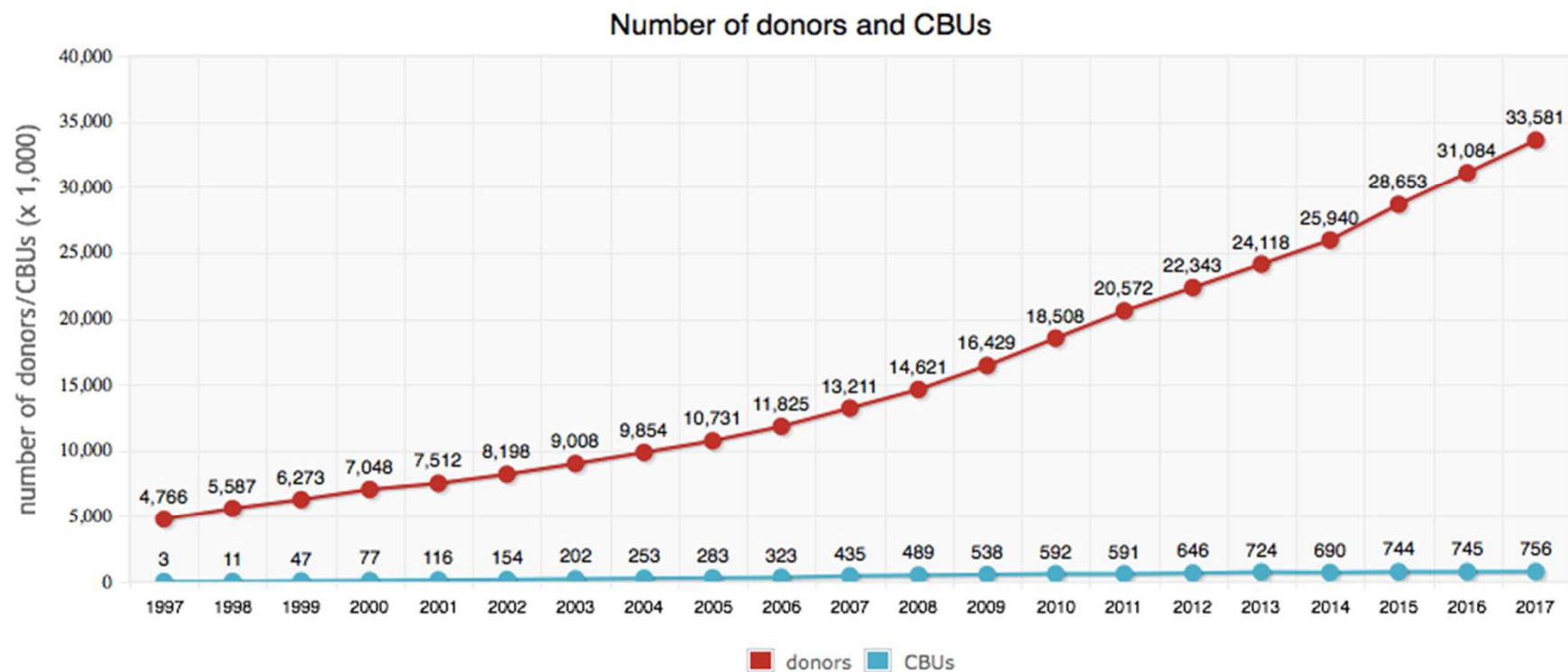


I Tools della ricerca ...o la ricerca del tools ?

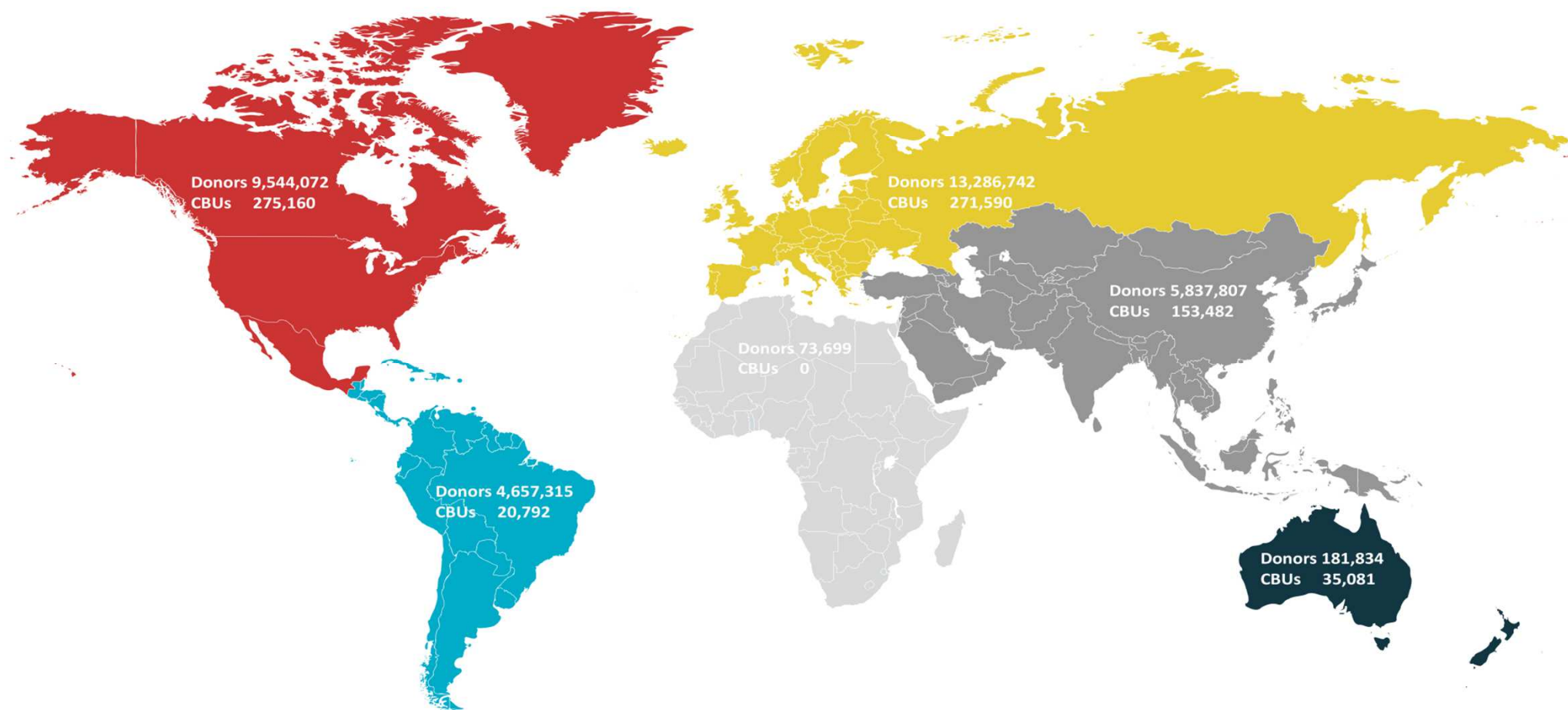


Nicoletta Sacchi - IBMDR

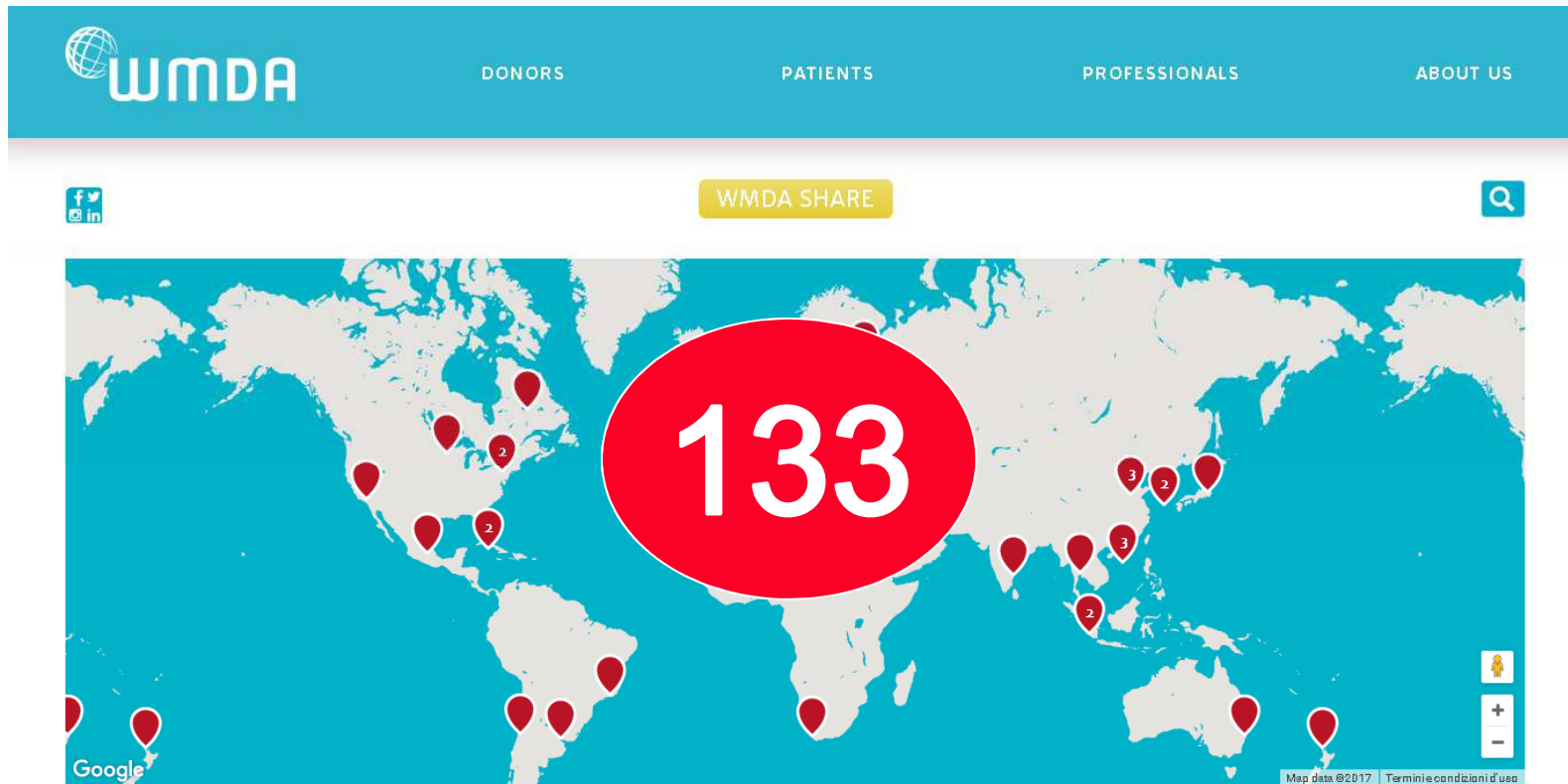
Quanti donatori nel mondo



Quanti donatori nel mondo



...e quanti registri / Banche

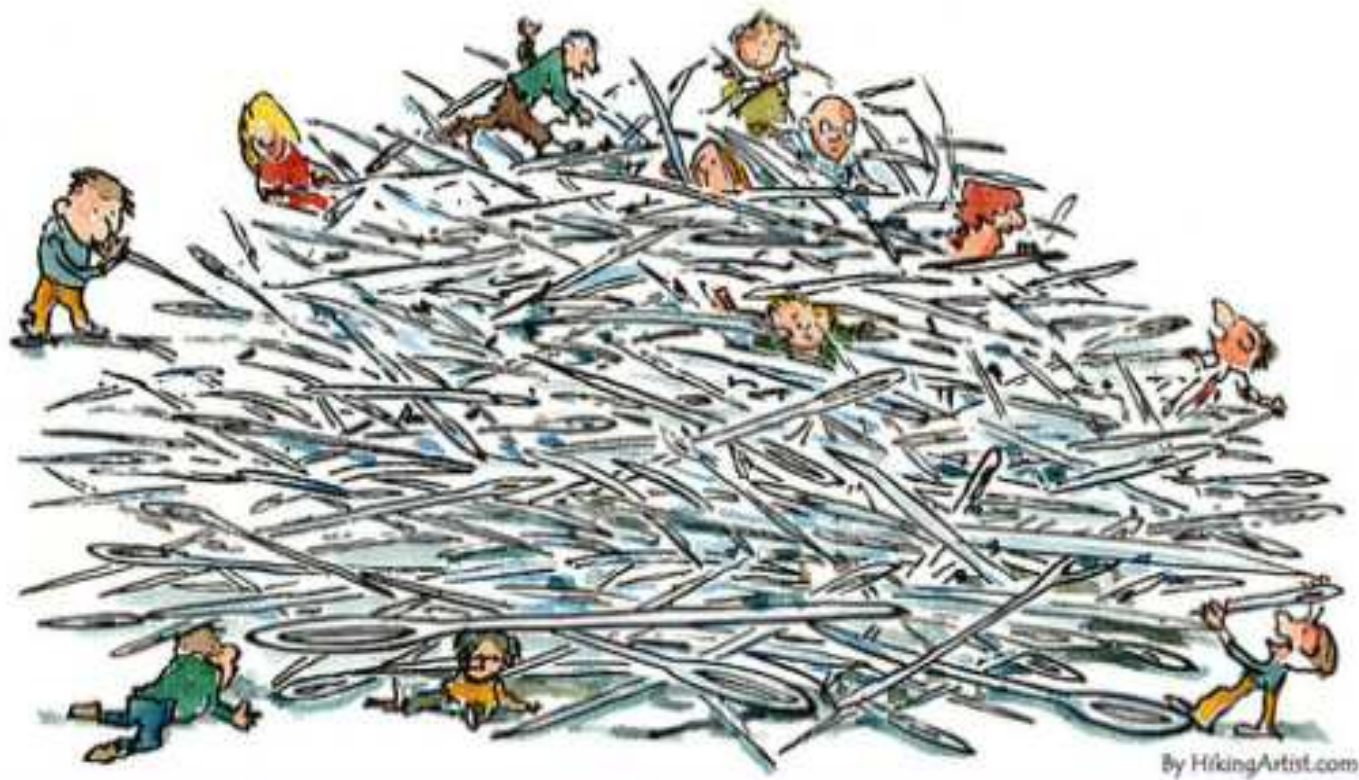


Serving blood stem cell organisation worldwide

**Dove e come trovo il donatore non familiare
migliore?**



Come cercare un ago in un pagliaio

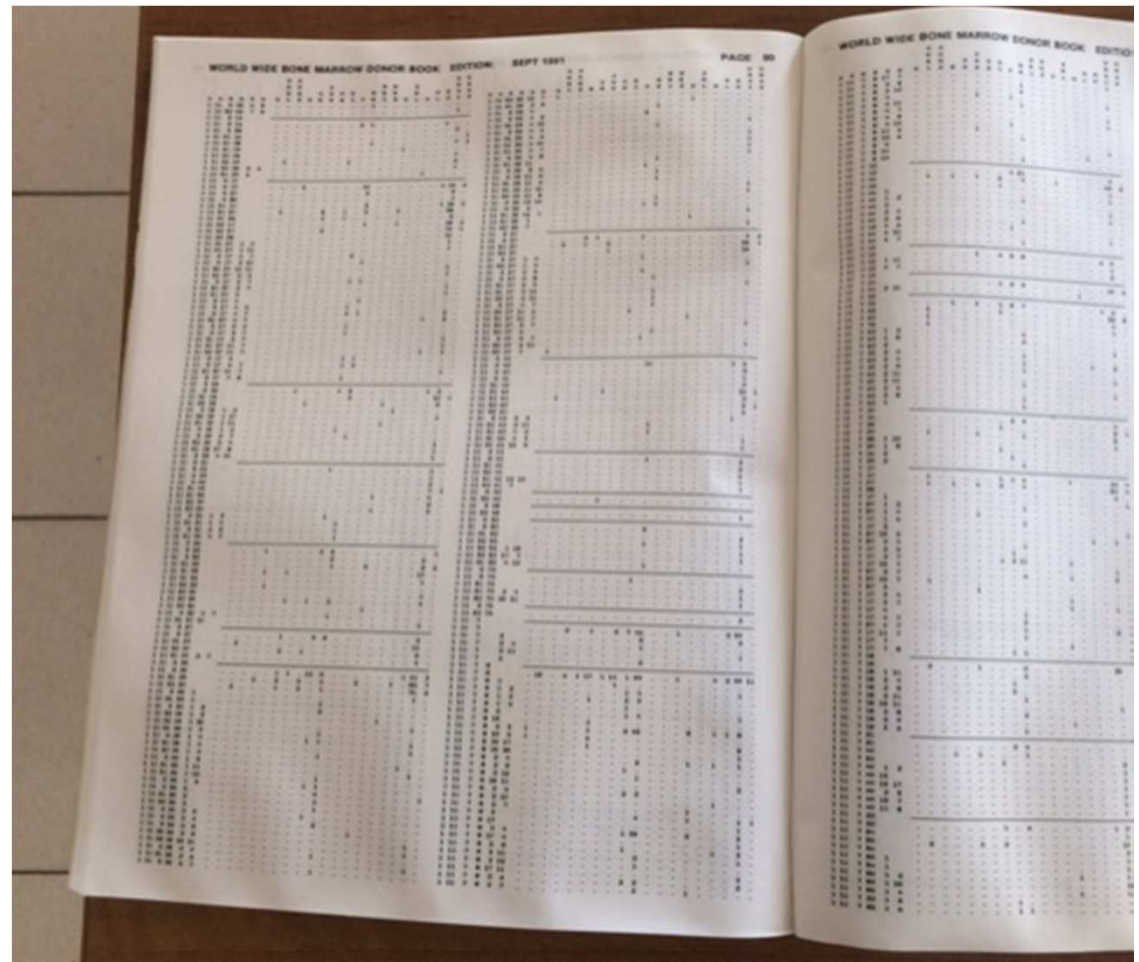


II BMDW



II BMDW

La prima stesura dell'archivio avvenne nel febbraio 1989 e fu fatta attraverso un libro (il Book) che contava la partecipazione dei 10 registri allora esistenti per un totale di 150.000 potenziali donatori.



Fino al 2000, il formato rimane cartaceo

II BMDW

E.O. Ospedali Galliera - I.B.M.D.R. X How to search for potential matches X Search & Match Service - WMDA X

https://www.wmda.info/professionals/optimising-search-match-connect/programme-services/ Cerca

Meetings JOIN US DONATE

WMDA PROFESSIONALS DONORS CORD BLOOD PATIENTS ABOUT US

Search & Match Service

Home > Professionals > Optimising 'Search, Match & Connect' > Search & Match Service

Search & Match Service

The Search & Match Service is a global database of life-saving donors. Operated by WMDA, it provides a fast preliminary search facility to find the best matched donor or cord blood unit in the world for a patient in need of a blood stem cell transplant.

In a glance

- Primary source of all haematopoietic stem cell donors and cord blood units worldwide.
- Lists over 30 million of donors and cord blood units from 54 countries.
- Allows the opportunity to find a donor as quickly as possible by providing:
 - user-friendly interface and functionalities;
 - probability matching for each donor/cord powered by OptiMatch; and
 - additional information on each donor and cord blood unit (if provided by the listing organisation).

Connect to the Search & Match Service, find out more:

- How to list donors or cord blood units in the global database; [information link](#)
- How to search for potential matches; [information link](#)
- How to get advice on searches; [information link](#)

OPTIMISING 'SEARCH, MATCH & CONNECT'

- Search & Match Service >
- Tools to operate a registry >
- WMDA forms >
- Organisation closure agenda >
- How to set up ICT in a registry >
- Bioinformatics in donor search >
- What to do about data privacy >
- Why a global donor identifier (GRID) >
- Governance: 'Search, Match & Connect' >

Total Donors : 32.359.194

Total Cord Blood Units: 752.013

Total Records : 33.111.207

Il Tool IBMDR



Software gestionale IBMDR - v. 1.0 RicercaCT

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Elenco pazienti CT

CT GE01 -- Stato Attivo

CT	Cog. paz.	Nom. paz.	Cod. paz.	Data di nascita	Stato	Ultimo agg. ric.
GE01					Attivo	? 2018-04-05 09:28:08
GE01					Attivo	? 2018-04-12 11:56:41
GE01					Attivo	? 2018-06-29 14:49:11
GE01					Attivo	? 2018-07-31 09:23:00
GE01					Attivo	? 2018-04-12 12:12:30
GE01					Attivo	? 2018-07-24 09:39:16
GE01					Attivo	
GE01					Attivo	
GE01					Attivo	
GE01					Attivo	
GE01					Attivo	? 2017-11-13 14:34:38
GE01					Attivo	
GE01					Attivo	
GE01					Attivo	? 2018-05-21 14:45:12
GE01					Attivo	
GE01					Attivo	? 2017-11-08 12:52:04
GE01					Attivo	
GE01					Attivo	? 2018-04-23 10:17:39
GE01					Attivo	? 2018-03-15 10:17:13
GE01					Attivo	? 2018-07-26 13:52:21

Utente collegato: Garbarino Lucia - Laboratorio di riferimento CT - GE01, GE02, PG01 - 31-07-2018 09:54

<https://donatori.galliera.it/ricerca>



Il Tool IBMDR

Fenotipo paziente

A/A* 02:01,68:01:02:02 - DR/DRB1* 04:02:01,08:01P
B/B* 39:06:02:01,49:01:01 - DQB1* 03:02,04:02
Cw/C* 07:01,07:02 - DPB1* 04:01:01:01,05:01



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Ricerca su BMDW (ita)

Privacy

Attivato sul CNC il 15.03.2018 09:31:39

Ricerca effettuata su BMDW aggiornato al 09.03.2018

Tipo	Score	Numero
MUD	8/8 10/10	2
MUD	7/8 9/10	360
MUD	7/8 8/10	3
MUD	6/8 8/10	4624
MUD	6/8 7/10	63
MUD	6/8 6/10	2
CBU	7/8	3
CBU	6/8	209
CBU	5/8	474
CBU	4/8	443

Sono esclusi dai risultati i donatori senza DR. La soglia per i MUD è 6/8, per i CBU è 5/8



I dettagli della ricerca sono stati cancellati in quanto si riferiscono ad una edizione del BMDW che risale a più di un mese fa

Utente collegato: Garbarino Lucia - Laboratorio di riferimento CT - GE01, GE02, PG01 - 31-07-2018 09:59



<https://donatori.galliera.it/ricerca>

Il Tool IBMDR

Fenotipo paziente

A/A* 03:01:01:01,24:02:01:01 - DR/DRB1* 11:01,15:01
B/B* 35:02,55:01:01 - DQB1* 03:01,06:02:01:01
Cw/C* 01:02:01:01,04:01:01:06 - DPB1* 02:01,04:01



Software gestionale IBMDR - v. 1.0 RicercaCT

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Ricerca su BMDW (ita)

Privacy

Attivato sul CNC il 26.07.2018 13:42:37

Ricerca effettuata su BMDW aggiornato al 24.07.2018

Tipo	Score		Numero
MUD	8/8	10/10	14
MUD	7/8	9/10	2021
MUD	7/8	8/10	18
MUD	6/8	8/10	23796
MUD	6/8	7/10	217
MUD	6/8	6/10	4

Sono esclusi dai risultati i donatori senza DR. La soglia per i MUD è 6/8, per i CBU è 5/8



Stampa risultati 8/8 MUD



<https://donatori.galliera.it/ricerca>

Il Tool IBMDR

Fenotipo paziente

A/A*	30:01:01,69:01:01	-	DR/DRB1*	03:01,11:04:01
B/B*	18:01:01:02,35:02:01	-	DQB1*	02:01:01,03:01
Cw/C*	04:01:01:06,12:03:01:01	-	DPB1*	02:01:02,04:01



Software gestionale IBMDR - v. 1.0 RicercaCT

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Ricerca su BMDW (ita)

Privacy

Attivato sul CNC il 24.07.2018 09:23:19

Ricerca effettuata su BMDW aggiornato al 17.07.2018

Tipo	Score	Numero
MUD	8/8 10/10	8
MUD	7/8 9/10	937
MUD	7/8 8/10	2
MUD	6/8 8/10	9739
MUD	6/8 7/10	25
MUD	6/8 6/10	1
CBU	7/8	48
CBU	6/8	415
CBU	5/8	931
CBU	4/8	906

Sono esclusi dai risultati i donatori senza DR. La soglia per i MUD è 6/8, per i CBU è 5/8



Stampa risultati 8/8 MUD



Stampa risultati 7/8 e 8/8 CBU



<https://donatori.galliera.it/ricerca>

Il Tool IBMDR

E. O. Ospedali Galliera - I.B.M.D.R.

How to search for potential ma

Search & Match Service - WMD

+

← → ↺ 🏠

🔒 https://donatori.galliera.it/cnc/gest/paz_ita_oggi_match_bmdw_dett.php?idmatch=4666&score_8=8/8&score_...

🔍 Cerca

≡

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Matchlist BMDW

Ricerca don./CBU su WMDA

Fenotipo paziente

A/A* 02:01P,02:01P - DR/DRB1* 14:54,07:01P - DPA1*

B/B* 44:02P,57:01 - DQA1* 01:01P,02:01 - DPB1*

C/C* 05:01,06:02 - DQB1* 05:03,03:03

Match allelico

Match NMDP

Match LR

Match antigenico

Potenz. match (vuoto)

Privacy

Ricerca effettuata su il 27.07.2018 su BMDW aggiornato al 24.07.2018

Scegli l'hub --- Locus C* --- Filtra:

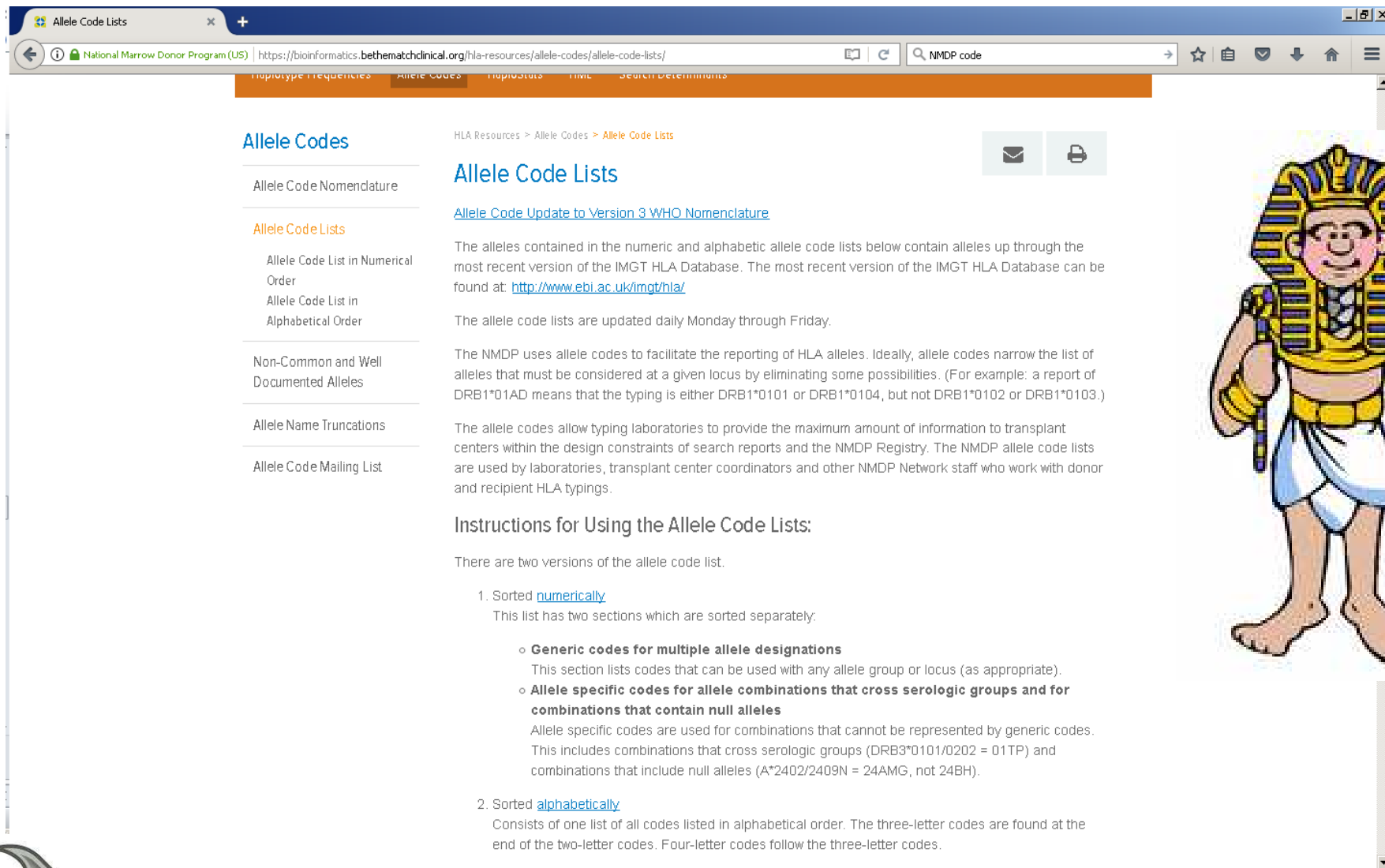
Ordina	A/A*	A/A*	B/B*	B/B*	C/C*	C/C*	DR/DRB1*	DR/DRB1*	DQB1*	DQB1*	Org. ▲	Sesso	Cod. don.	Età	CMV	Ab0
2			44	57			07:XX	14:XX	03:03	05:XX	A	M	AT49673	47		
02:01			44:XX	57:XX										31		BP
02:KBGH	02:KBGH		44:JXRA	57:JWJH										45		
02:FKXS	02:FKXS		44:FUZH	57:EJRM										35		AP
02:AYHWY	02:AYHWY		44:AZBCG	57:AWBVN										25		
02:AYCND	02:AYCND		44:AYWAV	57:BCGND										24		BN
02:GKEH	02:GKEH		44:XX	57:GKTJ										31		AP
02:XX	02:XX		44:XX	57:GKTJ										27		BN
02:XX	02:XX		44:XX	57:XX										53		
02:XX			44:XX	57:XX										37		AP
02:XX			57:XX	44:XX										44		AP
02:XX			44:XX	57:XX										34		AP
02:01:01G			44:02:01G	57:01:01	05:01:01G	06:02:01G	07:01:01G	14:01:01G			CND	F	CAR1001585223	18		
02:01:01G			44:02:01G	57:01:01G	05:01:01G	06:02:01G	07:01:01G	14:01:01G			CND	F	CAR1001292975	25		
02:VVDW	02:VVDW		44:VYPR	57:WEBW	05:WDFB	06:WECX	07:01	14:VCRV			CND	F	CAUB00613406	25		AP
02:AJEJN	02:AJEJN		44:AJGTH	57:AJGVN	05:AMADF	06:AKWNT	07:AJGEF	14:AECSS			CND	F	CAR1001490874	28		
02:ABVAT	02:ABVAT		44:ABVMK	57:ZNYN	05:ABWZF	06:ABVNS	07:ABXNU	14:ZJZZ			CND	M	CAUB00659641	35	N (2014-10-21)	OP
2			44	57			07:NZC	14:01			CND	F	CAUBM0334386	37		
02:01			44:02	57:01	05:01	06:02	07:01	14:54			D	F	DERKS-800036425	41		AP
02:01			44:02	57:01	05:01	06:02	07:01	14:54	03:03	05:03	D	F	DERKS-800036434	29	P (2012-08-29)	BP
02:01			44:02	57:01	05:01	06:02	07:01	14:54	03:03	05:03	D	M	DEWSZ-15890932	35	P (2014-10-02)	OP
02:01			44:02	57:01	05:01	06:02	07:01:01	14:54	03:03	05:03	D	M	DEDKM-2830264	31	N (2012-08-07)	AP
02:01			44:02	57:01:01	05:01	06:02	07:01:01	14:54	03:03:02	05:03:01	D	M	DEDKM-4144767	29	N (2014-11-21)	AP
02:01			44:02	57:01	05:01	06:02	07:01:01G	14:54:01	03:03:02G	05:03:01G	D	M	DEULM-80714	31	N (2012-09-14)	ON
02:01:01G			44:02:01G	57:01:01G	05:01:01G	06:02:01G	07:01:01	14:54:01	03:03:02	05:03:01	D	M	DEDKM-7450165	28		BP

JWJH

01/06/08/15/18/23/27/29/31/33/35/36/37/38/43

Utente collegato: Nicoletta Sacchi - 30-07-2018 11:38

Attenzione ai codici



Allele Code Lists

HLA Resources > Allele Codes > Allele Code Lists

Allele Code Lists

[Allele Code Update to Version 3 WHO Nomenclature](#)

The alleles contained in the numeric and alphabetic allele code lists below contain alleles up through the most recent version of the IMGT HLA Database. The most recent version of the IMGT HLA Database can be found at: <http://www.ebi.ac.uk/imgt/hla/>

The allele code lists are updated daily Monday through Friday.

The NMDP uses allele codes to facilitate the reporting of HLA alleles. Ideally, allele codes narrow the list of alleles that must be considered at a given locus by eliminating some possibilities. (For example: a report of DRB1*01AD means that the typing is either DRB1*0101 or DRB1*0104, but not DRB1*0102 or DRB1*0103.)

The allele codes allow typing laboratories to provide the maximum amount of information to transplant centers within the design constraints of search reports and the NMDP Registry. The NMDP allele code lists are used by laboratories, transplant center coordinators and other NMDP Network staff who work with donor and recipient HLA typings.

Instructions for Using the Allele Code Lists:

There are two versions of the allele code list.

1. Sorted [numerically](#)
This list has two sections which are sorted separately:
 - **Generic codes for multiple allele designations**
This section lists codes that can be used with any allele group or locus (as appropriate).
 - **Allele specific codes for allele combinations that cross serologic groups and for combinations that contain null alleles**
Allele specific codes are used for combinations that cannot be represented by generic codes. This includes combinations that cross serologic groups (DRB3*0101/0202 = 01TP) and combinations that include null alleles (A*2402/2409N = 24AMG, not 24BH).
2. Sorted [alphabetically](#)
Consists of one list of all codes listed in alphabetical order. The three-letter codes are found at the end of the two-letter codes. Four-letter codes follow the three-letter codes.



<https://bioinformatics.bethematchclinical.org/hla-resources/allele-codes/allele-code-lists/>



Il Tool IBMDR

←

→

↺

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🔒

https://donatori.galliera.it/ricerca/risultati_dett.php?idmatch=4612&score_8=8/8&score_10=10/10&isc...

📄

...

🔖

☆

🔍 Cerca

📁

📄

☰

Fenotipo paziente

A/A* 02:01:01:01,03:01:01:01 - DR/DRB1* 11:01:01,16:01:01

B/B* 44:02:01:01,44:27:01 - DQB1* 03:01,05:02

Cw/C* 05:01:01:02,07:04:01 - DPB1* 02:01:02,04:01

Match allelico

Match NMDP

Match LR

Match antigenico

Potenz. match (vuoto)



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Scegli l'hub

▼

 -- Locus C* ☐ -- Locus DPB1* permissivo ☐ -- Filtra:

it

Ordina	A/A*	A/A*	B/B*	B/B*	C/C*	C/C*	DR/DRB1*	DR/DRB1*	DQB1*	DQB1*	Org. ▲	Sesso	Cod. don.	Età	CMV	Ab0	DPB1*	DPB1*
.....	02:XX	03:XX	44:XX		05:XX	07:XX	11:01	16:01	03:XX	05:XX	I		IT886569216693436	37				

Utente collegato: Garbarino Lucia - Laboratorio di riferimento CT - GE01, GE02, PG01 - 31-07-2018 10:07

II Tool IBMDR

E. O. Ospedali Galliera - I.B.M.D.R.
+

https://donatori.galliera.it/ricerca/risultati_dett.php?idmatch=4612&score_8=8/8&score_10=10/10&iscr
Cerca

Fenotipo paziente
A/A* 02:01:01:01,03:01:01:01 - DR/DRB1* 11:01:01,16:01:01
B/B* 44:02:01:01,44:27:01 - DQB1* 03:01:05:02
Cw/C* 05:01:01:02,07:04:01 - DPB1* 02:01:02,04:01


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Match allelico

Match NMDP

Match LR

Match antigenico

Potenz. match (vuoto)

Privacy

Scegli l'hub --- Locus C* ☐ --- Locus DPB1* permissivo ☒ --- Filtra:

Ordina	A/A*	A/A*	B/B*	B/B*	C/C*	C/C*	DR/DRB1*	DR/DRB1*	DQB1*	DQB1*	Org.	Sesso	Cod. don.	Età	CMV	Ab0	DPB1*	DPB1*
.....	02:01:01	03:01:01	44:02:01G		05:01:01	07:04:01G	11:01:01G	16:01:01	03:01:01	05:02:01G	D		DEDUS-107664	41			04:01:01G	04:02:01G
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01G	16:01:01	03:01:01G	05:02:01G	D		DEVKS-601205505	38			02:01:02G	04:01:01G
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01G	16:01:01	03:01:01G	05:02:01G	D		DERKS-86018896	23			04:01:01G	
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-8417897	46			04:FNVS	04:HJMR
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-9375347	34		AP	04:01:01	
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-9615512	29	H (2018-06-19)	OP	02:01	04:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-9927713	31	Q (2017-07-27)	OP	02:01	04:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-6470002	24	Q (2018-06-08)		04:01:01	17:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-7204228	33		OP	04:01:01	
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-7252705	26		OP	04:01:01	
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-7630117	37	N (2017-05-08)	OP	03:FYKD	04:ADCGE
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-7696614	24	Q (2017-03-06)	OP	02:01:02G	04:01:01G
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-9085691	36		OP	01:AETTA	04:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-9064239	34		ON	02:01:02	10:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-7766162	43	Q (2014-12-31)	AP	02:01:02	04:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	D		DEDKM-8923143	51		ON	02:01:02	04:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	PL6		PLDKM-1575506	39		ON	02:01:02	04:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	PL6		PLDKM-1937734	41		BP	04:01:01	06:01:01
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	PL6		PLDKM-2307116	35	H (2018-03-08)	ABP	04:FNVS	04:HJMR
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	PL6		PLDKM-1547164	32		BP	04:01:01	
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	PL6		PLDKM-1482502	27		AP	02:01:02	
.....	02:01:01G	03:01:01G	44:02:01G		05:01:01G	07:04:01G	11:01:01	16:01:01	03:01:01	05:02:01	PL6		PLDKM-1435916	27	G (2017-05-15)	AP	03:FYKD	04:ADCGE

Fenotipo HLA raro o fuori linkage



Fenotipo raro o fuori linkage

Paziente : A **24:14**, **36:01**; B 40:02, 53:01; C 03:04, 04:01; DRB1 08:02,11:01

Origine: Venezuela

HLA > Allele Frequency Search > Classical

Please specify your search by selecting options from boxes. Then, click "Search" to find **selected**.

Locus: Starting Allele: Ending Allele: > (Type
Select specific alleles (If you want to pick specific alleles, make sure your alleles are with

A*36:01

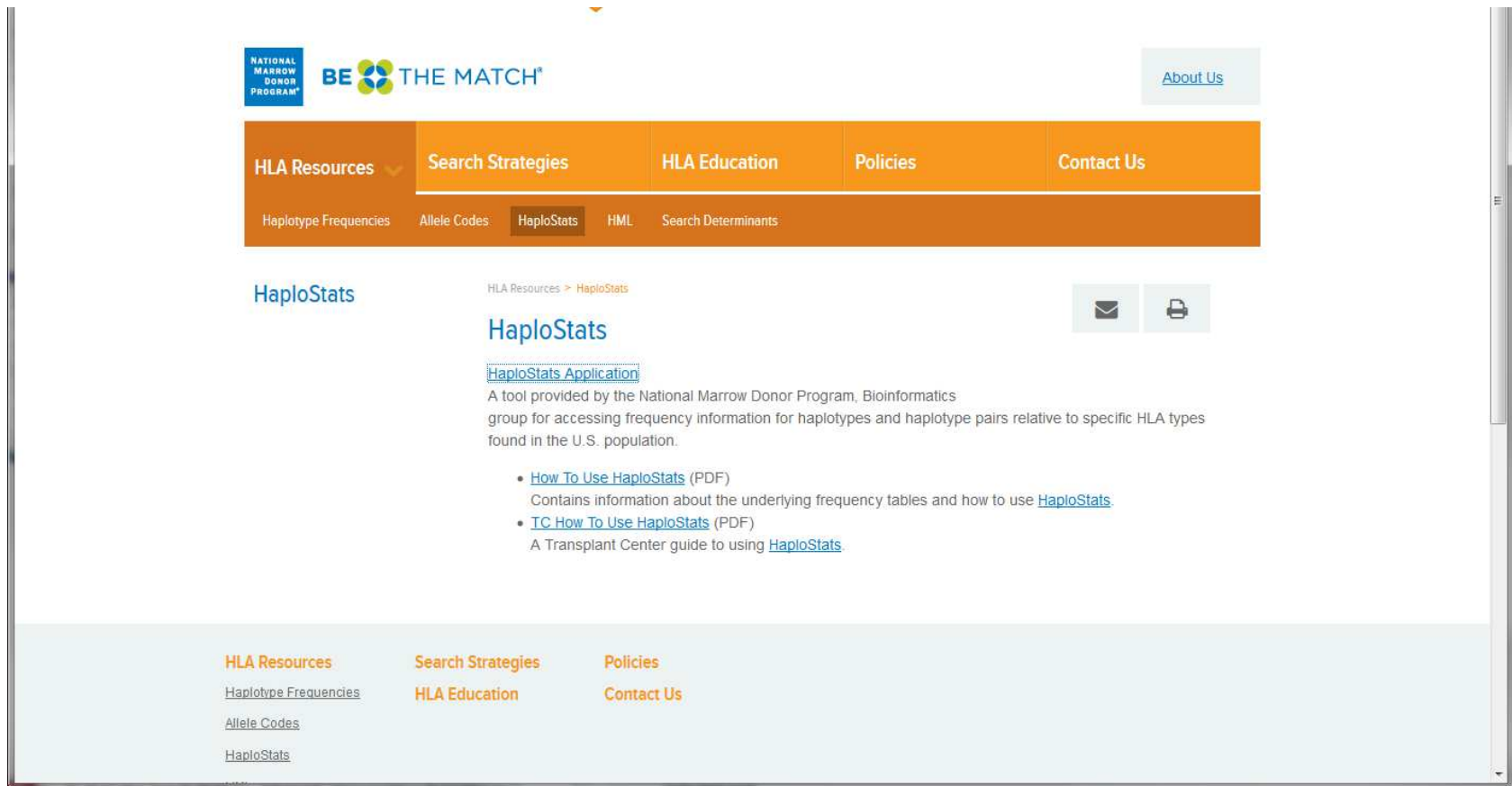
Allele reported 149 time(s) and present in 84 population(s).

Population	Phenotype Frequency (%)	Allele Frequency (in_decimals)	Sample Size
 Kenya		0.0700	144
 Sao Tome Island Angolar		0.0630	32
 USA African American Bethesda	7.9	0.0500	187
 Burkina Faso Mossi		0.0380	53
 Cameroon Beti		0.0370	174
 Zambia Lusaka		0.0350	44
 USA NMDP Caribbean Black		0.0335	33328
 USA African American		0.0320	252
 USA African American pop 3		0.0310	564
 Tunisia Ghannouch		0.0300	82
 Sao Tome Island Forro		0.0300	66
 Rwanda		0.0300	280
 Kenya Luo		0.0300	265
 USA NMDP African		0.0295	28557
 Uganda Kampala pop 2		0.0290	175
 Zimbabwe Harare Shona		0.0290	230
 Cameroon Bamileke		0.0260	77
 USA NMDP African American		0.0253	416581
 Kenya, Nyanza Province, Luo tribe	5.0	0.0250	100
 USA African American pop 4		0.0241	2411
 Jordan Amman		0.0240	146
 Cameroon Yaounde		0.0220	92
 Burkina Faso Fulani		0.0200	49



<http://www.allelefrequencies.net/default.asp>

Haplostats



The screenshot shows the HaploStats website. At the top left are the logos for the National Marrow Donor Program and BE THE MATCH. A navigation bar contains links for HLA Resources, Search Strategies, HLA Education, Policies, and Contact Us. Below this is a secondary bar with links for Haplotype Frequencies, Allele Codes, HaploStats (highlighted), HML, and Search Determinants. The main content area features the HaploStats title, a breadcrumb trail (HLA Resources > HaploStats), and a description of the tool as a resource for HLA frequency information. It includes links to 'How To Use HaploStats' (PDF) and 'TC How To Use HaploStats' (PDF). A footer section lists additional resources under HLA Resources, Search Strategies, and Policies.

NATIONAL MARROW DONOR PROGRAM BE THE MATCH®

About Us

HLA Resources Search Strategies HLA Education Policies Contact Us

Haplotype Frequencies Allele Codes HaploStats HML Search Determinants

HaploStats

HLA Resources > HaploStats

HaploStats

[HaploStats Application](#)

A tool provided by the National Marrow Donor Program, Bioinformatics group for accessing frequency information for haplotypes and haplotype pairs relative to specific HLA types found in the U.S. population.

- [How To Use HaploStats](#) (PDF)
Contains information about the underlying frequency tables and how to use [HaploStats](#).
- [TC How To Use HaploStats](#) (PDF)
A Transplant Center guide to using [HaploStats](#).

HLA Resources Search Strategies Policies

[Haplotype Frequencies](#) [HLA Education](#) [Contact Us](#)

[Allele Codes](#)

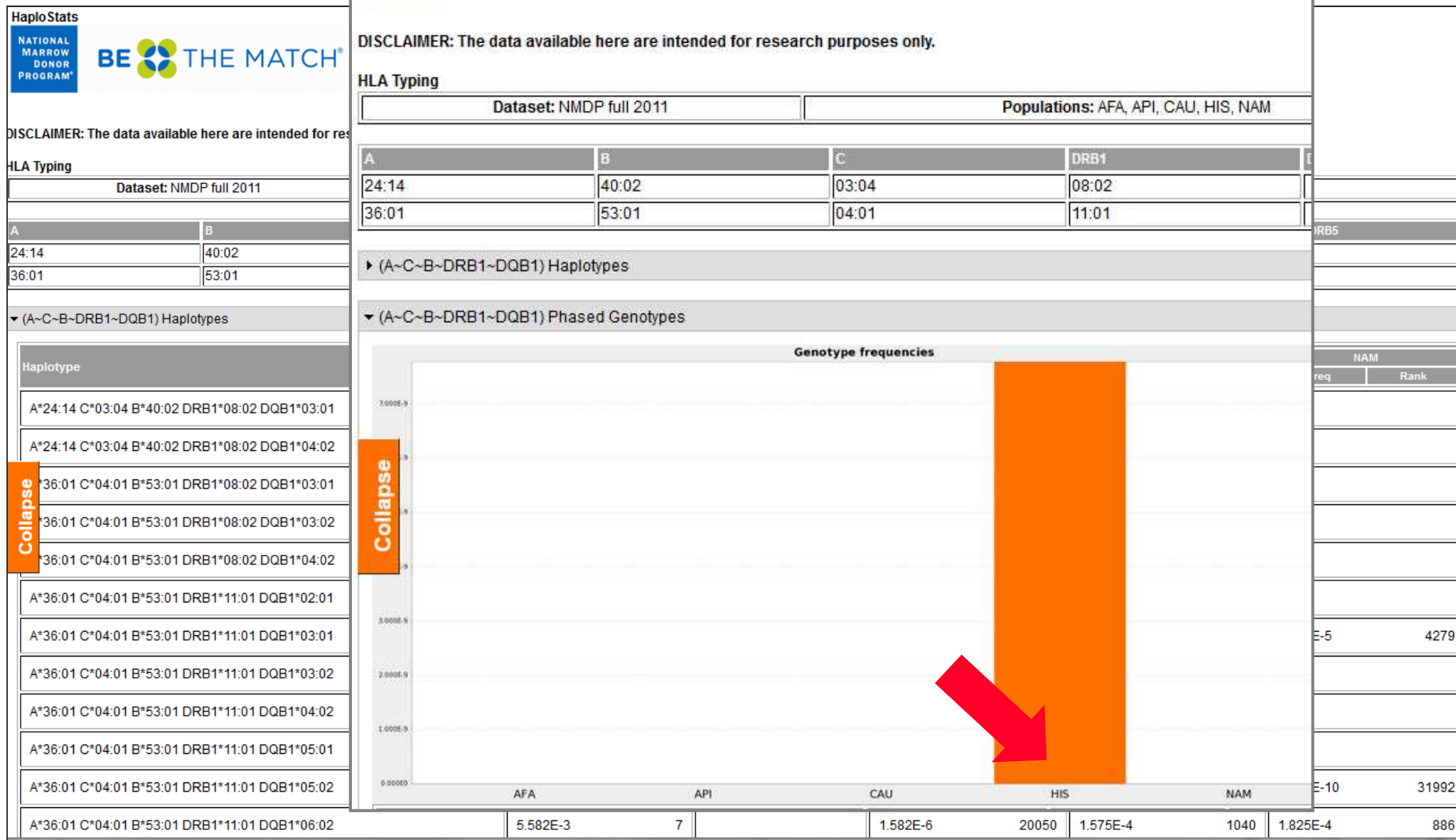
[HaploStats](#)



<https://www.haplostats.org/>

Fenotipo raro o fuori linkage

Paziente : A 2



Fenotipo raro o fuori linkage

Paziente : A **24:14**, **36:01**; B 40:02, 53:01; C 03:04, 04:01; DRB1 08:02,11:01

Origine: Venezuela

24	24:AWFBG	36	36:01	61	40:AWFBX	53	53:01:01G	03:06	04:AWFCF	11	11:01	8	08:02	04:02:01G	06:AVDDW	1	USA1
24	24:PWND	36	36:01	61	40:JWRU	53	53:01	03:06	04:MCDD	11	11:NVEX	8	08:BZGH	04:BC	06:ANK	1	USA1
24	24:TSY	36	36:01	61	40:PX $\overline{F}$	53	53:01			11	11:APWP	8	08:AS			1	USA1
24	24:02:01G	36	36:01	61	40:GWZH	53	53:ARGN			11	11:01	8	08:AS			1	USA1
24	24:CPDC	36	36:01	61	40:PX $\overline{F}$	53	53:01			11	11:APWP	8	08:02			1	USA1
24	24:XUTV	36	36:01	61	40:06	53	53:01	04:ZFZA	08:01:01G	11	11:NGCX	8	08:04	03:ZHAD		1	USA1
24	24:XX	36	36:XX	61	40:BXZZ	53	53:XX			11	11:04	8	08:AS			1	USA1

Fenotipi parziali dei donatori

Paziente: A 01:01, 24:02; B 08:01, 35:04; C 07:01, 07:02; DRB1 0301,1104

REG	A	A	B	B	C	C	DQB1	DQB1	DR/DRB1	DR/DRB1	Sex	BG	Age
BR	1	24	8	35	4				3	11			
D	1	24	8	35	4				3	11	Fem	O+	52
IBMDR	1	24	8	35					3	11	Mas	A+	53
E	1	24	8	35					3	11	Fem	B+	45
NL	1	24	8	35	4				03:XX	11:XX	Mas	B+	43
CND	1	24	8	35	4				03:XX	11:XX	Fem	B+	54

Fenotipi parziali dei donatori

Paziente: A 01:01, 24:02; B 08:01, 35:04; C 07:01, 07:02; DRB1 0301,1104

B*3504

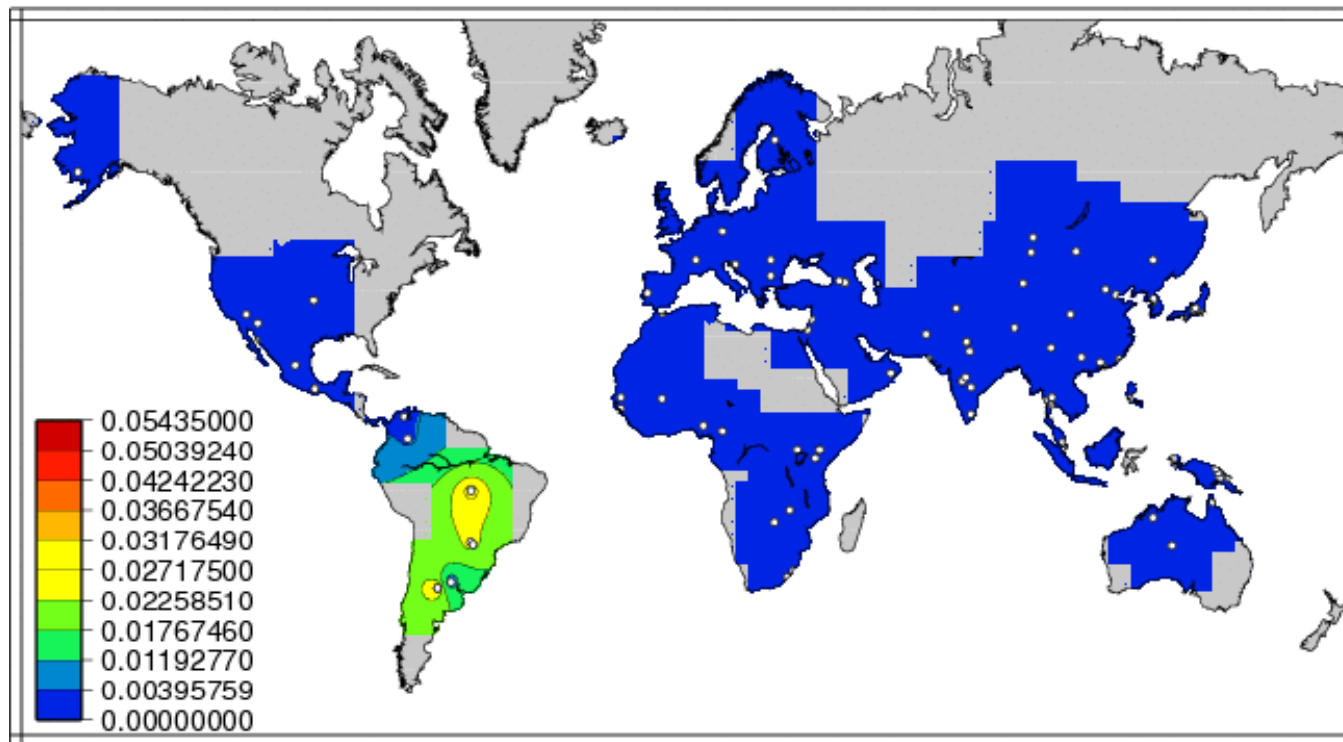


Image from Solberg et al. (2008) – see www.pypop.org/popdata for more info.



<http://www.igdawg.org/software/>

Il fenotipo errato



Errore typing

Pazienti attivati nel 2016: 2 riattivati per errore tipizzazione HLA

Pazienti attivati nel 2017: 7 riattivati per errore tipizzazione HLA

Pazienti attivati nel 2018: 1 riattivati per errore tipizzazione HLA

Paziente	A	A	B	B	C	C	DRB1	DRB1	DQB
1	02:01P	24:02P	07:02P	51:01P	07:02P	14:02P	11:04P	15:04	03:01P
2	24:02	30:02	18:01	35:01	04:01	05:01	03:01	13:02	02:01
3	01:01	02:01	08:04	18:07	07:01		03:01	11:04	02:01:01G
4	01:01P		15:17P	53:01:01	04:01P	07:01P	13:02P		06:04:01
5	03:01	33:01	13:02	58:01	03:02	06:02	01:02	07:01	02:02
6	68:01:01	68:01	40:01	40:02	03:04:01	07:04:01	04:04	11:01	03:01

Gli aplotipi più frequenti in Italia

Aplotipo					Freq	Rank
A	B	C	DR	DQ		
0101	0801	0701	0301	0201	0,026776	1
0201	1801	0701	1104	0301	0,013490	2
2402	3502	0401	1104	0301	0,012011	3
3001	1302	0602	0701	0201	0,011225	4
3301	1402	0802	0102	0501	0,009898	5
2902	4403	1601	0701	0201	0,009852	6
3002	1801	0501	0301	0201	0,008800	7
0301	0702	0702	1501	0602	0,008597	8
0301	3501	0401	0101	0501	0,007429	9
0101	5701	0602	0701	0303	0,005914	10
0201	3501	0401	1401	0503	0,005339	11
0201	1302	0602	0701	0201	0,005236	12
1101	3501	0401	0101	0501	0,005060	13
2301	4403	0401	0701	0201	0,004941	14
2402	1801	0701	1104	0301	0,004739	15
1101	3501	0401	1401	0503	0,004623	16
0201	0702	0702	1501	0602	0,004592	17
2402	1801	1203	1104	0301	0,004444	18
2301	4901	0701	1101	0301	0,003818	19
0205	5001	0602	0701	0201	0,003576	20
0201	0801	0701	0301	0201	0,003564	21
0201	5101	1502	1101	0301	0,003374	22
1101	5201	1202	1502	0601	0,003307	23
0201	1801	0501	0301	0201	0,003253	24
0101	3502	0401	1104	0301	0,002927	25
0201	4402	0501	1301	0603	0,002799	26
0205	5801	0701	1601	0502	0,002705	27
0101	1517	0701	1302	0604	0,002569	28
0201	1801	1203	1104	0301	0,002551	29
0201	5101	0102	1101	0301	0,002536	30

2501	1801	1203	1501	0602	0,002494	31
0201	4402	0501	1101	0301	0,002457	32
0101	5201	1202	1502	0601	0,002375	33
2402	1302	0602	0701	0201	0,002348	34
2601	3801	1203	1301	0603	0,002283	35
1101	3501	0401	1101	0301	0,002246	36
0201	4402	0501	0401	0301	0,002139	37
0201	5701	0602	0701	0303	0,002133	38
2402	0702	0702	1501	0602	0,002106	39
0101	3701	0602	1001	0501	0,002022	40
0101	0801	0701	1101	0301	0,002009	41
0201	3502	0401	1104	0301	0,001999	42
2402	0801	0701	0301	0201	0,001919	43
0201	1801	0701	1101	0301	0,001896	44
0201	4901	0701	1302	0604	0,001887	45
0301	0702	0702	1101	0301	0,001885	46
0201	5201	1202	1502	0601	0,001846	47
0201	3901	1203	1601	0502	0,001819	48
6801	4402	0704	1101	0301	0,001818	49
2402	1501	0303	1103	0301	0,001810	50
0201	1402	0802	0102	0501	0,001795	51
0201	3501	0401	1101	0301	0,001763	52
2301	4901	0701	1104	0301	0,001736	53
2601	3801	1203	1401	0503	0,001700	54
6802	5301	0401	1302	0604	0,001669	55
2402	1801	0701	1101	0301	0,001655	56
0201	5001	0602	0701	0201	0,001651	57
0201	1801	0701	1301	0603	0,001635	58
0201	3501	0401	0101	0501	0,001635	59
0201	4001	0304	1302	0604	0,001632	60

Errore typing

Paziente n 3 : A 01:01, 02:01; **B 08:04, 18:07**; C 07:01; DRB1 03:01,11:04

Origine: Italia

Aplotipo					Freq	Rank
A	B	C	DR	DQ		
0101	0801	0701	0301	0201	0,026776	1
0201	1801	0701	1104	0301	0,013490	2
2402	3502	0401	1104	0301	0,012011	3
3001	1302	0602	0701	0201	0,011225	4
3301	1402	0802	0102	0501	0,009898	5
2902	4403	1601	0701	0201	0,009852	6
3002	1801	0501	0301	0201	0,008800	7
0301	0702	0702	1501	0602	0,008597	8
0301	3501	0401	0101	0501	0,007429	9
0101	5701	0602	0701	0303	0,005914	10
0201	3501	0401	1401	0502	0,005230	11

Errore typing

Paziente n 3 : A 01:01, 02:01; **B 08:04, 18:07**; C 07:01; DRB1 0301,1104



Locus B	Freq.	Rank
0801	0,058585	4
0802	0,000032	119
0803	0,000006	182
0804	0,000013	156
0807	0,000006	183
0809	0,000006	184
08111	0,000006	185
0812	0,000006	186
0817	0,000019	137



locus B	Freq alle	Rank
1801	0,096360	2
1803	0,001756	43
1805	0,000108	80
1820	0,000102	83
1802	0,000051	104
1807	0,000070	93
1818	0,000108	81
1804	0,000134	76
1834	0,000013	162
1819	0,000032	121
1832	0,000006	199

Impatto sulla ricerca

Paziente n 3 : A 01:01, 02:01; **B 08:04, 18:07**; C 07:01; DRB1 0301,1104

al	dna_a1	a2	dna_a2	b1	dna_b1	b2	dna_b2	dna_c1	dna_c2	dr1	drb11	dr2	drb12	dqb11	dqb12	nr	regcode
1		2		8		18				7	07:01					1	AUS
1	01:01	2	02:01	8	08:01	18	18:01	07:WTR		7	07:01			02:02	03:03	1	D
1	01:01	2	02:17	8	08:01	18	18:01	07:01		7	07:01			02:02		1	D
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:01:01			02:02:01		1	D
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:01:01			02:02:01	03:03:02	1	D
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:01:01G			02:02:01		1	D
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:03	07:01:01G		7	07:01:01G			02:02:01	03:03:02G	1	D
1	01:01:01G	2	02:17:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:01:01G			02:02:01	03:03:02	1	D
1	01:KTKV	2	02:DFKP	8	08:XKT	18	18:RRG	07:CVAG		7	07:01			02:02	03:03:02	1	D
1	01:PAUK	2	02:NPHX	8	08:XKT	18	18:JDZZ	07:JECH	12:CNE	7	07:01			02:02		1	D
1	01:TFDW	2	02:TFES	8	08:XKT	18	18:JDZZ	07:JECH		7	07:01			02:02	03:03	1	D
1	01:XX	2	02:XX	8	08:XX	18	18:XX			7	07:01					1	D
1	01:XX	2	02:XX	8	08:XX	18	18:XX			7	07:01					1	D
1	01:ZAKM	2	02:ZAKP	8	08:YETY	18	18:TXYF	07:ZAMN		7	07:01:01			02:DYCD	03:ZAMY	1	D
1	01:01	2	02:01	8	08:01	18	18:01	07:01	12:03	7	07:01					1	F
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:01:01G			02:02:01		1	PL6
1	01:01	2	02:01	8	08:01	18	18:01	07:01	12:03	7	07:01			03:03		1	USA1
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	05:01:01G	07:01:01G	7	07:01					1	USA1
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:01			02:01:01G		1	USA1
1	01:NSCM	2	02:HGEU	8	08:MWSF	18	18:MDTG	07:MBEW		7	07:01		07:AM	02:01:01G	03:JWMA	1	U
1	01:XX	2	02:XX	8	08:XX	18	18:XX	05:XX	07:XX	7	07:XX					1	A
1	01:APUWR	2	02:JXWN	8	08:JYHH	18	18:JYJP			7	07:JZNA					1	E
1	01:DEHB	2	02:EAFH	8	08:DYSE	18	18:DHUH			7	07:DFYD					1	E
1	01:DEJM	2	02:CSVG	8	08:DHUG	18	18:DHUH			7	07:DFYD					1	BR
1	01:XX	2	02:XX	8	08:XX	18	18:XX			7	07:XX					1	BR
1		2		8		18				7	07:MT					1	D
1	01:01:01G	2	02:01:01G	8	08:01:01G	18	18:01:01G	07:01:01G		7	07:DFRJ			02:GKDU		1	D



Impatto sulla ricerca

Paziente n 3 : A 01:01, 02:01; **B 08:01, 18:01**; C 07:01; DRB1 0301,1104



Tipo	Score	Freq. / Num.
MUD	8/8 10/10	3534 (4583)
MUD	8/8 9/10	9 (9)
MUD	7/8 9/10	16486 (19723)
MUD	7/8 8/10	56 (56)
MUD	6/8 8/10	54645 (63665)
MUD	6/8 7/10	184 (185)
MUD	6/8 6/10	2 (2)
CBU	8/8	166 (166)
CBU	7/8	619 (619)
CBU	6/8	2011 (2011)

Dati anagrafici	Dati HLA
Cod. Lab. gestione : [REDACTED]	A (SD) : 1,2
Data di nascita : [REDACTED] 1976	B (SD) : 8,18
Sesso : M	Cw: 7
Gruppo etnico : C	DR (SD) : 11,17
Attivo ? : S	DQ : 2,7
	A* : 01:01P,02:01P
	B* : 08:01P,18:01P
	C* : 07:01P
	DRB1* : 03:01P,11:04P
	DRB3* :
	DRB4* :
	DRB5* :
	DQA1* :
	DQB1* :
	DPA1* :
	DPB1* :

Allele NULL

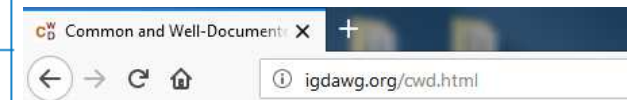


Alleli Null CWD

Null Allele	G Group
A*01:04N	A*01:01:01G
A*03:21N	A*03:01:01G
A*24:09N	A*24:02:01G
A*24:11N	A*24:02:01G
A*68:11N	A*68:01:02G
B*15:01:01:02N	B*15:01:01G
B*51:11N	B*51:01:01G
C*04:09N	C*04:01:01G



<http://igdawg.org/cwd.html>



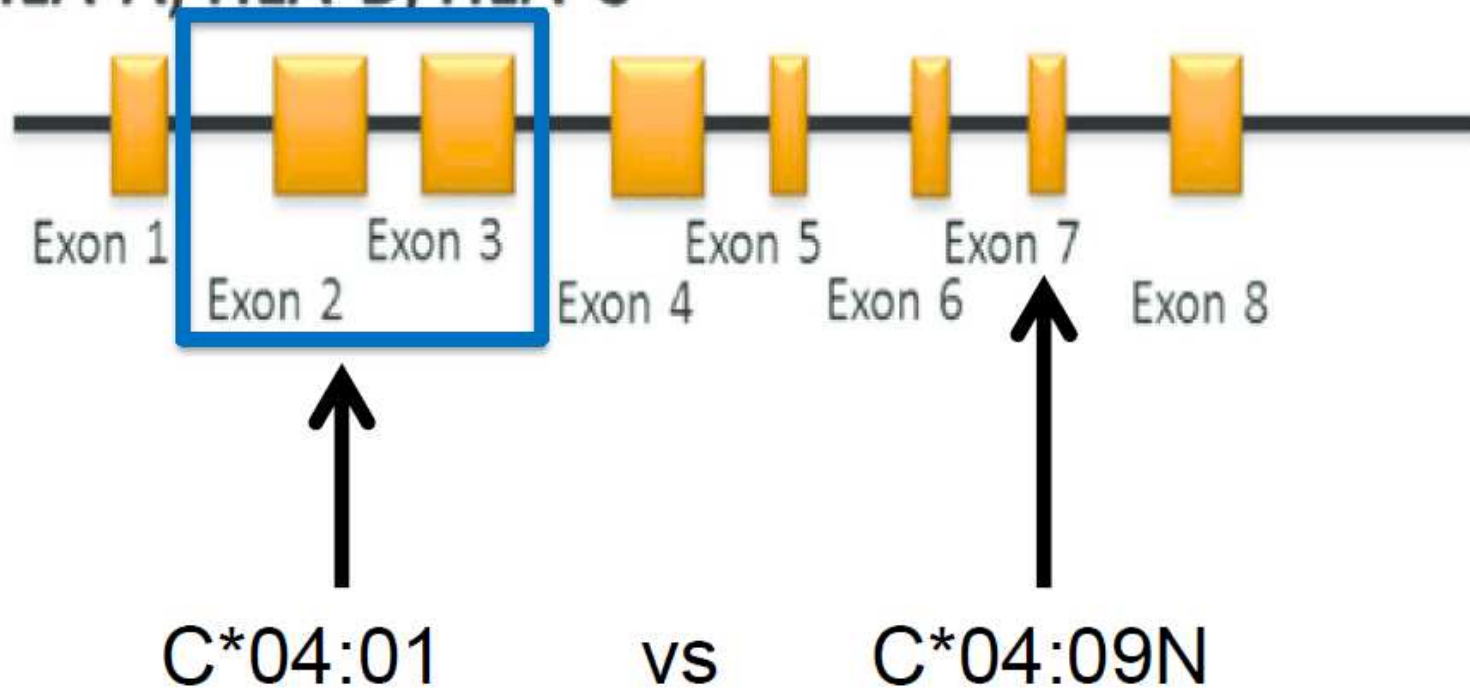
**Common
and
Well-Documented
Alleles**

Current Version: 2.0.0

Downloads

Fenotipo con allele Null

HLA-A, HLA-B, HLA-C



Fenotipo con allele NULL

Paziente : A 11:01:01, **24:185N**; B 18:01:01; C 01:02:01, 07:01:01; DRB1 11:04:01,12:01

Origine: Italia

Split identici ABDR compatibili (5 risultati)

al	dna_a1	a2	dna_a2	b1	dna_b1	b2	dna_b2	dna_c1	dna_c2	dr1	drb11	dr2	drb12	dqb11	dqb12	nr	regcode
11	11:01:01G			18	18:01:01G		18:03	07:XX	12:03:01G	11	11:04	12	12:01:01G	03:01:01G		1	USA1
11	11:01:01G			18	18:01:01G		18:03	01:02:01G	07:01:01G	11	11:04:01	12	12:JV	03:01:01		1	D
11	11:BDFZ			18	18:RRG			12:03		11	11:04:01	12	12:CVT			1	D
11	11:01:01G			18	18:01:01G		18:03	07:01:01G		11	11:04:01	12	12:JV	03:01:01		1	PL6
11	11:AGPFK			18	18:AGHXT		18:AGGEJ			11	11:AGTBJ	12	12:WBSR			1	BR

Split identici AB compatibili (50 risultati)

al	dna_a1	a2	dna_a2	b1	dna_b1	b2	dna_b2	dna_c1	dna_c2	dr1	drb11	dr2	drb12	dqb11	dqb12	nr	regcode	esporta
11				18												1	B	☐
11				18												1	CND	☐
11				18												1	CND	☐

Fenotipo con allele NULL

Paziente : A 11:01:01, **24:185N**; B 18:01:01; C 01:02:01, 07:01:01; DRB1 11:04:01,12:01

Origine: Italia

Potenziali donatori registrati su BMDW

Split identici ABDR compatibili (15 risultati)

a1	dna_a1	a2	dna_a2	b1	dna_b1	b2	dna_b2	dna_c1	dna_c2	dr1	drb11	dr2	drb12	dqb11	dqb12	nr	regcode
24	24:02:01	11	11:01:01	18	18:01:01			12:03:01		11	11:04:01	12	12:01:01	03:01:01		1	D
24	24:02	11	11:01P	18						11	11:04	12	12:01			1	I
24	24:02:01G	11	11:01:01G	18	18:01:01G			12:03:01G		11	11:04:01G	12	12:01:01G	03:01:01G		1	I
24	24:XX	11	11:XX	18	18:XX					11	11:04	12	12:XX			1	BR
24	24:02:01G	11	11:01:01G	18	18:01:01G			07:01:01G		11	11:04:01	12	12:JV	03:01:01		1	D
24	24:02:01G	11	11:01:01G	18	18:01:01G	18:03		07:01:01G		11	11:04:01	12	12:JV	03:01:01		1	D
24	24:DRZW	11	11:CRGR	18	18:03	18:RRG		07:CVAG		11	11:04:01	12	12:CVT			1	D
24	24:XX	11	11:XX	18	18:XX					11	11:NPU	12	12:BRZ			1	D
24		11		18						11		12				1	I
24	24:10	11	11:FVBW	18	18:CVP					11	11:DFYR	12	12:BJ			1	TH
24	24:10	11	11:XX	18	18:EKZB	18:EKZA				11	11:AMGC	12	12:BJ			1	TH
24	24:AJFBT	11	11:AJEZY	18	18:AJHNR	18:AJHNN	03:AHMHW	07:AHMJF		11	11:AHZSD	12	12:XX			1	TH
24	24:JZSE	11	11:NVXC	18	18:JZGU	18:JZGR				11	11:XX	12	12:SPC			1	TH
24	24:KYJH	11	11:XX	18	18:RBDE	18:RBDE				11	11:MWGZ	12	12:REWC			1	TH
24	24:WWVJ	11	11:XX	18	18:XMKW	18:XMKV				11	11:XX	12	12:VZTH			1	TH

Alleli G

The screenshot shows a web browser window with the URL hla.alleles.org/alleles/g_groups.html. The page title is "HLA Nomenclature". The left sidebar contains a navigation menu with links: "hla.alleles.org", "Nomenclature", "HLA Numbers", "Genes", "Alleles", "Proteins", "Antigens", "Dictionary", "WMDA", and "Definitions". The main content area is titled "Nomenclature for Factors of the HLA System" and "G Codes For Reporting of Ambiguous Allele Typings". It explains that HLA alleles with identical nucleotide sequences across the exons encoding the peptide binding domains (exon 2 and 3 for HLA class I and exon 2 only for HLA class II alleles) will be designated by an upper case 'G' which follows the first 3 fields of the allele designation of the lowest numbered allele in the group. The group designation will contain a minimum of six digits. A computer readable file of these codes, [hla_nom_g.txt](#), is available for download, please see the [WMDA](#) section for further details.

The algorithm used to generate the G groups does include alleles which contain unsequenced regions. For the alleles in question, the sequence of an alternate allele has been used to extend the sequence over this region. Where possible a genomic or silent variant of the unsequenced allele are used, when this is not possible an alternate allele from within the same first field groups used and only used when there is a high probability that the sequence used would be shown to be correct if the region was fully sequenced. The list of alleles containing unsequenced regions and the alternate alleles used to infer the missing sequence are detailed in the [Ambiguous Typing files](#) available at from the [IMGT/HLA Database](#).

Following the modification or deletion of an allele sequence a G group may contain only a single allele. In these cases the G group is retained and can refer to single allele, the G group may expand at a later date if new alleles are shown to have an identical nucleotide sequences across the exons encoding the peptide binding domains.

In the case of unsequenced regions that cannot be accurately be inferred from known sequences with a high level of confidence the allele has been omitted from the analysis.

We recognise that future sequencing of unsequenced regions may reveal disparity between the predicted sequence and the newly sequenced region. We therefore welcome any further information which will help improve analysis of these regions.

Group Designation	Alleles Within Group
A*01:01:01G	01:01:01:01/01:01:02N/01:01:01:03/01:01:01:04/01:01:01:05/01:01:01:06/01:01:01:07/01:01:01:08/01:01:01:09/01:01:01:10/01:01:01:11/01:01:01:12/01:01:38/1

http://hla.alleles.org/alleles/g_groups.html

 hla.alleles.org/alleles/g_groups.html

Cerca

 A*11:02:01G 11:02:01/11:02:03/11:02:05/11:02:06/11:77/11:110

A*11:03:01G 11:03/11:175

A*11:05:01G 11:05/11:248

A*23:01:01G 23:01:01:01/23:01:01:02/23:01:01:03/23:01:01:04/23:01:05/23:01:19/23:07N/23:17/23:18/23:20/23:58

A*24:02:01G 24:02:01:01/24:02:01:02L/24:02:01:03/24:02:01:04/24:02:01:05/24:02:01:06/24:02:01:07/24:02:01:08/24:02:01:09/24:02:01:10/24:02:01:11/24:02:01:12/24:02:01:14/24:02:03Q/24:02:10/24:02:13/24:02:31/24:02:40/24:02:43/24:02:44/24:02:56/24:02:65/24:02:79/24:02:80/24:02:81/24:02:82/24:02:83/24:02:101/24:02:102/24:02:103/24:09N/24:11N/24:40N/24:76/24:79/24:83N/24:144/24:150/24:153/24:154/24:155N/24:163N/24:183N/24:231/24:249/24:264/24:265/24:266/24:267/24:268/24:269/24:270/24:271/24:352/24:353/24:354/24:383/24:385/24:388N

A*24:02:34G 24:02:34

A*24:03:01G 24:03:01:01/24:03:01:02/24:33

A*24:05:01G 24:05:01/24:199

A*24:14:01G 24:14:01:01/24:14:01:02/24:14:01:03

A*24:20:01G 24:20:01:01/24:20:01:02

A*24:26:01G 24:26/24:314

A*25:01:01G 25:01:01:01/25:01:01:02/25:07

A*26:01:01G 26:01:01:01/26:01:01:02/26:01:01:03N/26:01:01:04/26:01:01:05/26:01:01:06/26:01:01:07/26:01:01:08/26:01:01:09/26:01:07/26:01:25/26:01:32/26:01:33/26:01:43/26:01:44/26:24/26:26/26:56/26:82/26:98/26:99/26:117

A*29:01:01G 29:01:01:01/29:01:01:02N/29:01:05

A*29:02:01G 29:02:01:01/29:02:01:02/29:02:01:03/29:02:01:04/29:02:07/29:02:20/29:26/29:46/29:75/29:95/29:100

A*29:02:17G 29:02:17:01/29:02:17:02