

A 3D molecular model of RNA polymerase, shown as a large, complex, greyish-blue structure with a red DNA double helix passing through it. The structure is composed of many subunits, with some highlighted in green and purple. The DNA is a red double helix.

RNA polymerase

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Structural Biology
2019-2020

SUMMARY

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- e. METHODS

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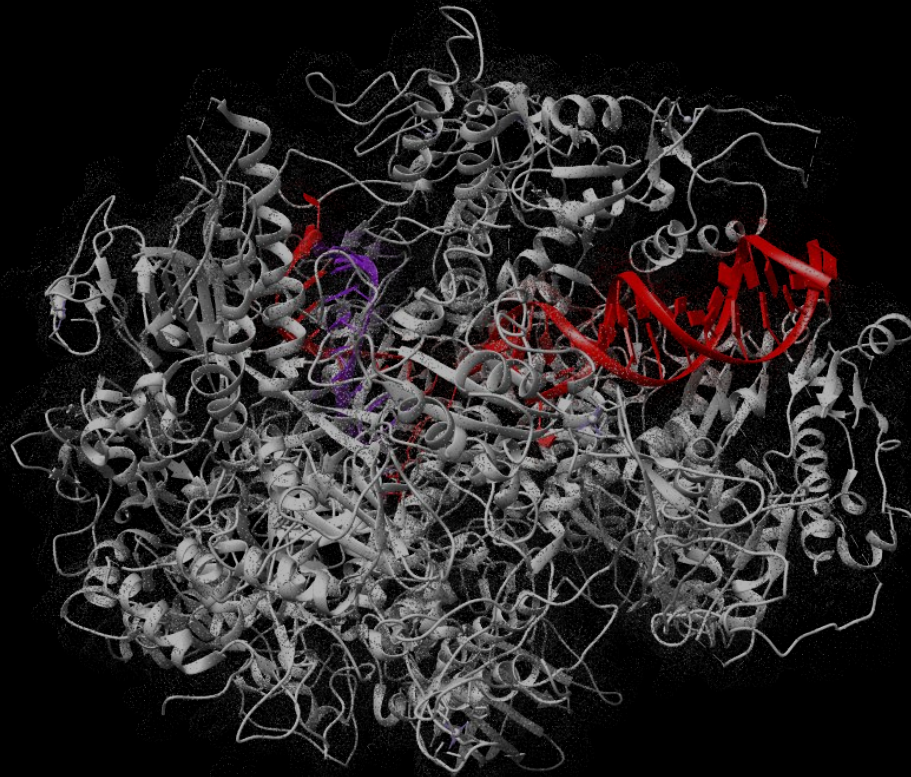
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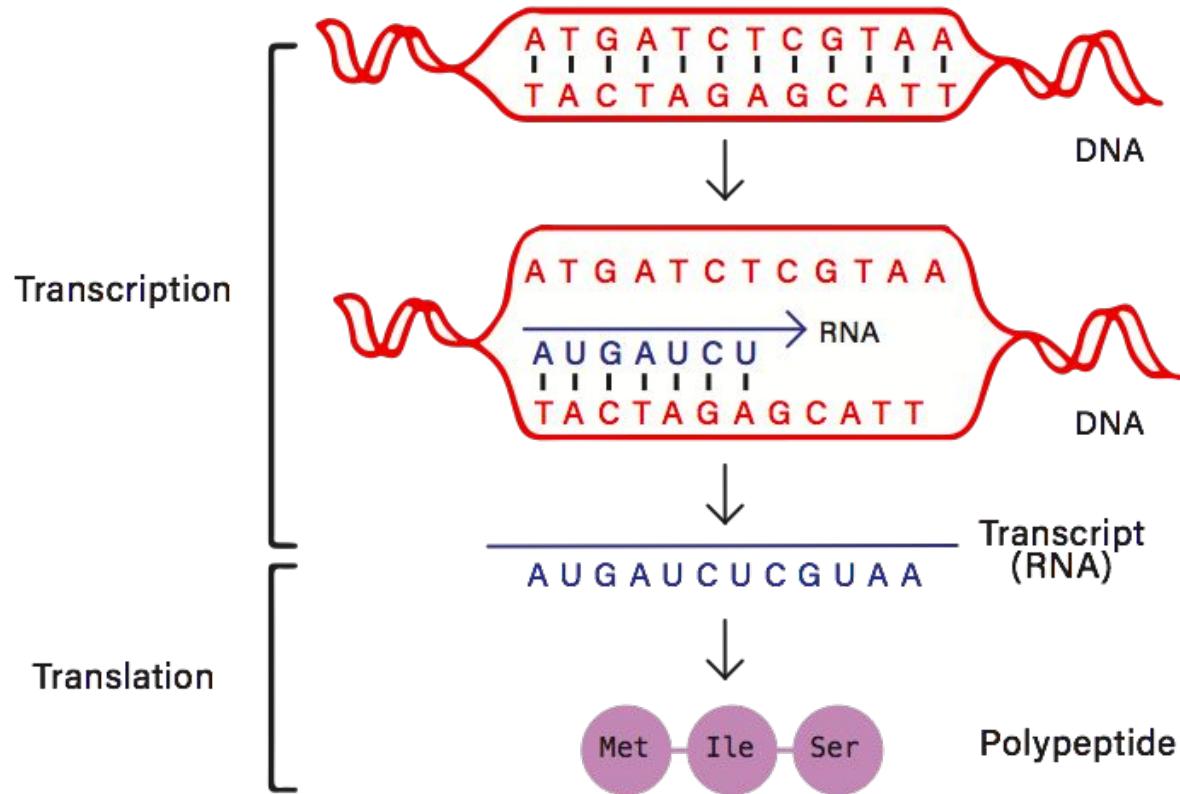
4. INHIBITOR: α -AMANITIN

5. CONCLUSIONS

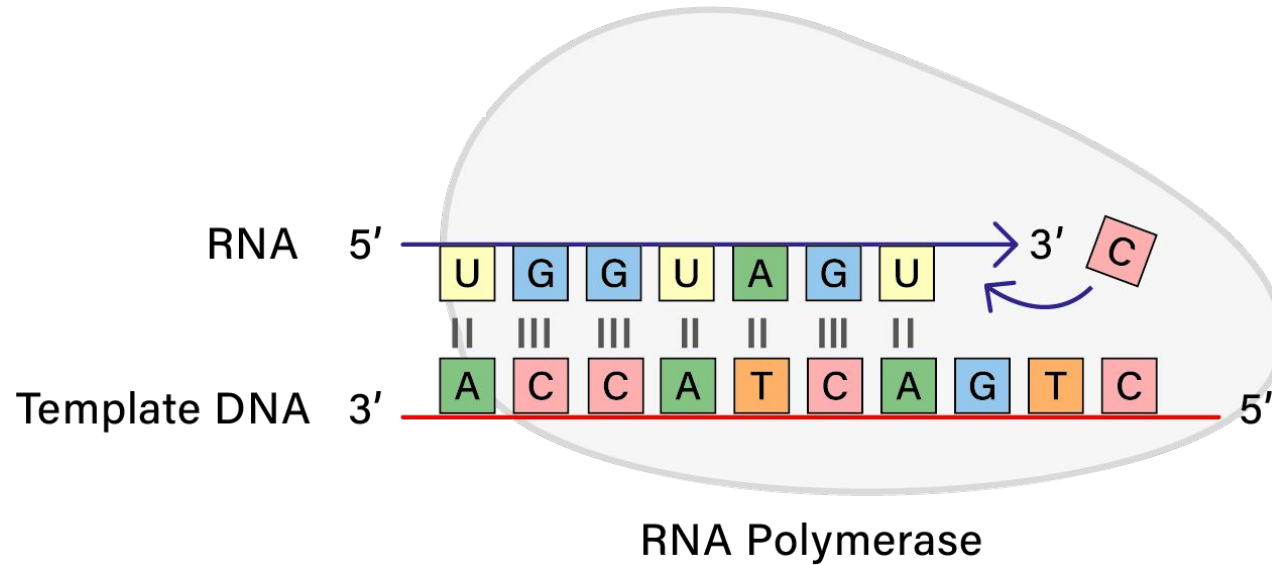


INTRODUCTION

TRANSCRIPTION



TRANSCRIPTION

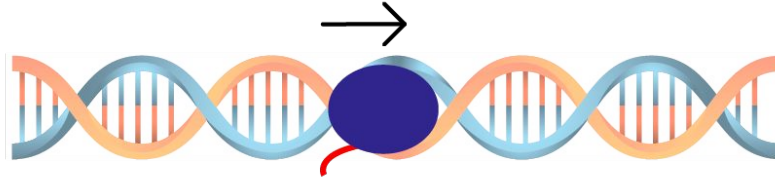


TRANSCRIPTION: Stages

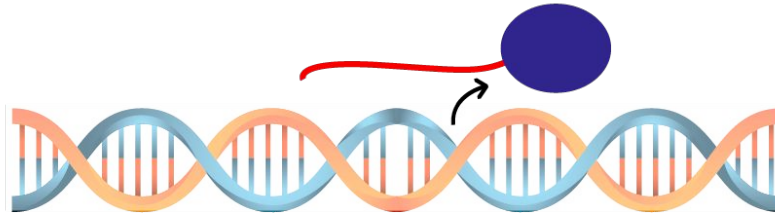
Initiation



Elongation



Termination



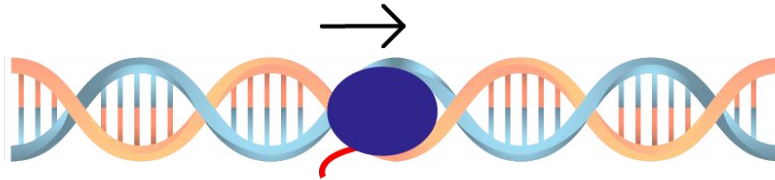
RNA POLYMERASES I, II and III

- DNA-dependent RNA polymerases
- *Bacteria* and *Archaea* → Only one RNA polymerase
- Present in all eukaryotes' **nucleus**

RNA polymerase I	RNA polymerase II	RNA polymerase III
rRNA	mRNA miRNA snRNA snoRNA	5S rRNA tRNA

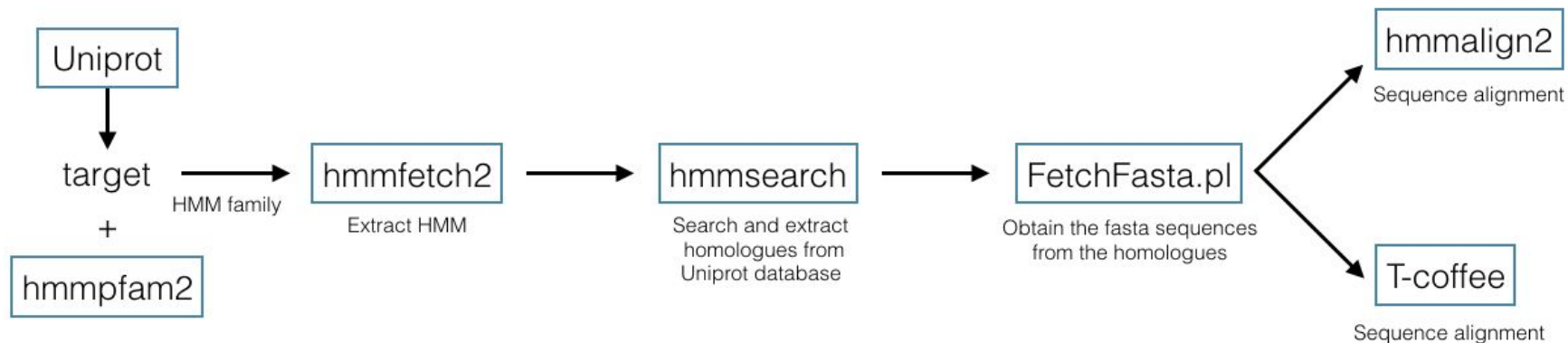
AIM OF THE PROJECT

- RNA polymerase II and Elongation cycle
- The aim of this project is:
 - To identify the main structures involved in the elongation cycle.
 - To find the residues whose interactions are essential for the enzyme function.
 - To analyze their conservation among different species' genome.

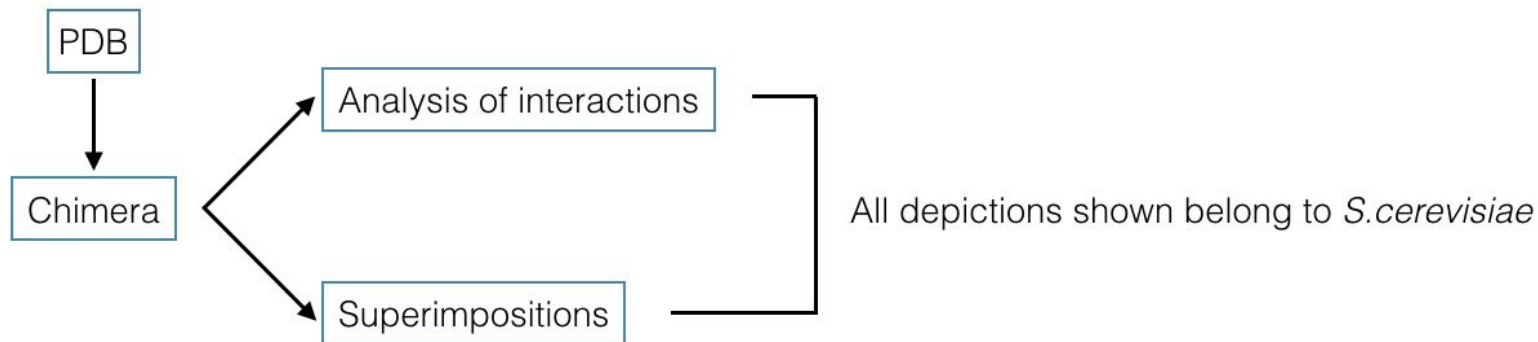


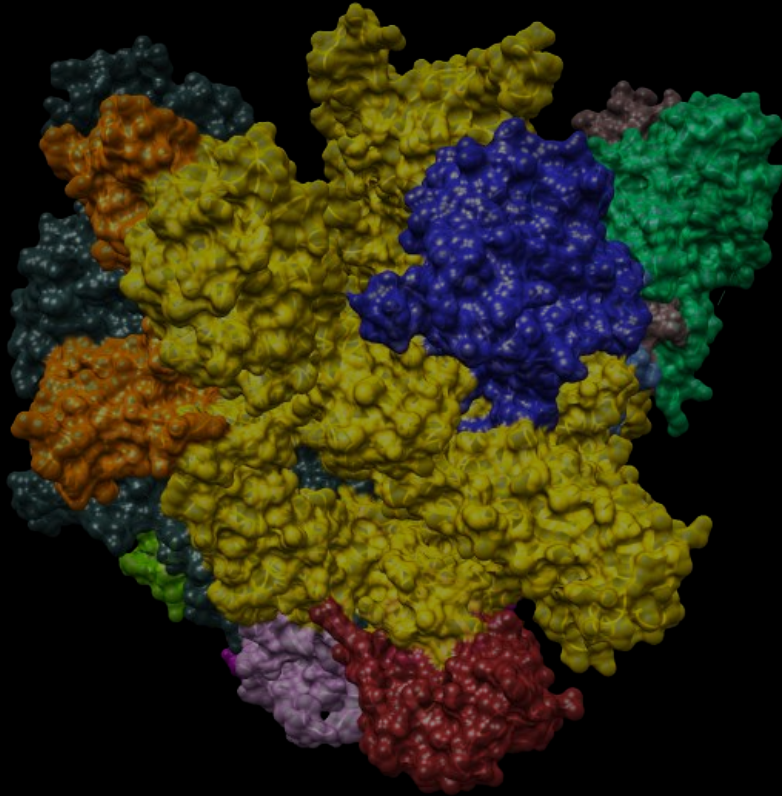
METHODS

Sequences



Structures

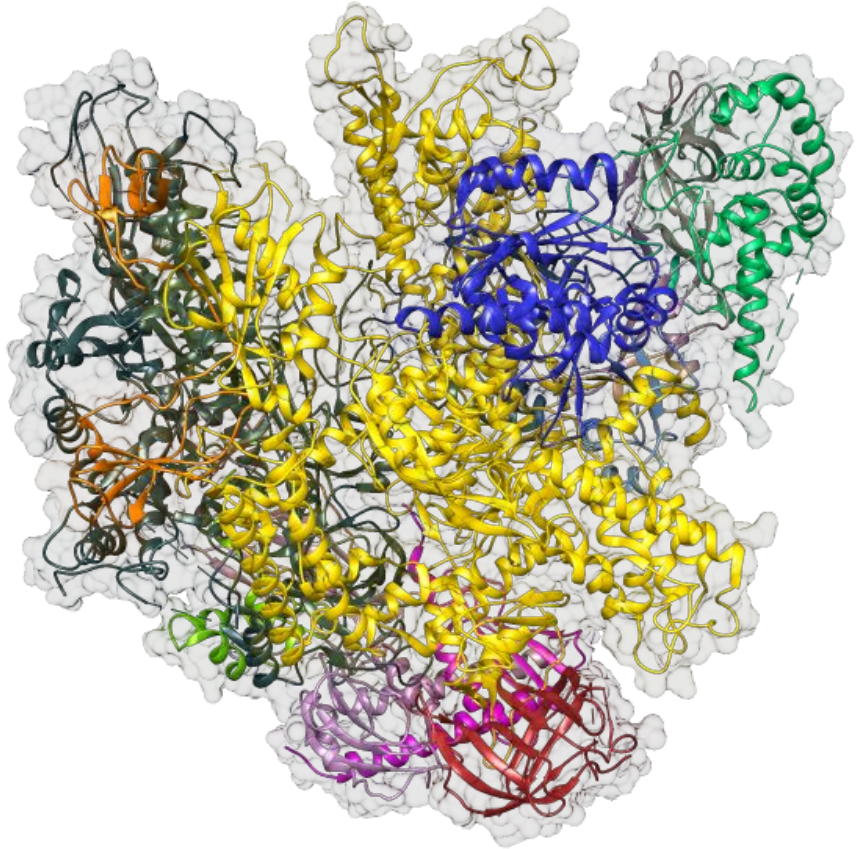
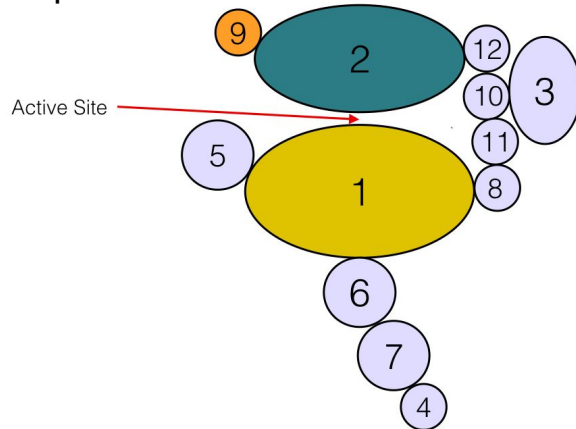




STRUCTURAL FEATURES OF
RNA POLYMERASE II

RNA polymerase II

- 550 kDa
- 12 subunits (Rpb1-Rpb12)
 - Rpb1
 - Rpb2
 - Rpb9

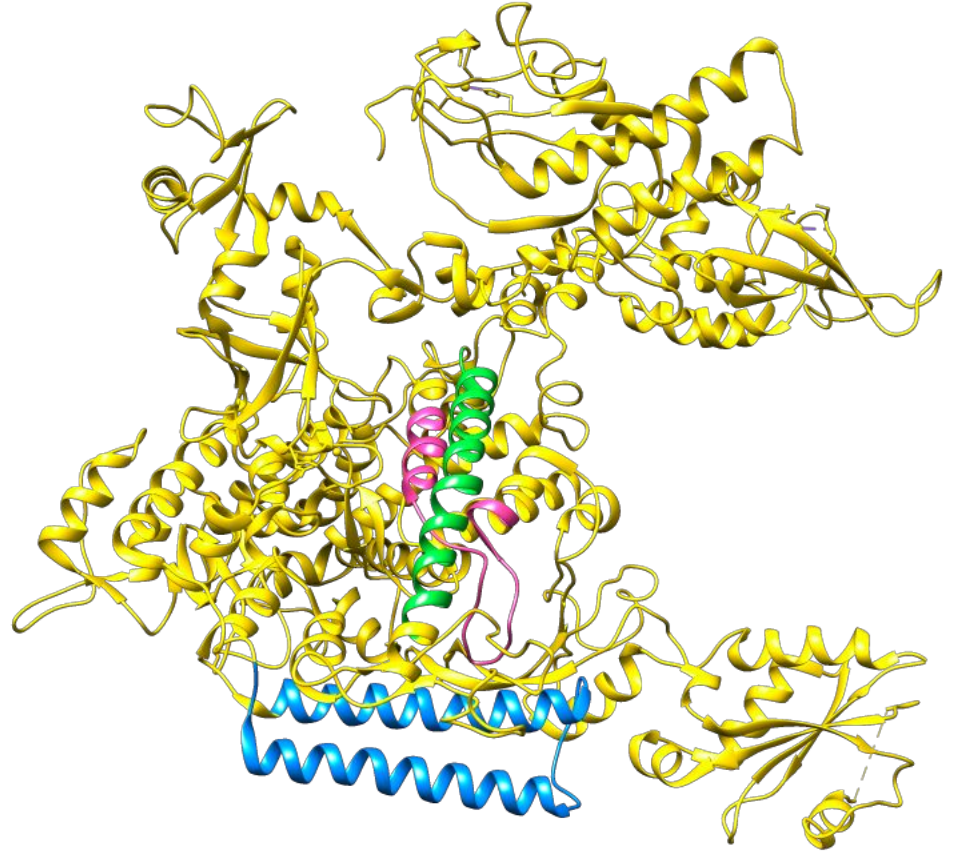


RNA polymerase II: Rpb1

- Largest subunit (220 kDa)

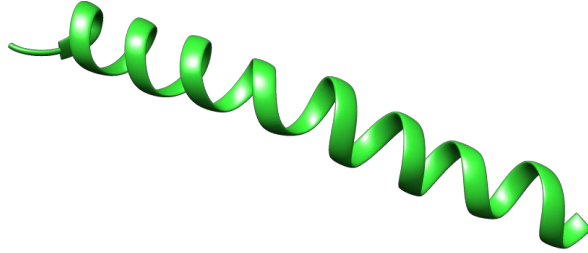
SCOP information:

- **Class:** Multi-domains protein
- **Fold:** Beta and beta-prime subunits of DNA-dependent RNA polymerase
- **Superfamily:** Beta and beta-prime subunits of DNA-dependent RNA polymerase
- **Family:** RNA polymerase beta-prime

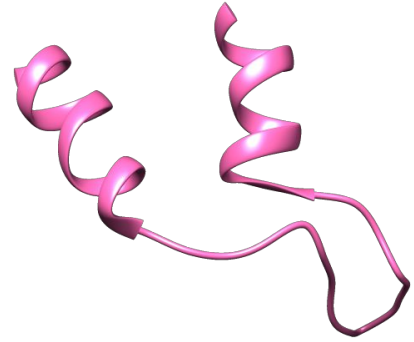


RNA polymerase II: Rpb1

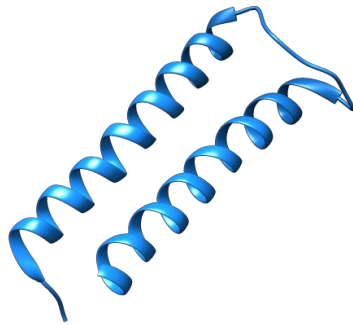
α -helix
(Bridge helix)



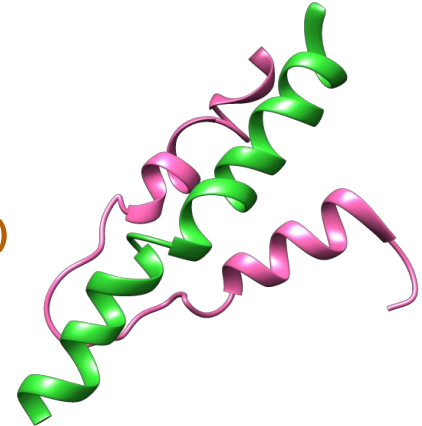
α -hairpin
(Trigger loop)



α -hairpin
($\alpha 20$ - $\alpha 21$)



three helix
bundle (BH+TL)

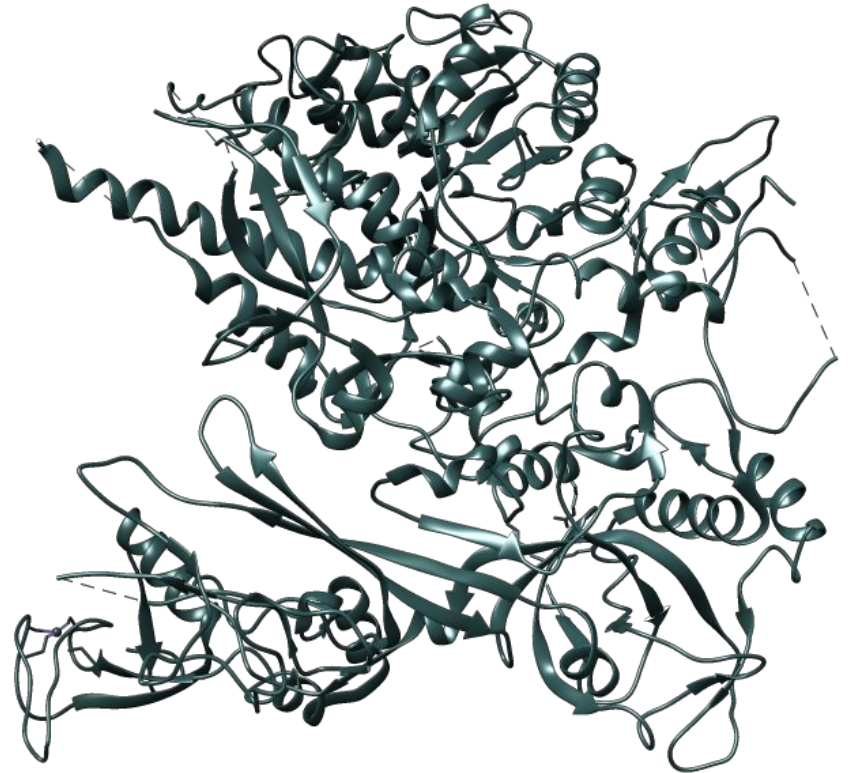


RNA polymerase II: Rpb2

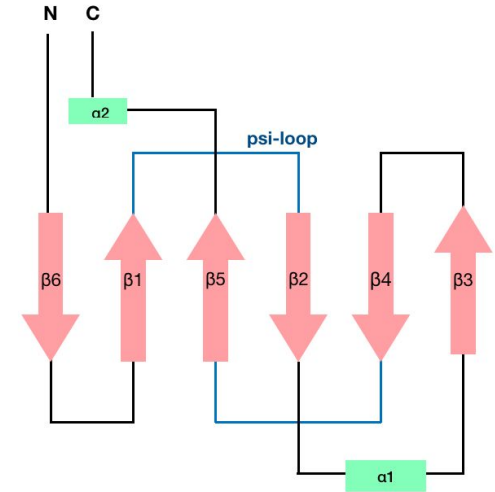
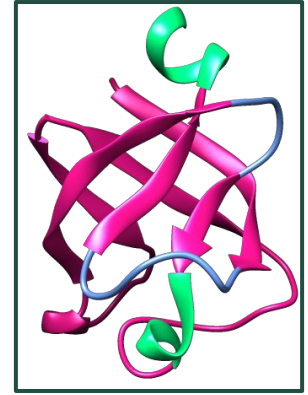
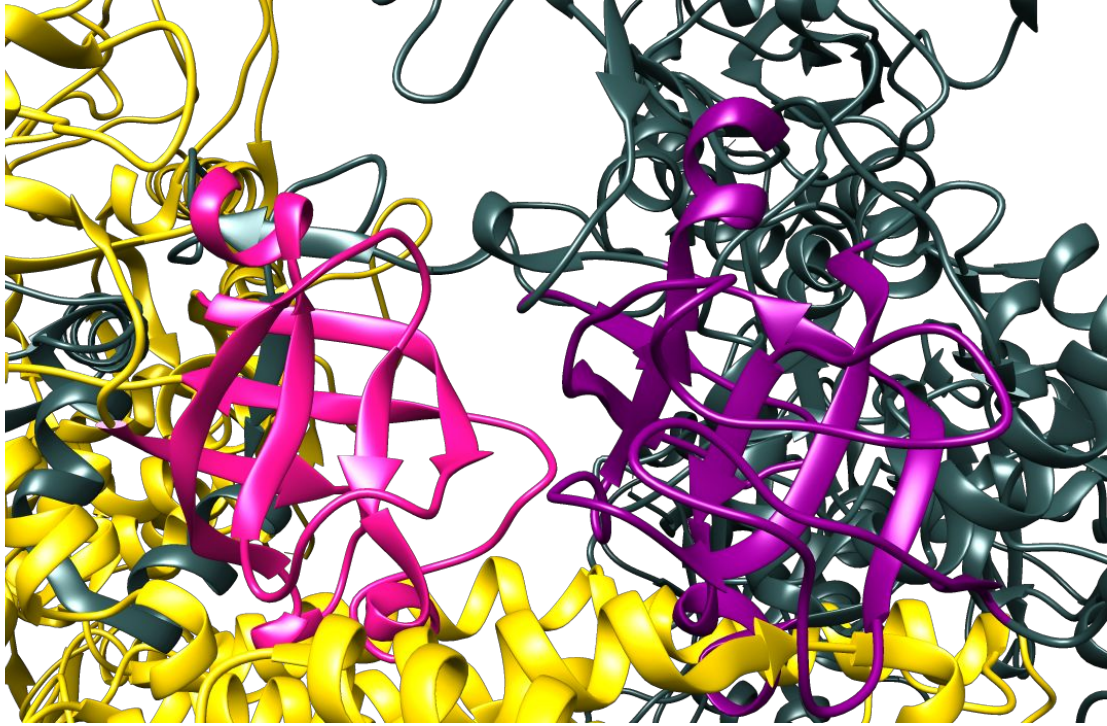
- 2nd largest subunit (140 kDa)

SCOP information:

- **Class:** Multi-domains protein
- **Fold:** Beta and beta-prime subunits of DNA-dependent RNA polymerase
- **Superfamily:** beta and beta-prime subunits of DNA-dependent RNA polymerase
- **Family:** RNA polymerase beta



RNA polymerase II: Rpb1 and Rpb2 double-psi β -barrels

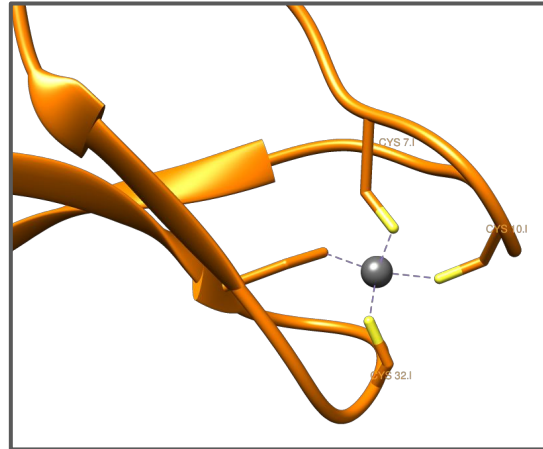
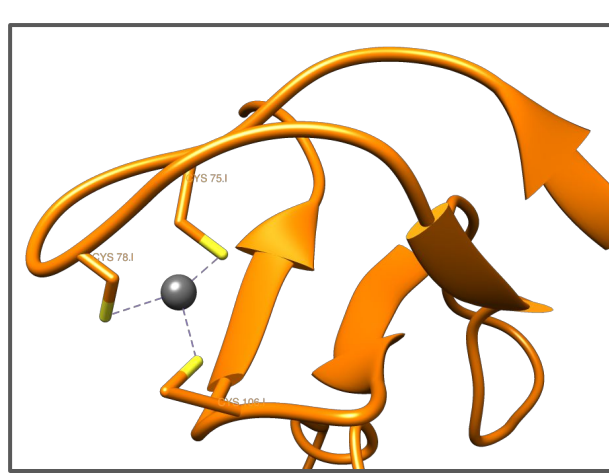


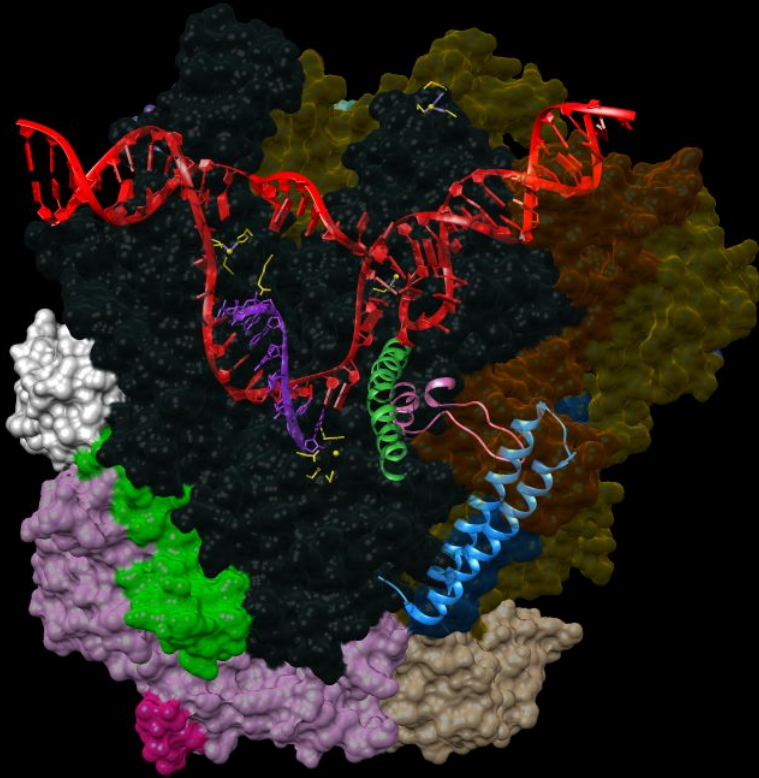
RNA polymerase II: Rpb9

- 14.5 kDa
- 2 Zn binding motifs

SCOP information:

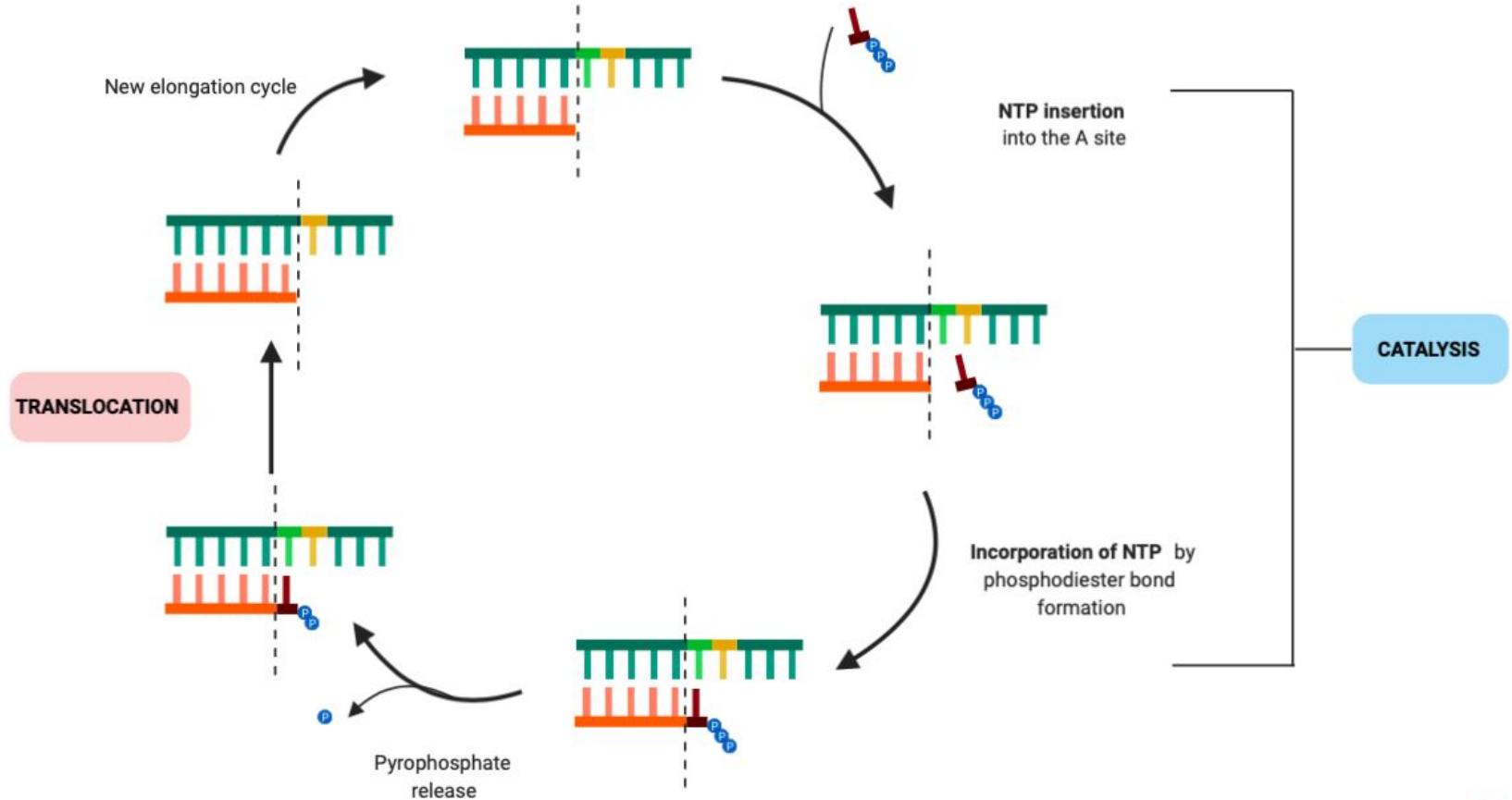
- **Class:** Small proteins
- **Fold:** Rubredoxin-like
- **Superfamily:** Zn beta-ribbon
- **Family:** Transcriptional factor domain



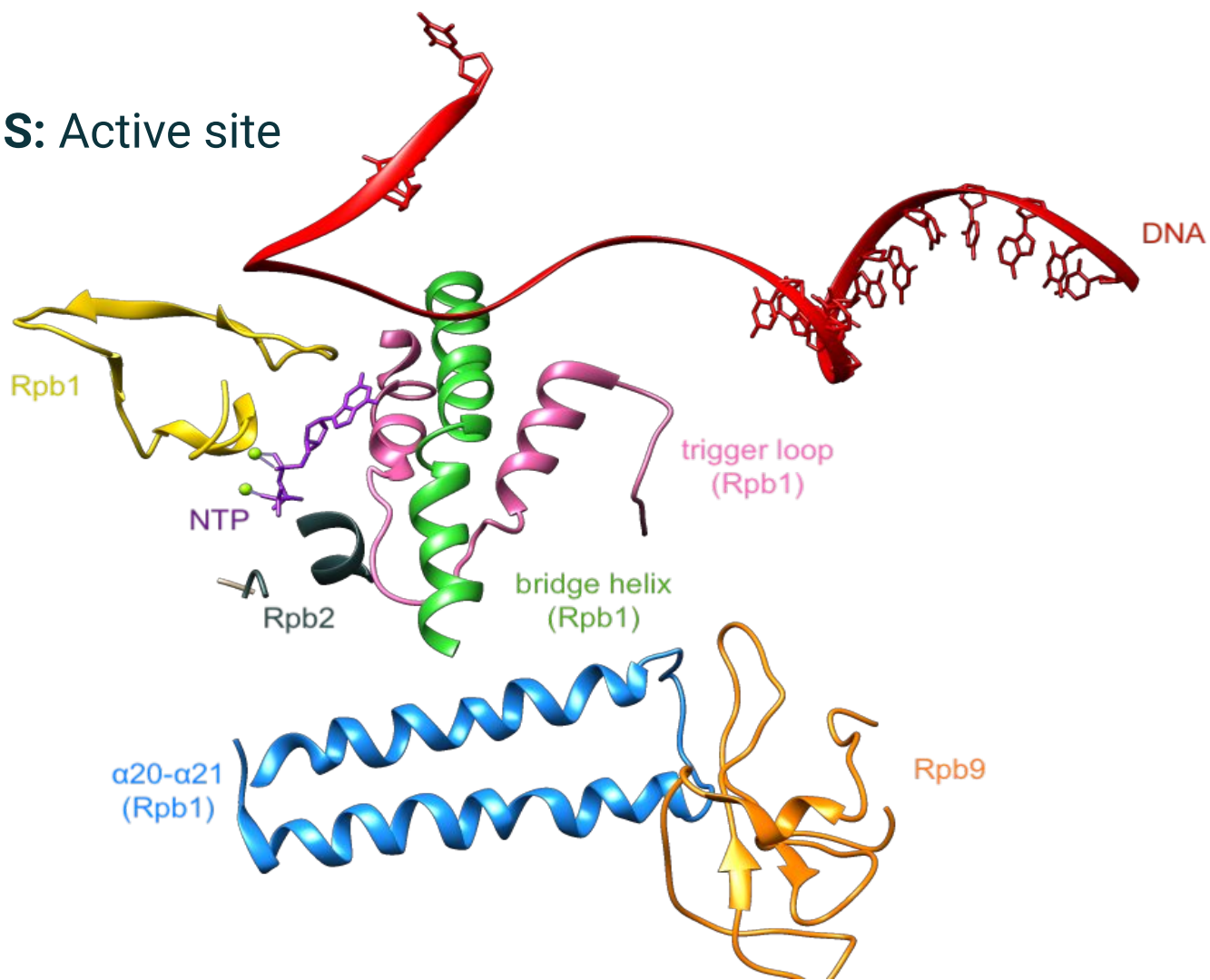


THE ELONGATION CYCLE

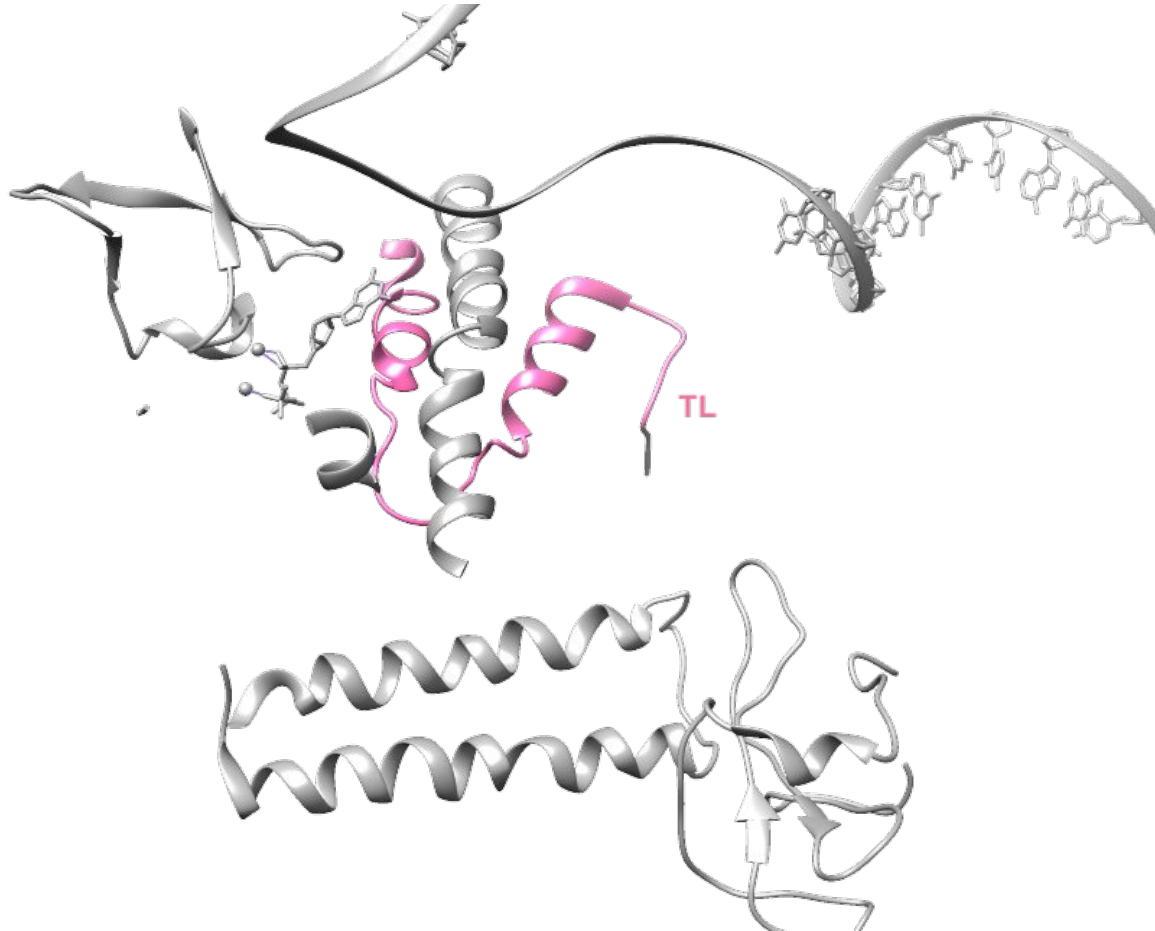
ELONGATION CYCLE



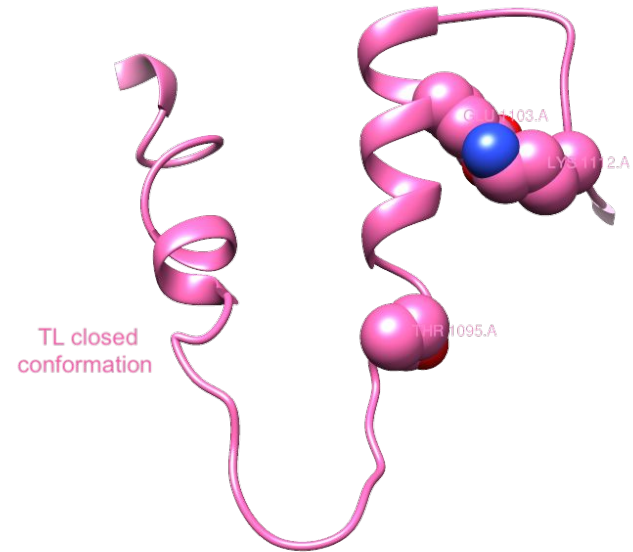
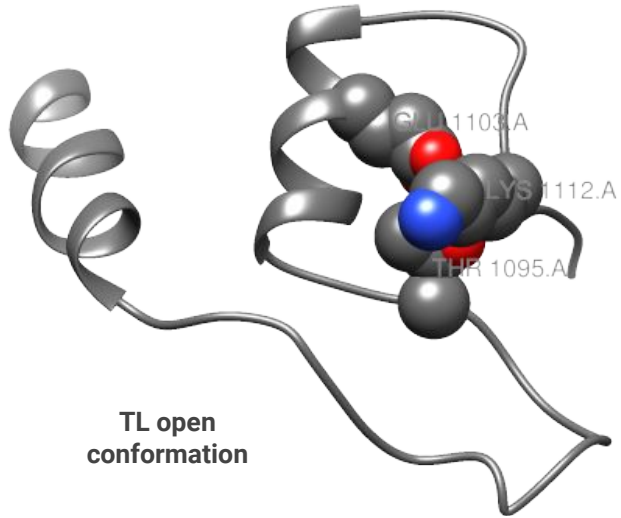
CATALYSIS: Active site



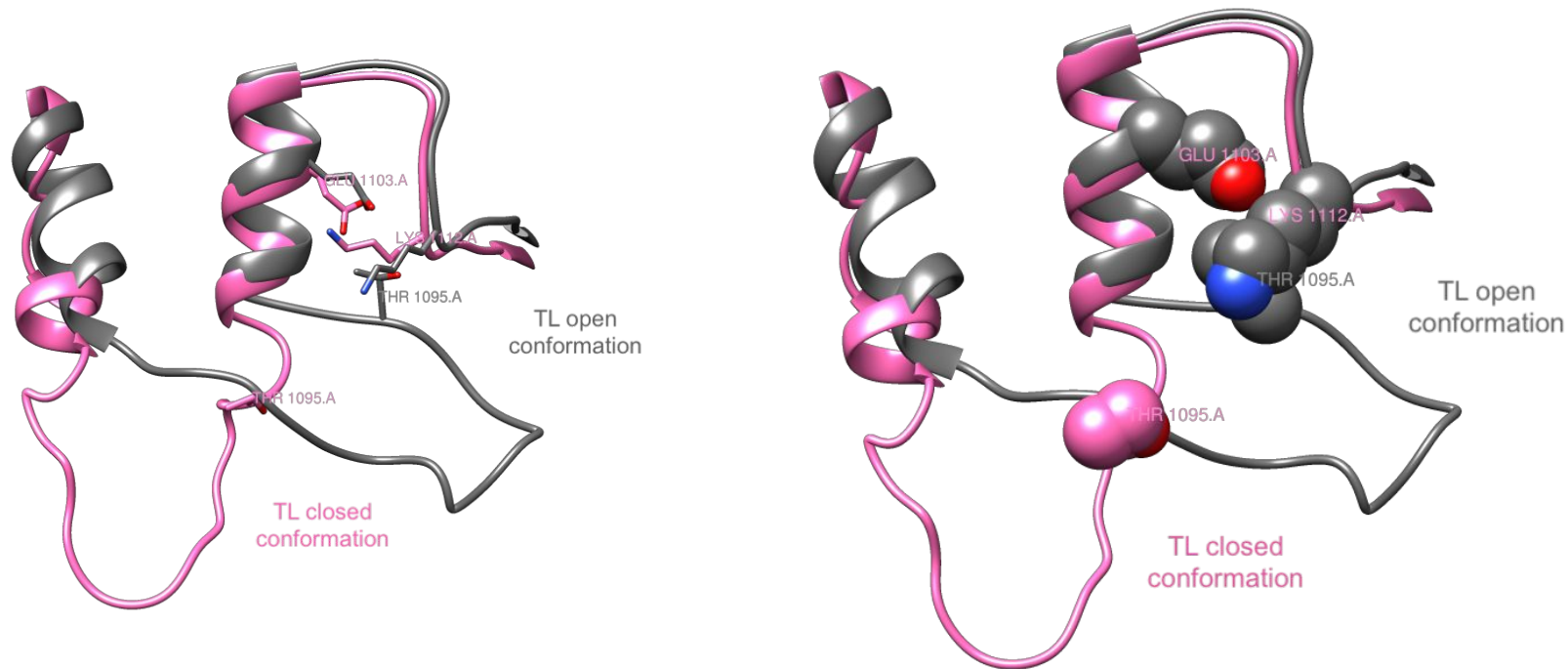
CATALYSIS: Trigger loop (TL) mobility



CATALYSIS: Trigger loop (TL) mobility

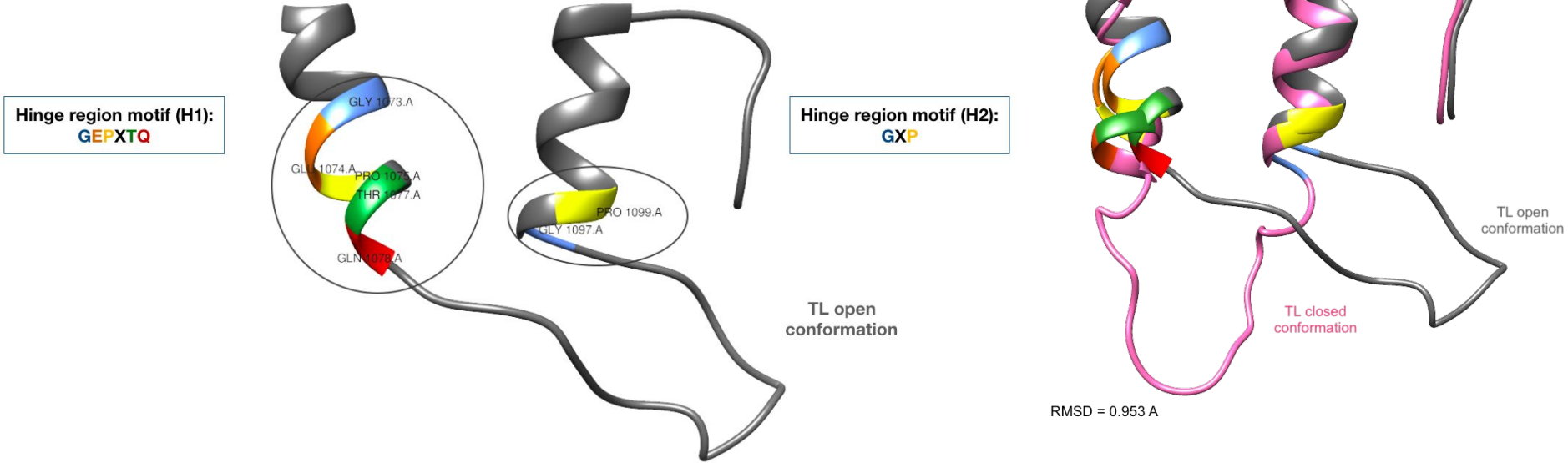


CATALYSIS: TL mobility (superimposition)

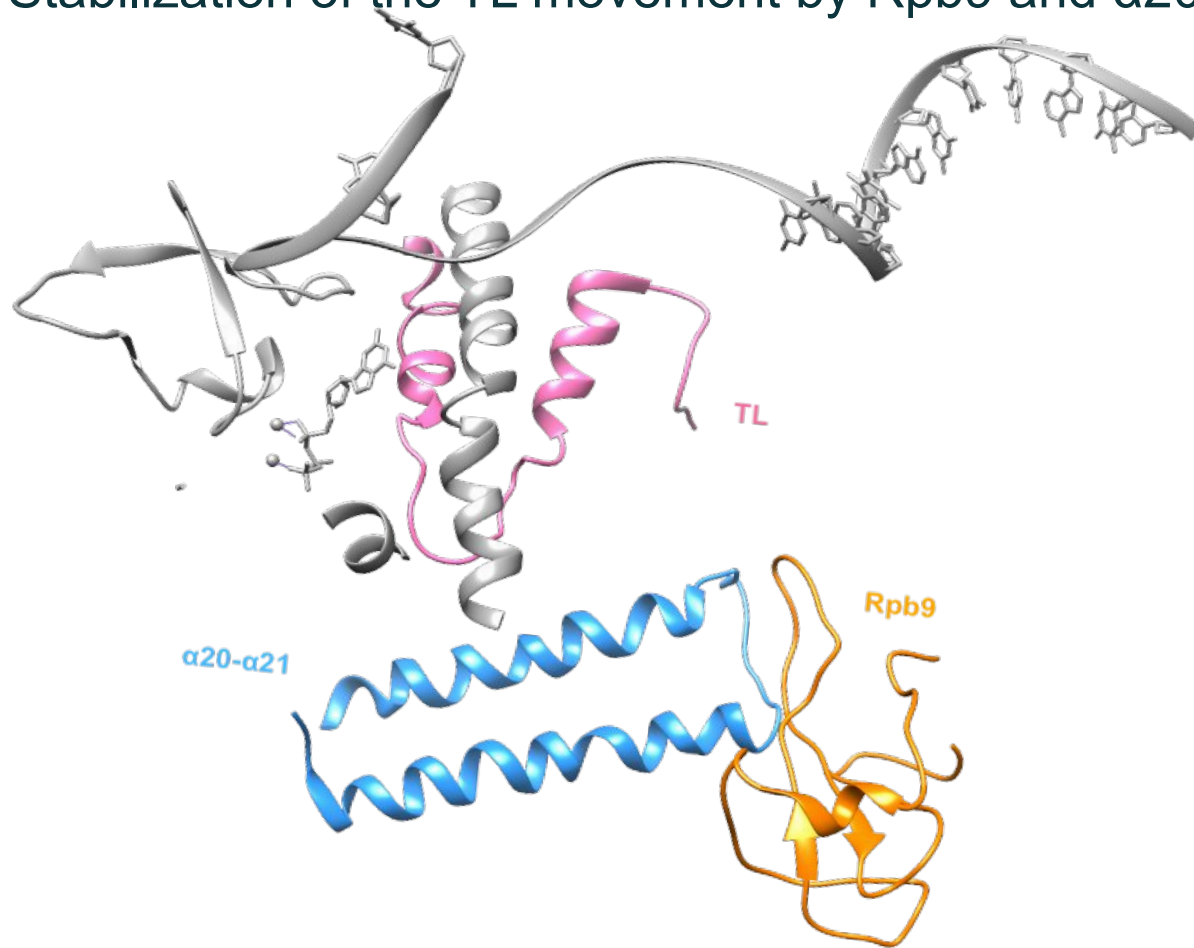


RMSD = 0.953 Å

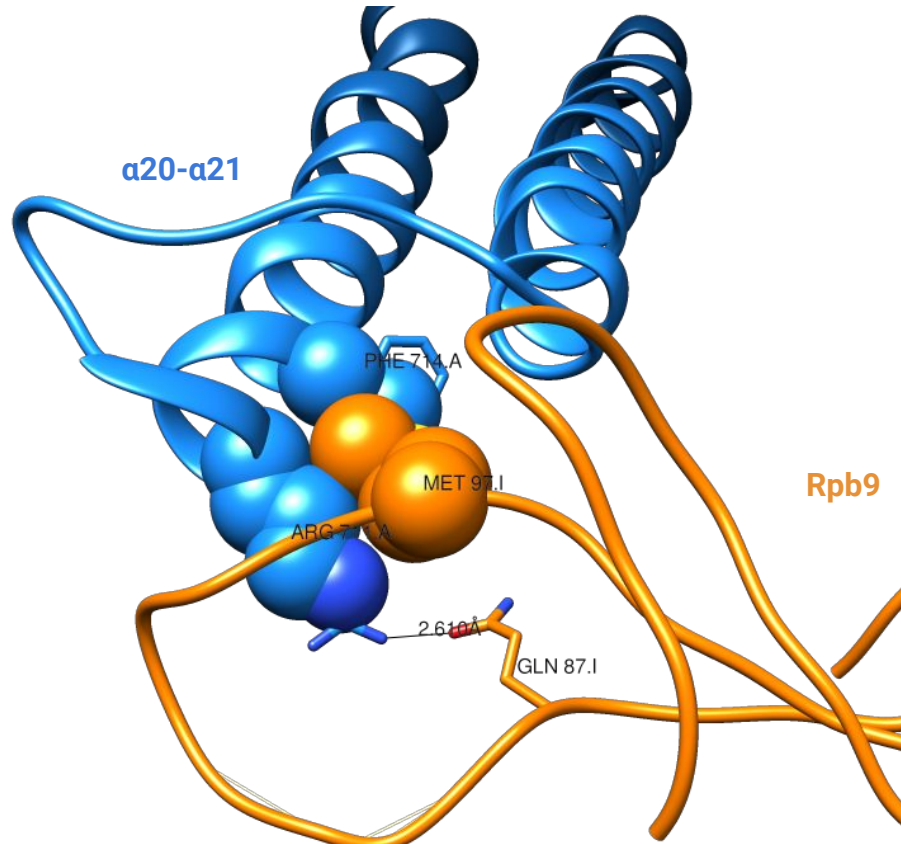
CATALYSIS: Hinge regions allow trigger loop mobility



CATALYSIS: Stabilization of the TL movement by Rpb9 and $\alpha 20$ - $\alpha 21$



CATALYSIS: Rpb9 stabilizes $\alpha 20$ and $\alpha 21$ from Rpb1



Rpb9

HUMAN
 PIG
 MOUSE
 BOVIN
 DROSOPHILA
 S. POMBE
 S. CEREVISIAE

87 97

KITHEVDEL TQIIADVSQDPTLPRTE DHPCQKCGHKEAVFFQSHSARAEDAMRLYYVCTA
 KITHEVDEL TQIIADVSQDPTLPRTE DHPCQKCGHKEAVFFQSHSARAEDAMRLYYVCTA
 KITHEVDEL TQIIADVSQDPTLPRTE DHPCQKCGHKEAVFFQSHSARAEDAMRLYYVCTA
 KITHEVDEL TQIIADVSQDPTLPRTE DHPCQKCGHKEAVFFQSHSARAEDAMRLYYVCTA
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 ELQSSNVENTTVSHDASTDPTLPR-SDKECPRCHQHEAVFYQTHSRRGDTMMTLIYVCVH
 ELITNIGETAGVVQDIGSDPTLPR-SDRECPKCHSRENVFFQSQRKDTSMVLFFVCLS
 :: . * : : * ***** .*: * :* :* **: *: * : * * : **

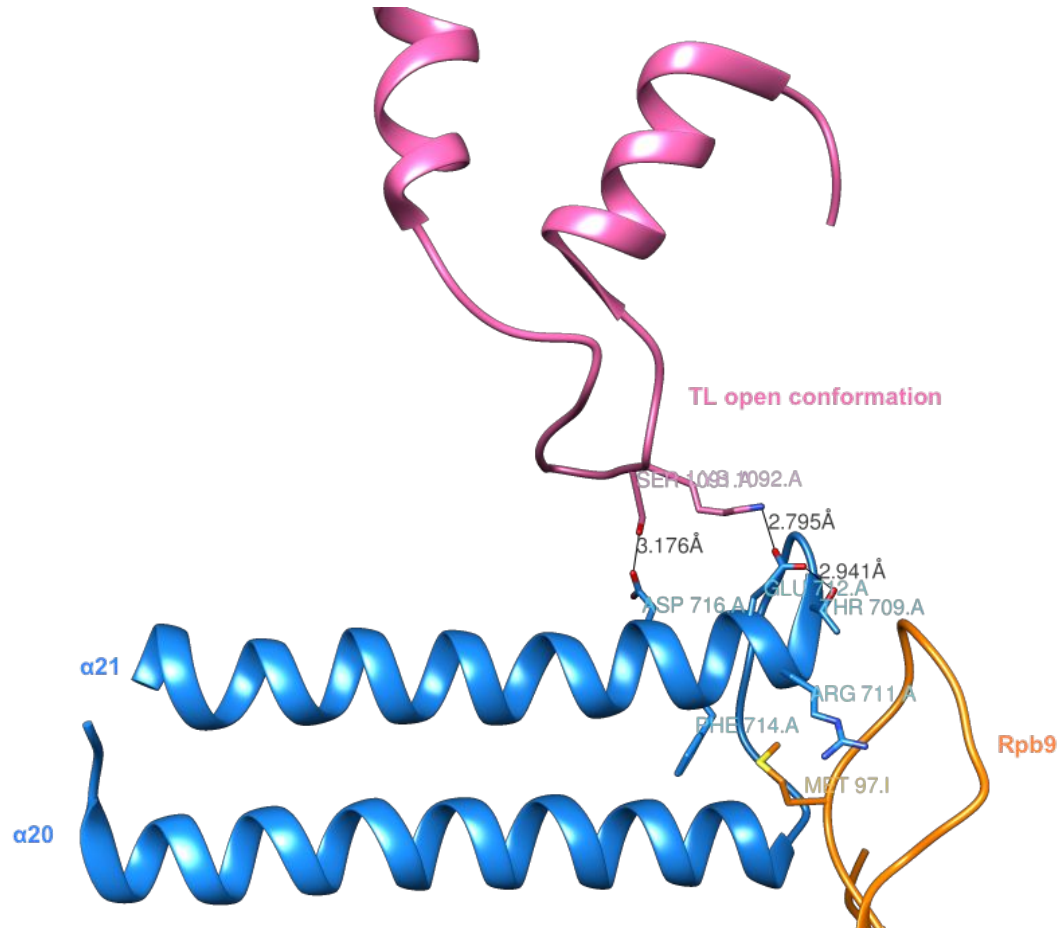
Rpb1

S. POMBE
 D. DISCOIDEUM
 C. ELEGANS
 MOUSE
 HUMAN
 DROSOPHILA
 ARCHEA
 S. CEREVISIAE
 #=GC RF

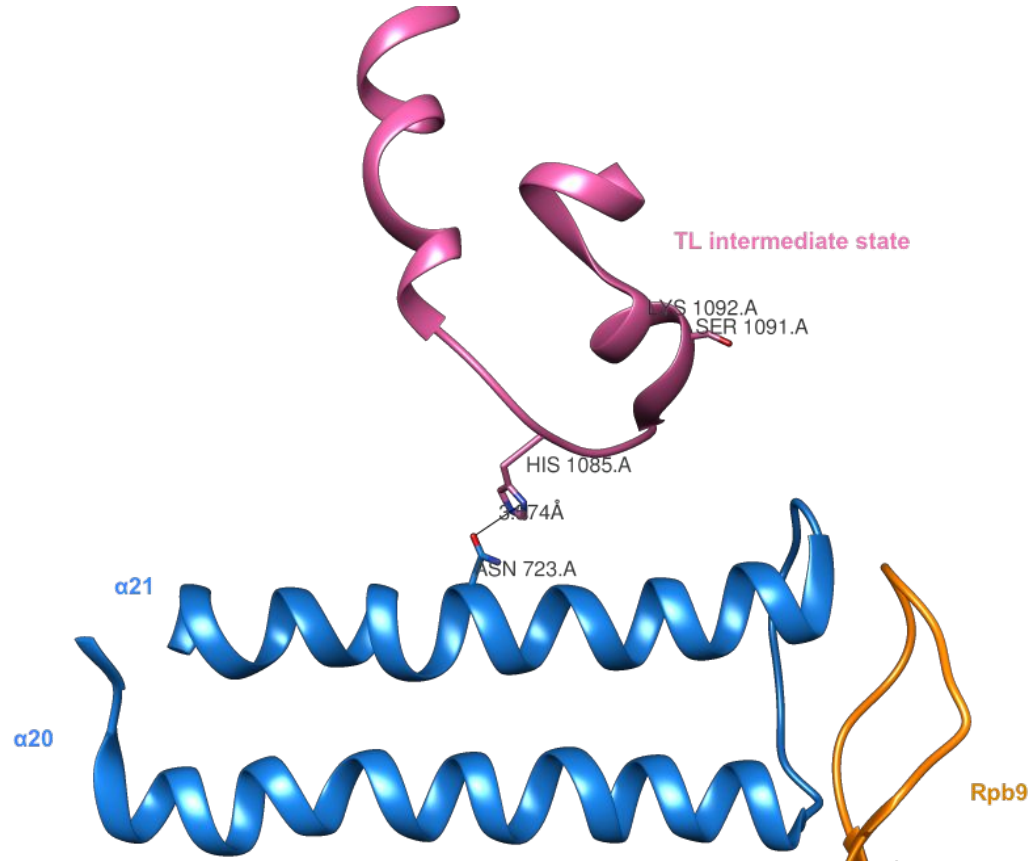
711 714

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 diqntikkakqdvievIEKAHN-NELEPTPGNTLRQTFENQVNRILNDAR
 eiqqaikkakddvinvIQKAHN-MELEPTPGNTLRQTFENKVNRIILNDAR
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

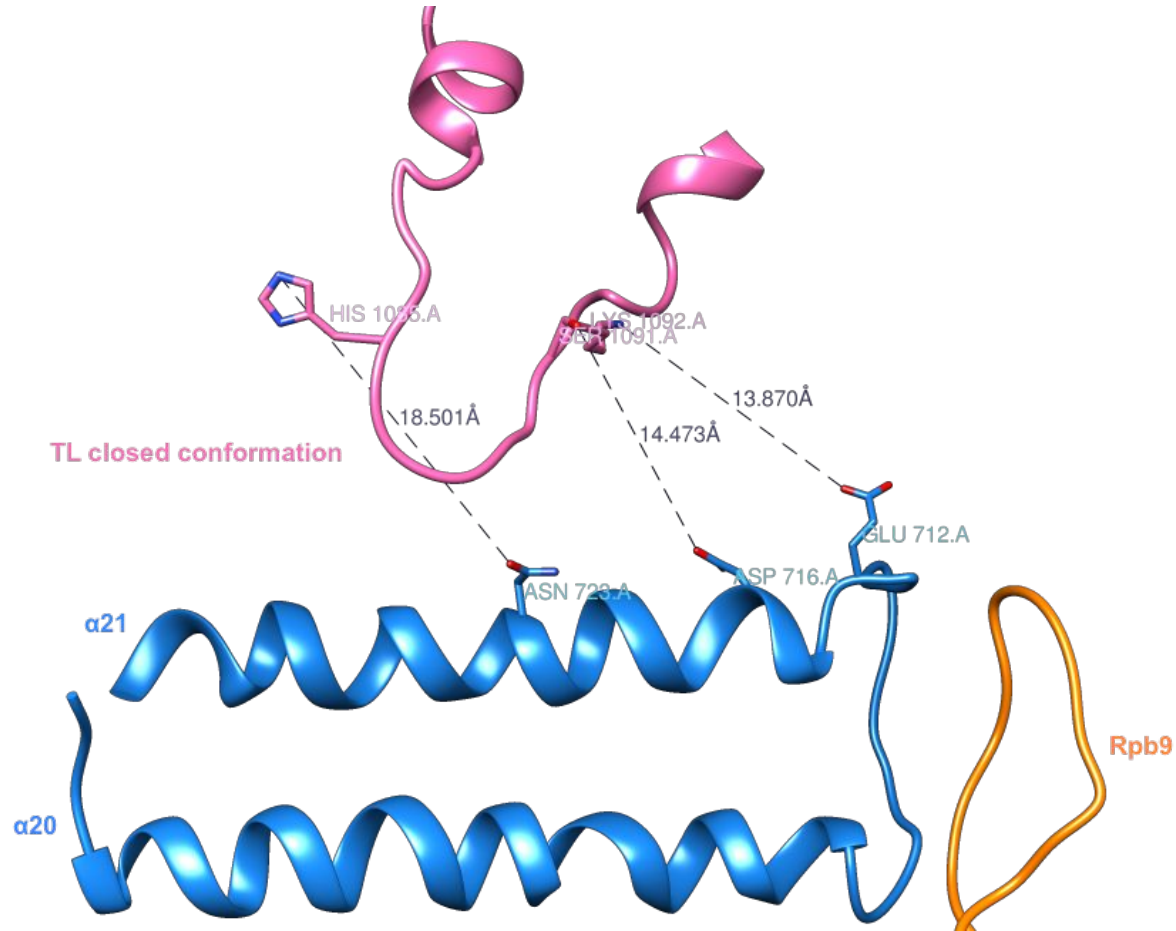
CATALYSIS: $\alpha 20$ and $\alpha 21$ stabilize TL movement



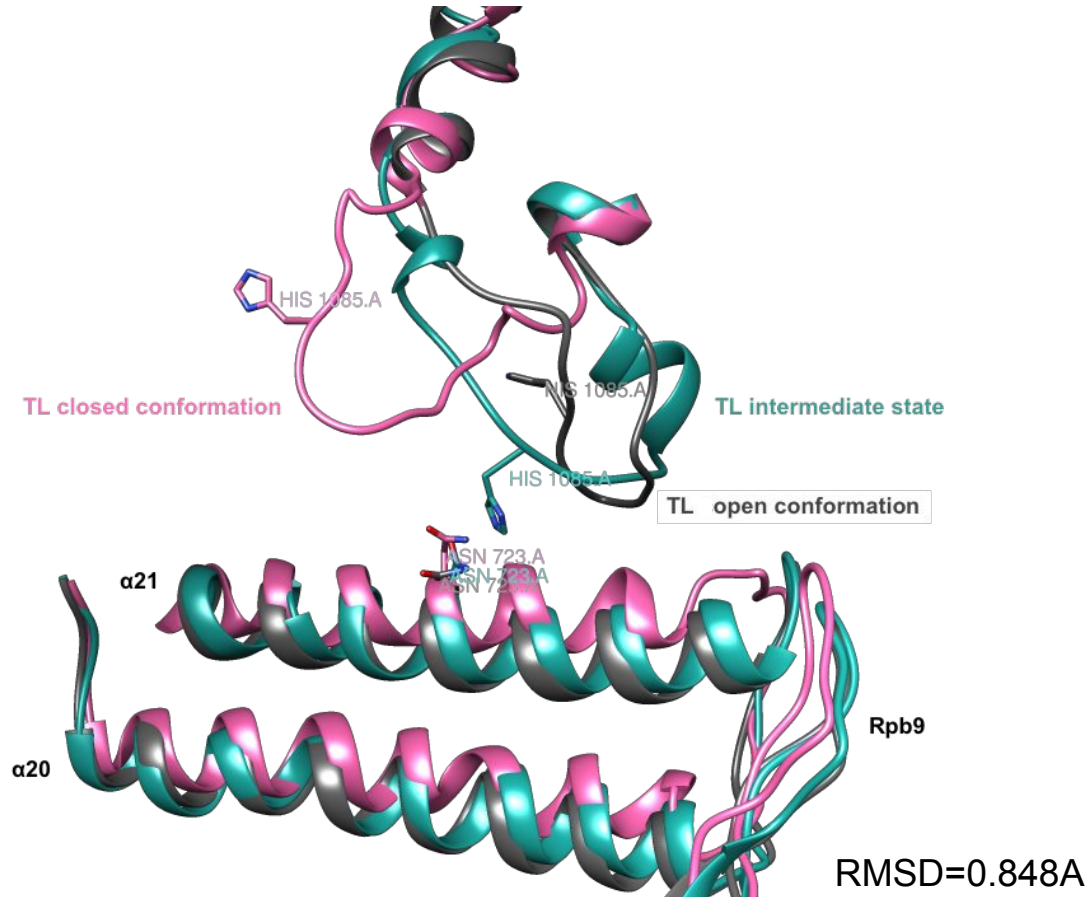
CATALYSIS: $\alpha 20$ and $\alpha 21$ stabilize TL movement



CATALYSIS: $\alpha 20$ and $\alpha 21$ stabilize TL movement



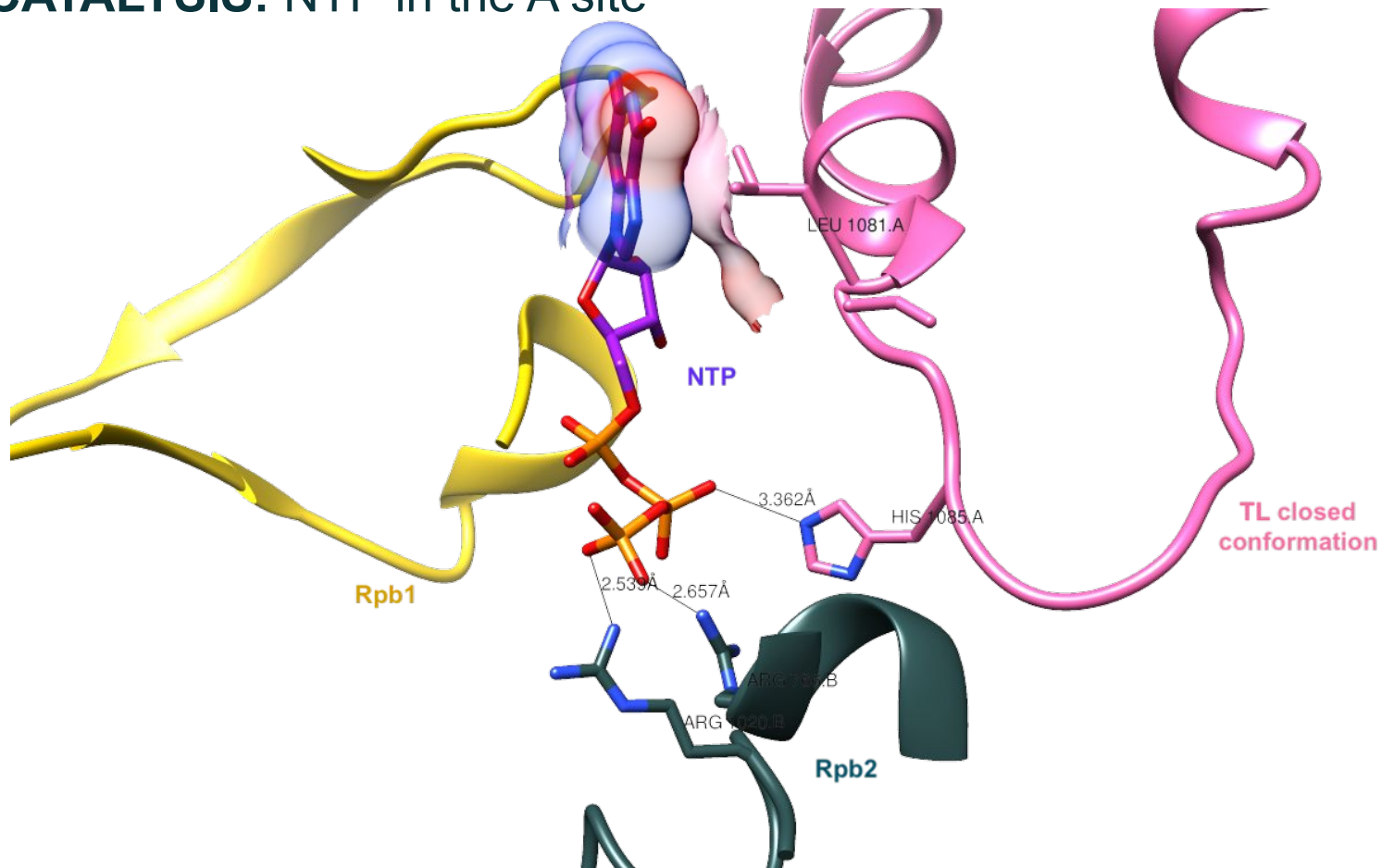
CATALYSIS: $\alpha 20$ and $\alpha 21$ stabilize TL movement (superimposition)



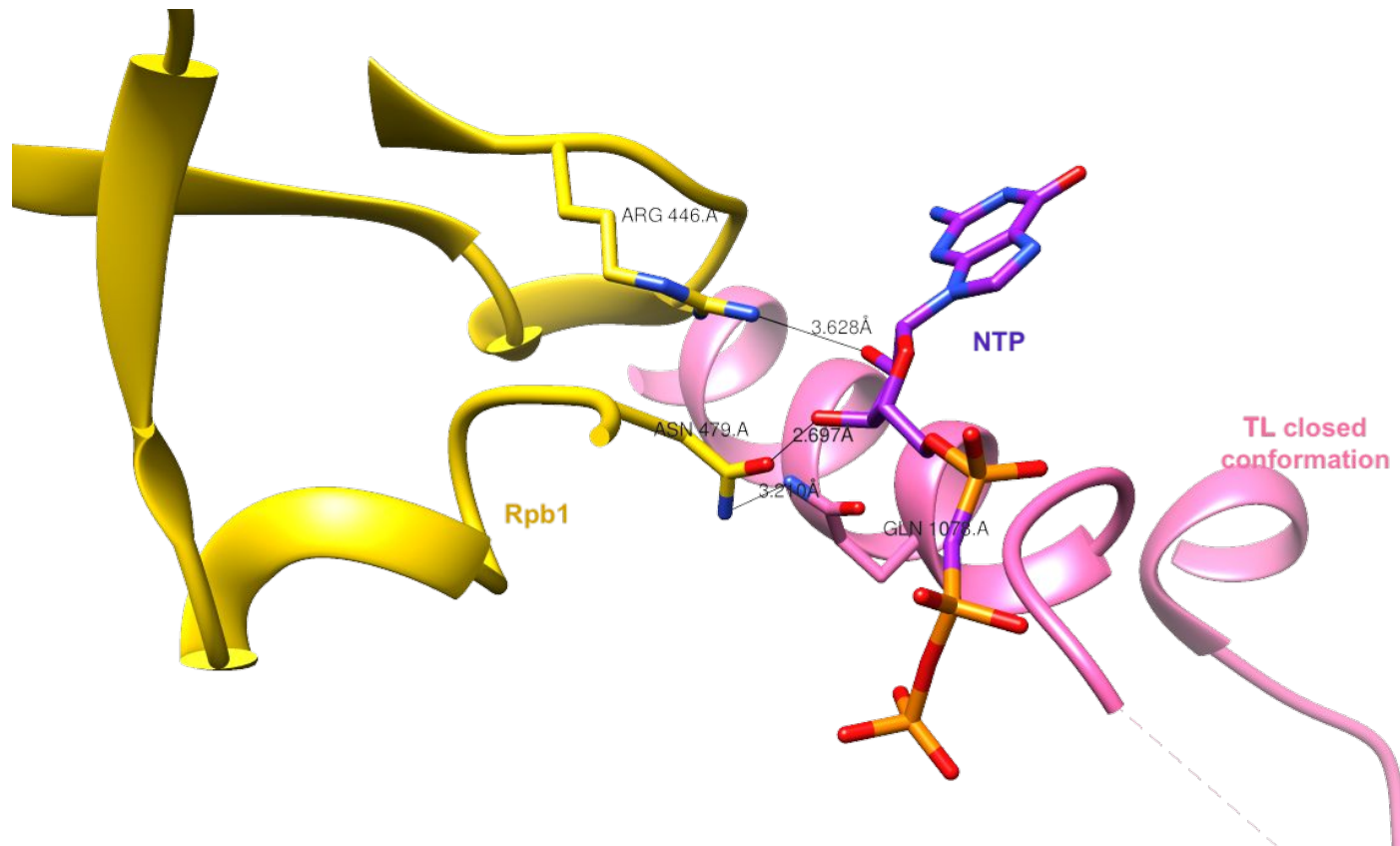
CATALYSIS: NTP in the A site



CATALYSIS: NTP in the A site



CATALYSIS: NTP in the A site



CATALYSIS: Residues that contact the NTP are conserved

Rpb1 (TL)

S. POMBE
DROSOPHILA
MOUSE
HUMAN
C. ELEGAN
D. DISCOIDEUM
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

1078 1081 1085

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AAQSLGEPATQMTLNTFFHAGVSSKNVTLGVPRLKEIINISKKPKAPSLT
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AAQSIGEPATQMTLNTFFHAGVASKVTSVLPRLKEILNVAKNMKTPSLT
XX

Rpb1

S. POMBE
D. DISCOIDEUM
C. ELEGANS
MOUSE
HUMAN
DROSOPHILA
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

446

----RVERHIRDGDVVIFNRQPS
----KVERHINDGDVVIFNRQPS
----RVERHMKDGDIIIVFNRQPT
----KVERHMCDDGDIVIFNRQPT
----KVERHMCDDGDIVIFNRQPT
----KVERHLRDDDLVIFNRQPT
----KVERHLQDGFVLFNRQPS
----DILDEVIREHPVLLNRAPT
----KVERHIMDNDPVLFNRRQPS
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

Rpb1

S. POMBE
D. DISCOIDEUM
C. ELEGANS
MOUSE
HUMAN
DROSOPHILA
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

479

SPYNADFDGDEMNMH
SPYNADFDGDEMNLH
SPYNADFDGDEMNLH
TPYNADFDGDEMNLH
TPYNADFDGDEMNLH
SPYNADFDGDEMNLH
SPYNADFDGDEMNMH
AAYNADFDGQMAVH
SPYNADFDGDEMNLH
XXXXXXXXXXXXXXXXXXXX

CATALYSIS: Residues that contact the NTP are conserved

Rpb2

766

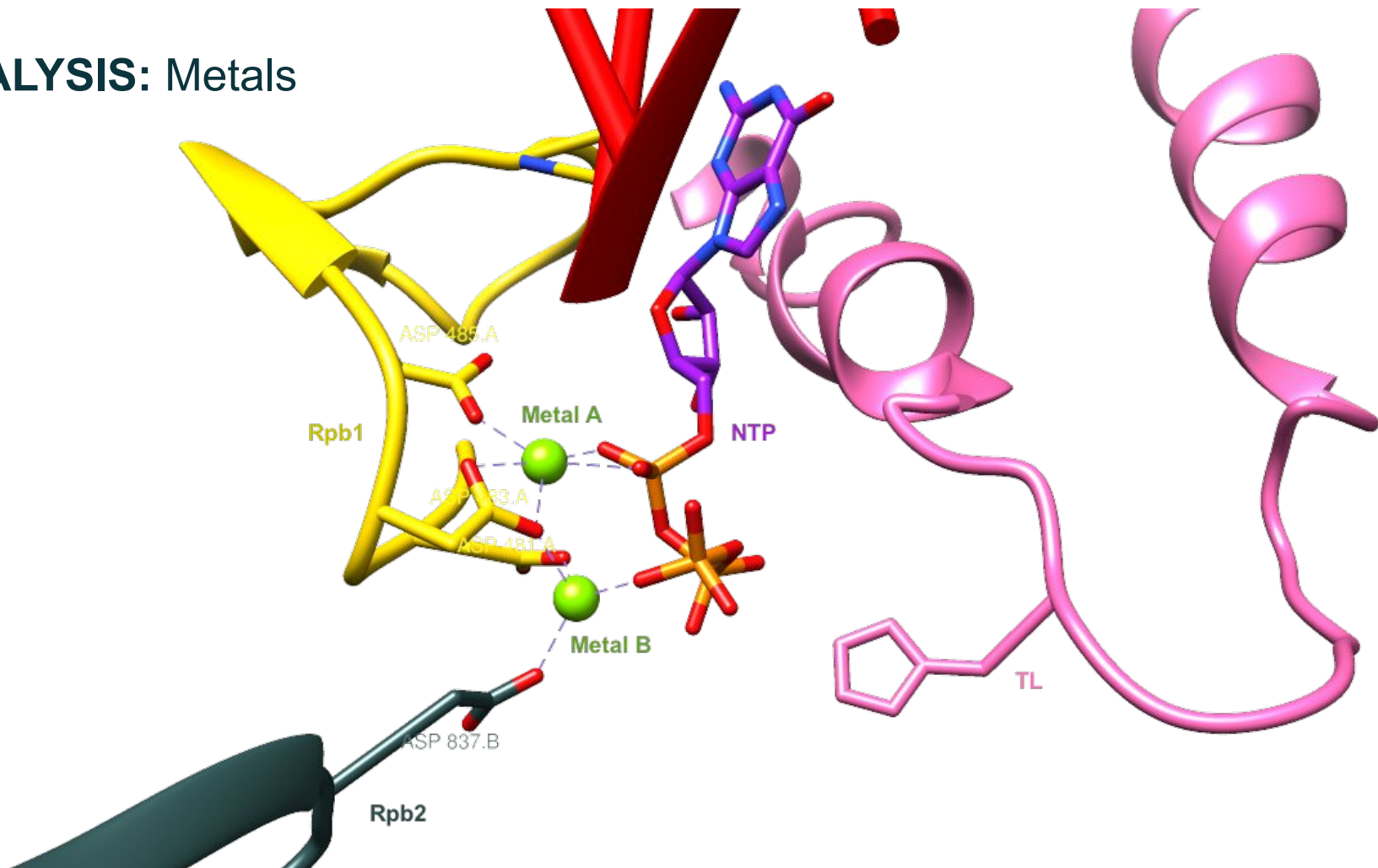
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S. POMBE	PH-----VHAWTHCEIHPAMILGILASIIPFPDHNQSPRNTYQSAMGKQA
HUMAN	AY-----CSTYTHCEIHPSMILGVCASIIPFPDHNQSPRNTYQSAMGKQA
D. DISCOIDEUM	QI-----VHTYTHCEIHPSMILGICCSIIPFPDHNQSPRNTYQAAMGKQA
C. ELEGANS	GY-----CDTHTHCEIHPAMILGVCASIIPFPDHNQSPRNTYQSAMGKQA
DROSOPHILA	AY-----CTTYTHCEIHPAMILGVCASIIPFPDHNQSPRNTYQSAMGKQA
E. COLI	GESSLFSRDQVDYMDVSTQQVVSVGASLIPFLEHDDANRALMGANMQRQA
S. CEREVISIAE	HH-----ATTFTHCEIHPSMILGVAASIIPFPDHNQSPRNTYQSAMGKQA
	: : : . : : : .*:*** :*::: * : * : **

Rpb2

1020

DROSOPHILA	LGPTYYYQLKHMVDDKIH SRARGPVQILVRQPMEGRARDGGLRFGEMERD
MOUSE	IGPTYYYQLKHMVDDKIH SRARGPIQILNRQPMEGRSRDGGLRFGEMERD
HUMAN	IGPTYYYQLKHMVDDKIH SRARGPIQILNRQPMEGRSRDGGLRFGEMERD
C. ELEGANS	FGPTYYYQLKHMVDDKIH SRARGPIQMMNRQPMEGRARDGGLRFGEMERD
S. POMBE	LGPTYYYQLKHLVDDKIH ARARGPVQILTRQPVEGRSRDGGLRFGEMERD
A. THALIANA	LGPTYYYQLKHMVDDKIH SRGRGPVQILTRQPAEGRSRDGGLRFGEMERD
E. COLI	VGMYMLKLNHLVDDKM HARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVD
D. DISCOIDEUM	IGPTYYYQLKHMVDDKIH SRSRGPVQILTRQPVEGRSRDGGLRFGEMERD
S. CEREVISIAE	FGPTYYYQLRHMVDDKIH ARARGPMQVLTRQPVEGRSRDGGLRFGEMERD
	. * * :*.*:*****:***. *. .:: :** *::: ** *****

CATALYSIS: Metals



CATALYSIS: Residues that contact Mg^{2+} are conserved

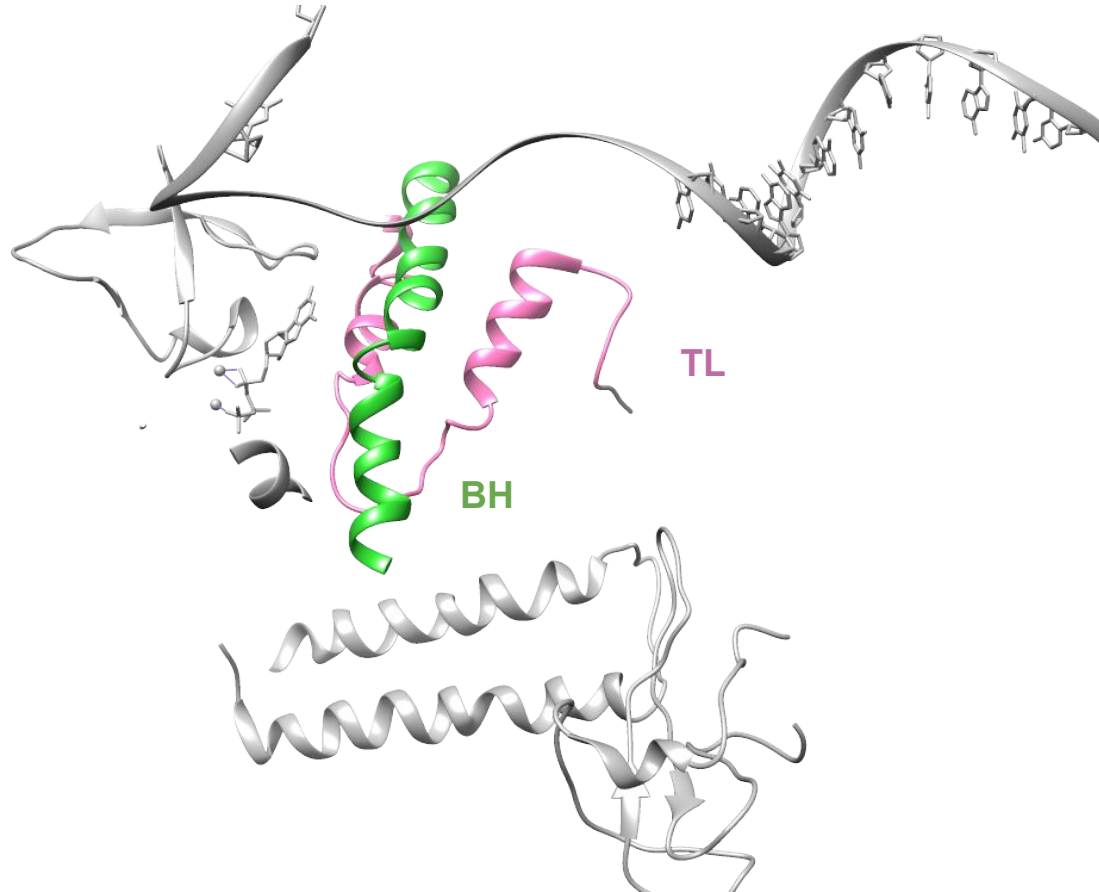
Rpb1

	481	483	485	
S. POMBE	SPYNAD	FDGD	EMNMHVPQSEETRAEIQEITMV	pkqivspqsnkpvmgivq
D. DISCOIDEUM	SPYNAD	FDGD	EMNLHVPQTLETRAEVIEIMMV	prqivspqsnrpvmgivq
C. ELEGANS	SPYNAD	FDGD	EMNLHLPQSLETRAIEEIAMV	prqlitpqankpvmgivq
MOUSE	TPYNAD	FDGD	EMNLHLPQSLETRAIEIQELAMV	prmiivtpqsnrpvmgivq
HUMAN	TPYNAD	FDGD	EMNLHLPQSLETRAIEIQELAMV	prmiivtpqsnrpvmgivq
DROSOPHILA	SPYNAD	FDGD	EMNLHVPQSMETRAEVENIHIT	prqiitpqankpvmgivq
A. THALIANA	SPYNAD	FDGD	EMNMHVPQSFETRAEVLELMMV	pkcivspqanrpvmgivq
E. COLI	AAYNAD	FDGD	QMAVHVPLTLEAQLERALMM	Stnnilspangepiivpsq
S. CEREVISIAE	SPYNAD	FDGD	EMNLHVPQSEETRAELSQLCAV	plqivspqsnkpcmgivq
#=GC RF	XXXXXXXXXXXXXXXXXXXXXXXXXXXX		

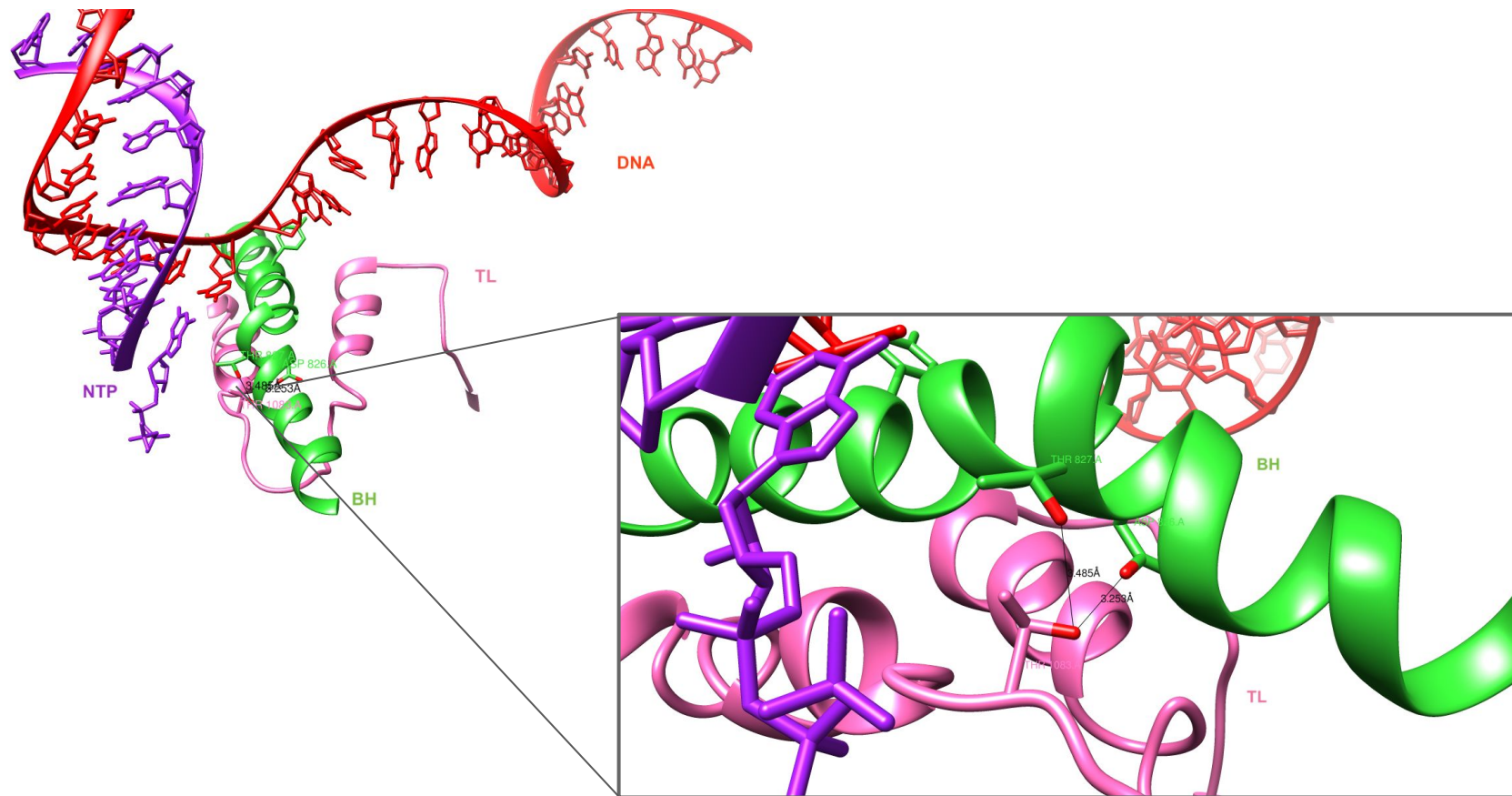
Rpb2

		837
CANDIDA_YEAST_	-----AMEYLKFRELPAQNAIVAIACYSGYNQ	DSMIMNQSSI
S. POMBE	-----SMEYLKFRELPAQNAIVAILCYSGYNQ	DSIIMNQASI
HUMAN	-----SMEYLRFRELPAGINSIVAIASYTGYNQ	DSVIMNRSV
D. DISCOIDEUM	-----SMEYLHFRELPAQNVCAIACYSGYNQ	DSVILNQSAI
C. ELEGANS	-----SMEYLRFNELPAGINAIVAILSYSYSGYNQ	DSVIMNNSAI
DROSOPHILA	-----SMEYLRFRELPAGINSIVAILCYTGYNQ	DSVILNASAV
E. COLI	GEPVERGDVLDGPSTDLGELALGQNMRFVAFMPWNGYNF	DSILVSEVV
S. CEREVISIAE	-----AMEYLKFRELPAQNAIVAIACYSGYNQ	DSMIMNQSSI
	: **. * * **: :.*** ***: :. :	

TRANSLOCATION: key role of bridge helix (BH)



TRANSLOCATION: BH and TL interaction



TRANSLOCATION: conservation of residues involved in BH and TL interaction

Rpb1 (TL)

1083

S. POMBE
DROSOPHILA
MOUSE
HUMAN
C. ELEGAN
D. DISCOIDEUM
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

```
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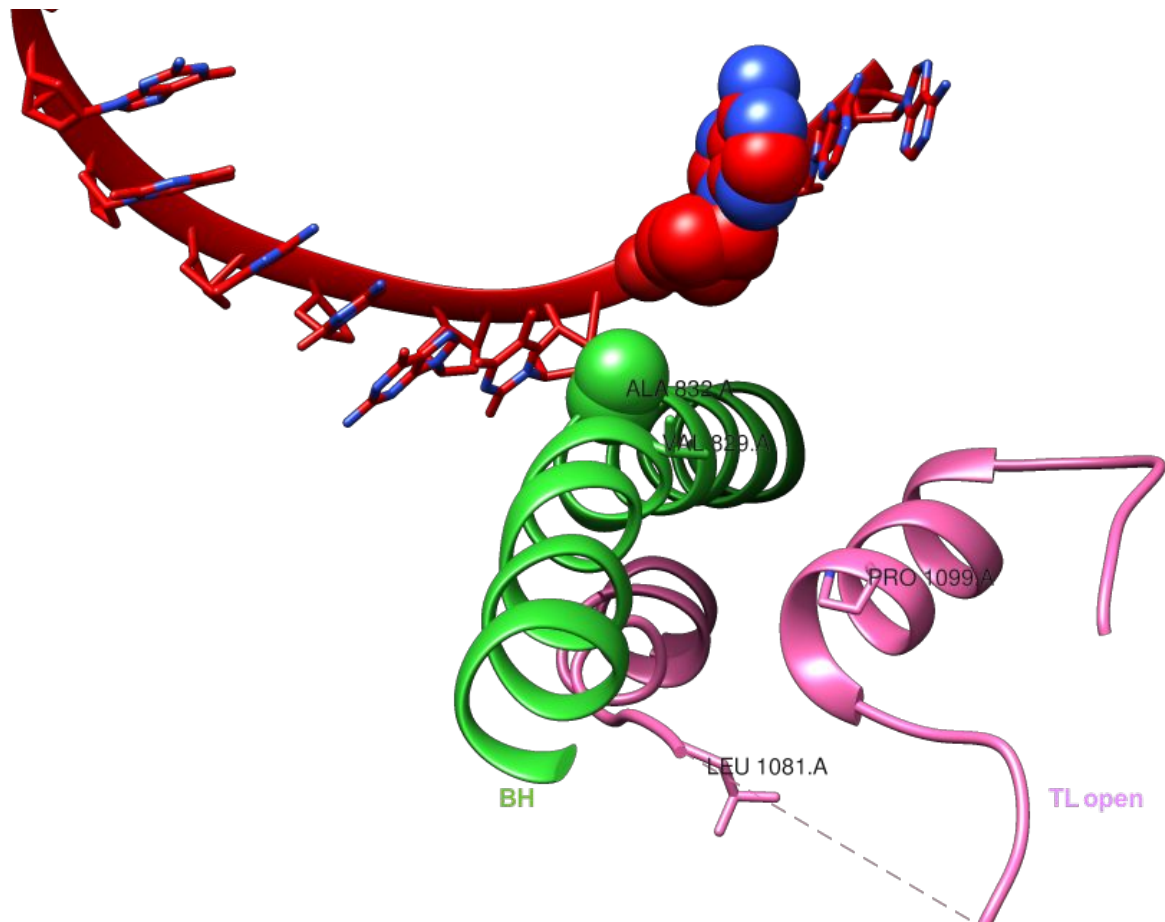
BH (Rpb1)

826-827

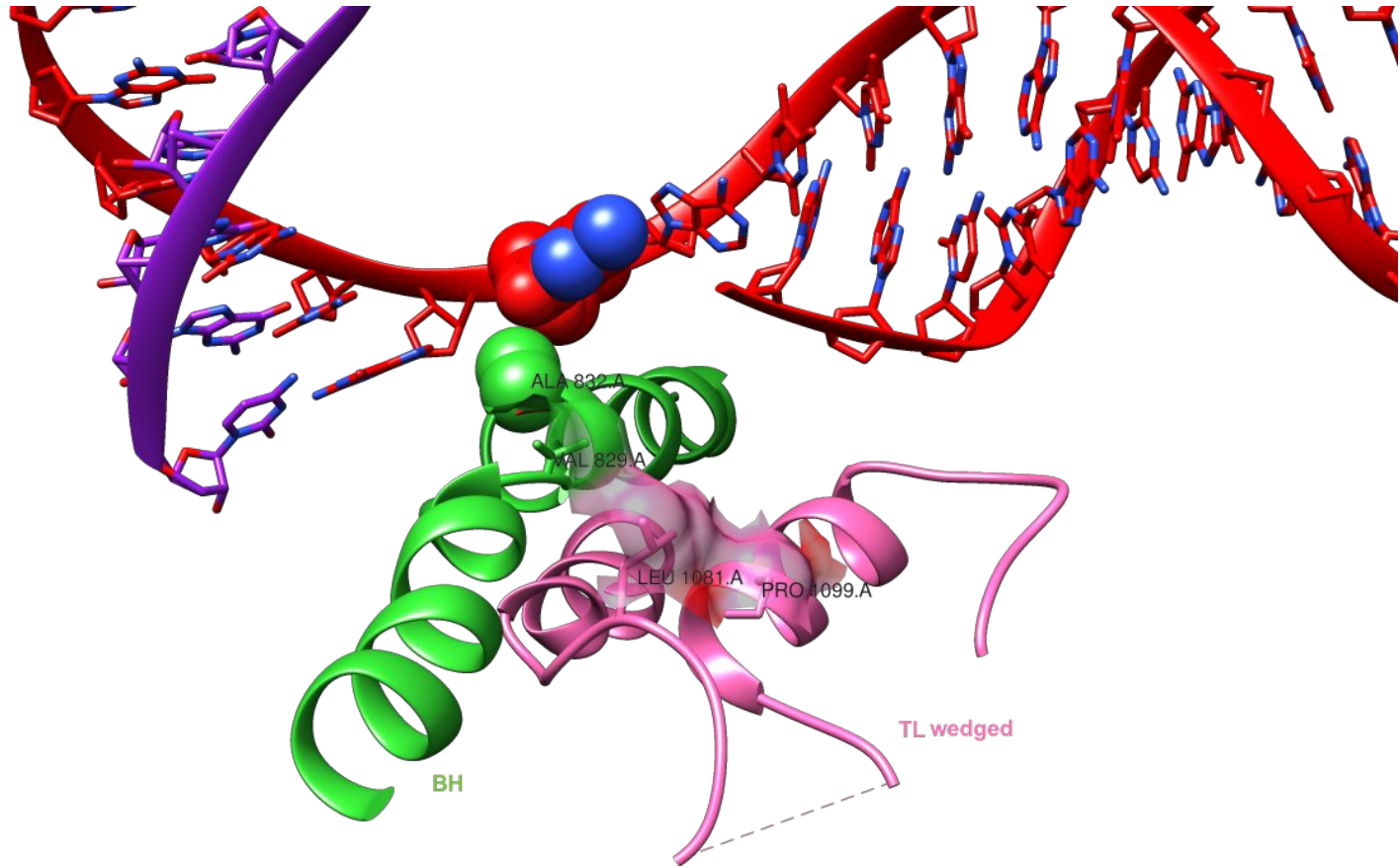
S. POMBE
DROSOPHILA
MOUSE
HUMAN
C. ELEGAN
D. DISCOIDEUM
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

```
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gfrhrctlphfikddygpeskrgfvensylaGLTPSEFFFHAMGGREGLIDT
gfgsrtlphftkddygpesrgfvensylrGLTPQEFFFHAMGGREGLIDT
gfdgrtlphftkddygpesrgfvensylrGLTPQEFFFHAMGGREGLIDT
irqlagmrglmakpdgsiietpitanfreGLNLVLYFISTHGARKGLADT
.....---PQEFFFHAMGGREGLIDT
.....XXXXXXXXXXXXXXXXXXXX
```

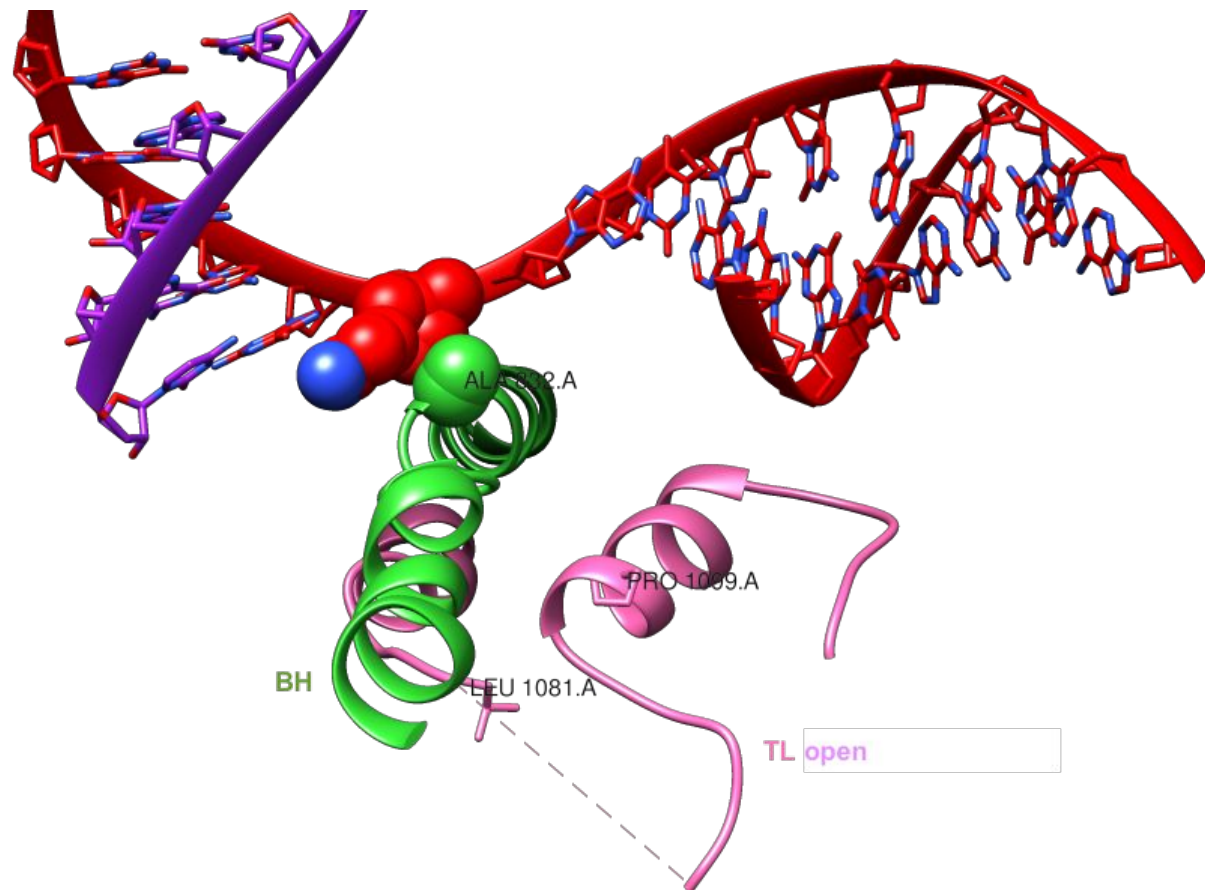
TRANSLOCATION: Pre-translocation



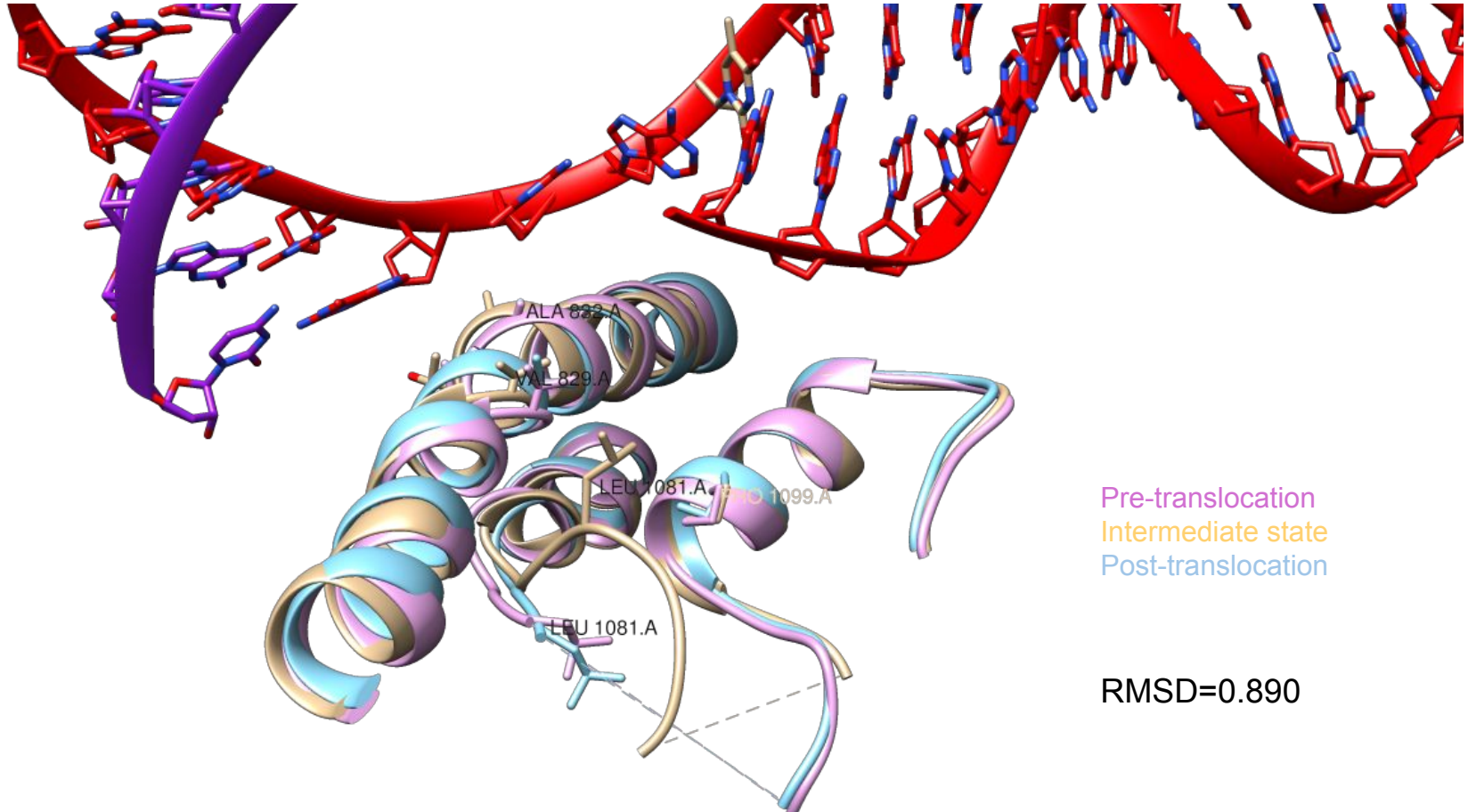
TRANSLOCATION: Intermediate state



TRANSLOCATION: Post-translocation



TRANSLOCATION: Superimposition of the three states



TRANSLOCATION: conservation of key residues

BH (Rpb1)

S. POMBE
DROSOPHILA
MOUSE
HUMAN
C. ELEGAN
D. DISCOIDEUM
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

829 832

```
GLTPQEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKAMEDVMVRYDGTVRNAMGDI
GLTPSEFYFHAMGGREGLIDTAVKTAETGYIQRRLIKAMESVMVNYDGTVRNSVGQL
GLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQV
GLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQV
GLTPSEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKAMESVMVNYDGTVRNSLAQM
GLTPQEFFFHAMGGREGLIDTAVKTSETGYIQRRLVKAMEDVSIKYDATVRNSLGDV
GLTPQEFFFHAMGGREGLIDTAVKTSETGYIQRRLVKAMEDIMVKYDGTVRNSLGDV
GLNVLQYFISTHGARKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMM
---PQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTRNSLGNV
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
```

Rpb1 (TL)

S. POMBE
DROSOPHILA
MOUSE
HUMAN
C. ELEGAN
D. DISCOIDEUM
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

1081

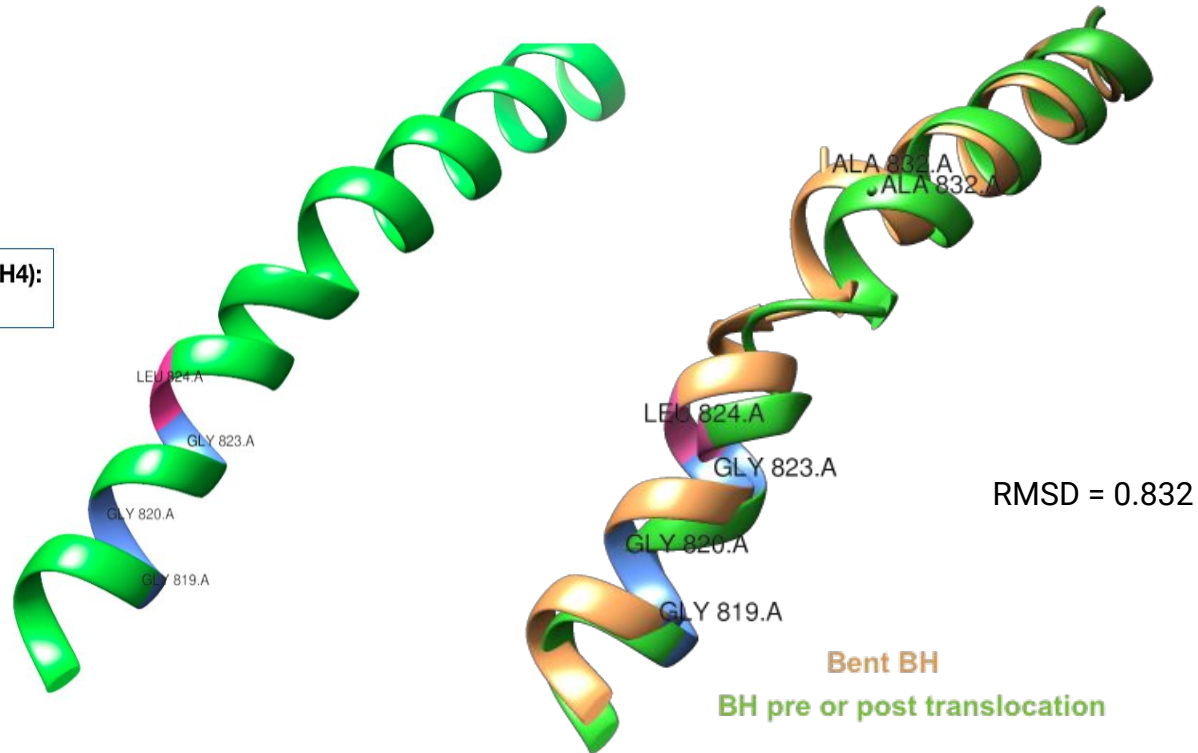
1099

```
AAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPRLKEILNVAKNIKTPSLT
AAQSLGEPATQMTLNTFHFAGVSSKNVTLGVPRLKEIINISKKPKAPSLT
AAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPRLKELINISKKPKTPSLT
AAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPRLKELINISKKPKTPSLT
AAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPRLKEIINVSKTLKTPSLT
AAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPRLKEIINIAKQVKTPSLT
AAQSIGEPATQMTLNTFHYAGVSAKNVTLGVPRLREIINVAKRIKTPSLS
AAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNVKSVVN
AAQSIGEPATQMTLNTFHFAGVASKKVTSGVPRLKEILNVAKNMKTPSLT
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
```

TRANSLOCATION: Hinge regions of BH

Hinge region motif (H3/H4):

GGXGL



TRANSLOCATION: Hinge regions of BH

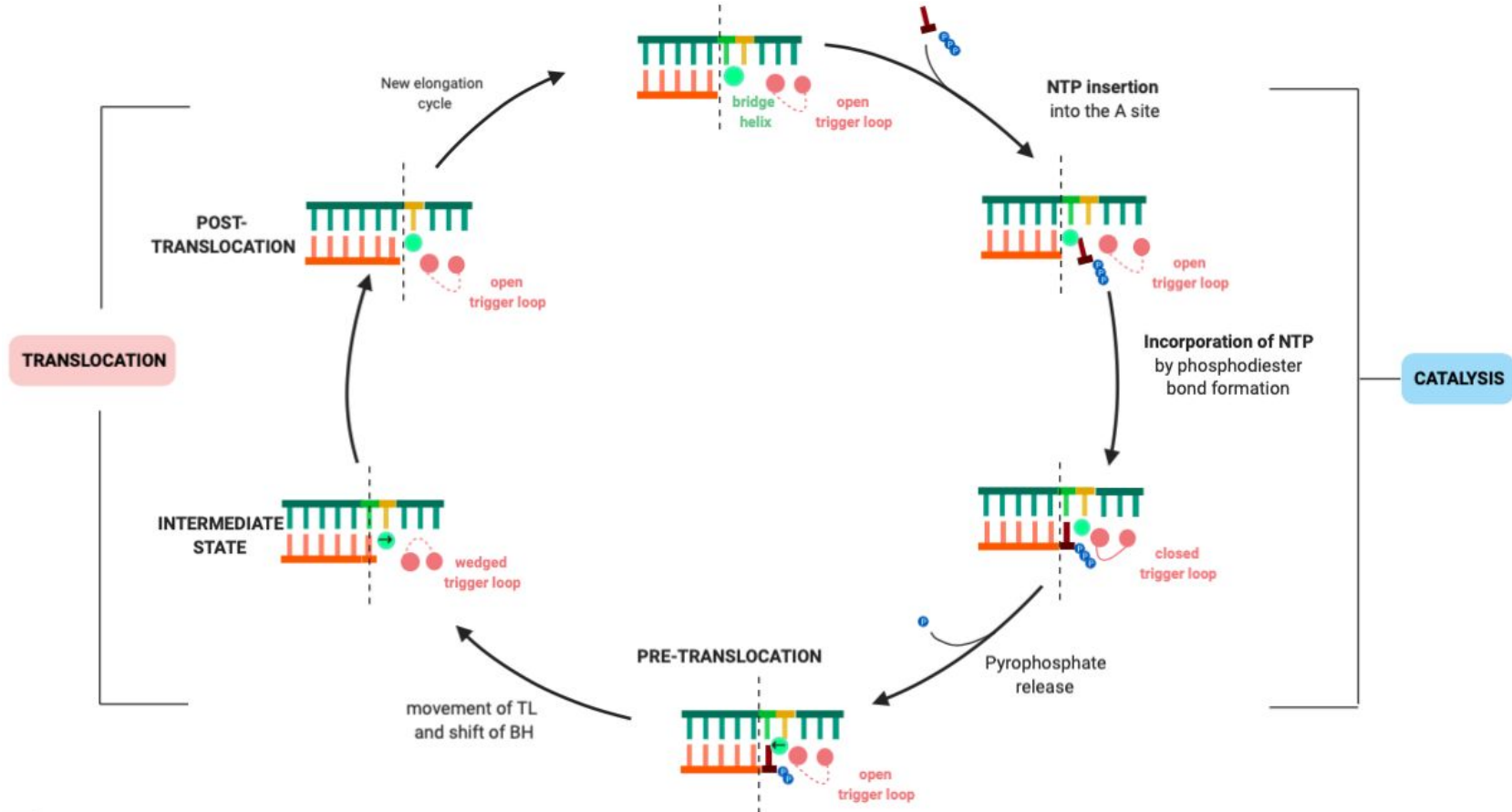
BH (Rpb1)

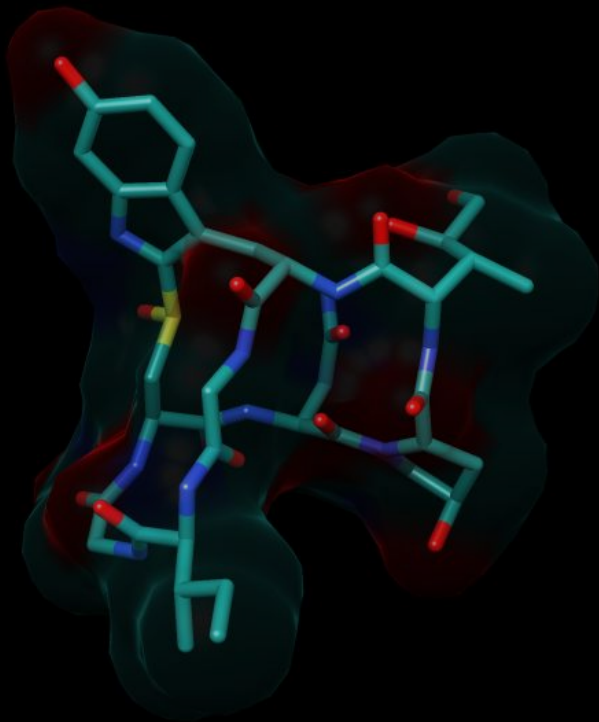
S. POMBE
DROSOPHILA
MOUSE
HUMAN
C. ELEGAN
D. DISCOIDEUM
A. THALIANA
E. COLI
S. CEREVISIAE
#=GC RF

819-820 823-824

[illegible]

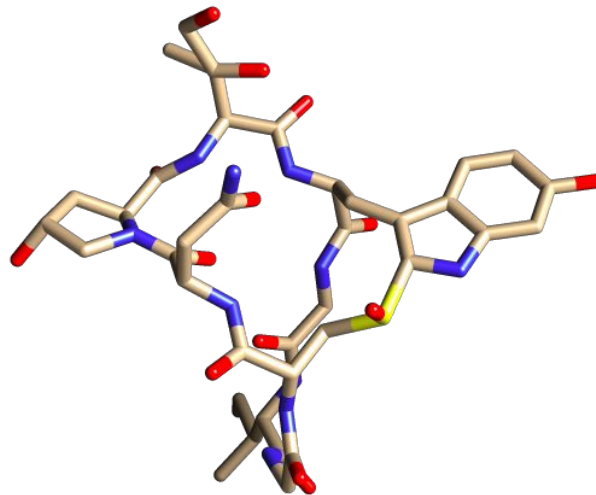
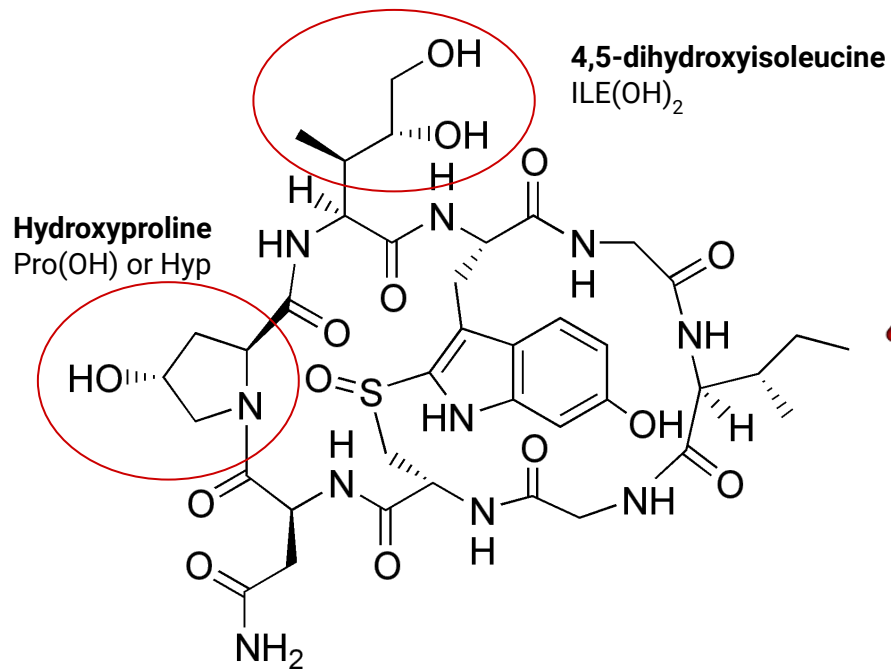
ELONGATION CYCLE: summary





INHIBITOR: α -AMANITIN

INHIBITOR: α -amanitin

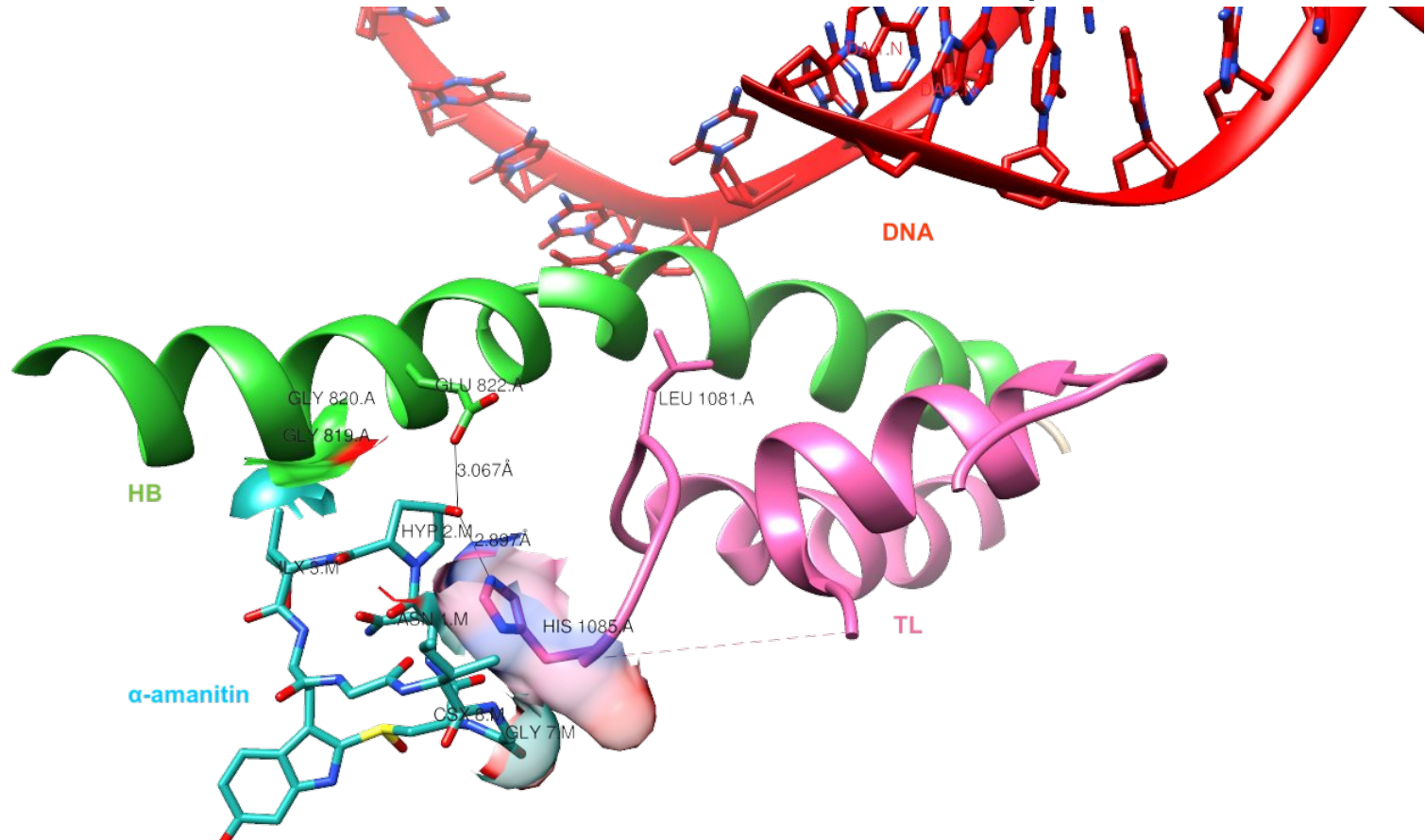


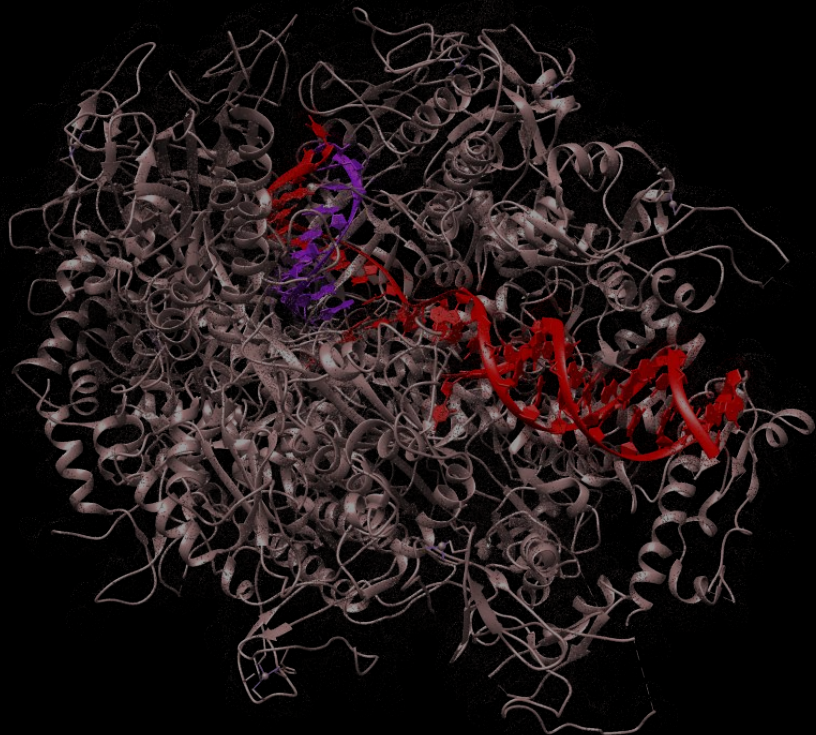
Death cap
(*A. phalloides*)



Destroying angel (*A. bisporigera*)

INHIBITOR: α -amanitin binds to the active site of RNA pol II

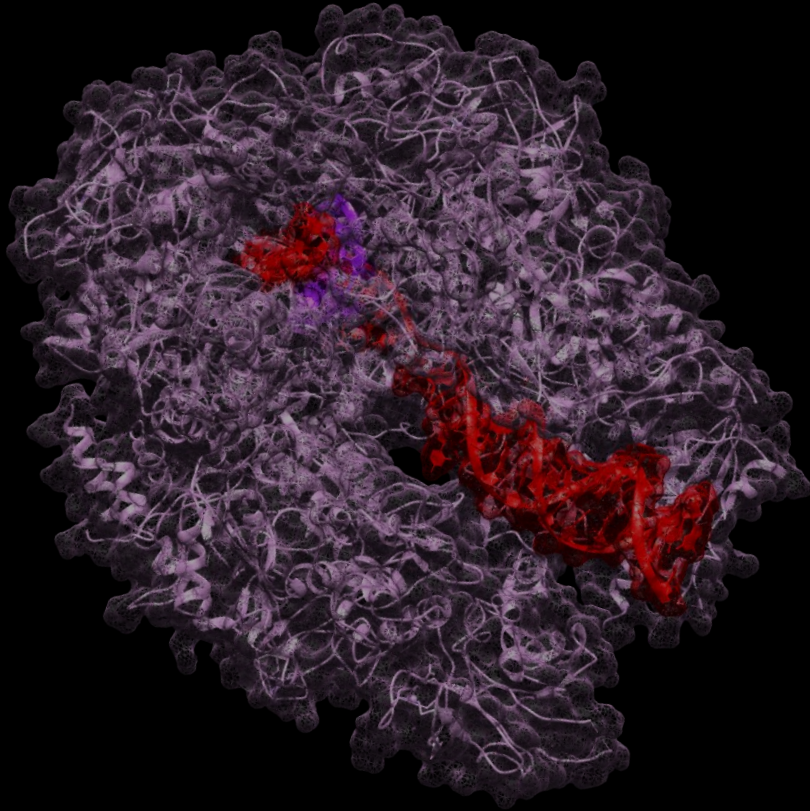




CONCLUSIONS

CONCLUSIONS

1. Transcription is an event that is **conserved** among all species and cell types.
2. There are different RNA polymerases but in eukaryotes, only **RNA polymerase II** transcribes protein coding genes.
3. RNA polymerase II is a multisubunit complex: subunits **Rpb1**, **Rpb2** and **Rpb9** form and/or stabilize the active site of the enzyme.
4. The **elongation cycle** is the process in which NTPs are added to the new RNA strand. It is divided in two phases: **catalysis** and **translocation**.
5. In **catalysis**, the **TL** has to **move** from open conformation to close conformation. In the active site, the **NTP** establishes interactions with the TL, other residues from Rpb1 and Rpb2.
6. In **translocation**, the TL moves from closed to open conformation and adopts an intermediate **wedged state**. The **BH bends** to move the next DNA nucleotide towards the active site.
7. **Amanitin** inhibits transcription by **blocking the TL** in the **wedged state** and not allowing translocation.
8. **Sequence alignments** show high conservation in key residues involved in transcription.



THANK YOU

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MULTIPLE CHOICE QUESTIONS

1. Which of the following structures is formed when the trigger loop (TL) and the bridge helix (BH) are together?

- a. TIM barrel
- b. Rossman folding
- c. Polymerase like folding
- d. Three helix bundle**
- e. Greek key

2. Select all the correct statements:

- 1. Rpb2 is the largest subunit of RNA polymerase II
 - 2. Rpb1 and Rpb2 share similar SCOP information
 - 3. Bridge helix and trigger loop can be found in subunit Rpb9
 - 4. RNA polymerase II is composed by 12 subunits
- a) 1, 2, 3
 - b) 1, 3
 - c) 2, 4**
 - d) 4
 - e) 1, 2, 3, 4

MULTIPLE CHOICE QUESTIONS

1. In RNA polymerase II, catalysis and translocation:

- a. **Require coordination of the main two structures involved in the processes (bridge helix and trigger loop).**
- b. They are independent processes so can happen simultaneously.
- c. In translocation, the NTP is incorporated to the RNA.
- d. Translocation is different from catalysis because it does not involve any structures from the active site.
- e. All of the above.

2. Select the correct statements about the metals of active site

- a. Both metals are always present in the active site
- b. Metal A is always present while metal B is present only when NTP is in the active site.
- c. These metals are both zinc ions.
- d. More polymerases have 2 metals in the active site
 - a) 1,2,3
 - b) 1,3
 - c) 2,4**
 - d) 4
 - e) 1,2,3,4

MULTIPLE CHOICE QUESTIONS

1. When the NTP is incorporated into the forming RNA strand:

- a. Trigger loop is in its open conformation
- b. **Trigger loop is in its closed conformation**
- c. Trigger loop is in its wedged conformation
- d. TL can have all the different conformations
- e. None of the statements above are correct

2. Select the false statement:

- a. **Rpb9 subunit contacts directly with TL**
- b. Rpb9 subunit modulates the TL movement
- c. $\alpha 20$ - $\alpha 21$ from Rpb1 are important for the mobility of the TL
- d. The TL mobility is allowed by the hinge regions which provide flexibility to the structure
- e. $\alpha 20$ - $\alpha 21$ interact with Rpb9 by VDW and hydrogen bond interactions.

MULTIPLE CHOICE QUESTIONS

1. In the wedged conformation of the trigger loop (TL), translocation:
 - a. It's over.
 - b. It's being carried out.**
 - c. It has not started yet.
 - d. All of the above.
 - e. None is correct.

2. In translocation of DNA to begin another elongation cycle:
 - a. The nucleotide is pulled to the active site by a hydrogen bond.
 - b. The DNA moves independently to arrive to the active site.
 - c. The DNA is translocated by a transcription factor.
 - d. When the bridge helix bends, it forms multiple hydrogen bonds with the following nucleotides.
 - e. When the bridge helix bends, an alanine can contact the dNTP through VDW interactions and can push it to the active site.**

MULTIPLE CHOICE QUESTIONS

1. About the hinge regions of the bridge helix:

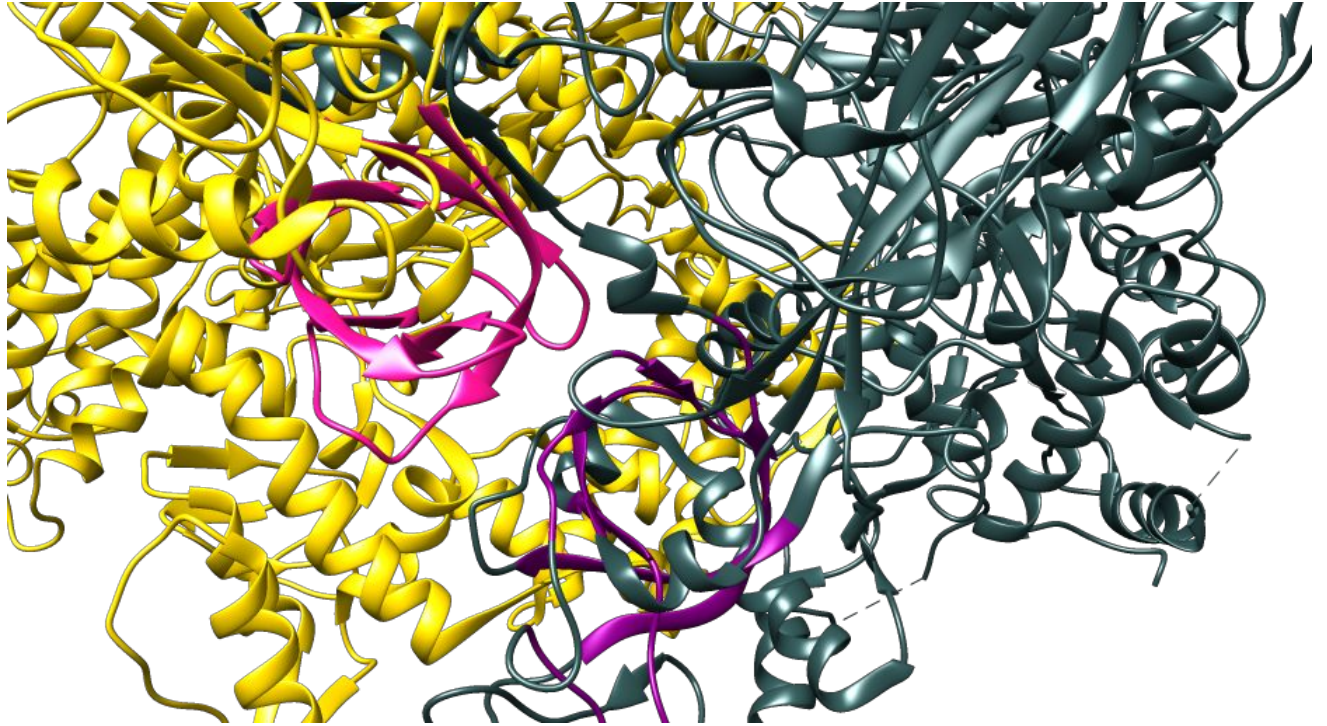
- a. They are regions that provide flexibility to the structure.
- b. Their sequence is highly conserved among species.
- c. Their residues cannot make hydrogen bonds.
- d. They allow the bridge helix bending.
- e. All of the above.**

2. About the inhibitor alpha-amanitin:

- a. Alpha-amanitin binds to the enzyme through the modified amino acids hydroxyproline and dihydroxyisoleucine.
- b. Trigger loop movement is blocked when alpha-amanitin interacts with the enzyme
- c. The two above are correct**
- d. Alpha-amanitin binds to the surface of the enzyme and causes a conformational change that blocks transcription
- e. All the above are correct

EXTRA SLIDES

EXTRA SLIDES



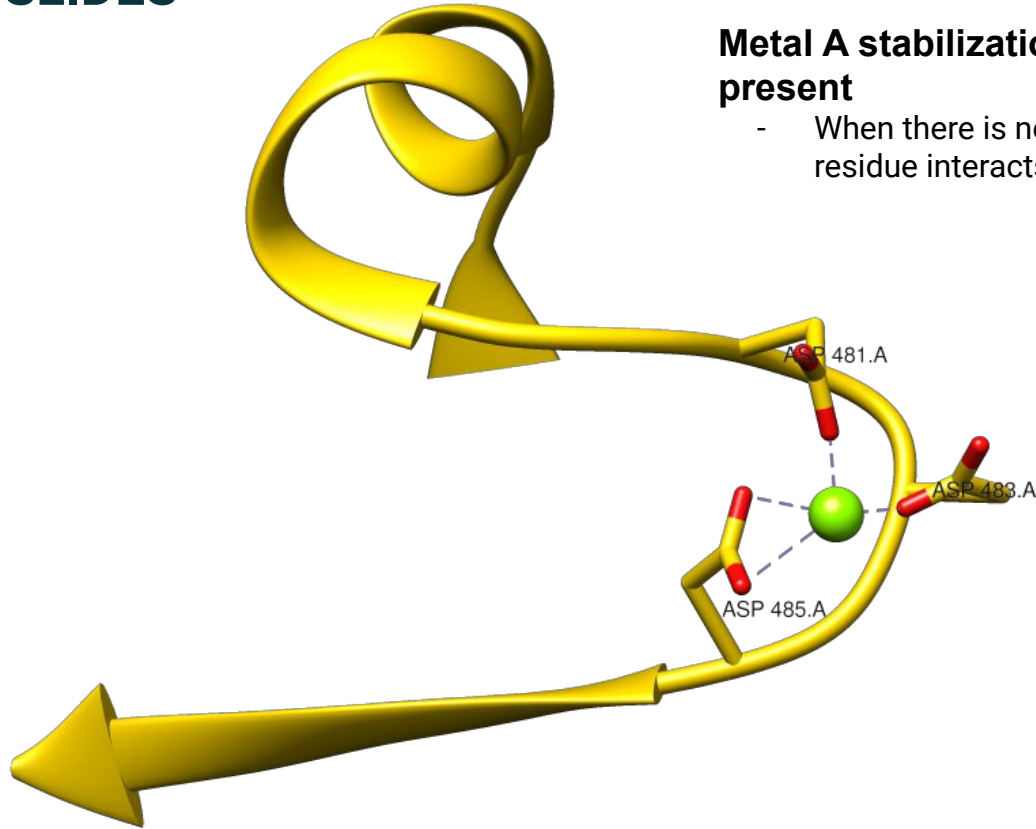
Double psi barrel

A different view.

EXTRA SLIDES

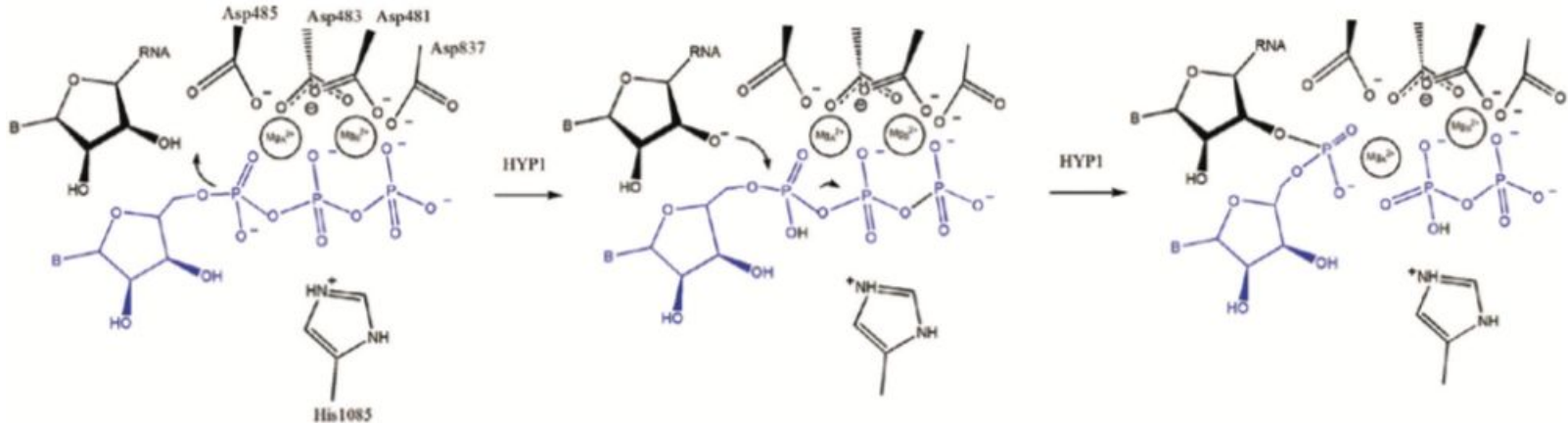
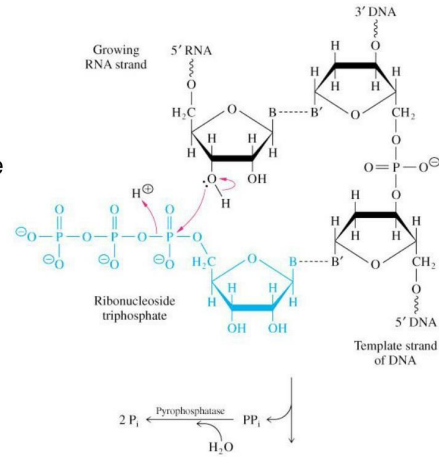
Metal A stabilization when NTP is not present

- When there is no NTP, a new aspartic acid residue interacts with the magnesium atom.

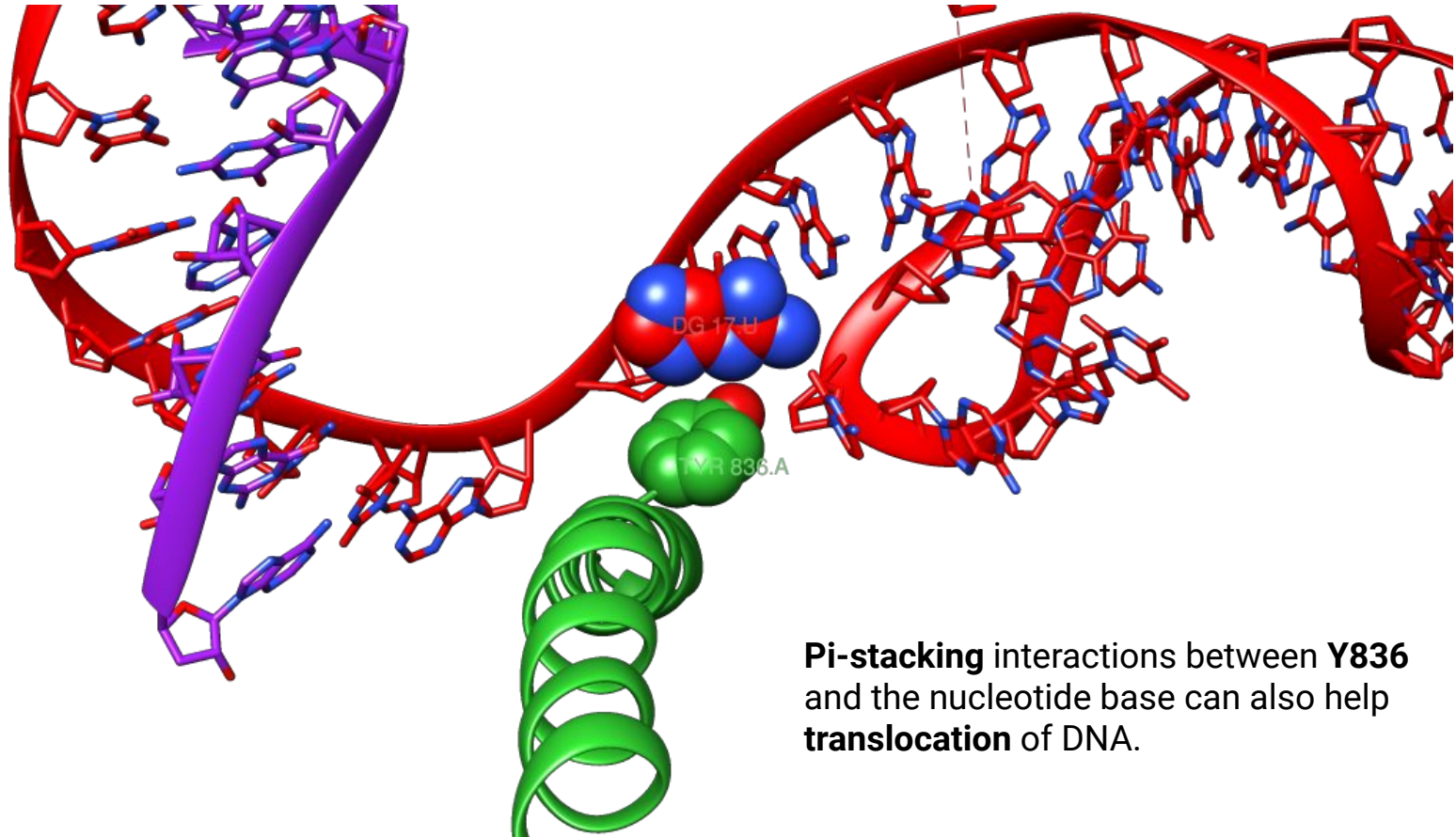


EXTRA SLIDES

- RNA polymerase reaction



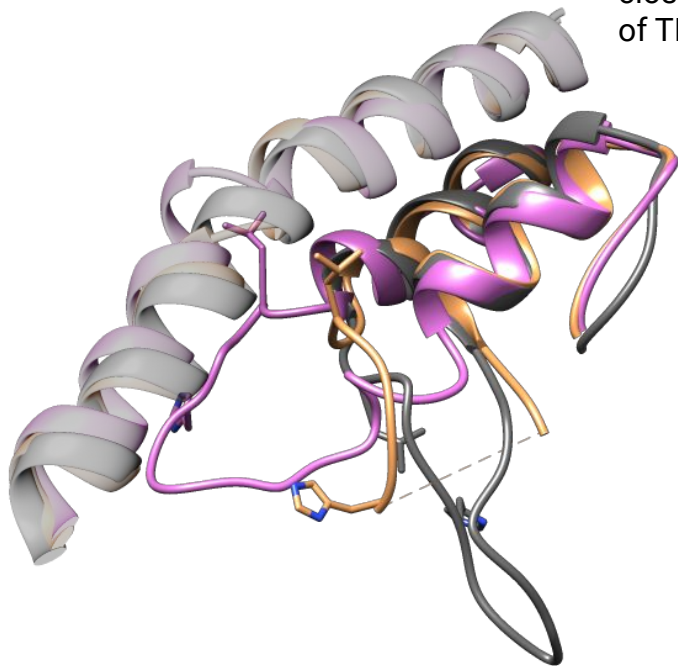
EXTRA SLIDES



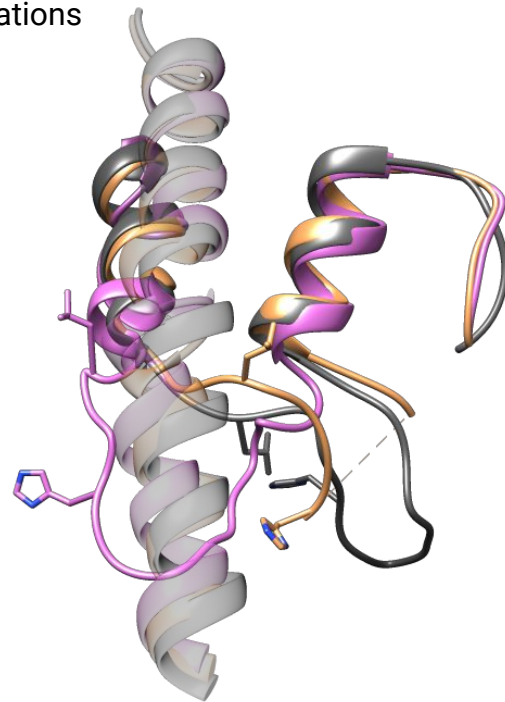
Pi-stacking interactions between Y836 and the nucleotide base can also help **translocation** of DNA.

EXTRA SLIDES

TL movement during translocation. A closer look to the different conformations of TL in translocation.

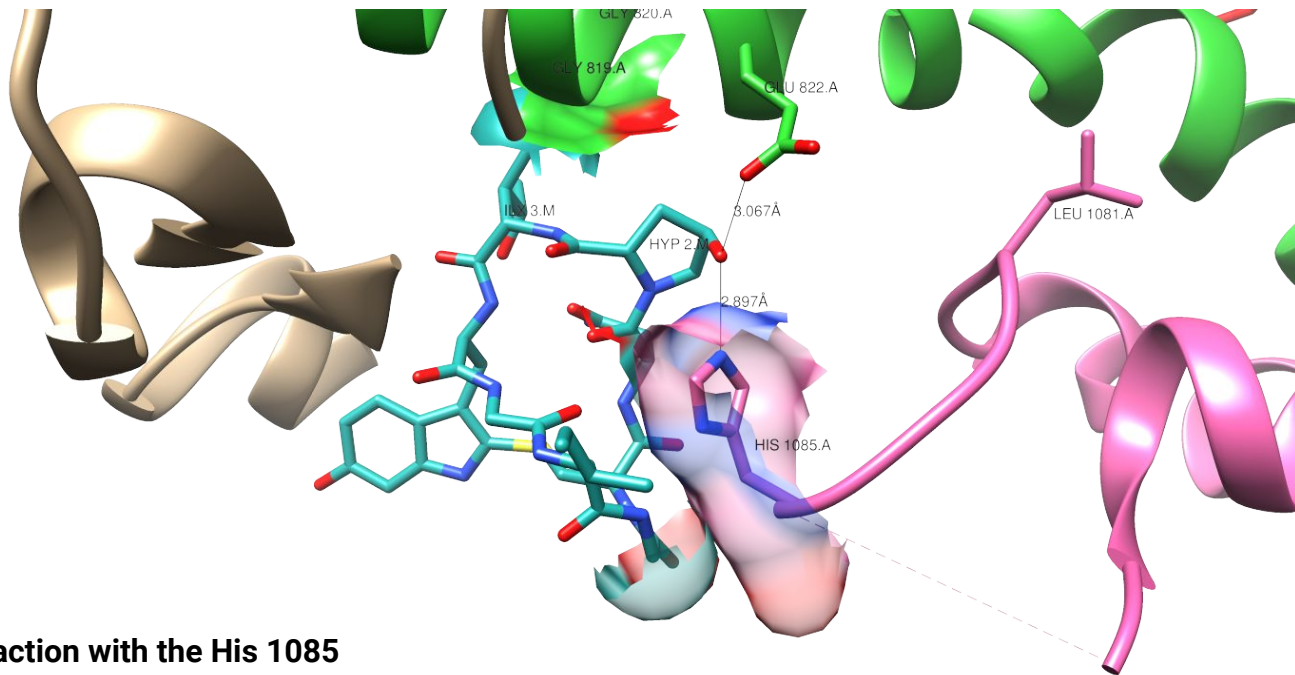


TL closed
TL wedged
TL open



RMSD= 0.826 Å

EXTRA SLIDES

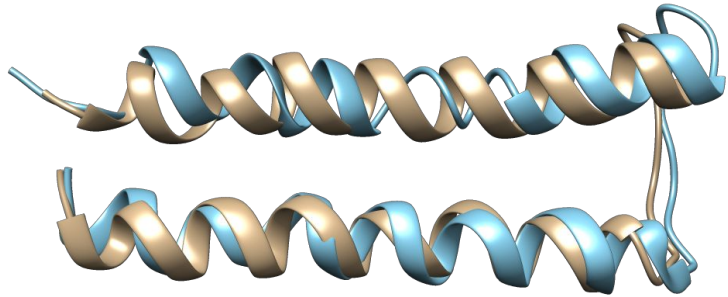


Amanitin interaction with the His 1085

Interaction of the OH of the hydroxyProline with:

- the NH of the His
- the NH2 of the Asp

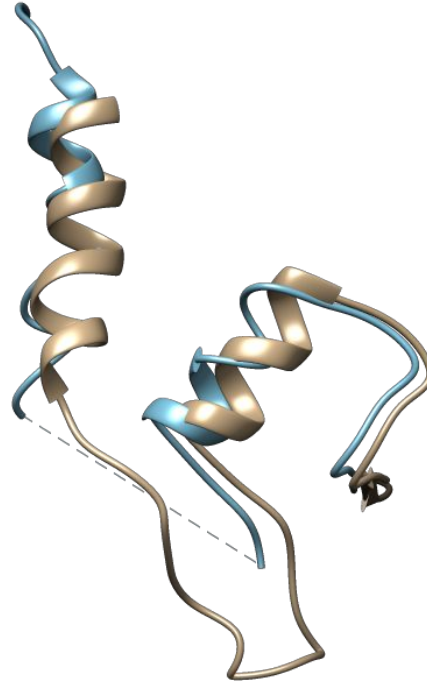
EXTRA SLIDES: superimposition human/*S.cerevisiae*



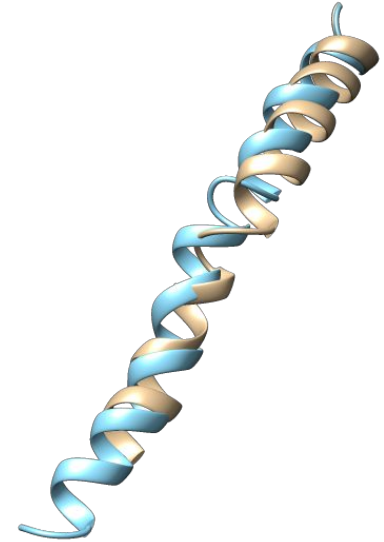
alfa20-21

RMSD=1.288 Å

Human
S.cerevisiae

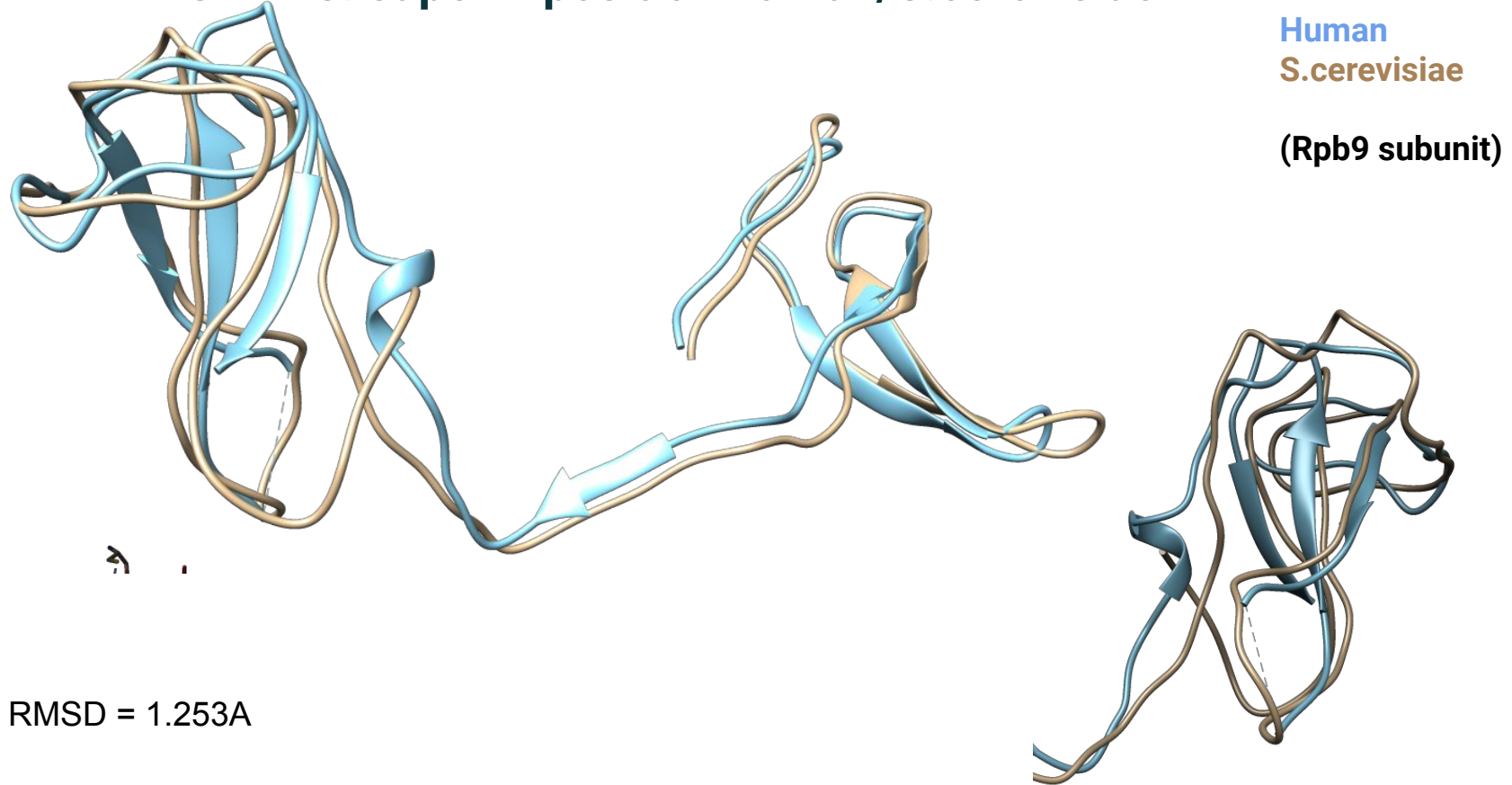


Trigger Loop



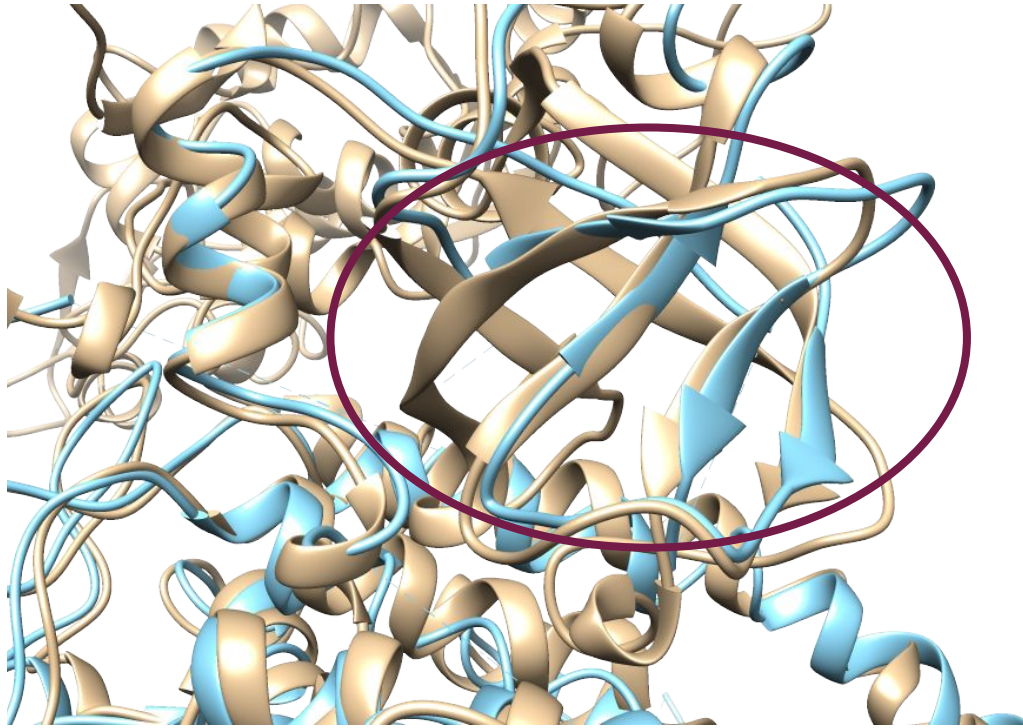
Bridge Helix

EXTRA SLIDES: superimposition human/*S.cerevisiae*



EXTRA SLIDES: superimposition human/*S.cerevisiae*

Human
S.cerevisiae



RMSE = 1.288Å

Human pdb is cut, some beta sheet are not present, it may be due to the crystallization process