



14<sup>th</sup>

International Donor Registry Conference  
& WMDA Meetings

25 – 29 June, 2024 – Cape Town, South Africa

*All patients & donors matter*

[www.capetownidrc.co.za](http://www.capetownidrc.co.za)

# Searching for the Most Suitable Donor: WMDA's Search & Match Service



**WMDA**

matching donors • serving patients

# Alicia Venter

Pillar 1: Optimising Search, Match & Connect

Project Coordinator



# Outline

01

## Bioinformatics in Unrelated Donor selection

- Probabilistic matching algorithms
- Haplotype frequencies



02

## Identifying a suitable stem cell product

- Leveraging technologies to save time
- Donor/cord blood unit Identification Tools



# Outline

01

## Bioinformatics in Unrelated Donor selection

- Probabilistic matching algorithms
- Haplotype frequencies



# Bioinformatics & Search & Match

**Bioinformatics** is the use of digital tools for computation and analysis in order to capture and interpret biological data. Bioinformatics is essential for **management of data** in modern biology and medicine, in particular when the data sets are **large and complex**, such as HLA.

**Search & Match Service (SMS)** is the **primary source** of all hematopoietic stem cell donors and cord blood units globally.

The database holds over 41 million donors and more than 790,000 cord blood units from 134 registries and cord blood banks across 57 countries.

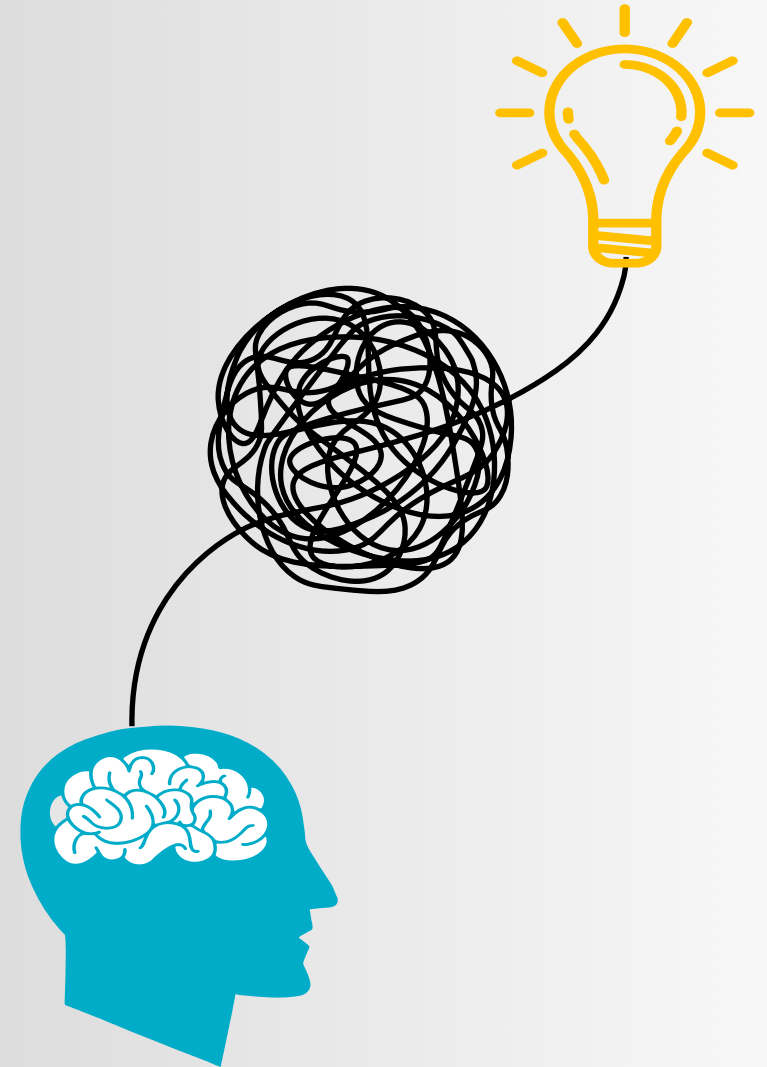
SMS provides a fast preliminary search facility to find the **best suitable cell source in the world** for a patient in need of a hematopoietic stem cell transplant.

# Probabilistic matching algorithms

An **algorithm** is simply a series of instructions that are followed, step by step, to **do** something useful or **solve a problem**.

For example, you could consider a cake recipe an **algorithm** for making a cake.

In computing, **algorithms** provide computers with a successive **guide to completing actions**.



# Probabilistic matching algorithms



The matching algorithms help to provide probability matching percentages using haplotype frequencies.



WMDA hosts the data from donors and cords worldwide on behalf of the listing organisations in a database to which the algorithm is also connected.



The data collected is used to periodically calculate Haplotype Frequency (HF) sets which are used by the algorithms to perform the probability matching.

# Haplotype frequency (HF)

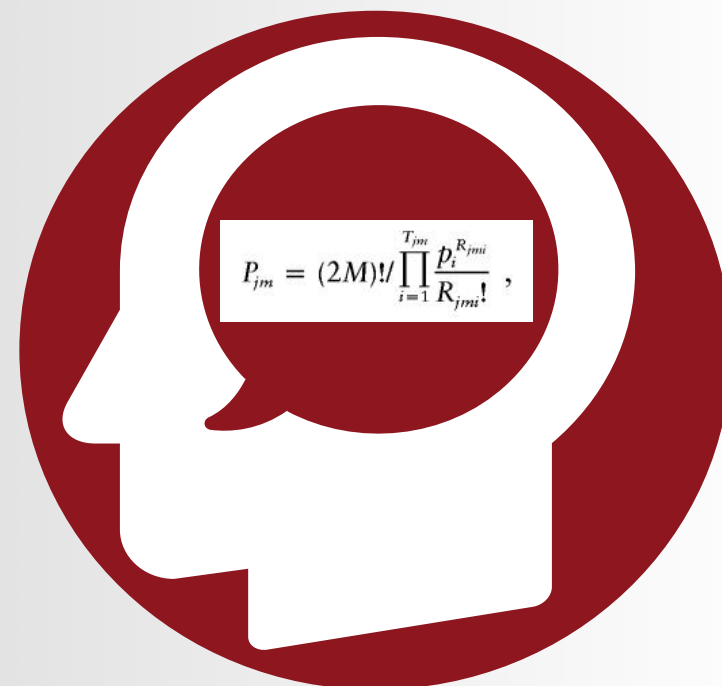
HF is defined as the **proportion of chromosomes** of that type in the population.

WMDA uses HF set configuration to better serve all patients and provide increased accuracy when selecting suitable donors and cord blood units to patients.

These frequency sets utilize high resolution typing results from organisations to extrapolate the haplotypes of the region or organisation.

Thus, an organisation or geographical region must meet a minimum threshold of number of donors and availability of high resolution typing to build usable and valuable frequency set.

For organisations or geographical regions that do not meet this minimum threshold, the global HF set is applied.



# Probabilistic matching algorithms

Probability of Mismatches ⓘ		A	B	C	DRB1	DQB1	DPB1	Registry	Sex	Age	Blood group
Patient details											
		03:01	07:02	04:01	04:02	03:DECZF	04:01		M	66	A+
		26:01	35:01	07:02	11:01	03:DWKVT	14:01				
10/10 (potential) allele matches											
# 12	GRID:	Status: <b>AV</b>		CMV:	No. of donations:		Ethnicity: <b>CA</b>		<a href="#">Full report</a>		
0: <b>99%</b>		<b>P</b>	<b>P</b>	<b>P</b>	<b>A</b>	<b>A</b>		3553 ✓	Female	58	☆
1: <b>1%</b>		<b>74%</b>	<b>55%</b>	<b>71%</b>	<b>100%</b>	<b>100%</b>	-				
2: <b>0%</b>		03:BJFRF	07:AREGZ	04:FEVX	04:02	03:ENWH					
		26:BTHM	35:EBZM	07:FEWC	11:01	03:02:01					
# 13	GRID:	Status: <b>AV</b>		CMV:	No. of donations:		Ethnicity: <b>MX</b>		<a href="#">Full report</a>		
0: <b>86%</b>		<b>P</b>	<b>P</b>	<b>P</b>	<b>P</b>	<b>P</b>		3553 ✓	Female	41	☆
1: <b>7%</b>		<b>100%</b>	<b>63%</b>	<b>71%</b>	<b>100%</b>	<b>65%</b>	-				
2: <b>7%</b>		03:AVWB	07:CUCE	?	04:02	?					
		26:PEU	35:BVSP		11:APWP						

# Outline

## 02

### Identifying a suitable stem cell product

- Leveraging technologies to save time
- Donor/cord blood unit Identification Tools



## Steps to identify a suitable cell source:

1. Go to WMDA website
2. Login with Multi Factor Authentication (MFA)
3. Add patient data - Consent?
4. Enter required fields HLA-A, -B, DRB1
5. Enter optional Class II loci HLA-DRB3/4/5, -DQA1, DPA1
6. Indicate the search you want

### Add Patient

Patient ID

#### HLA Details

[DNA type lookup tool](#)

##### Class I

HLA-A*	<input type="text"/>	<input type="text"/>
HLA-B*	<input type="text"/>	<input type="text"/>
HLA-C	<input type="text"/>	<input type="text"/>

##### Class II

HLA-DRB1*	<input type="text"/>	<input type="text"/>
HLA-DQB1	<input type="text"/>	<input type="text"/>
HLA-DPB1	<input type="text"/>	<input type="text"/>

Extra Class II loci

#### Medical Details

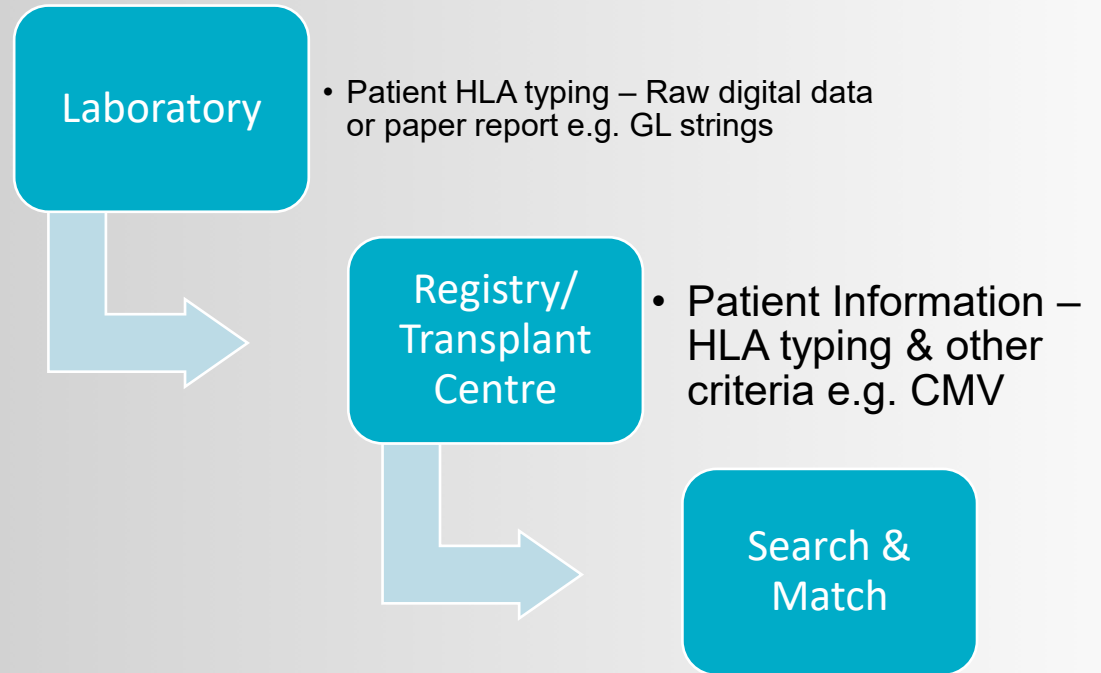
CMV Status	<input type="text" value="No Value"/>	Blood group, Rh	<input type="text" value="No Value"/>	<input type="text" value="No Value"/>
Ethnicity	<input type="text" value="No Value"/>	Weight	<input type="text"/>	
Birth Date	<input type="text" value="YYYY-MM-DD"/>	Sex	<input type="text" value="No Value"/>	
Diagnosis	<input type="text" value="No Value"/>	Disease Phase	<input type="text" value="No Value"/>	
Diagnosis Date	<input type="text" value="yyyy-mm-dd"/>	Pool Country Code	<input type="text" value="No Value"/>	
Diagnosis Text	<input type="text"/>	Transplant Center ID	<input type="text"/>	

#### Search details

Search type	<input checked="" type="checkbox"/> Run a donor search	Algorithm	<input checked="" type="checkbox"/> HAP-E
	<input type="checkbox"/> Run a cord search		

# ...alternatively

You can *Automatically transfer* patient data from your local system to Search & Match Service using the Patient API.



Patient ID

### HLA Details

[DNA type lookup tool](#)

Class I		Class II	
HLA-A*	<input type="text" value="01:01"/> <input type="text" value="23:01"/>	HLA-DRB1*	<input type="text" value="01:01"/> <input type="text" value="15:01"/>
HLA-B*	<input type="text" value="44:03"/> <input type="text" value="44:05"/>	HLA-DQB1	<input type="text" value="05:01"/> <input type="text" value="06:02"/>
HLA-C	<input type="text" value="02:02"/> <input type="text" value="04:01"/>	HLA-DPB1	<input type="text"/> <input type="text"/>

Extra Class II loci

### Medical Details

CMV Status	<input type="text" value="Negative"/>	Blood group, Rh	<input type="text" value="A"/> <input type="text" value="Positive"/>
Ethnicity	<input type="text" value="HICA - Central America, Caribbean"/>	Weight	<input type="text" value="86"/>
Birth Date	<input type="text" value="1983-04-24"/> <input type="text"/>	Sex	<input type="text" value="Female"/>
Diagnosis	<input type="text" value="AML - Acute Myelogenous Leukaemia"/>	Disease Phase	<input type="text" value="C2 - second complete remission"/>
Diagnosis Date	<input type="text" value="2019-04-24"/> <input type="text"/>	Pool Country Code	<input type="text" value="Netherlands(NL)"/>
Diagnosis Text	<input type="text" value="Acute Myeloid Leukemia"/>	Transplant Center ID	<input type="text" value="dr BM"/>

# Initiate Search

## Search details

### HAP-E

- Run a donor search
- Run a cord search

### ATLAS

- Run a donor search
- Run a cord search

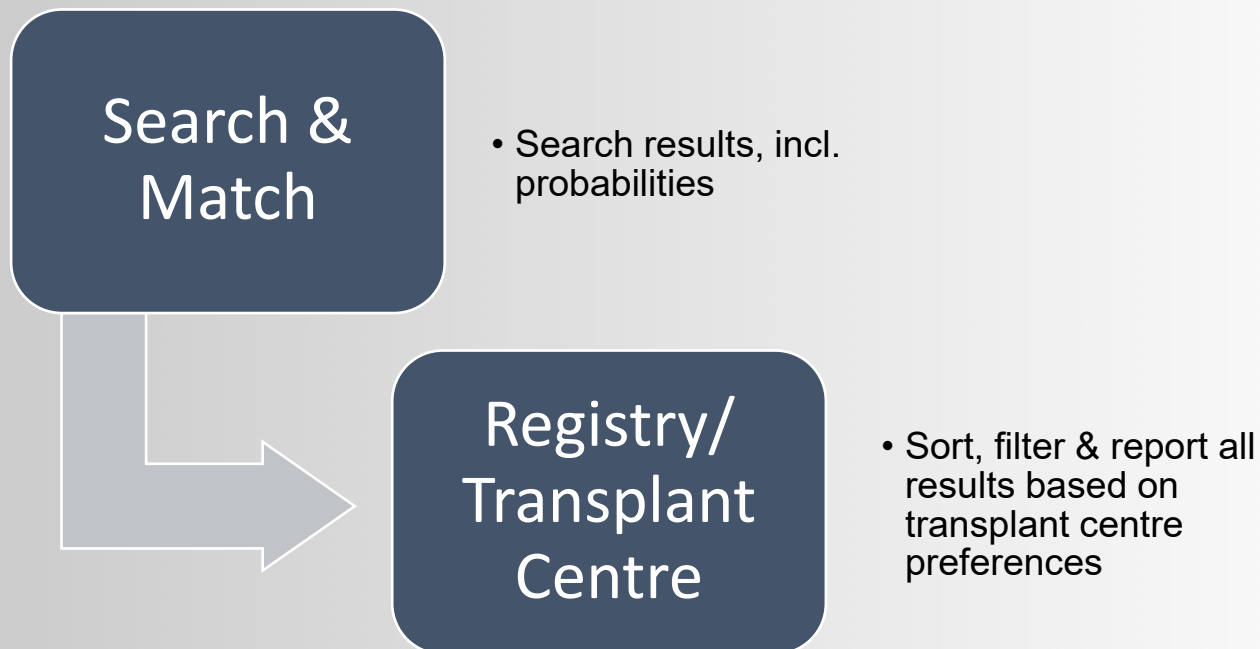
- I declare that the patient has been informed about the transmission of their information to the Search & Match Service.

Search

Probability of Mismatches ⓘ	A	B	C	DRB1	DQB1	DPB1	Registry	Sex	Age	Blood group
Patient details										
	01:01 23:17	08:01 41:02	07:01 17:01	07:01 11:01	02:02 06:02	104:01 105:01				
10/10 (potential) allele matches										
# 3	GRID: 4987 0000 0003 8224 836		Status: AV	CMV:	No. of donations: 0	Ethnicity:	<a href="#">Full report</a>			
0: 0%	<b>P</b>	<b>P</b>	<b>P</b>	<b>P</b>	<b>P</b>		4987 ✓ IL-Ezer Mizion	Male	53	☆
1: 1%										
2: 29%	<b>100%</b> 01:XX 23:XX	<b>59%</b> 08:XX 41:XX	<b>100%</b>	<b>100%</b> 07:XX 11:XX	<b>41%</b>	-				
9/10 (potential) allele matches										
# 4	GRID: 4987 0000 0002 0976 027		Status: AV	CMV:	No. of donations: 0	Ethnicity:	<a href="#">Full report</a>			
0: 0%	<b>P</b>	<b>P</b>	<b>P</b>	<b>P</b>	<b>P</b>		4987 ✓ IL-Ezer Mizion	Male	59	☆
1: 1%										
2: 29%	<b>100%</b> 01:XX 23:XX	<b>59%</b> 08:XX 41:XX	<b>100%</b>	<b>100%</b> 07:XX 11:XX	<b>41%</b>	-				
9/10 (potential) allele matches										
# 5	GRID: 6939 DKM0 0086 6391 004		Status: AV	CMV:	No. of donations: 0	Ethnicity: CAEU	<a href="#">Full report</a>			
0: 0%	<b>A</b>	<b>A</b>	<b>A</b>	<b>M</b>	<b>A</b>	<b>G</b>	5525 ✓ DE-DKMS	Female	29	B-
1: 100%										
2: 0%	- 01:01:01G 23:01:01G	- 08:01:01G 41:02:01	- 07:01:01G 17:01:01G	- 07:01:01 <b>(15:01:01)</b>	- 02:02:01 06:02:01	- <b>(04:01:01)</b> <b>(15:01:01)</b>				
9/10 (potential) allele matches										
# 6	GRID: 9968 DKM0 0000 1819 907		Status: AV	CMV: N 2020-12-10	No. of donations: 0	Ethnicity: CAEU	<a href="#">Full report</a>			
0: 0%	<b>A</b>	<b>A</b>	<b>A</b>	<b>A</b>	<b>M</b>	<b>G</b>	9968 ✓ GB-DKMS	Male	33	A+
1: 100%										
2: 0%	- 01:01:01G 23:01:01G	- 08:01:01G 41:02:01	- 07:01:01G 17:03:01	- 07:01:01G 11:01:01	- 02:02:01 <b>(03:01:01)</b>	- <b>(02:01:02)</b> <b>(02:01:02)</b>				



You can  
*Automatically download*  
donor and/or cord blood  
data from Search & Match  
Service to your local  
system using the Search  
API.



# Donor/CBU identification tools

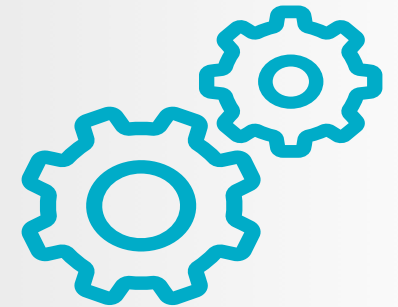
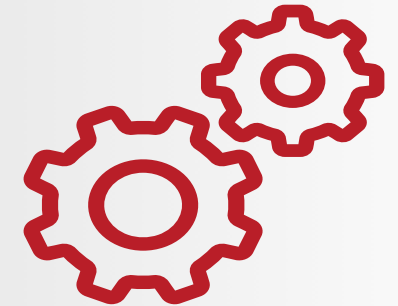
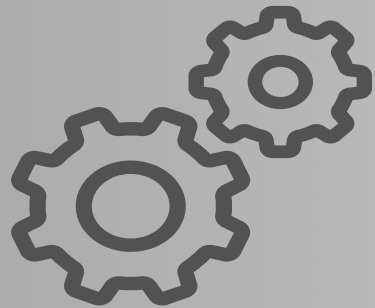


# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

---



# Donor Results

## Filters

### Match

Locus mismatch allowed

Select loci

DPB1 match grade

Select match grade

Number of mismatches allowed

Select number of mismatches...

Grouping/Sorting

- Standard  
 Sort by sum of probabilities

Inexplicable

Select Inexplicable

### Donor

Return only records with DRB1

Selected

Select Selection

CMV

Select CMV

Sex

Select sex

Blood group

Select blood group

Age



Donor status

Select Donor status

### Registry

Registry

Registry

Registry accreditation status

Select registry accreditation s...

Apply filters

Reset filters

# CBU Results

## Filters



### Match

Locus mismatch allowed

Select loci

DPB1 match grade

Select match grade

Number of mismatches allowed

Select number of mismatches...

Grouping/Sorting

- Standard  
 Sort by sum of probabilities

Secondary sort by

- TNC  
 CD34+

Inexplicable

Select Inexplicable

### Donor

Return only records with DRB1

Selected

Select Selection

CMV

Select CMV

Blood group

Select blood group

Age



Donor status

Select Donor status

### Registry

Registry

Registry

### Cord search filters

TNC

Minimum TNC  $\times 10^7$

CD34+

Minimum CD34+  $\times 10^6$

CBB accreditation status

Select CBB accreditation status

Apply filters

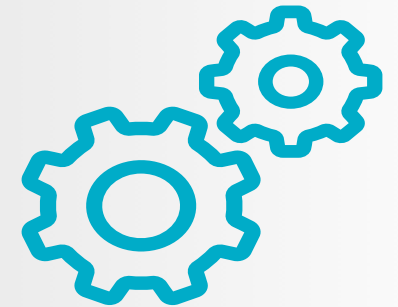
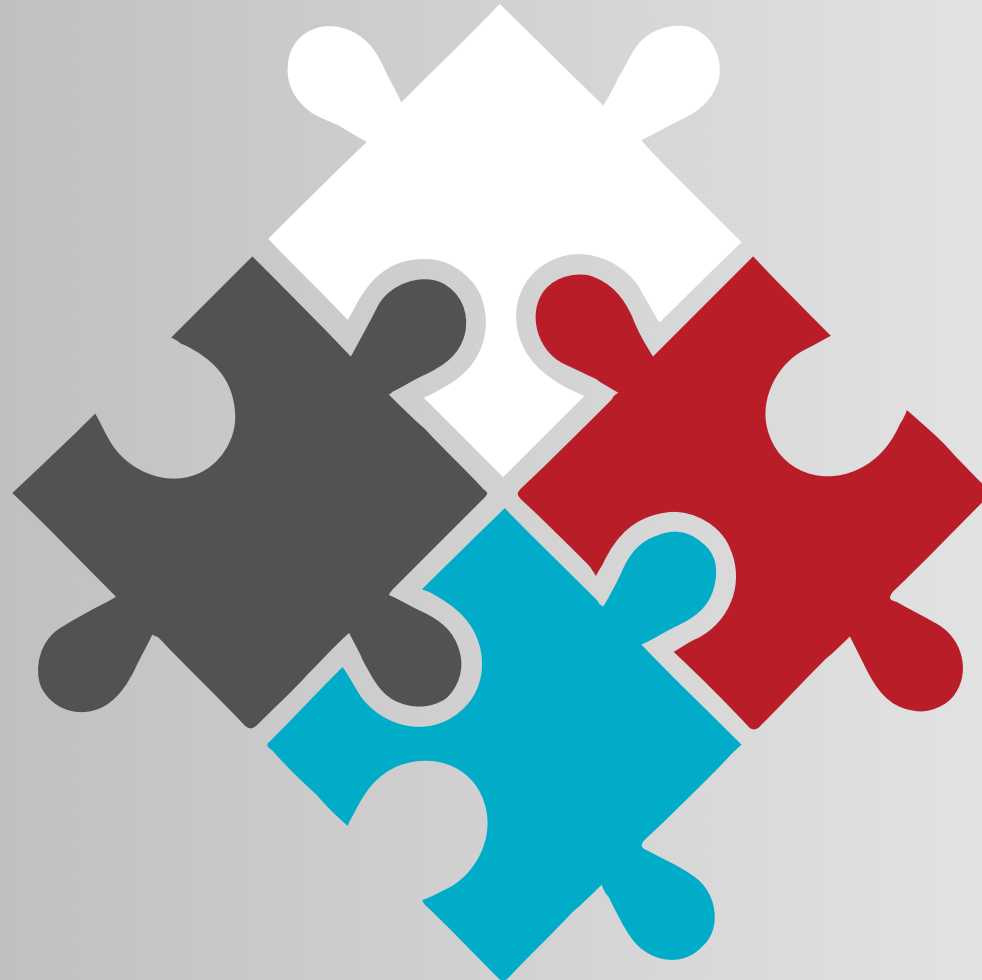
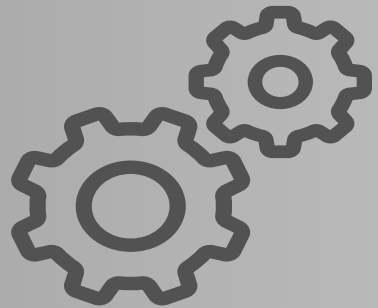
Reset filters

# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

---

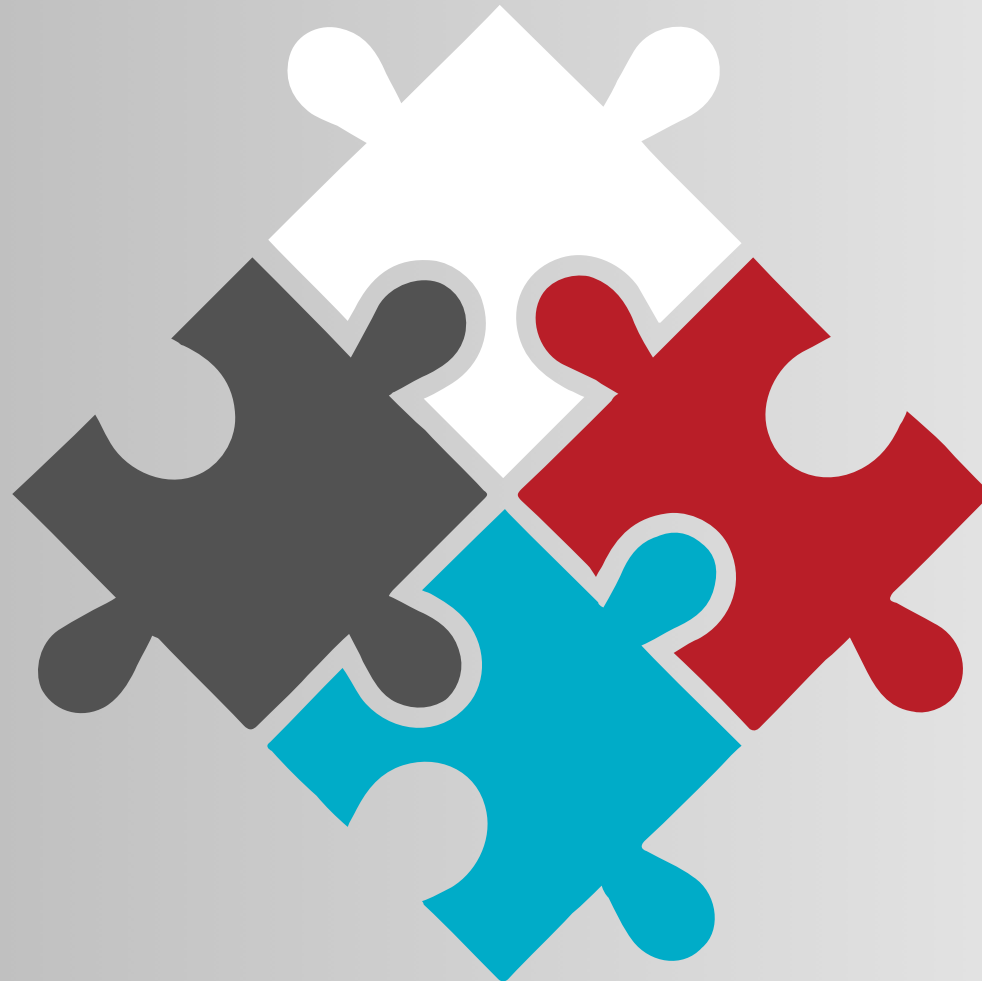
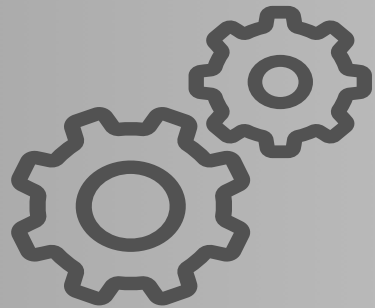


# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

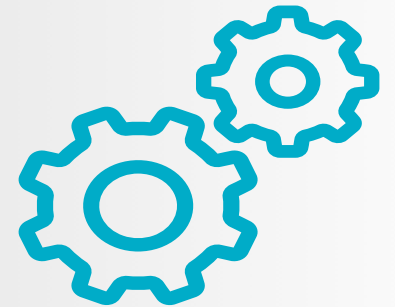
---



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**Automatic Updates** of active searches with notifications about changes in search results.

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Patient ID

Username

Results

Auto Refresh

Status Activity

IDRC - 550056

alicia.venter@wmda.info

Donor search | Hap-E | 10/10 | 33 potential donors  
Donor search | ATLAS | 10/10 | 31 potential donors  
Cord search | ATLAS | 10/10 | 0 potential cords  
Cord search | Hap-E | 10/10 | 0 potential cords  
Donor search | Hap-E | 9/10 | 1052 potential donors  
Donor search | ATLAS | 9/10 | 1026 potential donors  
Cord search | ATLAS | 9/10 | 39 potential cords  
Cord search | Hap-E | 9/10 | 39 potential cords



🕒 41 days until deactivation

IDRC - 550055

alicia.venter@wmda.info

Donor search | ATLAS | 10/10 | 0 potential donors  
Cord search | ATLAS | 10/10 | 0 potential cords  
Cord search | Hap-E | 10/10 | 0 potential cords  
Donor search | Hap-E | 10/10 | 0 potential donors  
Donor search | Hap-E | 9/10 | 95 potential donors  
Donor search | ATLAS | 8/10 | 4323 potential donors  
Cord search | ATLAS | 8/8 | 0 potential cords  
Cord search | ATLAS | 7/8 | 5 potential cords  
Cord search | ATLAS | 6/6 | 0 potential cords  
Cord search | ATLAS | 5/6 | 5 potential cords

🕒 38 days until deactivation

Probability of Mismatches ⓘ

A B C DRB1 DQB1 DPB1 Donor pool Sex Age Blood group

Patient details

03:01:01 07:02:01 03:04:01 04:01:01 03:02:01  
 24:02:01 15:01:01 07:02:01 15:01:01 06:02:01 04:01:01

10/10 (potential) allele matches

# 2 GRID: **5525 DKM0 0606 8459 935** Status: **AV** CMV: **O 2024-06-04** No. of donations: **0** Ethnicity: **CAEU** [Full report](#)

0: **100%** **A** **A** **A** **A** **A** **A** 5525 ✓ **DE-DKMS** Male 46 O+  
 1: **0%**  
 2: **0%** - - - - - -  
 03:01:01G 07:02:01G 03:04:01G 04:EACPF 03:EDYCS 04:ERTTH  
 24:02:01G 15:01:01G 07:02:01G 15:EKCEM 06:EEPNS 04:ERTTH

# 3 GRID: Status: CMV: No. of donations: Ethnicity: [Full report](#)

0: **100%** **A** **A** **A** **A** **A** **Pe** 0  
 1: **0%**  
 2: **0%** - - - - - -  
 03:AAAUY 07:TXXS 03:ACMGT 04:01:01 03:YGKM **(04:FNVS)**  
 24:ABGEW 15:ACMGN 07:ABGFN 15:01 06:AAAXA **(05:RGPW)**

☆  
+

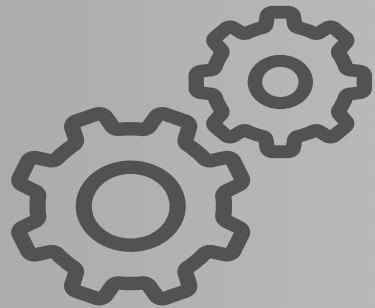
☆  
!

# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

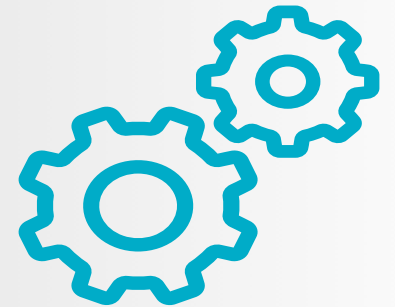
---



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**Automatic Updates** of active searches with notifications about changes in search results.

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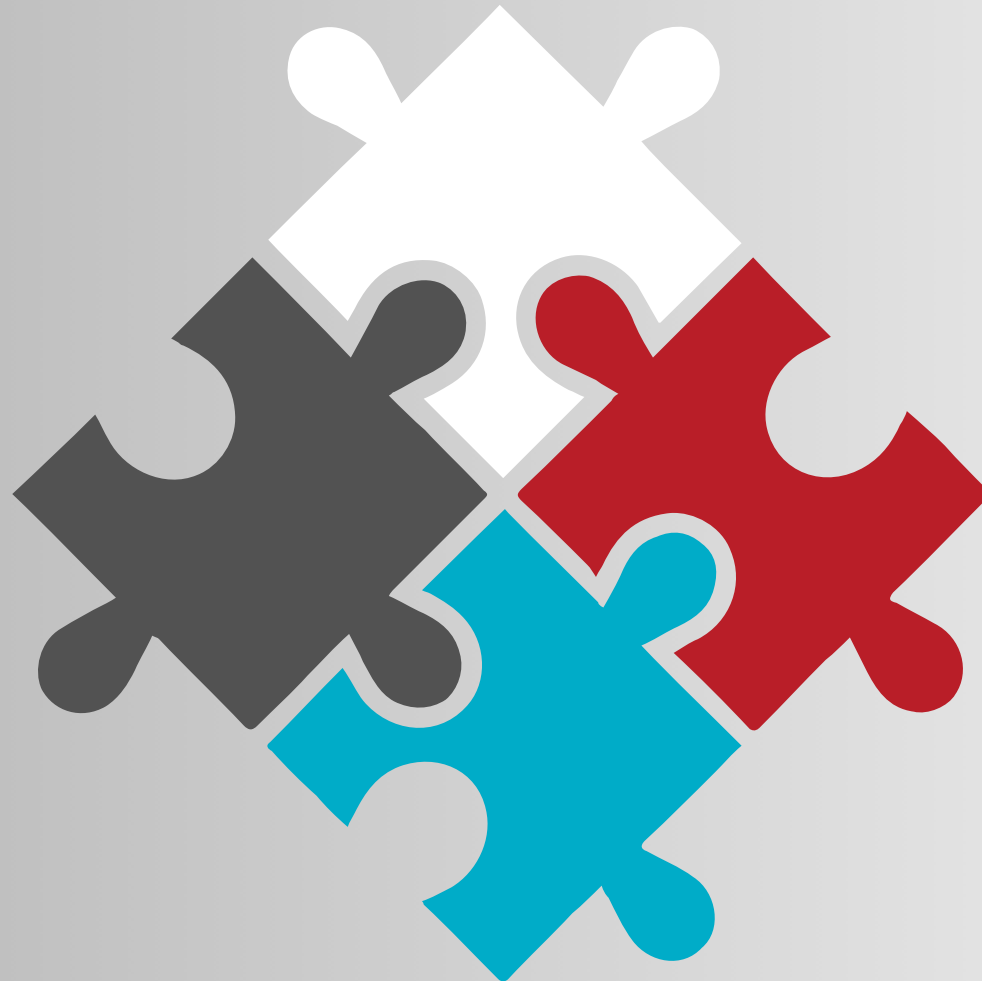
# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

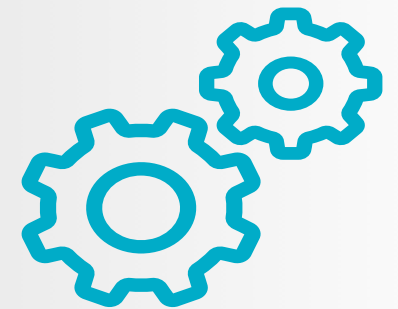
---

Grouping or sorting search results by match class or match probability.



---

**Automatic Updates** of active searches with notifications about changes in search results.



# Filters

## Match

Locus mismatch allowed

Select loci

DPB1 match grade

Select match grade

Number of mismatches allowed

Select number of mismatches...

Grouping/Sorting

Standard

Sort by sum of probabilities

Inexplicable

Select Inexplicable

Apply filters

Reset filters

## Donor

Return only records with DRB1

Selected

Select Selection

CMV

Select CMV

Sex

Select sex

Blood group

Select blood group

Age

Age slider

Donor status

Select Donor status

Filter:

CMV status

Registry

Blood group

Sex

Selected

All filters 1

815 filtered donor results

(Brackets) = mismatches (Bold) = antigen mismatches (Underlined) = allele mismatches *Italics* = uncertainty

Probability of Mismatches ⓘ

A B C DRB1 DQB1 DPB1 Registry Sex Age Blood group

Patient details

01:01 08:01 07:01 07:01 02:02 104:01  
23:17 41:02 17:01 11:01 06:02 105:01

+9/10 (potential) allele matches sorted by sum of probabilities

# 1 GRID: 6939 Status: AV CMV: No. of donations: 0 Ethnicity: CAEU Full report

0: 0%

1: 100%

2: 0%

A A A M A G 5525 DE-DKMS Female 29 B- ☆  
- - - - -  
01:01:01G 08:01:01G 07:01:01G 07:01:01 02:02:01 (04:01:01)  
23:01:01G 41:02:01 17:01:01G (15:01:01) 06:02:01 (15:01:01)

# 2 GRID: 9968 Status: AV CMV: N 2020-12-10 No. of donations: 0 Ethnicity: CAEU Full report

0: 0%

1: 100%

2: 0%

A A A A M G 9968 GB-DKMS Male 33 A+ ☆  
- - - - -  
01:01:01G 08:01:01G 07:01:01G 07:01:01G 02:02:01 (02:01:02)  
23:01:01G 41:02:01 17:03:01 11:01:01 (03:01:01) (02:01:02)

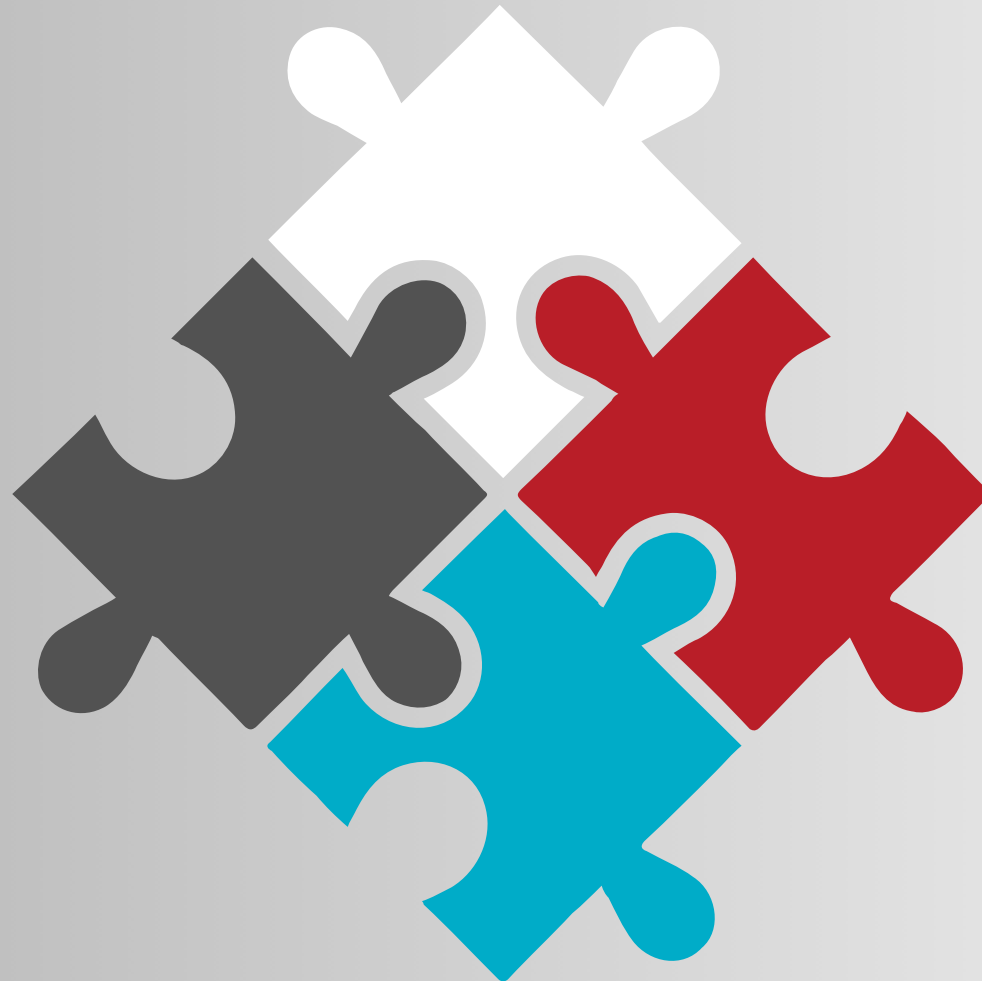
# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

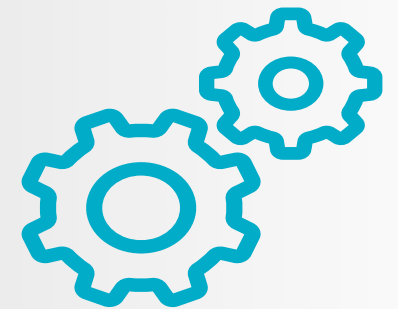
---

Grouping or sorting search results by match class or match probability.



---

**Automatic Updates** of active searches with notifications about changes in search results.



# Donor/CBU identification tools

---

Utilising various **filters** to narrow down the results based on TC preferences.

---

Grouping or sorting search results by match class or match probability.



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**Automatic Updates** of active searches with notifications about changes in search results.

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Set user or TC specific preferences as **search defaults**.

- Patient List


- Visible Tabs


- All tabs
    - Only “My patients” tab
    - Only “My organisation’s patients” tab

- Default visible tab

- My patients
    - My organisation’s patients



 Preferences


 Logout


- Search

- Default match engine for searches
  - Hap-E or ATLAS

- Default Donor search when patient HLA-A, B, C, DRB1, DQB1 is provided
  - 10/10 search (at HLA-A, B, C, DRB1, DQB1)
  - 8/8 search (at HLA-A, B, C, DRB1)

- Default Cord search when patient HLA-A, B, C, DRB1, DQB1 is provided
  - 10/10 search (at HLA-A, B, C, DRB1, DQB1)
  - 8/8 search (at HLA-A, B, C, DRB1)

 Preferences

 Logout

- Search Results

- Default sorting for 1/2 mismatch searches
  - Standard
  - Sum of probabilities

- Default secondary sorting
  - TNC
  - CD34+

**Search Results**

Default sorting for 1/2 mismatch searches

Standard ▾

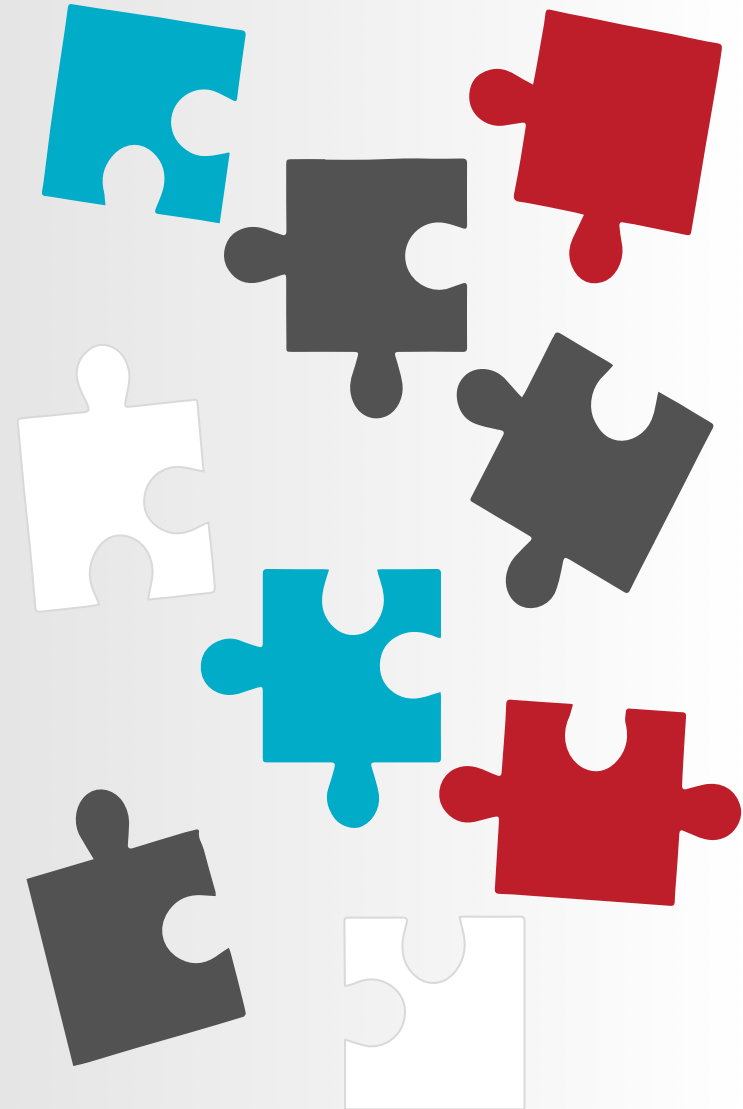
Default secondary sorting

TNC ▾

# WHAT DOES THE FUTURE HOLD?

## Central source of truth & communication solution

- New product: Adult Donor Cryopreserved Units (ADCU)
- New product feature: Extensively tested cord blood units
  - which includes post-thaw & verification typing data
- Match-Connect
  - New registry-to-registry communication solution
  - Registries can send requests automatically after identifying a suitable cell source
  - Place Health Availability Checks, VT/CT, ET, IDM and WU requests from your internal systems to ANY other connected registry in the world



**Thank you.**

