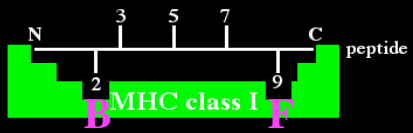
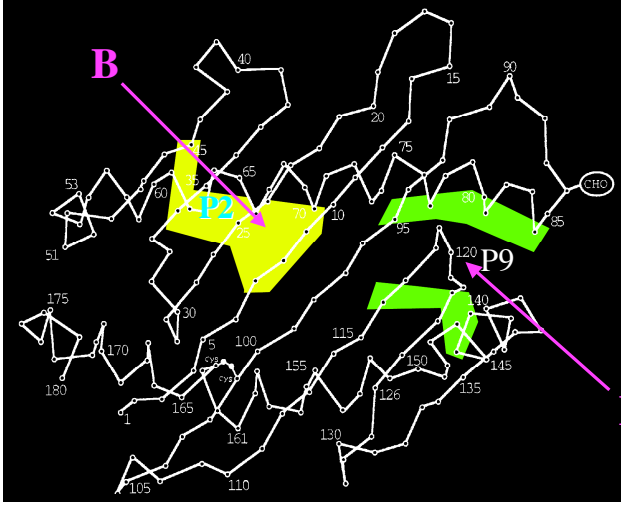
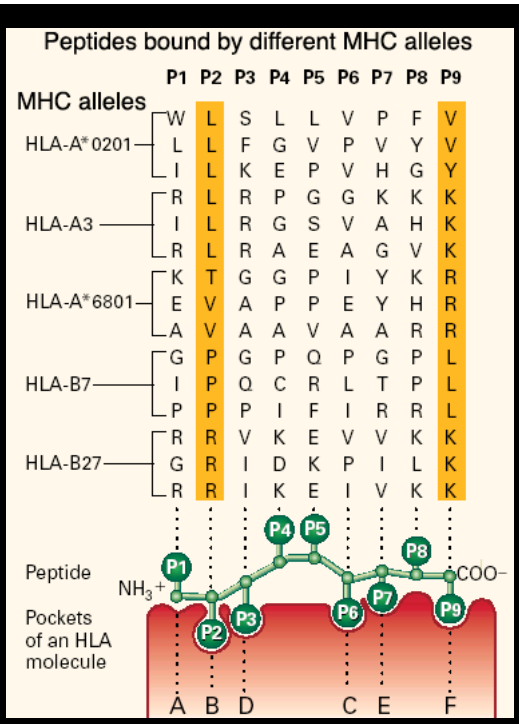
Different MHC alleles confer different functional properties on the adaptive immune system by specifying molecules that have different peptide binding abilities

Location of MHC class I pockets termed "B" and "F" that bind P2 and P9 amino acid side chains of the peptide





Amino acids of the MHC molecule that form the B and F pockets confer the main specificity for binding peptides through complementary interactions with amino acids at position P2 and P9 in the peptide



Key Concept

The difference in amino acid sequence around the peptide binding pockets of various allelic forms of MHC class I molecules confer the property of binding completely different self or non-self peptides

MHC alleles regulate immune responsiveness by influencing the number of peptides in a protein that can be recognized (Example HIV envelope protein)

Allele:	**HLA-B*27052**	**HLA-B*3501**	**HLA-B*0702**
Motif	XRXXXXXX[KRYL]	XPXXXXXXY	XPXXXXXXL

Peptides able to bind each allelic HLA molecule

IRGKVQKEY	KRRVVQREK	DPNPQEVVL
IRPVVSTQL	ARILAVERY	KPCVKLTPL
TRPNNNTRK	ERDRDRSIR	RPVVSTQLL
IRIQRGPGR	LRSLCLFSY	SPLSFQTHL
SRAKWNNTL	TRIVELLGR	IPRRIRQGL
LREQFGNNK	CRAIRHIPR	
FRPGGGDMR	IRQGLERIL	
WRSELYKYK		
# of peptides	**15**	**0**	**5**

What peptides are found in MHC molecules?

•Elution of peptides from MHC molecules reveals that class I molecules typically bind 2000-10,000 different peptides per cell

•Each of these peptides has a dominant motif reflecting the relatively conserved anchor residues, e.g. for HLA-B27

Motif XRXXXXXX[KRYL]

•Most peptides are fragments of conventional cell proteins, e.g.

```
HRAQVIYTR 40S ribosomal protein
RRIKEIVKK Heat shock protein 89
ARLFGIRAK Breast basic conserved protein
RRFFPYYVY Proteasome subunit C5
GRWPGSSLY Lamin B receptor
```

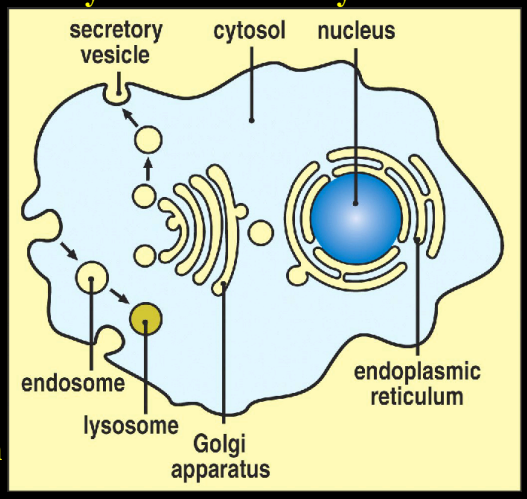
•Even the most abundant peptide species accounts for only 1% of the total peptides bound, so the T cell has its work cut out

How do peptides get loaded onto the proper kind of MHC molecule?

How do cytosolic peptides from virally infected cells get loaded only on class I, but not class II molecules, to trigger killing by CD8T cells?

How do peptides from endocytosed proteins get loaded on class II, but not class I molecules, to elicit macrophage activation and B cell help?

Class I peptide loading from peptides synthesized in the cytosol

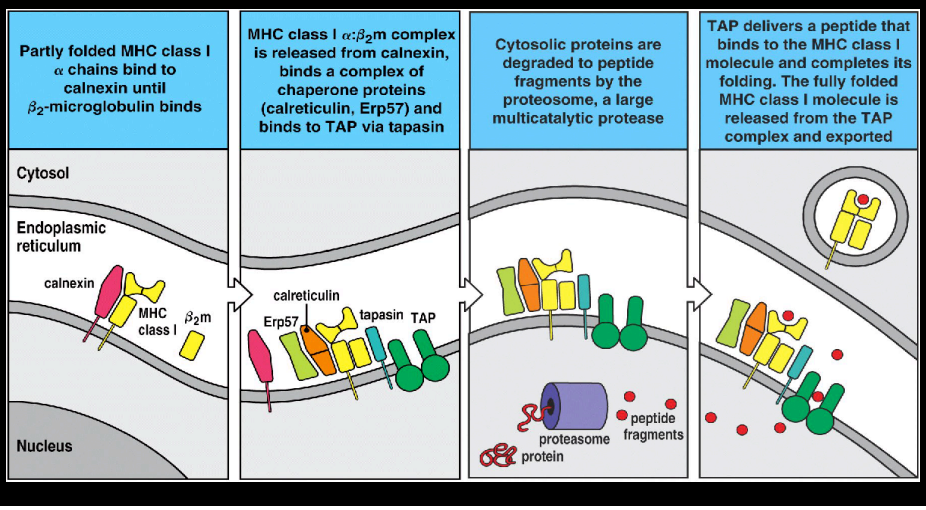


Class II peptide loading from peptides produced by lysosomal degradation of endocytosed organism

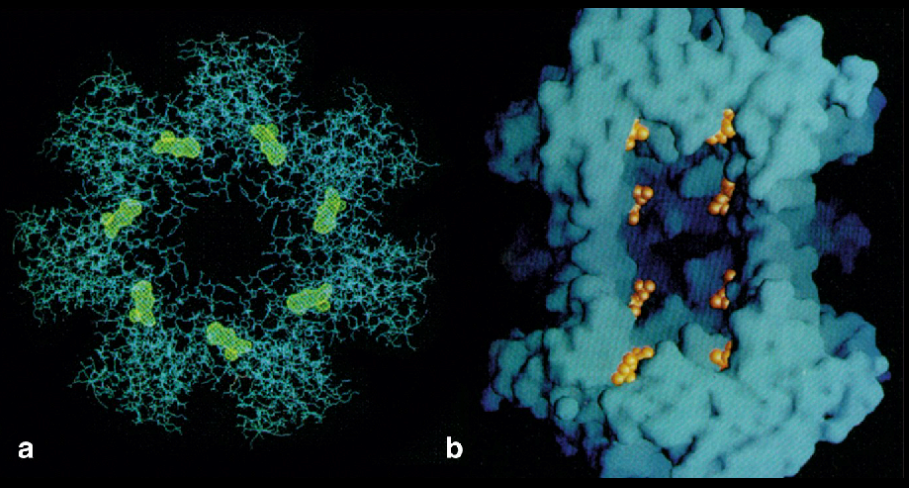
The endocytic and synthetic pathways are usually quite separate

Loading class I MHC molecules with cytosolic peptides

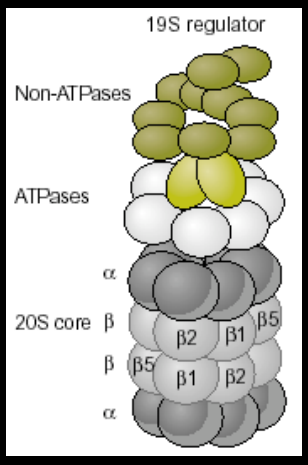
MHC class I molecules are synthesized and bind peptides derived from cytosolic molecules during assembly within the ER



Proteosome- digests ubiquitin-tagged cytosolic proteins



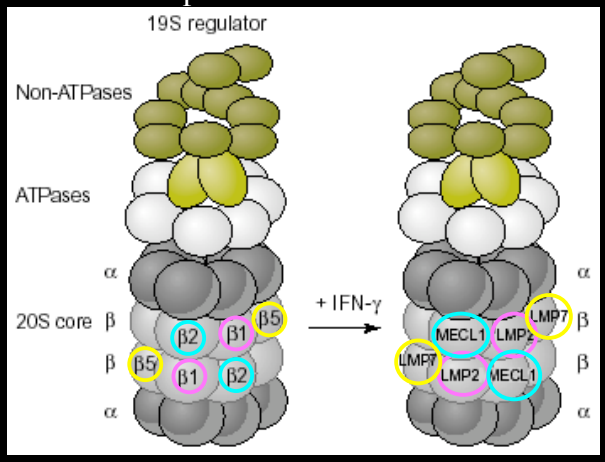
The proteasome is composed of the proteasome catalytic core and regulatory complexes that bind and unfold ubiquitinylated substrates



3 of the 7 subunits in each ring of the 20s core confer the proteolytic activity

Peptide processing changes in an immune response:

IFN-γ, made by NK, CD8 and some CD4 T cells, upregulates the synthesis of three new proteasome immunosubunits



LMP2, LMP7 and MECL-1 replace the constitutive β1, β5 and β2 subunits, and change proteasome specificity to make hydrophobic peptides with greater affinity for MHC pockets

Production of 9 AA peptides for class I MHC

The proteasome makes precise cuts only at the C termini of the peptides

Other peptidases, some in the e.r., nibble back the N termini until the peptide fits exactly, e.g. the IFN-γ-inducible leucine aminopeptidase (LAP)

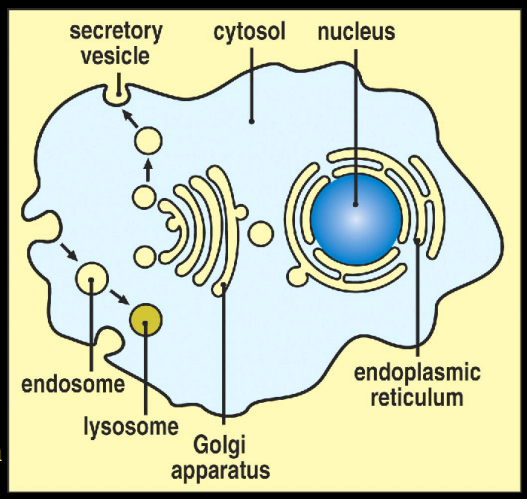
The peptide production system is not coordinated with the peptide binding specificity of the individual's MHC class I molecules

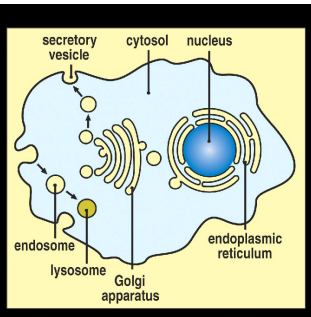
Peptide and β_2 microglobulin subunit are required to stabilize the MHC class I molecule

Empty MHC class I molecules are unstable

This prevents "friendly fire" killing of bystander cells by the uptake of random peptides by empty MHC molecules

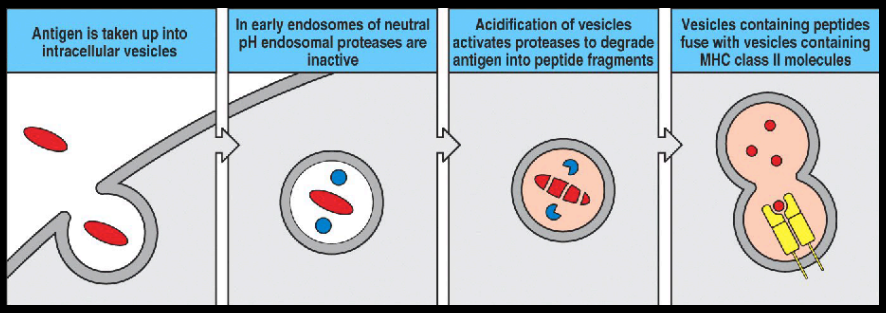
Class II peptide loading from peptides produced by lysosomal degradation of an endocytosed organism





Class II loading is centered in the vesicular system

Acidic endosomal proteases digest ingested proteins into peptides that will load MHC class II molecules



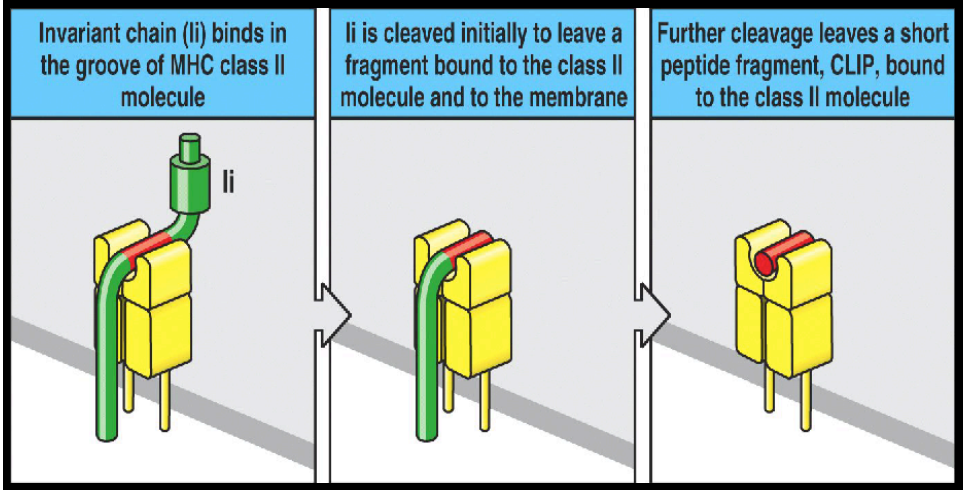
This process does not require the precise proteolysis needed in the class I system, since the peptide terminii are not constrained by MHC class II

Invariant chain (Ii)

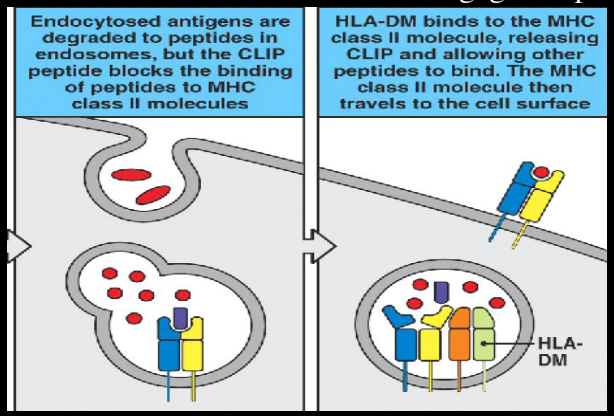
Class II MHC molecule peptide loading depends on the synthesis of Ii

- A chaperone that complexes with MHC class II molecules during their synthesis in the endoplasmic reticulum
- Ii Blocks the class II peptide binding groove of the newly synthesized MHC class II molecule in the e.r. and prevents loading by peptides destined for class I molecules
- A recognition sequence on the Ii transmembrane portion redirects the nascent MHC II molecule to traffic to the acidic endosomal compartment where it will be loaded with the degraded ingested exogenous peptides

Within the acidic endosome, Ii is first degraded to CLIP (Class II-associated invariant chain peptide) by specific endosomal acidic cysteine proteases (cathepsins)



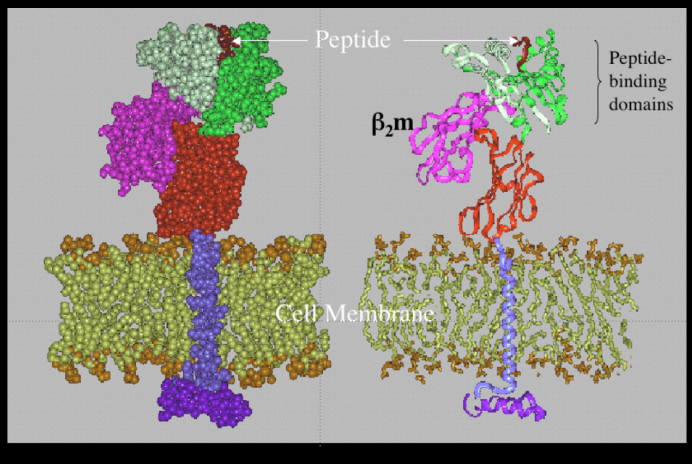
CLIP is only bound to the MHC groove by its peptide backbone and its side chains do not engage the pockets

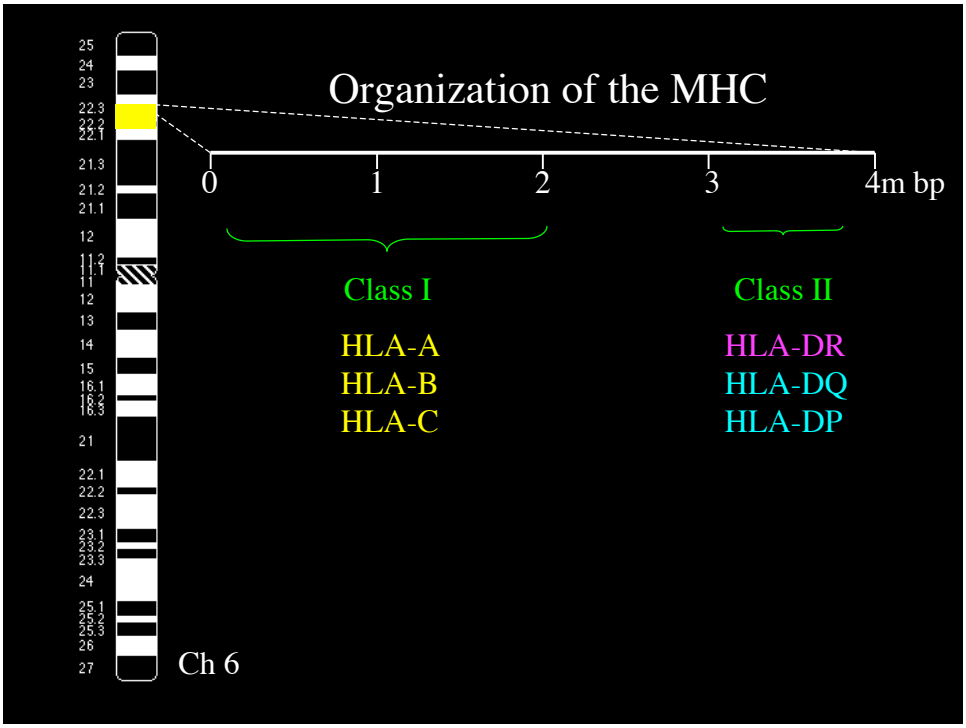


• HLA-DM, an ancient but non-classical class II molecule catalyzes the release of CLIP and the binding of high affinity peptides via interaction of peptide amino acid side-chains with MHC pockets

• Without Ii the MHC class II molecule now is free to traffic to the cell membrane

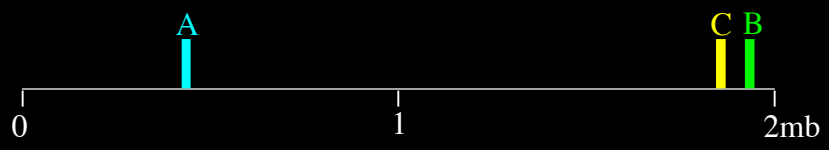
Expression MHC molecule on the cell surface





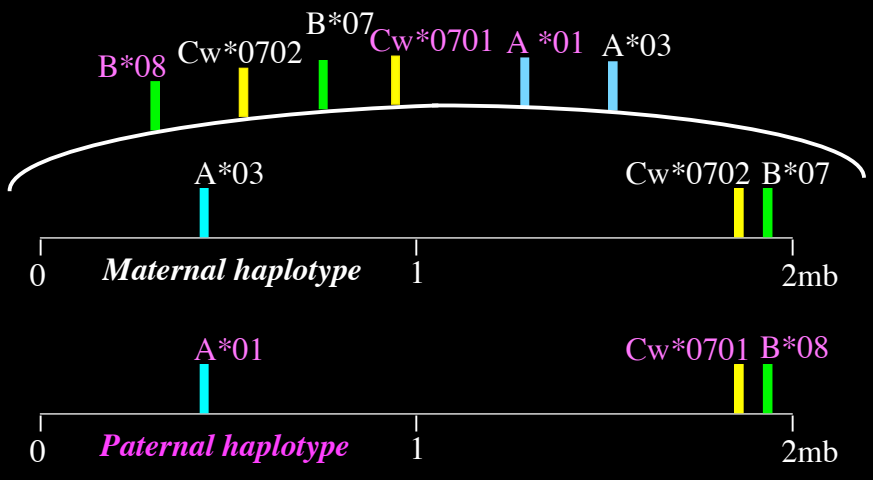
MHC class I (HLA-A,B,C) genes

MHC class I loci	Specificity (Antigen)	Allele designation	# of alleles
HLA-**A** α-chain	A1, A2,…	A*0101,…	451
HLA-**B** α-chain	B7, B8,…	B*0702,…	789
HLA-**C** α-chain	Cw1, Cw2...	Cw*0101,...	238



(β_2 microglobulin encoded on chromosome 15)

Codominant expression of MHC class I genes results in 6 different types of class I molecules on the surface of each cell

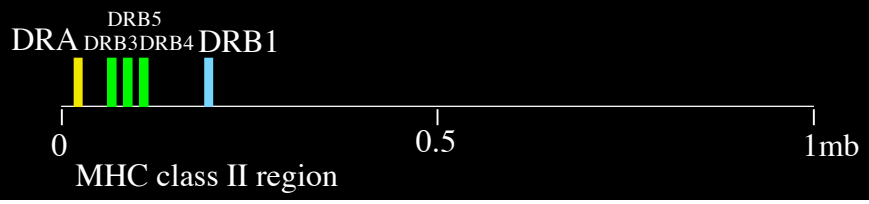


MHC class I region

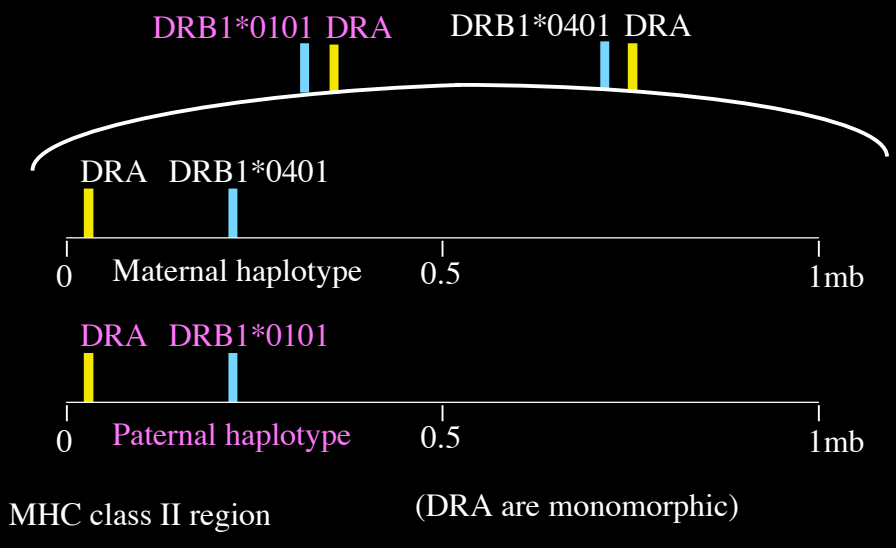
10-20,000 molecules of each type are present on most cells

Polygenic human MHC class II (HLA-DR) genes

MHC class II loci	Specificity (Antigen)	Allele designation	# of alleles
HLA-DRA α-chain		DRA*0101	2
HLA-DRB1 β-chain	DR1, 2,…	DRB1*0101,…	**522**



Codominant expression of MHC II genes gives 2 different HLA- DR molecules on the cell surface



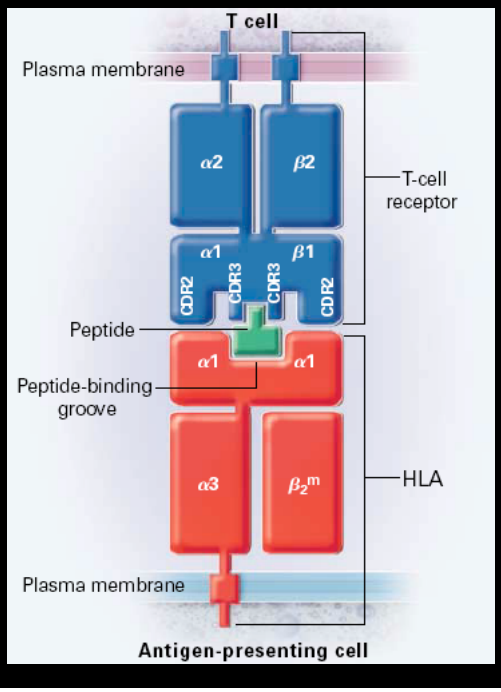
Maximum number of different types of HLA molecules expressed on the cell surface

	Nucleated cells	Antigen presenting cells
Class I (HLA-A)	2	2
Class I (HLA-B)	2	2
Class I (HLA-C)	2	2
Class II (HLA-DR)	0	2*
Class II (HLA-DQ)	0	4
Class II (HLA-DP)	0	4
Total	6	16

Each of these MHC molecules selects its *own T cell repertoire* that only recognizes peptides presented by that particular type of MHC molecule

Recognition of p-MHC by the TCR

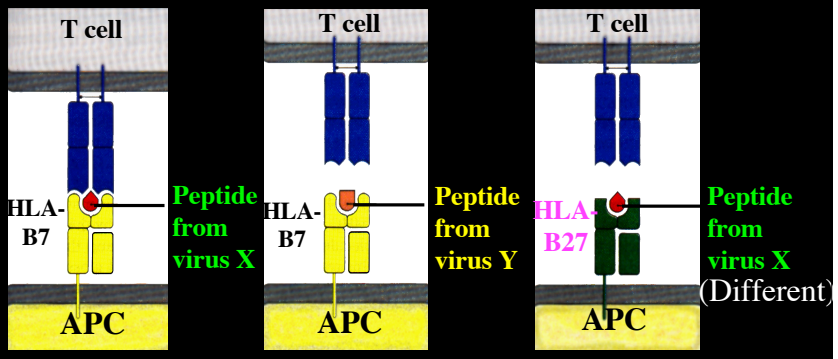
The classic Zinkernagel & Doherty experiment



T cell receptors interact both with the MHC molecule and with the bound peptide

MHC I-CD8 TCR ***CDR3 hypervariable regions*** of TCR α and β-chain primarily contact peptide

Because the TCR recognizes both peptide and MHC molecule, T cell recognition of MHC-peptide is both MHC restricted and specific for the immunizing peptide



(Different)

Target killed: ***Yes*** **No** **No**

In each experiment the T cell is from a HLA-B7 person who recovered from infection by virus "X".
The APC target cell is either infected with virus X or Y and is from an individual who is either HLA-B7 or HLA-B27

Summary points

•During development ~16 T cell repertoires are separately selected on self-peptides presented by 3 types of class I and 3 types of class II MHC molecules

• Later during an immune response these same T cells recognize "not quite self"/non self peptides presented on these MHC molecules and then clonally expand

•MHC molecules are codominantly expressed, with class I molecules found on the surface of all nucleated cells and class II molecules on professional antigen presenting cells

•The alleles of the MHC genes specify different amino acids in MHC pockets that bind peptide side chains, and this confers specificity on MHC molecules to bind different peptides

•As a consequence individuals vary markedly in what particular peptides the T cell recognizes

•Class I and class II MHC molecules differ markedly in the details of how they bind peptides and the biochemical pathways the peptides take to be loaded on the MHC. These differences assure that the correct CD4 or CD8 adaptive immune response is made to a peptide

•The fact that class I MHC molecules bind the CD8 molecule and class II MHC molecules bind the CD4 molecules assists in the discrimination

•The presence of a "not quite self"/non self peptide on a MHC class I molecule renders the cell a target of a cytotoxic CD8 T cell, while a peptide in a class II molecule evokes macrophage activation and B cell help