

一、送样前细胞 STR 信息检索：

- 1、送样前请先在 ICLAC(International Cell Line Authentication Committee, <https://iclac.org/>) 网站公布的**错误细胞系目录**中检索待检测细胞是否为已经确定的错误细胞系，如已确认，建议不必再检测。
- 2、在 <https://web.expasy.org/cellosaurus/> 网站或 <https://scicrunch.org/> 网站可检索待检测细胞信息，查看是否为红色标记的“**Problematic cell line**”。如果经检索您的细胞为错误细胞系或有问题细胞系，建议您在后续的实验中谨慎使用。

二、检测结果比对：

可将您的检测结果在 <https://www.dsmz.de/services/services-human-and-animal-cell-lines/online-str-analysis.html> 网站进行检索，比对查询您的样品来源。

也可在以下数据库进行检索：

[ATCC STR profile database](#) (search and compare STR profiles, login required)

[DSMZ STR profile database](#) (search and compare STR profiles, login required)

[CLIMA database](#) (search and compare STR profiles, version 2.1)

[Cellosaurus](#) database (search cell line name or description)

[NCBI BioSample](#) database (search cell line name or description)

三、计算自建细胞系与其来源的组织样品之间一致性的方法：

可参考 DSMZ 的计算方法（下图）或 ICLAC 提供的计算表格（见下页）。

How to compare STR profiles

$$I_{j,j'} = \frac{2 \times \sum_{i \in L_{j,j'}} |S_{i,j} \cap S_{i,j'}|}{\sum_{i \in L_{j,j'}} |S_{i,j}| + |S_{i,j'}|}$$

$S_{i,j} : \{\text{Unique alleles observed at locus } i, \text{ sample } j\}$
 $L_{j,j'} : \{\text{Loci at which assay succeeded for both } j \text{ and } j'\}$

$\frac{2 \times \text{shared alleles}}{(\text{total alleles in sample 1} + \text{total alleles in sample 2})}$

Source	Tracking ID	Cell Line Name	D16S539	D5S818	D7S820	vWA	TPOX	TH01	AMEL	CSF1PO	D13S317	
DSMZ	ACC 632	SK-N-BE(2)	9,11	12	9,10	18	8,11	6	X	10	11	
GNE	586645	SK-N-BE(2)	9,11	12	9,10	18	8,11	6,7	X,Y	10	11	
												Total
DSMZ Alleles			2	1	2	1	2	1	1	1	1	12
GNE Alleles			2	1	2	1	2	2	2	1	1	14
Intersecting Alleles			2	1	2	1	2	1	1	1	1	12

$$\frac{2 \times 12}{(12 + 14)} = 0.923 \text{ (92\% identity)}$$

total alleles = total number of unique, detected alleles. Does not assume samples are diploid.

www.dsmz.de

Sample Comparison

Table 3A: STR Profile Results

	Test Sample	Reference Sample
Cell line designation e.g. name and catalog number		
Date sample collected (if known)		
Passage or Population Doubling (if known)		
STR Profile Result (enter name of kit if used)		
D5S818		
D13S317		
D7S820		
D16S539		
vWA		
TH01		
Amelogenin		
TPOX		
CSF1PO		

Table 3B: Percent Match Calculations

TOTAL ALLELES in the Test Sample	
TOTAL ALLELES in the Reference Sample	
SHARED ALLELES, Test and Reference Samples	
Percent Match for Test and Reference Samples	

Percent Match can be calculated using an appropriate Match Algorithm (2.3). For this Worksheet:

$$\text{Match Algorithm} = \frac{\text{SHARED ALLELES} \times 2}{\text{TOTAL ALLELES in the Test Sample} + \text{TOTAL ALLELES in the Reference Sample}}$$

$$\text{Percent Match} = \text{Match Algorithm result} \times 100$$

Table 3C: Interpretation of Results

Are there multiple peaks that would be consistent with a mixture?	YES/NO
Is the percent match result in the range 0-55 %? This result is consistent with the two samples being unrelated (different donors).	YES/NO
Is the percent match result in the range 56-79 %? This result is indeterminate and may need further testing.	YES/NO
Is the percent match result in the range 80-100 %? This result is consistent with the two samples being related (same donor).	YES/NO