## Peter M. Schneider ISFG Fellowship – "STRNaming and STRidER" – Short Report

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The *STRs for identity ENFSI Reference database* (STRidER) is a freely accessible, forensic high-quality autosomal STR allele frequency database and online platform for genotype probability estimation, interpretation, and quality control (QC) hosted at https://strider.online by the Institute of Legal Medicine, Medical University of Innsbruck, under the umbrella of the ISFG. STRidER QC is mandatory before data upload on the database and publication in the ISFG-endorsed journals *FSI: Genetics* and *FSI: Reports*. STR datasets are scrutinized by a suite of software tools, optimized towards detecting common discrepancies, idiosyncrasies and implausibility. A broad range of error types and rates is encountered. STR allele frequencies deriving from CE are available on STRidER from 25 countries and 40 STR loci (Release 3). While a growing number of STR sequence datasets are being generated by the scientific community, the corresponding frequency data are not yet available on STRidER due to a lack of tools and harmonization. The ISFG Fellowship was used to promote the provision of high-quality STR sequencing data to the scientific community on STRidER.

The ISFG DNA Commission on STR Sequence Nomenclature has published recommendations for sequence-based STR nomenclature, including a minimum range for allele sequences in 2024. Along with further resources, the Commission endorsed the NFI-developed software STRNaming for conversion of allele strings into the recommended bracketed nomenclature. The ISFG Fellowship helped to exchange knowledge and facilitate crosstalk and cooperation between the two ISFG-recommended resources STRidER and STRNaming. The research visit enabled the implementation of practical needs from STRidER QC and databasing in the STRNaming software for its upcoming integration into STRidER and QC. A tool to extract the recommend minimum allele range from sequence data has recently been developed within STRNaming. Fruitful discussions resulted in steps forward in assessing the requirements for this extraction and sharing data with the community. The detailed tests were useful to expand the insight on software performance on some challenging details of sequence variation. These developments will help to provide high-quality STR sequencing data in the ISFG-recommended ranges and nomenclature, along with relevant tools, to the forensic community in a practical way, and will further support STR sequencing implementation.

I am very grateful to the ISFG and the host institution NFI for making this possible!

## Martin Bodner, March 2025