# Cell Line Authentication

## Analysis Report

Research use only

psomagen

## Basic Information

| | | | | | |
|---|---|---|---|---|---|
| Report Date | 0X/XX/20XX | Order Number | AC00XXXXXX | Service Type | CLA - Human |
| Client Name | NNN | Client ID | XX_X | Institution | XXX University |
| Option Number | Option 3 | Sample Type | Tissue | Quantity | 3 |

## Sample Description

| STR Profile No. | Sample | Sample Name | Passage Number | Sample Type | Cell Line /Identifier | DB Reference No. (Source) | Others |
|---|---|---|---|---|---|---|---|
| #1 | Query | Sample A | 5 | Tissue | MCF-7 | - | |
| | Subject | - | - | - | - | HTB-22 (ATCC) | |
| #2 | Query | Sample B | 20 | Tissue | HeLa | - | |
| | Subject | - | - | - | - | CVCL_0030 (Cellosaurus) | |
| #3 | Query | Test-150 | 150 | Tissue | HeLa | - | |
| | Subject | Test-1 | 10 | Tissue | HeLa | AC000XXXXX (Psomagen) | |

### Methodology

- **Twenty-four short tandem repeat** (STR) loci, including Amelogenin and two additional sex-determining markers, were amplified using the **ThermoFisher's CLA GlobalFiler™ Kit**. The cell line sample was processed on an ABI 3730/3730XL DNA Analyzer, and data were analyzed using **GeneMapper software** (Applied Biosystems).
- STR profile analysis was performed following the **ANSI/ATCC ASN-0002 2022 guidelines**.

## STR profile #1

| **STR Loci** | **Query** | | | | **Subject** | | | |
|---|---|---|---|---|---|---|---|---|
| | **Sample A** | | | | **HTB-22 (ATCC)** | | | |
| D8S1179 | 15 | 17 | | | 15 | 17 | | |
| D21S11 | 15 | 14 | | | 15 | 14 | | |
| D7S820 | 9 | 12 | | | 9 | 12 | | |
| CSF1PO | 13 | | | | 13 | | | |
| D3S1358 | 22 | 23 | | | 22 | 23 | | |
| TH01 | 9.3 | | | | 9.3 | | | |
| D13S317 | 18 | 17 | | | 18 | 17 | | |
| D16S539 | 16 | 17 | | | 16 | 17 | | |
| vWA | 30.2 | 31.2 | | | 30.2 | 31.2 | | |
| TPOX | 11 | 12 | | | 11 | 12 | | |
| D18S51 | 12 | 13 | | | 12 | 13 | | |
| D5S818 | 18 | 19 | | | 18 | 19 | | |
| FGA | 8 | 11 | | | 8 | 11 | | |
| Amelogenin | X | | | | X | | | |
| D2S1338 | 11 | 10 | | | NA* | | | |
| D19S433 | 20 | | | | NA | | | |
| SE33 | 11 | 13 | | | NA | | | |
| DYS391 | 15 | 17 | | | NA | | | |
| Yindel | 22 | 24 | | | NA | | | |
| D10S1248 | 12 | 13 | | | NA | | | |
| D1S1656 | 8 | 12 | | | NA | | | |
| D22S1045 | 12 | 14 | | | NA | | | |
| D2S441 | 30 | 33.2 | | | NA | | | |
| D12S391 | 9 | | | | NA | | | |
| Shared alleles between the query sample and the subject | | | | | | | | 14 |
| Matching % (Between query and the subject) | | | | | | | | 100 % |

*homozygous alleles count as one allele*

*NA* – Allele information not available.*

## Matching % Guideline

** Reference : ICLAC - Match Criteria for Human Cell Line Authentication*

If the percent match result falls within the range of 80% - 100%, it suggests that the two samples are related, likely originating from the same donor. If the result is between 56% and 79%, it is inconclusive and may require further testing to determine relatedness. If the percent match is between 0% and 55%, it indicates that the two samples are unrelated, likely derived from different donors.

## STR profile #2

| STR Loci | Query | | | | Subject | | | |
|---|---|---|---|---|---|---|---|---|
| | Sample B | | | | CVCL_0030 (Cellosaurus) | | | |
| D8S1179 | 15 | 17 | | | 15 | 17 | | |
| D21S11 | 15 | 14 | | | 15 | 14 | | |
| D7S820 | 9 | 12 | | | 9 | 12 | | |
| CSF1PO | 13 | | | | 13 | | | |
| D3S1358 | 22 | 23 | | | 10 | 11 | | |
| TH01 | 9.3 | | | | 7 | 9 | | |
| D13S317 | 18 | 17 | | | 18 | 17 | | |
| D16S539 | 16 | 17 | | | 2 | 17 | | |
| vWA | 30.2 | 31.2 | | | 30.2 | 31.2 | | |
| TPOX | 11 | 12 | | | 10 | 12 | | |
| D18S51 | 12 | 13 | | | 12 | 13 | | |
| D5S818 | 18 | 19 | | | 18 | 19 | | |
| FGA | 8 | 11 | | | 10 | 11 | | |
| Amelogenin | X | | | | X | Y | | |
| D2S1338 | 11 | 10 | | | NA* | | | |
| D19S433 | 20 | | | | NA | | | |
| SE33 | 11 | 13 | | | 11 | 15 | | |
| DYS391 | 15 | 17 | | | NA | | | |
| Yindel | 22 | 24 | | | 22 | 25 | | |
| D10S1248 | 12 | 13 | | | NA | | | |
| D1S1656 | 8 | 12 | | | NA | | | |
| D22S1045 | 12 | 14 | | | NA | | | |
| D2S441 | 30 | 33.2 | | | 7 | 8 | | |
| D12S391 | 9 | | | | 7 | | | |
| Shared alleles between the query sample and the subject | | | | | | | | 18 |
| Matching % (Between query and the subject) | | | | | | | | 83 % |

*homozygous alleles count as one allele*

*NA* – Allele information not available.*

## Matching % Guideline

** Reference : ICLAC - Match Criteria for Human Cell Line Authentication*

If the percent match result falls within the range of 80% - 100%, it suggests that the two samples are related, likely originating from the same donor. If the result is between 56% and 79%, it is inconclusive and may require further testing to determine relatedness. If the percent match is between 0% and 55%, it indicates that the two samples are unrelated, likely derived from different donors.

## STR profile #3

| STR Loci | Query | | | | Subject | | | |
|---|---|---|---|---|---|---|---|---|
| | Test-150 | | | | Test-1 (AC000XXXXX) | | | |
| D8S1179 | 11 | 12 | | | 11 | 12 | | |
| D21S11 | 10 | 11 | | | 10 | 11 | | |
| D7S820 | 30.2 | 31.2 | | | 30.2 | 31.2 | | |
| CSF1PO | 8 | | | | 8 | | | |
| D3S1358 | 30 | 33.2 | | | 30 | 33.2 | | |
| TH01 | 9 | | | | 9 | | | |
| D13S317 | 18 | 17 | | | 18 | 17 | | |
| D16S539 | 32.2 | | | | 32.2 | | | |
| vWA | 9.3 | | | | 9.3 | | | |
| TPOX | 11 | 14 | | | 11 | 14 | | |
| D18S51 | 22 | 23 | | | 22 | 23 | | |
| D5S818 | 12 | 16 | | | 12 | 16 | | |
| FGA | 12 | 14 | | | 12 | 14 | | |
| Amelogenin | X | | | | X | | | |
| D2S1338 | 29 | 31.2 | | | 29 | 31.2 | | |
| D19S433 | 7 | | | | 7 | | | |
| SE33 | 17 | 19 | | | 17 | 19 | | |
| DYS391 | 8 | 14 | | | 8 | 14 | | |
| Yindel | 12 | 14 | | | 12 | 14 | | |
| D10S1248 | 20 | | | | 20 | | | |
| D1S1656 | 22 | 23 | | | 22 | 23 | | |
| D22S1045 | 10 | 14 | | | 10 | 14 | | |
| D2S441 | 24 | | | | 24 | | | |
| D12S391 | 9 | | | | 9 | | | |
| Shared alleles between the query sample and the subject | | | | | | | | 24 |
| Matching % (Between query and the subject) | | | | | | | | 100% |

*homozygous alleles count as one allele*

*NA* – Allele information not available.*

## Matching % Guideline

** Reference : ICLAC - Match Criteria for Human Cell Line Authentication*

If the percent match result falls within the range of 80% - 100%, it suggests that the two samples are related, likely originating from the same donor. If the result is between 56% and 79%, it is inconclusive and may require further testing to determine relatedness. If the percent match is between 0% and 55%, it indicates that the two samples are unrelated, likely derived from different donors.

## Interpretation of Result

| STR Profile No. | Detail |
|---|---|
| **#1** | **Query** : Sample A **Subject :** HTB-22 (ATCC)<br>The submitted Query[**Sample A**] exhibits a **100%** match across all shared loci with the Subject[**HTB-22(ATCC)**]. Therefore, based on the STR analysis, **Sample A** is confirmed to be identical to **HTB-22(ATCC)**. |
| **#2** | **Query :** Con-1 **Subject :** CVCL_0030 (Cellosaurus)<br>The submitted Query[**Sample B**] exhibits an **83%** match across the shared loci with the Subject [**CVCL_0030 (Cellosaurus)**] However, inconsistencies were detected in the sex-determining loci, potentially attributable to the loss of the Y chromosome. While statistically, the Query and Subject may appear 'related,' the ANSI/ATCC ASN-0002-2022 guidelines regard inconsistencies in the sex-determining loci as a significant complication. Consequently, it is recommended that further examination be conducted to confirm the identity of **Sample B.** |
| **#3** | **Query :** Test-150 **Subject :** Test-1 (AC000XXXXX).<br>The submitted Query[**Test-150**] exhibits a **100%** match across all shared loci with the Subject[**Test-1 (AC000XXXXX)**]. Therefore, based on the STR analysis, **Test-150** is confirmed to be identical to **Test-1 (AC000XXXXX)**. |

### Note :

The Short Tandem Repeat (STR) profile analysis was conducted in accordance with the ANSI/ATCC ASN-0002 2022 guidelines. When using public databases (e.g., ATCC, Cellosaurus) as subject profiles, not all 24 STR loci included in Psomagen's test may be available. However, Psomagen adheres to the ANSI/ATCC ASN-0002-2022 guidelines, which recommend 13 core STR loci, along with Amelogenin, as the minimum requirement for human cell line authentication.

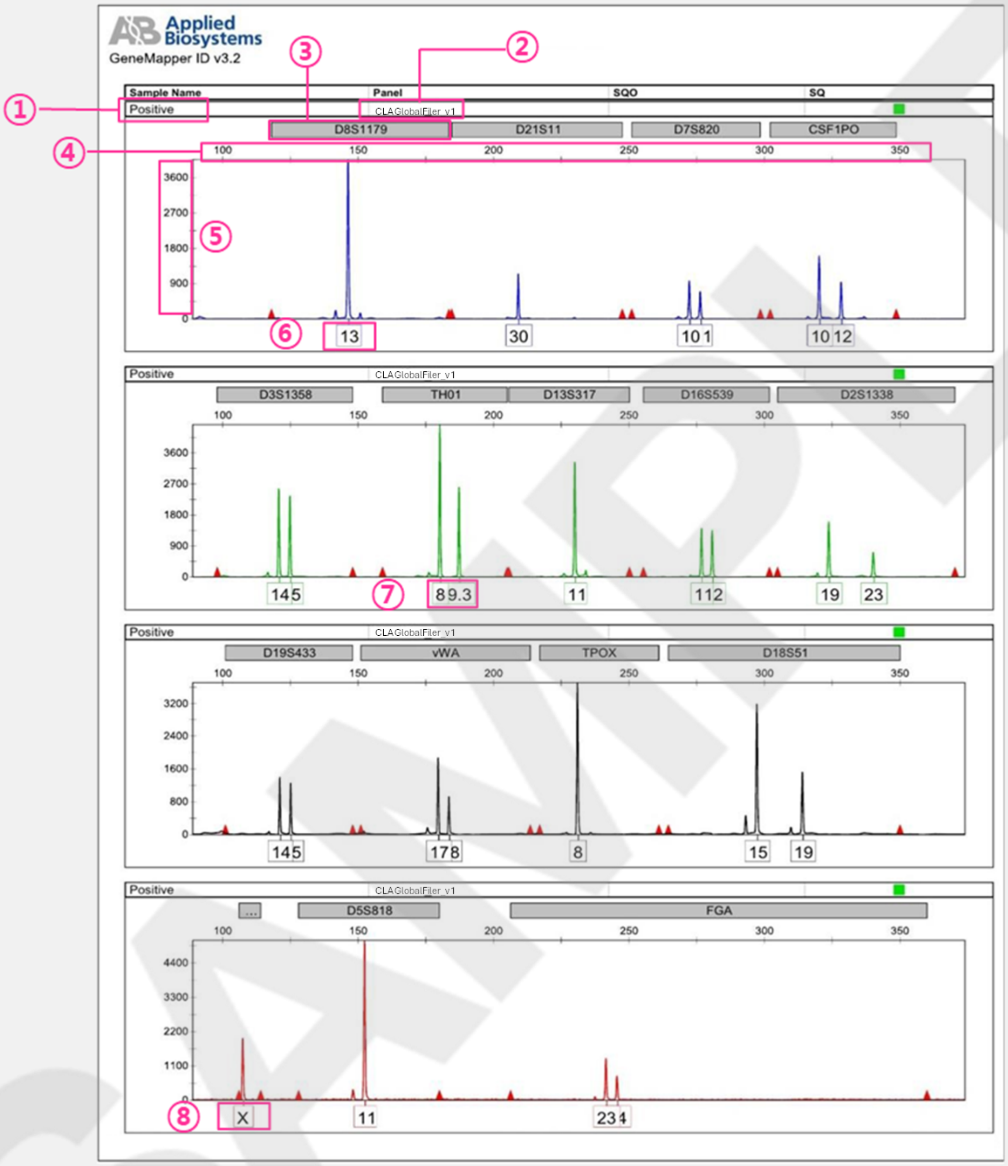
For the calculation of the matching percentage, Psomagen adheres to the match criteria for human cell line authentication as detailed in the publication "*Where do we draw the line?*" (International Journal of Cancer, 2012 Nov 8. DOI: 10.1002/ijc.27931). The matching percentage is determined by dividing the number of alleles that match between the query and the subject by the total number of shared loci in the STR profile. It is important to note that this calculation does not account for the loss of heterozygosity in the query profile, as specified in ANSI/ATCC ASN-0002-2022.

### Signature

| | | | |
|---|---|---|---|
| Test Performed By | Signiture, CLA Testing Personnel | Date | XX/XX/2025 |
| Test Reviewed By | Signiture, CLA Analyst | Date | XX/XX/2025 |

# Peak Plot Guide

(Electropherogram)



① Sample name

② STR amplification kit

③ STR marker

④ X axis: Fragment size

⑤ Y axis: Relative fluorescence units (RFU)

⑥ STR repeat number (13 = 13 repeats)

⑦ Decimal point (9.3 = ATGC ATGC …. ATGC ATG)

⑧ sex determining marker (Female: XX / Male: XY)

psomagen | **CLA-Human**
Cell Line Authentication

## Contact Us

customerservice@psomagen.com

Phone: (+1) 301-251-1007

bsi. ISO 9001 Quality Management

### Headquarters

1330 Piccard Dr Suite 103,
Rockville, MD 20850
Tel: 301-251-1007 Ext. 302
customerservice@psomagen.com

### Massachusetts Branch

10 Rogers Street Unit 1A,
Cambridge, MA 02142
Tel: 301-251-1007 Ext. 851
boslab@psomagen.com

### New York Branch

760 Parkside Ave. Suite 122,
Brooklyn, NY 11226
Tel: 301-251-1007 Ext. 303
nyclab@psomagen.com