

# How to interpret locus-specific match probabilities in the full report

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## Locus-specific match probabilities for ATLAS searches

Locus-specific match probabilities for p0, p1 and p2 are available in the full donor and CBU reports of ATLAS search results.

These results can be accessed by navigating to the full report by selecting the "full report" button that is displayed for every search result.

## Why are locus-specific match probabilities not available for Hap-E searches?

Because of the different [definitions](#) between match probabilities calculated by ATLAS and Hap-E and the nature of how match probabilities are displayed by Hap-E, it is not possible to display locus-specific match probabilities for p0, p1 and p2.

## How to interpret locus-specific match probabilities in the full report

### For Hap-E search results

Based on the type of search, the locus-specific match probability displays the **relative probability** that this locus is a match **in the next mismatch case**. Therefore, it is not possible to distinguish between p0, p1 and p2 locus-specific match probabilities.

For additional information about the definition of the match probabilities in Hap-E, please visit [this page](#).

### For ATLAS search results

The locus-specific match probabilities are defined for p0, p1 and p2 in the full donor and CBU reports of ATLAS search results:

- The match probability for p0 is defined as the **match** probability for a full match at a specific locus
- The match probability for p1 is defined as the **mismatch** probability for a single mismatch at a specific locus
- The match probability for p2 is defined as the **mismatch** probability for two mismatches at a specific locus

In the example below, the probabilities for a full match (no mismatches) for HLA-B and -DRB1 are 100%. For HLA-A and HLA-C, the matching probabilities are 98% and 1%, respectively.

Therefore, the match probabilities displayed for p0 are considered **match probabilities**.

The probability for a single mismatch at HLA-B and -DRB1 is 0%. For HLA-A and HLA-C, the probabilities for a single mismatch are 2% and 97%, respectively.

Therefore, the match probabilities displayed for p1 and p2 are considered **mismatch probabilities**.

HLA	Patient	CBU	Match grade	Match probability
HLA-A	01:01 02:01	01:XX 02:XX	P	0: <b>98%</b> 1: <b>2%</b> 2: <b>0%</b>
HLA-B	08:01 37:01	08:01 37:01	A	0: <b>100%</b> 1: <b>0%</b> 2: <b>0%</b>
HLA-C	03:EENEH 07:EEDAU		P	0: <b>1%</b> 1: <b>97%</b> 2: <b>3%</b>
HLA-DRB1	03:EEPXR 10:DEDFB	03:01 10:01	A	0: <b>100%</b> 1: <b>0%</b> 2: <b>0%</b>

1. Example locus-specific match probabilities ATLAS search