



# Cell Line Authentication Service

## STR Profile Report

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**ATCC Sales Order:** SOJ28485

**FTA Barcode:** STRA3083

**Cell Line Designation:** ARPE 19

**Date Sample Received:** April 26, 2016

**Report Date:** April 28, 2016

**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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### Technical questions?

ATCC Technical Support  
(800) 638-6597 / +1 703-365-2700  
STRTechSupport@atcc.org

### Ordering questions?

800-638-6597 or 703-365-2700  
Fax 703-365-2750  
Email: STRtesting@atcc.org



Test Results for Submitted Sample					ATCC Reference Database Profile			
Loci	Query Profile: ARPE 19				Database Profile: ARPE-19			
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  $\geq 80\%$  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 (ARPE-19)
- ☐ The submitted profile is similar to the following ATCC human cell line(s):

#### Additional Comments:

Submitted sample, STRA3083 (ARPE-19), is an exact match to ATCC cell line CRL-2302 (ARPE-19).

e-Signature, Technician:	Isander 04/28/16
e-Signature, Reviewer:	kkindig 04/28/16





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

% Match	ATCC® Cat. No.	Designation	D5S818	D13S317	D7S820	D16S539	vWA	TH01	AMEL	TPOX	CSF1PO
100	CRL-2302	ARPE-19	13	11,12	9,11	9,11	16,19	6,9,3	X,Y	9,11	11
100	N/A	ARPE 19	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.)



