



# Cell Line Authentication Service

## STR Profile Report

**Sample Submitted By:** University of Eastern Finland  
Mika Reinisalo

**Email Address:** mika.reinisalo@uef.fi

**ATCC Sales Order:** SO0340466

**FTA Barcode:** STRA11405

**Cell Line Designation:** ARPE-19

**Date Sample Received:** Thursday, January 03, 2019

**Report Date:** Tuesday, January 08, 2019

**Methodology:** Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

**Data Interpretation:** Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) Authentication of Human Cell Lines: Standardization of STR Profiling by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int. J. Cancer. 2012 Nov 8. doi: 10.1002/ijc.27931

### ATCC performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards.

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Fax 703-365-2750  
Email: sales@atcc.org



**Cell Line  
Authentication Service**  
STR Profile Report

FTA Barcode: STRA11405

ATCC Sales Order: SO0340466

| Test Results for Submitted Sample   |                        |     |  |  | ATCC Reference Database Profile                                     |     |  |     |
|---|------------------------|-----|--|--|---|-----|--|-----|
| Locus   | Query Profile: ARPE-19 |     |  |  | Database Profile: ARPE-19; Retinal Epithelium; Human (Homo sapiens) |     |  |     |
| D3S1358   | 14                     | 15  |  |  |   |     |  |     |
| TH01  | 6                      | 9.3 |  |  | 6   | 9.3 |  |     |
| D21S11  | 28                     | 29  |  |  |   |     |  |     |
| D18S51  | 12                     | 16  |  |  |   |     |  |     |
| Penta_E   | 7                      | 11  |  |  |   |     |  |     |
| D5S818  | 13                     |     |  |  | 13  |     |  |     |
| D13S317   | 11                     | 12  |  |  | 11  | 12  |  |     |
| D7S820  | 9                      | 11  |  |  | 9   | 11  |  |     |
| D16S539   | 9                      | 11  |  |  | 9   | 11  |  |     |
| CSF1PO  | 11                     |     |  |  | 11  |     |  |     |
| Penta_D   | 11                     | 13  |  |  |   |     |  |     |
| Amelogenin  | X                      | Y   |  |  | X   | Y   |  |     |
| vWA   | 16                     | 19  |  |  | 16  | 19  |  |     |
| D8S1179   | 13                     |     |  |  |   |     |  |     |
| TPOX  | 9                      | 11  |  |  | 9   | 11  |  |     |
| FGA   | 23                     |     |  |  |   |     |  |     |
| D19S433   | 12                     | 13  |  |  |   |     |  |     |
| D2S1338   | 19                     |     |  |  |   |     |  |     |
| Number of shared alleles between query sample and database profile:   |                        |     |  |  |   |     |  | 16  |
| Total number of alleles in the database profile:  |                        |     |  |  |   |     |  | 16  |
| Percent match between the submitted sample and the database profile:  |                        |     |  |  |   |     |  | 100 |
| <i>The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.</i>   |                        |     |  |  |   |     |  |     |
| <b>NOTE:</b> Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, <b>please do not publish</b> the allele calls from all the STR loci tested. Electropherograms showing raw data are attached. |                        |     |  |  |   |     |  |     |

**Explanation of Test Results**

Cell lines with 80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- ☐ The submitted sample profile is human, but not a match for any profile in the ATCC STR database.
- ☒ The submitted profile is an exact match for the following ATCC human cell line(s) in the ATCC STR database (8 core loci plus Amelogenin): CRL-2302
- ☐ The submitted profile is similar to the following ATCC human cell line(s):
- ☐ An STR profile could not be generated.

**Additional Comments:**

Submitted sample, STRA11405 (ARPE-19), is an exact match to ATCC cell line CRL-2302 (ARPE-19).

|                          |                     |
|--------------------------|---------------------|
| e-Signature, Technician: | snicholson 1/8/2019 |
| e-Signature, Reviewer:   | Bchase 1/8/2019     |





**Addendum: Comparative Output from the ATCC STR Profile Database**

| % Match | ATCC® Cat. No. | Designation                                       | D5S818 | D13S317 | D7S820 | D16S539 | vWA   | THO1  | AMEL | TPOX | CSF1PO |
|---------|----------------|---|--------|---------|--------|---------|-------|-------|------|------|--------|
| 100     | STRA11405      | ARPE-19   | 13     | 11,12   | 9,11   | 9,11    | 16,19 | 6,9.3 | X,Y  | 9,11 | 11     |
| 100     | CRL-2302       | ARPE-19; Retinal Epithelium; Human (Homo sapiens) | 13     | 11,12   | 9,11   | 9,11    | 16,19 | 6,9.3 | X,Y  | 9,11 | 11     |

**Definitions of terms used in this report:**

**Peak Area Difference (PAD):**

Refers to a heterozygous peak imbalance.

Two alleles at a single locus should amplify in a similar manner; and therefore produce peaks of similar height and area. Peaks which are above threshold (50 rfu) but are not of similar area, within 50% of each other, are referred to as a PAD. Due to their nature cell lines do not amplify in the same manner as a sample taken from a fresh buccal swab. PAD is far more common in cell line samples.

**Stutter:**

A stutter peak is a small peak which occurs immediately before the true peak. It is defined as being a single repeat unit smaller than the true peak. The stutter peak should be less than 15% of the true peak. The stutter is caused by the polymerase.

**+4 Peak:**

A +4 is similar to a stutter but occurs immediately after the true peak. A stutter peak should be less than 5% for a homozygous and 10% for a heterozygous.

**Below Threshold Peak(s):**

Cell lines can produce unusual profiles and occasionally a peak will amplify poorly and be below threshold. Where we find a below threshold peak which we believe is valid we indicate it as a below threshold peak. Our cell line analysis criteria, Homozygous and Heterozygous peaks must be equal to or above the set height threshold for it to be considered a true peak.

**Ladder/ Off Ladder Peak(s):**

The allelic ladder consists of most or all known alleles in the population and allows for precise assignment of alleles. Those which do not align are termed 'off ladder'.

**Artifact:**

A non-allelic product of the amplification process, an anomaly of the detection process, or a by-product of primer synthesis

**Pull-up:**

A term used to describe when signal from one dye color channel produces artificial peaks in another, usually adjacent, color.

**Spike:**

An extraneous peak resulting from dust, dried polymer, an air bubble, or an electrical surge.

**Dye blob:**

Free dye not coupled to primer that can be injected into the capillary (A known and documented dye blob is often found at the D3S1358 locus.)



# Cell Line Authentication Service

## STR Profile Report

**Sample Submitted By:** University of Eastern Finland  
Mika Reinisalo

**Email Address:** mika.reinisalo@uef.fi

**ATCC Sales Order:** SO0340466

**FTA Barcode:** STRA11406

**Cell Line Designation:** LEPI-1

**Date Sample Received:** Thursday, January 03, 2019

**Report Date:** Tuesday, January 08, 2019

**Methodology:** Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

**Data Interpretation:** Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) Authentication of Human Cell Lines: Standardization of STR Profiling by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int. J. Cancer. 2012 Nov 8. doi: 10.1002/ijc.27931

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**Cell Line  
Authentication Service**  
STR Profile Report

FTA Barcode: STRA11406

ATCC Sales Order: SO0340466

| Test Results for Submitted Sample   |                       |     |  |  | ATCC Reference Database Profile                                     |     |  |     |
|---|-----------------------|-----|--|--|---|-----|--|-----|
| Locus   | Query Profile: LEPI-1 |     |  |  | Database Profile: ARPE-19; Retinal Epithelium; Human (Homo sapiens) |     |  |     |
| D3S1358   | 14                    | 15  |  |  |   |     |  |     |
| TH01  | 6                     | 9.3 |  |  | 6   | 9.3 |  |     |
| D21S11  | 28                    | 29  |  |  |   |     |  |     |
| D18S51  | 12                    | 16  |  |  |   |     |  |     |
| Penta_E   | 7                     | 11  |  |  |   |     |  |     |
| D5S818  | 13                    |     |  |  | 13  |     |  |     |
| D13S317   | 11                    | 12  |  |  | 11  | 12  |  |     |
| D7S820  | 9                     | 11  |  |  | 9   | 11  |  |     |
| D16S539   | 9                     | 11  |  |  | 9   | 11  |  |     |
| CSF1PO  | 11                    |     |  |  | 11  |     |  |     |
| Penta_D   | 11                    | 13  |  |  |   |     |  |     |
| Amelogenin  | X                     | Y   |  |  | X   | Y   |  |     |
| vWA   | 16                    | 19  |  |  | 16  | 19  |  |     |
| D8S1179   | 13                    |     |  |  |   |     |  |     |
| TPOX  | 9                     | 11  |  |  | 9   | 11  |  |     |
| FGA   | 23                    |     |  |  |   |     |  |     |
| D19S433   | 12                    | 13  |  |  |   |     |  |     |
| D2S1338   | 19                    |     |  |  |   |     |  |     |
| Number of shared alleles between query sample and database profile:   |                       |     |  |  |   |     |  | 16  |
| Total number of alleles in the database profile:  |                       |     |  |  |   |     |  | 16  |
| Percent match between the submitted sample and the database profile:  |                       |     |  |  |   |     |  | 100 |
| <i>The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.</i>   |                       |     |  |  |   |     |  |     |
| <b>NOTE:</b> Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, <b>please do not publish</b> the allele calls from all the STR loci tested. Electropherograms showing raw data are attached. |                       |     |  |  |   |     |  |     |

**Explanation of Test Results**

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- ☐ The submitted sample profile is human, but not a match for any profile in the ATCC STR database.
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- ☐ The submitted profile is similar to the following ATCC human cell line(s):
- ☐ An STR profile could not be generated.

**Additional Comments:**

Submitted sample, STRA11406 (LEPI-1), is an exact match to ATCC cell line CRL-2302 (ARPE-19). Due to the low intensity of the peaks at some of the loci the alleles were called manually. Note the many peaks in the TRM-ET channel due to pull-ups from the internal lane standard.

|                          |                     |
|--------------------------|---------------------|
| e-Signature, Technician: | snicholson 1/8/2019 |
| e-Signature, Reviewer:   | Bchase 1/8/2019     |





**Addendum: Comparative Output from the ATCC STR Profile Database**

| % Match | ATCC® Cat. No. | Designation                                       | D5S818 | D13S317 | D7S820 | D16S539 | vWA   | THO1  | AMEL | TPOX | CSF1PO |
|---------|----------------|---|--------|---------|--------|---------|-------|-------|------|------|--------|
| 100     | STRA11406      | LEPI-1  | 13     | 11,12   | 9,11   | 9,11    | 16,19 | 6,9.3 | X,Y  | 9,11 | 11     |
| 100     | CRL-2302       | ARPE-19; Retinal Epithelium; Human (Homo sapiens) | 13     | 11,12   | 9,11   | 9,11    | 16,19 | 6,9.3 | X,Y  | 9,11 | 11     |

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**Pull-up:**

A term used to describe when signal from one dye color channel produces artificial peaks in another, usually adjacent, color.

**Spike:**

An extraneous peak resulting from dust, dried polymer, an air bubble, or an electrical surge.

**Dye blob:**

Free dye not coupled to primer that can be injected into the capillary (A known and documented dye blob is often found at the D3S1358 locus.)



# Cell Line Authentication Service

## STR Profile Report

**Sample Submitted By:** University of Eastern Finland  
Mika Reinisalo

**Email Address:** mika.reinisalo@uef.fi

**ATCC Sales Order:** SO0340466

**FTA Barcode:** STRA11407

**Cell Line Designation:** HRPEpiC

**Date Sample Received:** Thursday, January 03, 2019

**Report Date:** Friday, January 04, 2019

**Methodology:** Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

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**Cell Line  
Authentication Service**  
STR Profile Report

FTA Barcode: STRA11407

ATCC Sales Order: SO0340466

| Test Results for Submitted Sample   |                        |      |  |  | ATCC Reference Database Profile |  |  |    |
|---|------------------------|------|--|--|---------------------------------|--|--|----|
| Locus   | Query Profile: HRPEpiC |      |  |  | Database Profile:               |  |  |    |
| D3S1358   | 15                     | 18   |  |  |                                 |  |  |    |
| TH01  | 6                      | 7    |  |  |                                 |  |  |    |
| D21S11  | 32.2                   | 33   |  |  |                                 |  |  |    |
| D18S51  | 15                     | 18   |  |  |                                 |  |  |    |
| Penta_E   | 7                      | 11   |  |  |                                 |  |  |    |
| D5S818  | 8                      | 13   |  |  |                                 |  |  |    |
| D13S317   | 11                     | 12   |  |  |                                 |  |  |    |
| D7S820  | 10                     | 13   |  |  |                                 |  |  |    |
| D16S539   | 12                     |      |  |  |                                 |  |  |    |
| CSF1PO  | 10                     | 12   |  |  |                                 |  |  |    |
| Penta_D   | 8                      | 15   |  |  |                                 |  |  |    |
| Amelogenin  | X                      | Y    |  |  |                                 |  |  |    |
| vWA   | 13                     | 16   |  |  |                                 |  |  |    |
| D8S1179   | 14                     |      |  |  |                                 |  |  |    |
| TPOX  | 8                      | 11   |  |  |                                 |  |  |    |
| FGA   | 18                     | 26   |  |  |                                 |  |  |    |
| D19S433   | 13                     | 13.2 |  |  |                                 |  |  |    |
| D2S1338   | 21                     | 22   |  |  |                                 |  |  |    |
| Number of shared alleles between query sample and database profile:   |                        |      |  |  |                                 |  |  | NA |
| Total number of alleles in the database profile:  |                        |      |  |  |                                 |  |  | NA |
| Percent match between the submitted sample and the database profile:  |                        |      |  |  |                                 |  |  | NA |
| <i>The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.</i>   |                        |      |  |  |                                 |  |  |    |
| <b>NOTE:</b> Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, <b>please do not publish</b> the allele calls from all the STR loci tested. Electropherograms showing raw data are attached. |                        |      |  |  |                                 |  |  |    |

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- ☐ The submitted profile is similar to the following ATCC human cell line(s):
- ☐ An STR profile could not be generated.

**Additional Comments:**

Submitted sample, STRA11407 (HRPEpiC), is not a match to any cell line in either the ATCC or the DSMZ STR database. The cell line, (HRPEpiC), is not a part of the ATCC collection.

|                          |                     |
|--------------------------|---------------------|
| e-Signature, Technician: | snicholson 1/4/2019 |
| e-Signature, Reviewer:   | Bchase 1/4/2019     |







**Cell Line  
Authentication Service**  
STR Profile Report

FTA Barcode: STRA11407

ATCC Sales Order: SO0340466

**Addendum: Comparative Output from the ATCC STR Profile Database**

| % Match | ATCC® Cat. No. | Designation | D5S818 | D13S317 | D7S820 | D16S539 | vWA   | TH01 | AMEL | TPOX | CSF1PO |
|---------|----------------|-------------|--------|---------|--------|---------|-------|------|------|------|--------|
| 100     | STRA11407      | HRPEpiC     | 8,13   | 11,12   | 10,13  | 12      | 13,16 | 6,7  | X,Y  | 8,11 | 10,12  |

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