

Cell line authentication - Human | 900154

Given the prevalence of cross-contamination and misidentification, the authenticity of cells employed in scientific research projects is a major concern. It is estimated that about 15-20% of all cell line-based research is working with misidentified cell lines. Therefore, determining a cell line's profile using STR analysis is crucial for carrying out reliable and repeatable research. Additionally, a growing number of journals demand cell line verification before accepting an article.

Our service includes

- Cell line authentication
- Comparison with online databases
- Publication-ready analysis report

Easy-to-use

- Please download the [Cell Line Authentication Order Form](#) and add the filled out and printed sheet to your sample shipment.
- Please send us the samples in a padded envelope at room temperature.
- For gDNA please provide us with $\geq 50 \mu\text{l}$ of 50ng/ μl gDNA in Tris or EDTA (10 mM Tris, 0.1 mM EDTA).
- For Cell Pellets, please provide us with 1.0-5.0 million cells as a cell pellet. Please wash twice with PBS and resuspend in 0.5 ml of 70-90% ethanol.

Markers

- Human cells are typed with the PowerPlex System from Promega using 16 STR markers.
- Mouse cells are typed with 18 STR markers.
- Rat cells are typed with 14 STR markers and one sex-specific marker.
- Dog cells are typed with 11 STR markers.
- Hamster cells are typed with 10 STR markers.

Results

You will get the results within 2 weeks per email. The results include the comparison of the data with the Cellosaurus database. The cell line will be classified as authenticated or misidentified.

Short Tandem Repeats (STRs)

A DNA motif of 2-13 bases that is repeated up to several hundred times makes up a short tandem repeat (STR). Individual variability in the number of repetitions in an STR leads to variations in the length of the produced fragments when employing PCR. The cell lines are profiled using these variations in fragment lengths at several loci.

Detection of Cell Line Mixtures

It is possible to identify contamination of one cell line by one or more additional cell lines down to a 10% frequency of the contaminating cell line. Cell line combinations typically provide STR profiles with three or more peaks for a single or several loci.