
Europdonor Foundation

Bone Marrow Donors Worldwide

User Guide

Version 1.4, December 2011

Revision History

Date	Version	Description	Author
2005-04-15	1.0	First version	JB
2005-05-18	1.01	Minor corrections	JB
2005-09-30	1.1	Minor update	JB
2005-10-26	1.11	Minor corrections	JB
2006-09-13	1.12	Minor corrections	JB
2010-02-03	1.2	General update reflecting change requests (CRF025, CRF023, CRF018, CRF014, CRF012)	JB
2010-05-07	1.3	- Update for new nomenclature - A few minor corrections related to the implementation of additional change requests	JB
2011-12-08	1.4	- General update reflecting change requests (CRF001, CRF009, CRF029)	JB

Contents

1	Introduction	4
2	Accessing the on-line match programs	4
2.1	General	4
2.2	Requesting authorization	4
3	The main menu	5
3.1	Other menu options	6
4	Edit Recipient Details / Add New Recipient	6
5	User Preferences	7
5.1	Personal Information	7
5.2	Match preferences	7
5.2.1	Consider HLA-C/HLA-DQ when grading match results	7
5.2.2	Extended sorting on a locus	8
5.2.3	Sort cord blood units on TNC	8
5.2.4	Include additional data in match results	9
6	The search process	9
6.1	Pre-match selections	9
6.2	Searching	10
6.2.1	Match Categories	10
6.2.2	Matching grades	11
6.2.3	Grading of phenotypes	12
6.3	Search Results	12
7	References	14

User Guide

1 Introduction

The Bone Marrow Donors Worldwide (hereafter referred to as “BMDW”) on-line match programs provide a search facility to find the best matched haematopoietic stem cell donor or cord blood unit for a patient in need of a haematopoietic cell transplantation. This document is intended as an introduction to the new on-line match programs for BMDW.

The on-line match programs provide fast preliminary search results. Access to the match programs is restricted to authorized users only, and is primarily intended for unrelated stem cell donor search coordinators and transplant physicians of transplant centres and (national) stem cell donor registries and cord blood banks. Users of the on-line match programs must have a good knowledge of the HLA system in order to use BMDW optimally.

2 Accessing the on-line match programs

2.1 General

To access the on-line match programs, you need to click on the On-line Match Programs link in the menu on the BMDW web site. As an authorized user you have received a username and password, which you will need to log on.

2.2 Requesting authorization

BMDW's on-line facilities can be used by transplant centres and search coordinators. Authorization is given primarily by the national stem cell donor registries. People who are not professional members of the haematopoietic stem cell transplantation (HSCT) community will not be authorized.

Users that would like to be authorized can request authorization by filling out the form MR-10, and faxing this to either the national hub, or if none is available in the country of origin, directly to the BMDW Office. More information and the above mentioned form can be found on the BMDW website, by following the link “Authorization”.

3 The main menu

After logging on successfully, the main menu will be shown. Immediately after logging on, the system will show you when you have last logged on, and from what system; in addition it will show details of your current log on. This is an informational security warning and this section is only shown once. The next time during the session you return to the menu, this section will not be shown.

The next section of the menu page shows your registered recipients (if any). The grid with recipients is not shown if you have no recipients registered.

- Edit recipient details
 - Delete recipient
 - Select recipient for matching
 - Select recipient for Prognostic Match
 - Search Advice Request

Show: Sorted on:
 Ascending
 Descending

Recipient ID	Urgent	Last Name	First Name	Date of birth	Gender	Diagnosis	Weight (kg)	Last updated	Last searched
[REDACTED]								04-Jan-2010	03-Feb-2010
[REDACTED]								05-Aug-2009	03-Feb-2010
[REDACTED]								14-Oct-2009	
[REDACTED]								17-Jun-2009	03-Feb-2010
[REDACTED]								26-Aug-2008	
[REDACTED]								02-Dec-2009	
[REDACTED]								02-Oct-2009	
[REDACTED]								04-Dec-2007	

The icons after the ID's of the recipients are explained in the legend above and below the grid.

The meaning of the icons is:

- **Edit recipient details:** Modify all details for the given recipient - not just the details shown in the recipient grid, but also the HLA or DNA typing of the recipient.
- **Delete recipient:** Delete all information for the given recipient.
- **Select recipient for matching:** The recipient's details will be retrieved, and the user is taken to a page with match options.
- **Select recipient for Prognostic Match:** The recipient's details will be retrieved, and the prognostic match option is executed.
- **Search Advice Request:** In case of a difficult recipient, you may submit the recipient for a BMDW Search Advice.

The grid can be filtered and sorted. If a large number of recipients are registered for a user's account, you can filter the list of recipients on:

- “All recipient” – show all recipients for the user's account
- “Urgent recipients” – show only recipients that have an urgency flag set in their details
- “Non-urgent recipients” – show only recipients that do not have an urgency flag set in their details

The list of recipients can also be sorted on:

- “no sorting” – to list recipients in the order of their registration, so the recipient that was entered last is on top of the list.
- “Recipient ID” – recipients are listed ordered by the Recipient ID's.
- “Last name” – recipients are ordered according to their last names.
- “Last updated” – when recipient details are updated, this is stored in the database. This option orders the list of recipients on this column.

“Last searched” – recipients are listed on the date the recipient was last searched.

For all these options, sorting can be done either ascending or descending.

3.1 Other menu options

The other main menu options are:

- **Add new recipient:** Register the details for a recipient not yet registered.
- **User Preferences:** Set the user preferences for your account. See below for more details.
- **User Guide:** an online link to this document.
- **Log out:** Sign off and return to the BMDW homepage.

4 Edit Recipient Details / Add New Recipient

The form shown below is used for recipient registration and editing. When entering/updating a recipient, only the recipient ID and a valid HLA-A, -B, and -DRB1 phenotype are required.

Recipient ID: <input type="text"/>	Last name: <input type="text"/>	First name: <input type="text"/>		
Date of Birth: <input type="text"/> <input type="text"/> <input type="text"/>	Gender: <input type="radio"/> Male <input type="radio"/> Female	Weight: <input type="text"/> kg <input type="checkbox"/> Urgent		
Diagnosis: <input type="text"/>	Date of diagnosis: <input type="text"/> <input type="text"/>			
Class I - DNA typing	<u>A</u> ¹ <input type="text"/>	<u>B</u> ¹ <input type="text"/>	<u>C</u> <input type="text"/>	
	<input type="text"/>	<input type="text"/>	<input type="text"/>	
Class II - DNA typing	<u>DRB1</u> ¹ <input type="text"/>	<u>DRB3</u> <input type="text"/>	<u>DRB4</u> <input type="text"/>	<u>DRB5</u> <input type="text"/>
	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
	<u>DQA1</u> <input type="text"/>	<u>DQB1</u> <input type="text"/>	<u>DPA1</u> <input type="text"/>	<u>DPB1</u> <input type="text"/>
	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>

Notes: It is recommended that you enter the underlined fields.

¹ A complete HLA-A, -B, and -DR/DRB1 typing is required for matching.

² Date fields require 4 digit for the year value.

Things to consider when entering/updating recipient details:

- Search determinants will be generated from the DNA values entered. The search determinants will be used for matching.
- Dates need to be entered using four digits for the years.
- Use the Tab key to move from field to field. When using the Tab key on the HLA fields, the cursor will move as such that you can first enter both locus values, before moving to the next locus.
- After you are finished entering or updating the recipient's details, you can save the details by clicking the button below the form. After clicking the button the details will be validated.
- If no problems are detected during this validation, the details will be stored in the database.
- If there are any problems, these will be reported at the top of the form, and the form fields that need to be corrected are highlighted in red.
- For urgent recipients, the Urgent checkbox can be set. This checkbox does not affect the match functionality, but may be used to manage the list of recipients as described in section 3.

5 User Preferences

There are a number of settings available per user account. These settings include the user's contact details (i.e. email address), settings that affect the user interface, and settings that affect the behaviour of the match programs:

User Preferences

Personal Information

- [Change your password](#) (your password was last changed on 2010-06-08).
- [Update your contact details](#)

Other user settings

Default sort option
Default sorting method for the recipients:

Match Preferences

Option	Enabled
Consider HLA-C when grading match results *	<input checked="" type="checkbox"/>
Consider HLA-DQ when grading match results **	<input checked="" type="checkbox"/>
Extended sorting on locus **	<input type="radio"/> HLA-A <input type="radio"/> HLA-B <input type="radio"/> HLA-DRB1 <input checked="" type="radio"/> None
Sort cord blood units on TNC within each match category ***	<input checked="" type="checkbox"/>
Include additional data in the match results	<input checked="" type="checkbox"/>
Include 2 and 3 NIMA in match****	<input type="checkbox"/>

* If the recipient is not typed for HLA-C or HLA-DQ, then enabling these preferences do not effect the search process.
** Sorts donors and cords blood units with high-resolution DNA to the top of the match category they are in.
*** Only applies to the cord blood match. With this option enabled HLA of the cord blood units is not included in the sorting within each match category.
**** Only applies to the NIMA match. With this option enabled cord blood units with 2 or 3 NIMA's are also used.

! Important notice: the regular match program and the mismatch program provide results upto 1 antigen/allele mismatch (6/6 and 5/6 matches). When the options to consider HLA-C and HLA-DQ are used, a donor or CBU with one mismatch on HLA-A, -B, or -DRB1, and an additional mismatch on HLA-C or -DQ results in the donor or CBU no longer being shown on the search report, due to this second mismatch. See the user guide for more details.

5.1 Personal Information

The personal information section of the User Preferences allows you to change the password for your user account, and update your contact details.

An informational message will be shown to inform users when their passwords were changed last. Changing the password requires entering the current password, and a new password. In addition the new password needs to be confirmed.

Clicking on the “Update your contact details” link will show a form that allows updating of for example the user’s name and organisation, the email address, and the phone and fax numbers of the user.

5.2 Match preferences

The match preferences affect the behaviour of the match process and the results returned. These preferences are stored as part of the user profile, and will be used as default settings when a user selects a recipient for matching, however at that time the user can still overrule the settings for that particular match.

5.2.1 Consider HLA-C/HLA-DQ when grading match results

These two options affect the match process; and only if the recipient is typed for these loci: if the recipient is not typed for HLA-C (or HLA-DQ), considering HLA-C (or HLA-DQ) when grading match results is not possible.

With these options disabled, the match process only considers HLA-A, -B, and -DR (including DNA), when matching, and grading donors and/or cord blood units. Based on HLA-A, -B, and -DR, the donors are put in the proper match categories. With these options enabled, HLA-C and -DQ are included in the match process and may result in donors or cord blood units typed for HLA-C and HLA-DQ being put in different match categories.

This is perhaps best explained by an example. Let us assume we have a recipient with a DNA typing that includes C*04:01,07:06. Let us further assume that there are two donors available that are allele matched with the recipient for HLA-A, -B and -DRB1, and that the first of these donors is typed C*04:01,16:01, the second is not typed for HLA-C.

With the option to consider HLA-C is disabled, the above mentioned two donors would both be put in the “Allele matched” category: since the option to consider HLA-C is disabled, the mismatch on HLA-C for the second donor is ignored. When the option to consider HLA-C is enabled, the second donor that is not typed for HLA-C is still an “allele matched” donor – however, the first donor is now put in the “HLA-C Allele/Split Antigen Mismatched” category.



Without these options enabled the regular match program shows donors and cord blood units up to one allele/split antigen mismatch (6/6 and 5/6 matches). It is therefore important to note that when the options for HLA-C and -DQ are used, donors and cord blood units with one allele/antigen mismatch on HLA-A, -B, or -DR and an additional mismatch on HLA-C or -DQ will no longer be shown on the search report.

In summary the regular match program reports the following:

- with these options disabled: 6/6 and 5/6 matches
- with either the HLA-C or -DQ option enabled: 8/8 and 7/8 matches
- with both HLA-C and -DQ options enabled: 10/10 and 9/10 matches

The options affect the mismatch program as well – the same principle applies: with these options enabled, donors or cord blood units with a second mismatch on HLA-C or -DQ will no longer be listed, since the mismatch program shows only one antigen/allele mismatches. In summary the mismatch program reports the following:

- with these options disabled: 5/6 matches
- with either the HLA-C or -DQ option enabled: 7/8 matches
- with both HLA-C and -DQ options enabled: 9/10 matches

5.2.2 Extended sorting on a locus

In cases where you may have a recipient with a rare allele, you may find it hard to locate the one donor you are looking for. Donors that are for example typed with serology for HLA-A and -B, but with high-resolution DNA for DRB1, might be the best chance for a recipient, especially if for example a donor has the same rare allele as the recipient. However, due to the serology of this donor or cord blood unit, it is probably not on top of the match list.

This option allows extended sorting of donors and cords blood units with high-resolution DNA to the top of the match category they are in. The locus to sort on (either HLA-A, -B, or -DR/DRB1) can be selected.

5.2.3 Sort cord blood units on TNC

This match preference affects the results for the cord blood matches only: when this option is enabled, the cords that are listed in each match category will be ordered on the number of nucleated cells (TNC).

5.2.4 Include additional data in match results

Optionally extra donor or cord blood data can be shown in the match results: which results are shown with this option enabled or disabled is summarized in the table below:

<i>Regular and mismatch programs</i>	<i>Option enabled</i>	<i>Option disabled</i>
HLA typing (A, B, C, DR, DQ, DRB3/4/5)	✓	✓
Registry code	✓	✓
Number of donors for the given phenotype	✓	✓
Sex, Age, CMV data, blood group	✓	

Additionally, for users at registries and cord blood banks, the donor ID is also included in the additional data.

<i>Cord blood match program</i>	<i>Option enabled</i>	<i>Option disabled</i>
HLA typing (A, B, C, DR, DQ, DRB3/4/5)	✓	✓
Registry code and ID of the cord blood unit	✓	✓
Number of donors for the given phenotype	✓	✓
Nucleated cell count, volume, CD34+ cell count, mononucleated cell count	✓	✓
Sex, Age, CMV data, blood group	✓	

5.2.5 Include 2 and 3 NIMA in match

Specifically for the NIMA cord blood match option, this option includes 2 or 3 mismatched, but NIMA matched cords in the match results.

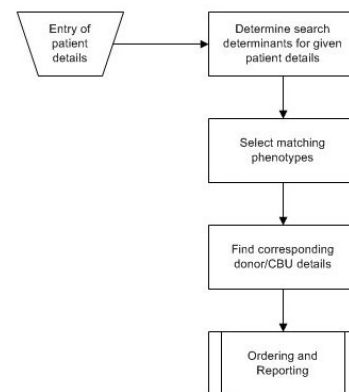
6 The search process

6.1 Pre-match selections

When the little magnifying glass (🔍) is selected from the grid of recipients on the main menu, the pre-match-selection page is shown.

On top of the pre-match-selection page the details for the selected recipient are shown.

In the next section, the search determinants for the recipient are shown. The search determinants are extracted by combining both serology (if given) and the serological equivalents for the provided DNA of the recipient. This process uses resources that include the HLA Dictionary [1], the World Health Organisation (WHO) Nomenclature for factors of the HLA system [2], and the World Marrow Donor Association (WMDA) IT Working Group HLA Standards [3]. The reference tables used are currently updated monthly, but will be updated more frequently in the near future.



The next section shows the same match preference options we've seen in the previous chapter. As mentioned, the defaults values for these options are loaded from the user profile, but can be changed for this specific match.

Also, for this match, there are two additional options:

- **Match on own donors (available for registry and cord blood bank users only):** filter the search results and present only those donors or cord blood units of the local registry / cord blood bank.
- **Do NOT paginate the output:** to force all search results into one long list, enable this option.
Warning: when many donors have been found, this may cause browser and printing problems.

Finally, at the bottom of the page the type of match to be done can be selected. In brief, the different match programs have to following functions:

- **Regular Match Program:** performs a match basically looking for identical donors, but this option also includes split antigen or allele mismatches.
Note: this match does not include cords blood units.
- **Mismatch on HLA-A/B/DR:** performs a match looking for one antigen/allele mismatches on either HLA-A, -B, or -DR. **Note:** this match does not include cords blood units.
- **CBU Match Program:** options to perform a cord blood match, looking for cord blood units up to two antigen/allele mismatches. You can search for either identical and one antigen/allele mismatches or cords with two antigen/allele mismatches.
- **NIMA Match Program:** performs a match on cord blood units, for which maternal HLA has been made available. The match program reports mismatched cord blood units that are matched on up to three NIMA's.

After selecting the desired match preferences and the type of match, the search button can be clicked to start the match process.

6.2 Searching

The search process itself is too complex to describe in detail in this user guide. In brief the process works as follows.

The search process selects donors and cord blood units based on the search determinants (extracted from the recipient's phenotype as provided by the user).

Matching (or mismatching) phenotypes are selected using the search determinants. If any additional donor or cord blood details are available these are added to the resulting dataset.

Finally the dataset is filtered in match categories and ordered based on the DNA, additional donor or cord blood details, and the user preferences. The flowchart to the right shows the search process in brief.

6.2.1 Match Categories

The following match categories are available. Only those categories, for which donors or cord blood units have been found, are shown in the search results.

- Allele matched
- Potentially (allele) matched

- HLA-A or -B Allele/Split Antigen Mismatched
- HLA-DR Allele/Split Antigen Mismatched
- HLA-C Allele/Split Antigen Mismatched
- HLA-DQ Allele/Split Antigen Mismatched

- HLA-A Antigen Mismatched

- HLA-B Antigen Mismatched
 - HLA-DR Antigen Mismatched
 - HLA-C Antigen Mismatched
 - HLA-DQ Antigen Mismatched
-
- Two Antigen Mismatched

The lines in this list of match categories show groups of categories: the first two match categories all contain potentially (allele) matched donors or cord blood units; the second block of categories contain donors or cord blood units that have an allele or split antigen mismatch (what we used to call “a minor mismatch”); the third block of categories contain donors or cord blood units with an antigen mismatch; and finally, a category only found in the cord blood match, to report donors or cord blood units with two antigen mismatches.

Specifically for the NIMA cord blood match, the following match categories are available:

- HLA-A or -B Allele/Split Antigen Mismatched / NIMA Matched
 - HLA-DR Allele/Split Antigen Mismatched / NIMA Matched
-
- HLA-A Antigen Mismatched / NIMA Matched
 - HLA-B Antigen Mismatched / NIMA Matched
 - HLA-DR Antigen Mismatched / NIMA Matched
-
- Two Allele/Antigen Mismatched / NIMA Matched
 - Three Allele/Antigen Mismatched / NIMA Matched

These categories are identical to the corresponding mismatch categories listed above, but the mismatched cord blood units are NIMA matched.

6.2.2 Matching grades

This section describes in brief, a bit of the internals of the match process. Please note that as a user of the match programs you will not see these (internal) match grades. If you have no interest in these details and are just a user of the program, you can skip this section and move on to section 6.3.

The so called “match plug-in” is the core of the search process. The match plug-in examines just two sets of antigens and/or alleles for one locus, and uses a finite state machine to quickly determine the match grade for the locus. The following match grades could be returned:

0. Unable to determine (i.e. when the recipient or the donor/cord blood unit is not typed for the locus)
1. Allele Matched
2. Potentially (allele) Matched
3. Broad Matched
4. HLA Allele/Split Antigen Mismatched
5. HLA Antigen Mismatched

The names for these match grades look similar to the overall match grades described in the previous section. The match plug-in determines a match grade for every locus that is included in the match. By default this is for HLA-A, -B, and -DR, but when the HLA-C and -DQ match preferences are used, also for these loci. With the results for each locus available, the match plug-in combines the match grades per locus, into an overall match grade for the phenotype. The overall match grade corresponds with the match categories as described in the previous section. As an example a match grade 1 for all HLA-A, HLA-B and HLA-DR will result in an overall match grade 1; a match grade HLA-A = 1, HLA-B = 3, HLA-DR = 1 will result in an overall match grade 3.

Finally, when combining the match grades for the loci, and considering the user preferences, the plug-in may also return one of the next overall match grades:

- -1 for impossible combinations, or
- -2 for more than two HLA-A/B/C/DR/DQ (allele) mismatches

It is important to note that for the **cord blood match program**, matching is done somewhat differently compared to the regular match program or the mismatch programs: for the cord blood match program the cord blood units are listed in the match category, by determining the match grade for HLA-A, and -B on serologic broad level, and for HLA-DR(B1) on serologic split level. If however, the cord blood unit has an allele or split mismatch on HLA-A or -B, then this allele or split antigen is highlighted in italic – so this allele or split antigen mismatch on HLA-A or -B does not affect in which match category the cord blood unit will be listed.

6.2.3 Grading of phenotypes

After the match plug-in has put the found donors and cord blood units into the correct match categories, the donors and cord blood units need to be ordered. Within each of the match categories donors and cord blood units are graded (ordered) according to the following rules:

- The “quality” of their typing: phenotypes that are typed at the highest resolution are put on top. For each locus this quality factor is determined. The more loci are typed at DNA level, the higher the phenotype is on the list. Phenotypes with high-resolution alleles are ranked higher than phenotypes with multiple allele codes; phenotypes with multiple allele codes are ranked higher than phenotypes with low-resolution alleles (e.g., B*39:XX).
- For each locus a weight factor is set to determine whether or not and how much the locus should be included in the grading. Currently HLA-A, -B, -DR, -C and -DQ have higher weight factors (value of 2) than the other loci (value of 1). So, as an example, if a donor is typed for HLA/DNA-C a value of 2 is added to the grade for this donor, raising this donor above a donor not typed for HLA/DNA-C on the search report (and identical on the other loci).
- If donors or cord blood units are typed for more loci than another donor or cord blood unit, the additional loci will cause this phenotype to be a bit higher on the list than an identical record without these additional loci, but still considering the above mentioned weight factors.
- For donors or cord blood units that are typed for serology only, split typed donors are ranked higher than broad typed donors.

6.3 Search Results

Once the match process is complete, the user is presented with the search results. As an example, a top section of a search report of the cord blood match is shown in the figure below:

■ HLA-C considered ■ HLA-DQ considered ■ Addition data included ■ Only identical and 1 allele/antigen mismatch ■ Sorted on TNC

A	B		C		DRB1	DQB1	Reg	#	Additional details	TNC	Vol.	CD34+MN	Sex	Age	CMV	CMV date	ABORh	
03:02	32:01	08:01	15:01	03:03	07:01	13	14	05:01	05:03	ID	(10 ⁷)	(ml)	(10 ⁵)	(10 ⁷)				
HLA-A Antigen Mismatched:																		
1	3	8	15			13:01	14:54			NYCB	211155	79	103	2.3	M	0		
HLA-B Antigen Mismatched:																		
3	32	8	35			13:01:01	14:BCAD			ECB	SPUCMAD0022136	149	81					
03:XX	32:XX	15:XX	—			13:GVA	14:PRK			LVCB	CB6132	91	96					
HLA-DR Antigen Mismatched:																		
03:02	32:01	08:01	15:BNJ			03:AH	13:XR			U1CB	998903752	95	54					

Registry Code Information:
 ECB: Spain CORD # U1CB: USA-NMDP CORD #
 LVCB: Belgium-Leuven CORD
 NYCB: USA-New York CORD

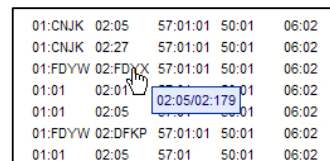
Multiple Allele Code Information:
 AH: 01/07 PRK: 01/07/26/39
 BCAD: 01/54 XR: 01/27
 BNJ: 15:01/15:04-15:07/15:20/15:24/15:25
 15:26N/15:27/15:28/ 15:30/15:32-15:35
 GVA: 01/02/16/28/35

= = CB registered in NetCord
 == = CB registry partly registered in NetCord

Hybrid cord blood banks are listed in bold and italic

Things you need to consider, when reviewing the search results:

- The links at the top (and the bottom) of the page include:
 - **Back to menu:** takes the user back to the main menu
 - **Select different match (options):** takes the user back to the pre-match selection form, to change match preferences, or select a different type of match for the currently selected recipient
 - **Show Summary:** shows a pop-up window with a summary of the match results
 - **Match on incomplete typings:** initially the regular match selects HLA-A, -B, and -DR typed donors and cord blood units. However, there is also still a large amount of donors in the database that are typed for just HLA-A and -B. In addition, registries might type for just two loci other than HLA-A and -B, for example just for HLA-B and -DR. This option will match on these donors and cord blood units.
Note: this option is only available for the regular match.
- Below these links you will find the ID and name of the recipient.
- On the next line, you will find the options that were used for this match. In the example above, you will see that for this match the option to include cord blood units was used. If the options to include a match on HLA-C or -DQ were used, that would be reported here as well.
- In the bar on top of the search results is the phenotype of the recipient. Below the phenotype of the recipient you will see the match categories for which donors or cord blood units have been found. Only the match categories, for which donors or cord blood units are found, are reported in the search results. Note that all match categories are shown in the summary. The bold number on the same lines as the name of the match category is the number of donors or cord blood units found in this match category.
- The search results contain NMDP allele codes. When you hover your mouse over the allele codes, a hint window will show the allele combination, the code represents. See the image to the right for an example.



- The search report was designed a minimum resolution of 1024x768 in mind. Due to this consideration of low screen resolution, the column for the registry a phenotype is found shows the shorthand code for the registries. Like with the allele codes, you may also hover over the registry codes with your mouse, to show the registry names.
- At the bottom of the report, all registry codes and allele codes are listed as found in the search results.

7 References

- [1] WMDA HLA Dictionary 2008, <http://hla.alleles.org/dictionary/index.html>
- [2] WHO Nomenclature for factors of the HLA system, <http://hla.alleles.org/>
- [3] World Marrow Donor Association (WMDA), <http://www.worldmarrow.org/>