

How to perform A, B Antigen, DRB1 ARD level CBU searches when using Hap-E

The [USA guidelines](#) for cord blood selection recommend a minimum 4/6 (HLA-A, -B antigen, -DRB1 allele/ARD) match as a suitable option for some patients. Some of the WMDA member organisations have implemented to run a routine HLA-A, -B antigen, -DRB1 allele/ARD cord search with up to two mismatches as a default. Therefore, WMDA has implemented this option as well in Search & Match Service.

- Allele matching is used to calculate overall and locus-specific match probabilities.
- Match class (e.g. 5/6, 4/6) is based on Antigen level matching at the A* and B* locus whereas regular matching at antigen recognition domain (ARD) level is used for DRB1.
- An antigen match is done according to method SI3 of [this paper](#).

Examples of antigen matches and mismatches can be found in this table:

patient	donor	Ag match?	patient	donor	Ag match?	patient	donor	Ag match?
B16	B16	yes	B39	B39	yes	B3901	B3901	yes
	B38	yes		B3901	yes		B39	yes
	B39	yes		B3902	yes		B16	yes
	B3901	yes		B16	yes		B3902	no
	B3902	yes		B38	no		B38	no

Match probabilities

Match probabilities for A, B Antigen, DRB1 ARD level CBU searches are calculated in the same way as "regular" searches. This means that the indicated overall and locus-specific match probabilities are based on ARD match, also for HLA-A and HLA-B.

HLA match grade categorisation

Whether a potential CBU is a 6/6, 5/6 or 4/6 considering the special rules for A, B Antigen, DRB1 ARD level CBU searches is determined by whether it is an antigen match at HLA-A and HLA-B and whether it is an ARD level match at DRB1. Allele mismatches are therefore not considered regarding the categorisation.

Sorting

Sorting is performed in the regular way based on the match probabilities as explained below.

1. HLA match grade (e.g. first 6/6 then 5/6, 4/6)
2. ARD level match probability in 10% intervals (descending)
3. Number of total nucleated cells (TNC, descending) or, if chosen, CD34 count, descending