

01

Major

Histocompatibility



- Every mammalian species possesses a tightly linked cluster of genes, the major histocompatibility complex (MHC)
- Products play roles in intercellular recognition and in discrimination between self and non-self
- A collection of genes arrayed within a long continuous stretch of DNA on chromosome 6 in humans and on chromosome 17 in mice
- MHC is referred to as the HLA complex in humans and as the H-2 complex in mice

MHC Gene Subtype

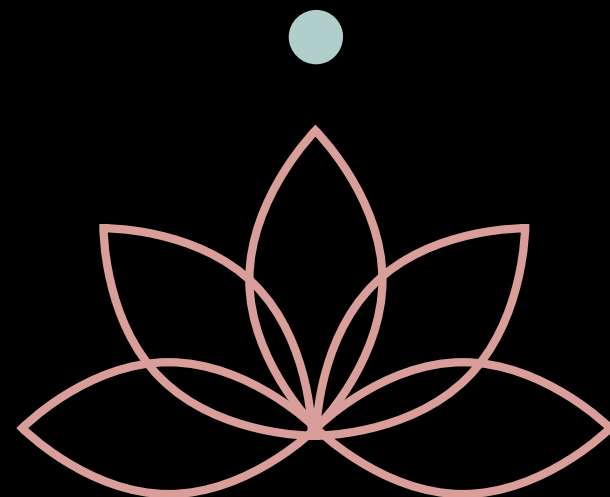
1) Class I

2) Class II

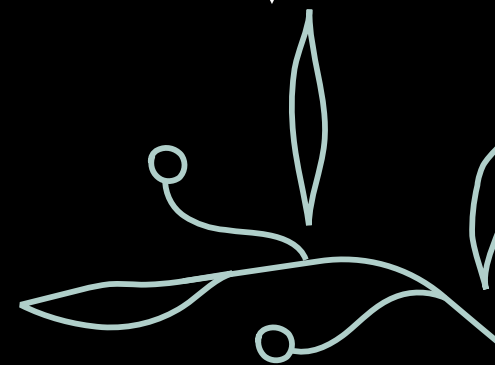
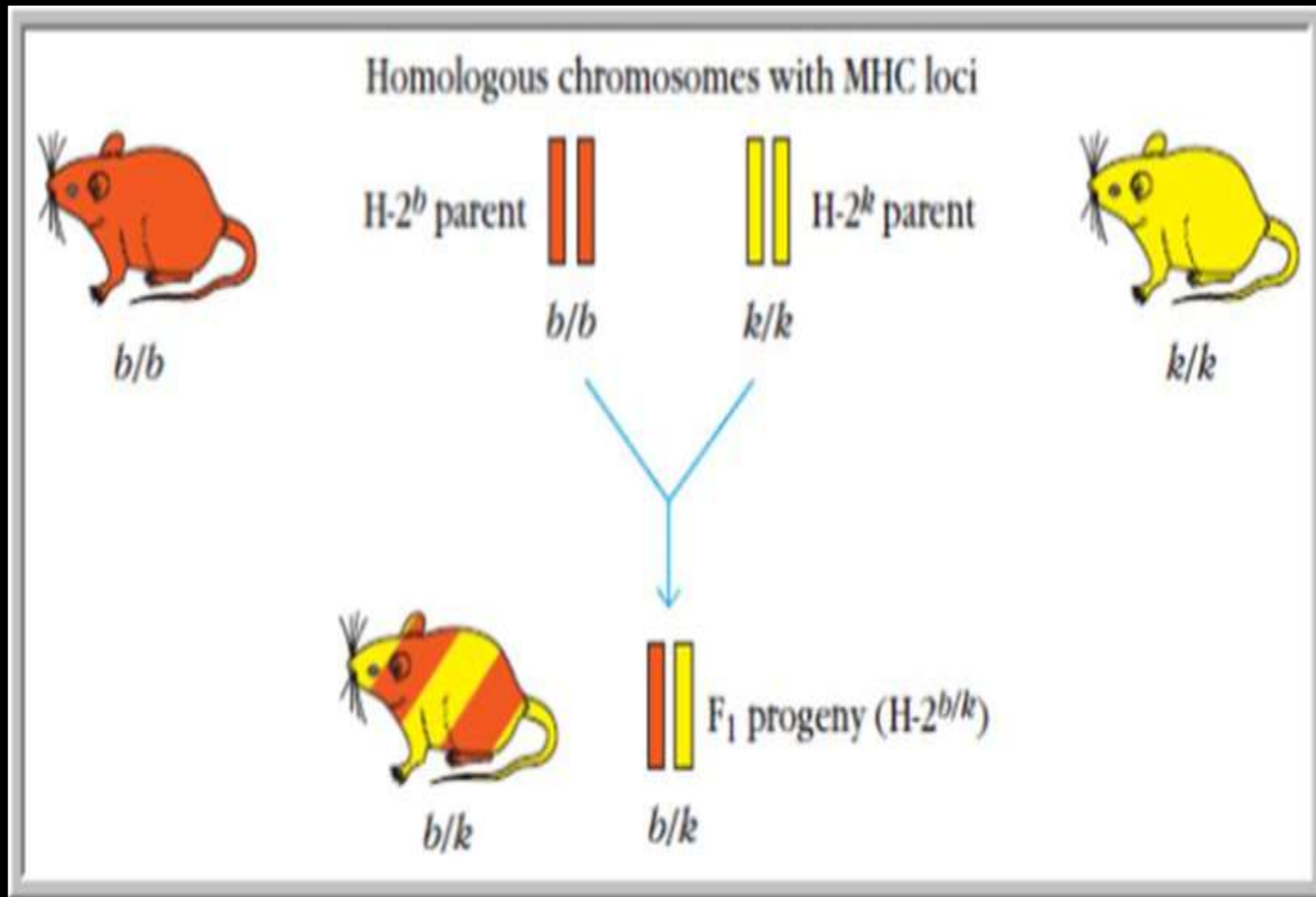
3) Class III



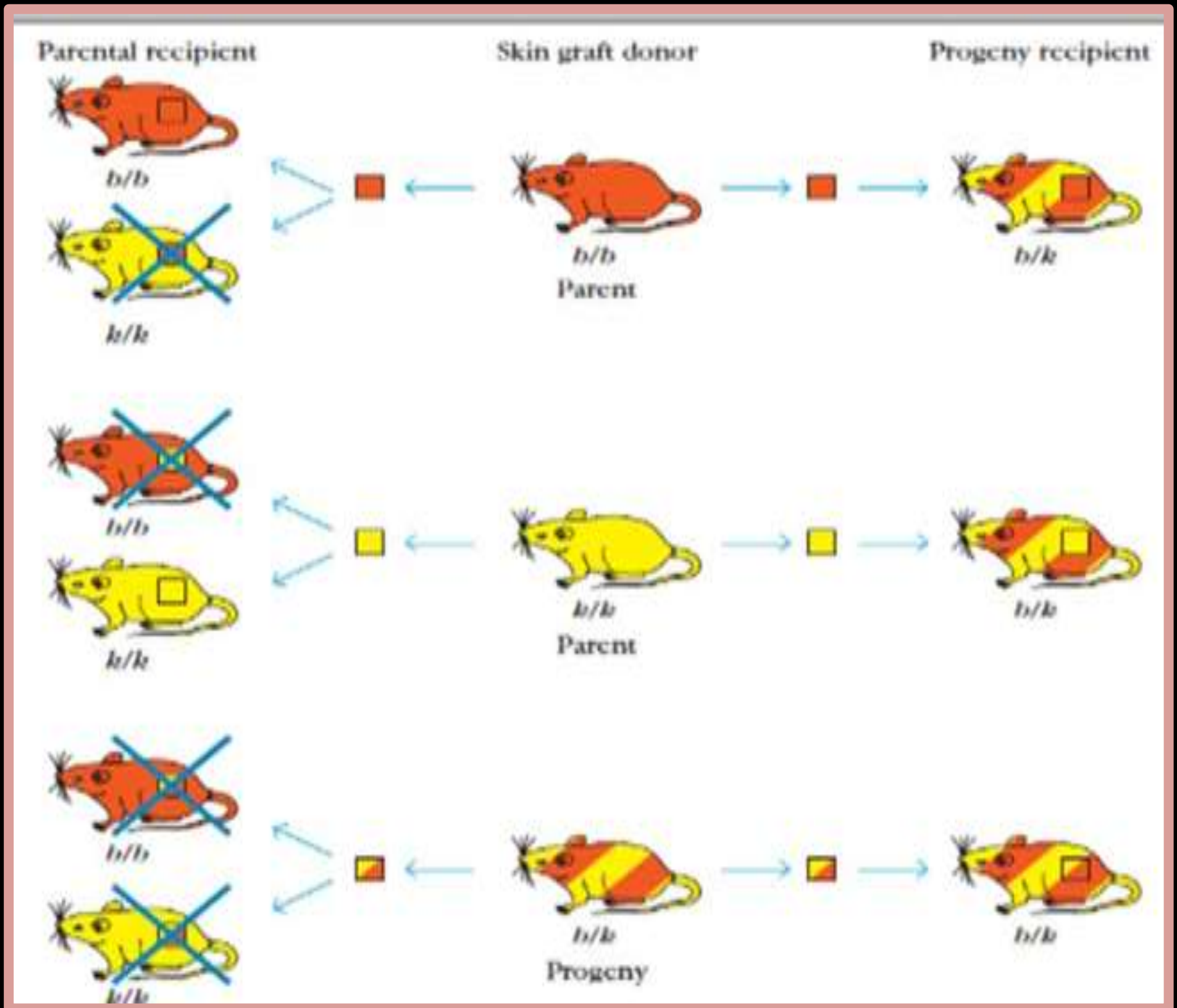
- *The loci is highly polymorphic*
- *The MHC loci is closely linked and many alleles exist at each locus.*
- *Each sets of alleles referred to as "haplotype".*
- *The alleles are co dominantly expressed.*



Inheritance of MHC haplotypes in inbred mouse strains



Inheritance of MHC haplotypes in inbred mouse strains



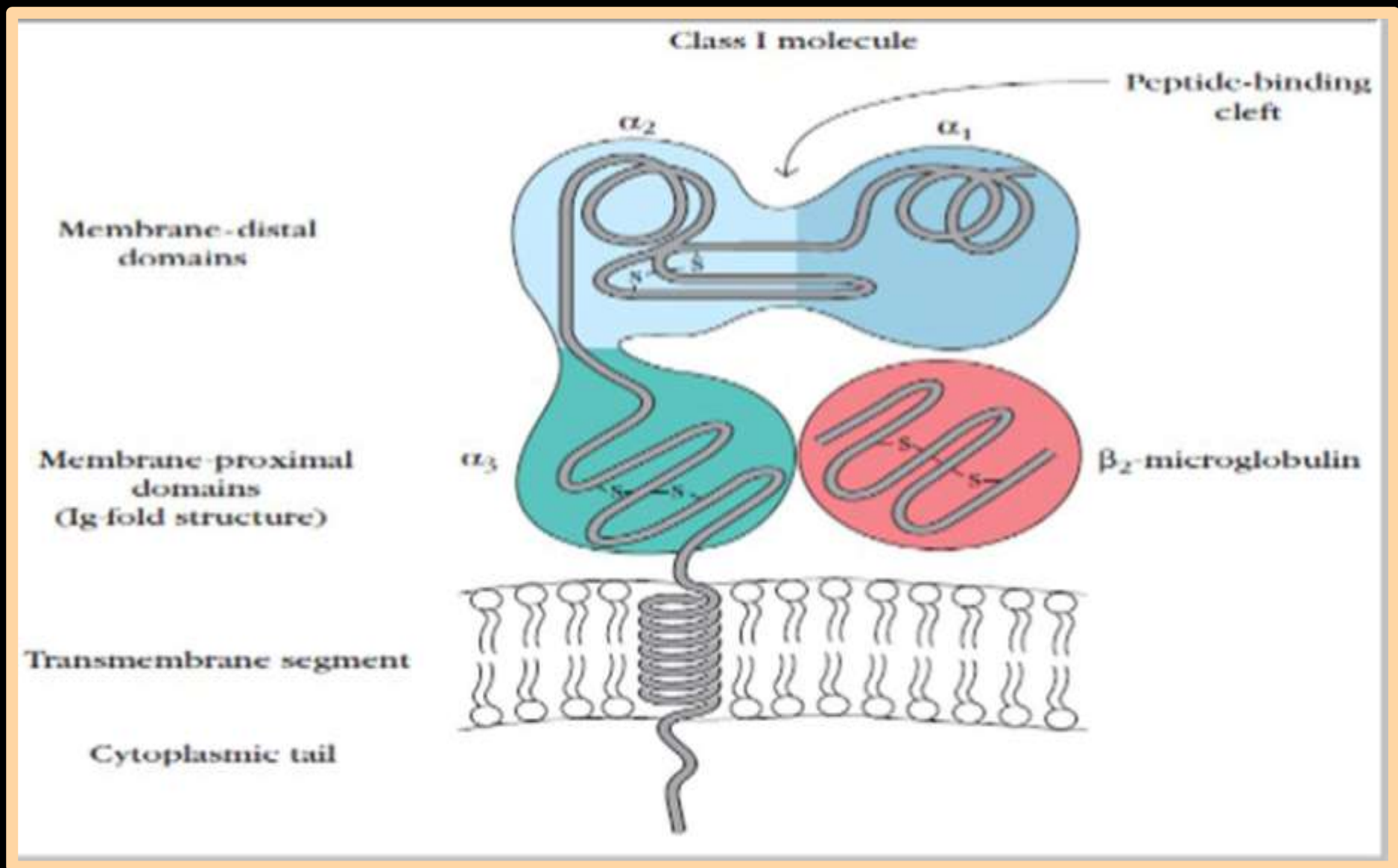
MHC Molecule

- Class I and class II MHC molecules are membrane-bound glycoproteins
- Are closely related in both structure and function
- Function as highly specialized antigen-presenting molecules that form unusually stable complexes with antigenic peptides, displaying them on the cell surface for recognition by T cells
- Class III MHC molecules are a group of unrelated proteins that do not share structural similarity and common function with class I and II molecules



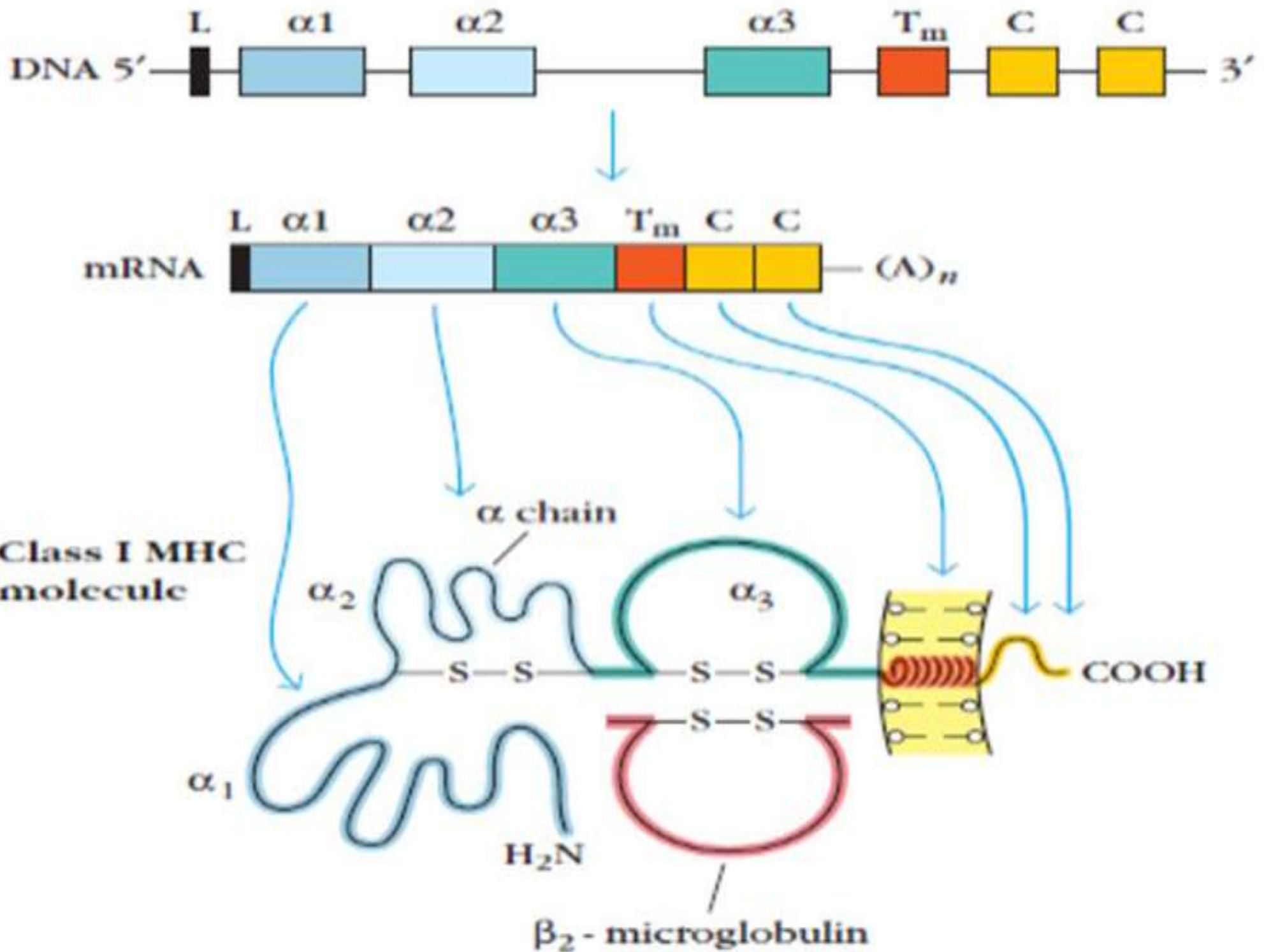
Structure of Class I MHC

- Class I MHC molecules contain a 45-kilodalton (kDa) α chain associated non-covalently with a 12-kDa β_2 -microglobulin molecule
- α -subunit is a glycoprotein encoded by A, B And C regions of HLA complex
- β_2 -Micro globulin is a protein encoded by a highly conserved gene located on a different chromosome
- α chain is organized into three external domains ($\alpha_1, \alpha_2, \alpha_3$) each approximately of 90 amino acids, a transmembrane domain of about 25 hydrophobic amino acids followed by short stretch of charged (hydrophilic) amino acids; and a cytoplasmic anchor segment of 30 amino acids



- Peptide binding cleft formed by α_1 and α_2 domains where 8-10 amino acid can bind
- α_3 - β_2 -microglobulin resembles Ig fold

Arrangement of exons in MHC gene

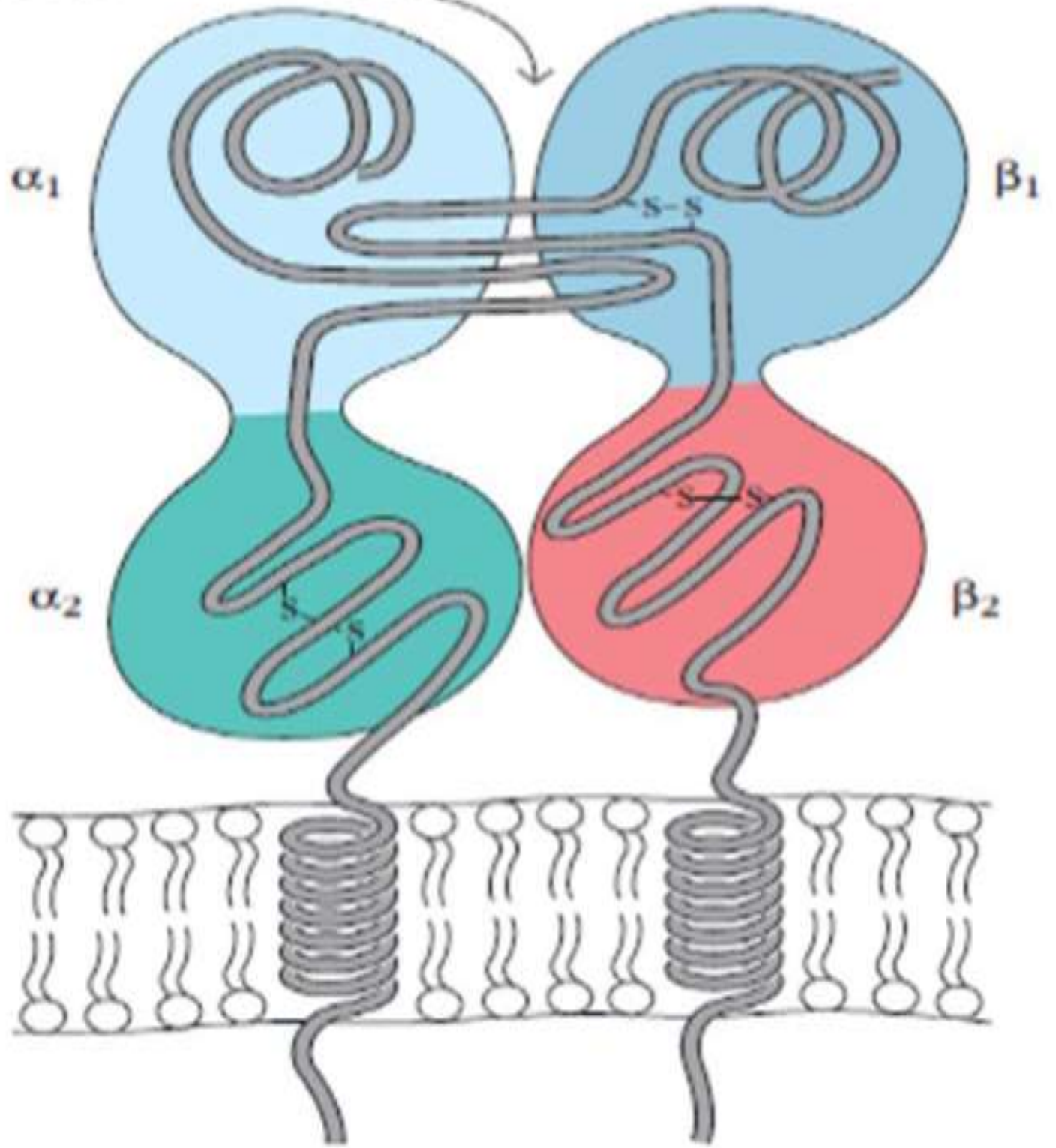


Structure of class II MHC

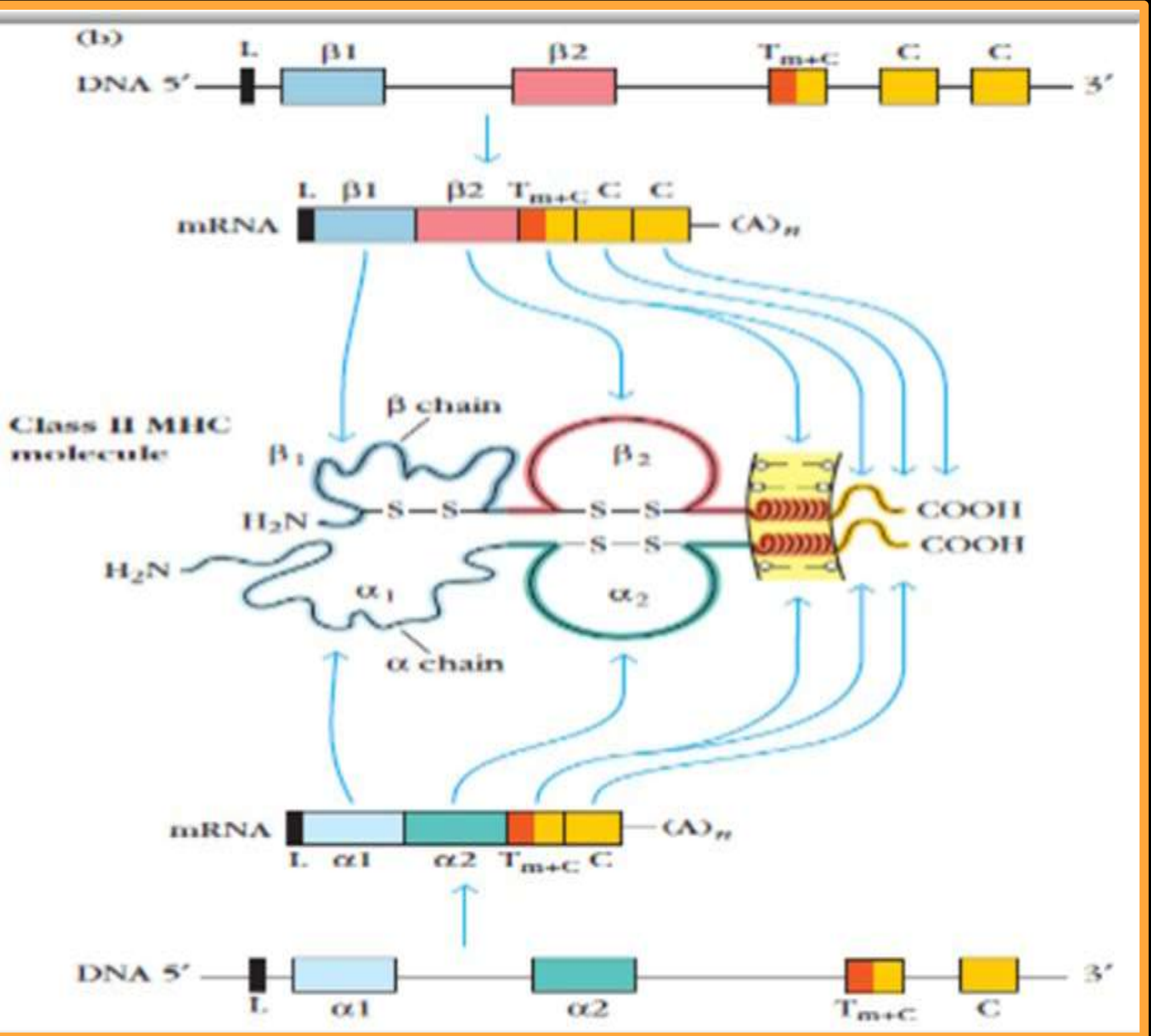
- Class II MHC molecules contain two different polypeptide chains (membrane bound glycoprotein), a 33-kDa α chain and a 28-kDa β chain, which associate by non covalent interactions
- Contain external domains, a transmembrane segment, and a cytoplasmic anchor segment
- Each chain contains two external domains: $\alpha 1$ and $\alpha 2$ domains in one chain and $\beta 1$ and $\beta 2$ domains in the other
- $\alpha 1$ and $\beta 1$ domains and forms the antigen-binding cleft for processed antigen. $\alpha 2$ and $\beta 2$ domains resembles Ig fold

Class II molecule

Peptide-binding cleft



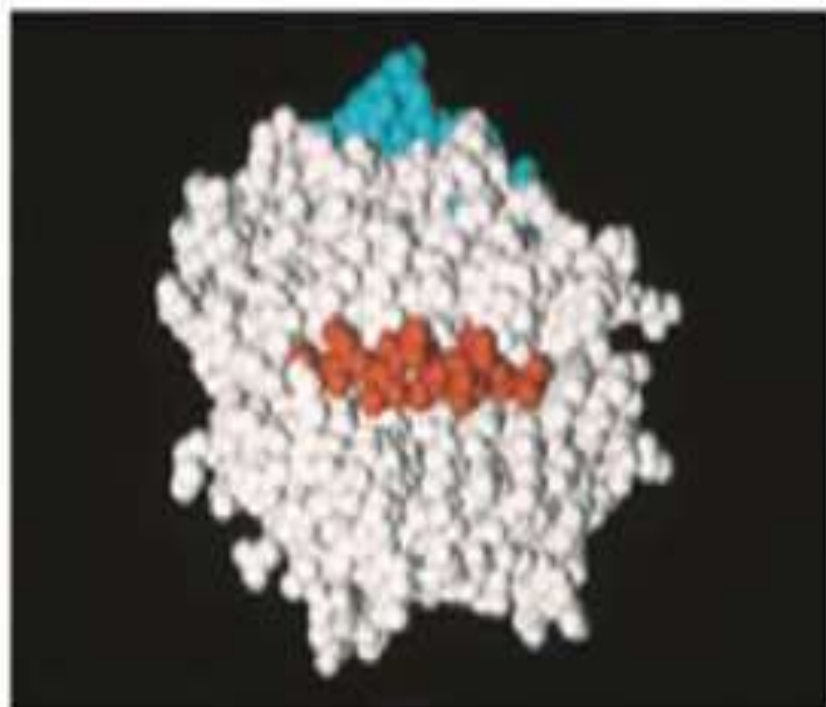
Arrangement of exons in MHC gene



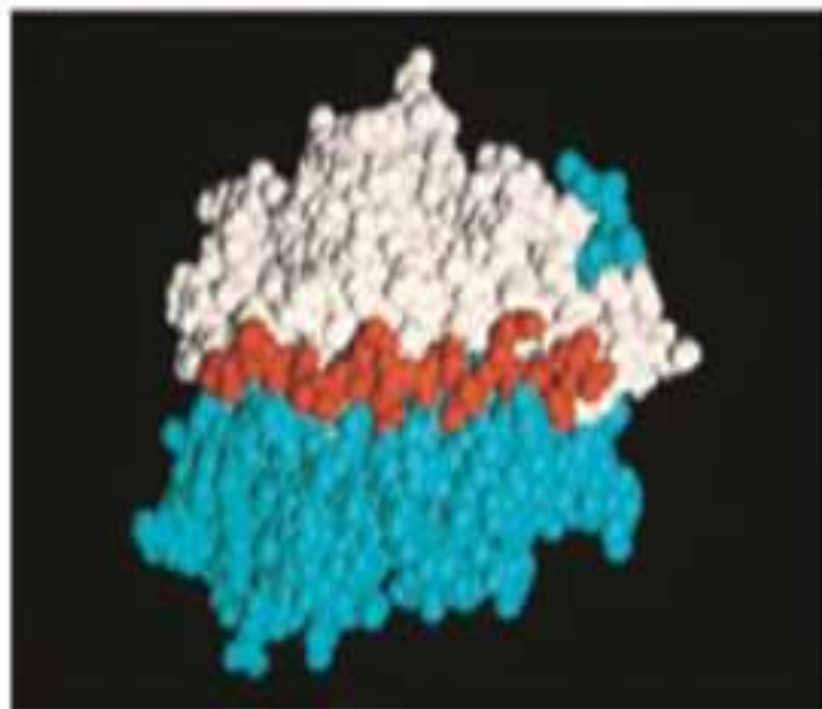
Peptide Binding By Class I and class II

| | Class I molecules | Class II molecules |
|--|---|--|
| Peptide-binding domain | $\alpha 1/\alpha 2$ | $\alpha 1/\beta 1$ |
| Nature of peptide-binding cleft | Closed at both ends | Open at both ends |
| General size of bound peptides | 8–10 amino acids | 13–18 amino acids |
| Peptide motifs involved in binding to MHC molecule | Anchor residues at both ends of peptide; generally hydrophobic carboxyl-terminal anchor | Anchor residues distributed along the length of the peptide |
| Nature of bound peptide | Extended structure in which both ends interact with MHC cleft but middle arches up away from MHC molecule | Extended structure that is held at a constant elevation above the floor of MHC cleft |

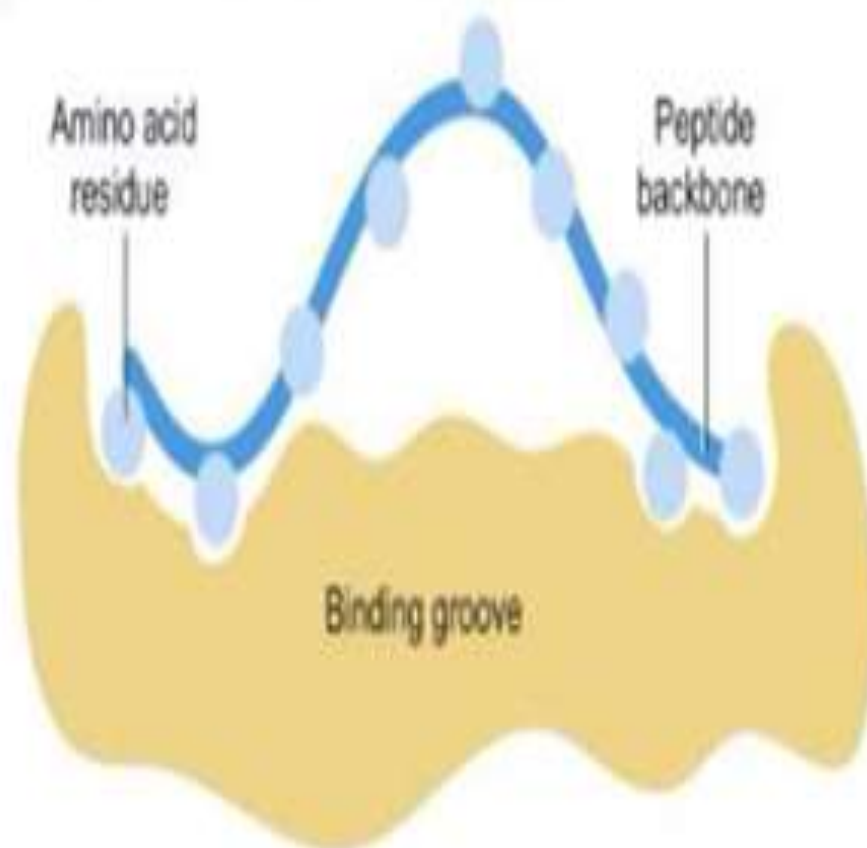
(a) Class I MHC



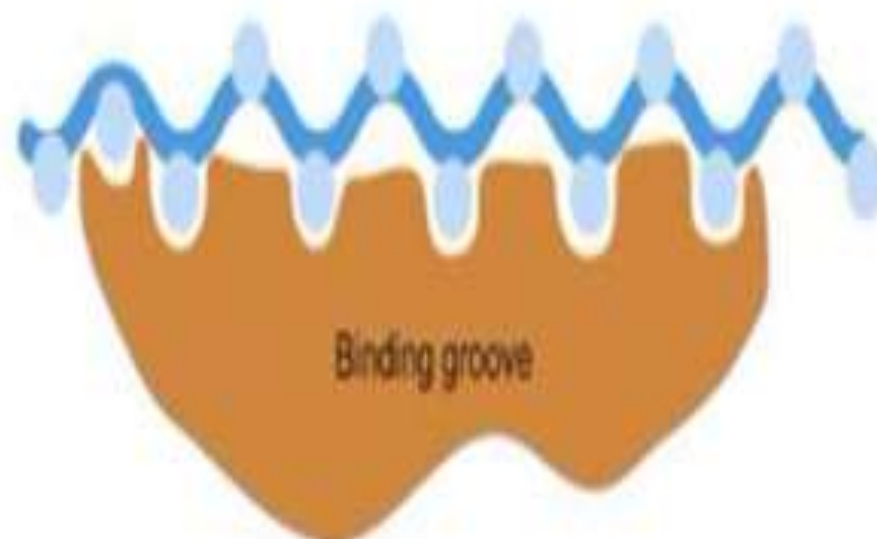
(b) Class II MHC



(A) Peptide in MHC Class I Binding Groove

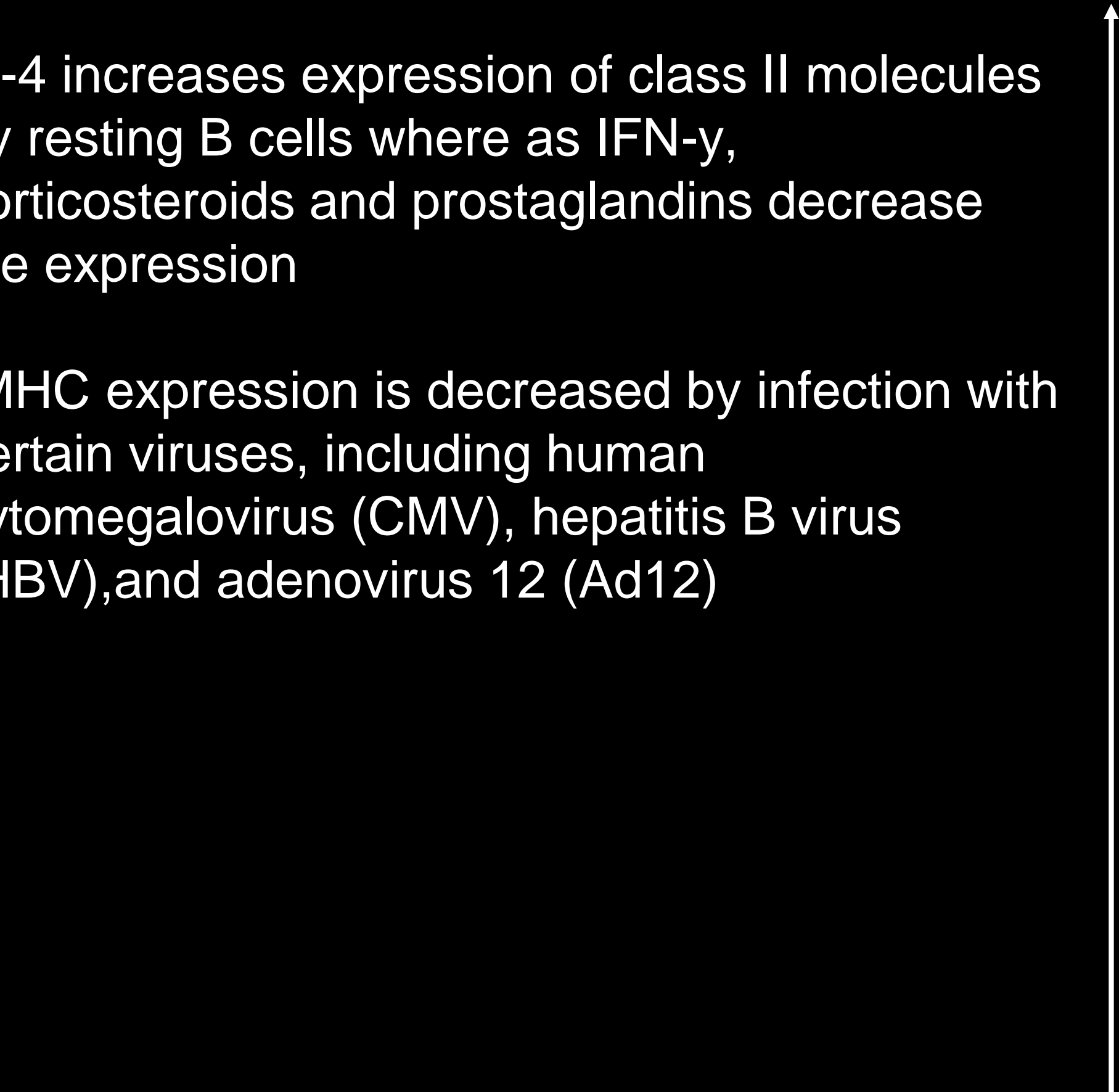


(B) Peptide in MHC Class II Binding Groove



Regulation of MHC Expression

- Transcriptional regulation of the MHC is mediated by both positive and negative elements - MHC II trans activator, called CIITA, and transcription factor, called RFX.
 - Cytokines - interferons (alpha, beta, and gamma) and tumor necrosis factor have each been shown to increase expression of class I MHC molecules on cells
 - IFN- γ also has been shown to induce expression of the class II transactivator (CIITA), thereby indirectly increasing expression of class II MHC molecules on a variety of cells, including non-antigen-presenting cells
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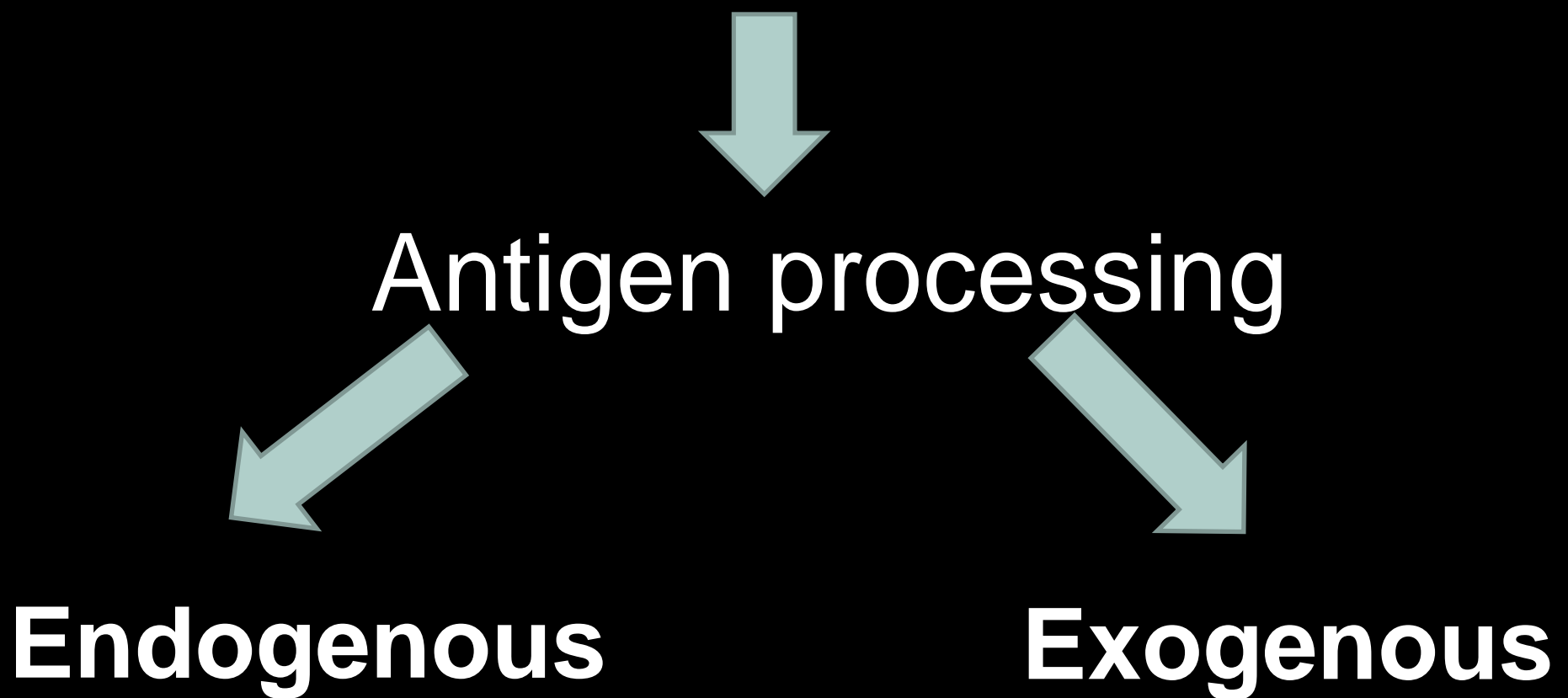
- IL-4 increases expression of class II molecules by resting B cells whereas IFN- γ , corticosteroids and prostaglandins decrease the expression
 - MHC expression is decreased by infection with certain viruses, including human cytomegalovirus (CMV), hepatitis B virus (HBV), and adenovirus 12 (Ad12)
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02

Antigen Processing
and Presentation



- T cells require antigenic peptides to be displayed by MHC on APC
- Antigenic protein degraded into peptides



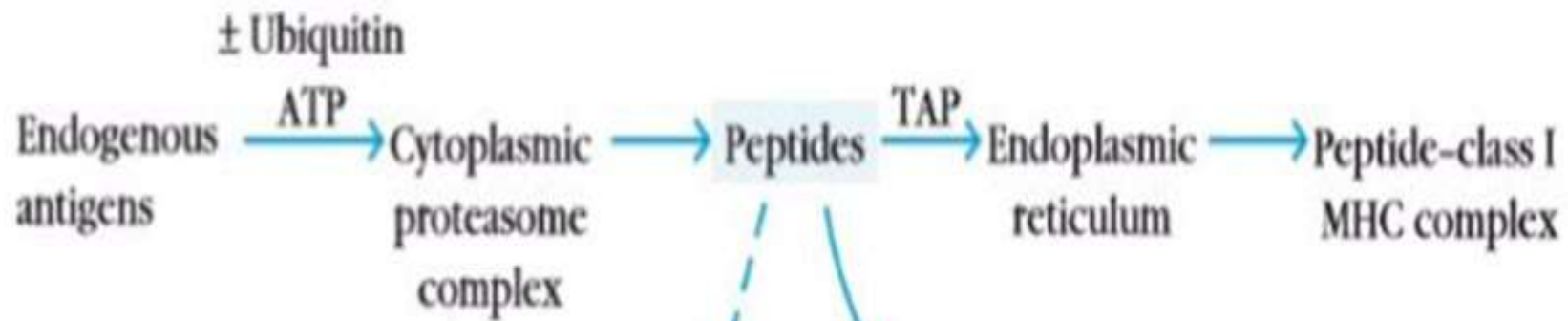
EXOGENOUS

- Exogenous antigens (phagocytosis)
- Processing done in the endocytic pathway
- Presented on the membrane with class II MHC molecules
Pathogen in APC

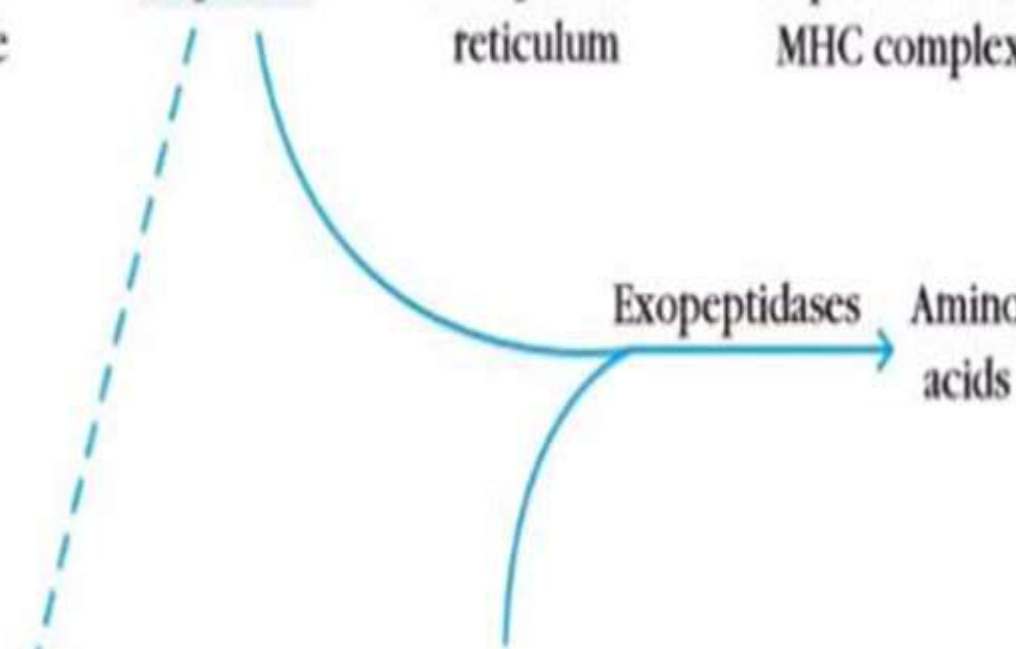
ENDOGENOUS

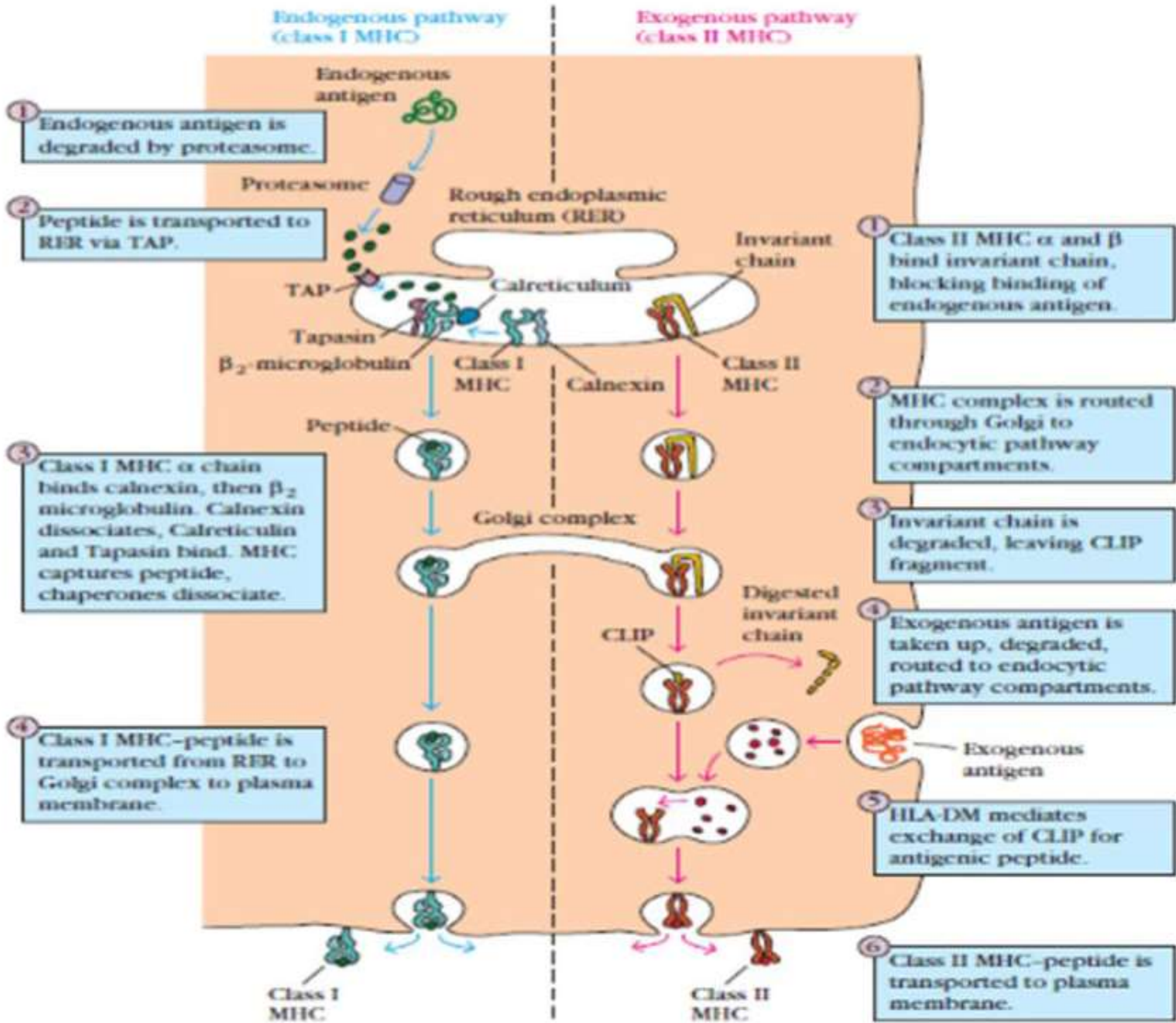
- Endogenous antigens processed within cell
- Processing done in the cytosolic pathway
- Presented on the membrane with class I MHC molecules
- Transcription factors. cyclins. denatured proteins. viral protein

CYTOSOLIC PATHWAY



ENDOCYTOTIC PATHWAY

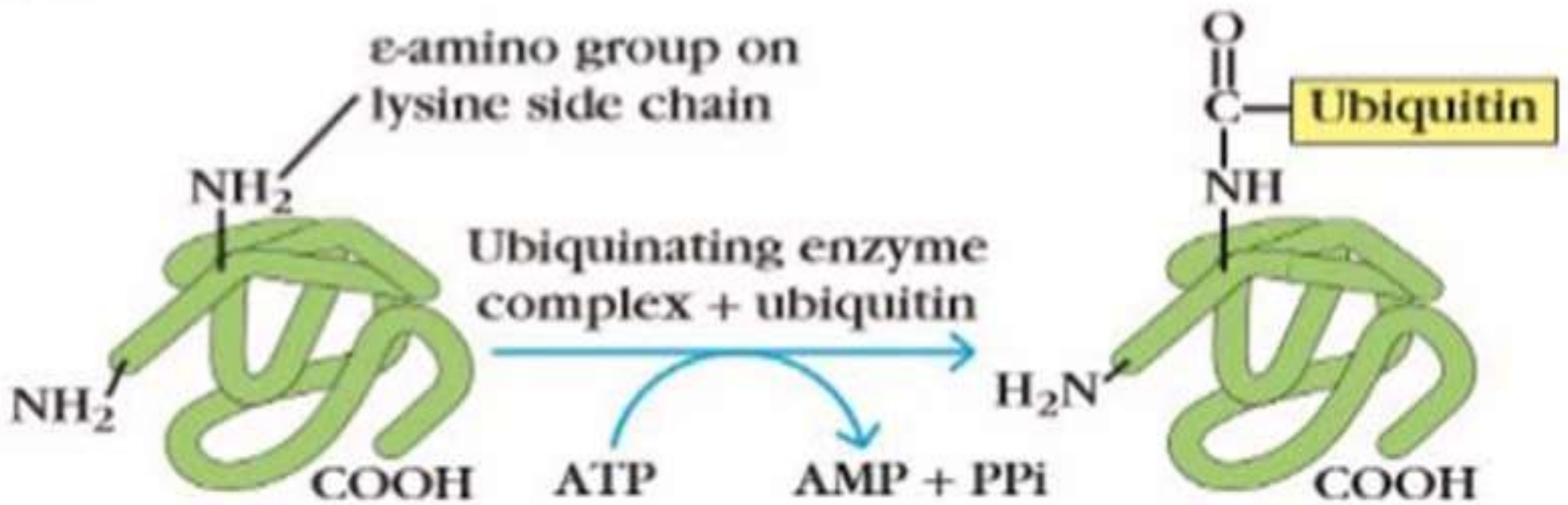




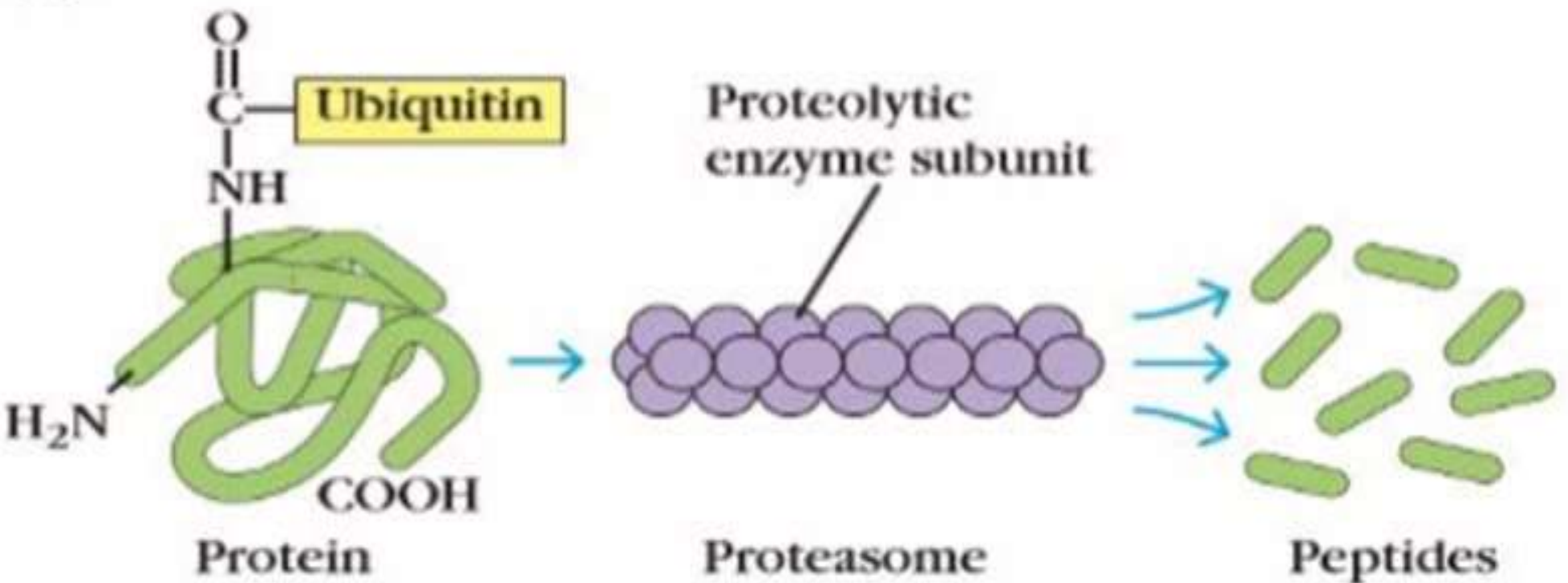
Cytosolic Pathway

- Peptide Generation
 - Intracellular proteins are degraded into short peptides by a cytosolic proteolytic system present in all cells
 - Proteins targeted for proteolysis often have a small protein, called ubiquitin, attached to them
 - Ubiquitin-protein conjugates can be degraded by a multifunctional protease complex called a proteasome
 - A proteasome can cleave peptide bonds between 2 or 3 different amino acid combinations in an ATP-dependent process

(a)



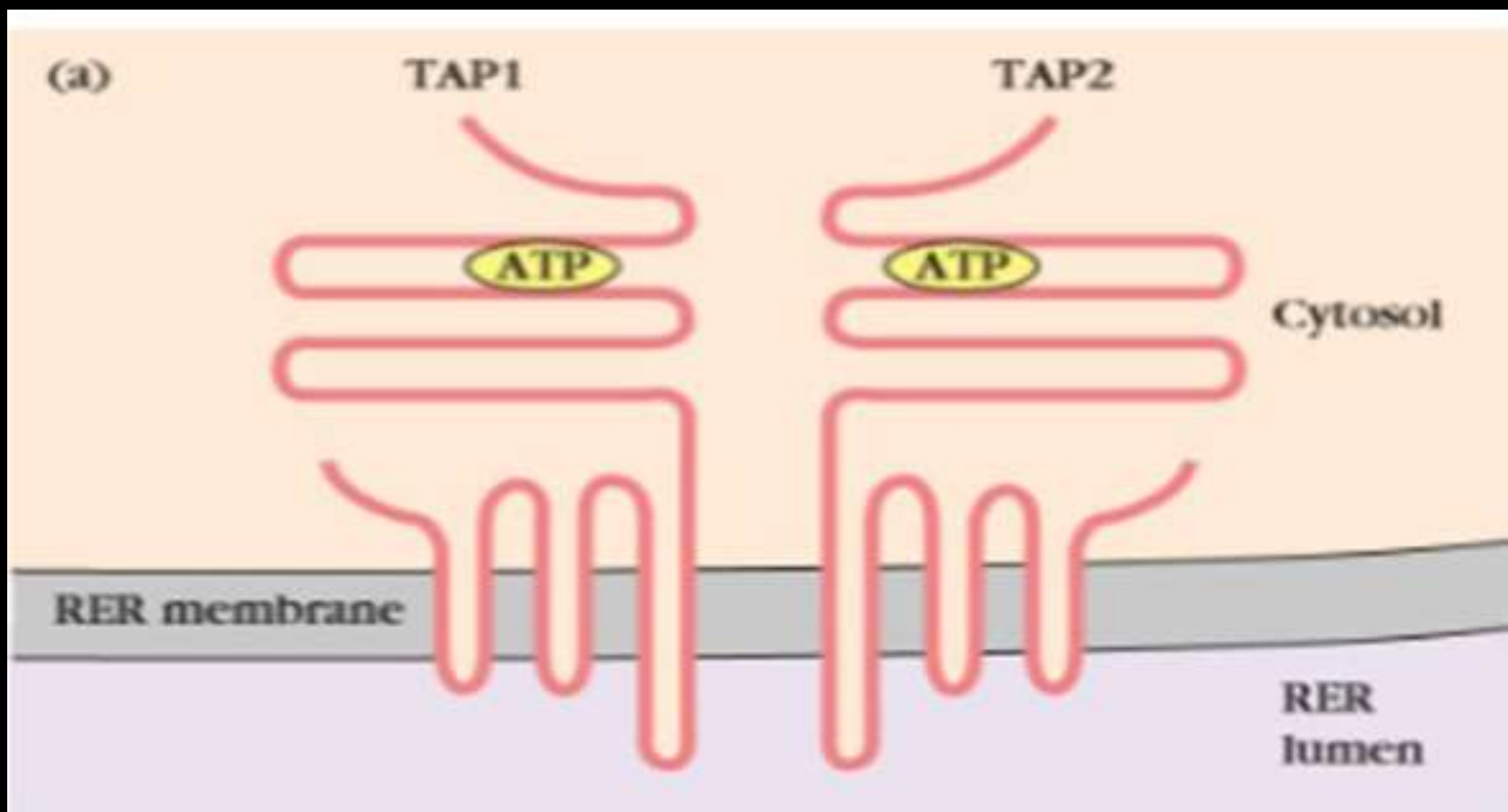
(b)



Peptide Transport to RER

- Peptides generated in the cytosol by the proteasome are trans located by TAP (transporter associated with antigen processing) into the RER by a process that requires the hydrolysis of ATP

TAP has the highest affinity for peptides containing 8-10 amino acids with hydrophobic or basic carboxyl-terminal amino acids



Peptide assembly with Class I

MHC

- ✓ Assembly of stable class I MHC molecular complex that can exit the RER requires the presence of a peptide in the binding groove of the class I molecule
- ✓ Calnexin associates with the free class I α chain and promotes its folding
- ✓ When B2-microglobulin binds to the α chain, calnexin is released and the class I molecule associates with the chaperone calreticulin and with tapasin
- ✓ Tapasin (TAP-associated protein) brings the TAP transporter into proximity with the class I molecule and allows it to acquire an antigenic peptide
- ✓ Now, the class I molecule displays increased stability and can dissociate from calreticulin and tapasin, exit from the RER

(b)

Protein

Cytosol

Amino acids

Peptides

ATP

ADP + Pi

TAP

Class I MHC

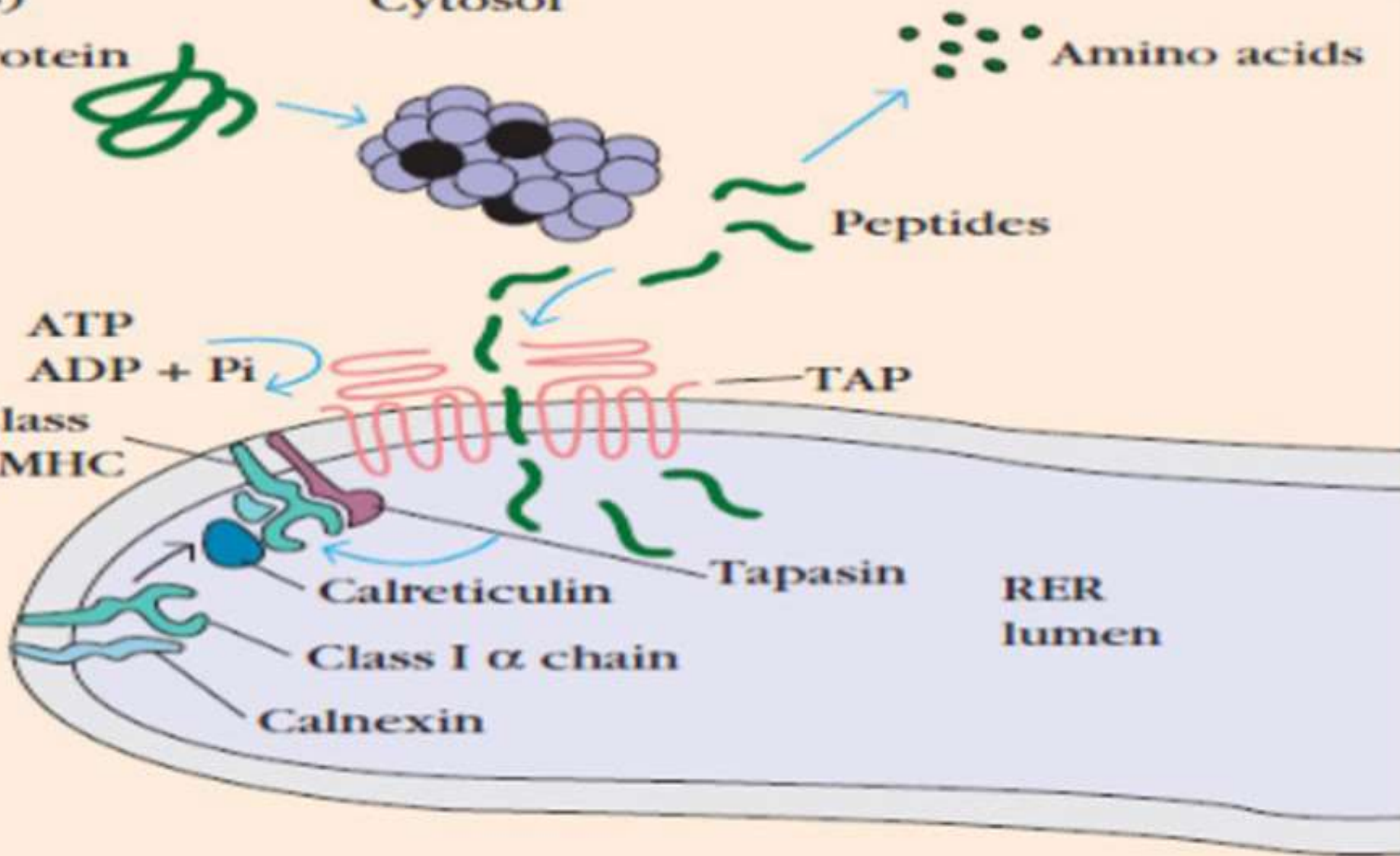
Calreticulin

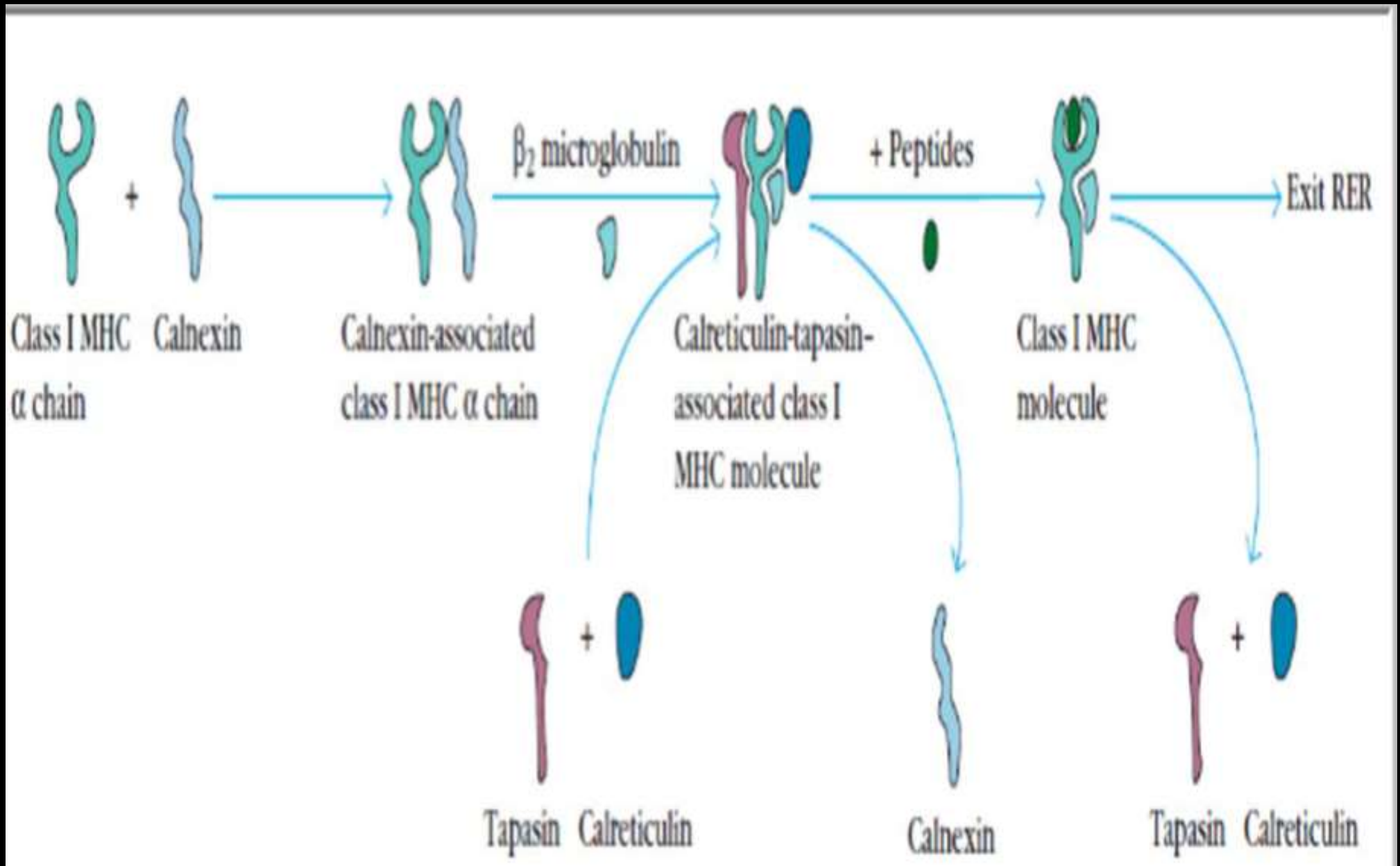
Tapasin

RER lumen

Class I α chain

Calnexin





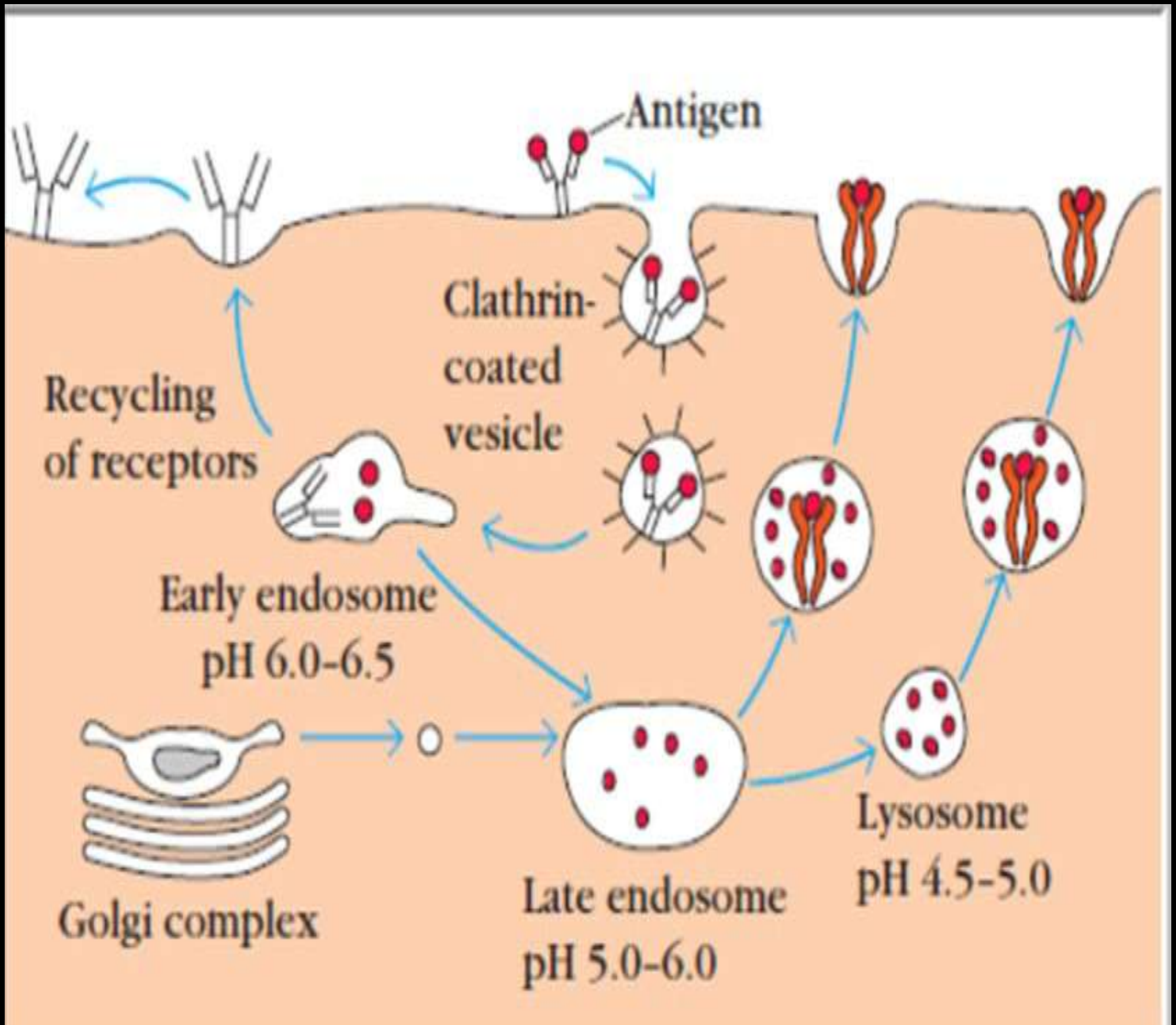
Endocytic Pathway

- Peptide Generation

1) An antigen is internalized by antigen-presenting cells it is degraded into peptides within compartments of the endocytic processing pathway

2) Internalized antigen moves from early to late endosomes and finally to lysosomes, encountering hydrolytic enzymes and a lower pH in each compartment

3) Antigen is degraded into oligo peptides of about 13-18 residues, which bind to class II MHC molecules

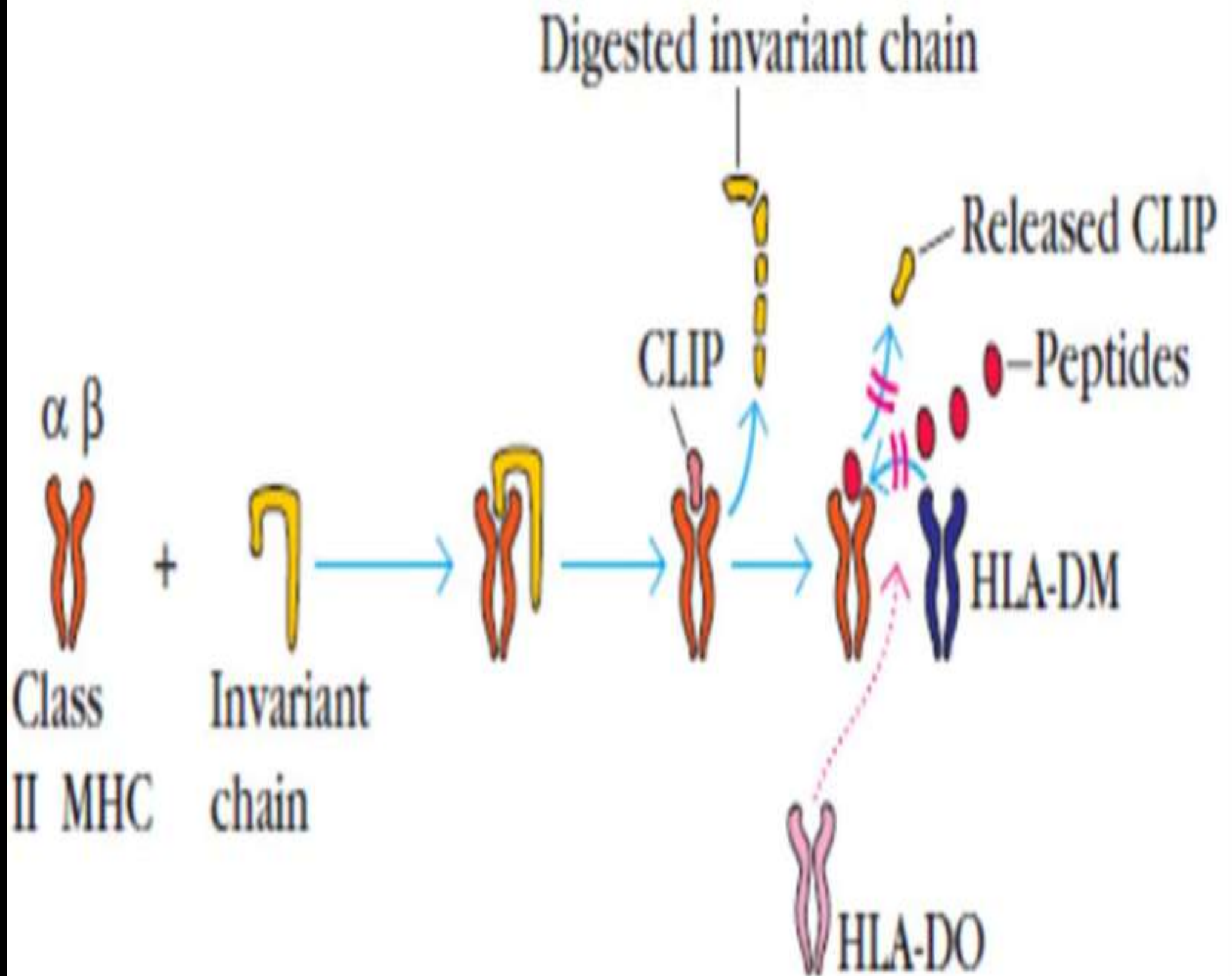


Transport of Class II MHC to Endocytic Compartment

- Class II MHC α and β bind invariant chain (trimeric protein)
- Interacts with the peptide-binding cleft of the class II molecules, preventing any endogenously derived peptides from binding to the cleft while the class II molecule is within the RER
- Also appears to be involved in the folding of the class II MHC
- Invariant chain helps in exit of Class II MHC from the RER, and the subsequent routing of class II molecules to the endocytic processing pathway from the trans-Golgi network

Peptide assembly with Class II MHC

- In the endocytic pathway, the invariant chain is gradually degraded by increasing proteolytic activity
- A short fragment of the invariant chain termed CLIP (for class II-associated invariant chain peptide) remains bound to the class II molecule in the peptide-binding groove
- A non classical class II MHC molecule called HLA-DM is required to catalyze the exchange of CLIP with antigenic peptides
- The peptide-class II complex is transported to the plasma membrane. where the neutral pH appears to enable the complex to assume a compact. stable form



THANKS!

