

Jennifer Cihlar, PhD  
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## Area of Expertise

Dr. Jennifer Cihlar's research interests lie in the development and application of human identification, population genetics analyses, and development of molecular biology technologies. Jennifer's current research projects focus on defining the molecular biology of library preparation and the chemistry of massively parallel sequencing technologies. The genetic markers of her primary interest are those of forensic relevance such as the mitochondrial genome, microsatellites, and single nucleotide polymorphisms. Jennifer is also directing the transfer of massively parallel sequencing into the operational laboratories of UNTHSC Center for Human Identification's Missing Persons Unit and Forensic Unit.

## Qualifications

BS in Biochemistry, Texas A & M University

PhD in Biomedical Sciences, University of Texas Graduate School of Biomedical Sciences

## Recent Publications

### **Developmental validation of a MPS workflow with a PCR-based short amplicon whole mitochondrial genome panel**

Cihlar, J. C., Amory, C., Lagacé, R., Roth, C., Parson, W. & Budowle, B., Nov 2020, In : *Genes*. 11, 11, p. 1-31 31 p., 1345.

### **Distinguishing mitochondrial DNA and NUMT sequences amplified with the precision ID mtDNA whole genome panel**

Cihlar, J. C., Strobl, C., Lagacé, R., Muenzler, M., Parson, W. & Budowle, B., Nov 2020, In : *Mitochondrion*. 55, p. 122-133 12 p.

### **The lot-to-lot variability in the mitochondrial genome of controls**

Cihlar, J. C., Peters, D., Strobl, C., Parson, W. & Budowle, B., Jul 2020, In : *Forensic Science International: Genetics*. 47, 102298.

### **Evaluation of mitogenome sequence concordance, heteroplasmy detection, and haplogrouping in a worldwide lineage study using the Precision ID mtDNA Whole Genome Panel**

Strobl, C., Churchill Cihlar, J., Lagacé, R., Wootton, S., Roth, C., Huber, N., Schnaller, L., Zimmermann, B., Huber, G., Lay Hong, S., Moura-Neto, R., Silva, R., Alshamali, F., Souto, L., Anslinger, K., Egyed, B., Jankova-Ajanovska, R., Casas-Vargas, A., Usaquén, W., Silva, D. & 10 others, Barletta-Carrillo, C., Tineo, D. H., Vullo, C., Würzner, R., Xavier, C., Gusmão, L., Niederstätter, H., Bodner, M., Budowle, B. & Parson, W., Sep 2019, In : *Forensic Science International: Genetics*. 42, p. 244-251 8 p.

### **Massively parallel sequencing-enabled mixture analysis of mitochondrial DNA samples**

Cihlar, J. C., Stoljarova, M., King, J. L. & Budowle, B., 1 Sep 2018, In : *International Journal of Legal Medicine*. 132, 5, p. 1263-1272 10 p.

### **Increasing the discrimination power of ancestry- and identity-informative SNP loci within the ForenSeq™ DNA Signature Prep Kit**

King, J. L., Churchill, J. D., Novroski, N. M. M., Zeng, X., Warshauer, D. H., Seah, L. H. & Budowle, B., Sep 2018, In : *Forensic Science International: Genetics*. 36, p. 60-76 17 p.

### **Erratum to "Population and performance analyses of four major populations with Illumina's FGx Forensic Genomics System" (*Forensic Sci. Int. Genet.* (2017) (30) (81–92)(S1872497317301369)(10.1016/j.fsigen.2017.06.004))**

Churchill, J. D., Novroski, N. M. M., King, J. L., Seah, L. H. & Budowle, B., Mar 2018, In : *Forensic Science International: Genetics*. 33, p. e17

**Parsing apart the contributors of mitochondrial DNA mixtures with massively parallel sequencing data**

Churchill, J. D., Stoljarova, M., King, J. L. & Budowle, B., Dec 2017, In : Forensic Science International: Genetics Supplement Series. 6, p. e439-e441

**Working towards implementation of whole genome mitochondrial DNA sequencing into routine casework**

Churchill, J. D., Peters, D., Capt, C., Strobl, C., Parson, W. & Budowle, B., Dec 2017, In : Forensic Science International: Genetics Supplement Series. 6, p. e388-e389

**Population and performance analyses of four major populations with Illumina's FGx Forensic Genomics System**

Churchill, J. D., Novroski, N. M. M., King, J. L., Seah, L. H. & Budowle, B., Sep 2017, In : Forensic Science International: Genetics. 30, p. 81-92 12 p.