| 6 | Optimized sample selection for cost-efficient long-read population sequencing. Genome Research, 2021, 31, 910-918. | 2.4 | 4 |
| 7 | Miscarriage matters: the epidemiological, physical, psychological, and economic costs of early pregnancy loss. Lancet, The, 2021, 397, 1658-1667. | 6.3 | 508 |
| 8 | Local adaptation and archaic introgression shape global diversity at human structural variant loci. ELife, $2021,10,.$ | 2.8 | 33 |
| 9 | Let the data do the talking: the need to consider mosaicism during embryo selection. Fertility and Sterility, 2021, 116, 1212-1219. | 0.5 | 20 |
| 10 | Haplotype-aware inference of human chromosome abnormalities. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 13 |
| 11 | Isolation of <i>Mycobacterium lepromatosis </i> i>and Development of Molecular Diagnostic Assays to Distinguish <i>Mycobacterium leprae </i> i>and <i>M. lepromatosis </i> i>. Clinical Infectious Diseases, 2020, 71, e262-e269. | 2.9 | 37 |
| 12 | Archaic hominin genomics provides a window into gene expression evolution. Current Opinion in Genetics and Development, 2020, 62, 44-49. | 1.5 | 9 |
| 13 | Single-cell analysis of human embryos reveals diverse patterns of aneuploidy and mosaicism. Genome Research, 2020, 30, 814-825. | 2.4 | 97 |
| 14 | Mathematical modeling of human oocyte aneuploidy. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10455-10464. | 3.3 | 16 |
| 15 | Chromosome errors in human eggs shape natural fertility over reproductive life span. Science, 2019, 365, 1466-1469. | 6.0 | 239 |
| 16 | Functional divergence among hominins. Nature Ecology and Evolution, 2019, 3, 1507-1508. | 3.4 | 1 |
| 17 | One hundred mosaic embryos transferred prospectively in a single clinic: exploring when and why they result in healthy pregnancies. Fertility and Sterility, 2019, 111, 280-293. | 0.5 | 143 |
| 18 | Quantifying the transcriptional impacts of aneuploidy in human blastocysts. Fertility and Sterility, 2019, 111, 888-889. | 0.5 | 1 |

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|----|---|------|-----------|
| 19 | Assessment of aneuploidy concordance between clinical trophectoderm biopsy and blastocyst. Human Reproduction, 2019, 34, 181-192. | 0.4 | 95 |
| 20 | Tripolar chromosome segregation drives the association between maternal genotype at variants spanning PLK4 and aneuploidy in human preimplantation embryos. Human Molecular Genetics, 2018, 27, 2573-2585. | 1.4 | 55 |
| 21 | Common variants associated with mitotic-origin of aneuploidy in human embryos. Reproductive BioMedicine Online, 2018, 36, e1. | 1.1 | 0 |
| 22 | Are blastocyst aneuploidy rates different between fertile and infertile populations?. Journal of Assisted Reproduction and Genetics, 2018, 35, 403-408. | 1.2 | 37 |
| 23 | Massive variation of short tandem repeats with functional consequences across strains of <i>Arabidopsis thaliana</i> . Genome Research, 2018, 28, 1169-1178. | 2.4 | 34 |
| 24 | Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. Science, 2018, 361, 511-516. | 6.0 | 56 |
| 25 | Impacts of Neanderthal-Introgressed Sequences on the Landscape of Human Gene Expression. Cell, 2017, 168, 916-927.e12. | 13.5 | 136 |
| 26 | Mosaicism in Preimplantation Human Embryos: When Chromosomal Abnormalities Are the Norm. Trends in Genetics, 2017, 33, 448-463. | 2.9 | 170 |
| 27 | Technology versus biology: the limits of preâ€implantation genetic screening. EMBO Reports, 2017, 18, 670-672. | 2.0 | 6 |
| 28 | Selection plays the hand it was dealt: evidence that human adaptation commonly targets standing genetic variation. Genome Biology, 2017, 18, 139. | 3.8 | 10 |
| 29 | Patterns of deleterious variation between human populations reveal an unbalanced load. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 809-811. | 3.3 | 2 |
| 30 | Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. Science, 2016, 352, 235-239. | 6.0 | 391 |
| 31 | Effects of maternal age on euploidy rates inÂa large cohort of embryos analyzedÂwith 24-chromosome single-nucleotide polymorphism–based preimplantation genetic screening. Fertility and Sterility, 2016, 105, 1307-1313. | 0.5 | 131 |
| 32 | Common Variants Spanning PLK4 Are Associated With Mitotic-Origin Aneuploidy in Human Embryos. Obstetrical and Gynecological Survey, 2015, 70, 451-452. | 0.2 | 0 |
| 33 | Evidence of Selection against Complex Mitotic-Origin Aneuploidy during Preimplantation Development. PLoS Genetics, 2015, 11, e1005601. | 1.5 | 170 |
| 34 | Common variants spanning <i>PLK4</i> are associated with mitotic-origin aneuploidy in human embryos. Science, 2015, 348, 235-238. | 6.0 | 106 |
| 35 | Illumina TruSeq Synthetic Long-Reads Empower De Novo Assembly and Resolve Complex, Highly-Repetitive Transposable Elements. PLoS ONE, 2014, 9, e106689. | 1.1 | 180 |
| 36 | The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nature Communications, 2014, 5, 4737. | 5.8 | 196 |

| # | | Article | lF | CITATIONS |
|---|---|---|-----|-----------|
| 3 | 7 | Genomic inference accurately predicts the timing and severity of a recent bottleneck in a nonmodel insect population. Molecular Ecology, 2014, 23, 136-150. | 2.0 | 40 |