شناسایی اهدا کننده مناسب سلولهای بنیادی در پیوند نقایص ایمنی اولیه و
گزارشی از مرکز پذیره نویسی اهدای سلولهای بنیادی مرکز تحقیقات ایمونولوژی، آسم و آلرژی

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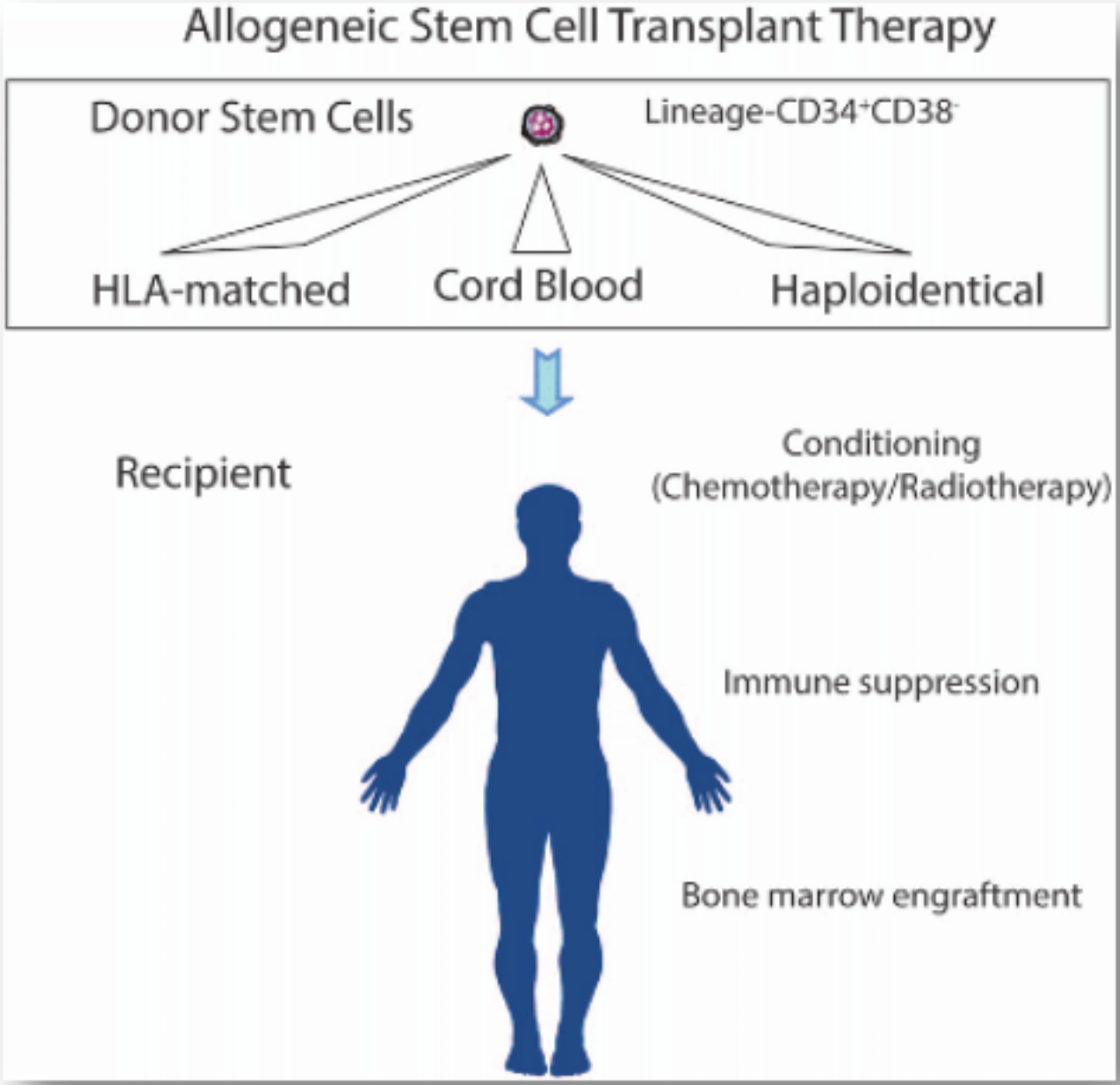
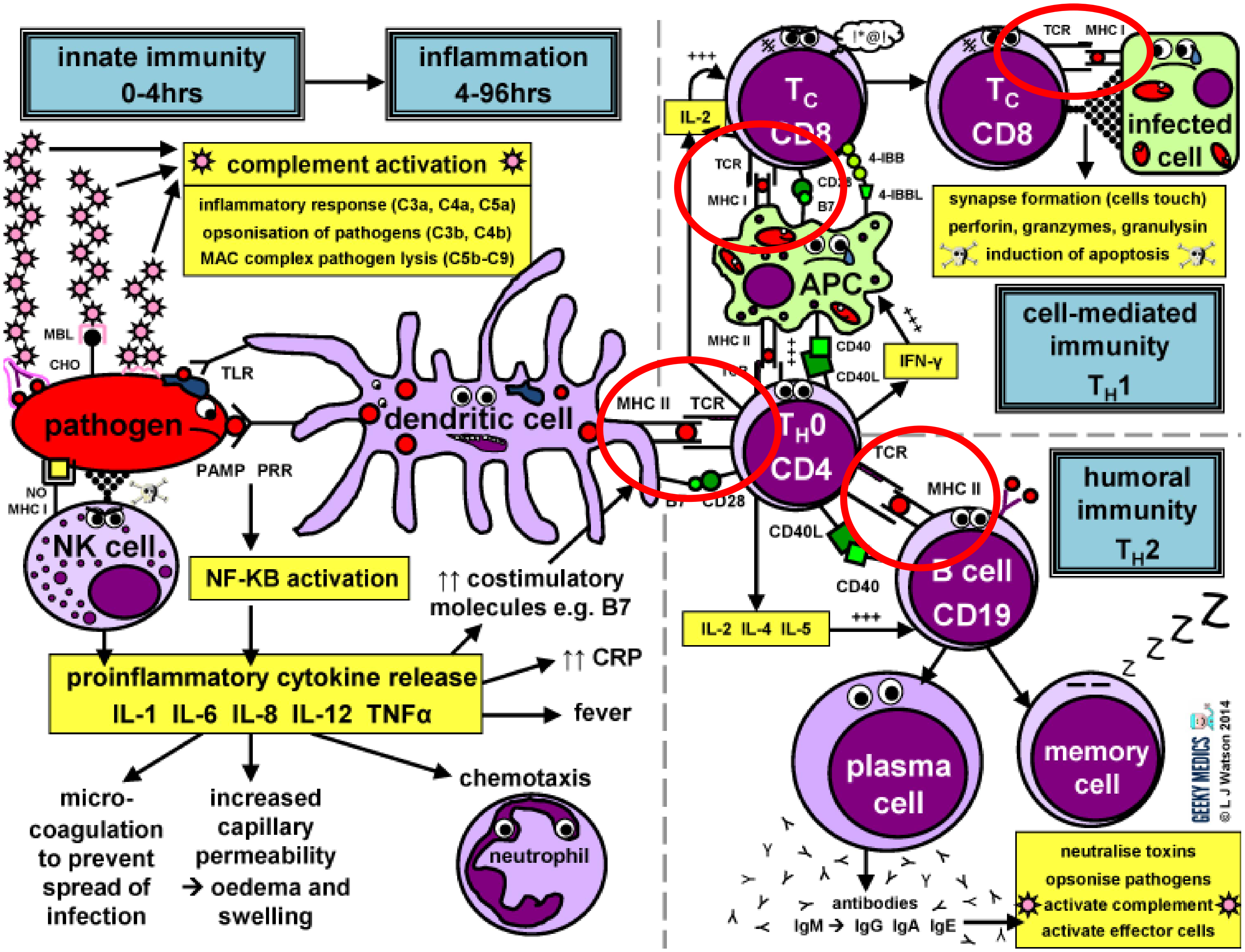
Assistant Prof.,
Immunology, Asthma and Allergy Research Institute (IAARI)
Tehran University of Medical Sciences (TUMS)

7 MARCH 2024

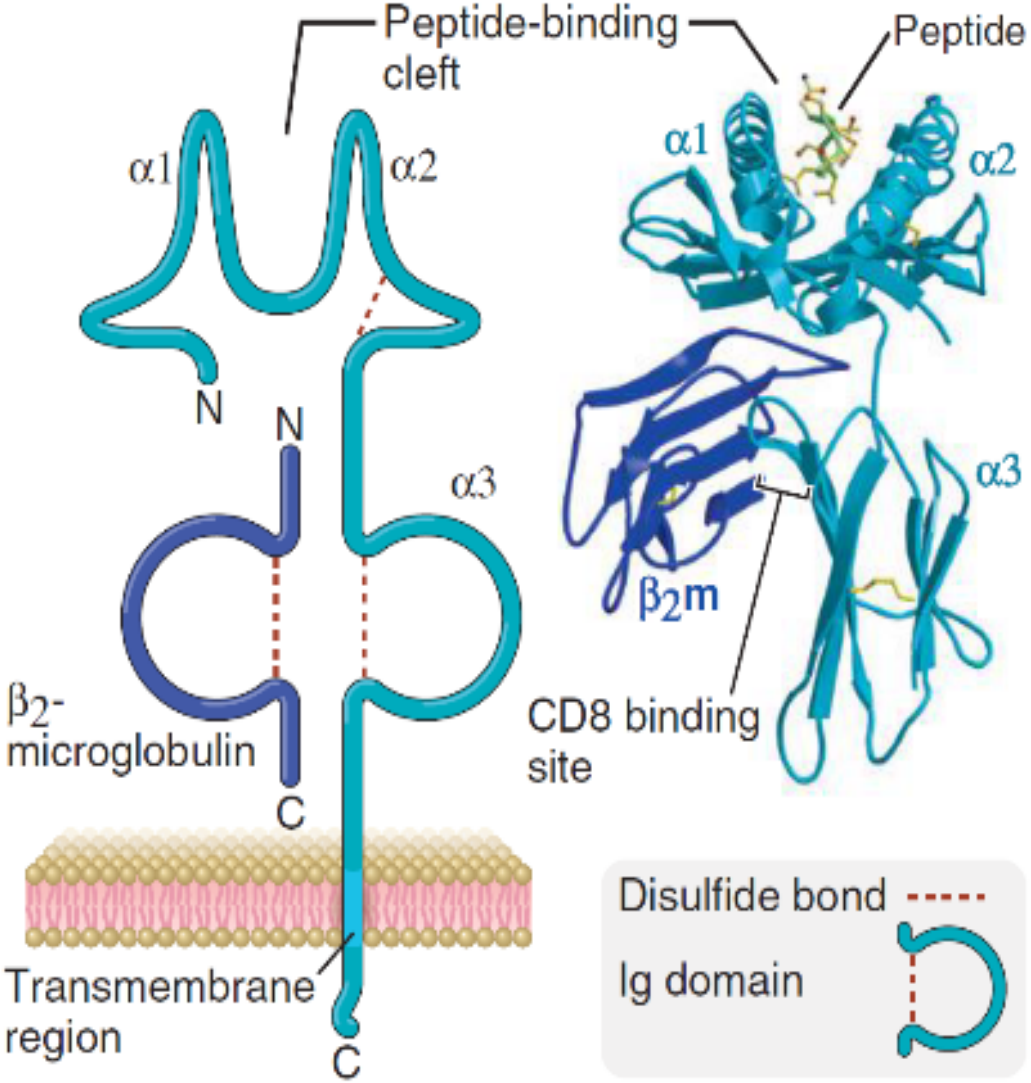

Allogeneic Stem Cell Transplant Therapy
Donor Stem Cells
Lineage-CD34+CD38-
HLA-matched
Cord Blood
Haploidentical
Recipient
Conditioning
(Chemotherapy/Radiotherapy)
Immune suppression
Bone marrow engraftment

What is HLA? What is it for?

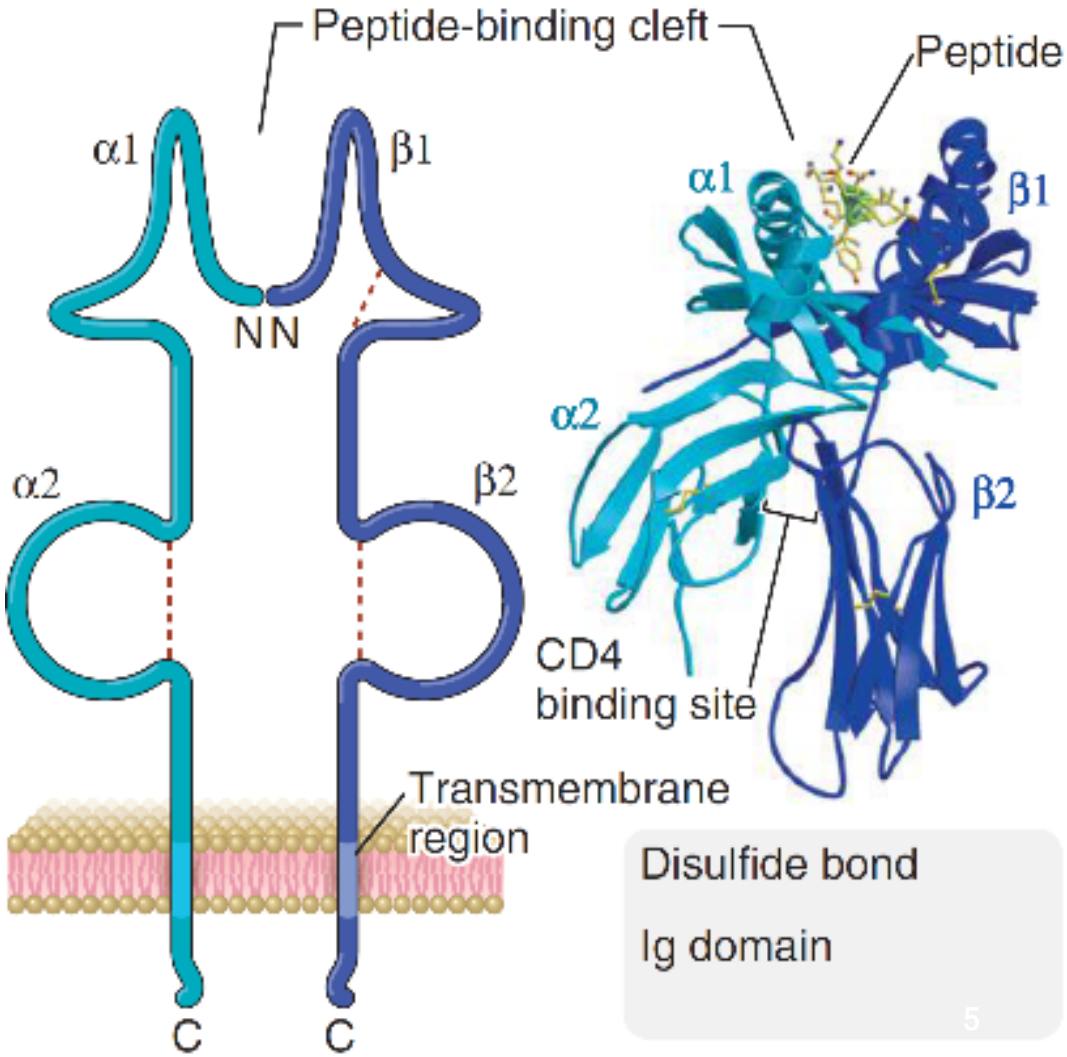
- Human Leukocyte Antigen
- Discovered: in mice (1937), humans (1954)
- Function: to present peptides to T cells, thus allowing elimination of foreign particles and recognition of self (so in transplants this has to be modulated)


innate immunity
0-4hrs
inflammation
4-96hrs
complement activation
inflammatory response (C3a, C4a, C5a)
opsonisation of pathogens (C3b, C4b)
MAC complex pathogen lysis (C5b-C9)
MBL
CHO
TLR
pathogen
PAMP PRR
dendritic cell
NO MHC I
NK cell
NF-KB activation
↑↑ costimulatory molecules e.g. B7
proinflammatory cytokine release
IL-1 IL-6 IL-8 IL-12 TNFα
↑↑ CRP
fever
micro-coagulation to prevent spread of infection
increased capillary permeability → oedema and swelling
chemotaxis
neutrophil
+++
IL-2
TC CD8
TCR
MHC I
CD28
B7
4-IBB
4-IBBL
APC
infected cell
synapse formation (cells touch)
perforin, granzymes, granulysin
induction of apoptosis
MHC II
CD40
CD40L
IFN-γ
cell-mediated immunity
TH1
MHC II TCR
TH0 CD4
B7 CD28
humoral immunity
TH2
B cell CD19
IL-2 IL-4 IL-5
plasma cell
memory cell
antibodies
IgM → IgG IgA IgE
neutralise toxins
opsonise pathogens
activate complement
activate effector cells
GEEKY MEDICS
© L J Watson 2014

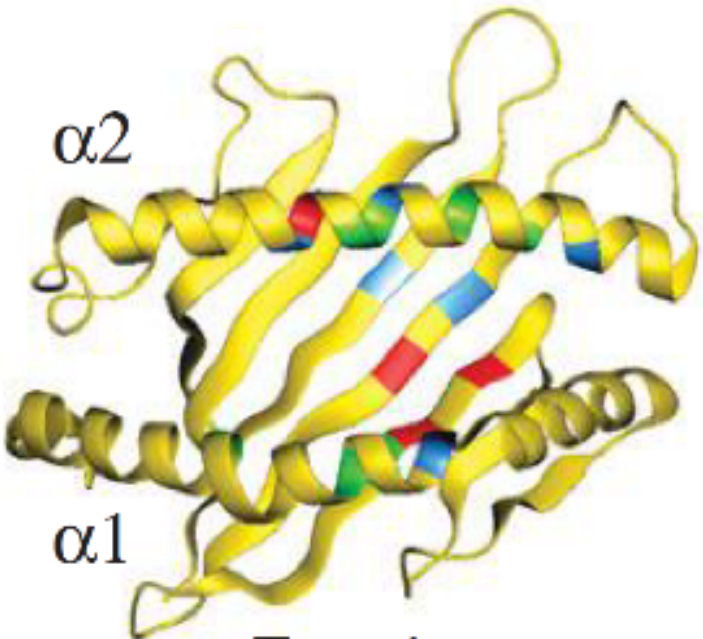
MHC class I expressing cells



MHC class II expressing cells



HLA class I

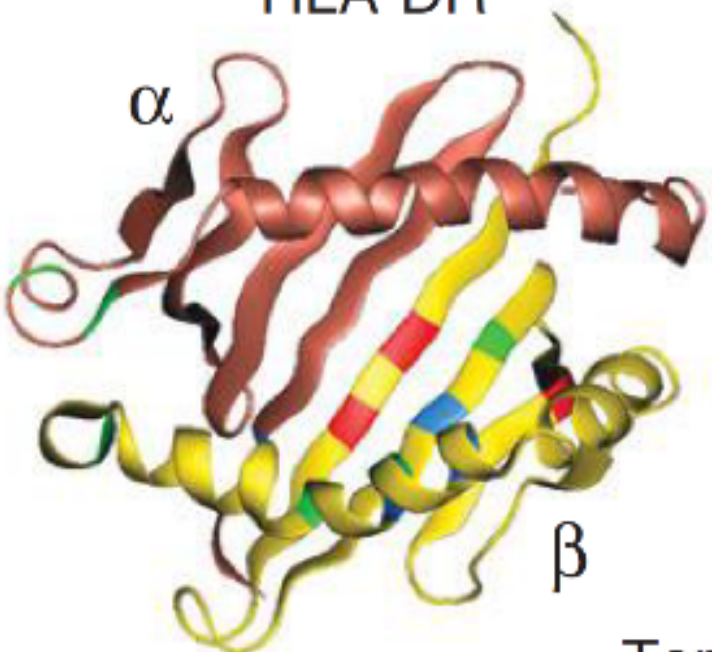


Top view

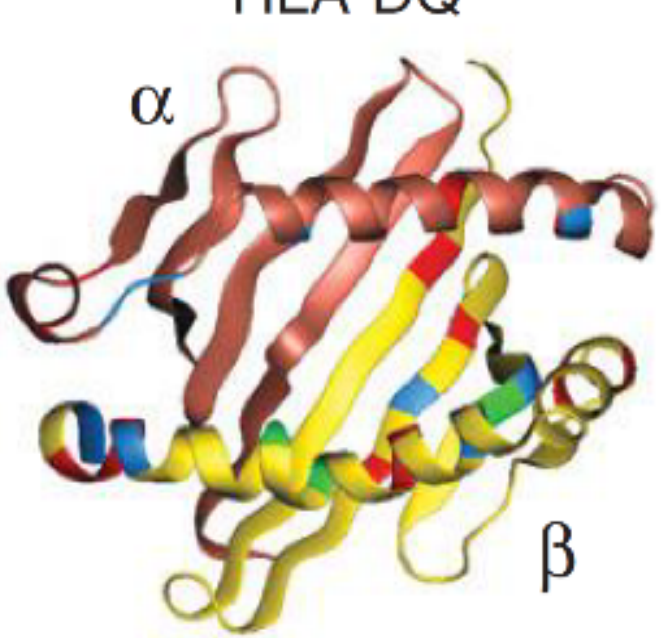
154'818 peptides
length 8 to 10 aa

HLA class II

HLA-DR



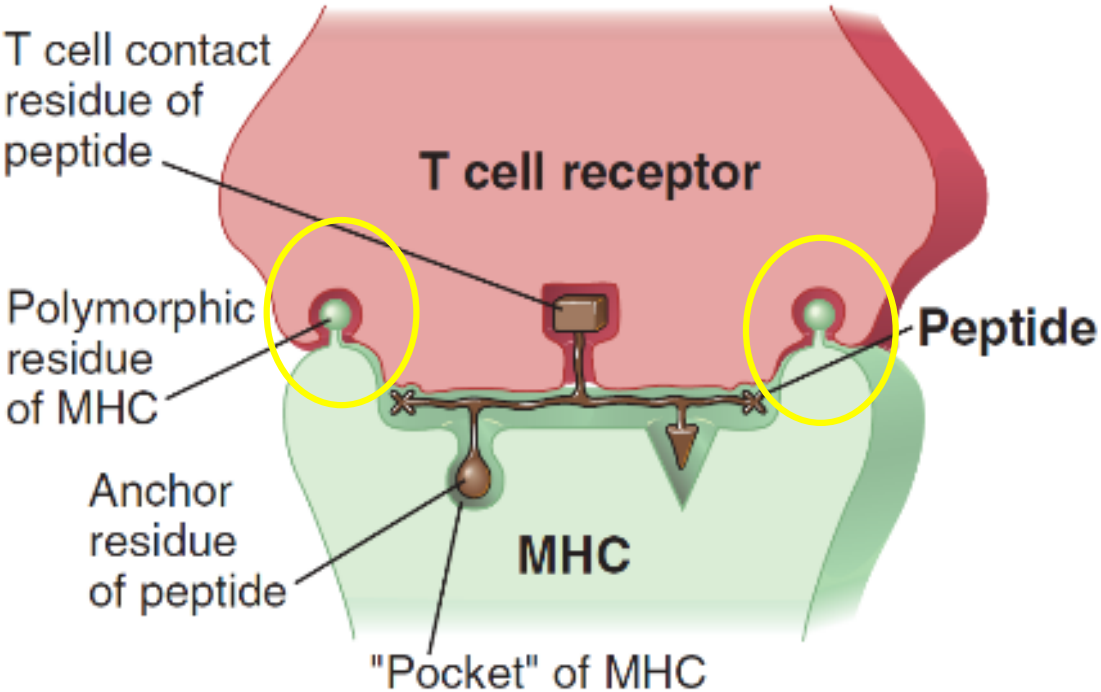
HLA-DQ

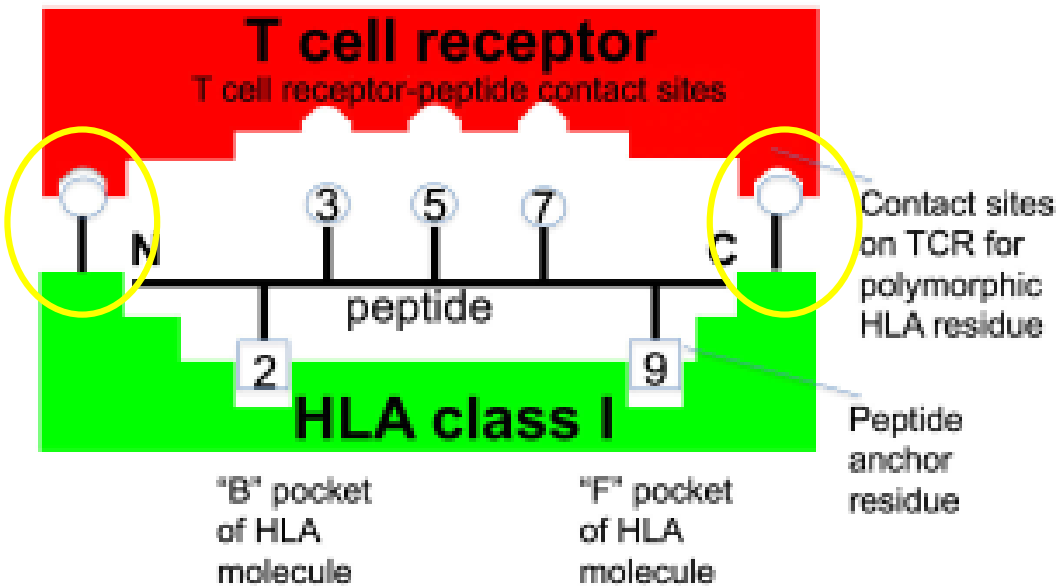


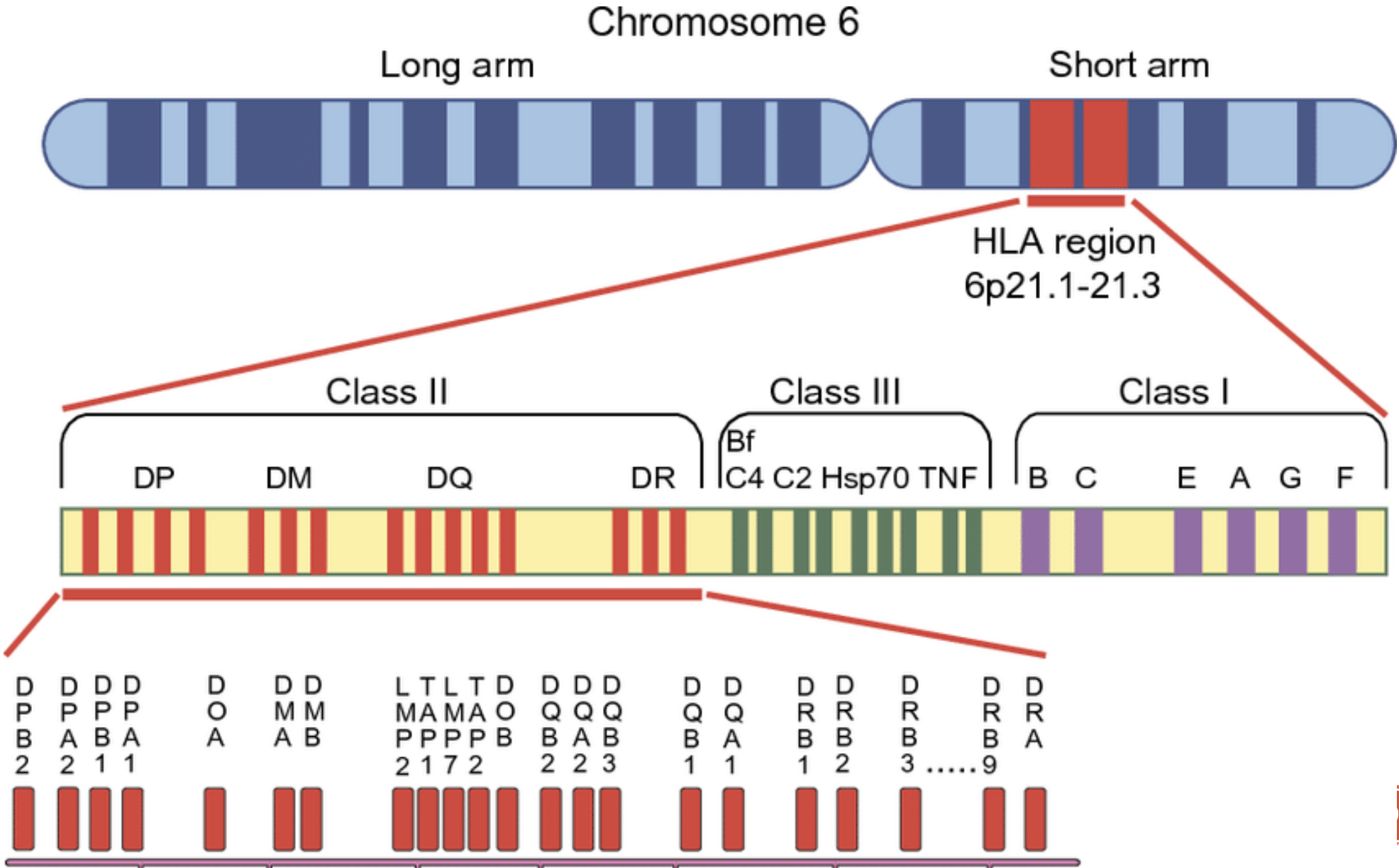
Top view

> 2000 peptides
length 12-24 aa

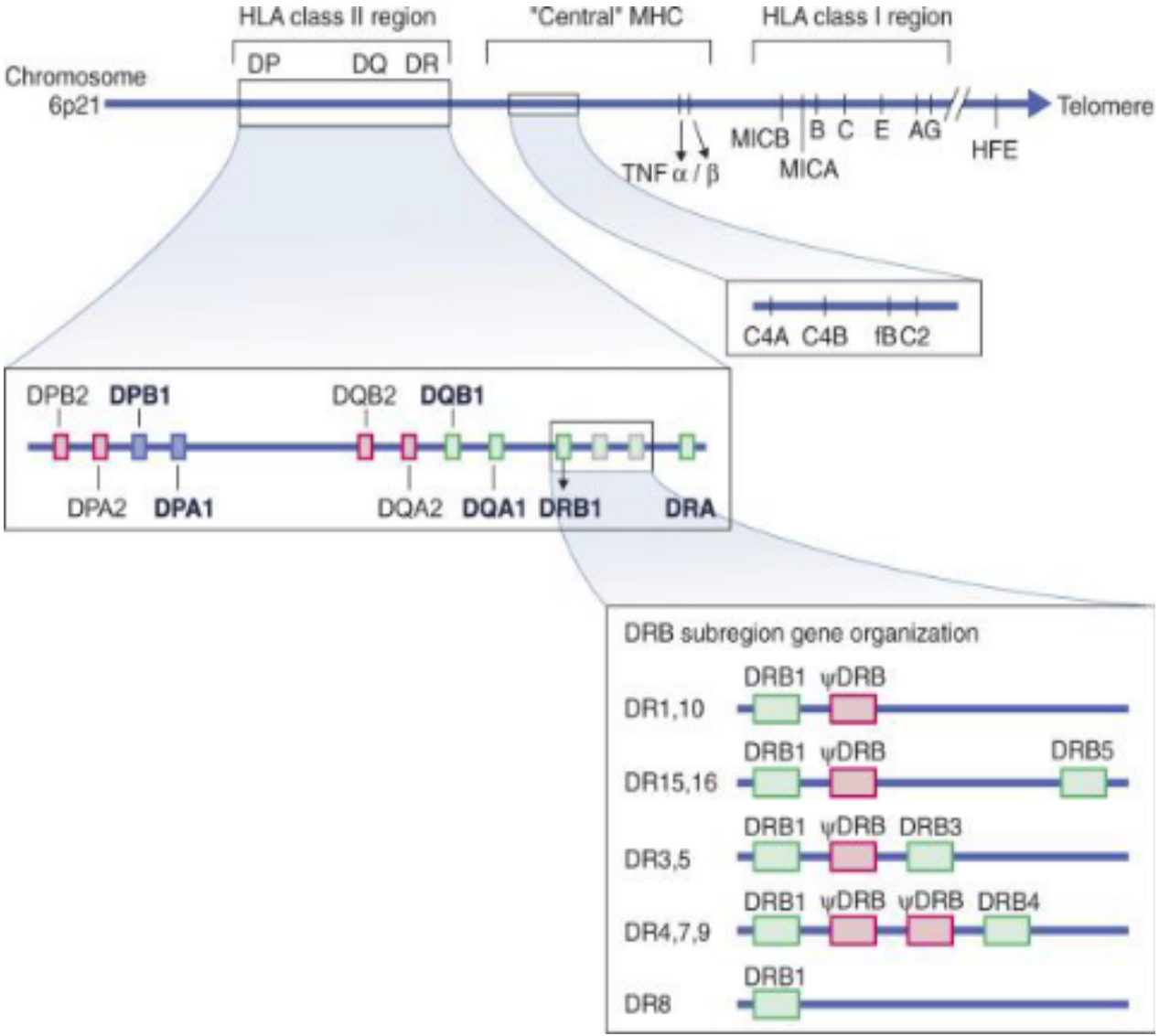
- MHC is the most highly polymorphic gene system in the body and hence in the population.
- This extensive polymorphism of MHC genes makes it very unlikely that two random individuals will express identical sets of MHC molecules.
- This polymorphism is the basis of rapid graft rejection between genetically different individuals.

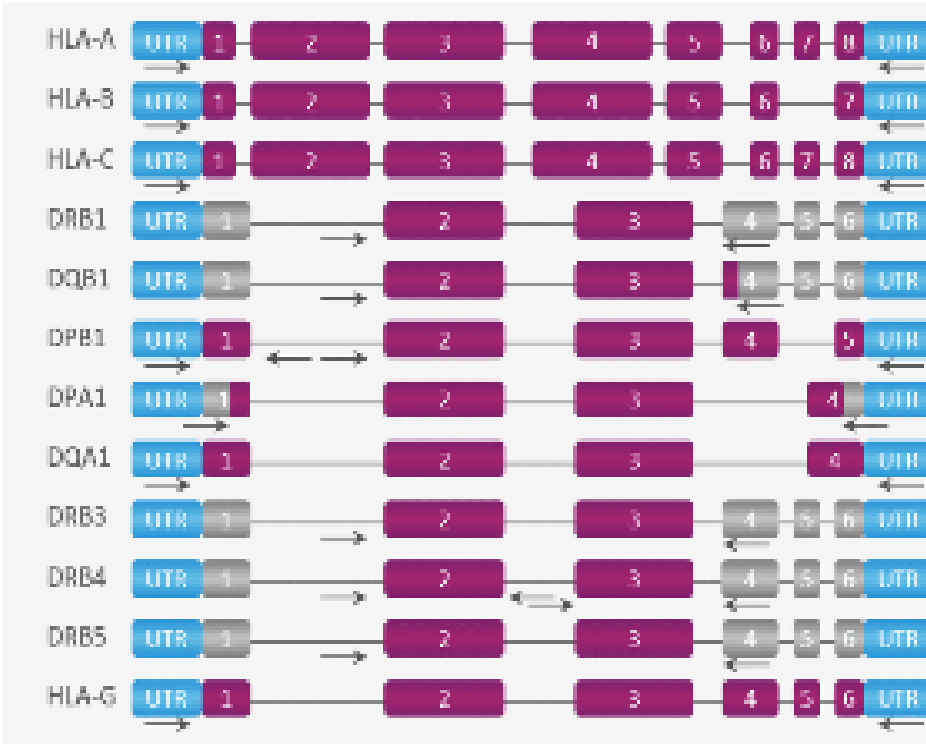

T cell contact residue of peptide
T cell receptor
Polymorphic residue of MHC
Peptide
Anchor residue of peptide
MHC
"Pocket" of MHC

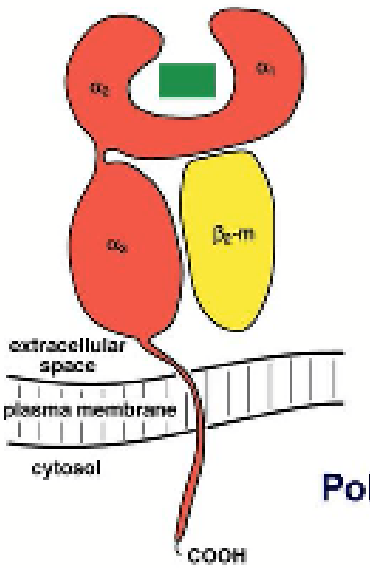

T cell receptor
T cell receptor-peptide contact sites
3
5
7
N
C
peptide
2
9
HLA class I
Contact sites on TCR for polymorphic HLA residue
Peptide anchor residue
"B" pocket of HLA molecule
"F" pocket of HLA molecule


Chromosome 6
Long arm
Short arm
HLA region
6p21.1-21.3
Class II
Class III
Class I
DP
DM
DQ
DR
Bf
C4 C2 Hsp70 TNF
B C E A G F
DPB2 DPA2 DPB1 DPA1 DOA DMA DMB LMP2 TAP1 LMP7 TAP2 DOB DQB2 DQA2 DQB3 DQB1 DQA1 DRB1 DRB2 DRB3 ..... DRB9 DRA

Human MHC Gene Loci



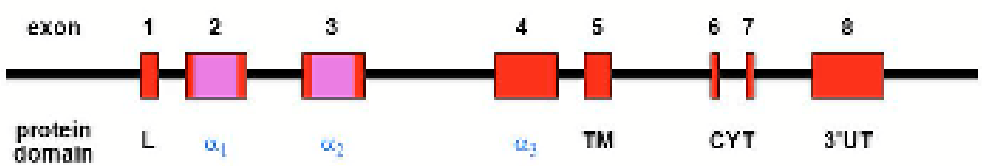


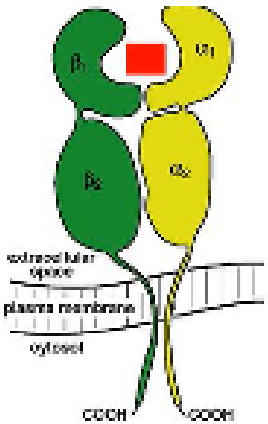


HLA Class I

- found on all nucleated cells

Polymorphism located in exons 2 & 3

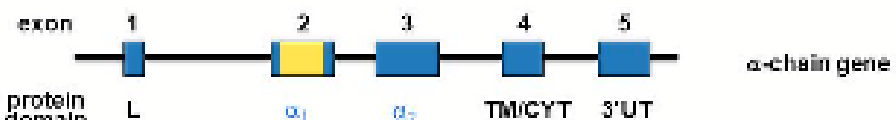




HLA Class II

- restricted to cells of the immune system

Polymorphism located in exon 2



Immuno Polymorphism Database

Overview | IMGT/HLA | KIR | MHC | NHKIR | HPA | ESTDAB

Welcome to IPD

Jan 2023, build 72

IPD was developed in 2003 to provide a centralised system for the study of polymorphism in genes of the immune system. The IPD project was established by the HLA Informatics Group of the Anthony Nolan Research Institute in close collaboration with the European Bioinformatics Institute.

IPD Resources

- Submission
- REST API
- Citations
- Contact
- Support

the **international ImMunoGeneTics project** (IMGT)

IPD-IMGT/HLA

Overview | IMGT/HLA | KIR | MHC | NHKIR | HPA | ESTDAB

HLA / IPD-IMGT/HLA / Release List / 3.55

Version report - 3.55 (2024-01)

4 Versions in a year
(Jan, April, July, Oct)

The following sequences have been submitted to the Nomenclature Committee since the previous release and have been assigned official allele designations.

For a complete release list, please visit the release list page.

New alleles

Allele	Accession	Assigned Date	EMBL/GenBank	Comments
A*01:01:01:116	HLA30086	2023-12	OR241664	Genomic Sequence
A*01:01:01:117	HLA30043	2023-12	OR664359	Genomic Sequence
A*01:01:153	HLA30122	2023-12	OR839577	Genomic Sequence

Summary

New alleles (499)

Modified alleles (128)

Suffix changes (1)

Deleted alleles (1)

Database Growth

The IPD-IMGT/HLA Database was first released in 1998 with 964 alleles. The latest version has 38909 distinct allelic variants.

The graph below indicates the numbers of alleles named and held in the IPD-IMGT/HLA Database since 1907 up to 2024-01-16.

HLA Alleles Assigned as of January 2024

HLA class I						
Gene	***A***	***B***	***C***	***E***	***F***	***G***
Alleles	8098	9656	8084	352	91	158
Proteins	4741	5745	4470	140	17	48
Nulls	420	339	362	10	2	6

HLA Alleles Assigned as of January 2024

HLA class II													
Gene	*DRA*	*DRB*	*DQA1*	*DQA2*	*DQB1*	*DQB2*	*DPA1*	*DPA2*	*DPB1*	*DPB2*	*DMA*	*DMB*	*DOA*	*DOB*
Alleles	67	4581	722	42	2510	41	639	6	2486	7	59	82	93	63
Proteins	15	3019	351	11	1524	9	311	0	1447	0	9	9	14	16
Nulls	0	200	21	0	111	1	26	0	130	0	0	0	1	0

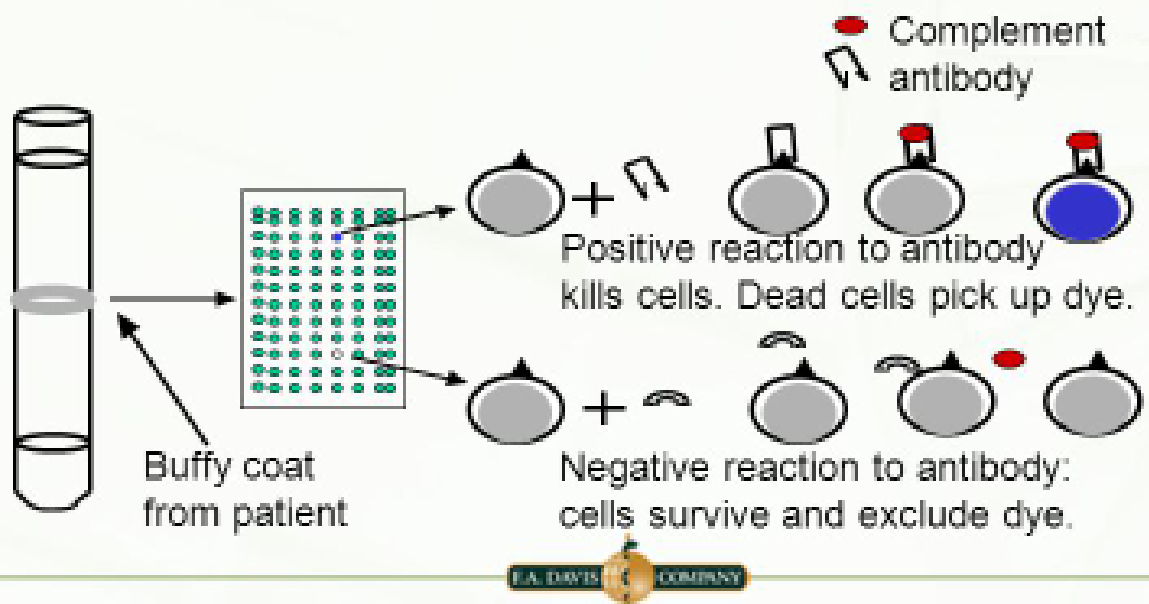
HLA class II - DRB Alleles								
Gene	*DRB1*	*DRB2*	*DRB3*	*DRB4*	*DRB5*	*DRB6*	*DRB7*	*DRB8*	*DRB9*
Alleles	3628	1	488	250	201	4	2	1	6
Proteins	2343	0	369	157	150	0	0	0	0
Nulls	124	0	24	27	25	0	0	0	0

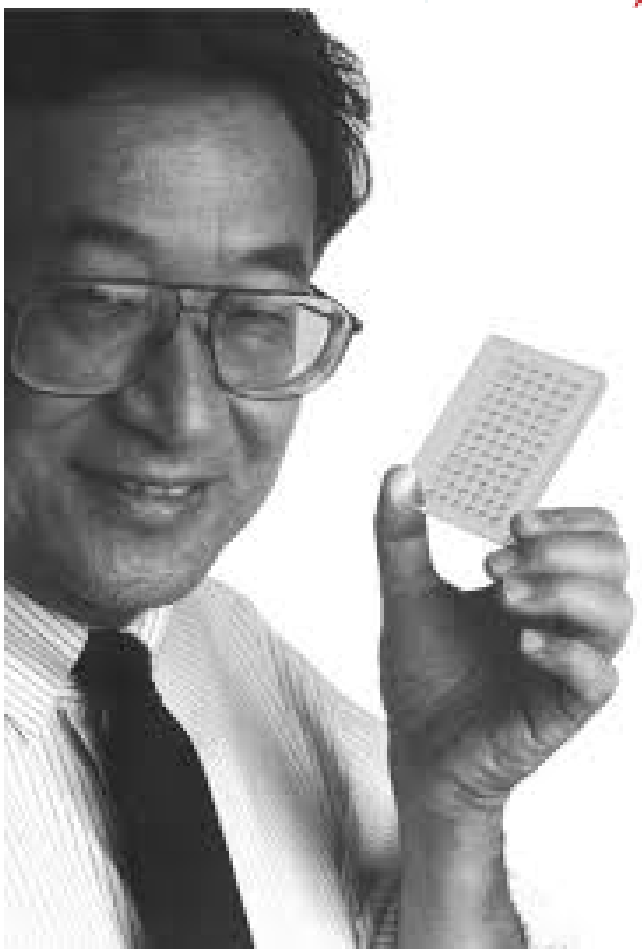
HLA TYPING METHODS

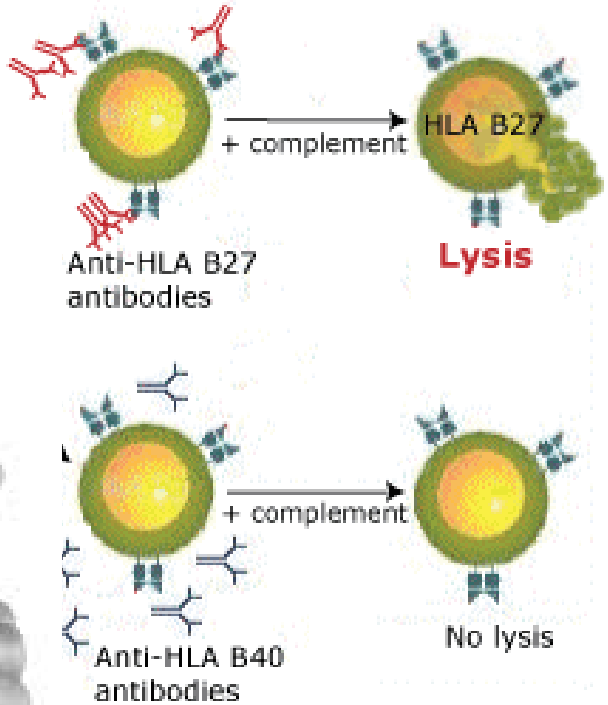
SEROLOGICAL TYPING

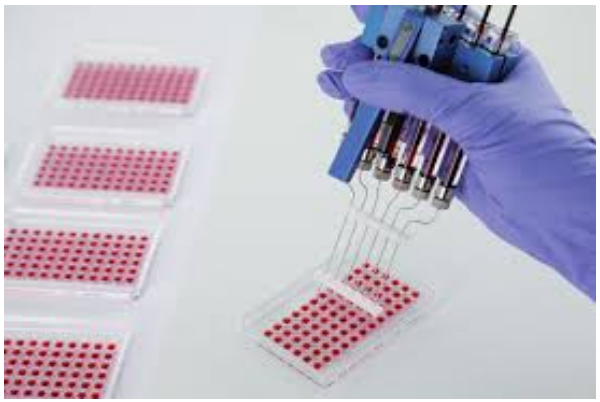
Serological Typing

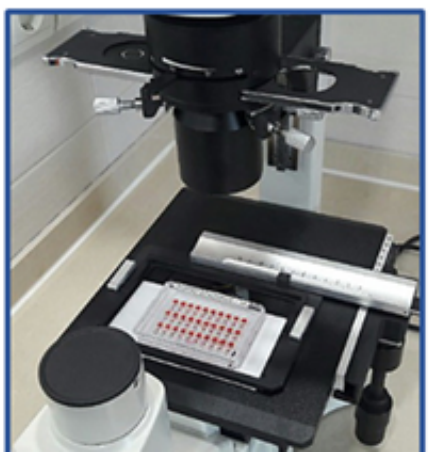
Lymphocytes are HLA-typed by crossmatching to panel reactive antibodies (PRA) using the complement-dependent cytotoxicity (CDC) test.

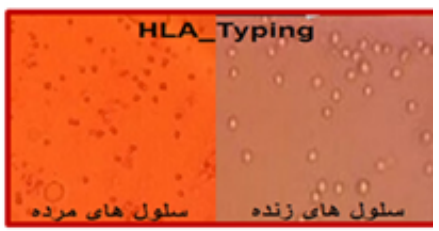





+ complement
HLA B27
Lysis
Anti-HLA B27
antibodies
+ complement
No lysis
Anti-HLA B40
antibodies






HLA_Typing
سلول های مرده
سلول های زنده

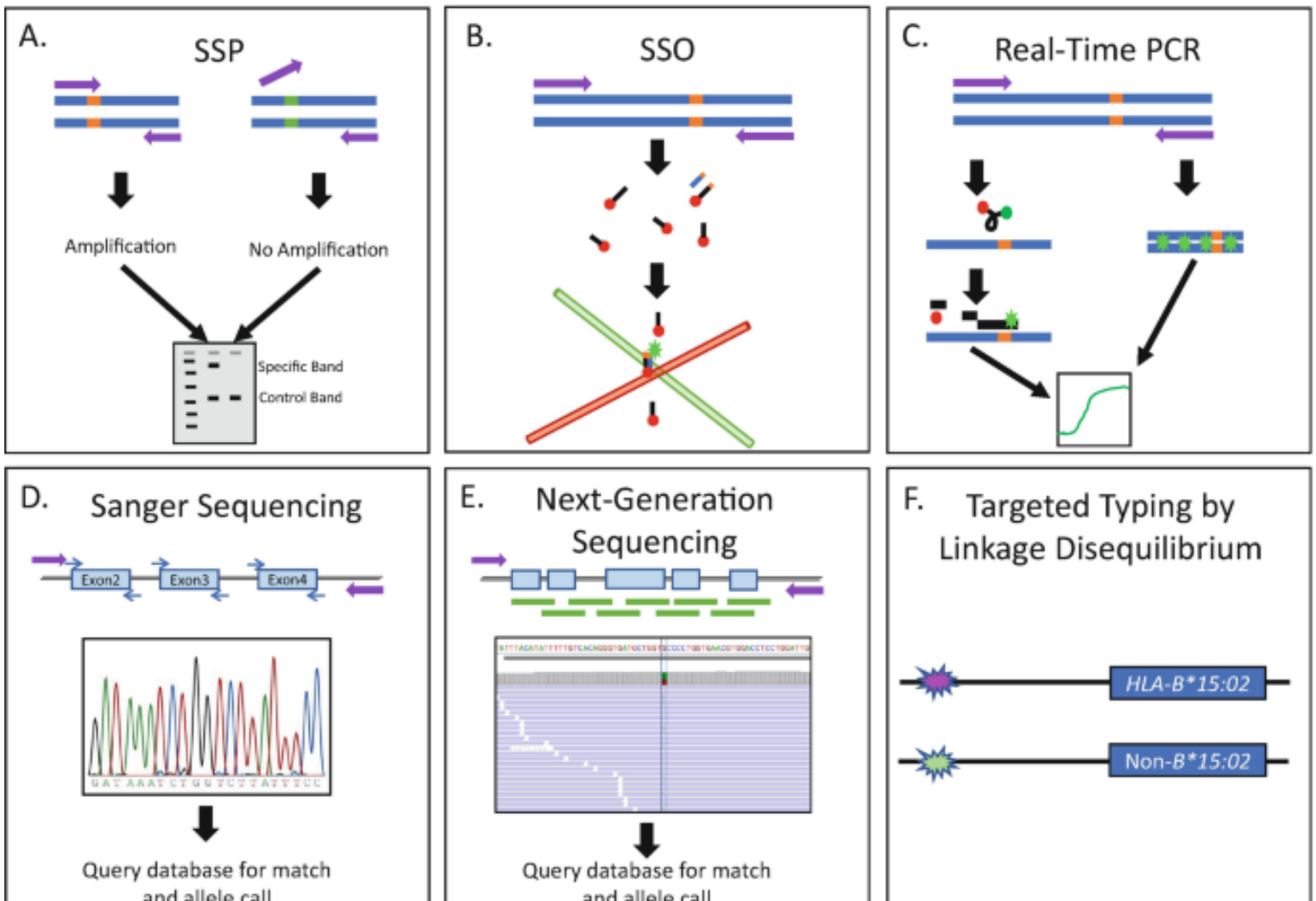
	Pos. *Well*	Serum *Lot*	Anti-HLA	Reaktion *Reaction*	Pos. *Well*	Serum *Lot*	Anti-HLA	Reaktion *Reaction*
TRAY ABC 144 / 1	1A	111 H 0150	pos. Control		7A	304 H 0080	A32	
	1B	110 H 0040	neg. Control		7B	304 H 0310	A32+25	
	1C	109 H 0400	A1+36		7C	105 P 0180	A32(25) s.t.wk	
	1D	109 H 0010	A1		7D	303 P 1050+	A32+74+1+3+11+36	
	1E	109 H 0630	A1		7E	106 P 0350	A33+10 (28, 11,B63)	
	1F	110 H 0070	A2		7F	110 H 0610	A33+34	
	2F	110 H 0080	A2		8F	106 H 0410	A33+31 (29)	
	2E	105 P 0430	A2+69		8E	204 P 0850	A33	
	2D	306 H 0390	A3		8D	204 P 1700	A34	
	2C	304 H 0250 +	A3		8C	110 H 0430	B 51	
	2B	109 P 0220	A3 (11)		8B	108 H 0380	B 51	
	2A	109 P 0110	A 23		8A	111 H 0130	B5[51+52]	
	3A	109 P 0120	A 23		9A	109 H 0650	B5 [51+52]	
	3B	403 H 1040	A9[23+24]+80		9B	105 H 0540	B5[51+52]+53 (B49, A25)	
	3C	111 H 0190	A 24+2403 s.t.wk		9C	106 H 0580	B7 (81)	
	3D	208 H 0160	A 24+2403		9D	110 H 0130	B7	
	3E	110 P 0210	A 25		9E	105 H 0820	B7+27+81+73+42	
	3F	110 H 0260	A 25		9F	110 H 0280	B8	
	4F	112 P 0200	A10[25+26+34+66]+43		10F	106 H 0550	B8+59	
	4E	112 H 0310	A 25+26+66		10E	106 H 0530	B8+14+39	
	4D	104 H 1340	A 26+wk 66		10D	110 P 0250	B 44	
	4C	105 P 0350	A 26		10C	110 H 0470	B 44	

HLA DICTIONARY

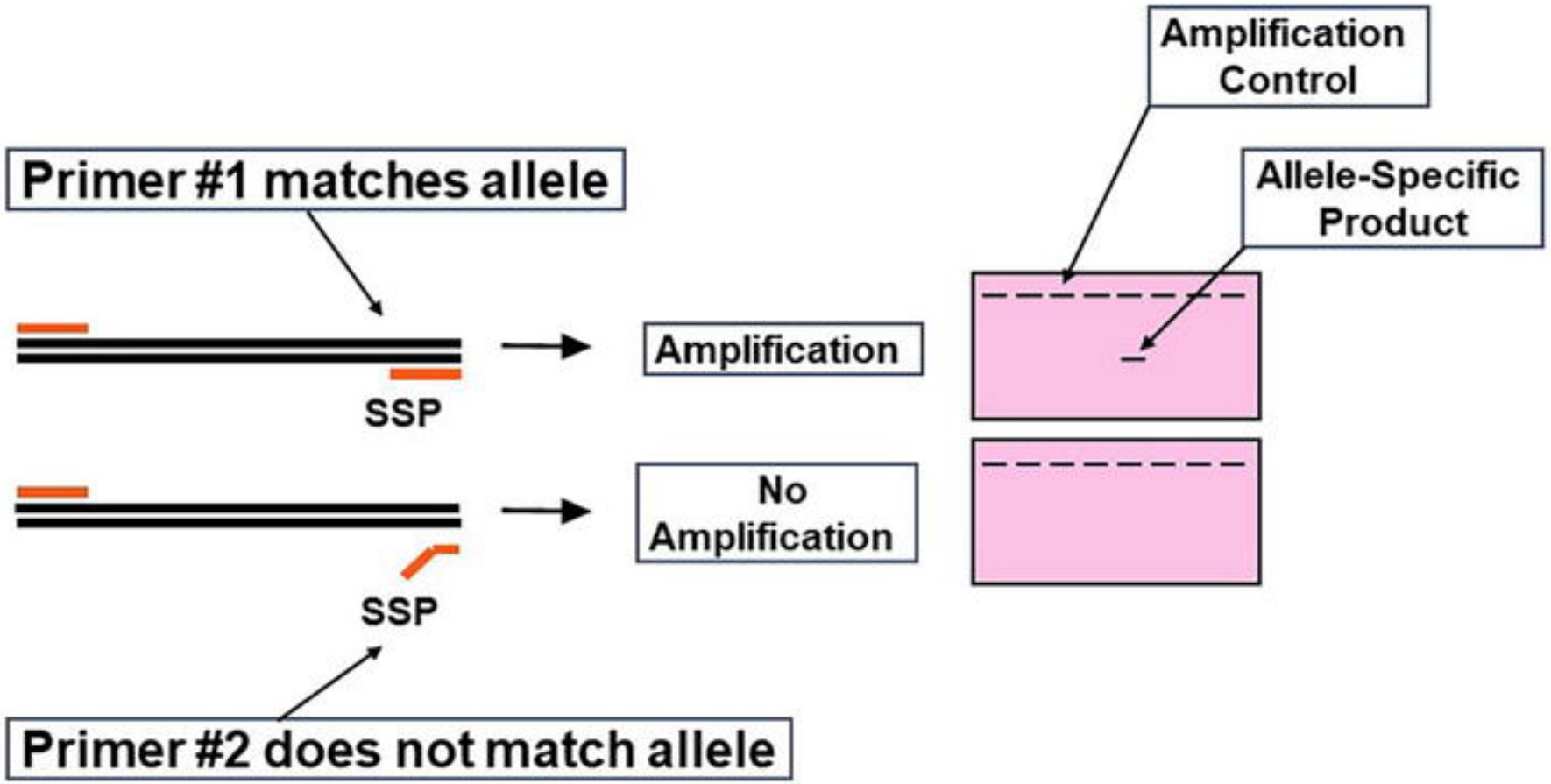
- Serologic : B15 : B62, B63, B75, B76, B77 Molecular: B*15
- Serologic: B70: B71, B72 Molecular: B*15
- Serologic: A28: A68, A69 Molecular: A*68 or A*69
- Serologic: B40: B60, B61 Molecular: B*40

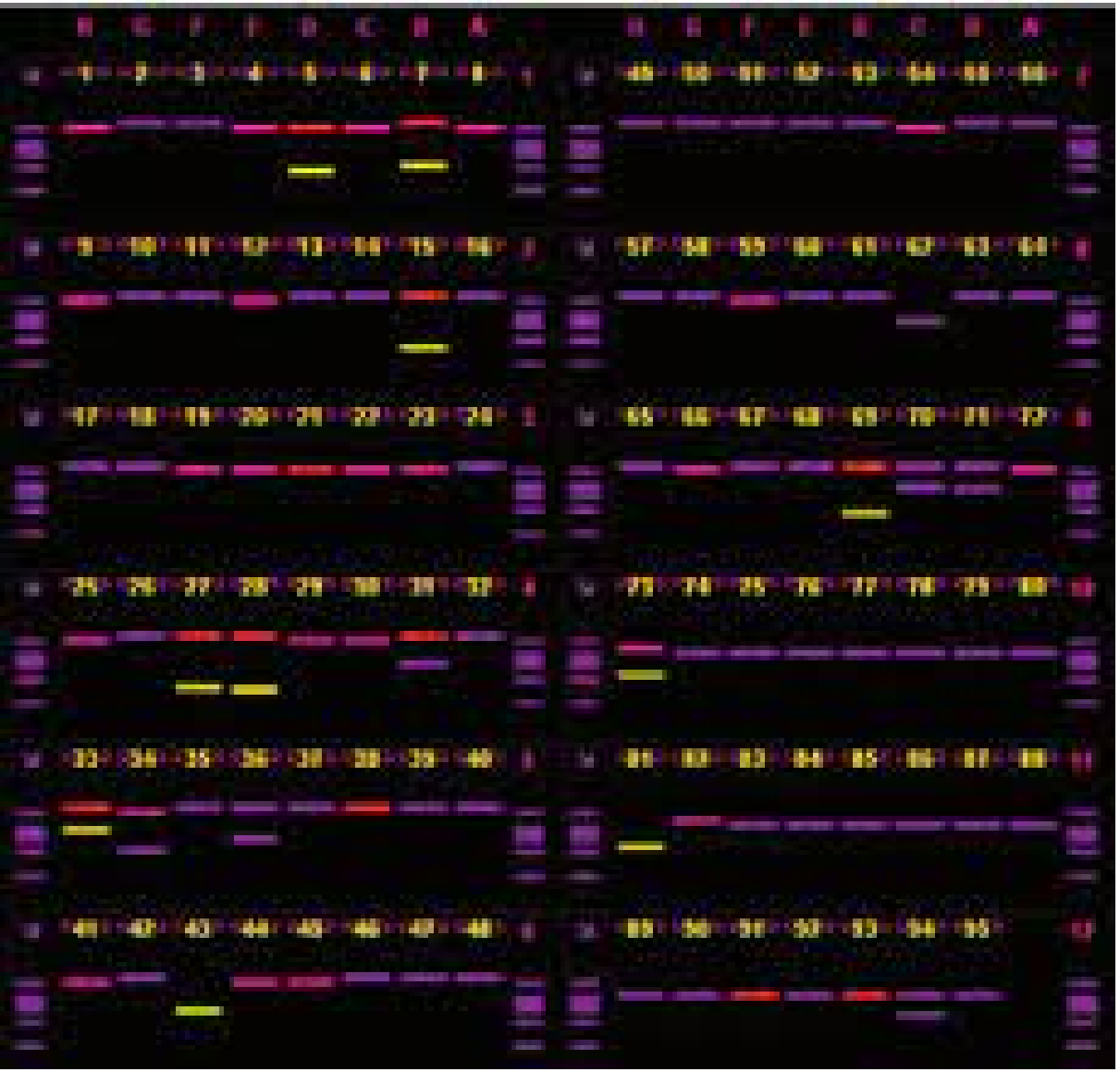
LIMITATIONS

MOLECULAR TYPING METHODS



PCR- SEQUENCE-SPECIFIC PRIMERS (PCR-SSP)

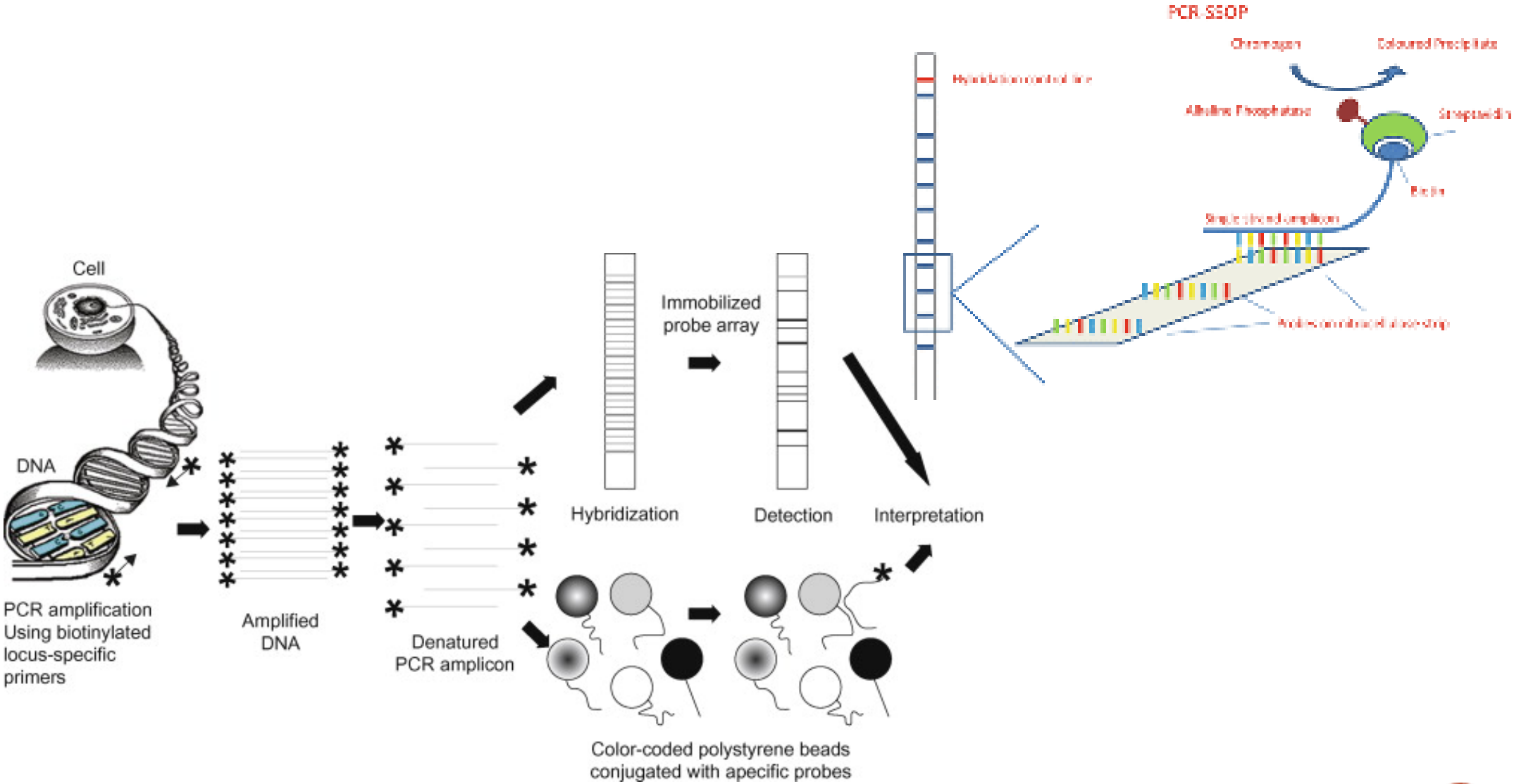




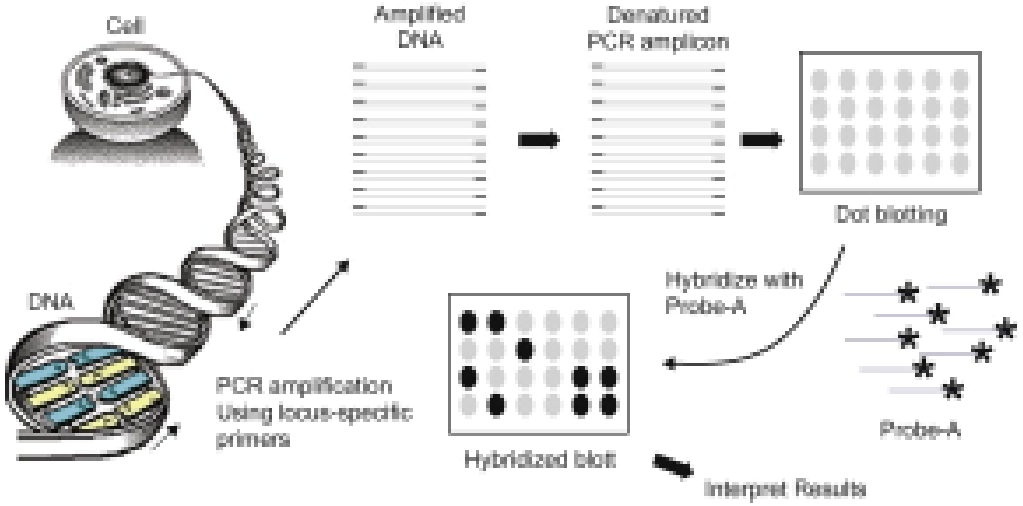

-20°C
-20°C
Taq

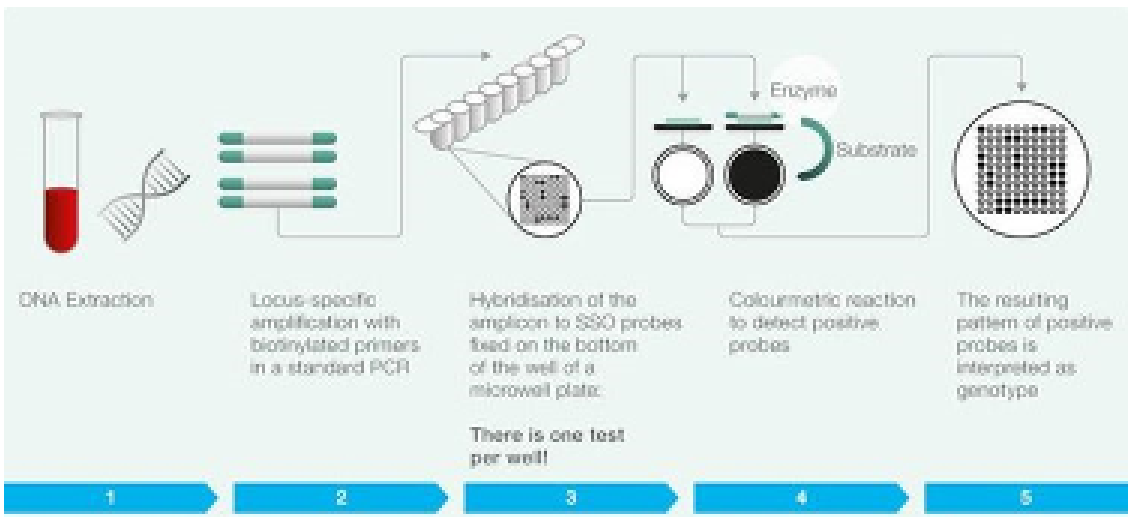

SCORE
Sequence Compilation and Rearrangement Evaluation
for research only

Polymerase chain reaction Sequence-specific Oligonucleotides Probes (PCR-SSOP)

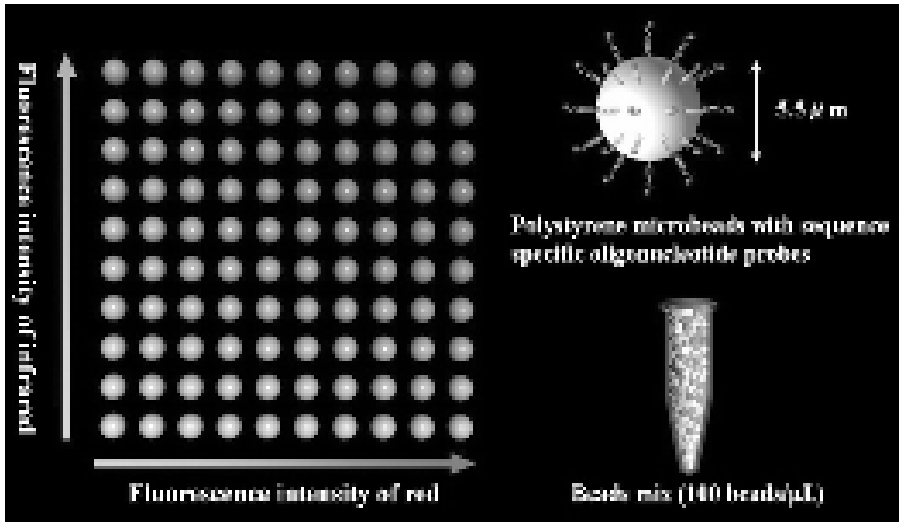

PCR SSOP
Cell
DNA
PCR amplification
Using biotinylated
locus-specific
primers
Amplified
DNA
Denatured
PCR amplicon
Immobilized
probe array
Hybridization
Detection
Interpretation
Color-coded polystyrene beads
conjugated with apecific probes

Enzyme-based Protocols





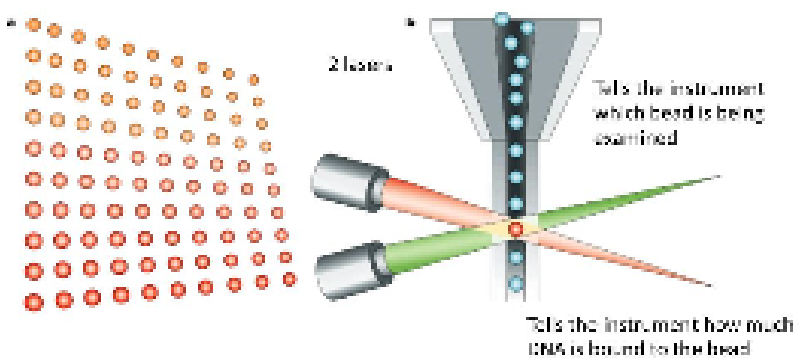
HLA Typing by SSO using Fluorescence



HLA typing by SSO using Luminex platform

100 types of microspheres distinguished by fluorescence emission signature

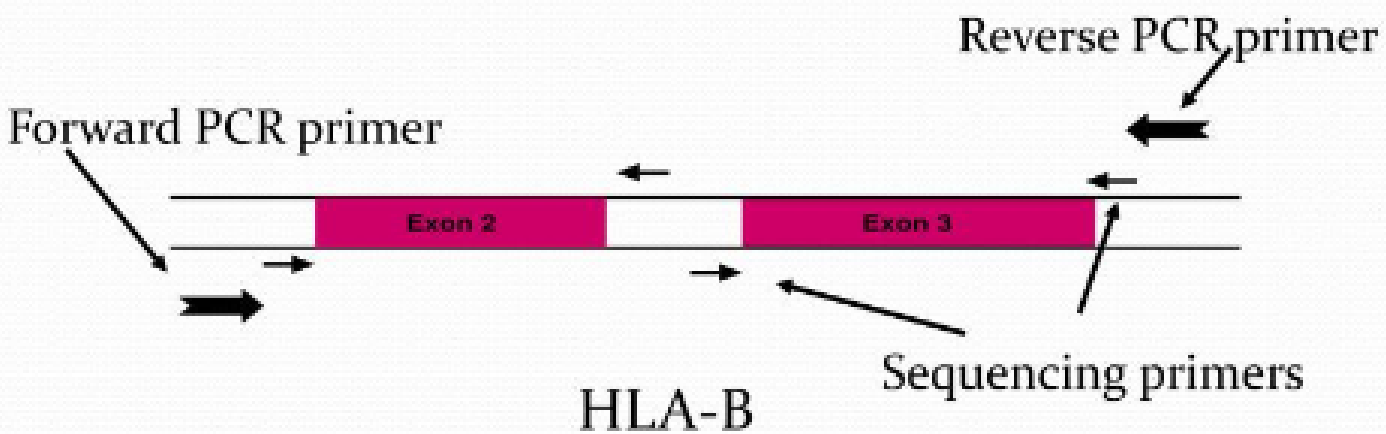
Each microsphere type is coated with different sequence specific oligonucleotide (HLA allele)

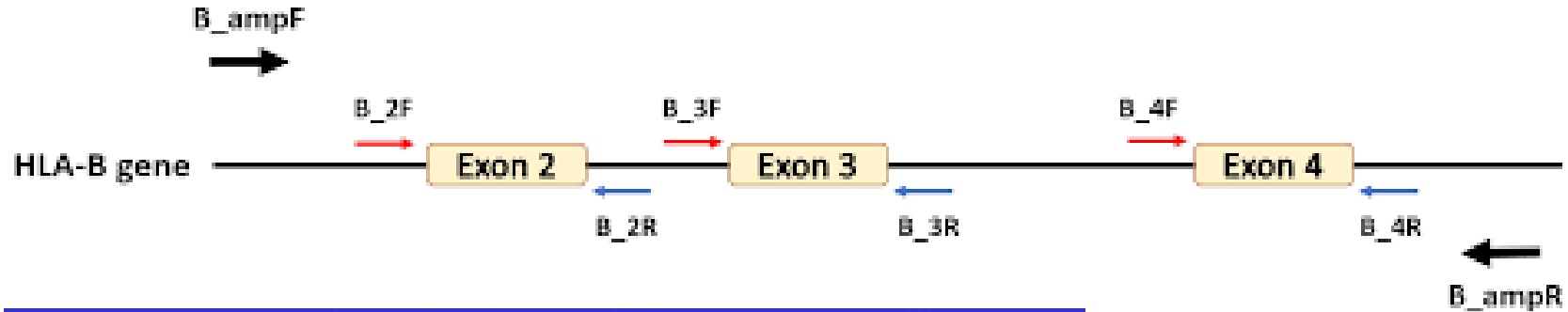


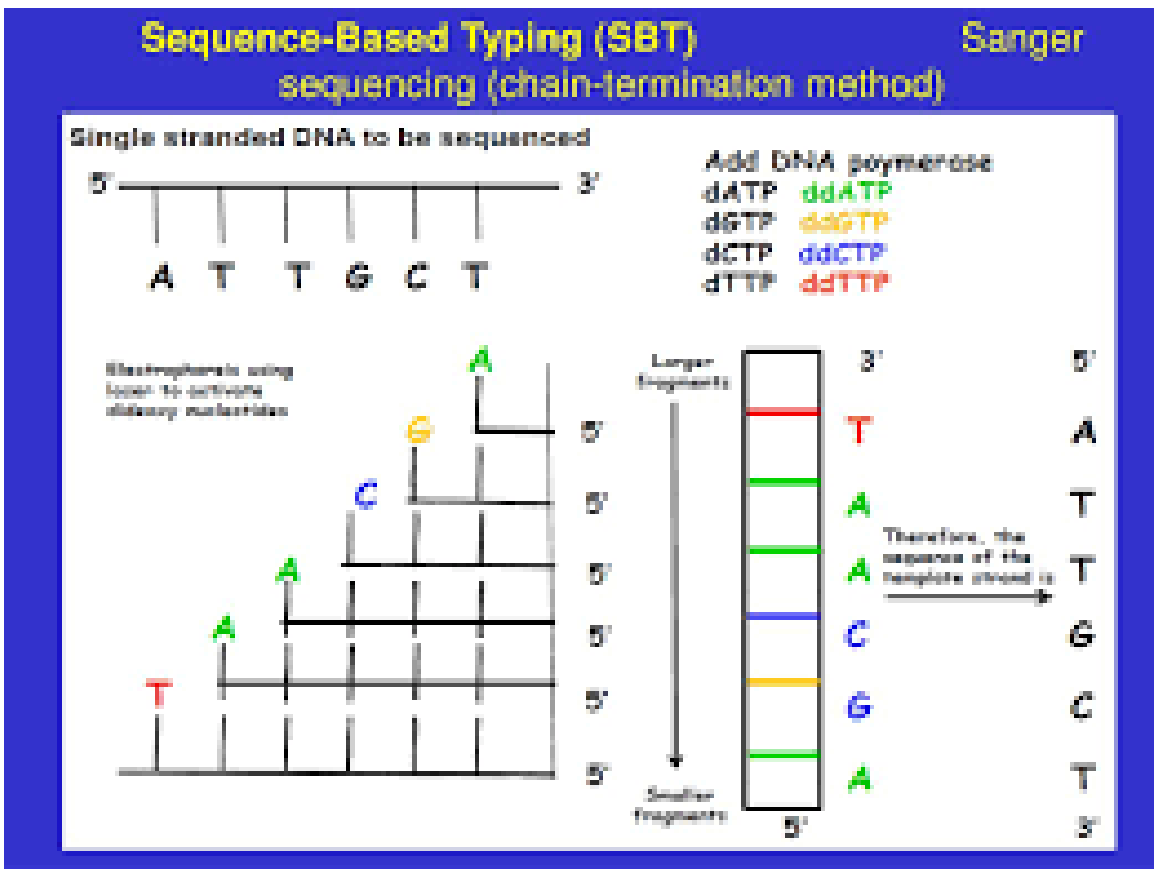
Polymerase chain reaction-Sequencing Based Typing (PCR-SBT)

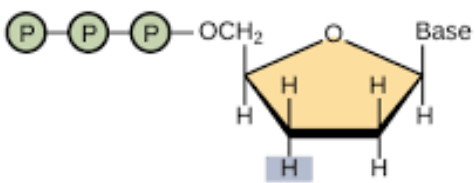
DNA-Based Typing Methods: Sequence-Based Typing

- Sequence-based typing (SBT) is high resolution.
- Polymorphic regions are amplified by PCR and then sequenced.

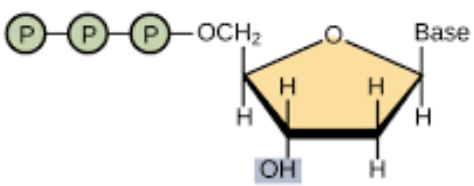




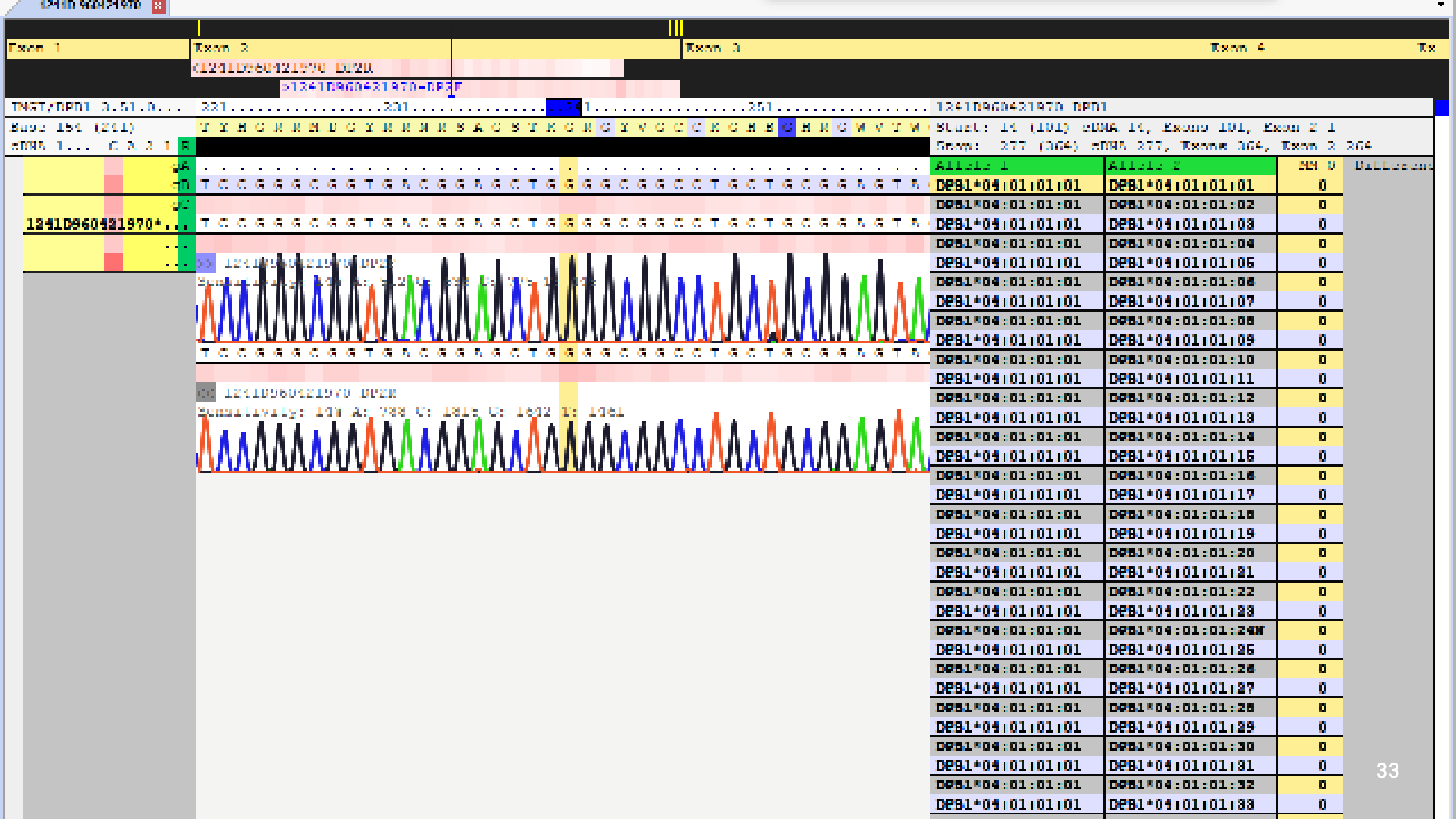




Dideoxynucleotide (ddNTP)



Deoxynucleotide (dNTP)


Exon 1
Exon 2
Exon 3
Exon 4
Allele 1
Allele 2
DPB1*04:01:01:01
DPB1*04:01:01:02
DPB1*04:01:01:03
DPB1*04:01:01:04
DPB1*04:01:01:05
DPB1*04:01:01:06
DPB1*04:01:01:07
DPB1*04:01:01:08
DPB1*04:01:01:09
DPB1*04:01:01:10
DPB1*04:01:01:11
DPB1*04:01:01:12
DPB1*04:01:01:13
DPB1*04:01:01:14
DPB1*04:01:01:15
DPB1*04:01:01:16
DPB1*04:01:01:17
DPB1*04:01:01:18
DPB1*04:01:01:19
DPB1*04:01:01:20
DPB1*04:01:01:21
DPB1*04:01:01:22
DPB1*04:01:01:23
DPB1*04:01:01:24N
DPB1*04:01:01:25
DPB1*04:01:01:26
DPB1*04:01:01:27
DPB1*04:01:01:28
DPB1*04:01:01:29
DPB1*04:01:01:30
DPB1*04:01:01:31
DPB1*04:01:01:32
DPB1*04:01:01:33

Next generation sequencing (NGS)

Roche/454 FLX
Pyrosequencing

Illumina

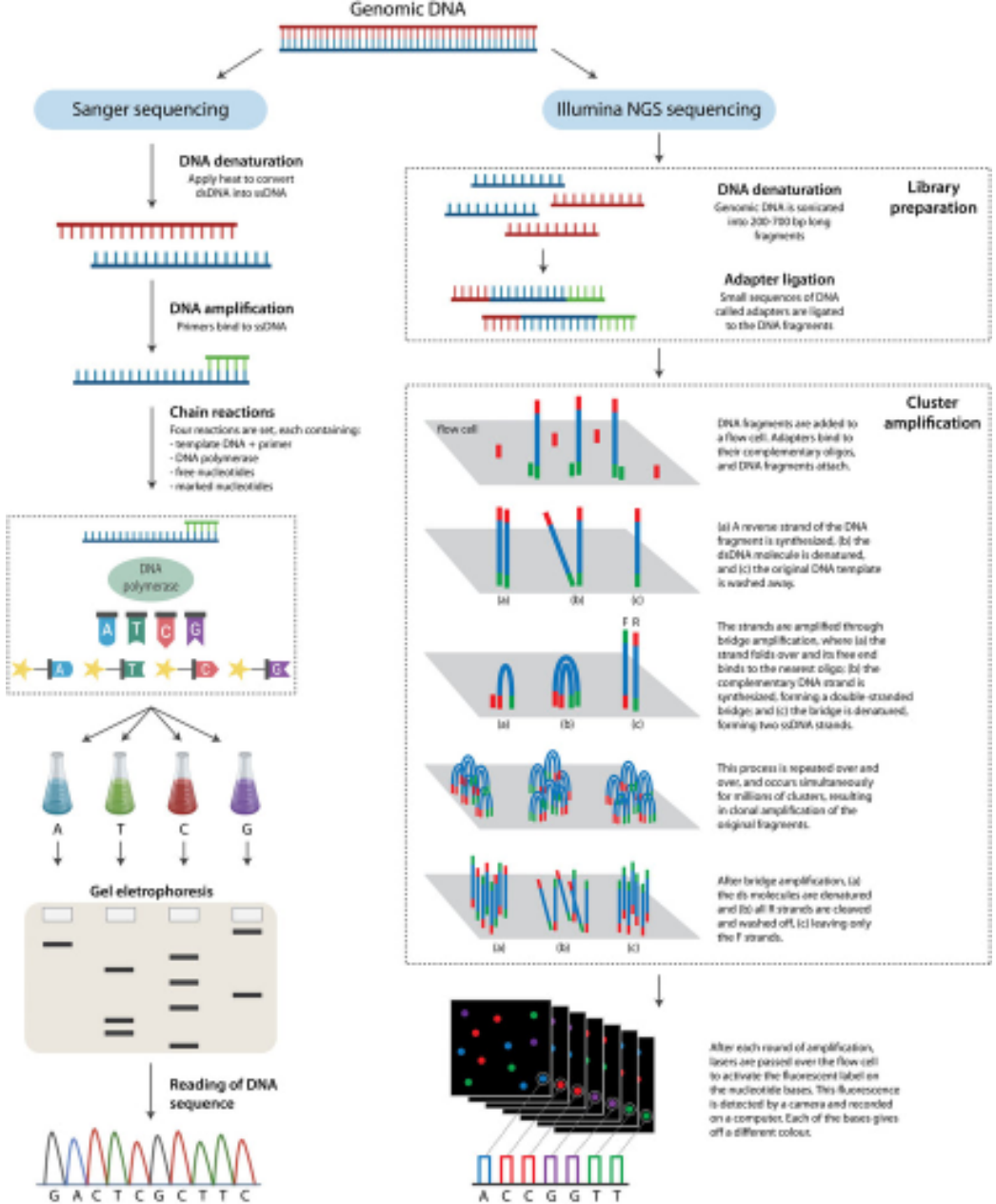
Ion Torrent

ROCHE/454 FLX PYROSEQUENCING

- The GS FLX system utilizes forward and reverse PCR primers fused to adaptors that enable the capture of a single-stranded DNA to a bead in the well of a picotiter plate (PTP).
- The PTP has 1.6×10^6 wells, one bead per well where water-in-oil emulsion PCR occurs.
- After PCR, each well will contain millions of copies of the same DNA strand.
- A number of enzymes (polymerase, luciferase, sulphurylase and apyrase) are added to the wells by the GS FLX system followed by sequential addition of nucleotides.
- Incorporation of one or more nucleotides results in the release of pyrophosphate, which is converted to ATP by sulphurylase. ATP is used by luciferase to create light.
- The sequential addition of nucleotides and the release of light are monitored by a CCD camera, and a flowgram is produced, similar to a sequencing chromatogram, showing the order of A, C, G, T.
- Through clonal PCR and massively parallel pyrosequencing, unambiguous HLA typing is achievable.

ION TORRENT

- Ion Torrent's Personal Genome Machine™ detects H^+ released upon the sequential addition of (unlabelled, natural) nucleotides.
- Release of a proton causes a change in pH, producing an electrical signal that can be measured.
- This technology therefore does not require any optical detection system or enzymatic amplification cascades and thus eliminates sources of sequencing errors while delivering highly uniform genome coverage in a very short time (2h)


Genomic DNA
Sanger sequencing
Illumina NGS sequencing
DNA denaturation
Apply heat to convert dsDNA into ssDNA
DNA amplification
Primers bind to ssDNA
Chain reactions
Four reactions are set, each containing:
- template DNA + primer
- DNA polymerase
- free nucleotides
- marked nucleotides
DNA polymerase
A T C G
Gel eletrophoresis
Reading of DNA sequence
G A C T C G C T T C
DNA denaturation
Genomic DNA is sonicated into 200-700 bp long fragments
Library preparation
Adapter ligation
Small sequences of DNA called adapters are ligated to the DNA fragments
Cluster amplification
Flow cell
DNA fragments are added to a flow cell. Adapters bind to their complementary oligos, and DNA fragments attach.
(a) A reverse strand of the DNA fragment is synthesized. (b) the dsDNA molecule is denatured, and (c) the original DNA template is washed away.
F R
The strands are amplified through bridge amplification, where (a) the strand folds over and its free end binds to the nearest oligo; (b) the complementary DNA strand is synthesized, forming a double-stranded bridge; and (c) the bridge is denatured, forming two ssDNA strands.
This process is repeated over and over, and occurs simultaneously for millions of clusters, resulting in clonal amplification of the original fragments.
After bridge amplification, (a) the ds molecules are denatured and (b) all R strands are cleaved and washed off, (c) leaving only the F strands.
After each round of amplification, lasers are passed over the flow cell to activate the fluorescent label on the nucleotide bases. This fluorescence is detected by a camera and recorded on a computer. Each of the bases gives off a different colour.
A C C G G T T

A new generation of molecular sensing technology

Explore the nanopore portfolio of flow cells, compatible devices, manual and automated library prep, and data analysis solutions.

Oxford NANOPORE Technologies

PREPARE
your library

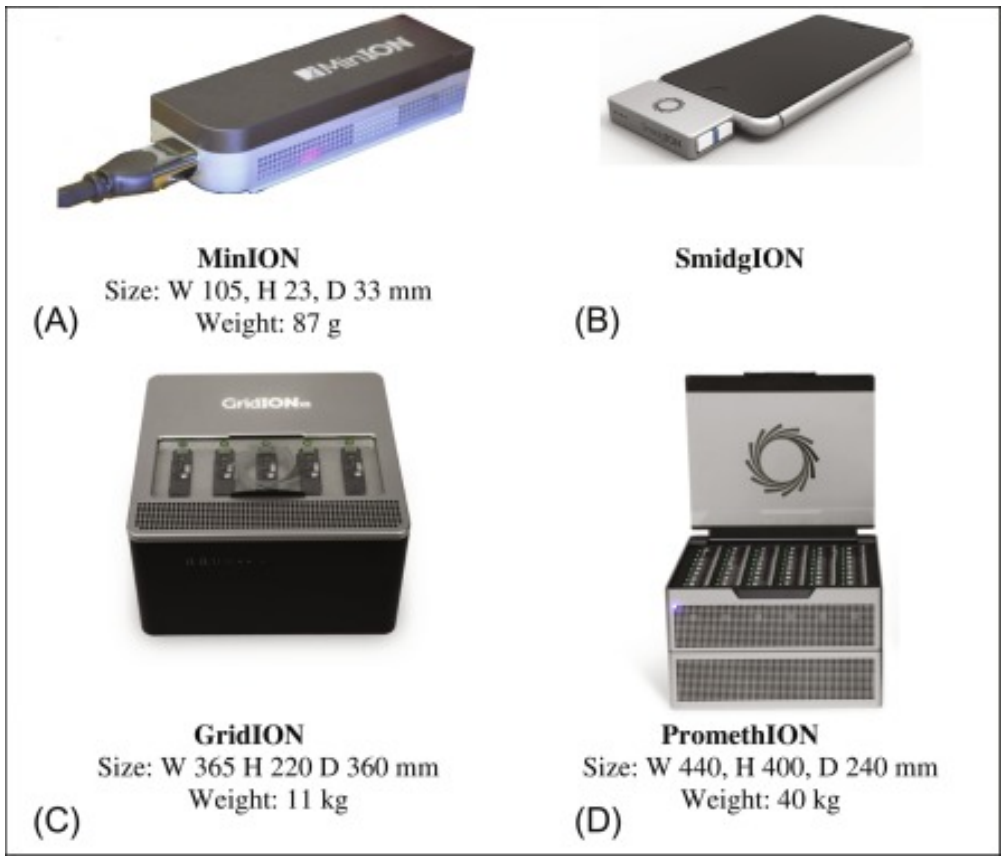
Explore >

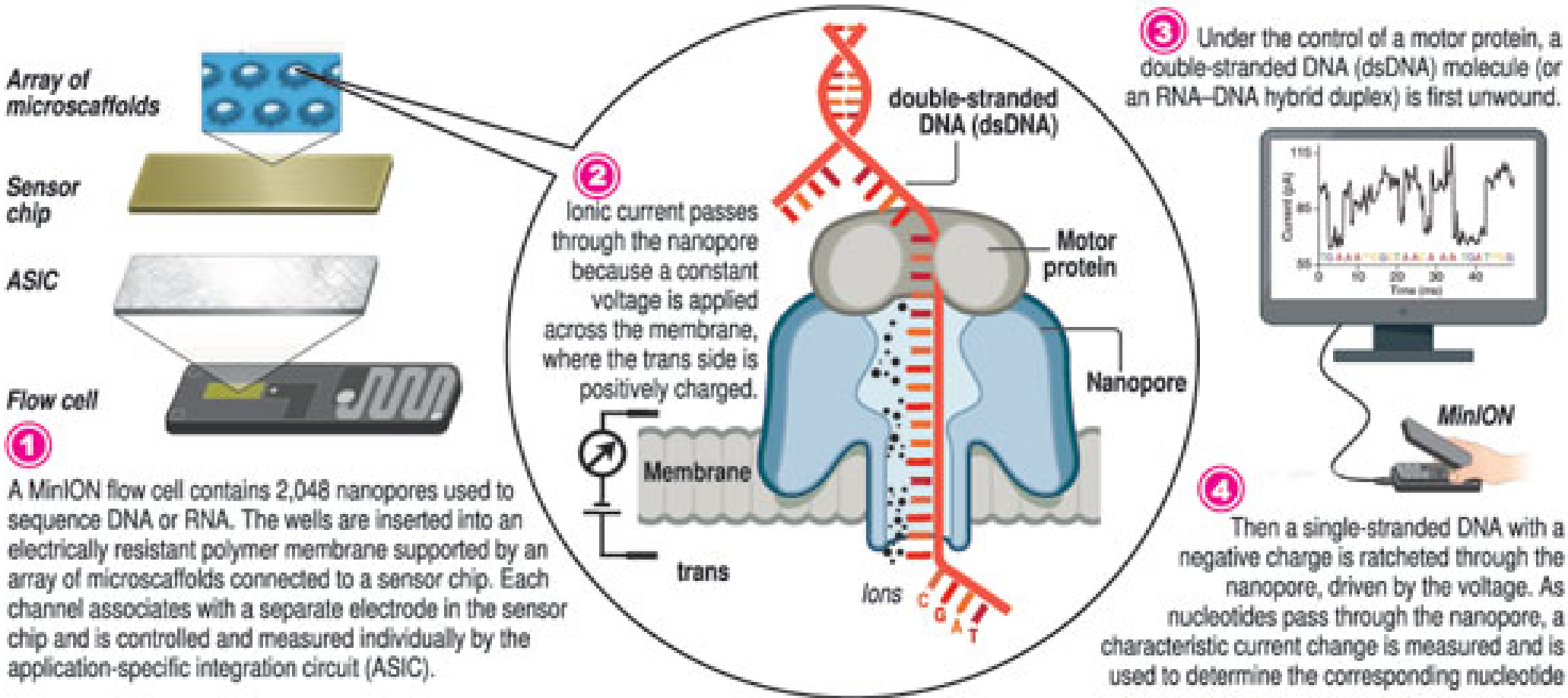
SEQUENCE
with flow cells & devices

Explore >

ANALYSE
your data

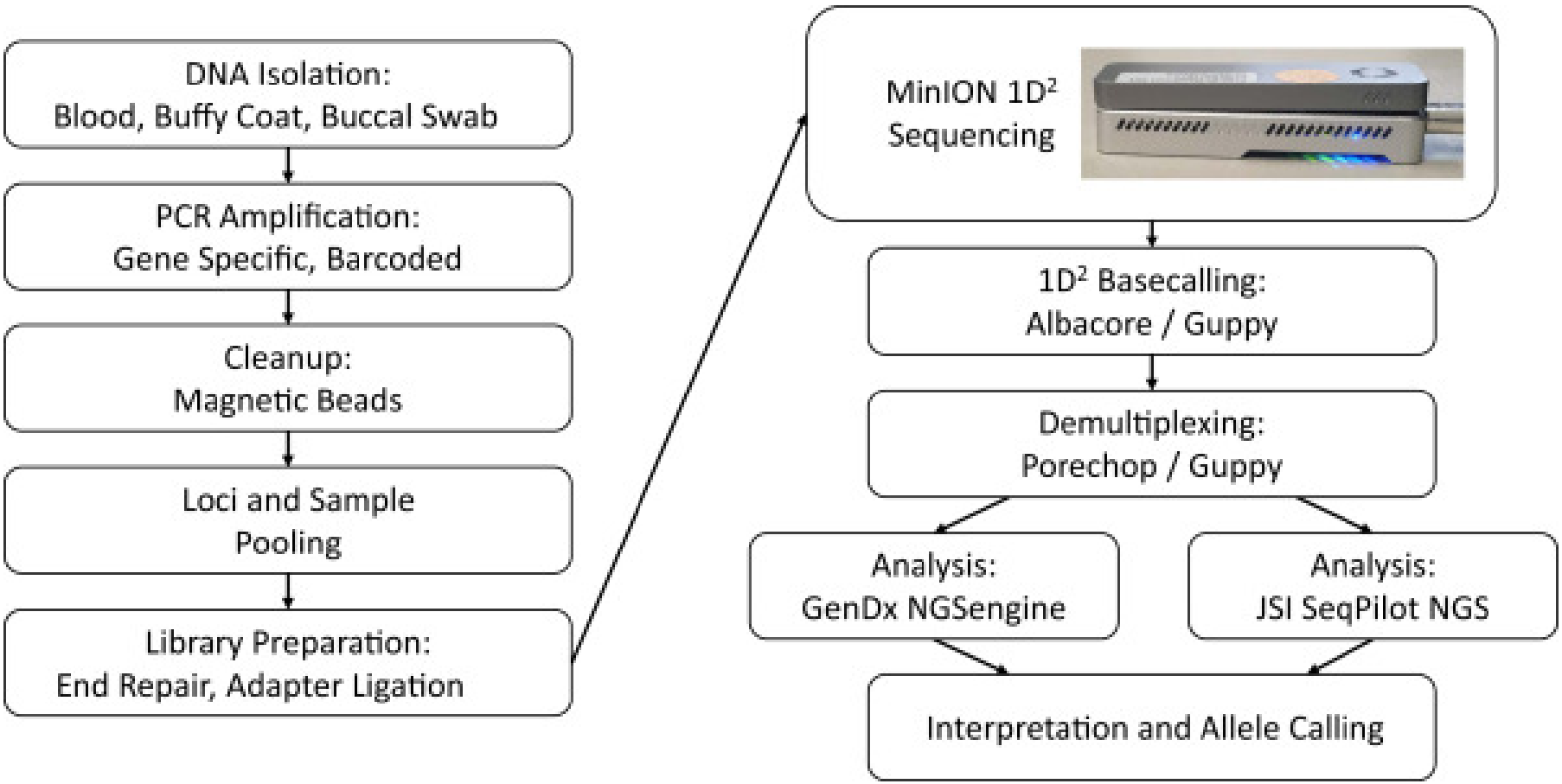
Explore >

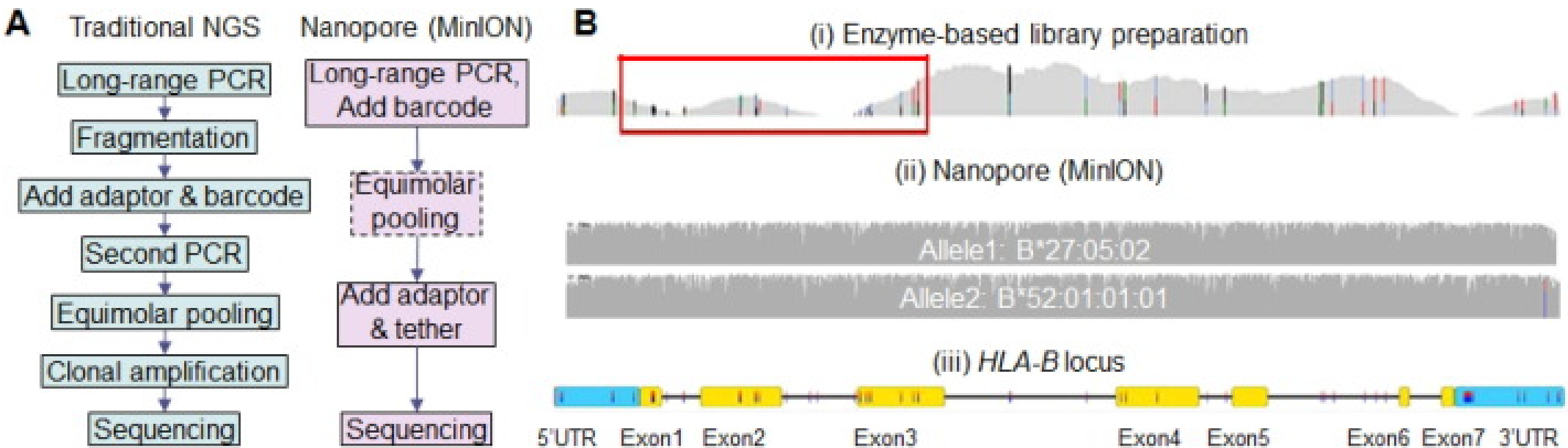

MinION
Size: W 105, H 23, D 33 mm
Weight: 87 g
(A)
SmidgION
(B)
GridION
Size: W 365 H 220 D 360 mm
Weight: 11 kg
(C)
PromethION
Size: W 440, H 400, D 240 mm
Weight: 40 kg
(D)


Array of microscaffolds
Sensor chip
ASIC
Flow cell
1
A MinION flow cell contains 2,048 nanopores used to sequence DNA or RNA. The wells are inserted into an electrically resistant polymer membrane supported by an array of microscaffolds connected to a sensor chip. Each channel associates with a separate electrode in the sensor chip and is controlled and measured individually by the application-specific integration circuit (ASIC).
2
Ionic current passes through the nanopore because a constant voltage is applied across the membrane, where the trans side is positively charged.
double-stranded DNA (dsDNA)
Motor protein
Nanopore
Membrane
trans
Ions
3
Under the control of a motor protein, a double-stranded DNA (dsDNA) molecule (or an RNA–DNA hybrid duplex) is first unwound.
MinION
4
Then a single-stranded DNA with a negative charge is ratcheted through the nanopore, driven by the voltage. As nucleotides pass through the nanopore, a characteristic current change is measured and is used to determine the corresponding nucleotide sequence.

OXFORD NANOPORE TECHNOLOGY

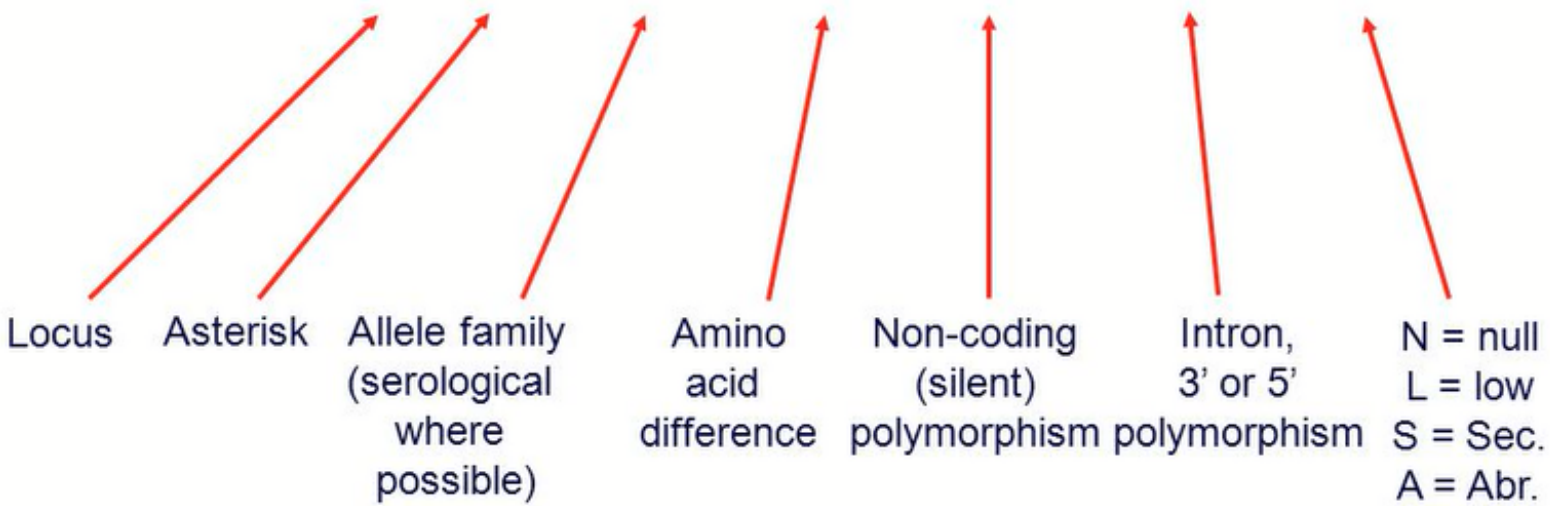
- Oxford Nanopore Technologies (Oxford, UK) utilize an engineered protein nanopore, alpha-haemolysin, adapted so that the identity of DNA bases can be ascertained as they pass through the nanopore by measuring variations in an ionic current passing through the pore.
- The company is developing two methods –'exonuclease' sequencing where individual bases are cleaved by the enzyme and passed through the nanopore in sequence and 'strand' sequencing where an ssDNA molecule is ratcheted through the nanopore by the enzyme


DNA Isolation:
Blood, Buffy Coat, Buccal Swab
PCR Amplification:
Gene Specific, Barcoded
Cleanup:
Magnetic Beads
Loci and Sample
Pooling
Library Preparation:
End Repair, Adapter Ligation
MinION 1D²
Sequencing
1D² Basecalling:
Albacore / Guppy
Demultiplexing:
Porechop / Guppy
Analysis:
GenDx NGSengine
Analysis:
JSI SeqPilot NGS
Interpretation and Allele Calling


A
Traditional NGS
Long-range PCR
Fragmentation
Add adaptor & barcode
Second PCR
Equimolar pooling
Clonal amplification
Sequencing
Nanopore (MinION)
Long-range PCR, Add barcode
Equimolar pooling
Add adaptor & tether
Sequencing
B
(i) Enzyme-based library preparation
(ii) Nanopore (MinION)
Allele1: B*27:05:02
Allele2: B*52:01:01:01
(iii) HLA-B locus
5'UTR
Exon1
Exon2
Exon3
Exon4
Exon5
Exon6
Exon7
3'UTR

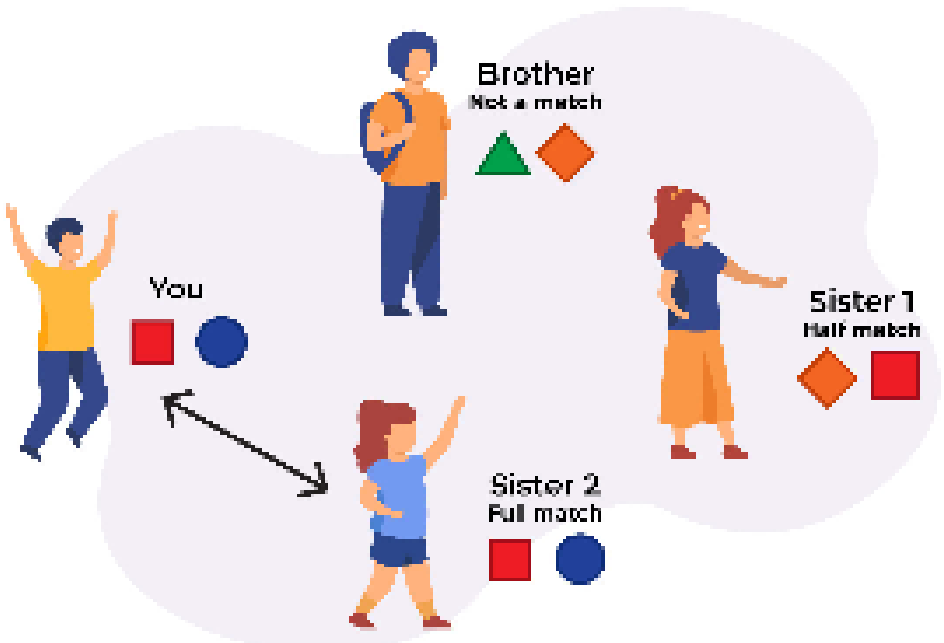
HLA Allele Nomenclature

HLA - A * 24 02 01 01
HLA - A * 24 02 01 02 L

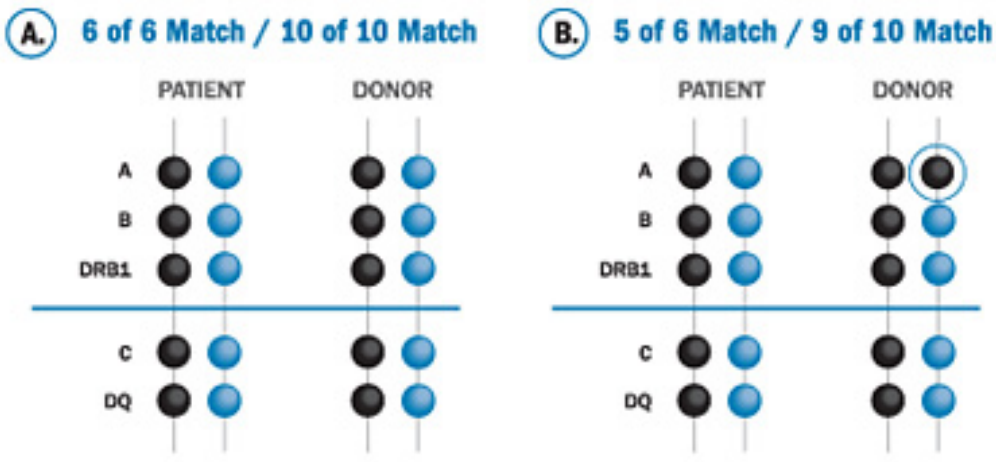


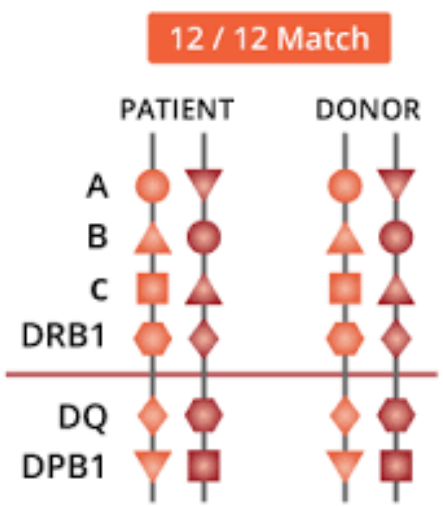
HLA MATCHING

BEST MATCHED DONOR

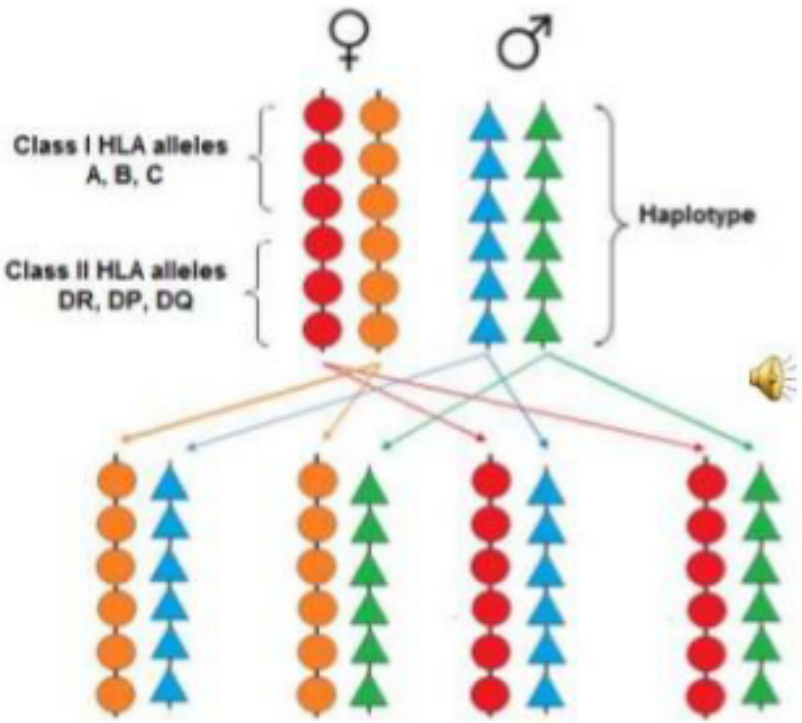


Related



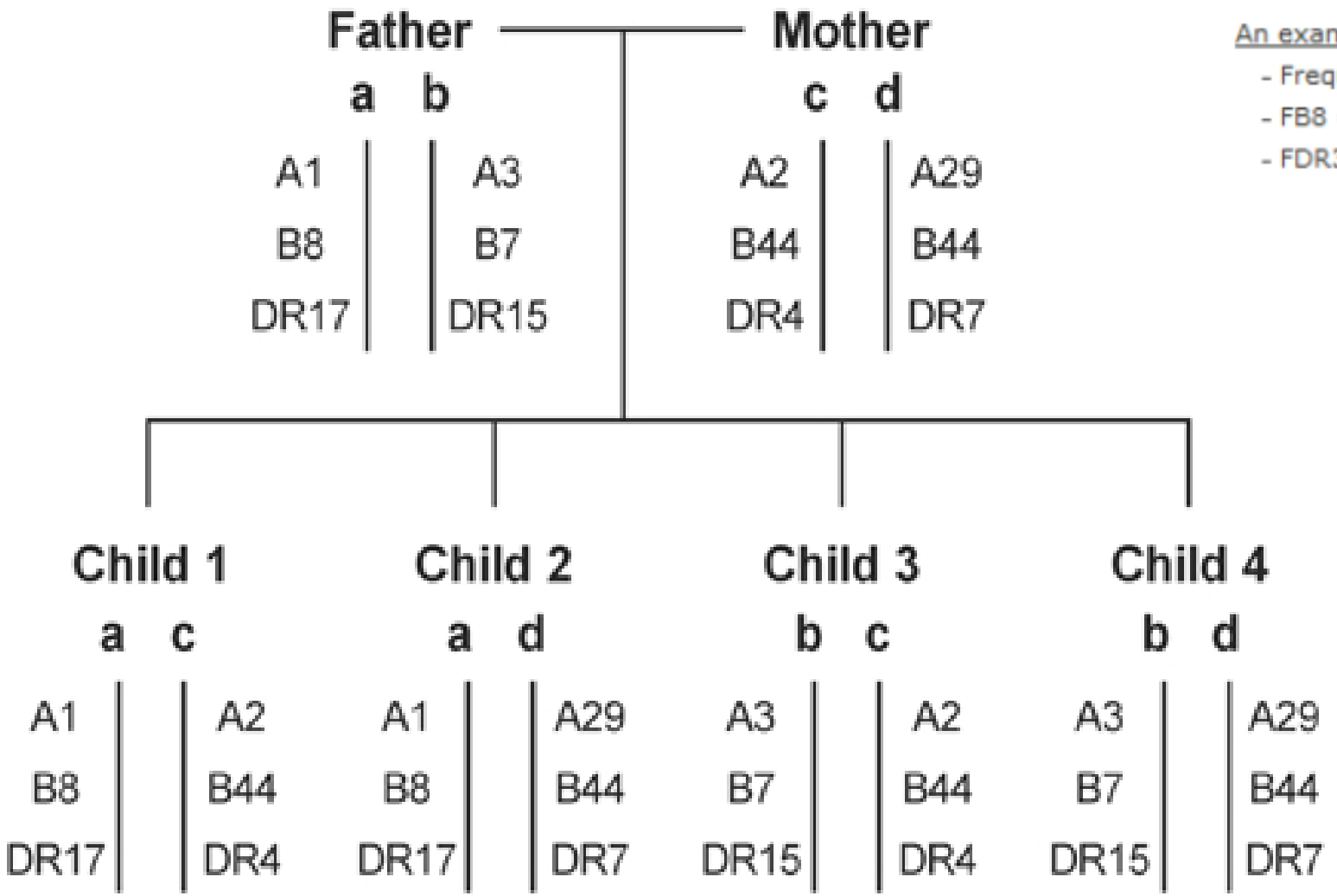


HLA inheritance and familial matching



- 'Haplotype': a combination of alleles at adjacent loci on a chromosome that are inherited together.
- Breeding between two heterozygous individuals results in children with 4 possible genotypes
- There is a 1 in 4 chance of a complete match between two siblings

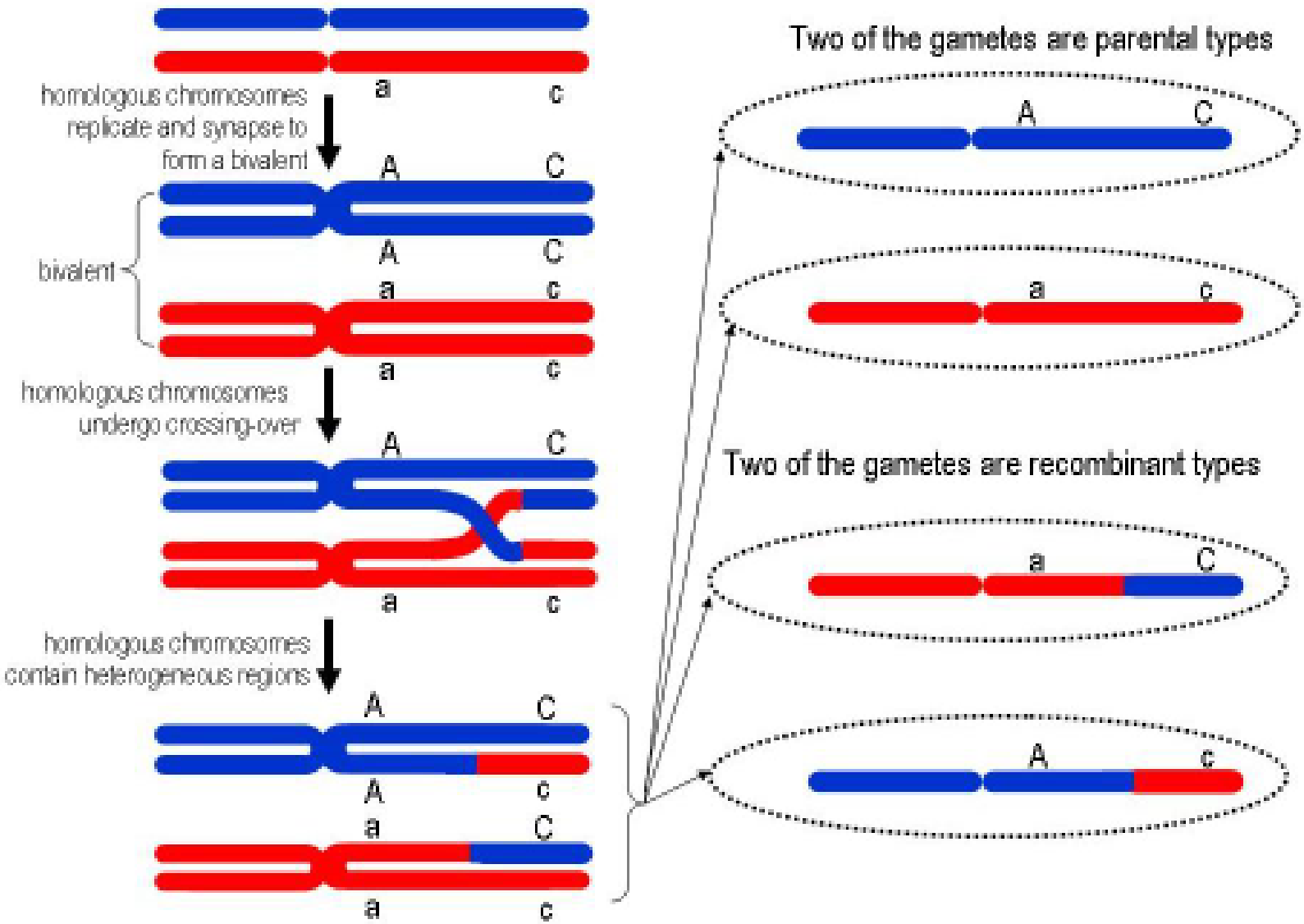
Linkage Disequilibrium



An example: Haplotype A1-B8-DR3

- Frequency of A1 (FA1) = 0.137
- FB8 = 0.103
- FDR3 = 0.11
  - $F_{expected}$ of A1-B8-DR3 = **0.0015**
  - $F_{observed}$ = **0.025**

RECOMBINATION (CROSSING OVER)



Classic HLA loci

High expression loci (HEL)

- A
- B
- C
- DRB1

Low expression loci (LEL)

- DRB3
- DRB4
- DRB5
- DQA1
- DQB1
- DDPA1
- DPB1

Matched sibling donors

- Primary low resolution typing for all available first degree relatives.
- Low or high resolution confirmatory typing of the patient and phenotypically matched donor based on HLA pedigree.
- In most cases high resolution typing is not needed.

Matched other related donors

- Typing of second degree relatives or beyond based on intra familial marriages.
- Low or high resolution confirmatory typing of the patient and phenotypically matched donor based on HLA pedigree.
- In most cases high resolution typing is needed.

Results

- Overall, outcomes for patients treated from a 1-antigen/allele mismatch related donor were significantly worse than from a MUD, primarily because of increased NRM.
- Overall survival (OS) rates at 3 years for 1-antigen/allele mismatched related donor and MUD transplant recipients were 19% and 45% (P =.007), and NRM rates were 40% and 26% (P =.05), respectively.
- Patients with class I mismatches appeared to have poorer OS than did patients with class II mismatches.
- A higher incidence of graft rejection was identified in the mismatched related donor group (P=.02).

An Apparently 8/8 But Really Haploidentical Donor

- Patient and his uncle:

A*02,*24; B*35,*51; C*04,*16; DRB1*11,*12

- High resolution HLA typing results:
- Patient: A*24:02:01 B*35:01 DRB1*11:04
- Uncle: A*24:02:01 B*35:02 DRB1*11:01

Split HLA Antigens

- A9: A23, A24
- A10: A25, A26, A34, A66
- A19: A29, A30, A31, A32, A33, A74
- A28: A68, A69
- B5: B51, B52
- B12: B44, B45
- B14: B64, B65
- B15: B62, B63, B75, B76, B77
- B16: B38, B39
- B17: B57, B58
- B21: B49, B50
- B22: B54, B55, B56
- B40: B60, B61
- B70: B71, B72

Linkage Disequilibrium/ Haplotypes

- LD: Alleles occur together with a greater frequency than would be expected by chance
  - B/C strong, DR/DQ strong, A less strong, DP weak
  - e.g. B*0801 - 99% will be Cw*0701
  - But B*1801 either Cw*0501, *0701
  - e.g DRB1*1501 - will be DQB1*0602
  - But DRB1*0401 either Cw*0301, *0302
- Haplotype: A group of genes inherited together
  - e.g. A*0101,B*0801,Cw*0701,DRB1*0301,DQB1*0201

Example

- Patient:
  - A*0201, B*1801, DRB1*0401

- Finding a donor:
  - Less strong LD - therefore ‘ NOT predictable’ i.e. equal chance of C being *0701, *0501, *1203; DQB1 50/50 chance of *0301, *0302
  - At low resolution (A2, B18, DRB4) unable to predict this will match

G CODES FOR REPORTING OF AMBIGUOUS ALLELE TYPING

- HLA alleles that have 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*02:01:01G

- A*02:01:01:01/A*02:01:01:02L/A*02:01:01:03/A*02:01:01:04/A*02:01:01:05/A*02:01:01:06/A*02:01:01:07/A*02:01:01:08/A*02:01:01:09/A*02:01:01:10/A*02:01:01:11/A*02:01:01:12/A*02:01:01:13/A*02:01:01:14/A*02:01:01:15/A*02:01:01:16/A*02:01:01:17/A*02:01:01:18/A*02:01:01:19/A*02:01:01:20/A*02:01:01:21/A*02:01:01:22/A*02:01:01:23/A*02:01:01:24/A*02:01:01:25/A*02:01:01:26/A*02:01:01:27/A*02:01:01:28/A*02:01:01:29/A*02:01:01:30/A*02:01:01:31/A*02:01:01:32/A*02:01:01:33/A*02:01:01:34/A*02:01:01:35/A*02:01:01:36/A*02:01:01:37/A*02:01:01:38/A*02:01:01:39/A*02:01:01:40/A*02:01:01:41/A*02:01:01:42/A*02:01:01:43/A*02:01:01:44/A*02:01:01:45/A*02:01:01:46/A*02:01:01:47/A*02:01:01:48/A*02:01:01:49/A*02:01:01:50/A*02:01:01:51/A*02:01:01:52/A*02:01:01:53/A*02:01:01:54/A*02:01:01:55/A*02:01:01:56/A*02:01:01:57/A*02:01:01:58/A*02:01:01:59/A*02:01:01:60/A*02:01:01:61/A*02:01:01:62/A*02:01:01:63/A*02:01:01:64/A*02:01:01:65/A*02:01:01:66/A*02:01:01:67/A*02:01:01:68/A*02:01:01:69/A*02:01:01:70/A*02:01:01:71/A*02:01:01:72/A*02:01:01:73/A*02:01:01:74/A*02:01:01:75/A*02:01:01:76/A*02:01:01:77/A*02:01:01:78/A*02:01:01:79/A*02:01:01:80/A*02:01:01:81/A*02:01:01:82/A*02:01:01:83/A*02:01:01:84/A*02:01:01:85/A*02:01:01:86/A*02:01:01:87/A*02:01:01:88/A*02:01:01:89/A*02:01:01:90/A*02:01:01:91/A*02:01:01:92/A*02:01:01:93/A*02:01:01:94/A*02:01:01:95/A*02:01:01:96/A*02:01:01:97/A*02:01:01:98/A*02:01:01:99/A*02:01:01:100/A*02:01:01:101/A*02:01:01:102/A*02:01:01:103/A*02:01:01:104/A*02:01:01:105/A*02:01:01:106/A*02:01:01:107/A*02:01:01:108/A*02:01:01:109/A*02:01:01:110/A*02:01:01:111/A*02:01:01:112/A*02:01:01:113/A*02:01:01:114/A*02:01:01:115/A*02:01:01:116/A*02:01:01:117/A*02:01:01:118/A*02:01:01:119/A*02:01:01:120/A*02:01:01:121/A*02:01:01:122/A*02:01:01:123/A*02:01:01:124/A*02:01:01:125/A*02:01:01:126/A*02:01:01:127/A*02:01:01:128/A*02:01:01:129/A*02:01:01:130/A*02:01:01:131/A*02:01:01:132/A*02:01:01:133/A*02:01:01:134Q/A*02:01:01:135/A*02:01:01:136/A*02:01:01:137/A*02:01:01:138/A*02:01:01:139/A*02:01:01:140/A*02:01:01:141/A*02:01:01:142/A*02:01:01:143/A*02:01:01:144/A*02:01:01:145/A*02:01:01:146/A*02:01:01:147/A*02:01:01:148/A*02:01:01:149/A*02:01:01:150/A*02:01:01:151/A*02:01:01:152/A*02:01:01:153/A*02:01:01:154/A*02:01:01:155/A*02:01:01:156/A*02:01:01:157/A*02:01:01:158/A*02:01:01:159/A*02:01:01:160/A*02:01:01:161/A*02:01:01:162/A*02:01:01:163/A*02:01:01:164/A*02:01:01:165/A*02:01:01:166/A*02:01:01:167/A*02:01:01:168/A*02:01:01:169/A*02:01:01:170/A*02:01:01:171/A*02:01:01:172/A*02:01:01:173/A*02:01:01:174/A*02:01:01:175/A*02:01:01:176/A*02:01:01:177/A*02:01:01:178/A*02:01:01:179/A*02:01:01:180/A*02:01:01:181/A*02:01:01:182/A*02:01:01:183/A*02:01:01:184/A*02:01:01:185/A*02:01:01:186/A*02:01:01:187/A*02:01:01:188/A*02:01:01:189/A*02:01:01:190/A*02:01:01:191/A*02:01:01:192/A*02:01:01:193/A*02:01:01:194/A*02:01:01:195/A*02:01:01:196/A*02:01:01:197/A*02:01:01:198/A*02:01:01:199/A*02:01:01:200/A*02:01:01:201/A*02:01:01:202/A*02:01:01:203/A*02:01:01:204/A*02:01:01:205/A*02:01:01:206/A*02:01:01:207/A*02:01:01:208/A*02:01:01:209/A*02:01:01:210/A*02:01:01:211/A*02:01:01:212/A*02:01:01:213/A*02:01:01:214/A*02:01:01:215/A*02:01:01:216/A*02:01:01:217/A*02:01:01:218/A*02:01:01:219/A*02:01:01:220/A*02:01:01:221/A*02:01:01:222/A*02:01:01:223/A*02:01:01:224/A*02:01:01:225/A*02:01:01:226/A*02:01:01:227/A*02:01:01:228/A*02:01:01:229/A*02:01:01:230/A*02:01:01:231/A*02:01:01:232/A*02:01:01:233/A*02:01:01:234/A*02:01:01:235/A*02:01:01:236/A*02:01:01:237/A*02:01:01:238/A*02:01:01:239/A*02:01:01:240/A*02:01:01:241/A*02:01:01:242/A*02:01:01:243/A*02:01:01:244/A*02:01:01:245/A*02:01:01:246/A*02:01:01:247/A*02:01:01:248/A*02:01:11/A*02:01:14Q/A*02:01:15/A*02:01:21/A*02:01:48/A*02:01:50/A*02:01:79/A*02:01:80/A*02:01:89/A*02:01:97/A*02:01:98/A*02:01:99/A*02:01:104/A*02:01:130/A*02:01:131/A*02:01:132/A*02:01:133/A*02:01:134/A*02:01:135/A*02:01:136/A*02:01:143/A*02:01:148/A*02:01:149/A*02:01:151/A*02:01:154/A*02:01:156/A*02:01:159/A*02:01:160/A*02:01:161/A*02:01:163/A*02:01:164/A*02:01:166/A*02:01:167/A*02:01:168/A*02:01:169/A*02:01:170/A*02:01:181/A*02:01:182/A*02:01:183/A*02:01:184/A*02:01:185/A*02:01:186/A*02:01:188/A*02:01:191/A*02:01:192/A*02:01:193/A*02:01:194/A*02:01:195/A*02:01:196/A*02:01:197/A*02:01:198/A*02:01:199/A*02:01:200/A*02:01:201/A*02:01:202/A*02:01:203/A*02:01:204/A*02:01:205/A*02:01:206/A*02:01:208/A*02:01:209/A*02:01:211/A*02:01:213/A*02:01:215/A*02:09:01:01/A*02:09:01:02/A*02:09:01:03/A*02:09:01:04/A*02:43N/A*02:66/A*02:75/A*02:83N/A*02:89:01/A*02:89:02/A*02:97:01/A*02:97:02/A*02:132/A*02:134/A*02:140/A*02:241/A*02:252/A*02:256/A*02:266/A*02:291/A*02:294/A*02:305N/A*02:327/A*02:329/A*02:356N/A*02:357/A*02:397/A*02:411/A*02:446/A*02:455/A*02:469/A*02:481/A*02:538/A*02:559/A*02:607/A*02:608N/A*02:614/A*02:629/A*02:642/A*02:665/A*02:675N/A*02:685/A*02:686/A*02:687/A*02:689/A*02:690/A*02:691N/A*02:692/A*02:704/A*02:716/A*02:719/A*02:720/A*02:722/A*02:724/A*02:726/A*02:739/A*02:740/A*02:742/A*02:744/A*02:753/A*02:755/A*02:761/A*02:762/A*02:763/A*02:765/A*02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HLA-A		HLA-B		HLA-C		HLA-DRB1		HLA-DRB345		HLA-DQB1		HLA-DPB1	
A*01:04N*	WD	B*07:67N	WD	C*02:38N	WD	DRB1*07:10N	WD	DRB4*01:03:01:02N*	WD	DQB1*02:18N	WD	DPB1*61:01N	WD
A*01:15N	WD	B*07:181N	WD	C*02:92N	WD	DRB1*07:26N	WD	DRB4*01:16N	WD	DQB1*02:20N	WD	DPB1*64:01N	WD
A*01:16N	WD	B*14:07N	WD	C*04:09N*	I	DRB1*12:24N	WD	DRB4*02:01N	WD	DQB1*03:118N	WD	DPB1*120:01N	WD
A*01:57N	WD	B*15:01:01:02N*	WD	C*04:93N	WD			DRB4*03:01N	WD	DQB1*06:26N	WD	DPB1*154:01N	WD
A*01:123N	WD	B*15:79N	WD	C*04:95N	WD			DRB5*01:08N*	WD	DQB1*06:75N	WD	DPB1*161:01N	WD
A*02:53N	WD	B*15:181N	WD	C*05:07N	I			DRB5*01:10N	WD	DQB1*06:77N	WD	DPB1*218:01N	WD
A*02:83N*	WD	B*15:190N	WD	C*05:99N	WD					DQB1*06:144N	WD	DPB1*357:01N	WD
A*02:94N	WD	B*35:165N	WD	C*06:16N	WD							DPB1*570:01N	WD
A*02:113N	WD	B*37:03N	WD	C*06:79N	WD								
A*02:125N	WD	B*37:42N	WD	C*07:32N	WD								
A*02:227N	WD	B*39:40N	WD	C*07:33N	WD								
A*02:514N	WD	B*40:22N	WD	C*07:55N	WD								
A*03:21N*	WD	B*40:142N	WD	C*07:61N	WD								
A*11:21N*	WD	B*40:155N*	WD	C*07:104N	WD								
A*11:109N	WD	B*44:23N	WD	C*07:198N	WD								
A*23:11N	WD	B*51:11N*	WD	C*07:227N	WD								
A*23:19N	WD			C*07:452N	WD								
A*24:09N*	WD			C*08:127N	WD								
A*24:11N*	WD			C*15:122N	WD								
A*24:36N	WD			C*16:30N	WD								
A*24:84N	WD												
A*24:90N	WD												
A*24:252N	WD												
A*25:12N	WD												
A*30:70N	WD												
A*30:78N	WD												
A*31:14N*	WD												
A*31:60N	WD												
A*32:27N	WD												
A*32:45N	WD												
A*34:10N	WD												
A*68:18N	WD												

HLA disease association

Panel #	Disease or Hypersensitivity	Page #	Associated HLA Allele
1	Abacavir Hypersensitivity	3	HLA B*57:01
2	Allopurinol Hypersensitivity	4	HLA B*58:01
3	Spondyloarthropathies (Ankylosing Spondylitis,Reactive Arthritis, Juvenile Arthritis)	7	HLA-B27
4	Eye Disease HLA Association (Acute Anterior UveitisHLA-B27, Behçet's Disease HLA-B51, Birdshot chorioretinopathy HLA-A29)	11	HLA-B27 HLA-B51, HLA-A29
5	Carbamazepine Hypersensitivity	16	HLA-B*15:02, HLA-A*31:01
6	Celiac Disease (Celiac Genetics)	18	HLA-DQA1 and HLA-DQB1associated alleles and DQ2/DQ8 heterodimers
7	Narcolepsy	24	HLA-DQB1*06:02, DQA1*01:02
8	Pediatric Acute-onset Neuropsychiatric Syndrome(PANS)	27	HLA-B38, HLA-B5, HLA-B51, HLA-B52, HLA B27, HLA-Bw4
9	Psoriasis	29	HLA-B27, HLA-Cw6
10	IL-1 and IL-6 inhibitors Hypersensitivity	32	HLA-DRB1*15:01, HLA-DRB5*01:01 HLA-DQB1*06:02, HLA-DQA1*01:02,

مرکز پذیره نویسی اهداکنندگان سلولهای بنیادی و بانک HLA

مرکز تحقیقات ایمونولوژی، آسم و آلرژی

11. تهران، مرکز پذیره نویسی اهداکنندگان سلولهای بنیادی خونساز مرکز تحقیقات ایمونولوژی، آسم و آلرژی، مرکز طبی کودکان دانشگاه علوم پزشکی تهران

تهران، انتهای بلوار کشاورز خیابان دکترقریب، بیمارستان مرکز طبی کودکان، ساختمان شماره3، طبقه 4.

۰۲۱-۶۶۹۳۵۸۵۵،۰۲۱۶۶۹۰۷۴۱۵


خروج
تغییر رمز
مریم نوری زاده
صفحه اصلی
مراکز
جستجو
مرکز تحقیقات ایمونولوژی، آسم و آلرژی دانشگاه علوم پزشکی تهران
صفحه اصلی
پذیرش
لیست پذیرش
درخواست جستجو
درخواستها
لیست پذیرش
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011 1397/1/21
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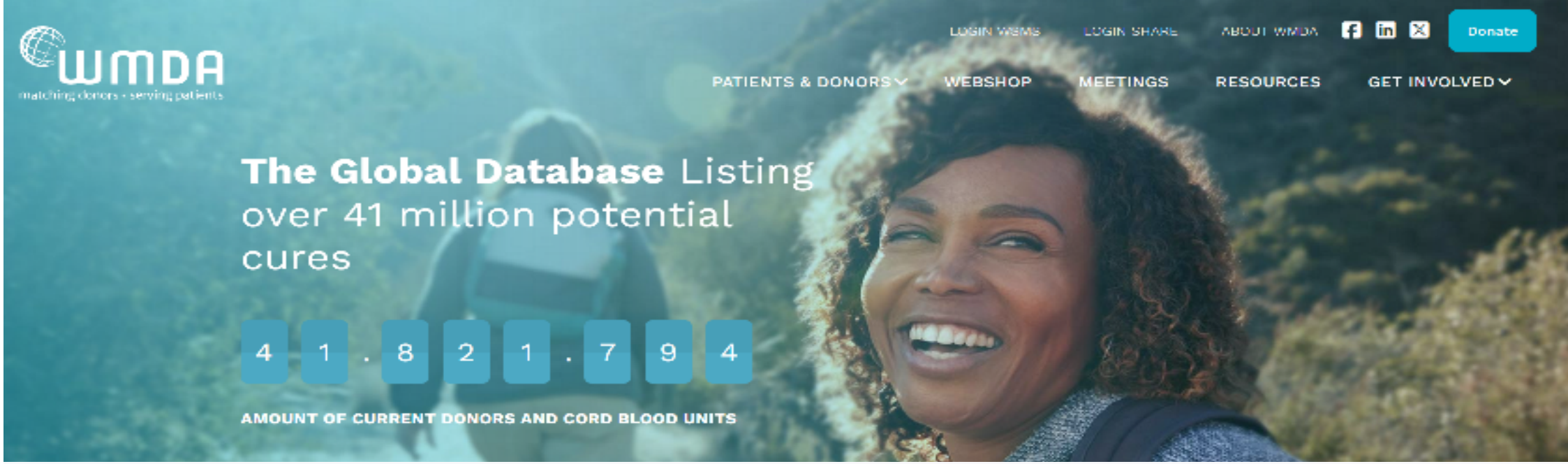
013 1397/1/21
014 1397/1/21
015 1397/1/21
016 1397/1/21
017
018 1397/1/21

جمهوری اسلامی ایران
وزارت بهداشت، درمان و آموزش پزشکی

شبکه ملی اهداکنندگان سلول های بنیادی خونساز ایران

Iranian National Stem Cell Donor Network

صفحه اصلی | درباره ما | گالری | متخصصین | اهداکنندگان | بیماران | حامیان و خیرین



ZKRD Zentrales Knochenmarkspender-Register Deutschland

ZKRD | Stem cell donation | Finding a donor | News

... from A for orders and billing to K for coordination, T for transport and Z for customs clearance make us a competent partner with a lot of know-how in the search for the most suitable donor for all patients worldwide.

Donor registration

German donor centers

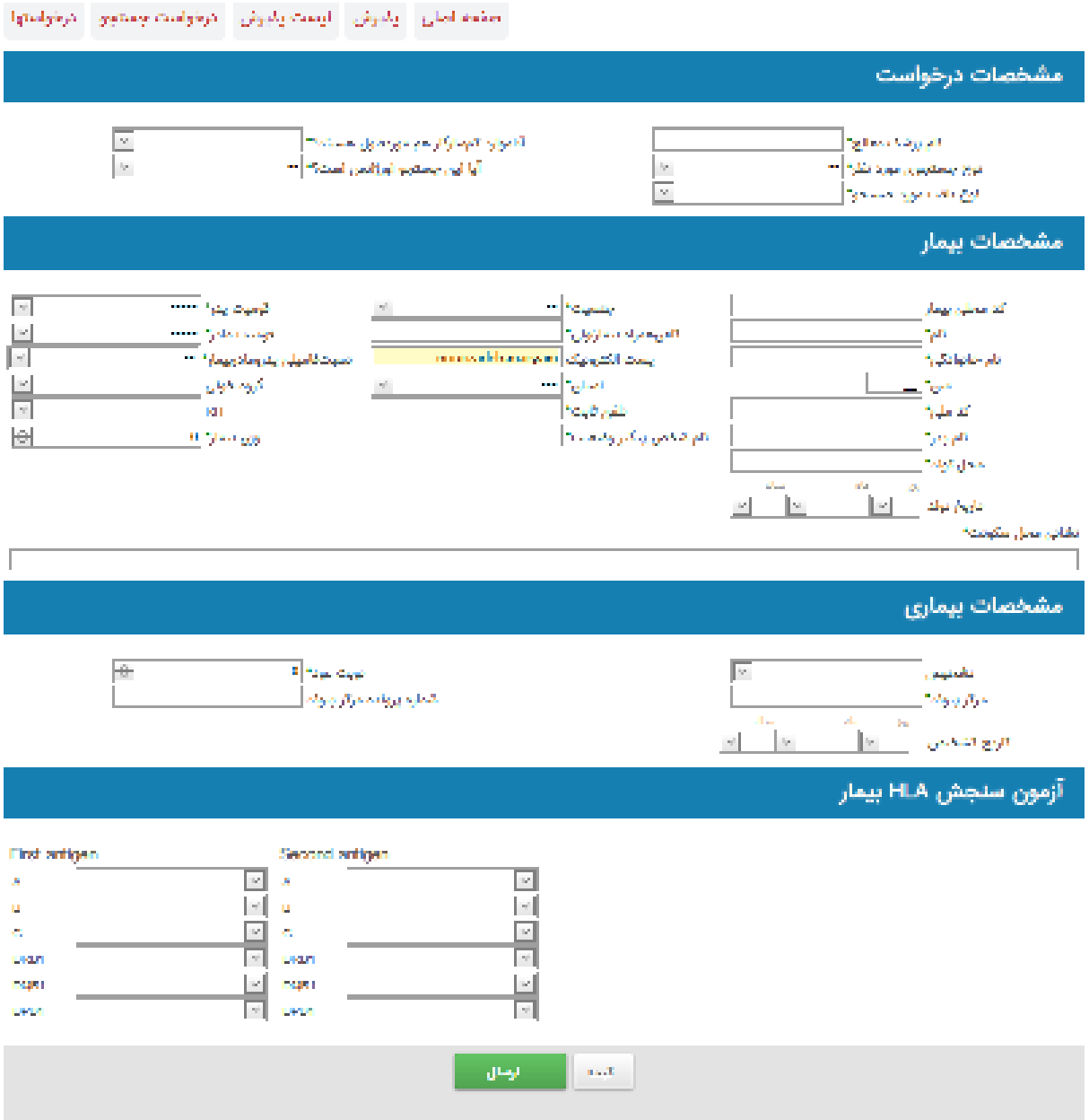
Current donor numbers: 10.254.730

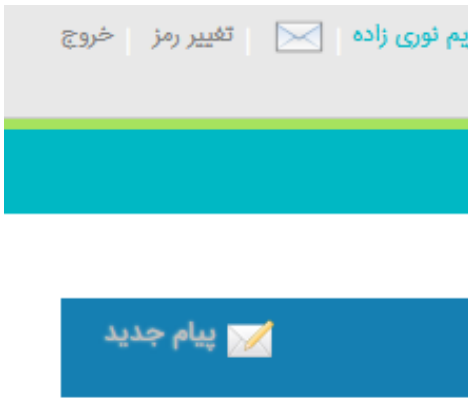
Support us

ZKRD for professionals

وبسایت

ماز ایران





بازگشت | چاپ

Search Report

Search ID: 20189
Search Date: 1402/12/14 12:56:33
Type: ALL

نام: [illegible]
کدملی: [illegible]

	Patient / Donor Sex Age BG Rh CMV Status CCR5	A 01:01:01 02:05:01	B 14:02:01 15:17:01	C 07:01:02 08:02:01	DRB1 01:07:01 13:03:01	DQB1 05:01:01 05:05:01	DPB1 04:01:01 47:01
10/10 Match Grade							
1	INSC002000125109 M 34	01 07	14 15		01 13		
9/10 Match Grade							
2	INSC002000124980 M 30	01 31	14 15		01 13		
3	INSC055000074203 M 30	01 02	14 15		01 15		
4	INSC002000154481 M 31	01 07	14 39		01 13		
5	INSC055000133430 M 37	01 33	14 15		01 13		
6	INSC005000099190 F 31	01:XX 31:XX	14:XX 15:XX		01:XX 13:XX		
7	INSC002000152451 M 33	01 66	14 15		01 13		
8	INSC002000154273 M 36	01 33	14 15		01 13		
9	INSC002000151565 M 37	01 31	14 15		01 13		
10	INSC002000156920 M 37	01 02	14 15		01 11		
11	INSC002000124501 M 38	02 01	14 15		01 13		
12	INSC055000112109 M 39	01:XX 33:XX	14:XX 15:XX		01:XX 13:XX		

مراحل بعدی:

- ارسال درخواست پیگیری اهدا کننده سازگار از وزارت بهداشت
- تماس با اهدا کننده(گان) سازگار ثبت شده در مرکز پذیره نویسی مرکز IAARI برای مراجعه ایشان به منظور انجام تستهای تاییدی و تکمیلی (نیاز به پیگیری های مکرر و برنامه ریزی دقیق دارد، خصوصا در زمانیکه بایستی تست کراس مچ انجام شود)
- پیگیری نامه نگاری ها با بخش پیوند و بیمارستان
- پیگیری مسایل مالی و دریافت ارز دولتی و راهنمایی بیماران در این خصوص (فعلا ارز دولتی لغو شده است)
- پیگیری وضعیت بیماران

محدودیت ها و موانع پیش رو در مرکز پذیره نویسی:

- عدم اطلاع رسانی کافی در مورد اهدا و پیوند سلولهای بنیادی به ویژه در مناطق بدون مراکز پذیره نویسی
- عدم تامین منابع مالی به منظور تهیه کیت و مواد لازم برای انجام HLA Typing برای اهداکننده گان
- گران بودن تست HLA Typing به ویژه نوع High Resolution که بیمه به آن تعلق نمیگیرد
- عدم حمایت نهادهای دولتی به ویژه وزارت بهداشت از بیماران در قبال تهیه کیت HLA Typing High Resolution با نرخ دولتی
- عدم تامین ارز دولتی کافی به منظور سلولگیری و انتقال آن ازاهداکنندگان خارجی
- به روز نبودن اطلاعات مربوط به اهداکنندگان داخلی در سایت مربوط به وزارت بهداشت
- عدم برنامه ریزی درست در مورد ساماندهی مراکز پذیره نویسی به منظور استفاده مراکز از سیستم اتوماسیون مراکز درمانی در جهت هماهنگی های بیشتر بین بخش های درگیر در پیوند
- عدم امکان انجام سرچ بانکهای جهانی در مراکز پذیره نویسی و انباشت درخواستها در شبکه ملی و در نتیجه تاخیر در ارائه نتیجه سرچ به بیماران