



FREQUENTLY ASKED QUESTIONS – ATCC STR PROFILING SERVICE

1. HOW DOES THE ATCC STR PROFILING SERVICE COMPARE TO OTHER PROFILING SERVICES?

The ATCC STR Profiling Service includes a signed Cell Line Authentication Report containing an easy-to-understand Short Tandem Repeat (STR) allele table, electropherograms that support the allele calls at each locus, a comprehensive interpretation of the results, and a comparison of the cell's profile against the ATCC STR Profile database. Our expertise, internal database, FTA sample submission process, quick turn-around, and mission focus, provides unmatched analysis, insight, and support. To view a sample profile, please click [here](#).

2. IS A SIGNED CELL LINE AUTHENTICATION REPORT REQUIRED FOR EITHER GRANT SUBMISSIONS OR SUBMISSION INTO A JOURNAL?

In recent years, Cell Line Authentication has become mandatory for many funding sources and publications. Complete authentication requirements for any specific publication or grant submission are dependent upon the conditions set by the deciding or governing entity. A very basic authentication requirement is a signed STR profile report showing the loci and qualified allele calls from an electropherogram which establishes the "identity" of the cells. The advantage of a signed report from ATCC is that our STR scientists are fully trained to analyze and report on raw STR data; their analysis includes, but is not limited to, interpretation of stutter, off-ladder alleles, and various artifacts. Be sure to contact the journal or grant administrator for guidelines and details.

3. WHAT IS "KNOWN REFERENCE PROFILING AGAINST THE ATCC STR PROFILE DATABASE"?

We will run the STR profile of your cell sample against all of the baseline STR profiles in the ATCC STR Profile database. Unlike other service providers, ATCC has an enhanced STR Profile database which includes cell lines that have been de-accessioned and/or confirmed to be misidentified, and no longer appear on the ATCC website. The ATCC STR Profile database continues to grow in complexity as STR profiles are updated and new profiles are added.

4. IF OUR CELL LINES ARE NOT FROM ATCC, WILL YOU STILL DO A COMPREHENSIVE INTERPRETATION OF RESULTS?

Yes. The profile of your cells will be compared to all other STR profiles in the ATCC database, as well as other STR Profile databases if necessary. The results are confidential.

5. CAN I SUBMIT A CELL PROFILE FROM ANOTHER SERVICE OR SOURCE AND COMPARE THIS TO THE DATABASE?

You can run your own profiles using ATCC's public STR profile database by registering and entering the loci calls (https://www.atcc.org/STR_Database.aspx). However, we strongly encourage researchers to use ATCC's STR profiling service as our experts are able to give you a comprehensive interpretation of your results, which may be very important for acceptance of your cell line for funding or publications.

6. HOW CAN I BE ASSURED OF ACCURATE RESULTS?

To ensure the best quality results, carefully follow the instructions in the sample submission pack for preparing the FTA cards. The quality of a profile is directly related to the quantity and quality of the sample provided.

7. DOES ATCC RETURN THE FTA CARDS WITH DNA BACK TO THE CUSTOMER?

ATCC keeps FTA cards for up to 6 months for re-assay, if necessary. Following this time period, they are properly disposed of.

8. DOES ATCC HAVE GUIDELINES FOR DETERMINING WHETHER A CELL LINE IS AUTHENTIC?

In 2012, ANSI Standard (ASN-0002), Authentication of Human Cell Lines: Standardization of STR Profiling was published by the ATCC Standards Development Organization detailing recommendations for the use of STR profiling in authenticating human cell lines. ATCC uses guidelines from this standard when determining the relationship between cell lines. Cell lines with $\geq 80\%$ match are considered to be related; i.e., derived from a common ancestry. Cell lines with a match ranging between 55% and 80% require further profiling for authentication of relatedness. Please also see: Capes-Davis A, et al. Match criteria for human cell line authentication: where do we draw the line? *Int J Cancer* 132(11): 2510-2519, 2013. PubMed: 23136038.

9. WHY IS CELL AUTHENTICATION IMPORTANT?

Misidentified cell lines lead to invalidation of published results and lost time, money, and effort. Authentication of human cell lines is now recommended by NIH and many journals before grant approval and/or acceptance for publication.

10. WHAT PLATFORM IS USED AND WHAT ARE THE BENEFITS?

Through our relationship with Promega, ATCC uses the PowerPlex® 18D kit. It is the only kit specifically designed to use FTA paper punches, which adds simplicity and consistency to sample handling. The core loci covered using this kit can be applied to the authentication standard. The alleles at additional loci can be used to look for changes when comparing your own cell profiles over time.

11. IS A PROMEGA KIT REQUIRED OR RECOMMENDED FOR JOURNAL OR GRANT SUBMISSIONS?

Journals and granting agencies neither specify nor promote any one specific STR kit. The basic STR requirement is a signed report showing the loci and qualified allele calls from an electropherogram in comparison to a set of standards; such a report establishes the “identity” of the cells.

12. WILL YOU ATTEMPT ANALYSIS FROM AN FTA CARD MORE THAN ONCE, OR IS IT A ONE TRY ATTEMPT?

In cases where the signal is overly weak or strong, a second run may be attempted to generate useable data; depending on the prior result, ATCC can re-run a sample with adjustments.

13. DOES ATCC SHARE MY RESULTS WITH ANYONE ELSE?

Profiles run using the ATCC STR Profiling Service become part of the ATCC internal database as part of the process of evaluating the data. The data produced by the ATCC STR Profiling Service is strictly confidential and is not used for comparison to samples from other customers. It may be used for comparison to your previously submitted samples, upon request. ATCC and Promega will not provide your results to any other customer or organization.

14. HOW CAN I OBTAIN THE STR PROFILE FOR A CELL LINE?

As part of our continuing efforts to fully characterize and authenticate the cell lines in our collection, ATCC has developed a comprehensive database of STR profile loci for all of our human cell lines. To find the STR profile for a certain cell line, log in to the STR Profile Database on the ATCC website. Search the database either by selecting an ATCC® number or by entering your own numeric values of each allele designation. Note: you will need to enter at least 7 of the 8 STR loci in order to return any possible matches. Amelogenin is not a true STR, but is a marker used for gender determination.

15. WHAT IS THE DIFFERENCE BETWEEN STR PROFILES AND DNA FINGERPRINTS?

Although STR profiles are often called fingerprints, STR profiles are different from DNA fingerprints [such as those generated from Variable Number Tandem Repeat (VNTR)] because STRs have a finite number of possible alleles. With fragments ranging in size from 700 bp to over 15 kb (determined via RFLPs), VNTRs are called fingerprints since the copy combinations on such large fragments are considered “infinitely” large.

16. HOW DO I USE THE ATCC PUBLIC STR DATABASE TO CONFIRM THE IDENTITY OF MY HUMAN CELLS?

The cell line STR profiles listed in our website catalog descriptions are included in the STR database. If you have an STR profile for your cell line, you can input the values for each locus into the allele table using at least 7 of the 8 loci: D5S818, D13S317, D7S820, D16S539, vWA, TH01, TPOX, and CSF1PO. Please read through our brief tutorial for details. The matching criterion ATCC uses is based on an algorithm that compares the number of shared alleles between two cell line samples, expressed as a percentage. Cell lines with ≥80% match are considered to be related; derived from a common ancestry. Cell lines with a match ranging from 55% to 80% require further analysis for authentication of relatedness. If you are unfamiliar with the process, we recommend using our STR profiling service which includes expert interpretation of your results.

17. I THINK THERE MAY BE MULTIPLE CELL TYPES IN MY CULTURE. CAN YOU TELL ME THE TYPES OF CELLS?

STR profiles are genetic fingerprints of the cell sample supplied. All cell types from the same individual generally have the same genetic make-up. STR profiling will determine the genetic origin of the cells, but it does not determine the phenotype (cell type) of the cells in the sample.

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