



# Cell Line Authentication Service

## STR Profile Report

**Sample Submitted By:** Ball State University  
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**ATCC Sales Order:** SO0492921

**FTA Barcode:** STRB1569

**Cell Line Designation:** HEK 293 A

**Date Sample Received:** Monday, September 30, 2019

**Report Date:** Thursday, October 03, 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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### **Technical questions?**

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

### **Ordering questions?**

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



Test Results for Submitted Sample				ATCC Reference Database Profile			
Locus	Query Profile: HEK 293 A			Database Profile: 293; Embryonic Kidney; Human (Homo sapiens)			
D3S1358	15	17					
TH01	7	9.3		7	9.3		
D21S11	28	30.2					
D18S51	17						
Penta_E	7	15					
D5S818	8			8	9		
D13S317	12	14		12	14		
D7S820	11			11	12		
D16S539	9	13		9	13		
CSF1PO	12			11	12		
Penta_D	9						
Amelogenin	X			X			
vWA	16	19		16	19		
D8S1179	12	14					
TPOX	11			11			
FGA	23						
D19S433	15	18					
D2S1338	19						
Number of shared alleles between query sample and database profile:							13
Total number of alleles in the database profile:							16
Percent match between the submitted sample and the database profile:							81
<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):
- The submitted profile is similar to the following ATCC human cell line(s): CRL-1573
- An STR profile could not be generated.

**Additional Comments:**

Submitted sample, STRB1569 (HEK 293 A), is a similar match to ATCC cell line CRL-1573 (293).

e-Signature, Technician:	wklein 10/3/2019
e-Signature, Reviewer:	Bchase 10/3/2019





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

% Match	ATCC® Cat. No.	Designation	D5S818	D13S317	D7S820	D16S539	vWA	TH01	AMEL	TPOX	CSF1PO
100	STRB1569	HEK 293 A	8	12,14	11	9,13	16,19	7,9,3	X	11	12
81	CRL-1573	293; Embryonic Kidney; Human (Homo sapiens)	8,9	12,14	11,12	9,13	16,19	7,9,3	X	11	11,12

**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.)