

TELOMERI E COMPLESSI DEL TELOMERO

Telomeres are the terminal **nucleoprotein** structures located at the ends of eukaryotic chromosomes.

These structures function as

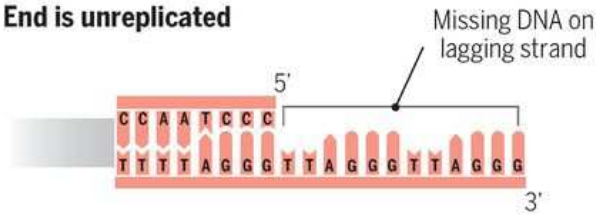
A **guardians of genome stability** by **limiting unwanted DNA repair** activity at chromosome ends, and in human cells,

B by **controlling the total number of times a cell can divide**, thereby limiting the accumulation of genomic instability in actively cycling cells

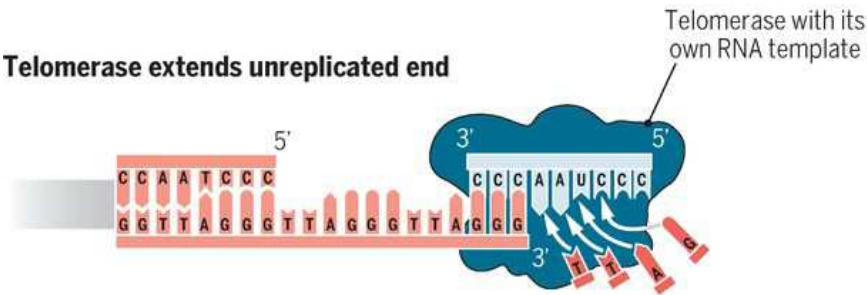
Long-term maintenance of telomeric DNA length requires telomerase.

A

End is unreplicated



Telomerase extends unreplicated end



Again, telomerase extends unreplicated end



Lagging strand is completed

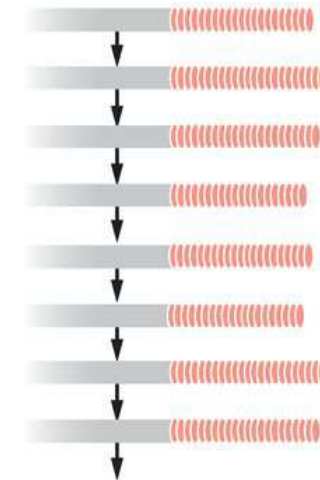
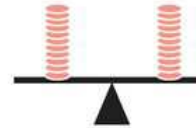


Long-term maintenance of telomeric DNA length requires telomerase.

B

Abundant telomerase as cell divides

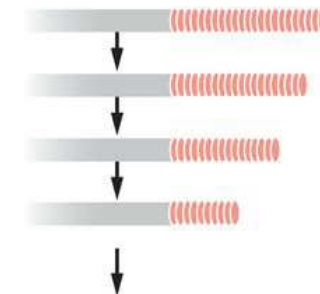
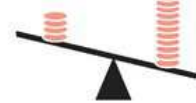
Addition and shortening stay balanced



Cells keep dividing
Most human cancers

C

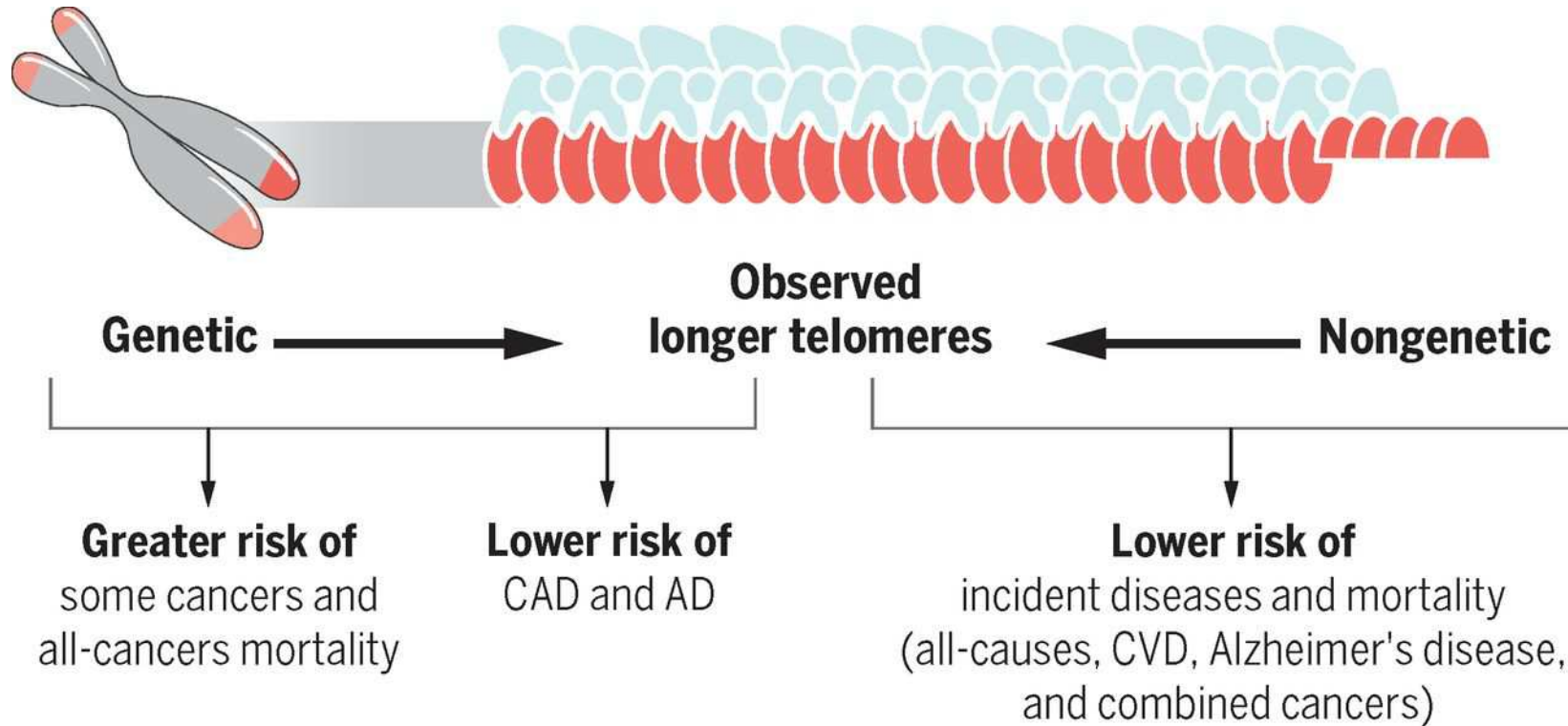
Insufficient telomerase as cell divides



Cell division STOPS after a delay
Senescence; cell malfunctions; genomic instability
Mitochondrial malfunction, pro-inflammatory,
tumorigenic factors



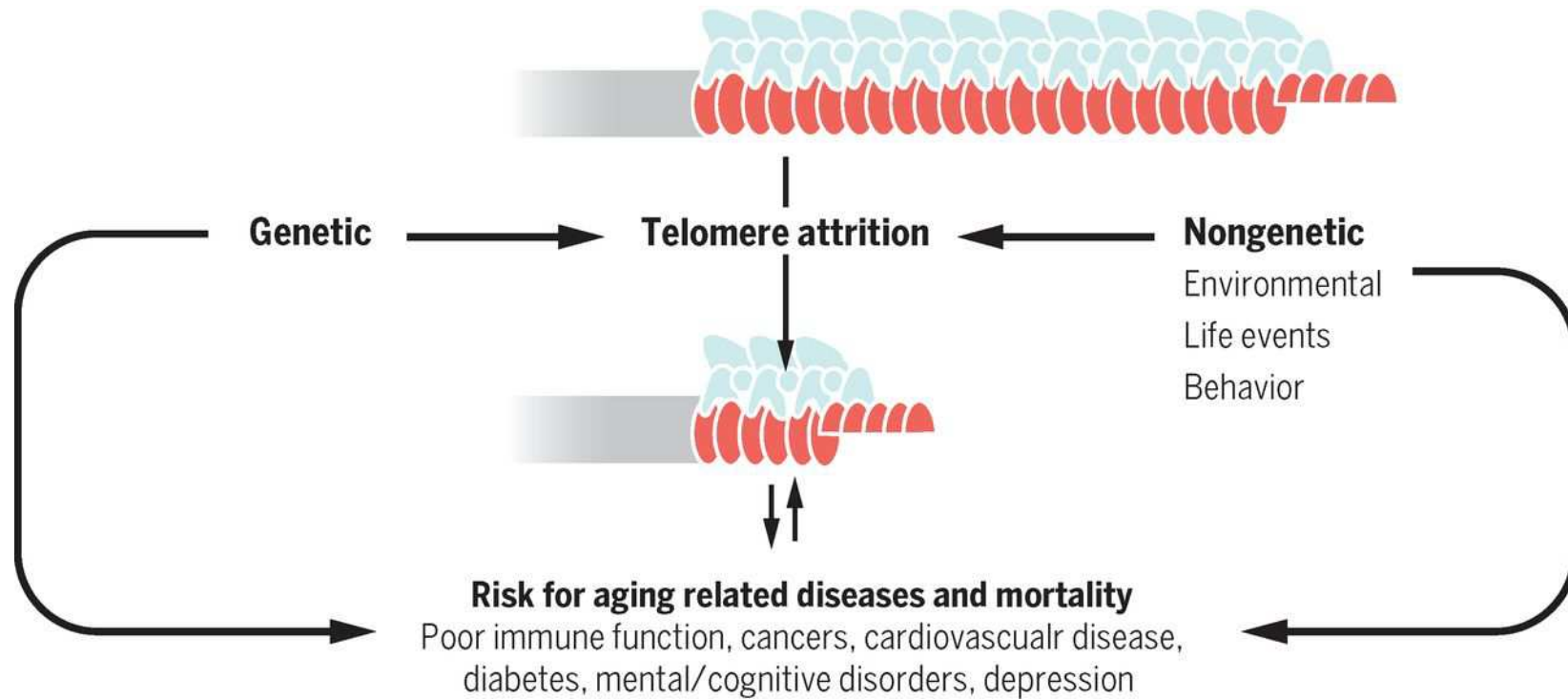
Different inputs to telomere maintenance have disease-specific consequences.



Elizabeth H. Blackburn et al. *Science* 2015;350:1193-1198



Relationship of telomere attrition to human aging-related diseases.



Elizabeth H. Blackburn et al. *Science* 2015;350:1193-1198



IL DNA Telomerico e le sue strutture alternative

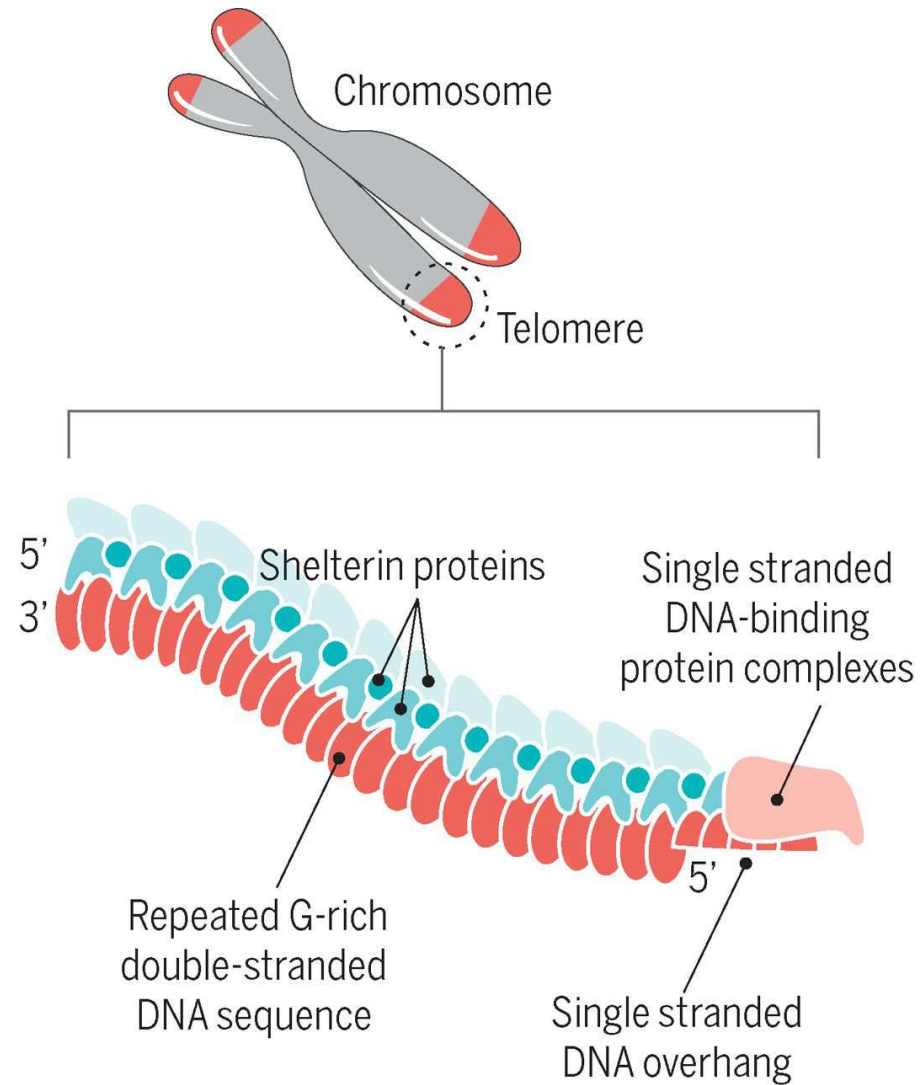
SEQUENZA TELOMERICA



5–15 kb in humans, ~48 kb in mice

Watson et al., BIOLOGIA
MOLECOLARE DEL GENE,
Zanichelli editore S.p.A.
Copyright © 2005

Telomere general structure.



Elizabeth H. Blackburn et al. *Science* 2015;350:1193-1198



The single-stranded 3' overhang folds back into the telomeric DNA, invades the double-helix, and anneals with the C-rich strand, forming a loop known as T-loop, thus hiding the very ends of chromosomal DNA.

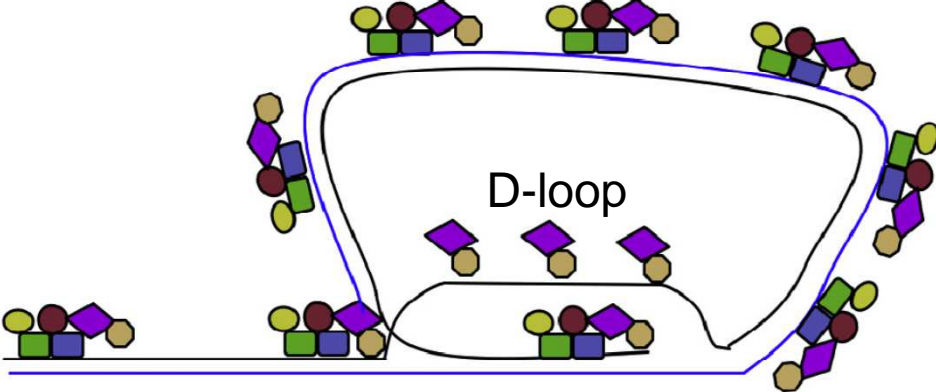


TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG-3'

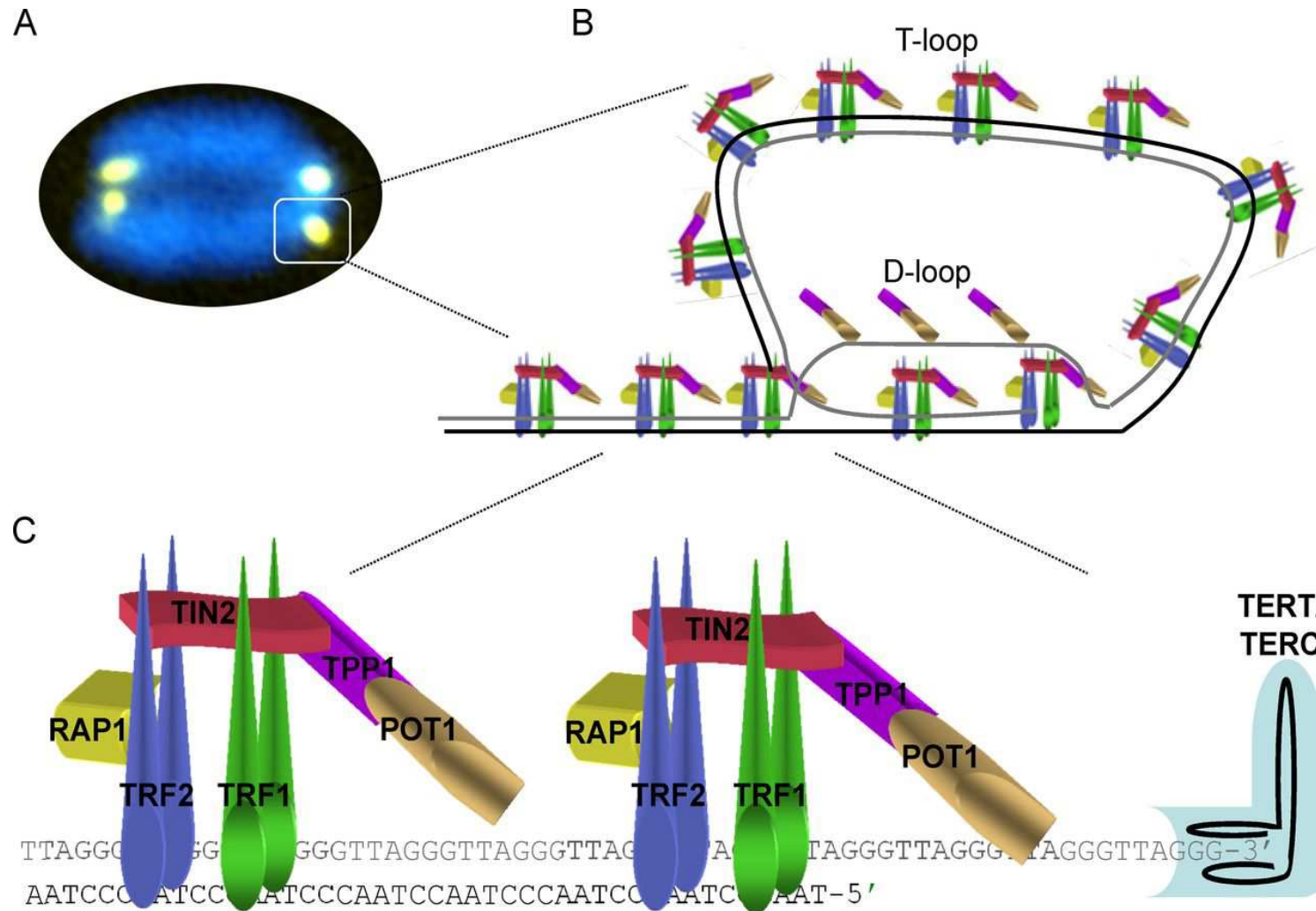
AATCCCAATCCCAATCCCAATCCAATCCCAATCCCAATCCCAATCCCAATC-5'

T-loop

D-loop



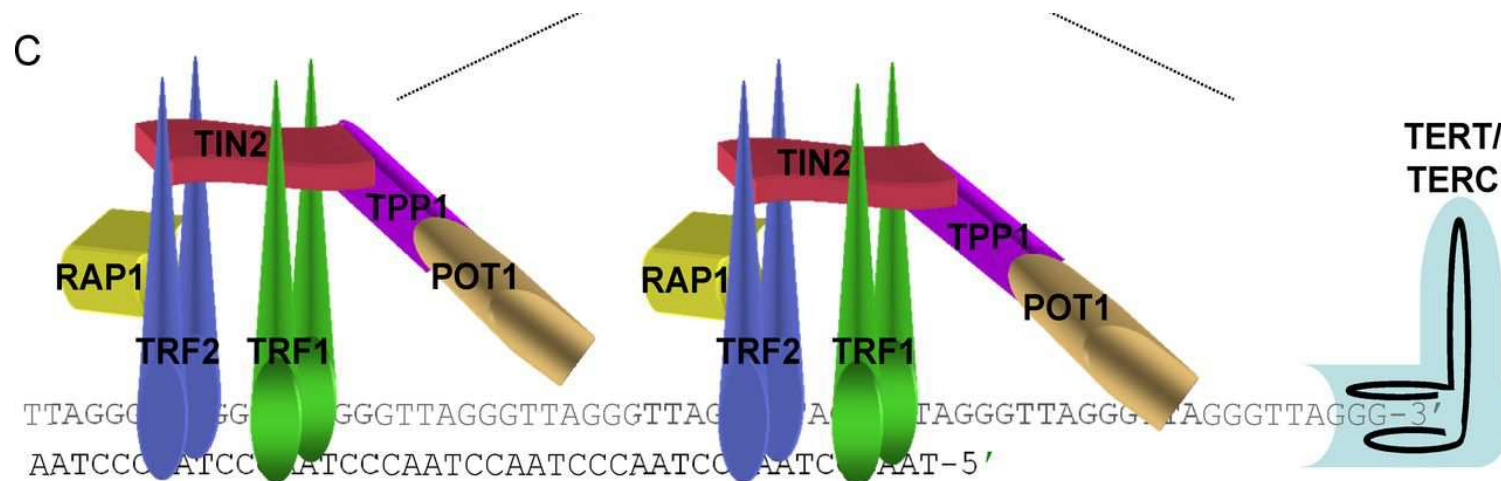
The shelterin complex and the structure of telomeres.



Paula Martínez, and Maria A. Blasco *J Cell Biol*
 doi:10.1083/jcb.201610111

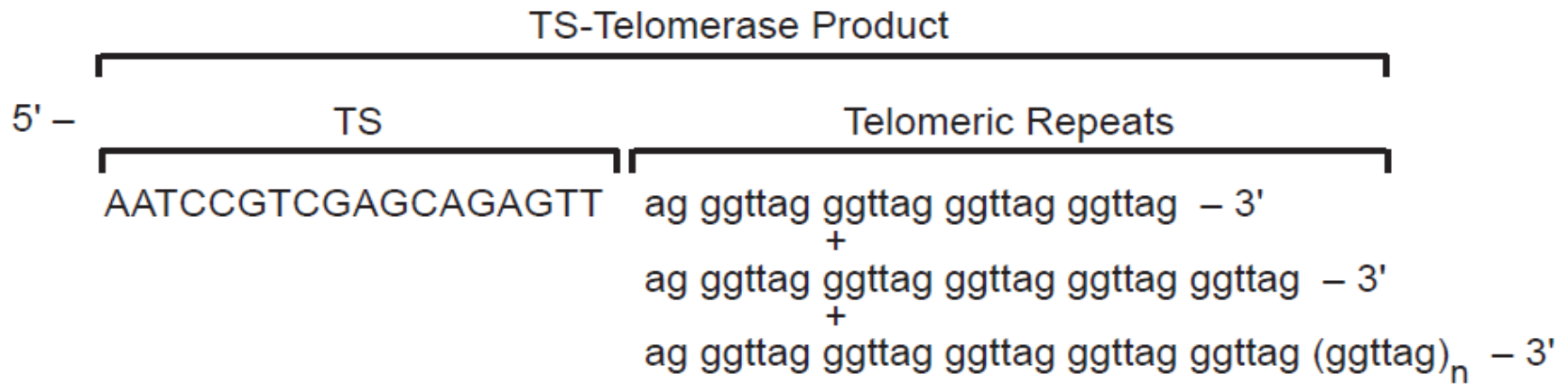
The shelterin complex and the structure of telomeres.

telomeric repeat binding factor 1 (TRF1)
telomeric repeat binding factor 2 (TRF2)
repressor-activator protein 1 (RAP1)
protection of telomeres protein 1 (POT1)
POT1-TIN2 organizing protein (TPP1)
TIN2

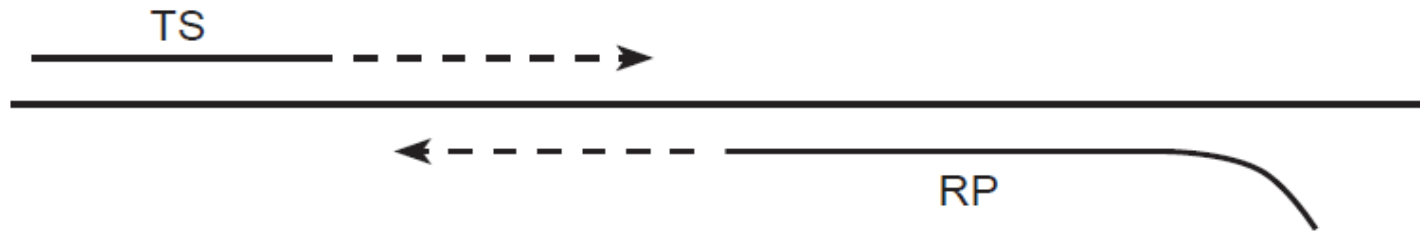


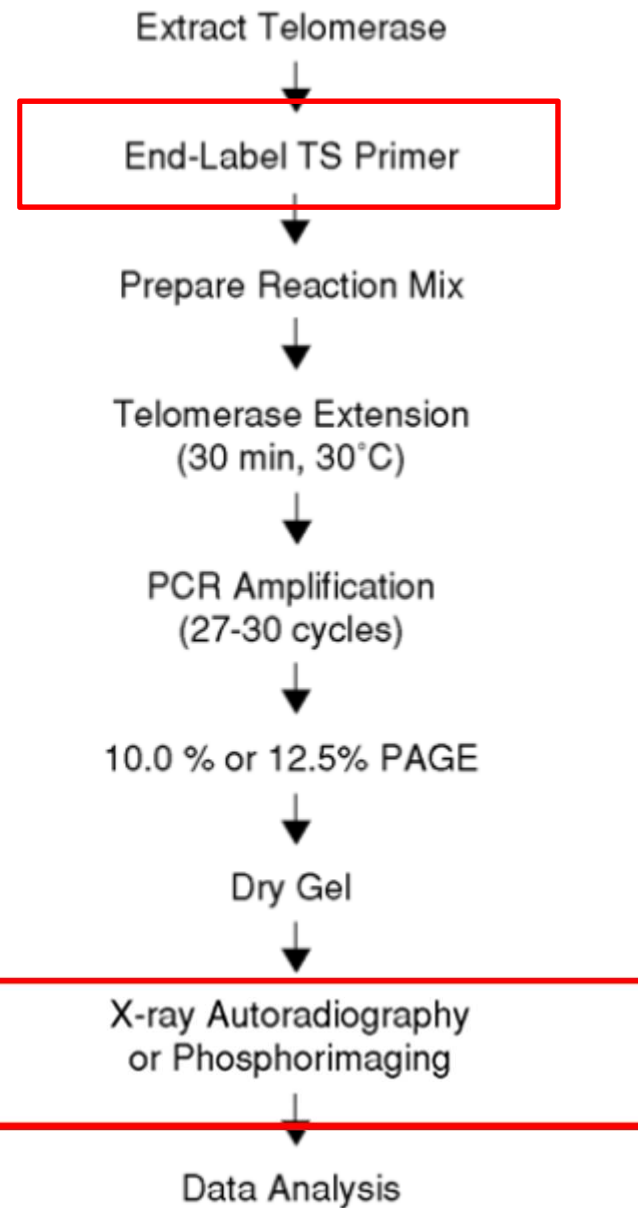
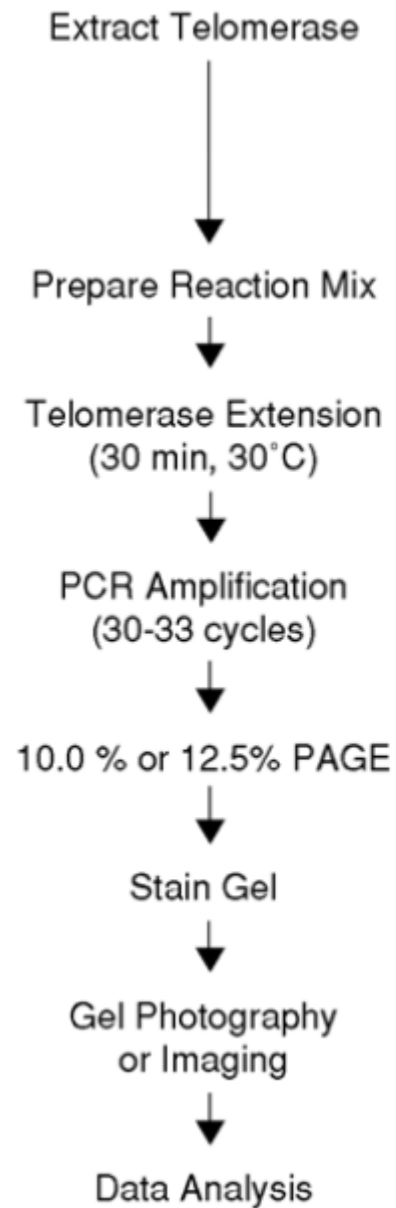
Paula Martínez, and Maria A. Blasco *J Cell Biol*
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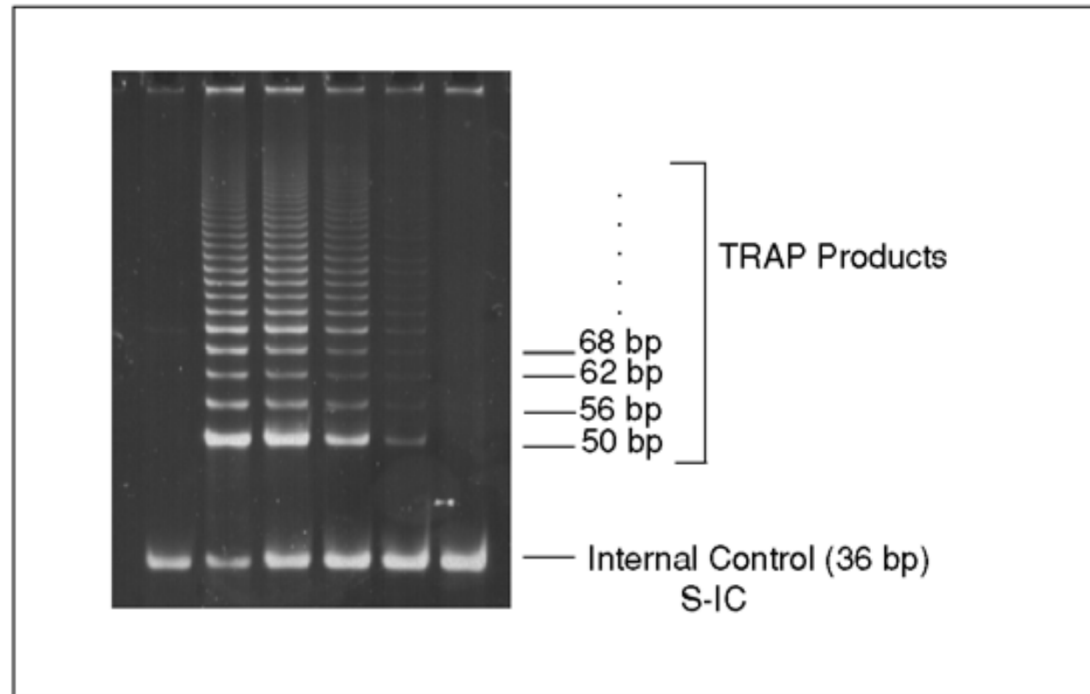
Metodi per lo studio dell'attività telomerasica



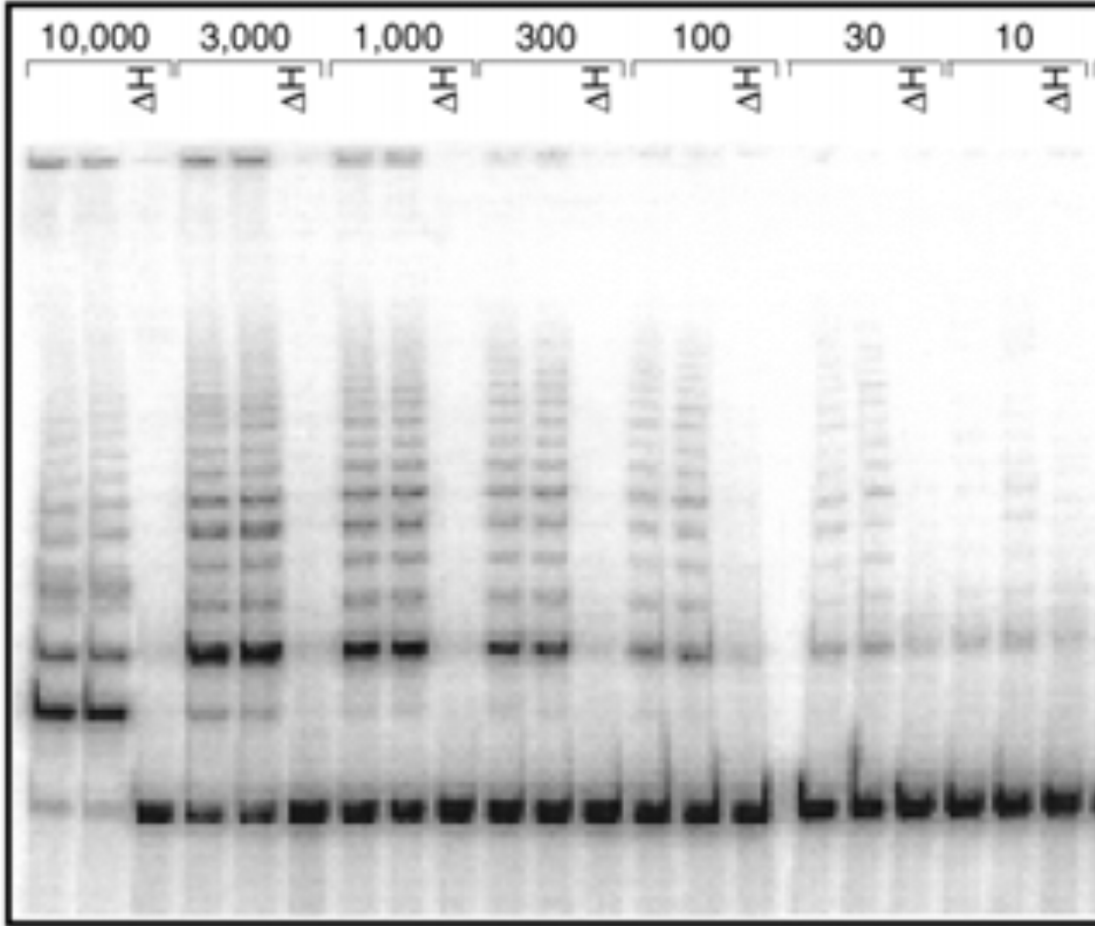
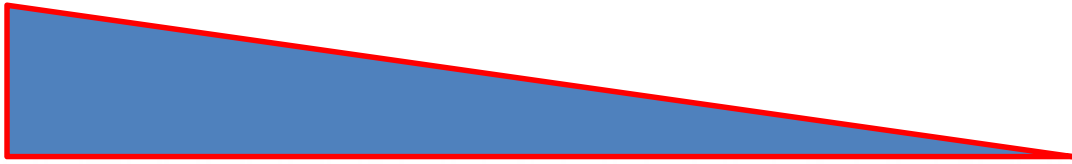
STEP 2. Amplification of TS-Telomerase Product By PCR





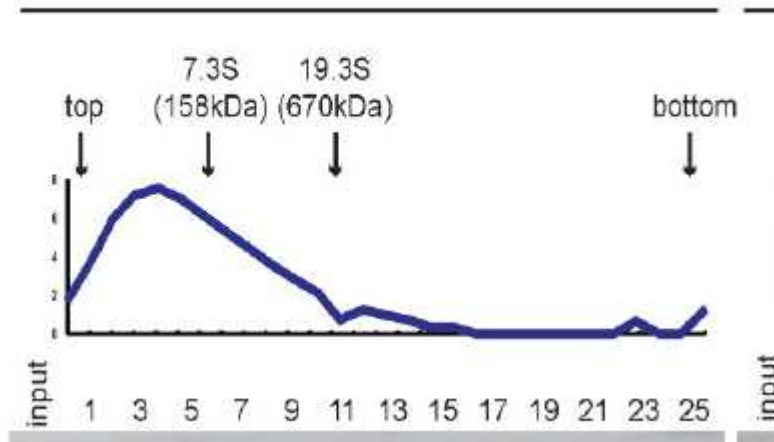


Telomeric Repeat Amplification Protocol



10-30% glycerol gradients

HeLa

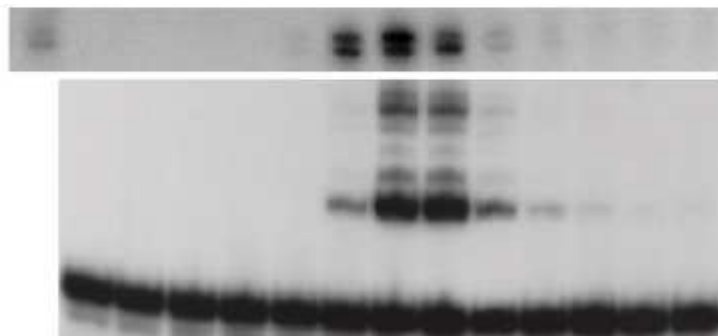


COMPLESSI TELOMERICI

Total protein

NB: TERC

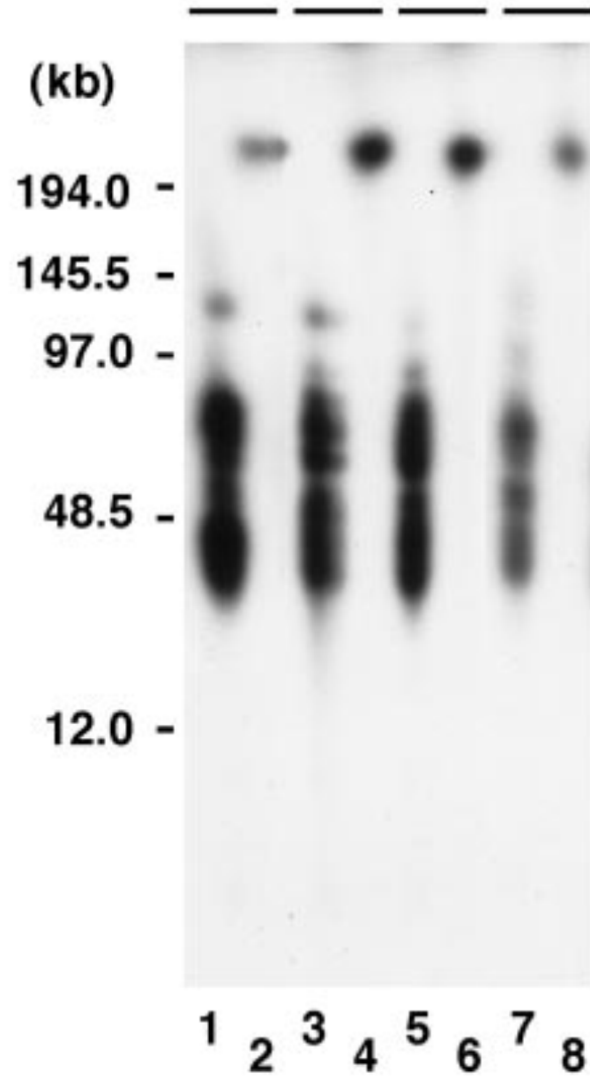
TRAP



Telomeric Repeat Amplification Protocol

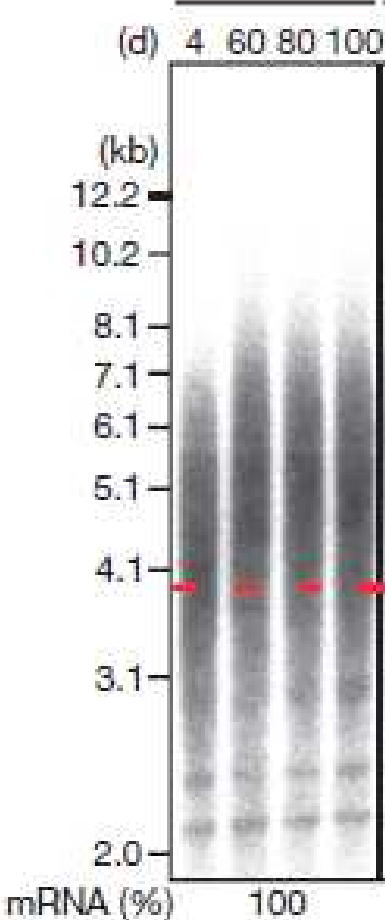
Metodi per lo studio dello stato dei telomeri

DNA TELOMERIC



digested with RsaI and Hinf - Odd lanes
pulse-field gel electrophoresis
hybridized with the telomeric specific [TTAGGG]₃ probe

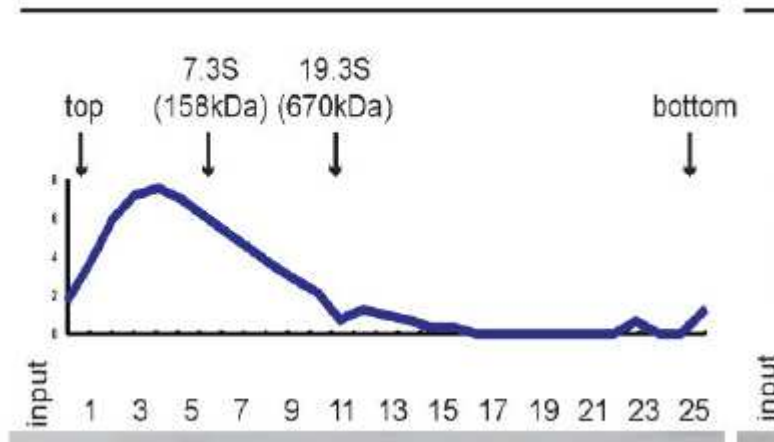
DNA TELOMERICO



Complessi macromolecolari associati al Telomero: funzioni

10-30% glycerol gradients

HeLa

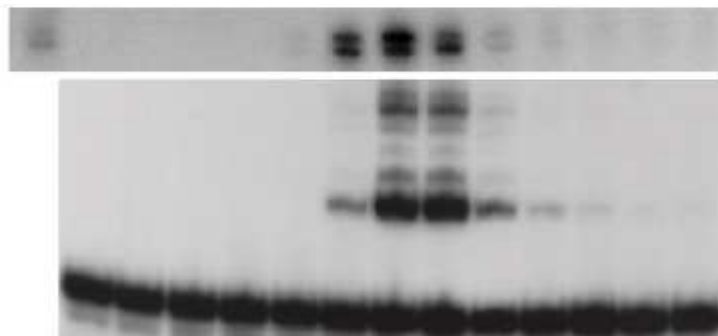


COMPLESSI TELOMERICI

Total protein

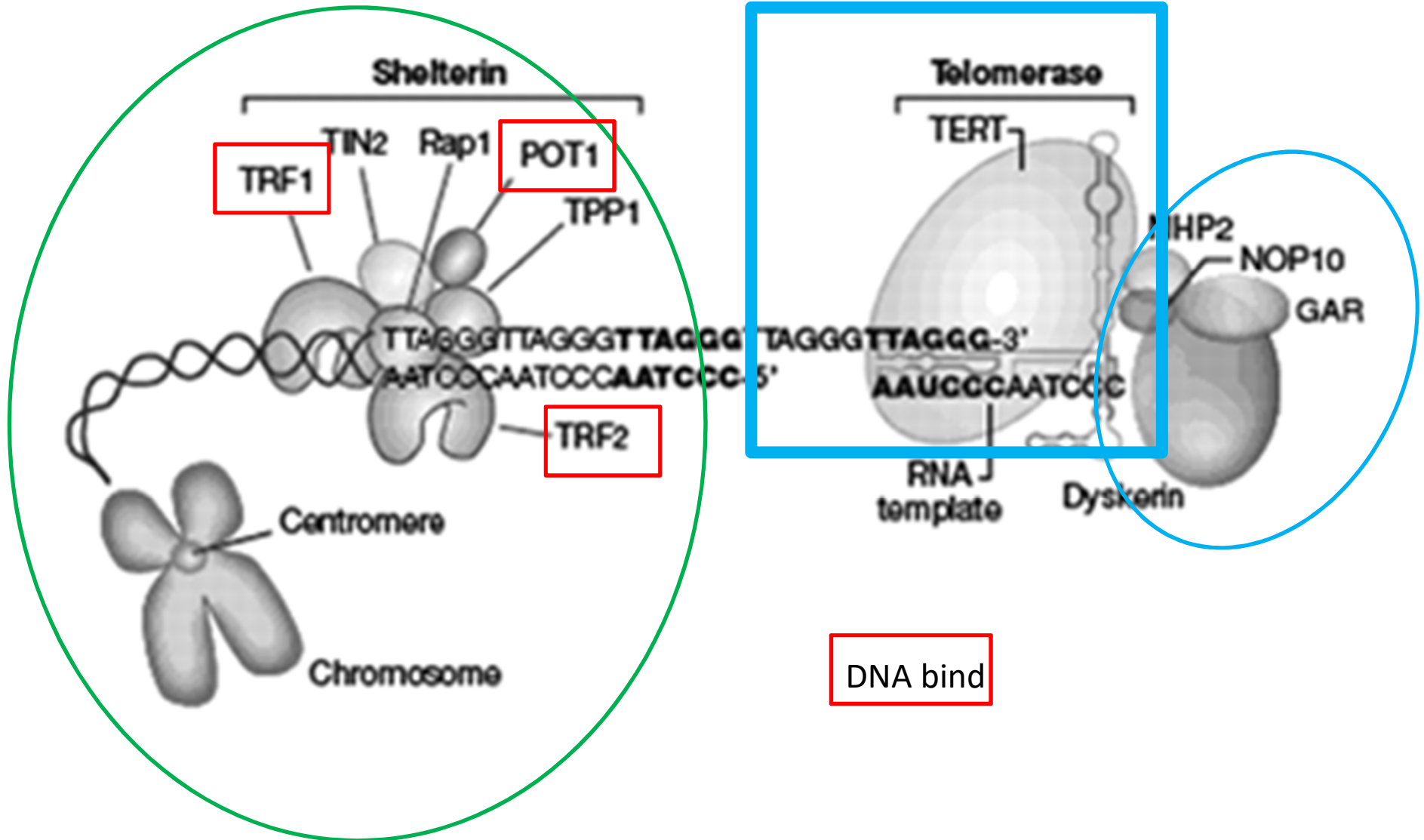
NB: TERC

TRAP



Telomeric Repeat Amplification Protocol

Complessi macromolecolari associati al Telomero ed alla Telomerasi

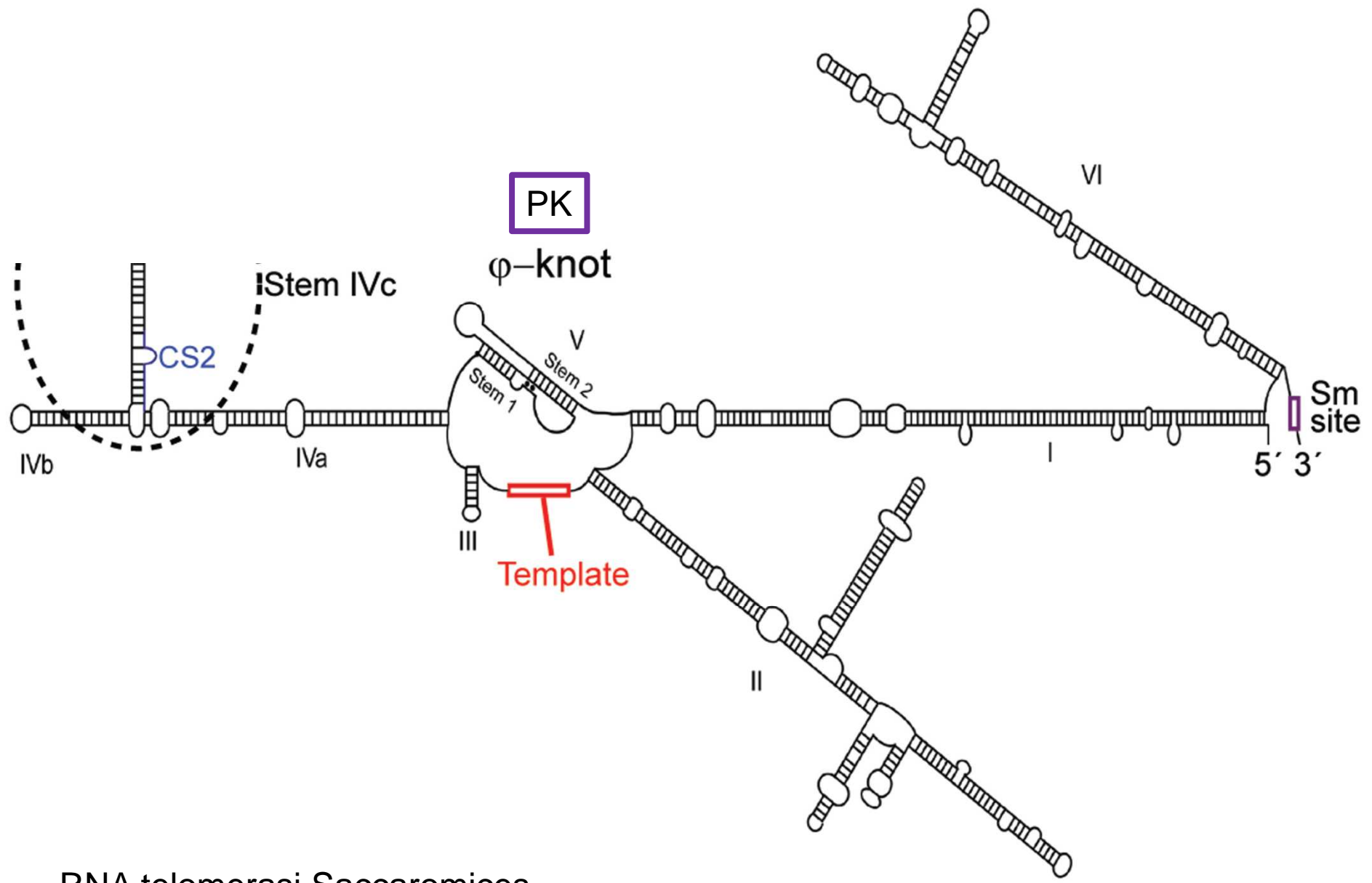


RNA TEMPLATO DELLA TELOMERASI

hTR is a 451-nucleotide RNA

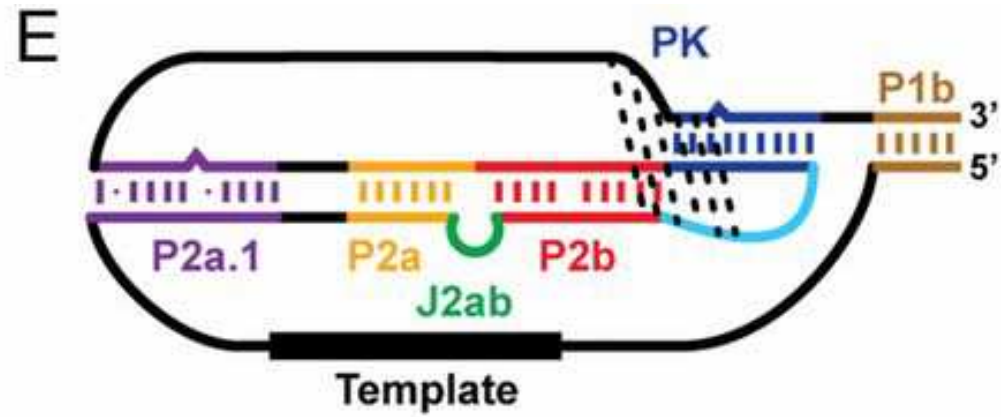
contains a box H/ACA motif at its 3' end essential for hTR stability and for its assembly with hTERT mediated by the presence of the box H/ACA-binding dyskerin complex, which is composed of four proteins:

dyskerin, NOP10, NHP2 and GAR1.

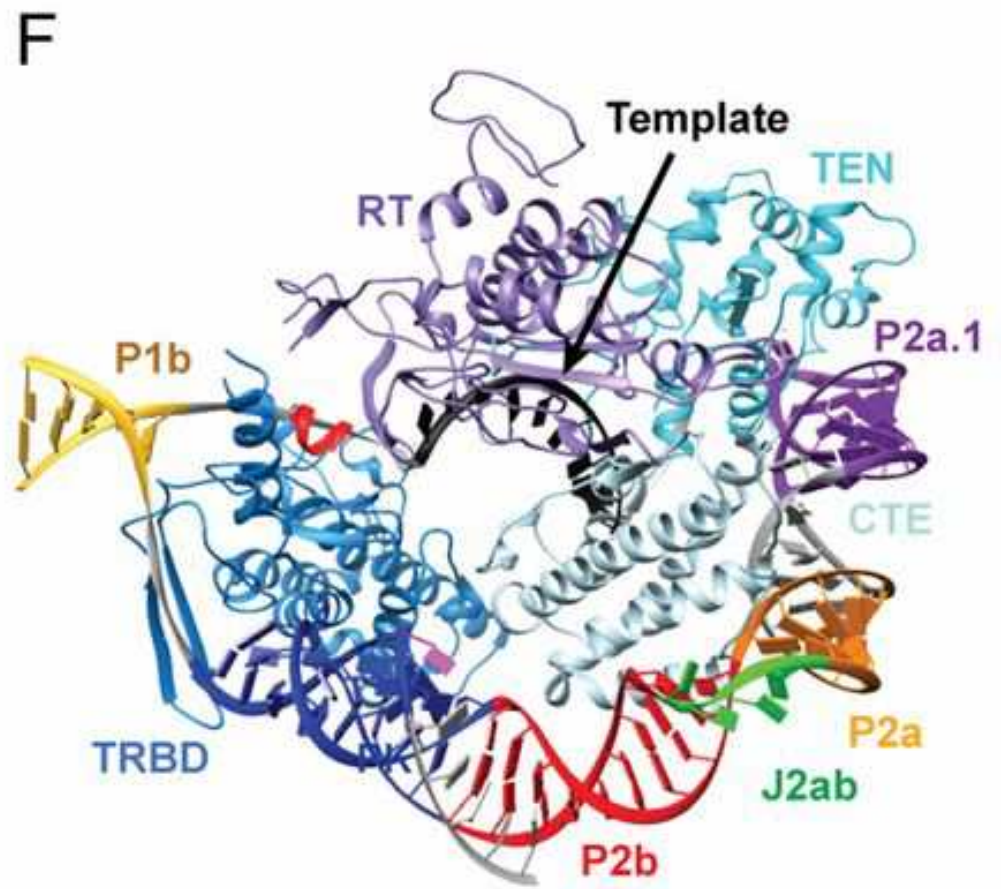
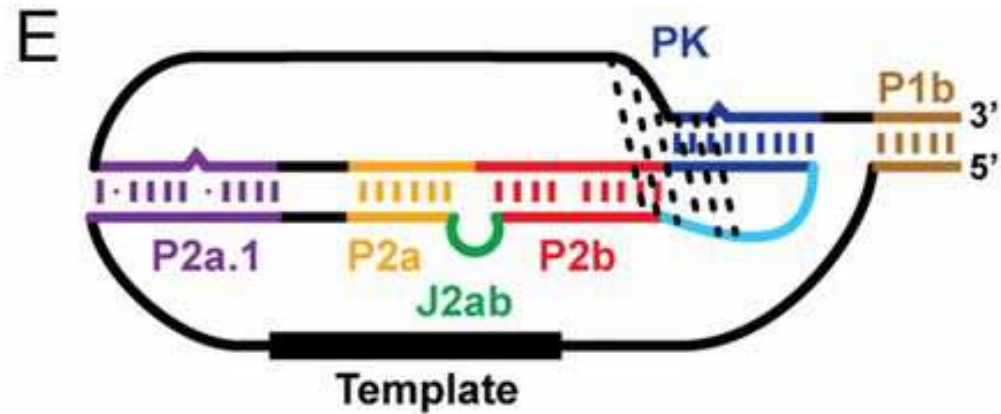


RNA telomerasi Saccharomices

human TERT-t/PK.

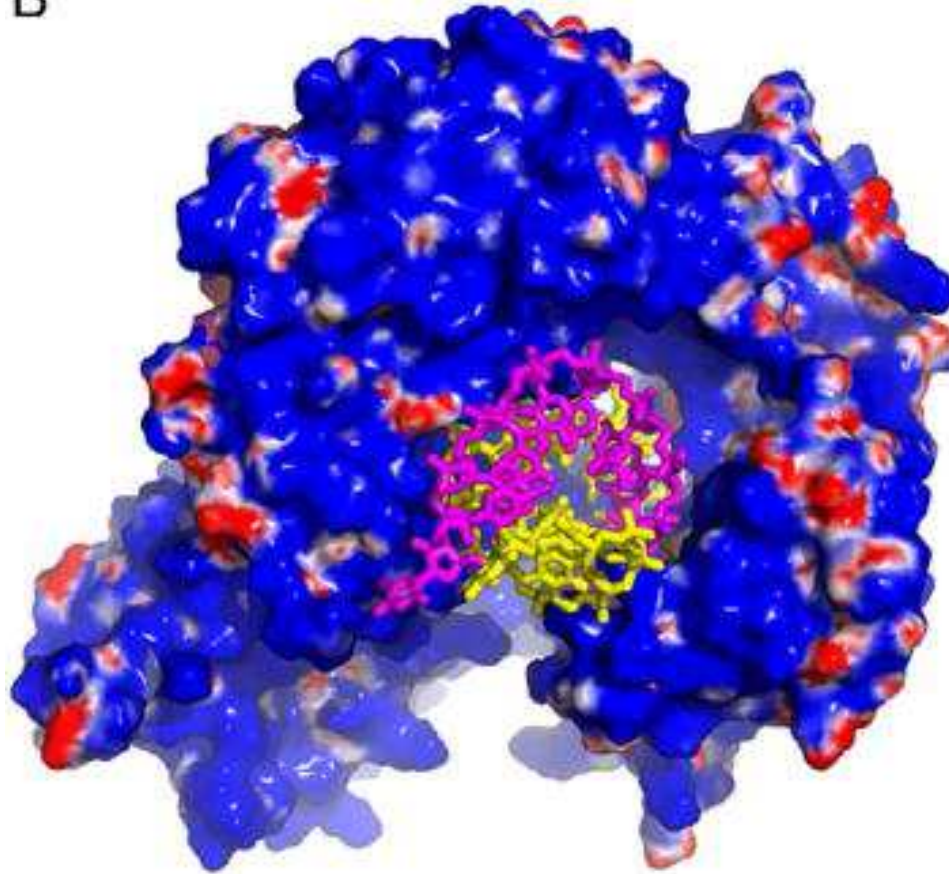


human TERT-t/PK.



RNA (magenta stick)–DNA (yellow stick) hairpin cocrystallized with tcTERT

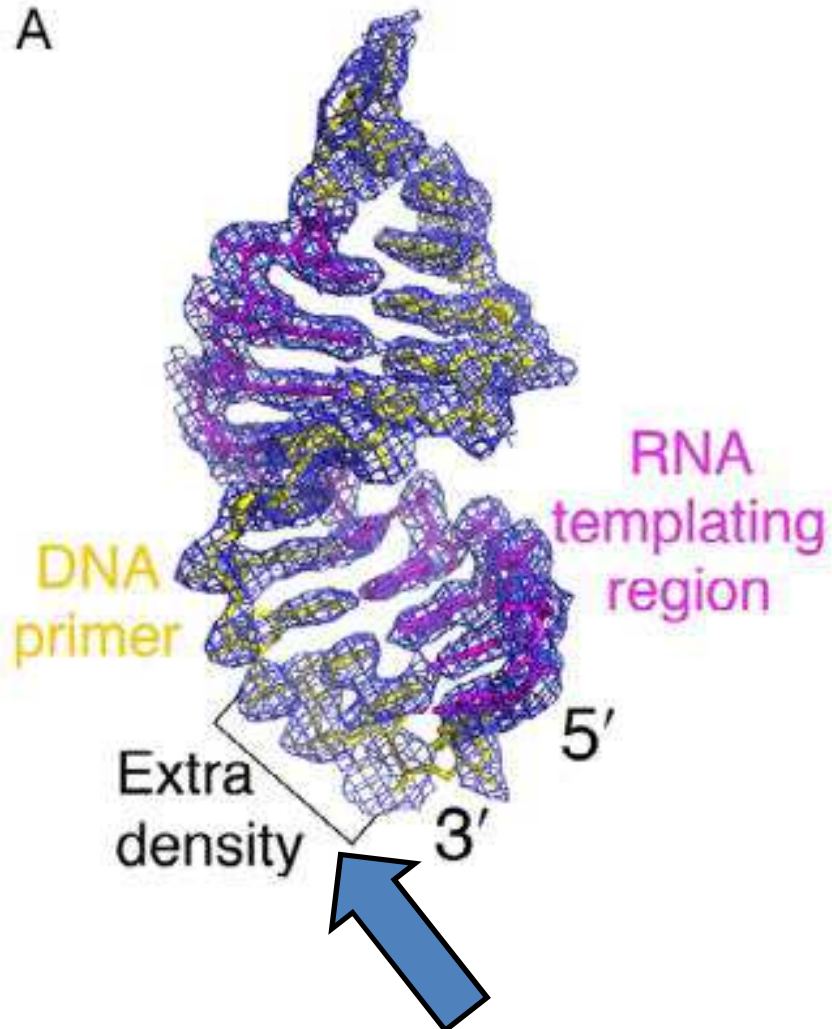
B



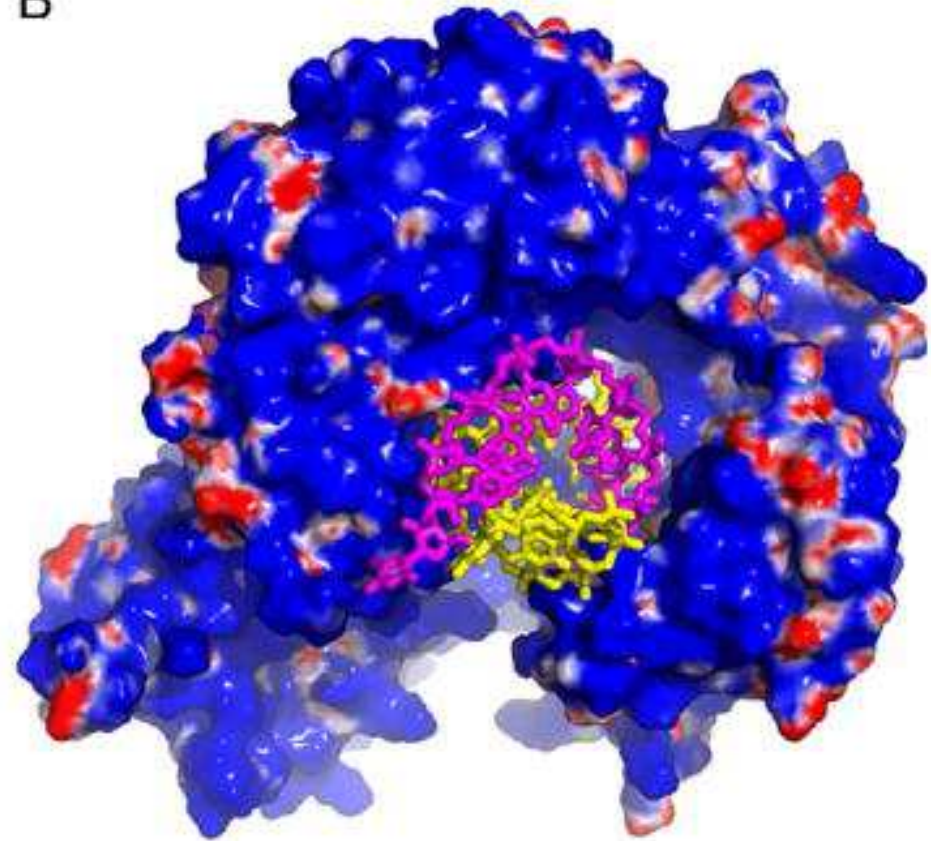
tcTERT surface charge representation,
the RNA–DNA hybrid (stick) docked in the
interior cavity of the TERT ring

RNA (magenta stick)–DNA (yellow stick) hairpin cocrystallized with tcTERT

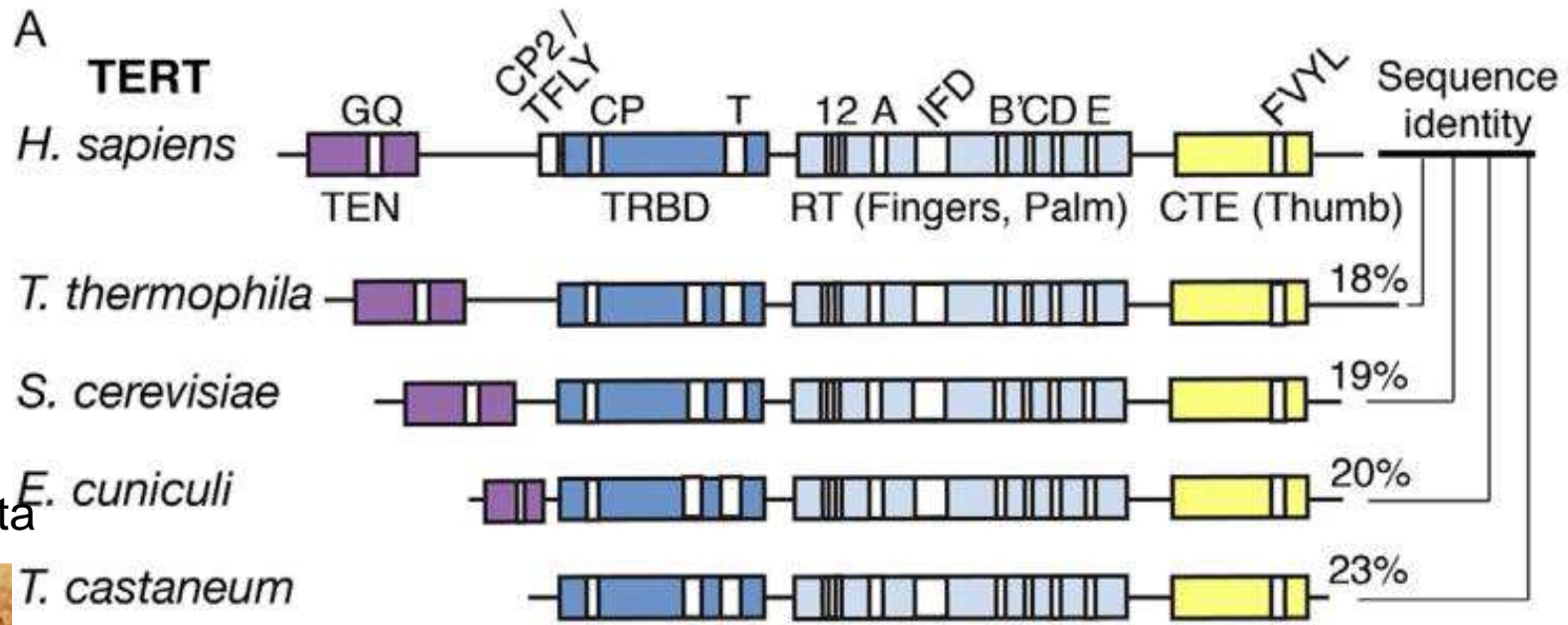
A



B



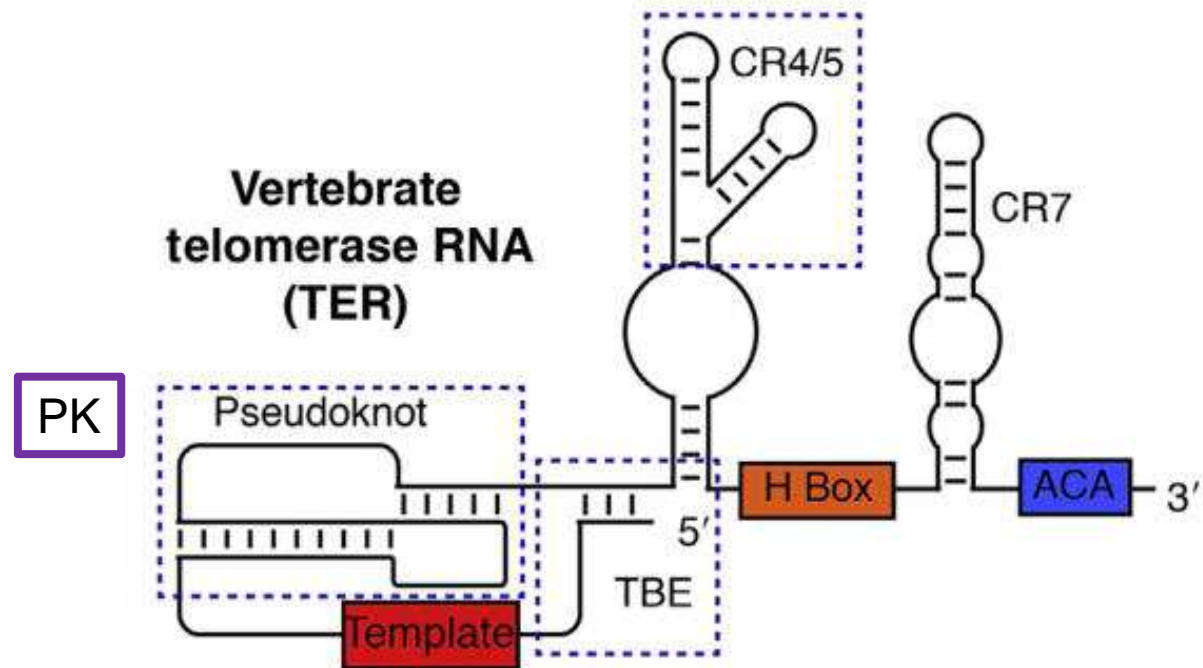
three additional nucleotides at the 3'-end of the telomeric DNA !!



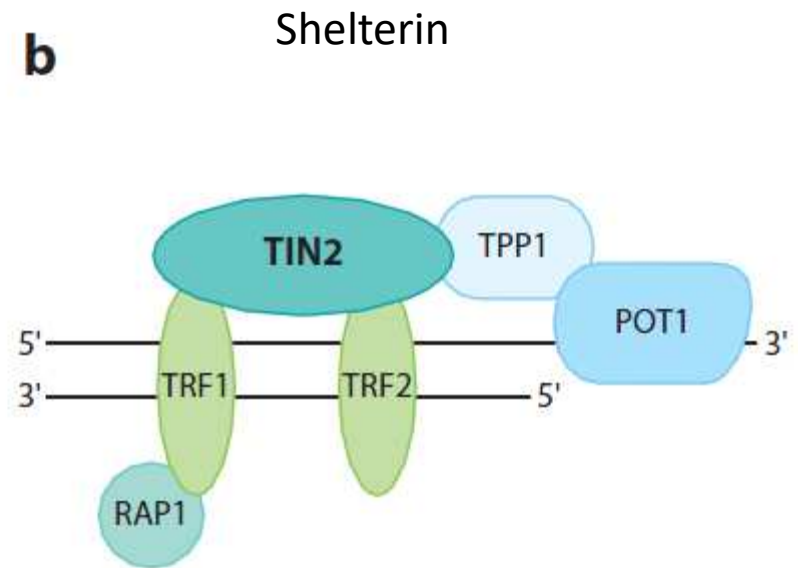
Fungo
parassita



B



Complessi macromolecolari associati al Telomero



Telomeres are coated by a group of at least six proteins, collectively called **shelterin**

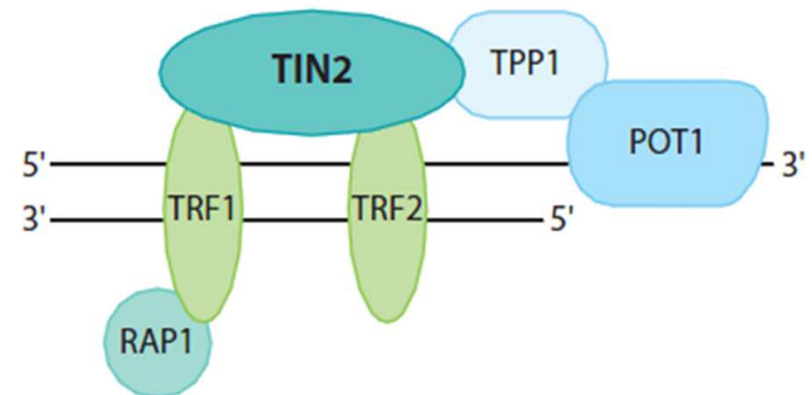
Three proteins, TRF1, TRF2, and POT1(single-stranded repeats) directly recognize and bind to TTAGGG repeats

TIN2 TPP1, and Rap1, interconnect the telomere-binding proteins to form the entire complex

Shelterin serves as a signal that allows the cellular DNA repair machinery to distinguish telomeres from DNA double-stranded breaks

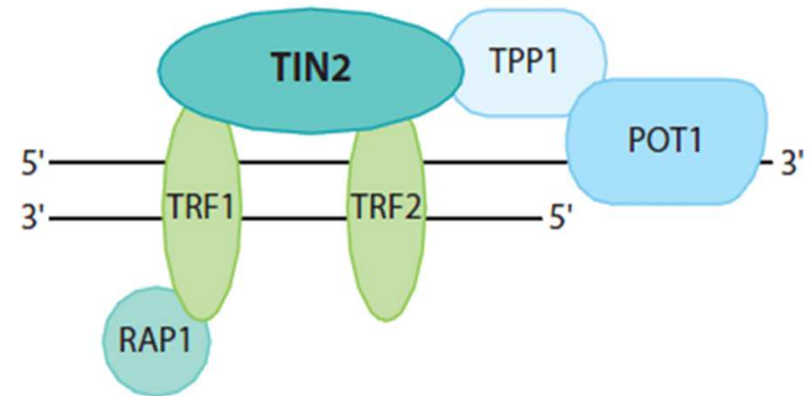
MUTATIONS IN TELOMERIC PROTEINS AND CANCER

Protein	Cancer(s)
Shelterin	
TRF1/TRF2	Gastric
POT1	Leukemia (CLL) Melanoma Glioma
TPP1	DC Melanoma
TIN2	DC
RAP1	Melanoma



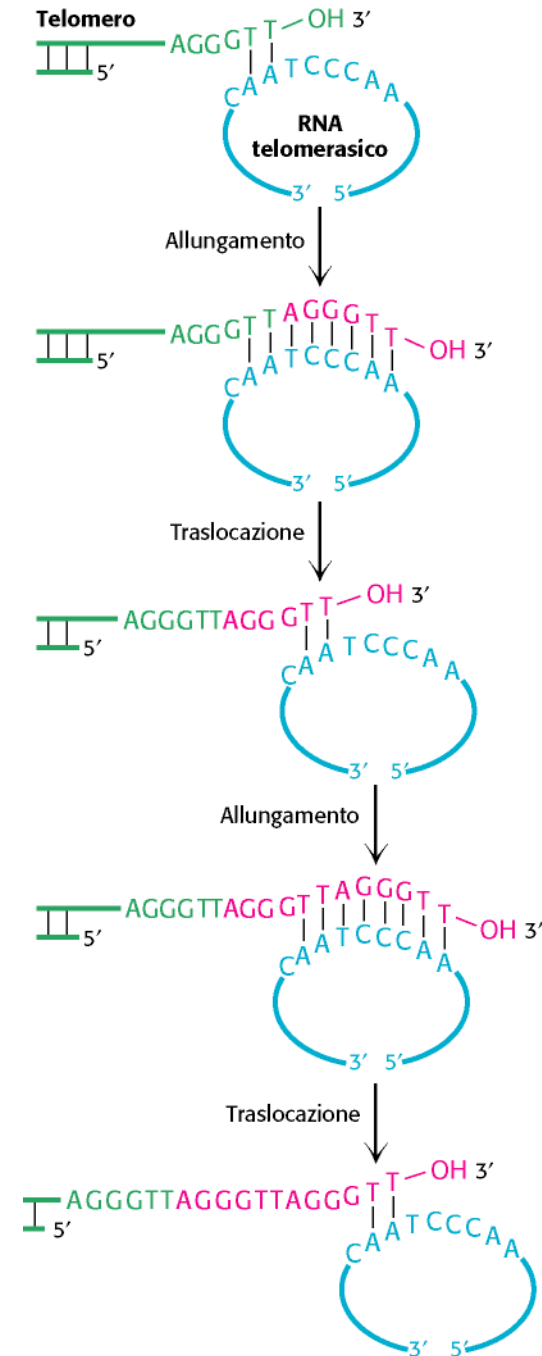
MUTATIONS IN TELOMERIC PROTEINS AND CANCER

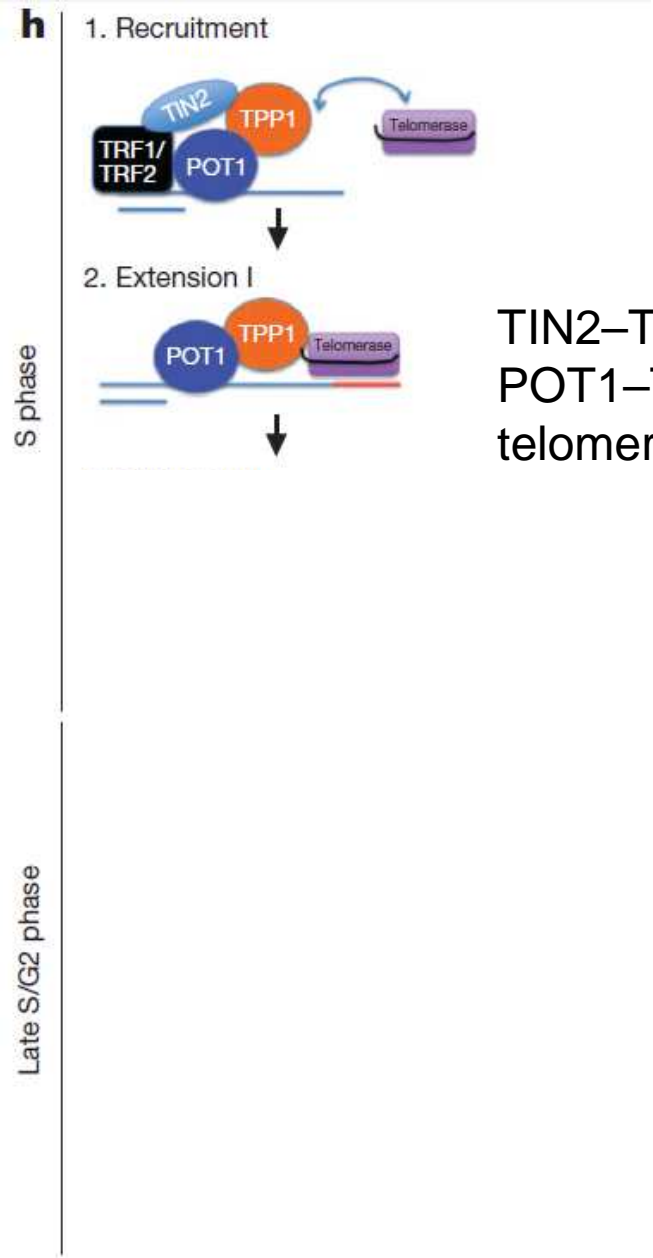
Protein	Cancer(s)
Shelterin	
TRF1/TRF2	Gastric
POT1	Leukemia (CLL) Melanoma Glioma
TPP1	DC Melanoma
TIN2	DC
RAP1	Melanoma
Telomere elongation	
TERT	Glioma Bladder Thyroid Melanoma Breast/ovarian
TERC	MDS



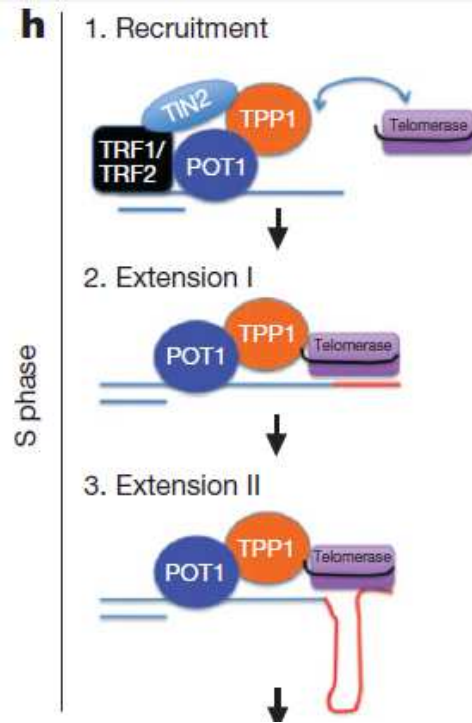
L'allungamento del telomero modello riassuntivo

During every cell division, telomeres are potentially shortened by 50–200 bp due to the end replication problem





TIN2–TPP1 recruits telomerase and POT1–TPP1 promotes processive telomere elongation



TIN2–TPP1 recruits telomerase and POT1–TPP1 promotes processive telomere elongation

IL RECLUTAMENTO DELLA TELOMERASI

TPP1 recruits telomerase to telomeres

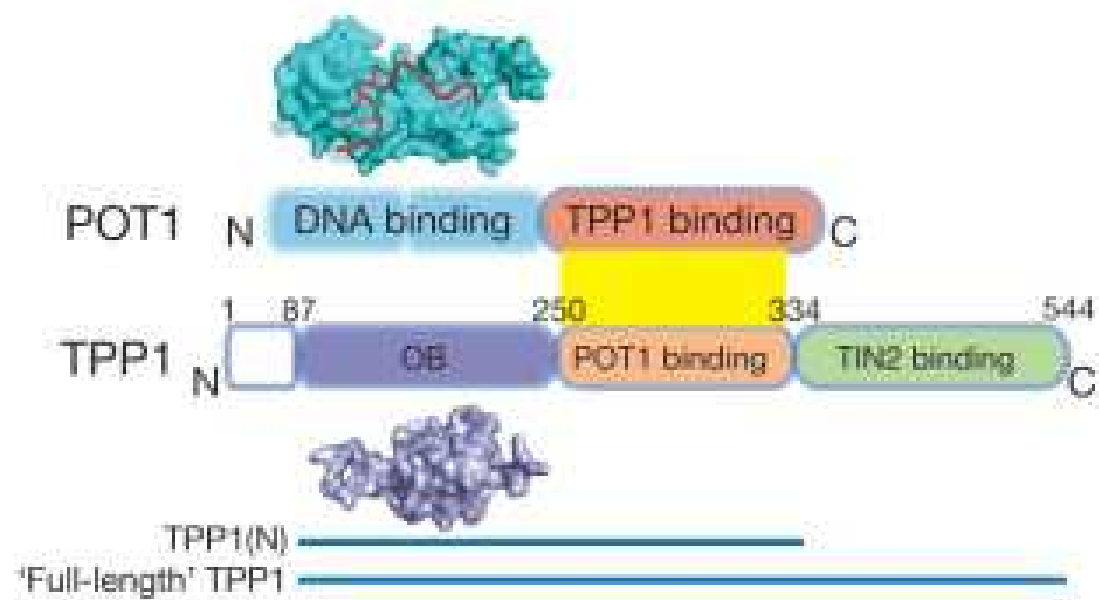
Telomere synthesis involves trafficking of telomerase and telomerase is thought to be recruited to telomeres through interactions with telomere-binding proteins.

The OB-fold domain of the telomere-binding protein TPP1 recruits telomerase to telomeres through an association with the telomerase reverse transcriptase, TERT.

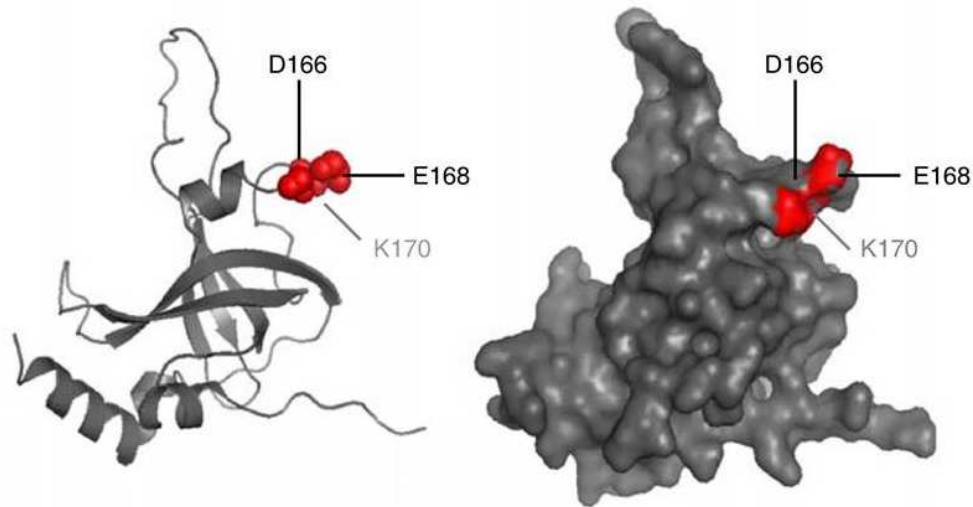
The TPP1 OB-fold domain is sufficient to recruit telomerase to a heterologous chromatin locus.

A minimal TPP1 OB-fold inhibits telomere maintenance by blocking access of telomerase to its binding site at telomeres.

A specific loop residues within the TPP1 OB-fold is necessary for association with critical residues in TERT Telomerase, including those mutated in pulmonary fibrosis patients, which defines the interface required for telomerase-TPP1 interaction.

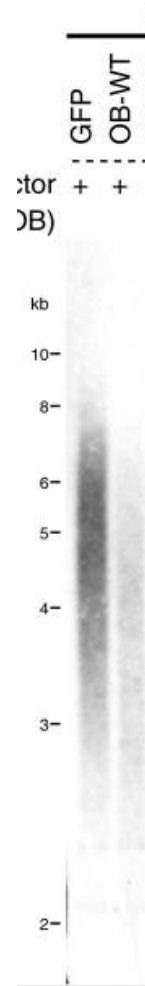
a**c****nature**

the OB-fold domain of the telomere-binding protein TPP1 recruits telomerase to telomeres through an association with the telomerase reverse transcriptase, TERT

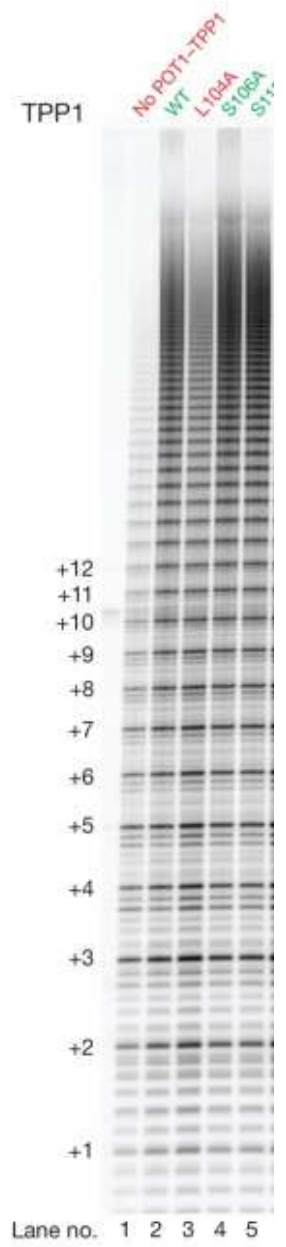


Structural representation of TPP1-OB domain (PDB 2i46).
Residues required for telomerase interaction shown in red

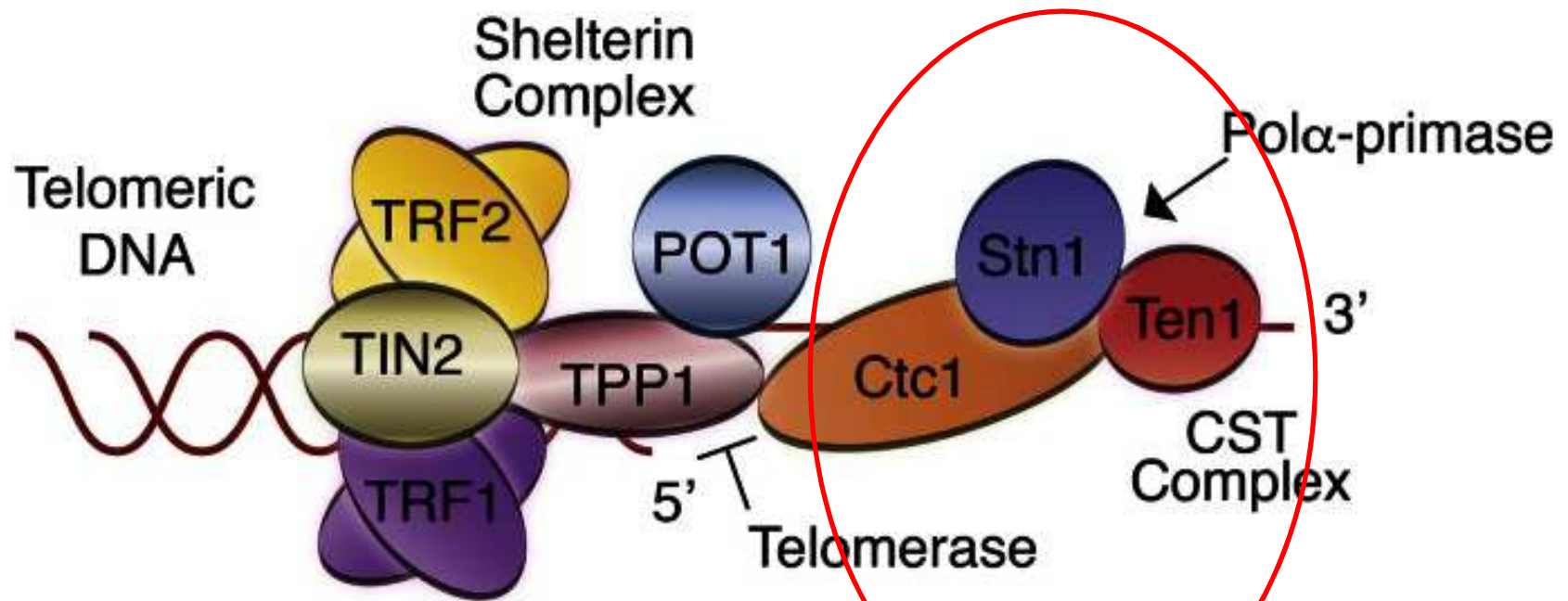
TPP1-OB inhibits telomere length maintenance by telomerase and blocks endogenous telomerase recruitment



Direct telomerase activity assay
of lysates from cells
co-transfected with
TR plasmid
TERT
POT1



nature

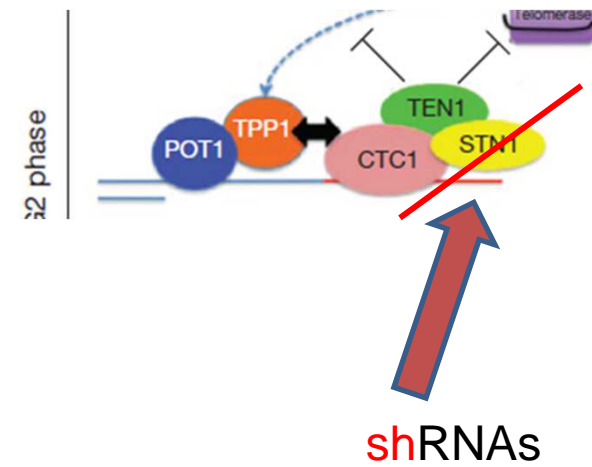
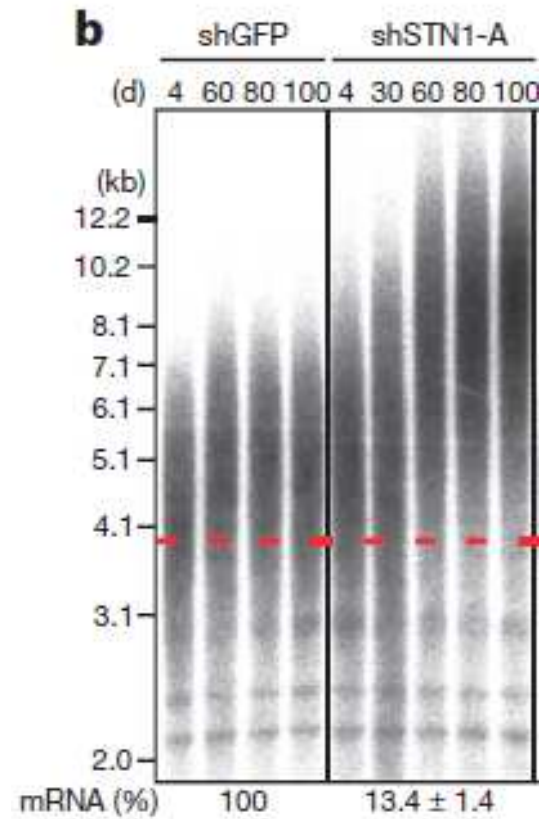


CST localizes specifically to the single-stranded telomeric DNA

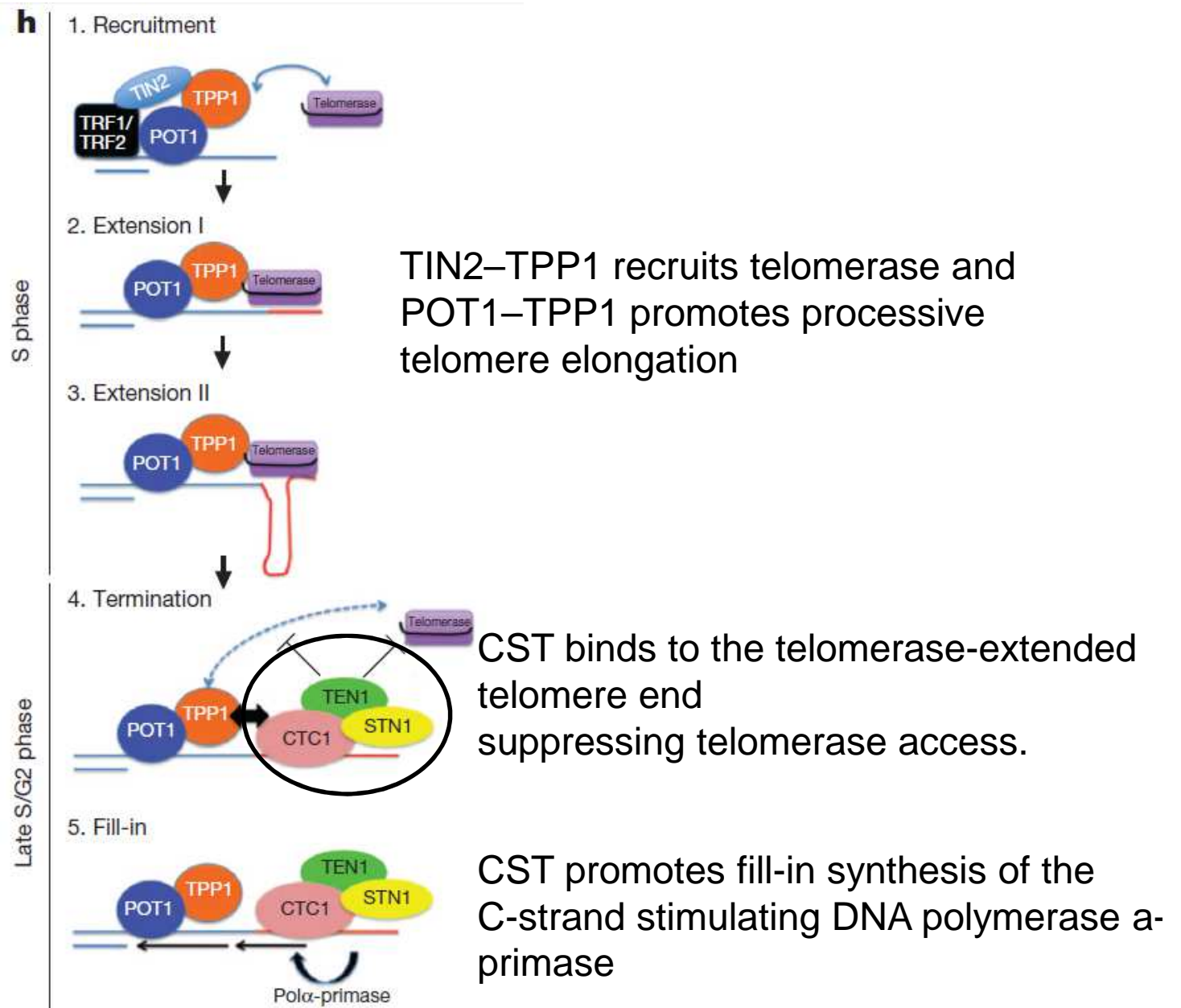
chromosome end capping and telomere length regulation

The CST complex limits telomere elongation

HT1080
human cancer cells



The CST complex is a terminator of telomerase activity



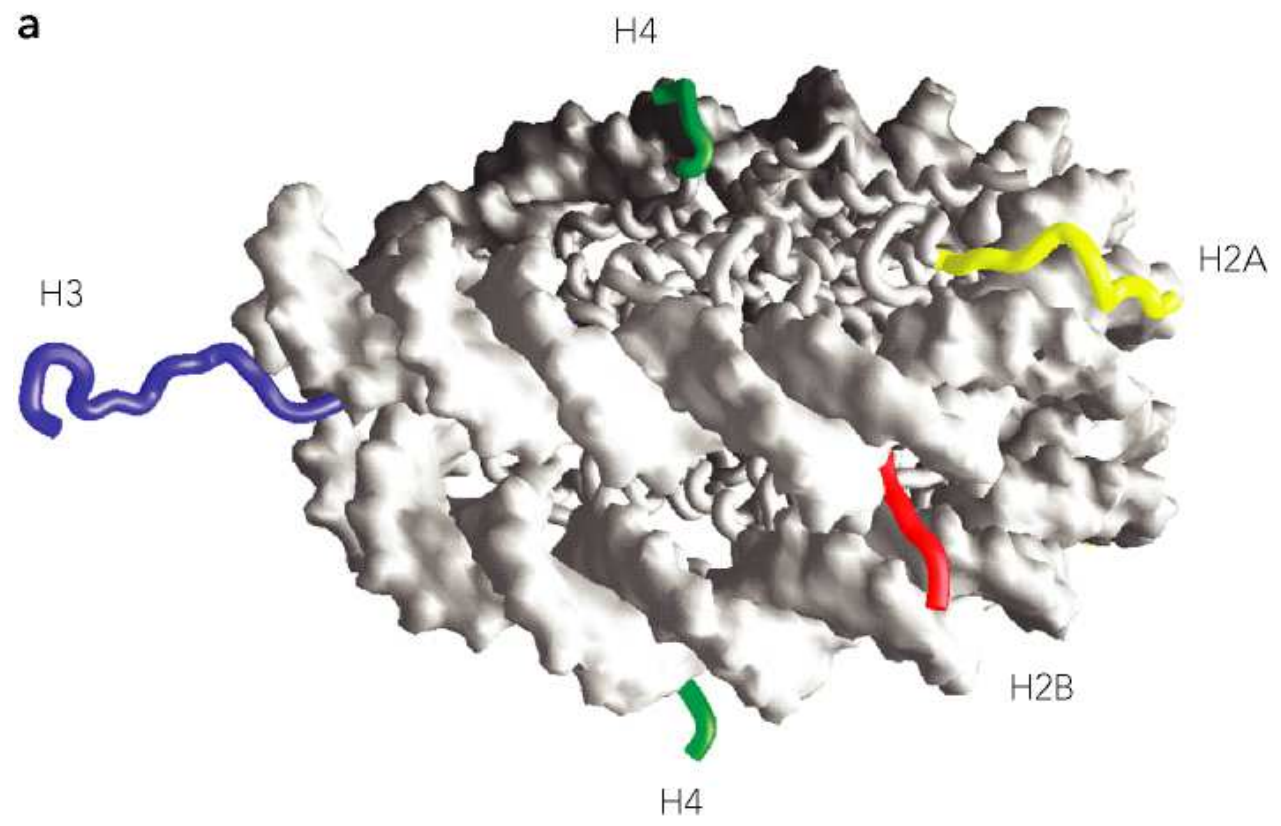
La cromatina telomerica e la sua modificazione

Telomeres also bind to nucleosomes, which are rich in modified histones.

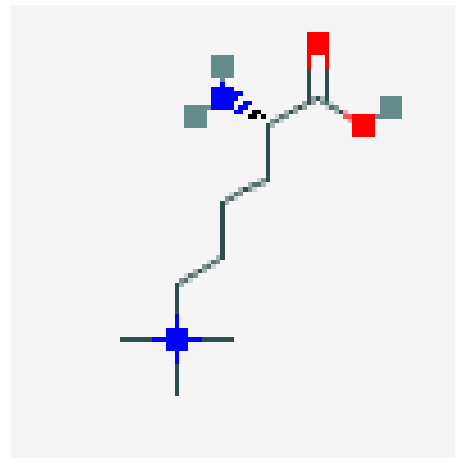
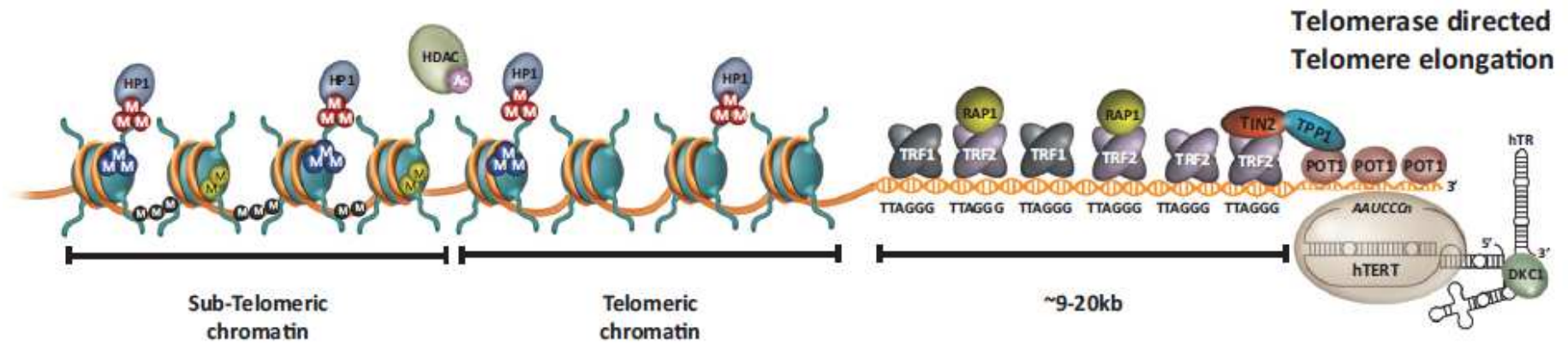
Major histone modifications *found in telomeres are*

-H3K9 and H4K20 trimethylation

-low abundance of acetylated H3 and H4



Telomeres in germ and stem cells



Kme3 = trimethyllysine

Key: M DNA Methylation M M M H3K9me3 M M M H4K20me3 M M H3K79me2 Ac Histone acetylation S Protein sumoylation

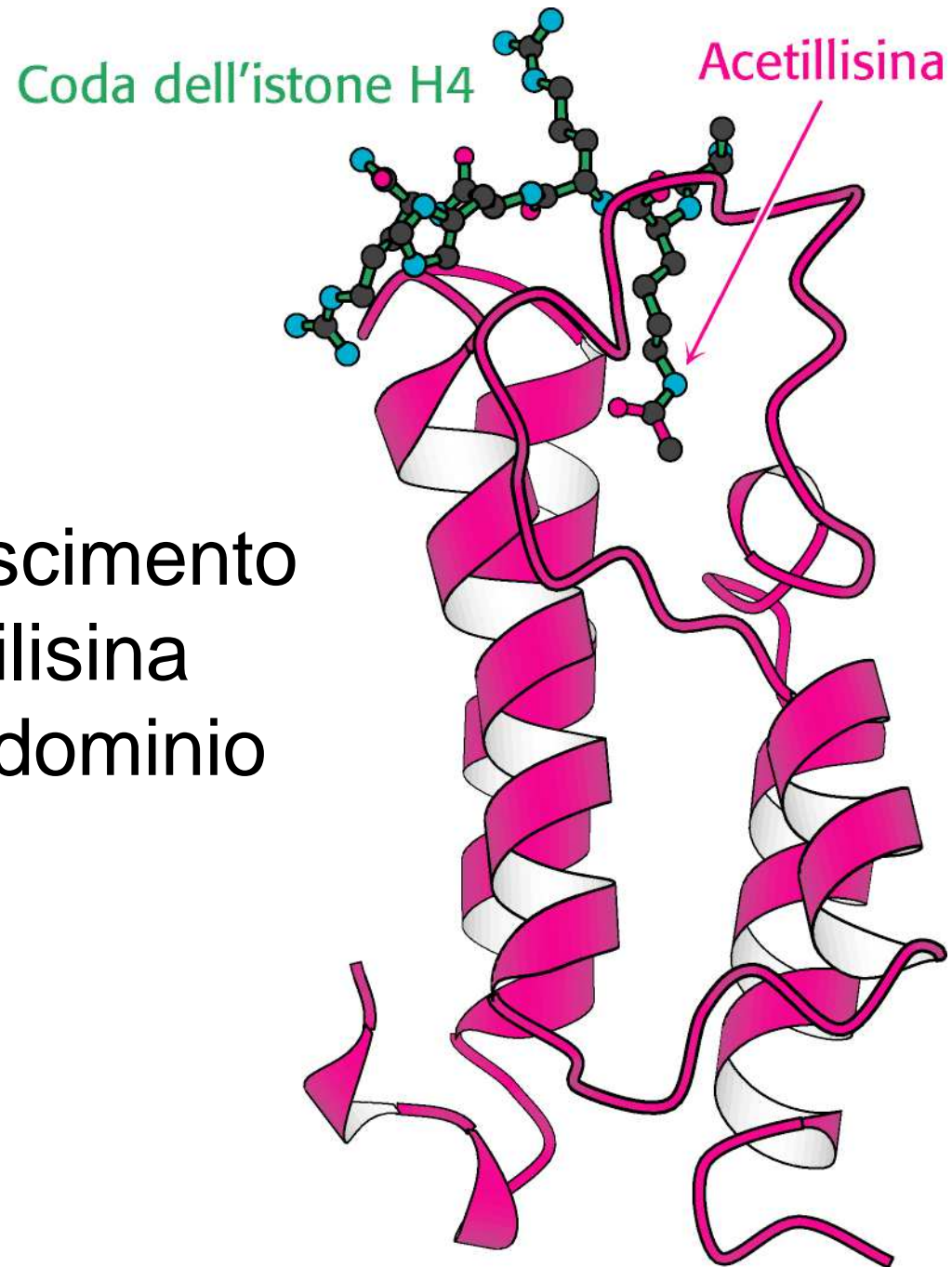
Telomeres also bind to nucleosomes, which are rich in modified histones.

Major histone modifications *found in telomeres are*

-H3K9 and H4K20 trimethylation

-low abundance of acetylated H3 and H4

Riconoscimento
acetilisina
bromodominio



Un enzima deacetilante specifico: SIRT6

SIRT6 is a histone H3 lysine 9 deacetylase that modulates telomeric chromatin

The Sir2 deacetylase regulates chromatin silencing and lifespan in *Saccharomyces cerevisiae*.

In mice, deficiency for the Sir2 family member SIRT6 leads to a shortened lifespan and a premature ageing-like phenotype.

SIRT6 is a chromatin-associated NAD⁺-dependent, histone H3 lysine 9 (H3K9) deacetylase that modulates telomeric chromatin.

SIRT6 is a histone H3 lysine 9 deacetylase that modulates telomeric chromatin

SIRT6 contributes to the propagation of a specialized chromatin state at mammalian telomeres,

Deacetylation is required for proper telomere metabolism and function.

chromatin regulation by SIRT6 is linked to telomere maintenance and a human premature ageing syndrome

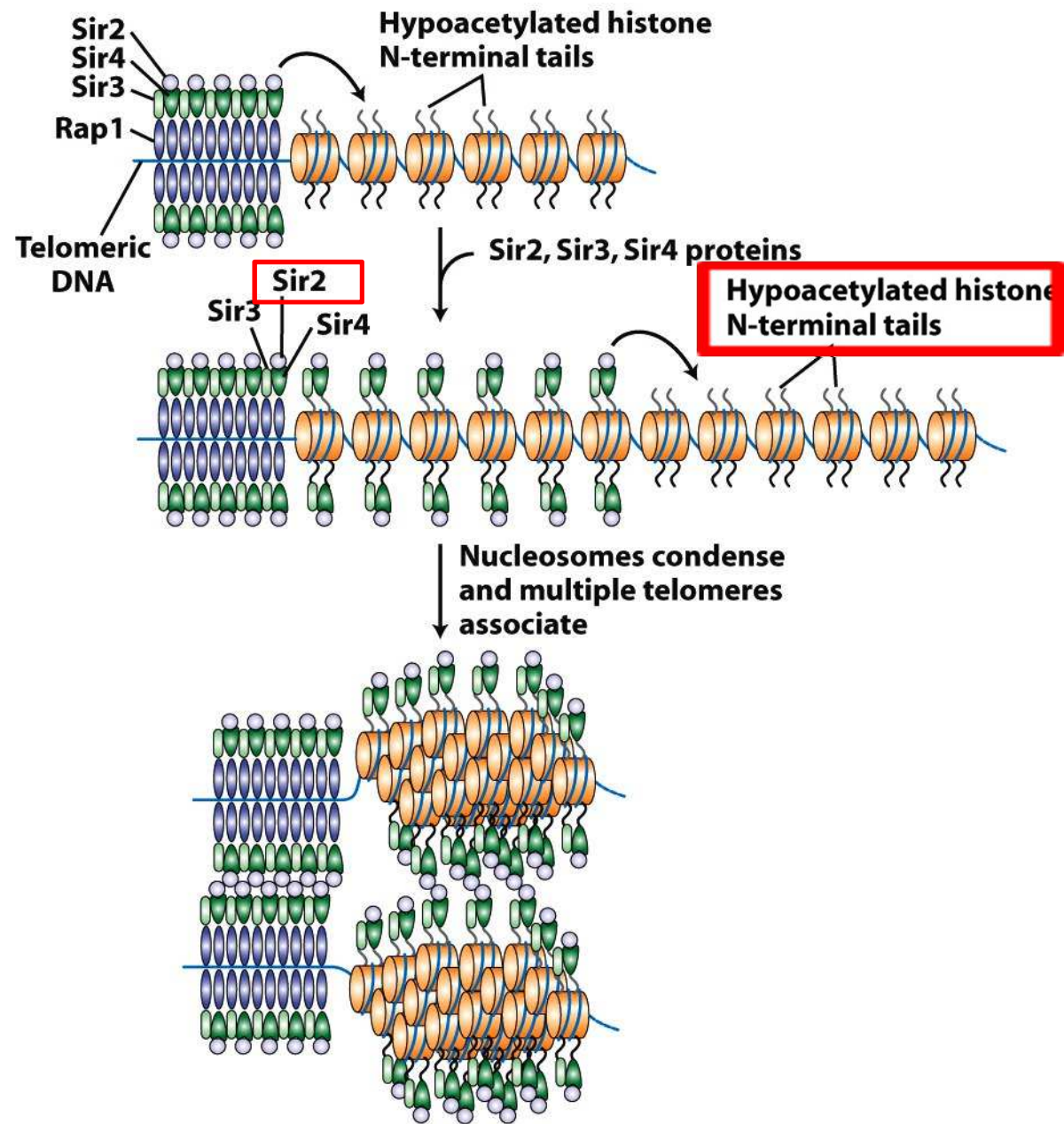


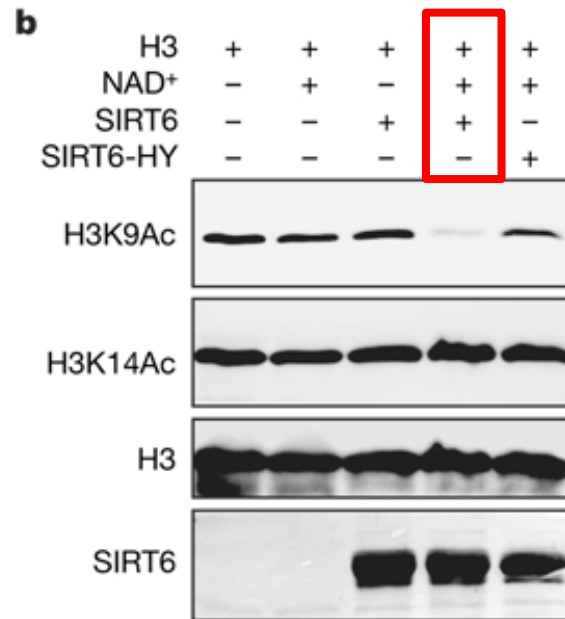
Figure 7-35
Molecular Cell Biology, Sixth Edition
 © 2008 W. H. Freeman and Company

SIRT6 (sir 2) deacetylates lysine 9 of histone H3 at telomeric chromatin

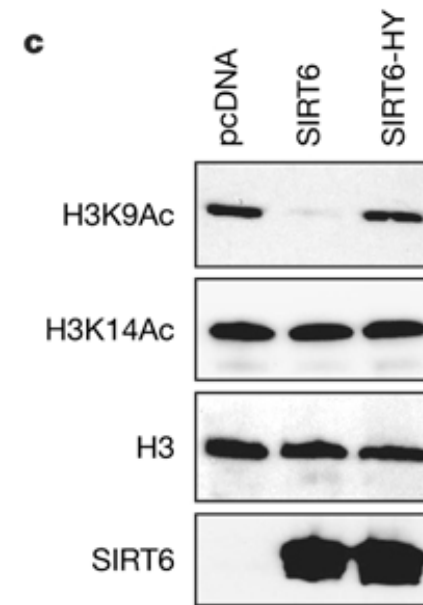
a

Peptide	Activity
H2AK5Ac	-
H2AK13Ac	-
H2BK5Ac	-
H2BK12Ac	-
H2BK15Ac	-
H2BK20Ac	-
H3K9Ac	+
H3K14Ac	-
H3K27	-
H4K5Ac	-
H4K8Ac	-
H4K12Ac	-
H4K16Ac	-

histone tail peptides



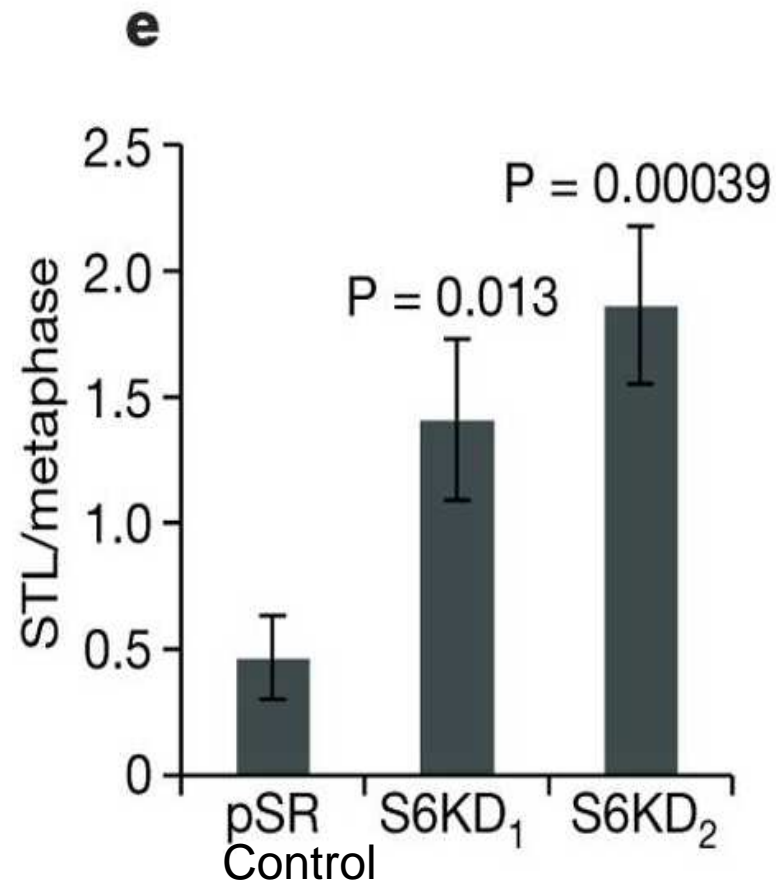
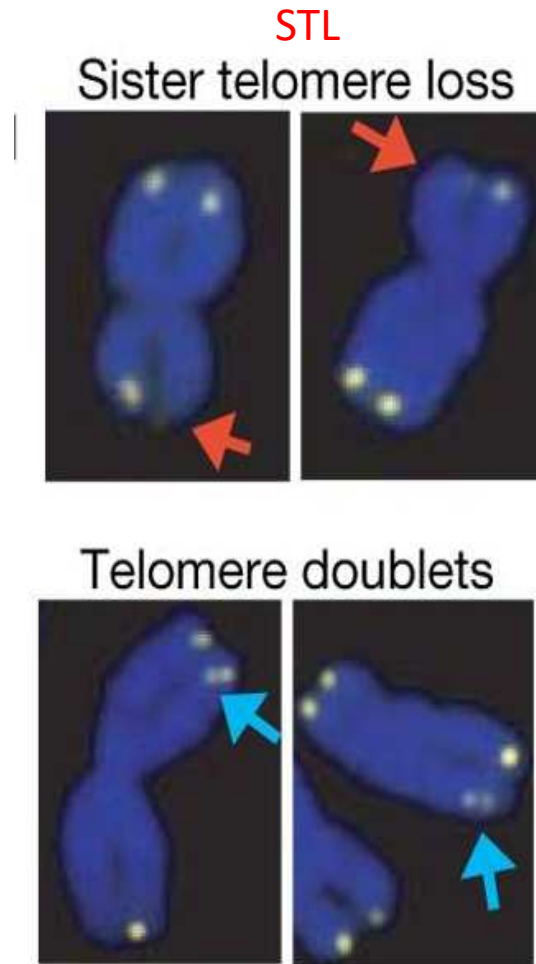
full-length histone H3



293T cells overexpressing SIRT6

SIRT6-HY: *catalytic H133Y SIRT6 mutant protein*

SIRT6 knockdown (S6KD) cells



d, Representative S6KD metaphases showing aberrant telomere signals. Red arrows, sister telomere loss; blue arrows, telomere doublets. e, Quantification of sister telomere loss

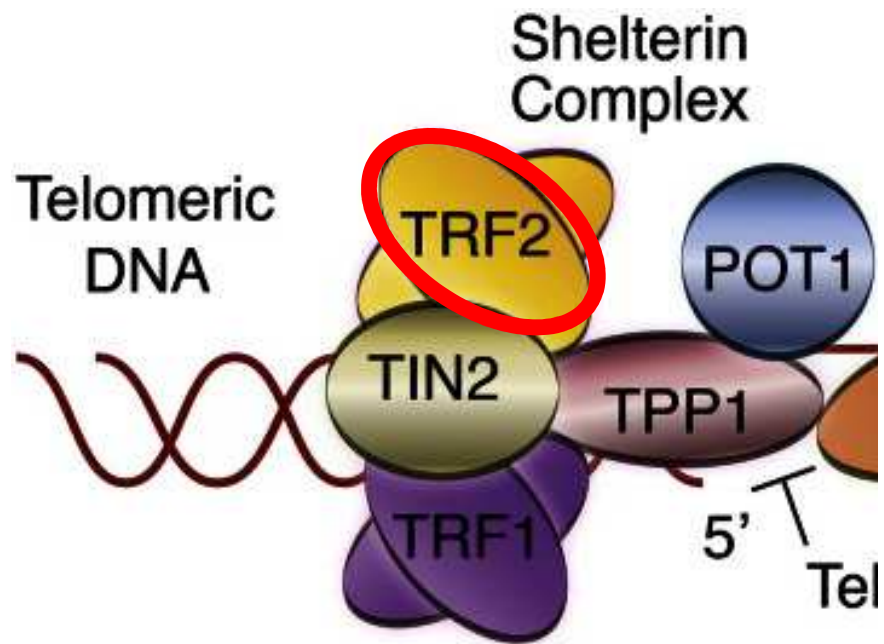
SIRT6 is a histone H3 lysine 9 deacetylase that modulates telomeric chromatin

SIRT6 associates specifically with telomeres

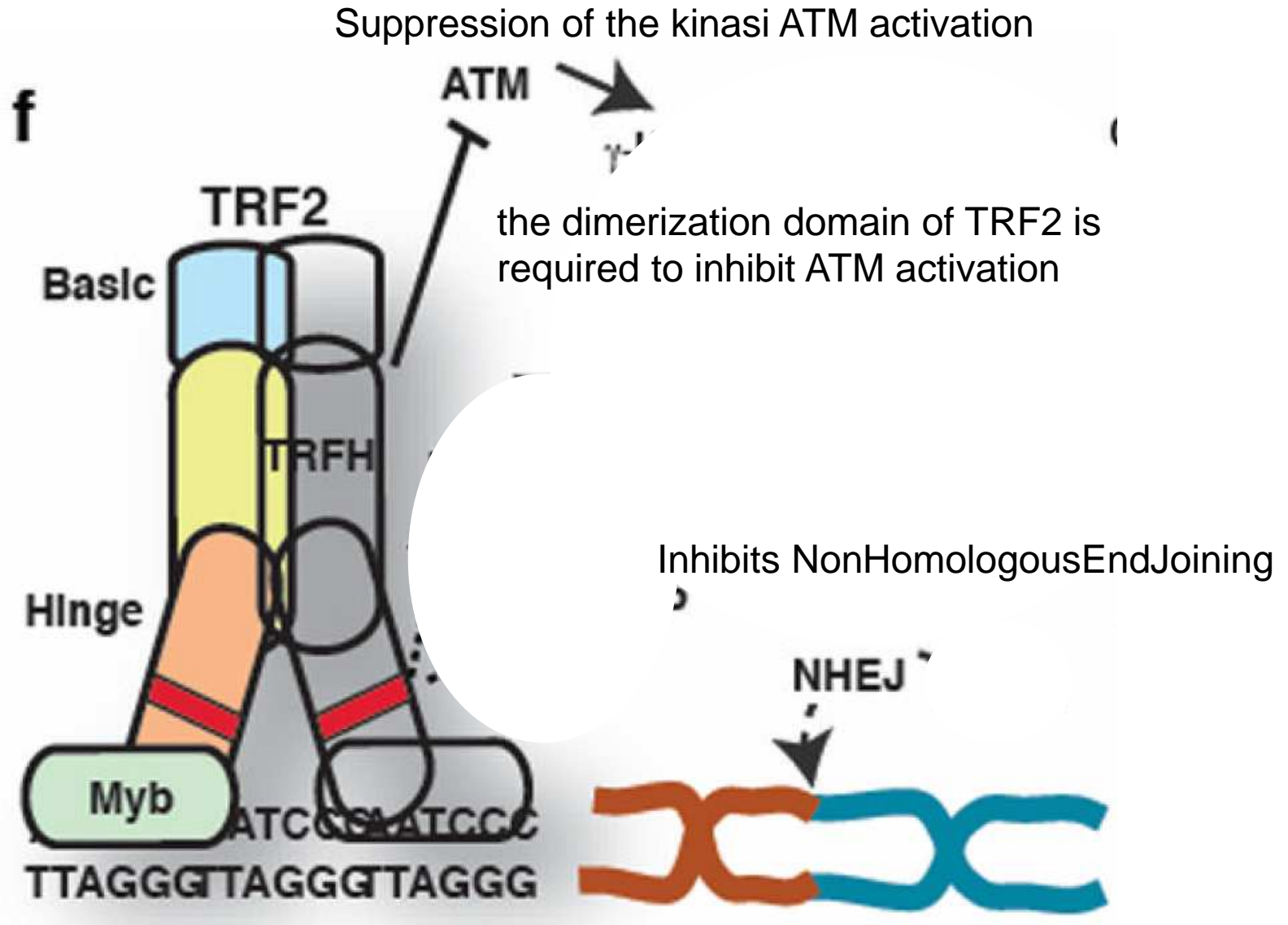
SIRT6 depletion leads to telomere dysfunction with end-to-end chromosomal fusions and premature cellular senescence.

SIRT6-depleted cells exhibit abnormal telomere structures

PROTEZIONE DEL TELOMERO



mechanism for TRF2-mediated chromosome end protection

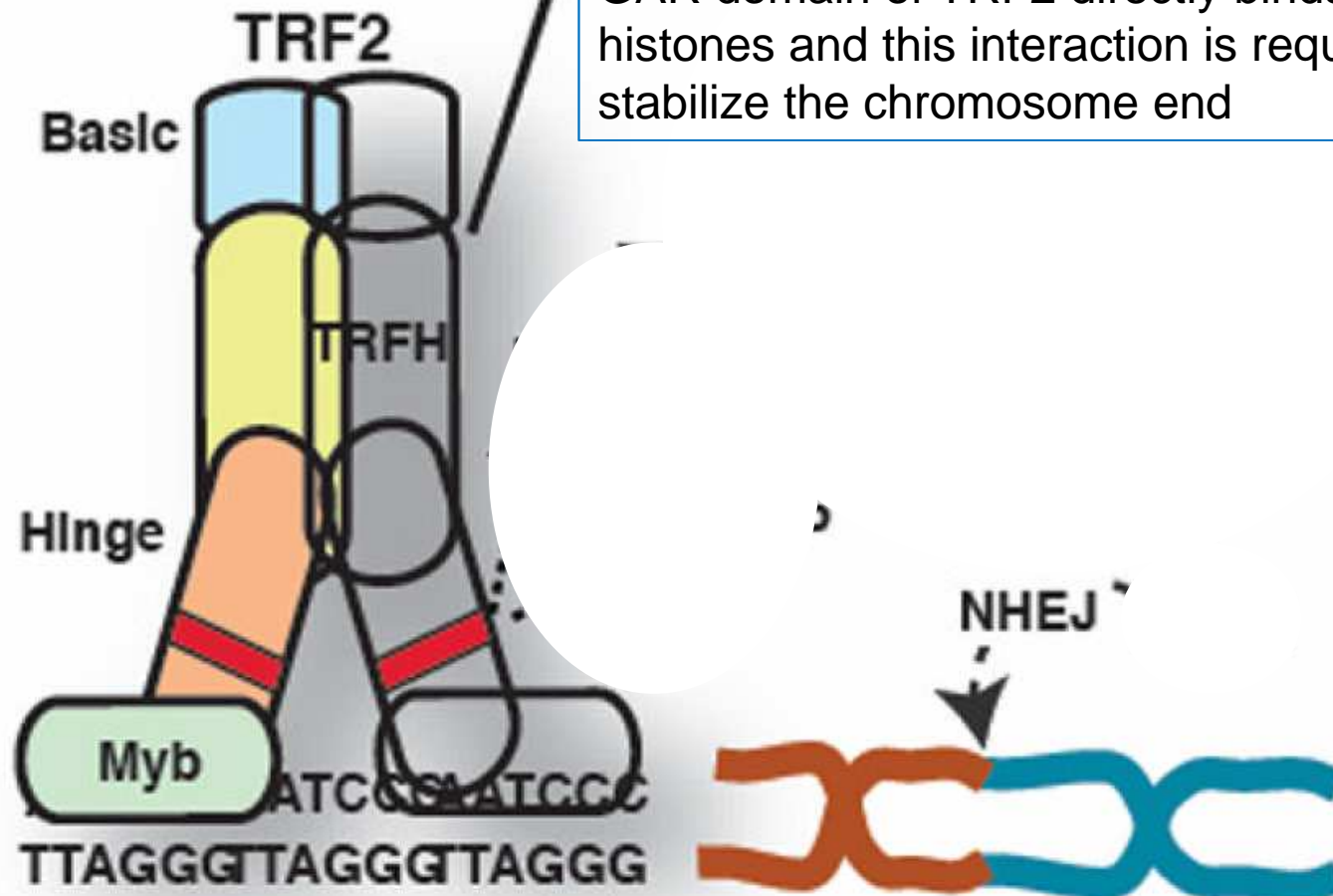


mechanism for TRF2-mediated chromosome end protection

The GAR/Basic domain, which is located at the N terminus of TRF2, is rich in Gly/Arg residues and highly basic

ATM

GAR domain of TRF2 directly binds to core histones and this interaction is required to stabilize the chromosome end



Telomeric nucleosomes

Telomeric nucleosomes are hypersensitive to micrococcal nuclease.

Reconstituted nucleosomes on TTAGGG repeats show higher mobility than on other sequences.

Telomeric chromatin is enriched for heterochromatin modification, such as trimethylation of H3K9 and H4K20, and loss of these marks affects telomere length regulation.

Direct binding of the GAR domain of TRF2 and core histones.

In vitro binding assay for the GAR domain of TRF2 and core histones.

Core histones:

mono-nucleosomes were purified using from HeLa cell nuclei digested with micrococcal nuclease-

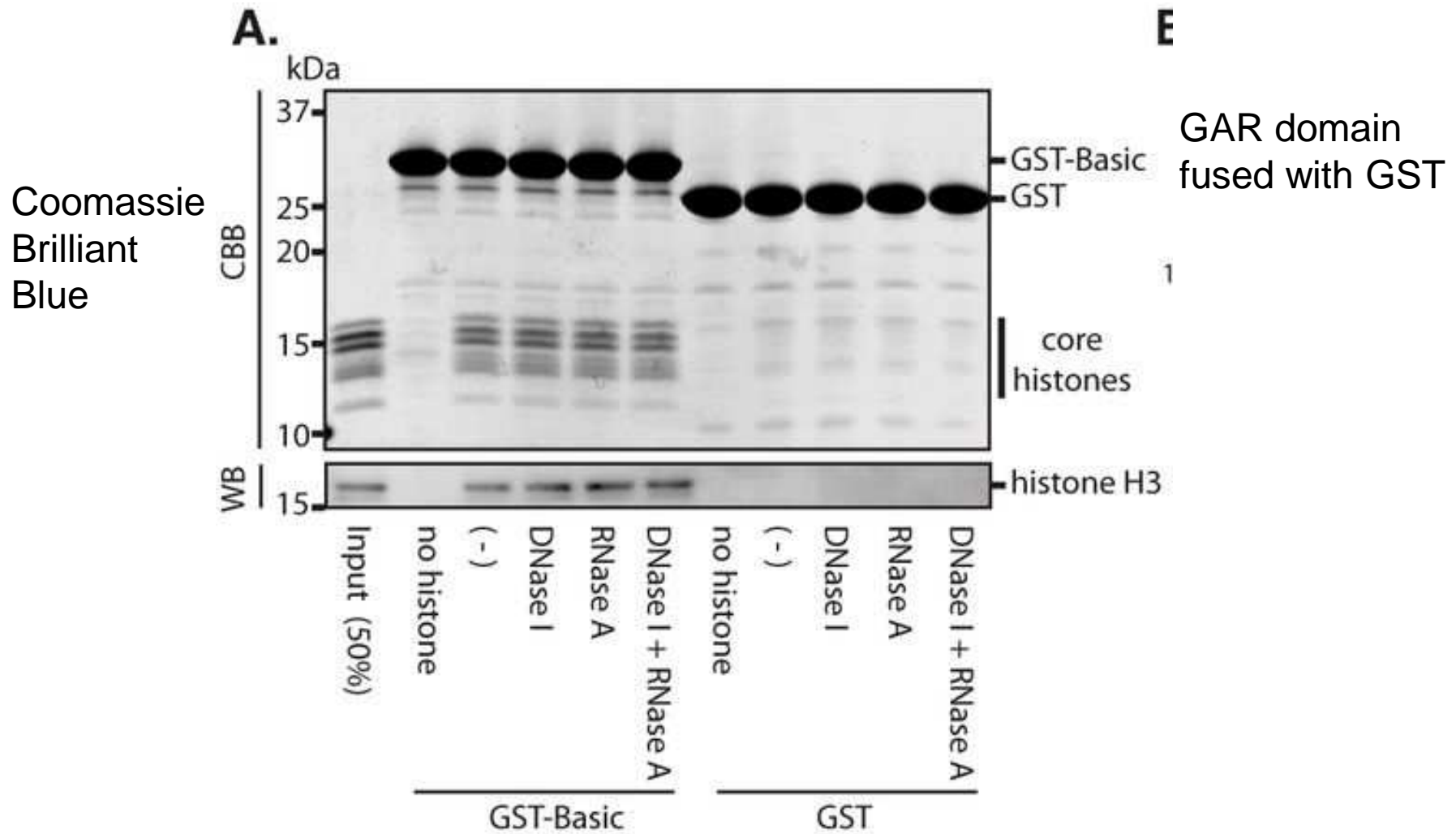
mono-nucleosome peaks were collected and partially digested with trypsin to generate the **tailless** histones

Recombinant GST-fused TRF2

GAR domain (GST-Basic) and GST protein (GST) were captured by glutathione-conjugated beads and incubated with core histones purified from HeLa cells.

Beads were washed extensively and then subjected to SDS-PAGE.

Direct binding of the GAR domain of TRF2 and core histones.



Direct binding of the GAR domain of TRF2 and core histones.

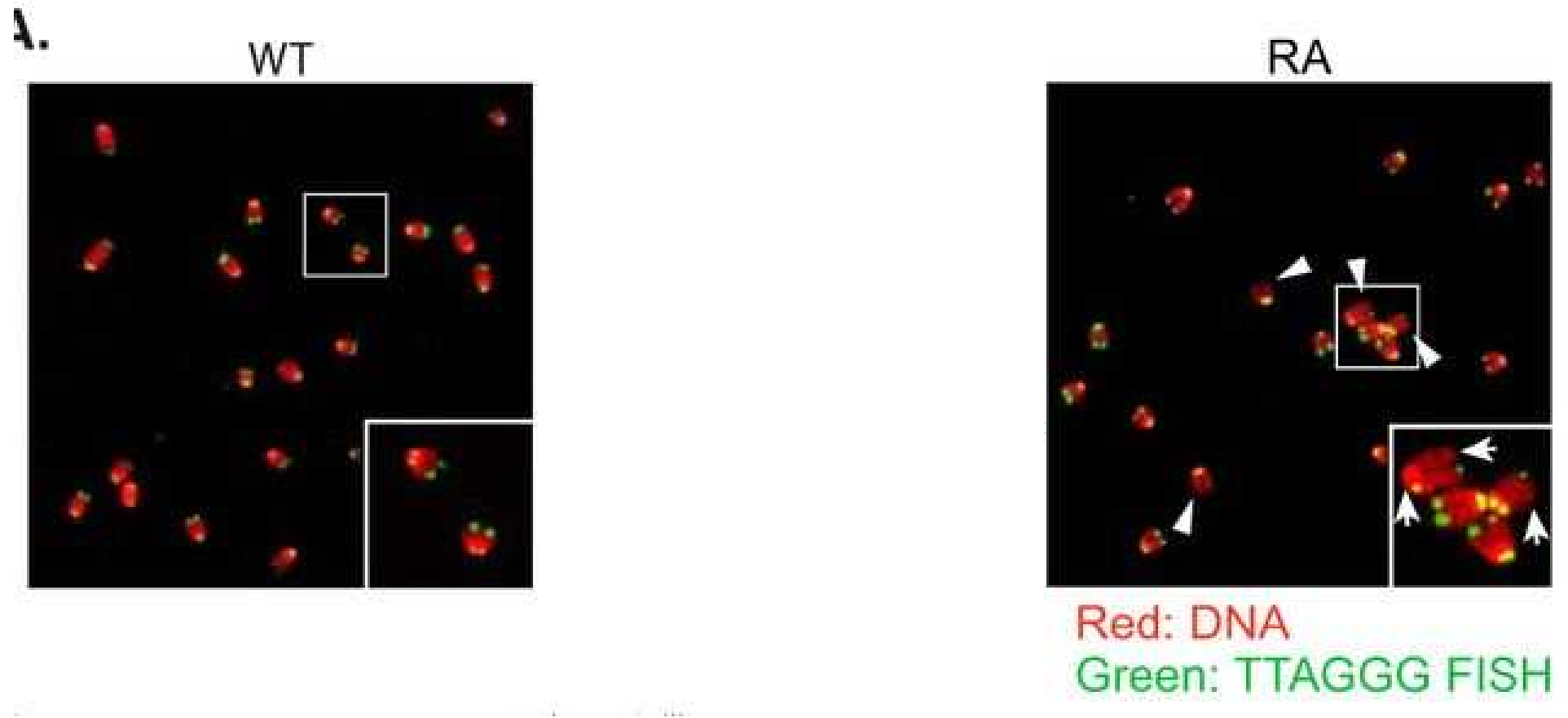
basic domain

E.

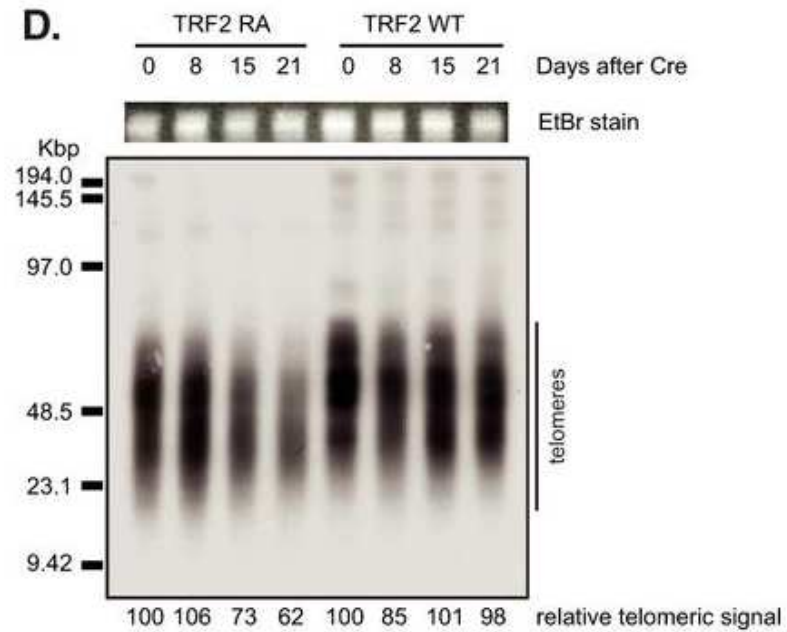
		* * *	
		MAPP <u>GMRLRSGR</u> ---STGAPLTRGSC	
LANA			
hTRF2	MAGGGGSSDGS	GRAAGRRASRSSGRARRGRHEPGLGGPAERGAGEARLEEAVNRW	
mTRF2	MAGGGGSSDSS	GRAASRRASRSGRARRGRHEPGLGGAAERGAGEARLEEAVNRW	
Basic2-45	AGGGGSSDGS	GRAAGRRASRSSGRARRGRHEPGLGGPAERGAGE	(+)
Basic2-24	AGGGGSSDGS	GRAAGRRASRSSG	(-)
Basic2-30	AGGGGSSDGS	GRAAGRRASRSSGRARRGR	(+)
Basic10-37		GSGRAAGRRASRSSGRARRGRHEPGLGG	(+)
			core histone binding
Basic RA	AGGGGSSDGS	GRAAGRRASRSSGAAAGAHEPGLGGPAERGAGE	

latency-associated nuclear antigen (LANA)
viral element essential for the DNA replication and genome maintenance
during latency

Rapid telomere DNA loss by loss of histone binding of TRF2.



Rapid telomere DNA loss and t-circle generation by loss of histone binding of TRF2.



Akimitsu Konishi et al. *J. Biol. Chem.* 2016;291:20798-20810