

Risposte quesiti 1° Parte corso

Elementi Mobili

Elementi mobili LINE1:

- ORF1, ci sono due domini, un Recognition Motif ed un Coiled Coil.
Quali sono le funzioni del Coiled Coil Domain ?

(a)

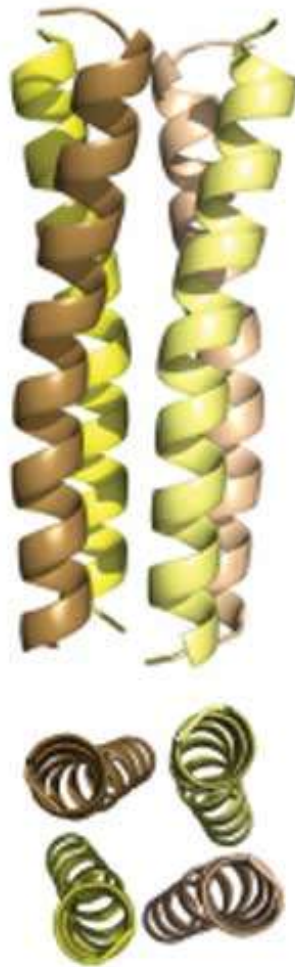
Dimer



Trimer



Parallel Tetramer



Antiparallel Tetramer



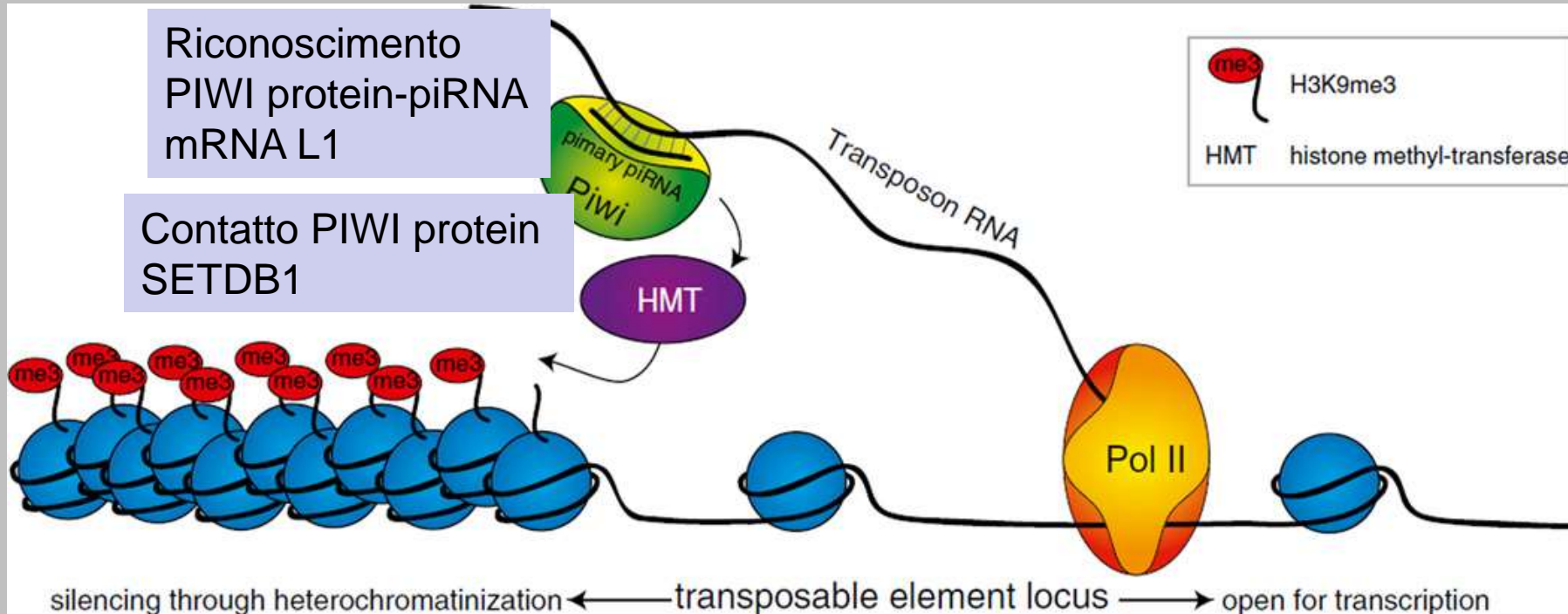
Pentamer



Silenziamento Elementi Mobili

- Silenziamento dei trasposoni: - La metil-transferasi SETDB1 compie la trimetilazione della lisina 9 H3, o richiama la proteina HP1?
- -

nuclear function of the piRNA pathway



SETDB1 = HMT Histone Methyl Transferase

Riconoscimento
H3K9 – HP1 (Cromodominio)

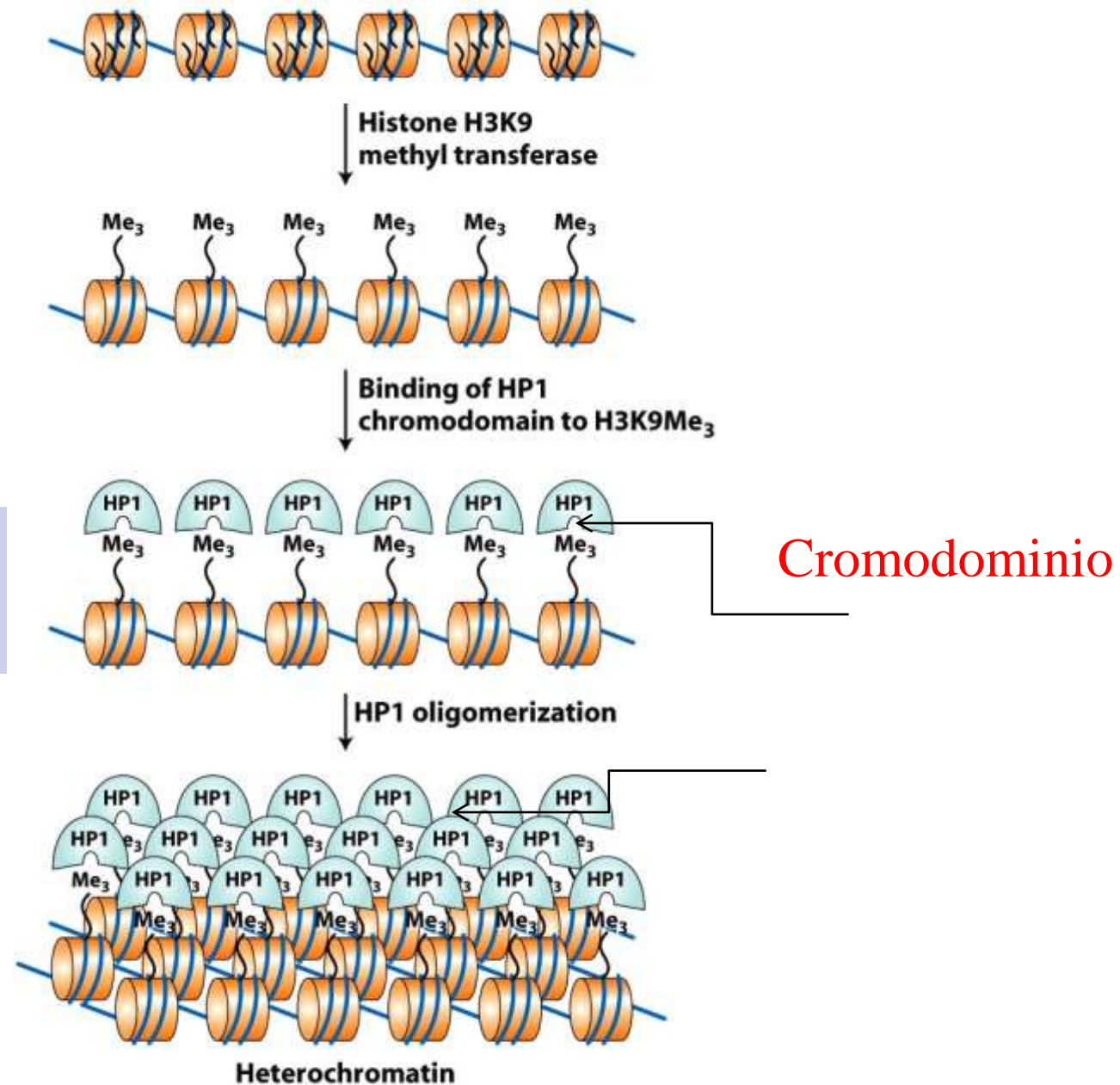


Figure 6-34a
Molecular Cell Biology, Sixth Edition
© 2008 W. H. Freeman and Company

Inibizione Elementi Mobili - PIWI proteins

- Le PIWI sono geni?

Sono proteine codificati da mRNA trascritti dalla RNA pol II da geni corrispondenti, e che vanno ad interagire con i pi-RNA

- Non ho compreso la differenza fra i piRNAs, PIWI, MIWI

transcriptional gene regulation (TGS) or post-transcriptional gene regulation (PTGS) by PIWI –piRNA complexes

Contatto PIWI protein
SETDB1

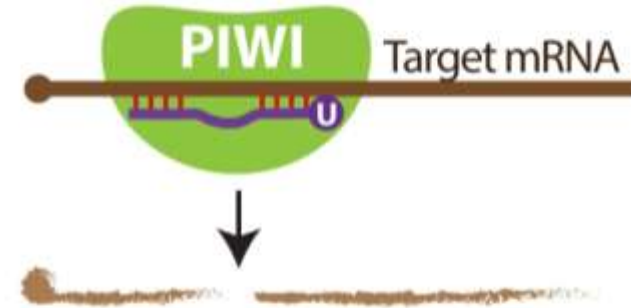
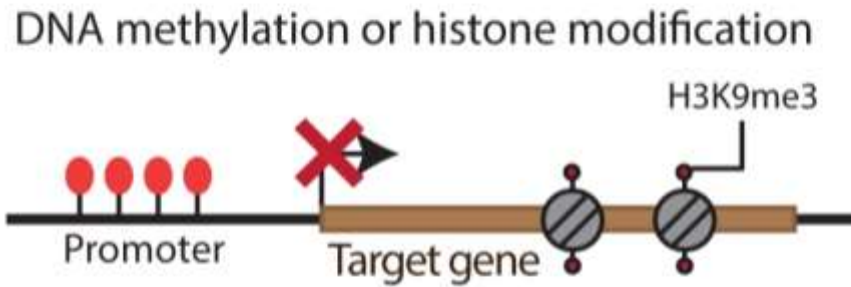
Contatto PIWI protein
DNMT



Riconoscimento
PIWI protein-piRNA
mRNA L1

TGS in the nucleus

PTGS in the cytoplasm



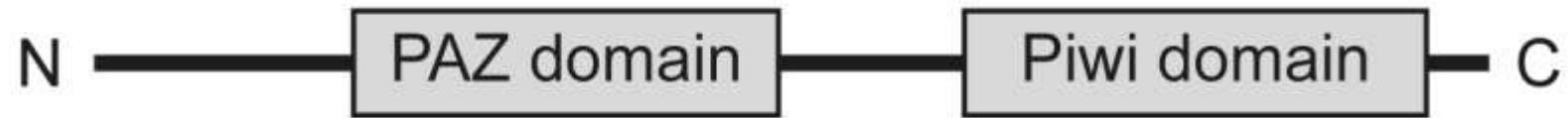
Riconoscimento
H3K9 – HP1

Nuclear silencing



mRNA cleavage

Inactivation of transposable elements
or
silencing of endogenous gene expression

A PIWI protein



B

 Human	 Mouse
PIWIL1 (HIWI)	PIWIL1 (MIWI)
PIWIL2 (HILI)	PIWIL2 (MILI)
PIWIL3 (HIWI3)	—
PIWIL4 (HIWI2)	PIWIL4 (MIWI2)

Inibizione Elementi Mobili - piRNA

- **Maturazione Pi RNA?**

E' una via quella di maturazione molto complessa e con grandi differenze tra organismi

“piRNA is the most diverse class of regulatory RNAs in general. According to piRBase, the number of unique piRNA sequences in the mouse is **over 68 million**”

Inibizione Elementi Mobili - Tudor Domains

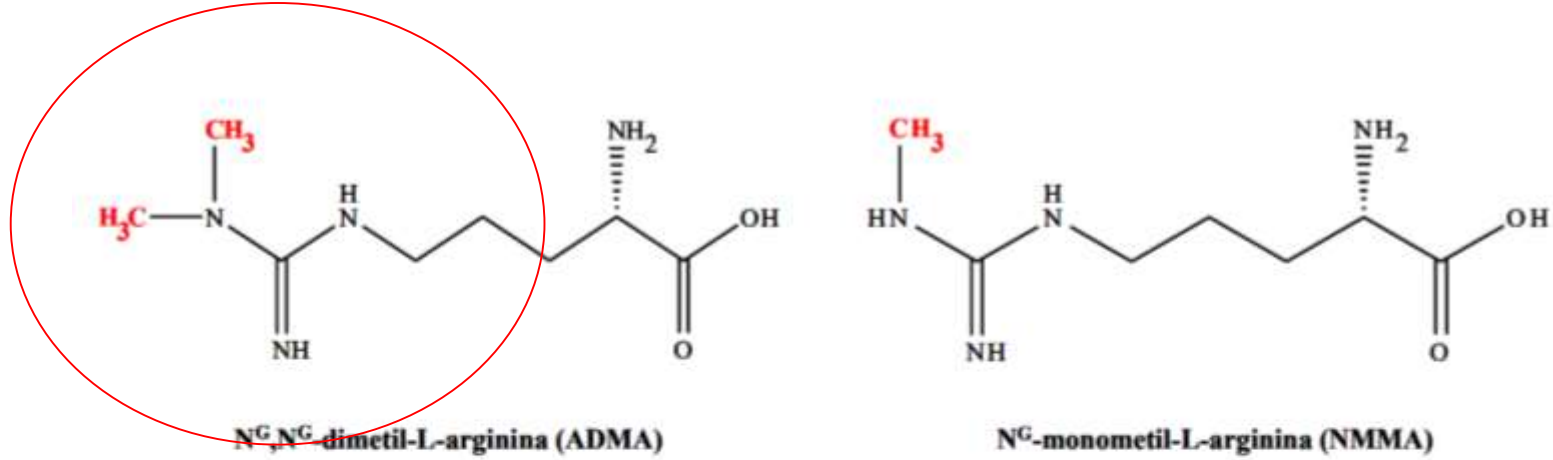
- Non ho compreso la differenza fra i piRNAs, PIWI, MIWI e la connessione con le proteine TUDOR.
- Linee germinali e contributo delle proteine appartenenti alla famiglia di Tdrd.
- In che modo i domini Tudor partecipano alla biogenesi dei pi-RNA in relazione alla dimetilazione asimetrica delle Arginine?

Inibizione Elementi Mobili - Tudor Domains

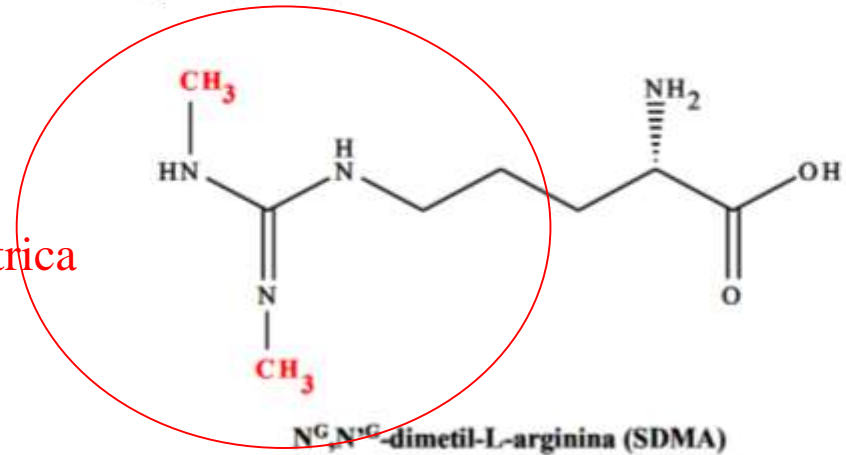
- I domini tudor permettono un riconoscimento proteina proteina tra gli enzimi che maturano i piRNA. In particolare le proteine con le Arg di-metilate in modo simmetrico.
- l'espressione sia dei messaggeri per PIWI proteins che dei piRNA è particolarmente efficiente nella linea germinale
- Quando si interrompe il riconoscimento (es trd12 KO) si interrompe il processo e ci sono disastri come l'atrofia testicolare (esempio modello murino)

Di-metil arginina asimmetrica (ADMA) e simmetrica (SDMA)

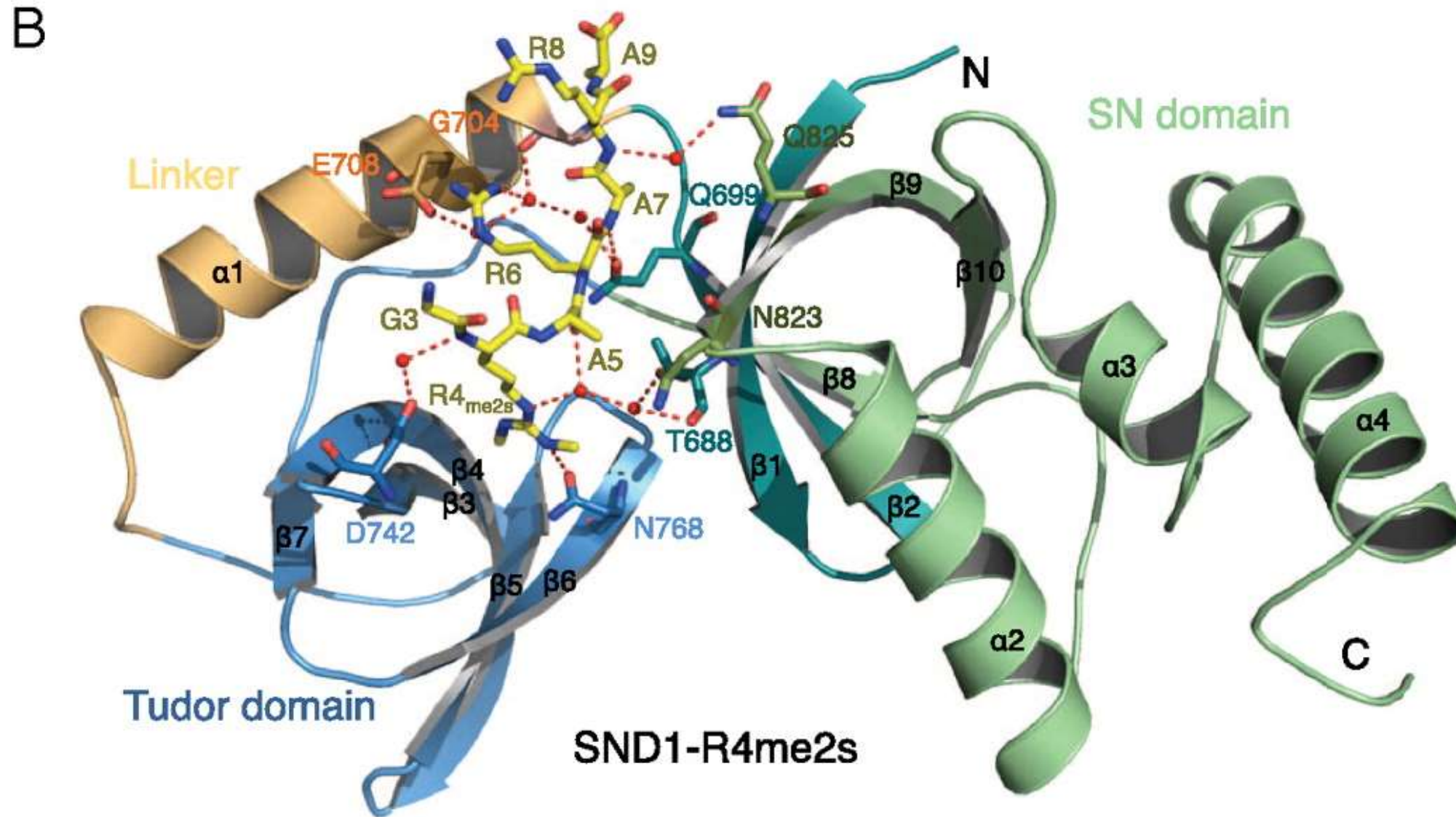
Asimmetrica

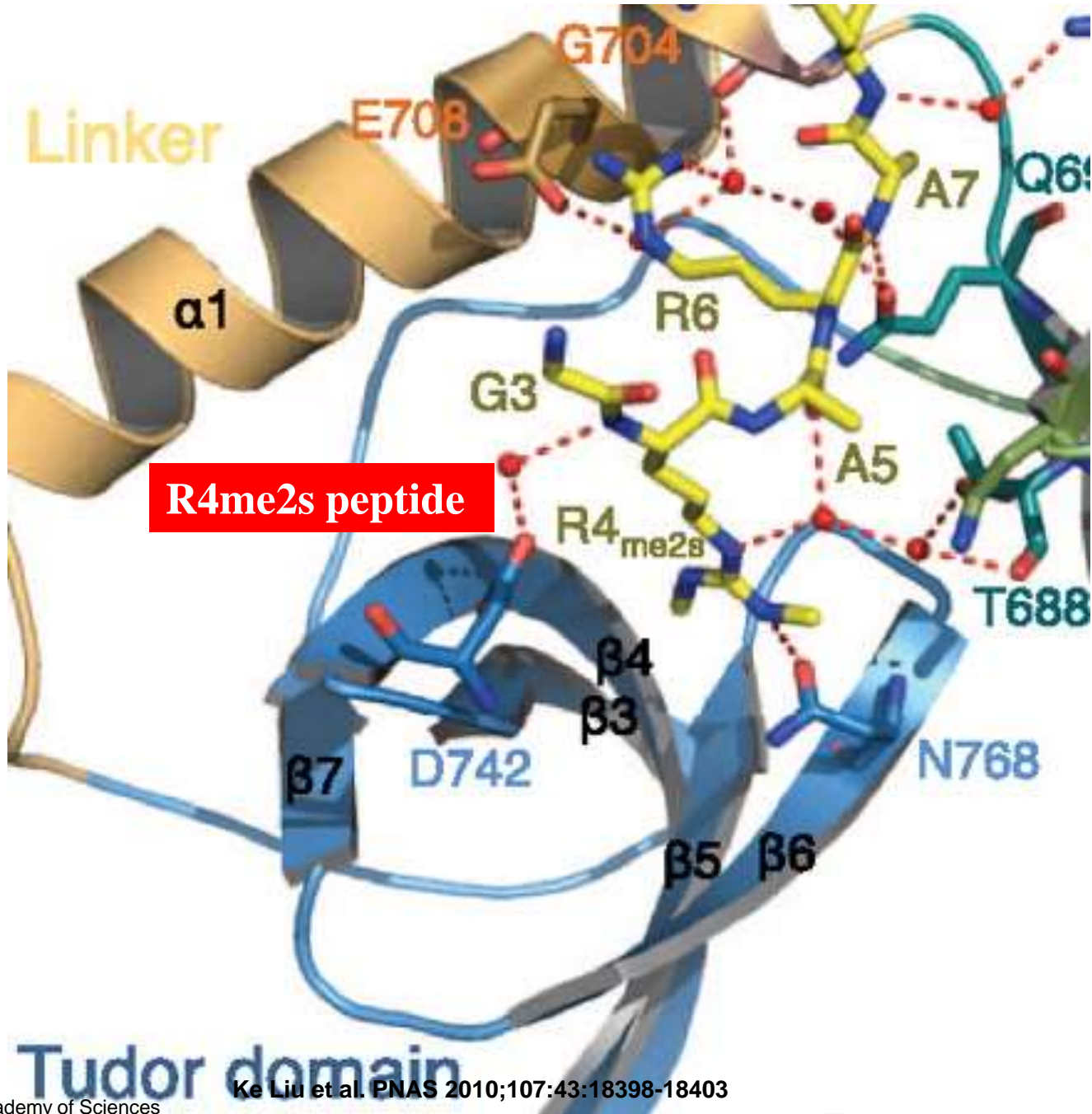


Simmetrica

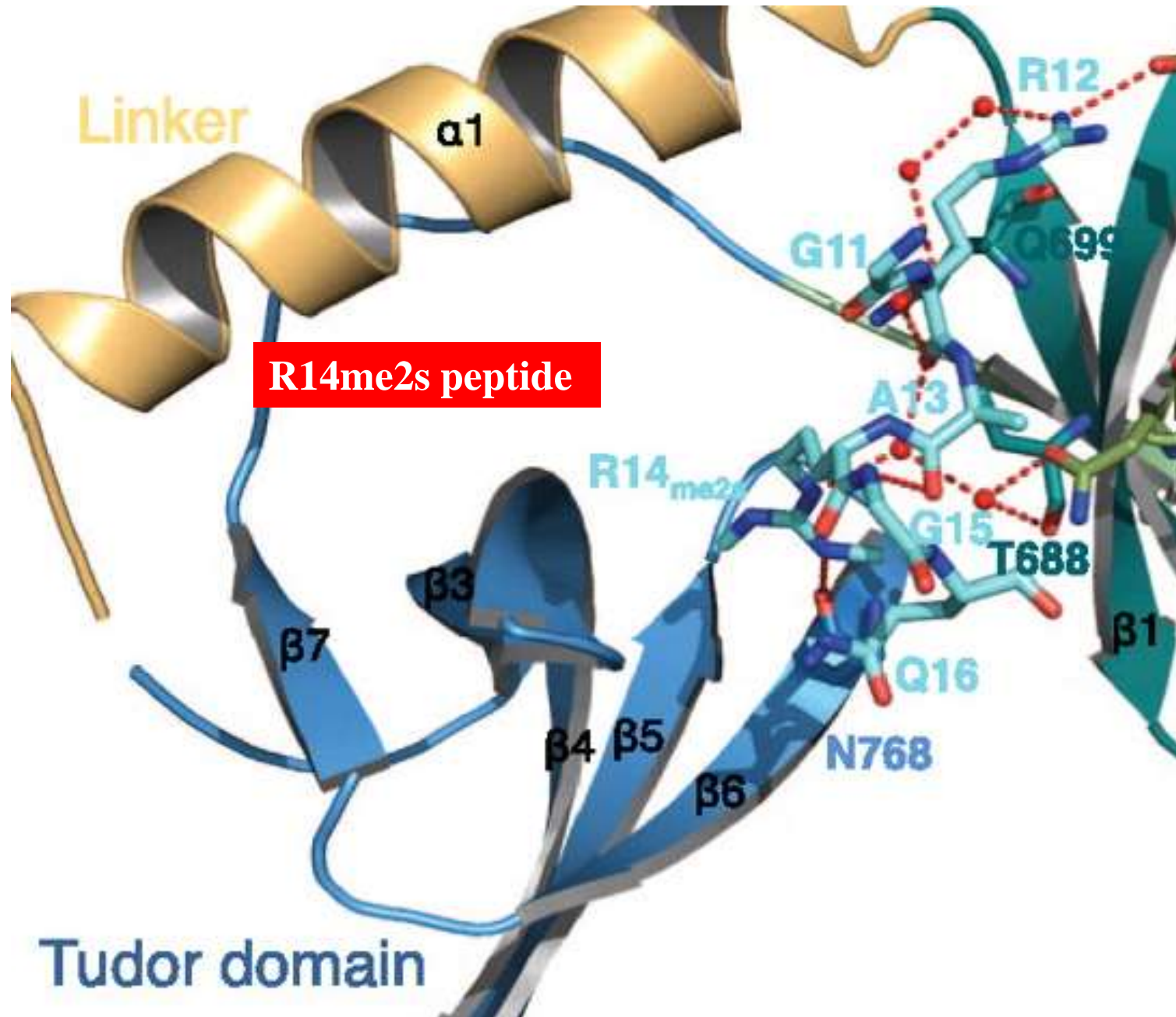


Crystal structures of human extended Tudor domain protein in complex with PIWIL1 peptides.





Crystal structures of human extended Tudor domain in complex with PIWIL1 peptides.



Extended Tudor domain preferentially binds Piwi peptides with symmetrical methylation of Arg R me2s

Peptide name	Sequence	Kd (μM) (pH 7.5, 50mM NaCl)	Kd (μM) (pH 7.5, 150mM NaCl)
R4me2s	TGRARARARGRARGQE	10 \pm 1	47 \pm 6
R4me2a	TGRARARARGRARGQE	42 \pm 2	188 \pm 38
R4me1	TGRARARARGRARGQE	19 \pm 1	97 \pm 20

Nessun legame agli istoni metilati!

Histone H3K4me1/2/3	ARTKQTARKST	No detectable binding	No detectable binding
Histone H3K9me1/2/3	ARTKQTARKSTGGKA	No detectable binding	No detectable binding

R: modified arginine; K: modified lysine; *: all Kd are measured by fluorescence polarization except H4R3me2s, which was measured by ITC. Ke Liu et al. PNAS 2010;107:43:18398-18403

Coronavirus - Proteasi

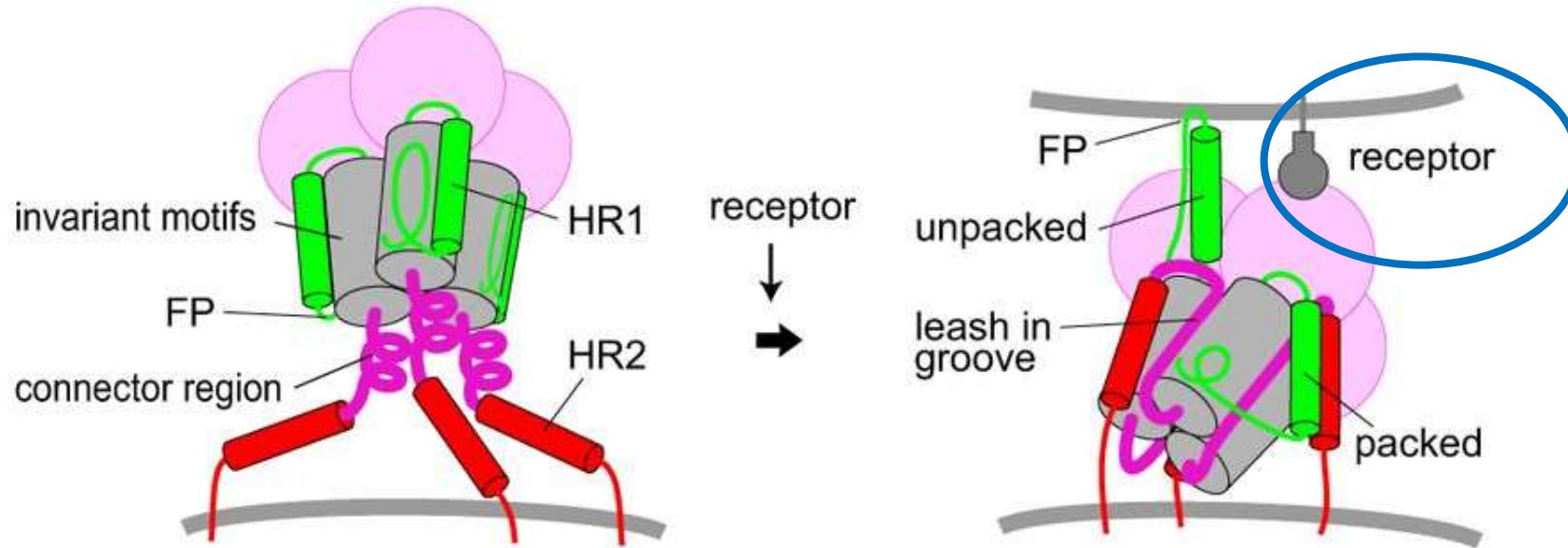
- Non mi è chiaro il concetto di protein priming

Schematic diagram of S protein activation.

A

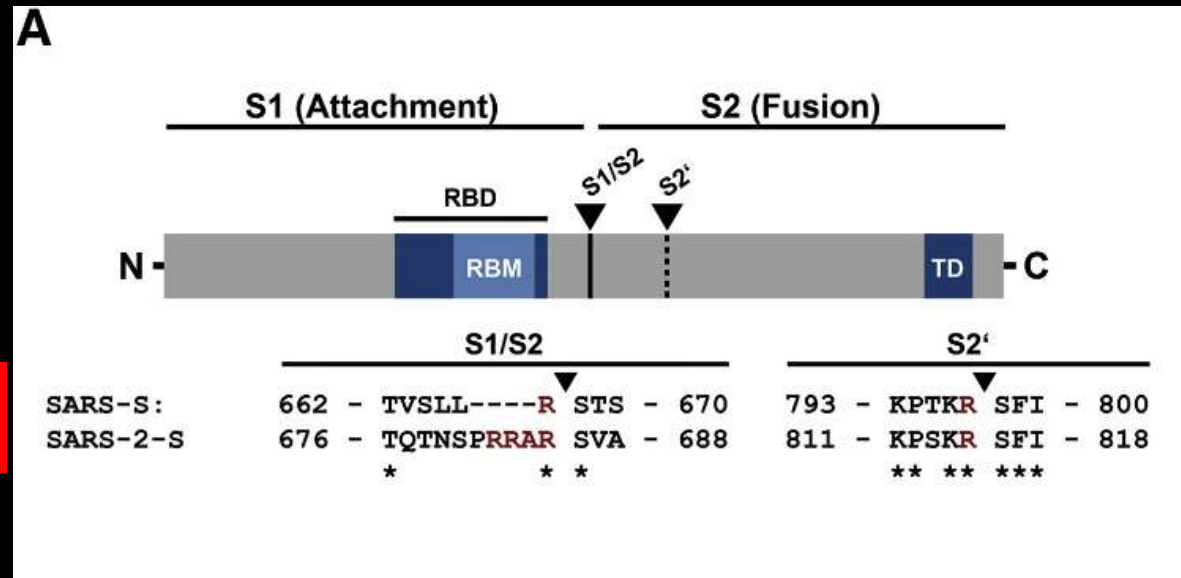
(i) pre-fusion

«liposome-binding activity»



Miyuki Kawase et al. J. Virol. 2019; doi:10.1128/JVI.00785-19

Figure 1



SARS-CoV
SARS-CoV-2

Virus entry requires **S protein priming** by cellular proteases, which cleave S protein at the **S1/S2** and the **S2'** site and allows fusion of viral and cellular membranes, a process driven by the S2 subunit

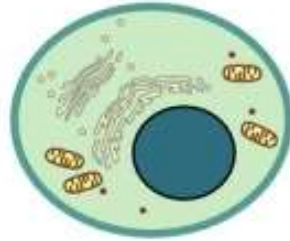
Coronavirus - Proteasi

- Proteasi dell'ospite FURINA e TMPRSS2 hanno la medesima funzione nella maturazione dello Spike in tessuti diversi o sono molecole diverse? non ho compreso bene la differenza fra le due.

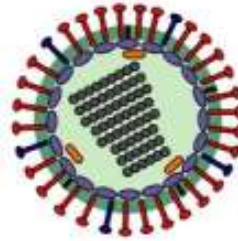
Furin



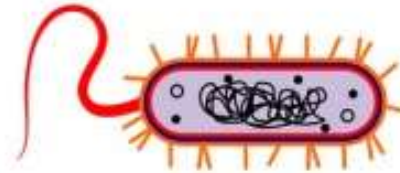
**Mammalian
substrates**



**Viral
substrates**



**Bacterial
substrates**

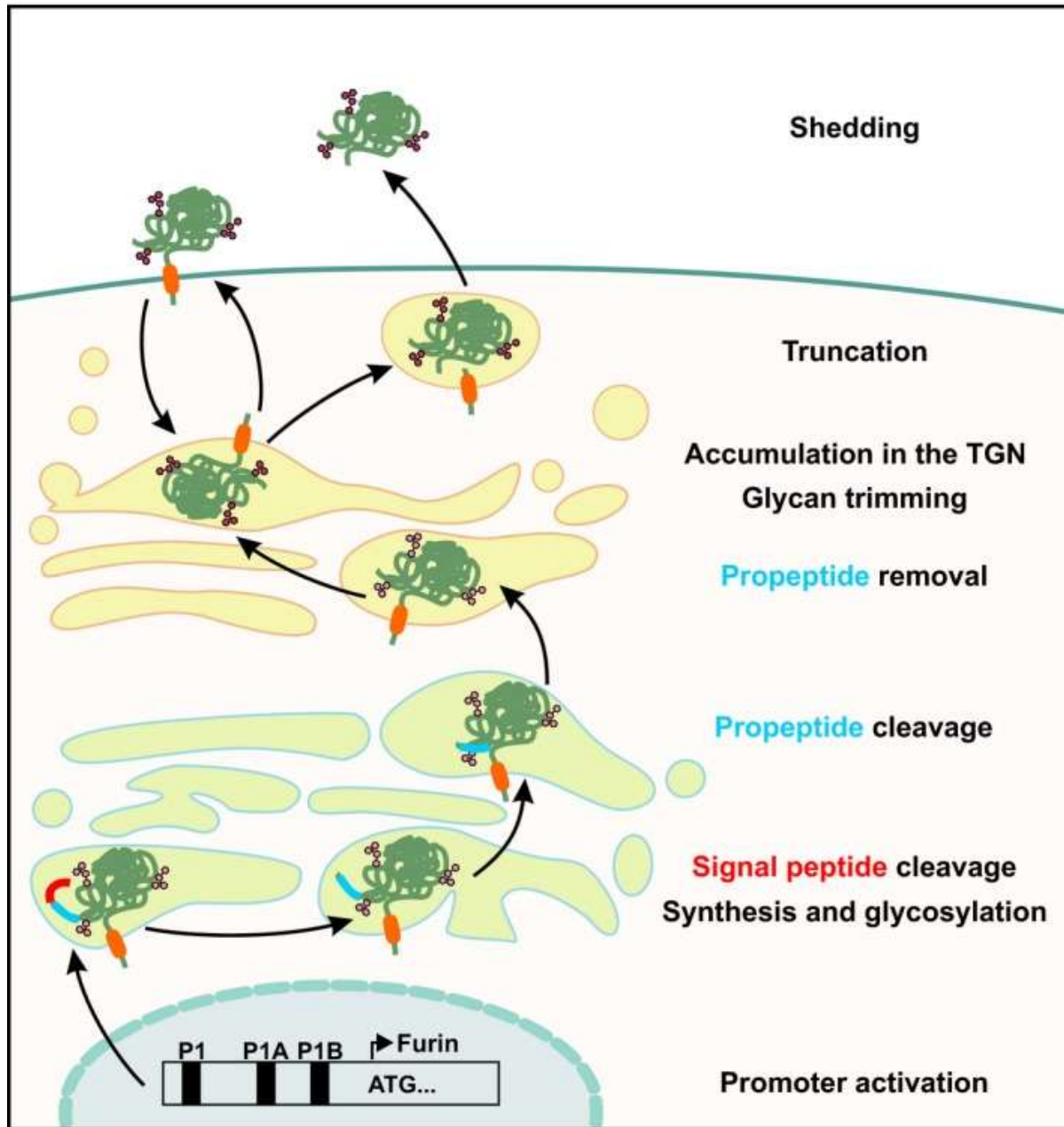


Proteolytic activation

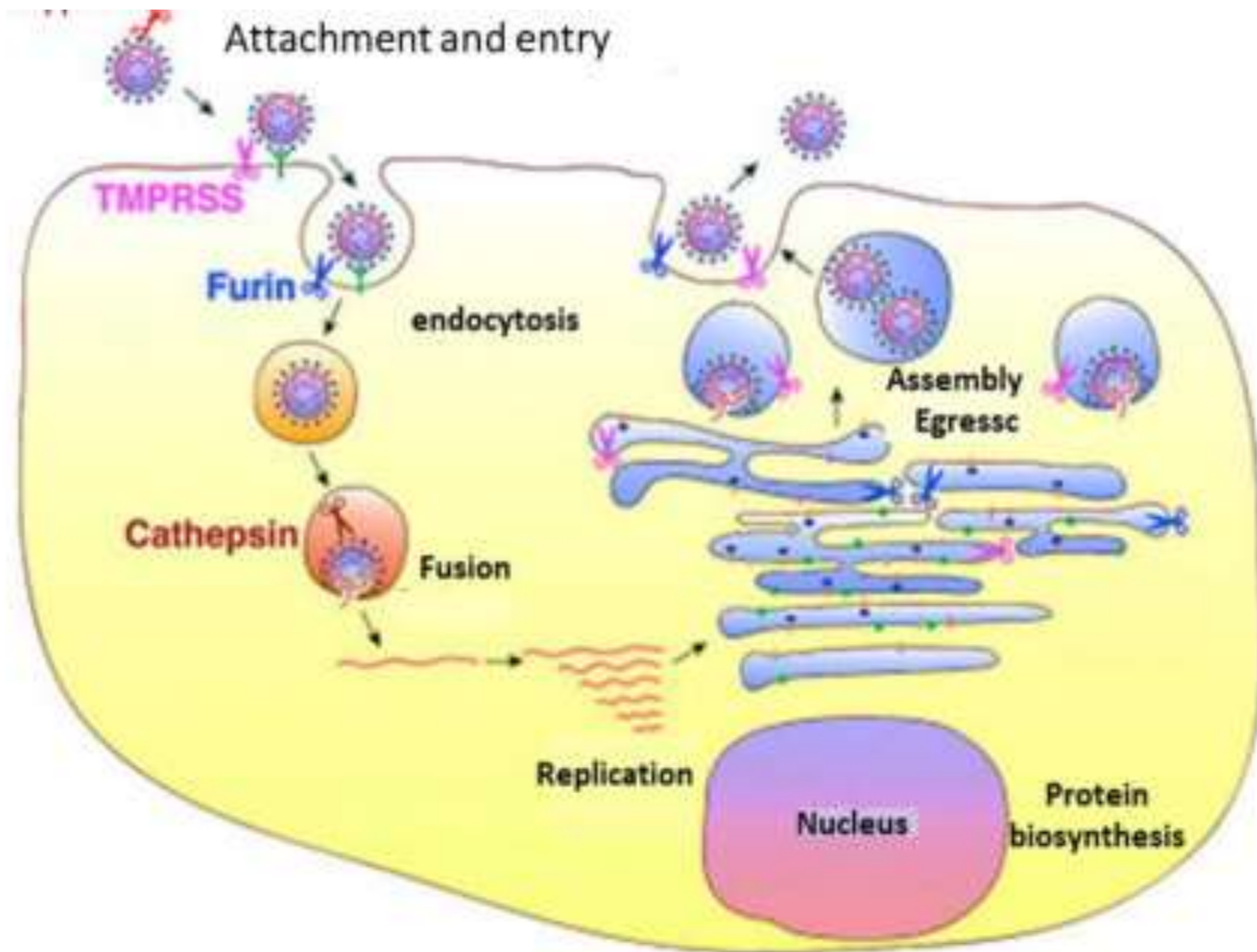
Hormones
Growth factors
Receptors
Adhesion molecules
Enzymes

Herpesvirus gB
Coronavirus S
Flavivirus prM
Togavirus E2
Bornavirus GP

Anthrax toxin
Diphtheria toxin
Pseudomonas exotoxin A
Shiga toxin
Shiga-like toxins



FURINA



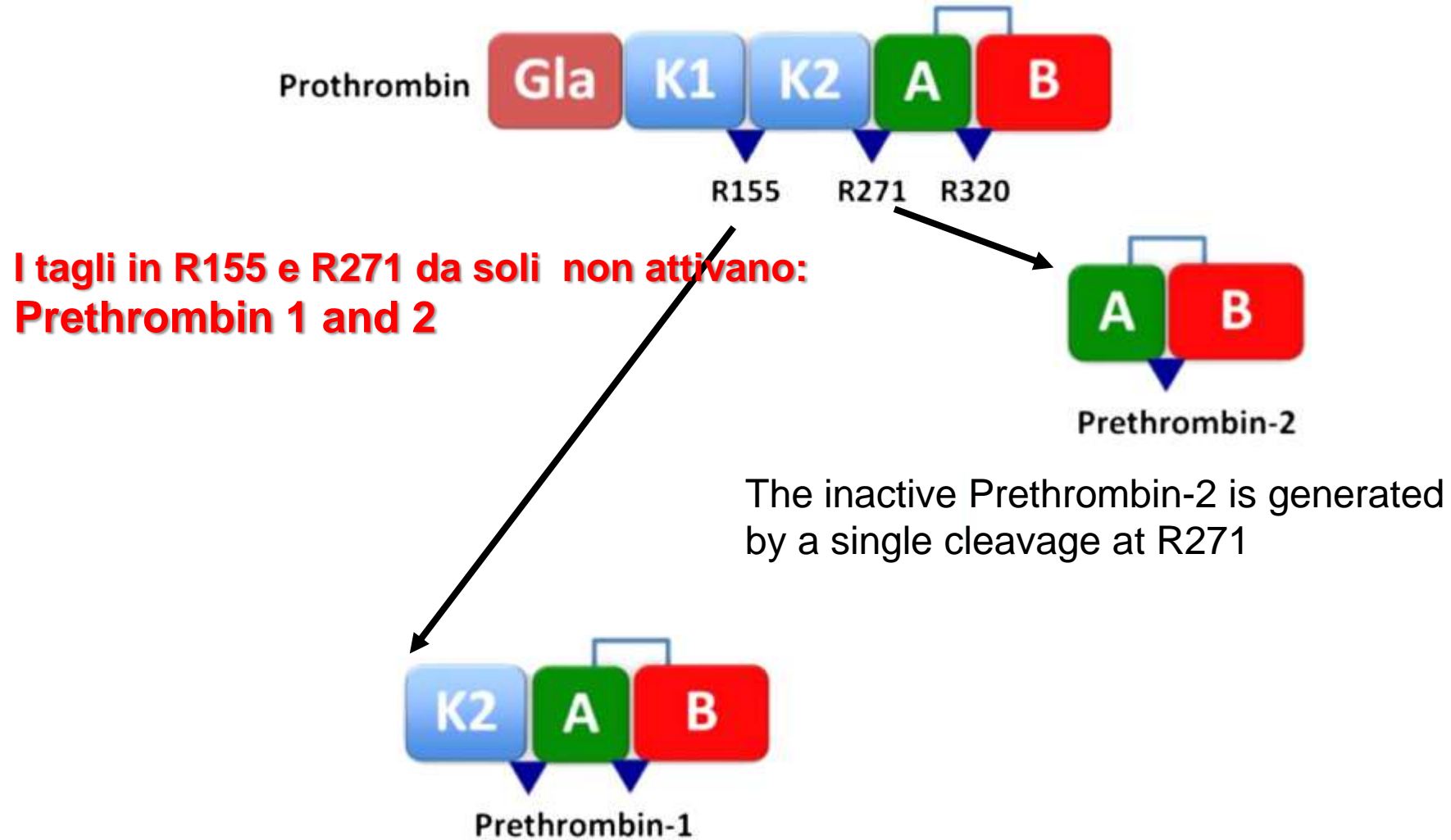
Coronavirus - Proteasi

- Stavo rivedendo la lezione 6 nella parte riguardo l'inibizione della proteina Tmprss2 per ridurre lo sviluppo virale; non riesco a capire come questa proteina possa interagire con lo spike, si trova vicino al sito di interazione tra ace2 e spike?

Trombina Attività ed attivazione

- Lei ha detto che questo enzima possiede due specifici siti di taglio riconosciuti dal complesso protrombinasi e attraverso una ricerca personale ho scoperto che questi siti sono rispettivamente
 - - tra arginina e triptofano in pozione N terminale
 - - tra arginina e isoleucina in posizione C terminale
- Volevo chiederle se fossero informazioni corrette poiché nella sua lezione ha parlato di un'esposizione (a seguito del taglio) della porzione ammino-terminale che corrisponde ad una isoleucina-valina nel nuovo peptide libero...

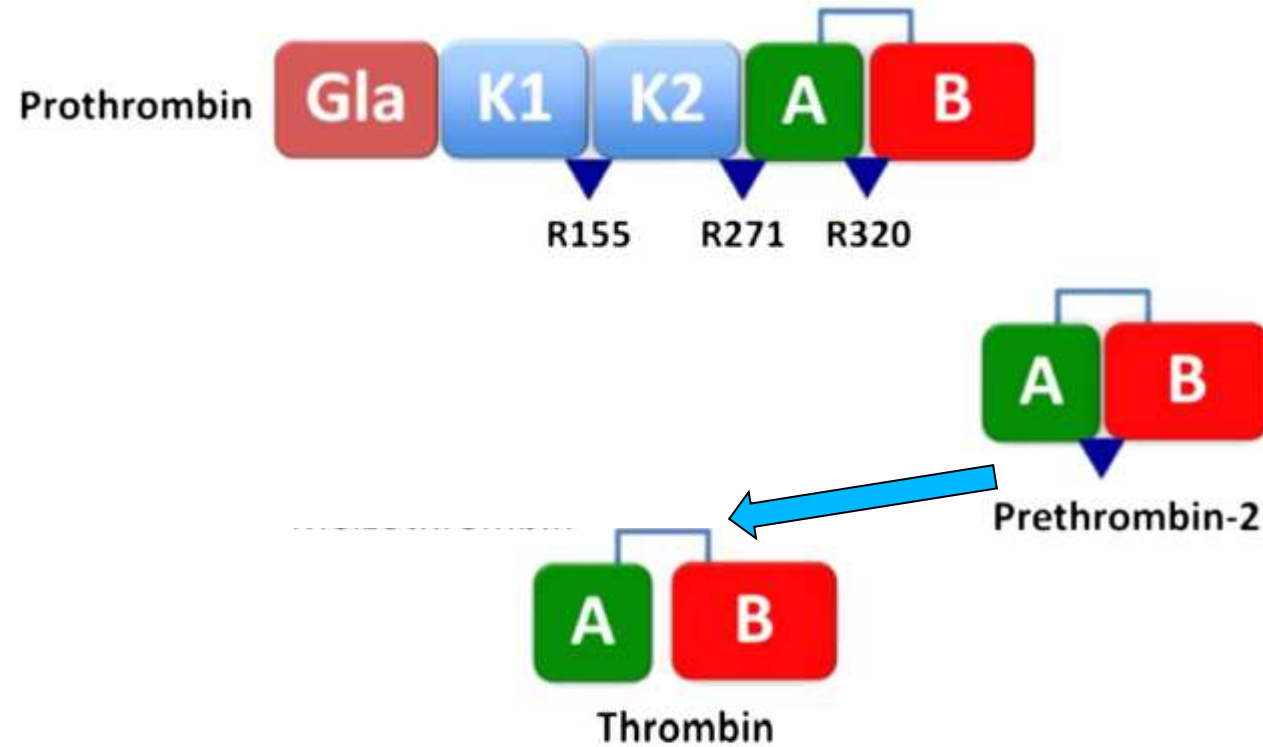
Schematic representation of prothrombin activation.



Zhiwei Chen et al. PNAS 2010;107:45:19278-19283

PNAS

Cleavage at R271 and R320 produce Thrombin



Cleavage at R320 separates the A and B chains and generates an active protease.

The inactive Prethrombin-2 is generated by a single cleavage at R271

Prothrombin is activated to thrombin by two proteolytic cleavages

Exosite-driven substrate specificity and function in coagulation 55

Table 1 Sites of cleavage in the human vitamin K-dependent zymogens*

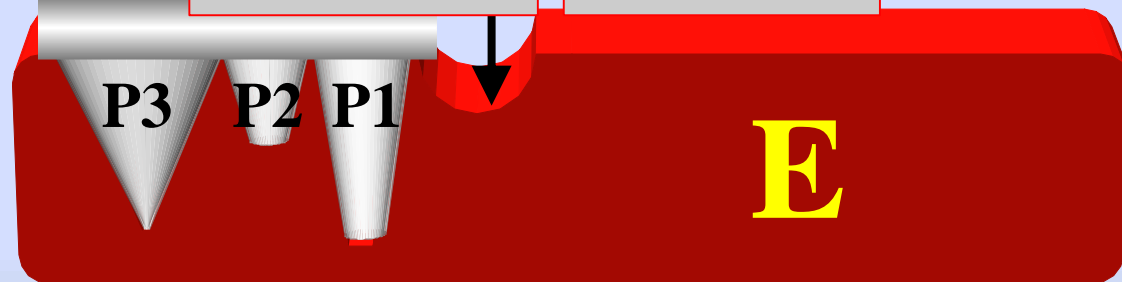
Enzyme	Substrate†	P ₄	P ₃	P ₂	P ₁	↓	P ₁ '	P ₂ '	P ₃ '	P ₄ '
Xa/Va	II	I	E	G	R		T	A	T	S
	II ₍₁₅₋₁₆₎	I	D	G	R		I	V	E	G

R271

Enzyme	Substrate†	P ₄	P ₃	P ₂	P ₁	↓	P ₁ '	P ₂ '	P ₃ '	P ₄ '
Xa/Va	II	I	E	G	R		T	A	T	S
	II ₍₁₅₋₁₆₎	I	D	G	R		I	V	E	G

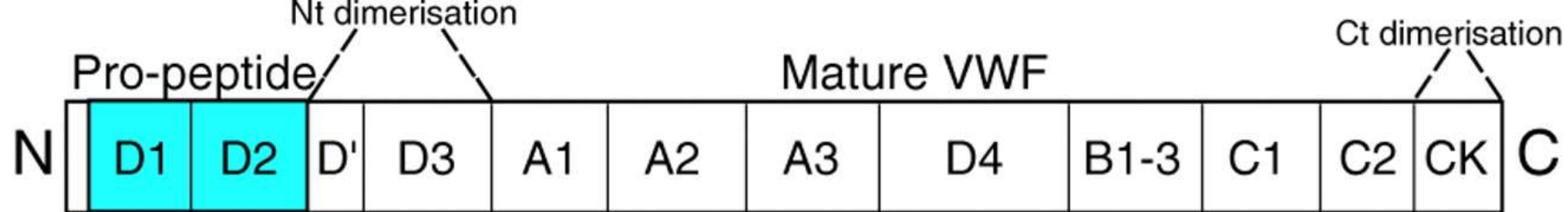
R320 alias R15

I321 alias I16



Fattore von Willebrand

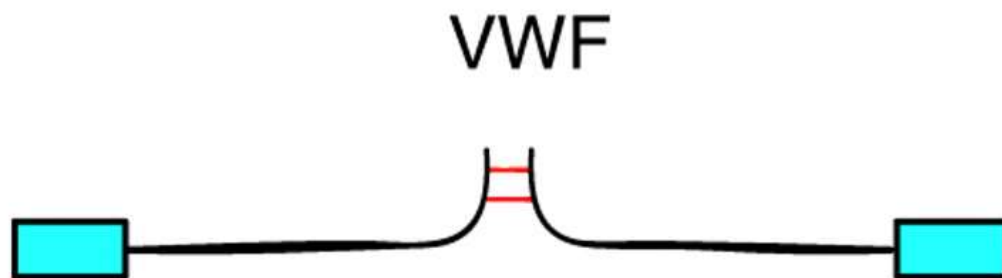
- VWF: - Può riesplorare, passaggio per passaggio, la biosintesi del Fattore di Von Willebrand come al minuto 49 della lezione del 27 aprile, dal pre-poli-peptide al multimerico maturo?

A**B**

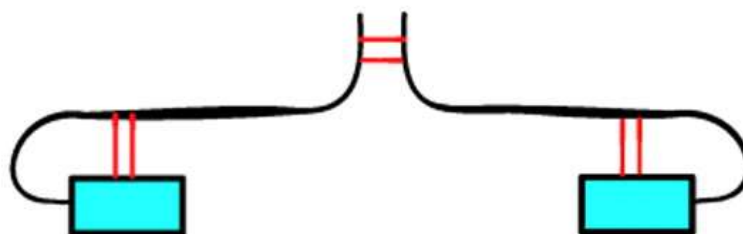
Location and process

ER

C-terminal dimerisation

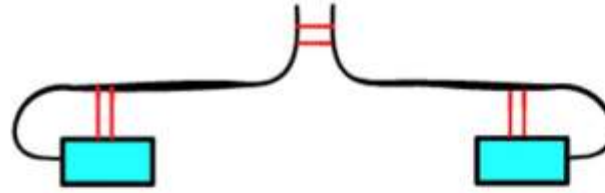
**ER and Golgi**

N-terminal intrachain
disulphide bonds form



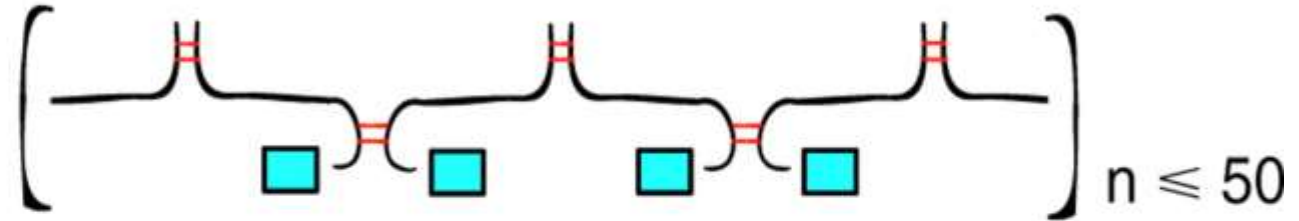
ER and Golgi

N-terminal intrachain disulphide bonds form



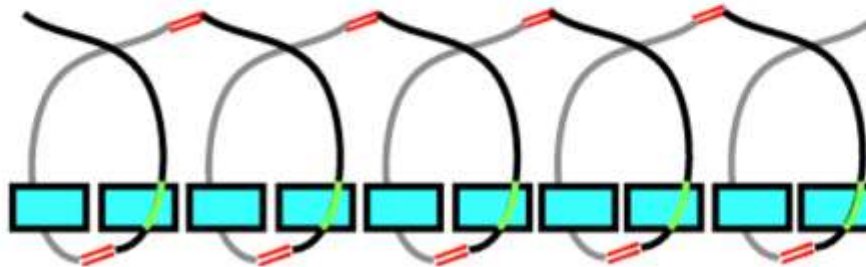
Golgi and TGN

N-terminal interchain disulphide bonds replace intrachain disulphide bonds and cleavage of pro-peptide



TGN and WPB

Ionic interaction between mature VWF and pro-peptide occurs, resulting in tubulation



Key:

 Propeptide  mature VWF  Disulphide bond  Ionic interaction

Biosynthesis of VWF

