User manual
STEP
(10may2022)

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1. Register an incompatible/altruistic living donor
Living donor -> Living kidney donor basic

Click on ‘Add new’

1.1. Basic donor parameters
You can now start with the data entry. Donornumber will be assigned after you have saved the data.
A few parameters are obligatory to register before you can save the data. The obligatory parameters are sex, country, birth-date, Tx. center, AB0 blood group, relation code and organ type. Organ type is found under the “Preop.” tab.

Relation code: For incompatible living donors select ‘STEP-donor’ as relation code, as the code is related to the possible transplantation and not the incompatible related-recipient.
Clinical data: GFR, sitting untreated BP, Diabetes and Proteinuria must be register on the donor to fulfil the requirements outlined in the STEP guidelines.

1.2. Linkage between donor and recipient

Create a link between the incompatible donor-recipient pair by clicking in the STEP relation field:

Bring forward the recipient by searching on Scandia number or person number, click on the specific patient and save

1.3. HLA typing on Living donor

The donor must be typed and registered with 2nd field resolution on HLA-A, B, C, DRB1, DRB3, DRB4, DRB5, DQA1, DQB1, DPA1 and DPB1. If it is not possible to exclude ambiguities please register CWD alleles and state this by selecting from ‘Haplotype/CWD alleles’ list and/or add a comment.
2. Update information on recipient

Recipient -> All Recipients

The recipient must be on the kidney waiting list (active/on hold) to be part of the STEP program.

2.1. Recipient ABO acceptance

The default setting is that the recipient is allowed to receive kidneys of all blood groups. If you want to add restrictions you need to add the blood groups that the recipient cannot accept, this is done on the waiting list under ‘Non-accepted ABO’.
2.2. HLA typing on recipient

The recipient must be typed and registered with 2\textsuperscript{nd} field resolution on HLA-A, B, C, DRB1, DRB3, DRB4, DRB5, DQA1, DQB1, DPA1 and DPB1. If it is not possible to exclude ambiguities please register CWD alleles and state this by selecting from ‘Haplotype/CWD alleles’ list and/or add a comment.

<table>
<thead>
<tr>
<th>Serological/serological equivalent</th>
<th>HLA Typing</th>
<th>Antibody Screen Test</th>
<th>Fusion</th>
<th>Acceptable Antibodies</th>
<th>Previous Mismatches</th>
<th>Death</th>
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<tr>
<td>Bon&amp;blod: w4</td>
<td>B: 57</td>
<td>62</td>
<td>Cw: 19</td>
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<td>Genomic</td>
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<td>B: 5702</td>
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<td>DQB1: 0302</td>
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</tbody>
</table>

2.3. HLA antibody data on recipient

MFI/bead data on recipients with HLA antibodies must be transferred from Fusion software to YASWA to define if there are any donor specific antibodies (DSA) against the donors enrolled in the program. Separate manuals describing this procedure is found on the homepage.

Bead information in the Fusion tab is isolated and currently only used for STEP match runs. Data found in ‘Antibody screen test’ and ‘Previous mismatches’ have no effect on these data.

Default setting is that antigens/beads with MFI ≥ 2000 are regarded as positive. If you wish to view/change default values select the most recent sample in the ‘Fusion’ tab.
If you click on the status field you are able to change a positive MFI/bead to ‘A: Acceptable’ or a negative bead to ‘U: unacceptable’.

Previous mismatches/non-acceptable antigens must be given separately in the Fusion tab or as an non acceptable antigen in YASWA.

Before each match run it is important to check that the most recent sample in the Fusion tab is updated with correct information, as it is this information that is used in the match algorithm.

If a new sample has been exported from Fusion to YASWA and you wish to bring forward manually conclusions made on a previous sample, that deviate from the default conclusion, you click on the ‘Add conclusions’ button.

This will bring forward the conclusions made on the previous sample, which you will now be able to modify and save.

2.4. Non-acceptable antigens on recipient
In some cases it is necessary to block a whole antigen, the reason for this can be common antigens where no bead exists and/or the DQ/DP matching on dimers.
Examples:
- There is currently no bead for HLA-C*07:01 and if you know that you will not accept any C*07 subtypes for a specific recipient you add HLA-Cw7 as an non-acceptable antigen.
- Your recipient has strong antibodies against DQB1*05 and you don’t want to accept any combinations of DQA with DQB1*05 you block HLA-DQ5.
2.5. Add recipient to match run

When you are ready to add the recipient/pair to the match run, you enter the waiting list and select the specific match run from the list:
In the menu ‘Recipient’ -> ‘STEP’ -> ‘Participating pairs’ you are able to get an overview of what recipients/pairs are included in which match run from your own center.