# Deanne M Taylor

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3976947/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 115 papers | 4,839 citations | 159525 30 h-index | 110317 64 g-index |
| 135 all docs | 135 docs citations | 135 times ranked | 6657 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Powerful SNP-Set Analysis for Case-Control Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 929-942. | 2.6 | 541 |
| 2 | Blastocyst biopsy with comprehensive chromosome screening and fresh embryo transfer significantly increases inÂvitro fertilization implantation and delivery rates: a randomized controlled trial. Fertility and Sterility, 2013, 100, 697-703. | 0.5 | 517 |
| 3 | InÂvitro fertilization with single euploid blastocyst transfer: a randomized controlled trial. Fertility and Sterility, 2013, 100, 100-107.e1. | 0.5 | 445 |
| 4 | Development and validation of an accurate quantitative real-time polymerase chain reactionâ€“based assay for human blastocyst comprehensive chromosomal aneuploidy screening. Fertility and Sterility, 2012, 97, 819-824.e2. | 0.5 | 219 |
| 5 | Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration. Cell, 2020, 183, 1162-1184. | 13.5 | 185 |
| 6 | Single embryo transfer with comprehensive chromosome screening results in improved ongoing pregnancy rates and decreased miscarriage rates. Human Reproduction, 2012, 27, 1217-1222. | 0.4 | 183 |
| 7 | Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. Cell, 2020, 183, 1185-1201.e20. | 13.5 | 161 |
| 8 | Evaluation of targeted next-generation sequencingâ€“based preimplantation genetic diagnosis ofÂmonogenic disease. Fertility and Sterility, 2013, 99, 1377-1384.e6. | 0.5 | 159 |
| 9 | Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066. | 2.6 | 137 |
| 10 | Telomere DNA Deficiency Is Associated with Development of Human Embryonic Aneuploidy. PLoS Genetics, 2011, 7, e1002161. | 1.5 | 117 |
| 11 | A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205. | 13.7 | 114 |
| 12 | Orientation of Amide-Nitrogen-15 Chemical Shift Tensors in Peptides:Â A Quantum Chemical Study. Journal of the American Chemical Society, 2001, 123, 914-922. | 6.6 | 91 |
| 13 | A Recurrent Missense Variant in AP2M1 Impairs Clathrin-Mediated Endocytosis and Causes Developmental and Epileptic Encephalopathy. American Journal of Human Genetics, 2019, 104, 1060-1072. | 2.6 | 78 |
| 14 | Splice variants of the relaxin and INSL3 receptors reveal unanticipated molecular complexity. Molecular Human Reproduction, 2005, 11, 591-600. | 1.3 | 72 |
| 15 | Massively Systematic Transcript End Readout, â€œMASTERâ€• Transcription Start Site Selection, Transcriptional Slippage, and Transcript Yields. Molecular Cell, 2015, 60, 953-965. | 4.5 | 72 |
| 16 | CapZyme-Seq Comprehensively Defines Promoter-Sequence Determinants for RNA 5â€² Capping with NAD+. Molecular Cell, 2018, 70, 553-564.e9. | 4.5 | 64 |
| 17 | Multiplexed protein-DNA cross-linking: Scrunching in transcription start site selection. Science, 2016, 351, 1090-1093. | 6.0 | 62 |
| 18 | Retention of CD19 intron 2 contributes to CART-19 resistance in leukemias with subclonal frameshift mutations in CD19. Leukemia, 2020, 34, 1202-1207. | 3.3 | 61 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. Journal of Medical Internet Research, 2021, 23, e22219. | 2.1 | 61 |
| 20 | Aggressive triple negative breast cancers have unique molecular signature on the basis of mitochondrial genetic and functional defects. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 1060-1071. | 1.8 | 57 |
| 21 | The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29. | 3.1 | 57 |
| 22 | Clinically recognizable error rate after the transfer of comprehensive chromosomal screened euploid embryos is low. Fertility and Sterility, 2014, 102, 1613-1618. | 0.5 | 52 |
| 23 | Role of miR-2392 in driving SARS-CoV-2 infection. Cell Reports, 2021, 37, 109839. | 2.9 | 52 |
| 24 | Uniparental disomy in the human blastocyst is exceedingly rare. Fertility and Sterility, 2014, 101, 232-236. | 0.5 | 47 |
| 25 | Genome-Wide Association Studies and Meta-Analyses for Congenital Heart Defects. Circulation: Cardiovascular Genetics, 2017, 10, e001449. | 5.1 | 47 |
| 26 | Genetic Polymorphisms ofPeptidase Inhibitor 3(Elafin) Are Associated with Acute Respiratory Distress Syndrome. American Journal of Respiratory Cell and Molecular Biology, 2009, 41, 696-704. | 1.4 | 46 |
| 27 | Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver. Scientific Reports, 2019, 9, 19195. | 1.6 | 46 |
| 28 | Variability of Gene Expression Identifies Transcriptional Regulators of Early Human Embryonic Development. PLoS Genetics, 2015, 11, e1005428. | 1.5 | 45 |
| 29 | Rare copy number variants and congenital heart defects in the 22q11.2 deletion syndrome. Human Genetics, 2016, 135, 273-285. | 1.8 | 43 |
| 30 | Prolonged, Controlled Daytime versus Delayed Eating Impacts Weight and Metabolism. Current Biology, 2021, 31, 650-657.e3. | 1.8 | 42 |
| 31 | Aberrant splicing in B-cell acute lymphoblastic leukemia. Nucleic Acids Research, 2018, 46, 11357-11369. | 6.5 | 39 |
| 32 | Computational analysis of 10,860 phenotypic annotations in individuals with SCN2A-related disorders. Genetics in Medicine, 2021, 23, 1263-1272. | 1.1 | 38 |
| 33 | Interactions between RNA polymerase and the core recognition element are a determinant of transcription start site selection. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2899-905. | 3.3 | 36 |
| 34 | Sphingosine-1-phosphate receptor 3 in the medial prefrontal cortex promotes stress resilience by reducing inflammatory processes. Nature Communications, 2019, 10, 3146. | 5.8 | 36 |
| 35 | Fusion Oncogenes Are Associated With Increased Metastatic Capacity and Persistent Disease in Pediatric Thyroid Cancers. Journal of Clinical Oncology, 2022, 40, 1081-1090. | 0.8 | 36 |
| 36 | International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. JAMA Network Open, 2021, 4, e2112596. | 2.8 | 33 |

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|---|---|---|---|
| 37 | Modulation of CD22 Protein Expression in Childhood Leukemia by Pervasive Splicing Aberrations: Implications for CD22-Directed Immunotherapies. Blood Cancer Discovery, 2022, 3, 103-115. | 2.6 | 31 |
| 38 | Next Generation Sequencing-Based Comprehensive Chromosome Screening in Mouse Polar Bodies, Oocytes, and Embryos1. Biology of Reproduction, 2016, 94, 76. | 1.2 | 30 |
| 39 | Identification and characterization of Aurora kinase B and C variants associated with maternal aneuploidy. Molecular Human Reproduction, 2017, 23, 406-416. | 1.3 | 30 |
| 40 | The Genomics Research and Innovation Network: creating an interoperable, federated, genomics learning system. Genetics in Medicine, 2020, 22, 371-380. | 1.1 | 30 |
| 41 | A New Era for Space Life Science: International Standards for Space Omics Processing. Patterns, 2020, 1, 100148. | 3.1 | 28 |
| 42 | Guidelines for reporting single-cell RNA-seq experiments. Nature Biotechnology, 2020, 38, 1384-1386. | 9.4 | 27 |
| 43 | Transient stabilization, rather than inhibition, of MYC amplifies extrinsic apoptosis and therapeutic responses in refractory B-cell lymphoma. Leukemia, 2019, 33, 2429-2441. | 3.3 | 24 |
| 44 | System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522. | 3.3 | 24 |
| 45 | Preclinical validation of a targeted next generation sequencing-based comprehensive chromosome screening methodology in human blastocysts. Molecular Human Reproduction, 2018, 24, 37-45. | 1.3 | 21 |
| 46 | Effect of gabapentin on sexual function in vulvodynia: aÂrandomized, placebo-controlled trial. American Journal of Obstetrics and Gynecology, 2019, 220, 89.e1-89.e8. | 0.7 | 21 |
| 47 | PANP - a New Method of Gene Detection on Oligonucleotide Expression Arrays. , 2007, , . | | 20 |
| 48 | Optical mapping of the 22q11.2DS region reveals complex repeat structures and preferred locations for non-allelic homologous recombination (NAHR). Scientific Reports, 2020, 10, 12235. | 1.6 | 20 |
| 49 | XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing. Molecular Cell, 2020, 79, 797-811.e8. | 4.5 | 20 |
| 50 | NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. IScience, 2021, 24, 102361. | 1.9 | 20 |
| 51 | NASA GeneLab Platform Utilized for Biological Response to Space Radiation in Animal Models. Cancers, 2020, 12, 381. | 1.7 | 18 |
| 52 | Analysis of Dipolar-Coupling-Mediated Coherence Transfer in a Homonuclear Two Spin-12 Solid-State System. Journal of Magnetic Resonance, 1999, 141, 18-28. | 1.2 | 16 |
| 53 | Four hour 24 chromosome aneuploidy screening using high throughput PCR SNP allele ratio analyses. Fertility and Sterility, 2009, 92, S49-S50. | 0.5 | 15 |
| 54 | Dual Targeting of Tumor and Endothelial Cells by Gonadotropin-Releasing Hormone Agonists to Reduce Melanoma Angiogenesis. Endocrinology, 2010, 151, 4643-4653. | 1.4 | 15 |

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|---|---|---|---|
| 55 | Rare copy number variants in patients with congenital conotruncal heart defects. Birth Defects Research, 2017, 109, 271-295. | 0.8 | 15 |
| 56 | Gene-based genome-wide association studies and meta-analyses of conotruncal heart defects. PLoS ONE, 2019, 14, e0219926. | 1.1 | 15 |
| 57 | Ten simple rules for providing effective bioinformatics research support. PLoS Computational Biology, 2020, 16, e1007531. | 1.5 | 15 |
| 58 | Gonadotropin-Releasing Hormone Agonists Sensitize, and Resensitize, Prostate Cancer Cells to Docetaxel in a p53-Dependent Manner. PLoS ONE, 2014, 9, e93713. | 1.1 | 14 |
| 59 | Antiinflammatory effects of aprepitant coadministration with cART regimen containing ritonavir in HIV-infected adults. JCI Insight, 2017, 2, . | 2.3 | 14 |
| 60 | Targeting CD123 in blastic plasmacytoid dendritic cell neoplasm using allogeneic anti-CD123 CAR T cells. Nature Communications, 2022, 13, 2228. | 5.8 | 14 |
| 61 | The interplay between lncRNAs, RNA-binding proteins and viral genome during SARS-CoV-2 infection reveals strong connections with regulatory events involved in RNA metabolism and immune response. Theranostics, 2022, 12, 3946-3962. | 4.6 | 14 |
| 62 | Betacoronavirus-specific alternate splicing. Genomics, 2022, 114, 110270. | 1.3 | 12 |
| 63 | A comparison of survival analysis methods for cancer gene expression RNA-Sequencing data. Cancer Genetics, 2019, 235-236, 1-12. | 0.2 | 11 |
| 64 | Personas for the translational workforce. Journal of Clinical and Translational Science, 2020, 4, 286-293. | 0.3 | 11 |
| 65 | Chromosomal characteristics at cleavage and blastocyst stages from the same embryos. Journal of Assisted Reproduction and Genetics, 2015, 32, 781-787. | 1.2 | 9 |
| 66 | Scedar: A scalable Python package for single-cell RNA-seq exploratory data analysis. PLoS Computational Biology, 2020, 16, e1007794. | 1.5 | 9 |
| 67 | Improved sensitivity to detect recombination using qPCR for Dyskeratosis Congenita PGD. Journal of Assisted Reproduction and Genetics, 2014, 31, 1227-1230. | 1.2 | 8 |
| 68 | The association of elevated maternal genetic risk scores for hypertension, type 2 diabetes and obesity and having a child with a congenital heart defect. PLoS ONE, 2019, 14, e0216477. | 1.1 | 8 |
| 69 | Gene-based analyses of the maternal genome implicate maternal effect genes as risk factors for conotruncal heart defects. PLoS ONE, 2020, 15, e0234357. | 1.1 | 8 |
| 70 | Trophectoderm DNA fingerprinting by quantitative real-time PCR successfully distinguishes sibling human embryos. Journal of Assisted Reproduction and Genetics, 2014, 31, 1421-1425. | 1.2 | 7 |
| 71 | Derivation of a metabolic signature associated with bacterial meningitis in infants. Pediatric Research, 2020, 88, 184-191. | 1.1 | 6 |
| 72 | Abstract 2464: Gabriella Miller Kids First Data Resource Center: Harmonizing clinical and genomic data to support childhood cancer and structural birth defect research. Cancer Research, 2019, 79, 2464-2464. | 0.4 | 6 |

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|---|---|---|---|
| 73 | pathVar:a new method for pathway-based interpretation of gene expression variability. PeerJ, 2017, 5, e3334. | 0.9 | 6 |
| 74 | A transcriptome-based classifier to determine molecular subtypes in medulloblastoma. PLoS Computational Biology, 2020, 16, e1008263. | 1.5 | 6 |
| 75 | Differentiating children with sepsis with and without acute respiratory distress syndrome using proteomics. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2022, 322, L365-L372. | 1.3 | 6 |
| 76 | Development and validation of a next-generation sequencing (NGS)-based 24-chromosome aneuploidy screening system. Fertility and Sterility, 2013, 100, S82. | 0.5 | 5 |
| 77 | Lack of association of KATNAL1 gene sequence variants and azoospermia in humans. Journal of Assisted Reproduction and Genetics, 2014, 31, 1065-1071. | 1.2 | 5 |
| 78 | An interdomain helix in IRE1Î± mediates the conformational change required for the sensor's activation. Journal of Biological Chemistry, 2021, 296, 100781. | 1.6 | 5 |
| 79 | A subset of the cumulus cell transcriptome is predictive of euploid human oocyte reproductive potential. Fertility and Sterility, 2010, 94, S34-S35. | 0.5 | 4 |
| 80 | Promoter-sequence determinants and structural basis of primer-dependent transcription initiation in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 4 |
| 81 | Coherence transfer through homonuclear dipolar coupling in an unoriented two spin-1/2 solid-state system. Journal of Molecular Structure, 2002, 602-603, 115-124. | 1.8 | 3 |
| 82 | Comparative expression analysis of four breast cancer subtypes versus matched normal tissue from the same patients. Journal of Steroid Biochemistry and Molecular Biology, 2008, 109, 207-211. | 1.2 | 3 |
| 83 | Comprehensive chromosome screening (CCS) results in significantly higher pregnancy rates and lower loss rates from single embryo transfer (SET) in a poor prognosis population. Fertility and Sterility, 2011, 96, S17. | 0.5 | 3 |
| 84 | Copy number variations in individuals with conotruncal heart defects reveal some shared developmental pathways irrespective of 22q11.2 deletion status. Birth Defects Research, 2019, 111, 888-905. | 0.8 | 3 |
| 85 | The accuracy of blastocoel fluid comprehensive chromosomal screening (CCS) is dependent on amplification yield and sequencing depth when using nextgen sequencing. Fertility and Sterility, 2014, 102, e308-e309. | 0.5 | 2 |
| 86 | Visualizing electromagnetic fields in metals by MRI. AIP Advances, 2017, 7, 025310. | 0.6 | 2 |
| 87 | Common Variation in Cytoskeletal Genes Is Associated with Conotruncal Heart Defects. Genes, 2021, 12, 655. | 1.0 | 2 |
| 88 | Gene-Interaction-Sensitive enrichment analysis in congenital heart disease. BioData Mining, 2022, 15, 4. | 2.2 | 2 |
| 89 | Characterizing the relationship between morphologic embryonic development and ploidy status as assessed by 24 chromosome microarray PGD. Fertility and Sterility, 2010, 94, S122-S123. | 0.5 | 1 |
| 90 | Development of a novel next-gen sequencing (NGS) methodology for accurate characterization of genome-wide mitochondrial heteroplasmy in human embryos. Fertility and Sterility, 2012, 98, S58-S59. | 0.5 | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | High cellularity of trophectoderm biopsy adversely affects pregnancy outcomes. Fertility and Sterility, 2014, 102, e176-e177. | 0.5 | 1 |
| 92 | 0036 The Impact of Nighttime Eating: A Randomized Controlled Trial of Daytime vs. Delayed Eating on Weight and Metabolism in Adults of Normal Weight. Sleep, 2019, 42, A15-A15. | 0.6 | 1 |
| 93 | Limits of Spatial Resolution of Phase Encoding Dimensions in MRI of Metals. Journal of Physical Chemistry Letters, 2019, 10, 375-379. | 2.1 | 1 |
| 94 | Translational Personas and Hospital Library Services. Journal of Hospital Librarianship, 2020, 20, 204-216. | 0.4 | 1 |
| 95 | Genome-Wide Association Studies of Conotruncal Heart Defects with Normally Related Great Vessels in the United States. Genes, 2021, 12, 1030. | 1.0 | 1 |
| 96 | Detection of contamination by quantitative real-time (q)PCR. Fertility and Sterility, 2013, 100, S206. | 0.5 | 0 |
| 97 | Targeted deep sequencing of maternal cohesin genes as putative biomarkers for increased risk of embryonic aneuploidy. Fertility and Sterility, 2013, 100, S53. | 0.5 | 0 |
| 98 | Development of a SNP array based methodology for mouse single cell comprehensive chromosomal aneuploidy screening. Fertility and Sterility, 2013, 100, S133. | 0.5 | 0 |
| 99 | Creation of a DNA bank from patients with infertility: a powerful resource for advancing the biology of reproduction. Fertility and Sterility, 2013, 100, S484-S485. | 0.5 | 0 |
| 100 | Tagging SNP genotyping and targeted next-generation sequencing of the katnal gene to investigate a putative genetic association with azoospermia. Fertility and Sterility, 2013, 100, S29. | 0.5 | 0 |
| 101 | Use of whole genome sequencing to identify chromosome-specific egg aneuploidy in a mouse model of natural reproductive aging. Fertility and Sterility, 2014, 102, e330. | 0.5 | 0 |
| 102 | Characterizing the uterine microbiome: next generation sequencing of the V4 region of the 16S ribosomal gene. Fertility and Sterility, 2014, 102, e135-e136. | 0.5 | 0 |
| 103 | Embryonic Aneuploidy Does Not Differ Amongst Major Ethnicities as Determined by Genotyping. Fertility and Sterility, 2015, 103, e21. | 0.5 | 0 |
| 104 | Markers of Ovarian Reserve Do Not Differ Amongst Major Ethnicities as Determined by Genotyping. Fertility and Sterility, 2015, 103, e6. | 0.5 | 0 |
| 105 | Genetic Mutation that May Contribute to Failure of Prolapse Surgery in White Women: A Case-Control Study. Journal of Minimally Invasive Gynecology, 2016, 23, 726-730. | 0.3 | 0 |
| 106 | 0022 MICRORNAS ARE CROSS-SPECIES MARKERS OF SLEEP LOSS IN HUMANS AND RATS. Sleep, 2017, 40, A8-A8. | 0.6 | 0 |
| 107 | TBIO-27. GABRIELLA MILLER KIDS FIRST DATA RESOURCE CENTER ADVANCING GENETIC RESEARCH IN CHILDHOOD CANCER AND STRUCTURAL BIRTH DEFECTS THROUGH LARGE SCALE INTEGRATED DATA-DRIVEN DISCOVERY AND CLOUD-BASED PLATFORMS FOR COLLABORATIVE ANALYSIS. Neuro-Oncology, 2018, 20, i186-i186. | 0.6 | 0 |
| 108 | TMOD-19. GABRIELLA MILLER KIDS FIRST DATA RESOURCE CENTER: LARGE-SCALE HARMONIZED CLINICAL AND GENOMIC DATA PLATFORM TO SUPPORT CHILDHOOD CANCER AND STRUCTURAL BIRTH DEFECT RESEARCH. Neuro-Oncology, 2019, 21, ii125-ii125. | 0.6 | 0 |

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|---|---|---|---|
| 109 | Aneuploid Human Oocytes and Embryos Possess Significantly Reduced Quantities of Telomere DNA.. Biology of Reproduction, 2010, 83, 10-10. | 1.2 | 0 |
| 110 | Abstract 2465: Genomic harmonization of the Data Resource Center for Gabriella Miller Kids First Pediatric Research Program. , 2019, , . | | 0 |
| 111 | Efficacy Proof of Concept for Allogeneic CD123 Targeting CAR T-Cells Against Primary Blastic Plasmacytoid Dendritic Cell Neoplasm (BPDCN): Efficient Control of Tumor Progression in PDX Model and Potential Loss of CD123 Expression in Relapsed Disease. Blood, 2019, 134, 2659-2659. | 0.6 | 0 |
| 112 | Title is missing!. , 2020, 15, e0234357. | | 0 |
| 113 | Title is missing!. , 2020, 15, e0234357. | | 0 |
| 114 | Title is missing!. , 2020, 15, e0234357. | | 0 |
| 115 | Title is missing!. , 2020, 15, e0234357. | | 0 |