

ELONGATION FACTOR COMPLEX eEF1A/eEF1Bα

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4th Human Biology
Structural Biology

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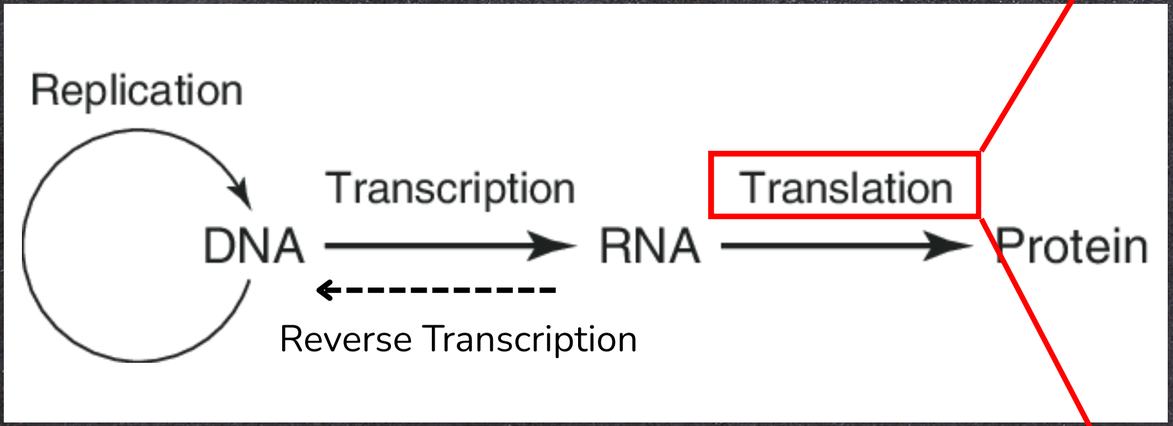
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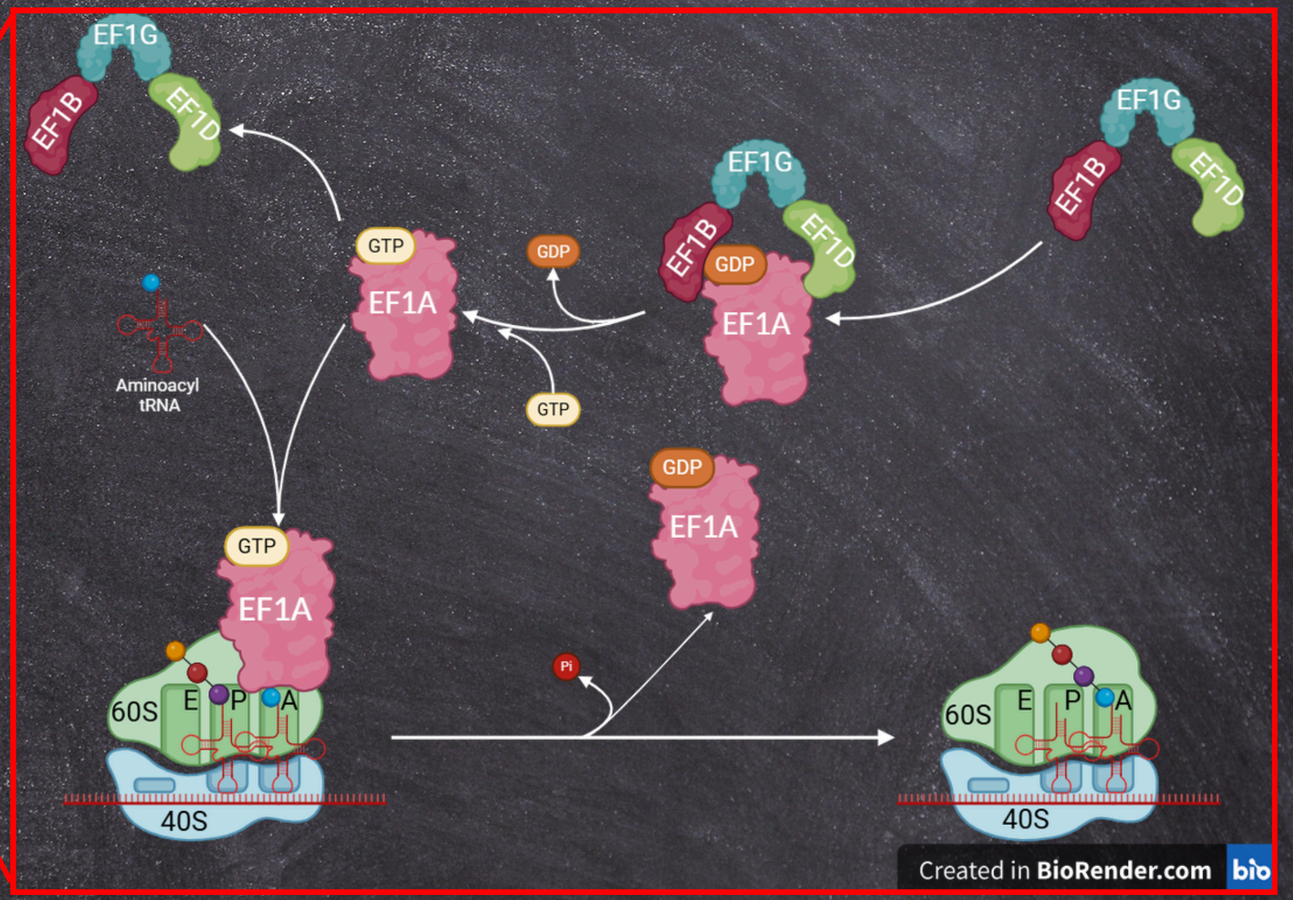
PDB | 1F60 | *S. cerevisiae*

1. INTRODUCTION

EUKARYOTIC TRANSLATION PROCESS



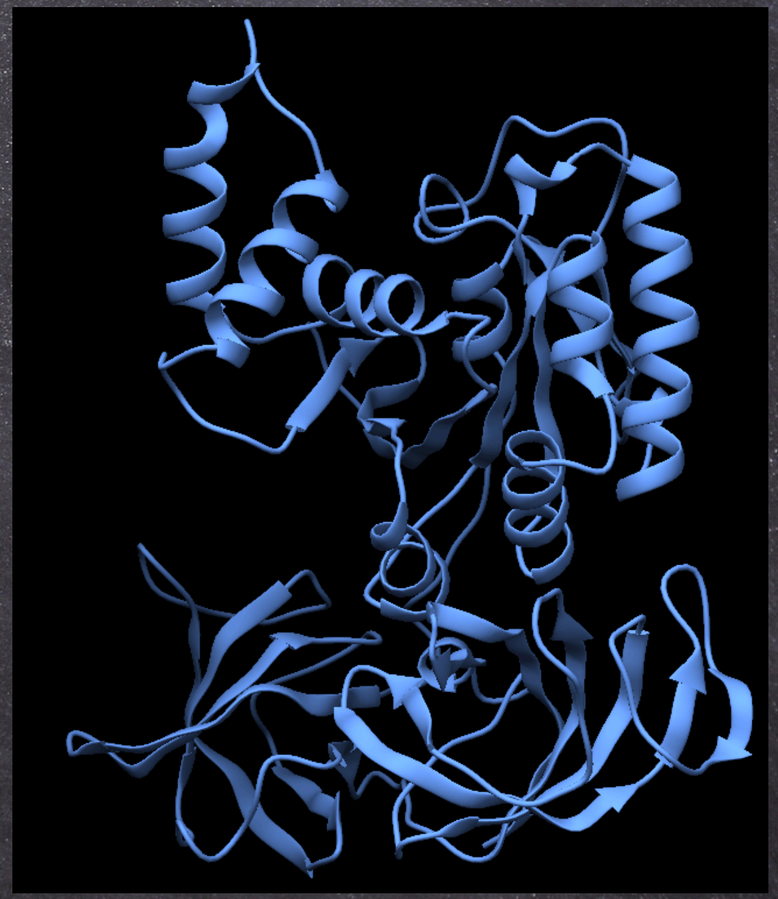
- Initiation → Elongation → Termination
- Components:
  - mRNA / Ribosomes / tRNAs / Amino acids
  - Protein factors (eIFs, eEFs, eRFs)
  - Energy molecules: GTP



Eukaryotic **Elongation process**

eEF1A (eukaryotic Elongation Factor 1A)

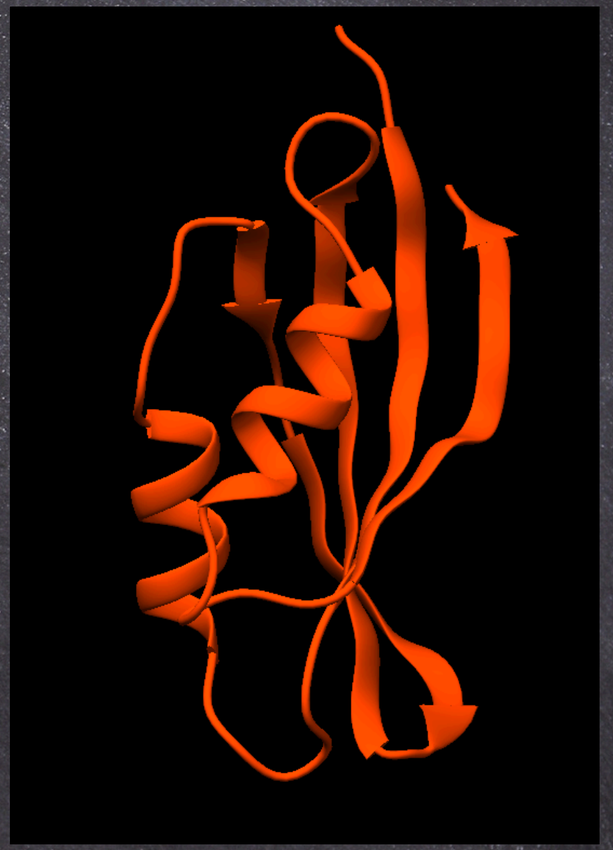
- eEF1A
  - GTP-dependent G protein
  - GTPase activity
  - Moonlighting protein (multiple functions)
- Function classification:
  - Canonical
    - Complex with GTP to bind aa-tRNA and deliver it to the ribosomal A-site during translation elongation
  - Non-canonical
    - Cytoskeleton organization (actin binding and bundling)
    - Regulation of cell survival (apoptosis and autophagy signaling)
    - Nuclear export and tRNA transport
- Cellular localization:
  - Cytoplasm (translation machinery-associated)
  - Actin cytoskeleton



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eEF1B (eukaryotic Elongation Factor 1B)

- eEF1B
  - GEF complex
  - GDP–GTP exchange
  - Regulator of translation elongation
  - Multi-subunit protein (α, γ, δ)
- Function classification:
  - Canonical
    - Guanine nucleotide exchange on eEF1A
  - Non-canonical (Secondary functions)
    - Regulatory, cytoskeletal, stress-related
    - Diverse and context-dependent
- Cellular localization
  - Cytoplasm (translation machinery-associated)



PDB | 1F60 | *S. cerevisiae*

SCOP CLASSIFICATION

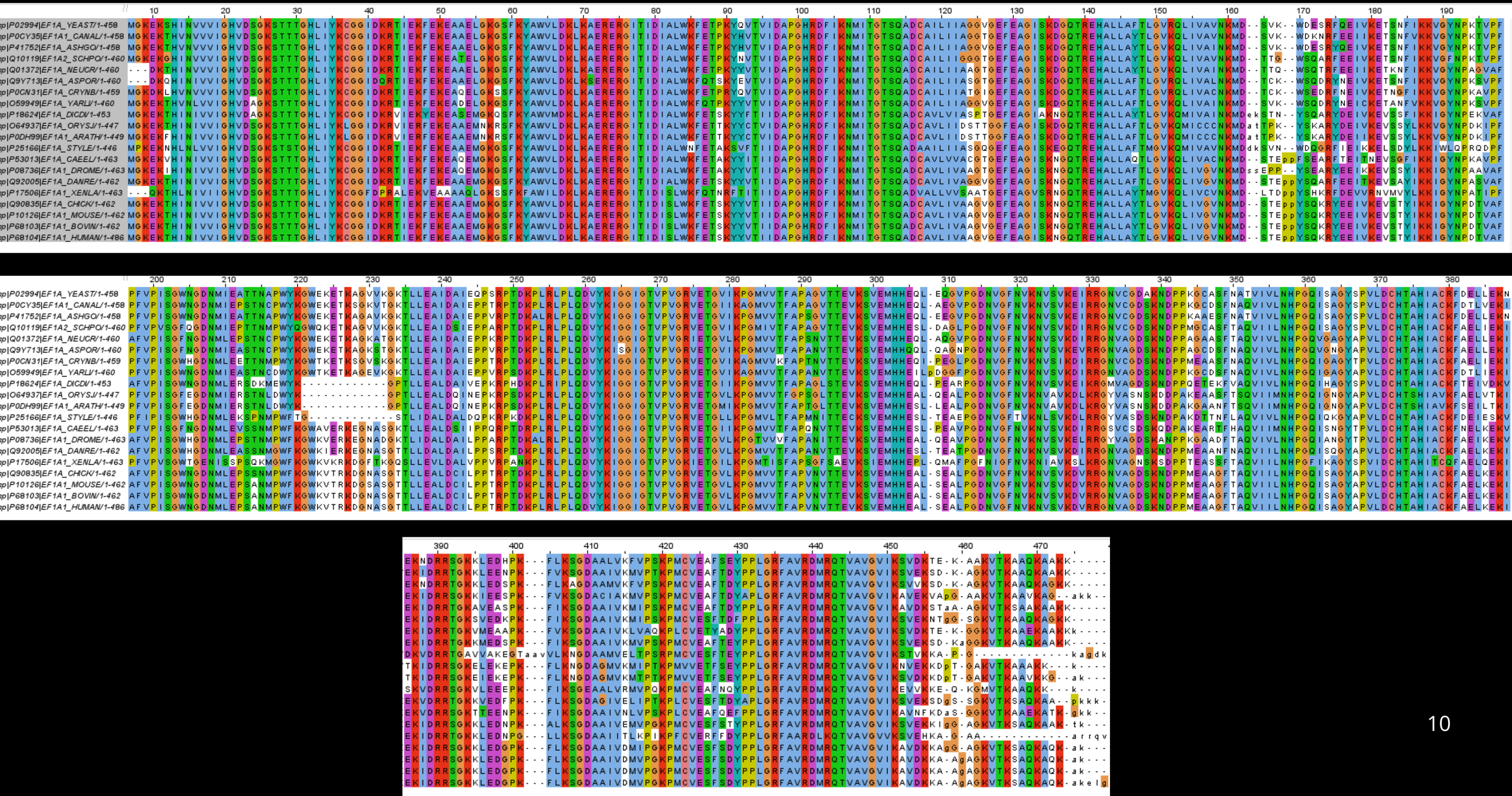
Chains	Domain Info	Class	Fold	Superfamily	Family	Domain	Species
A	Domain 2	All beta proteins	Reductase/isomerase/elongation factor common domain	Translation proteins	Elongation factors	Elongation factor eEF-1alpha, domain 2	(Saccharomyces cerevisiae) [TaxId: 4932],
A	Domain 3	All beta proteins	Elongation factor/aminomethyltransferase common domain	EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain	EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain	Elongation factor eEF-1alpha, C-terminal domain	(Saccharomyces cerevisiae) [TaxId: 4932],
A	Domain 1	Alpha and beta proteins (a/b)	P-loop containing nucleoside triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	G proteins	Elongation factor eEF-1alpha, N-terminal (G) domain	(Saccharomyces cerevisiae) [TaxId: 4932],
B	eEF1Bα	Alpha and beta proteins (a+b)	Ferredoxin-like	eEF-1beta-like	eEF-1beta-like	Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta	baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932],

2. HMM MSA

eEF1A MSA

Uniprot code	Species	Domain
O64937	Oryza sativa	Plant
P0DH99	Arabidopsis thaliana	Plant
P02994	Saccharomyces cerevisiae	Yeast
P0CY35	Candida albicans	Yeast
P41752	Ashbya gossypii	Yeast
Q10119	Schizosaccharomyces pombe	Yeast
Q01372	Neurospora crassa	Yeast
Q9Y713	Aspergillus oryzae	Yeast
P0CN31	Cryptococcus neoformans	Yeast
O59949	Yarrowia lipolytica	Yeast

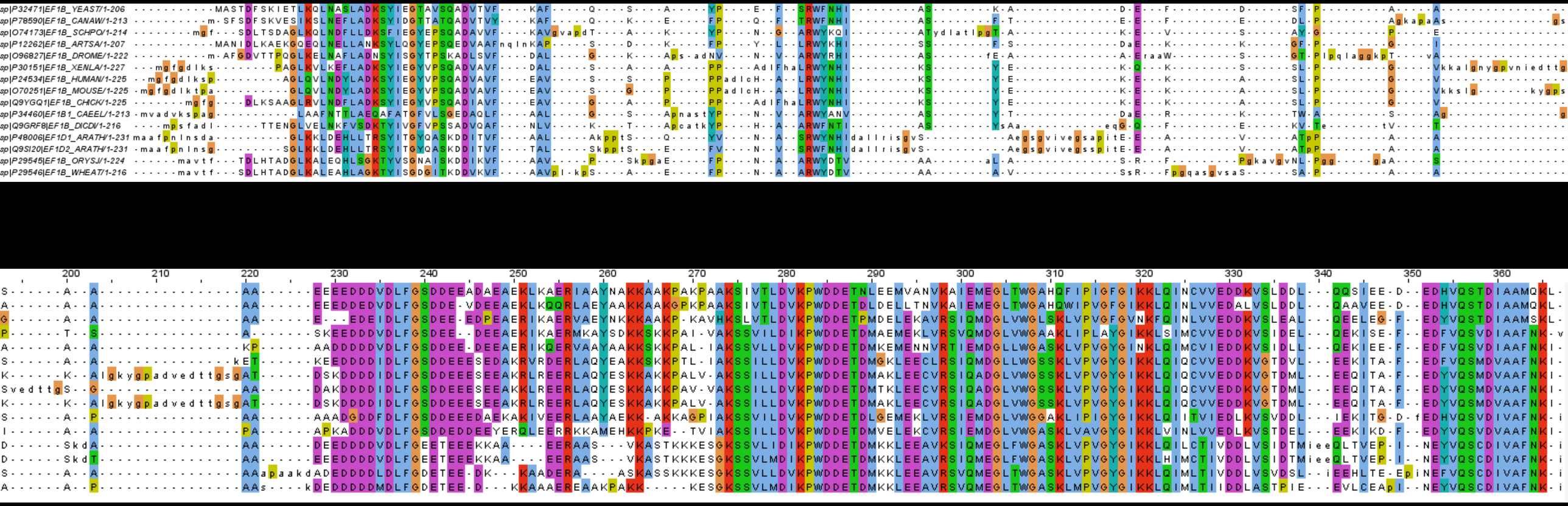
Uniprot code	Species	Domain
P18624	Dictyostelium discoideum	Amoeba
P25166	Stylonychia lemnae	Cilophora
P08736	Drosophila melanogaster	Artropode
P53013	Caenorhabditis elegans	Nematode
P10126	Mus musculus	Vertebrates
Q92005	Danio rerio	Vertebrates
P17506	Xenopus laevis	Vertebrates
Q90835	Gallus gallus	Vertebrates
P68103	Bos taurus	Vertebrates
P68104	Homo sapiens	Vertebrates


sp|P02994|EF1A_YEAST/1-458
sp|P0CY35|EF1A1_CANAL/1-458
sp|P41752|EF1A_ASHGO/1-458
sp|Q10119|EF1A2_SCHPO/1-460
sp|Q01372|EF1A_NEUCR/1-460
sp|Q9Y713|EF1A_ASPOR/1-460
sp|P0CN31|EF1A_CRYNB/1-459
sp|O59949|EF1A_YARLI/1-460
sp|P18624|EF1A_DICDV/1-453
sp|O64937|EF1A_ORYSJ/1-447
sp|P0DH99|EF1A1_ARATH/1-449
sp|P25166|EF1A_STYLE/1-446
sp|P53013|EF1A_CAEEL/1-463
sp|P08736|EF1A1_DROME/1-463
sp|Q92005|EF1A_DANRE/1-462
sp|P17506|EF1A1_XENLA/1-463
sp|Q90835|EF1A_CHICK/1-462
sp|P10126|EF1A1_MOUSE/1-462
sp|P68103|EF1A1_BOVIN/1-462
sp|P68104|EF1A1_HUMAN/1-486

eEF1B MSA

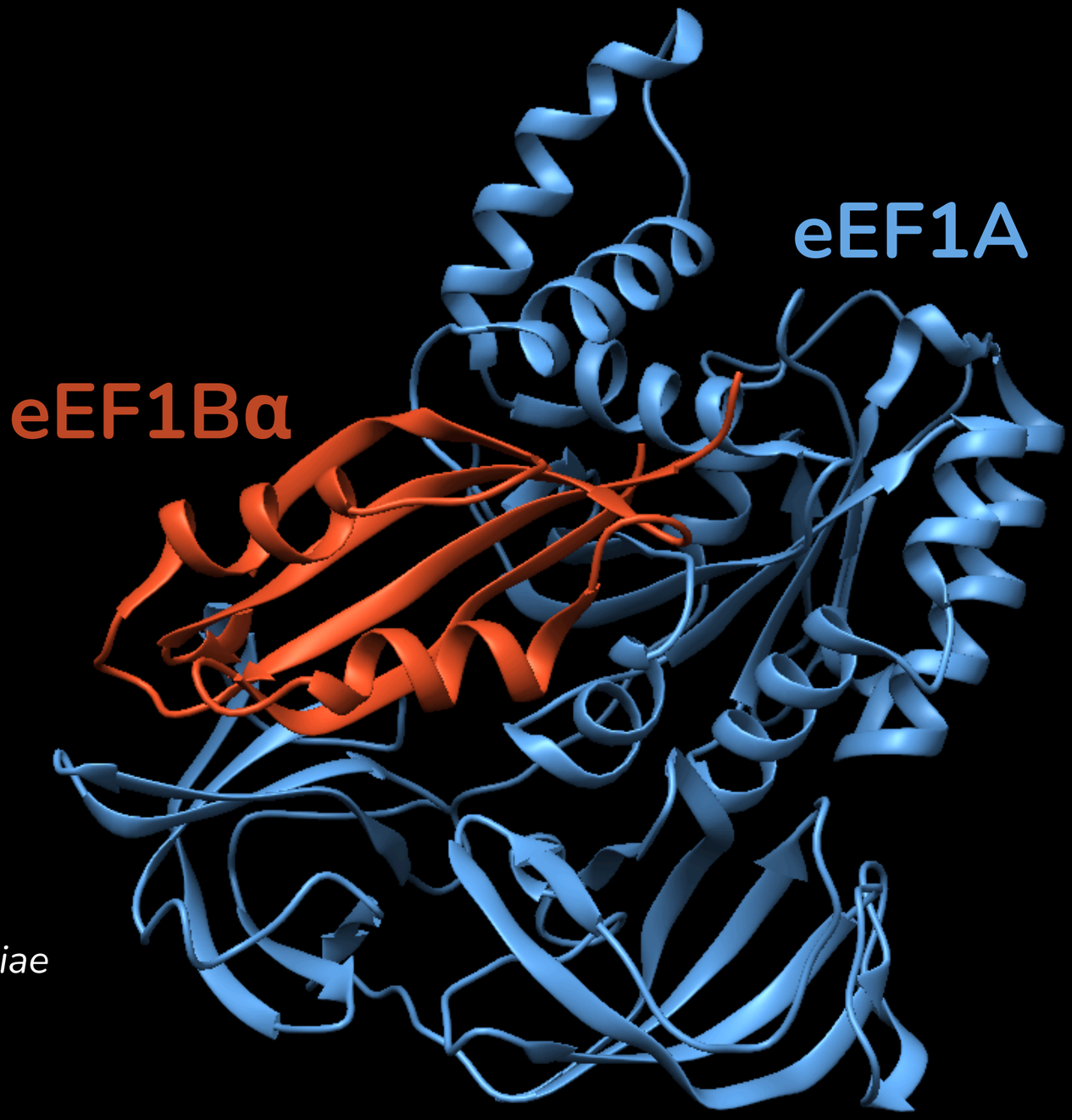
Uniprot code	Species	Domain
Q9SI20	Arabidopsis thaliana	Plant
P29545	Oryza sativa	Plant
P29546	Triticum aestivum	Plant
P32471	Saccharomyces cerevisiae	Yeast
P78590	Candida albicans	Yeast
O74173	Schizosaccharomyces pombe	Yeast
Q9GRF8	Dictyostelium discoideum	Amoeba

Uniprot code	Species	Domain
P34460 – Caenorhabditis elegans	Caenorhabditis elegans	Nematode
O96827	Drosophila melanogaster	Artropode
P12262	Artemia salina	Artropode
P30151	Xenopus laevis	Vertebrates
Q9YGQ1	Gallus gallus	Vertebrates
O70251	Mus musculus	Vertebrates
P24534	Homo sapiens	Vertebrates


sp|P32471|EF1B_YEAST/1-206
sp|P78590|EF1B_CANAW/1-213
sp|O74173|EF1B_SCHPO/1-214
sp|P12262|EF1B_ARTSA/1-207
sp|O96827|EF1B_DROME/1-222
sp|P30151|EF1B_XENLA/1-227
sp|P24534|EF1B_HUMAN/1-225
sp|O70251|EF1B_MOUSE/1-225
sp|Q9YGQ1|EF1B_CHICK/1-225
sp|P34460|EF1B1_CAEEL/1-213
sp|Q9GRF8|EF1B_DICDI/1-216
sp|P48006|EF1D1_ARATH/1-231
sp|Q9SI20|EF1D2_ARATH/1-231
sp|P29545|EF1B_ORYSJ/1-224
sp|P29546|EF1B_WHEAT/1-216
200
210
220
230
240
250
260
270
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290
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310
320
330
340
350
360

3. STRUCTURE

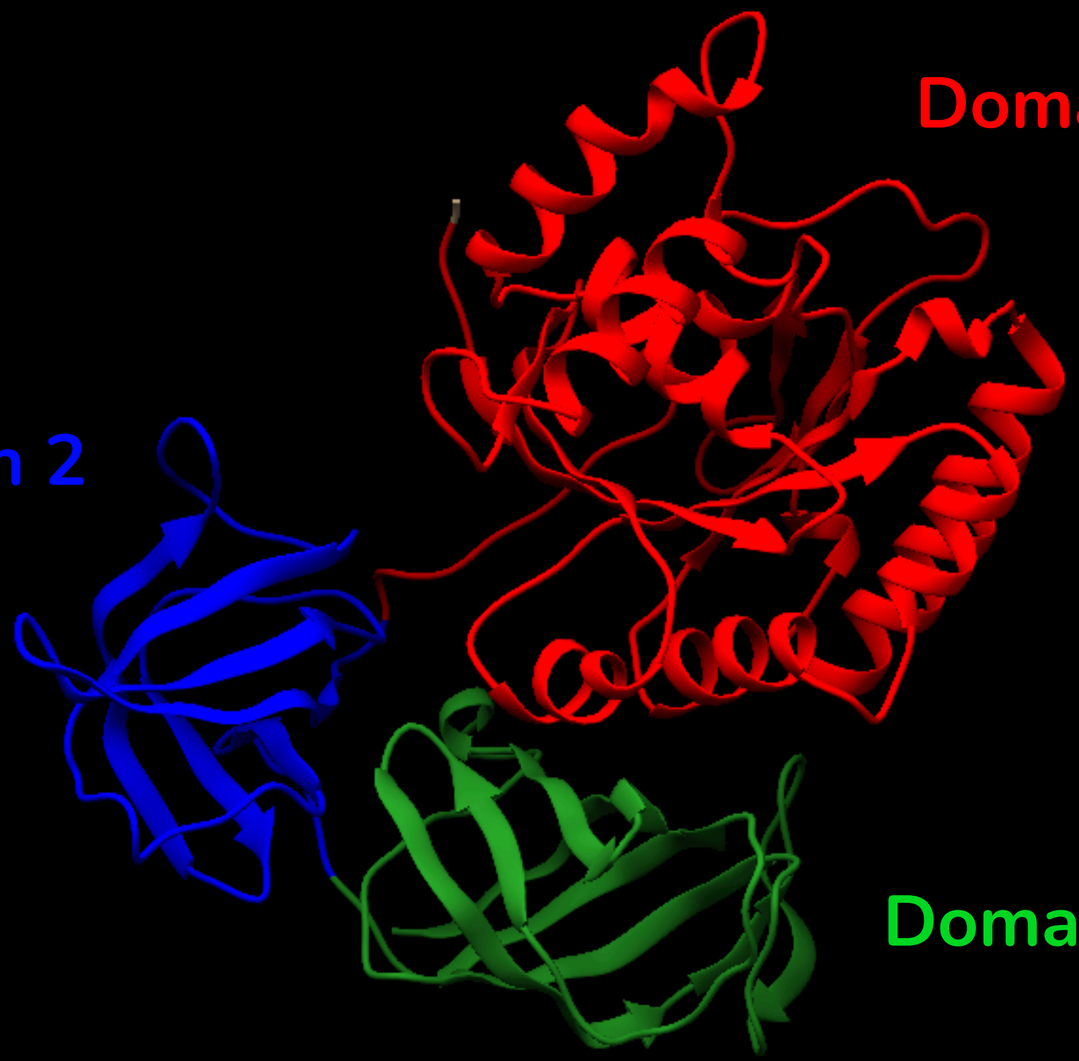
GLOBAL STRUCTURE - eEF1A:eEF1Bα



PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

GLOBAL STRUCTURE- *e*EF1A



PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

eEF1A DOMAIN 1

(N-terminal, residues: 1 - 240)

-It has a classic GTPase fold consisting of a central β sheet surrounded by 8 α helices (A, A, A', B, C*, C, D, and F).*

-It is the core of the GTPase activity of the elongation factor: the binding site for guanine nucleotides (GDP/GTP).

-Is primarily responsible for the conformational change between the active and inactive states.



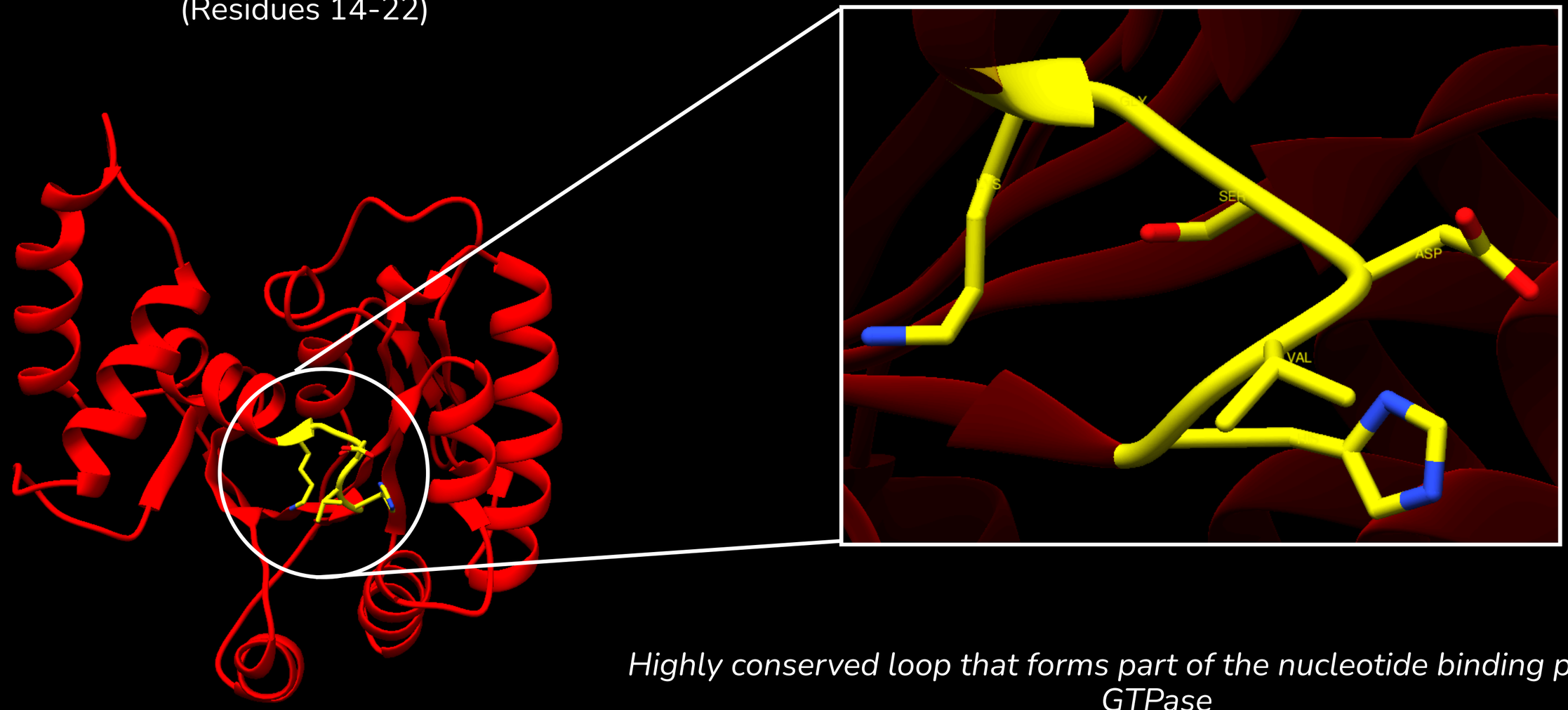
PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

eEF1A DOMAIN 1 P-LOOP

(Residues 14-22)

GXXXXGK Motif



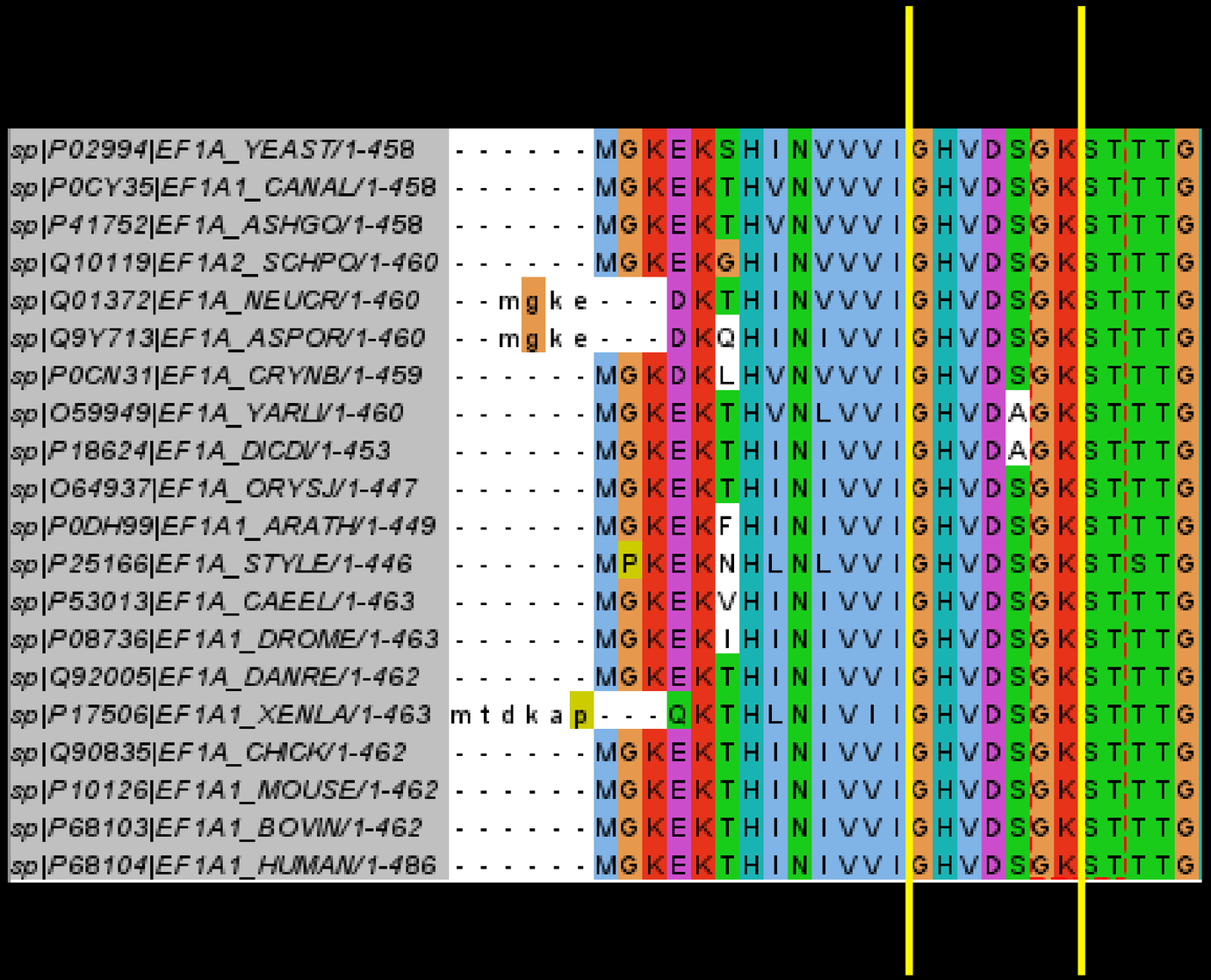
PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

Highly conserved loop that forms part of the nucleotide binding pocket of GTPase

Its main function is to closely coordinate the GTP molecule.

eEF1A DOMAIN 1 P-LOOP

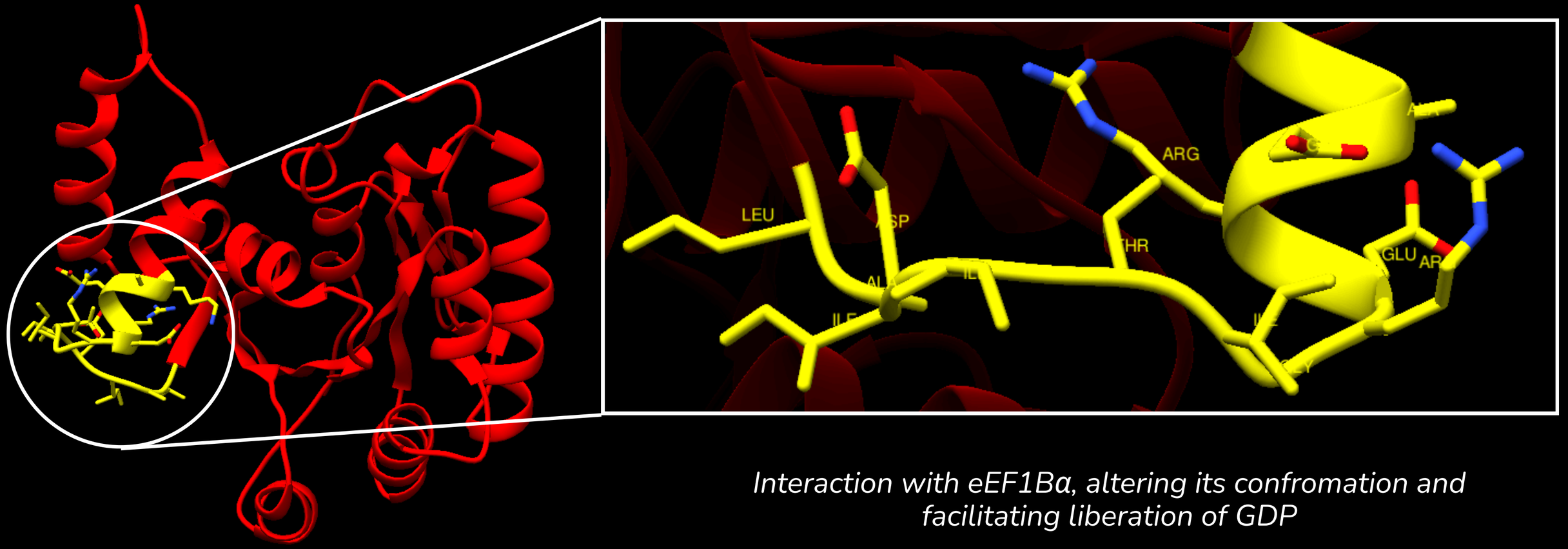


GXXXXGK Motif
Highly conserved among all Eukaryotes

eEF1A DOMAIN 1 - SWITCH-I

(Residues 64-77)

70-GITIDIAL-77 motif



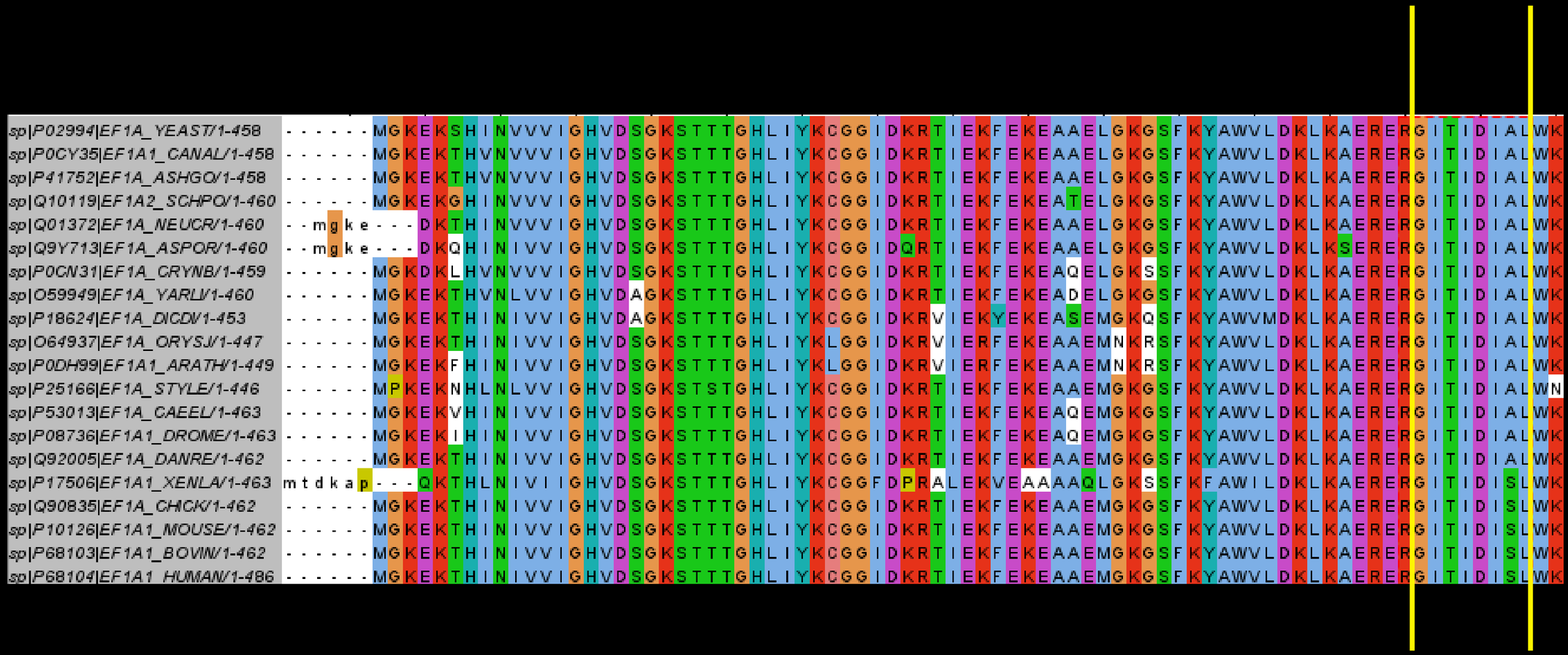
PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

Interaction with eEF1Bα, altering its confromation and facilitating liberation of GDP

Essential for the union of the GTP

eEF1A DOMAIN 1 - SWITCH-I

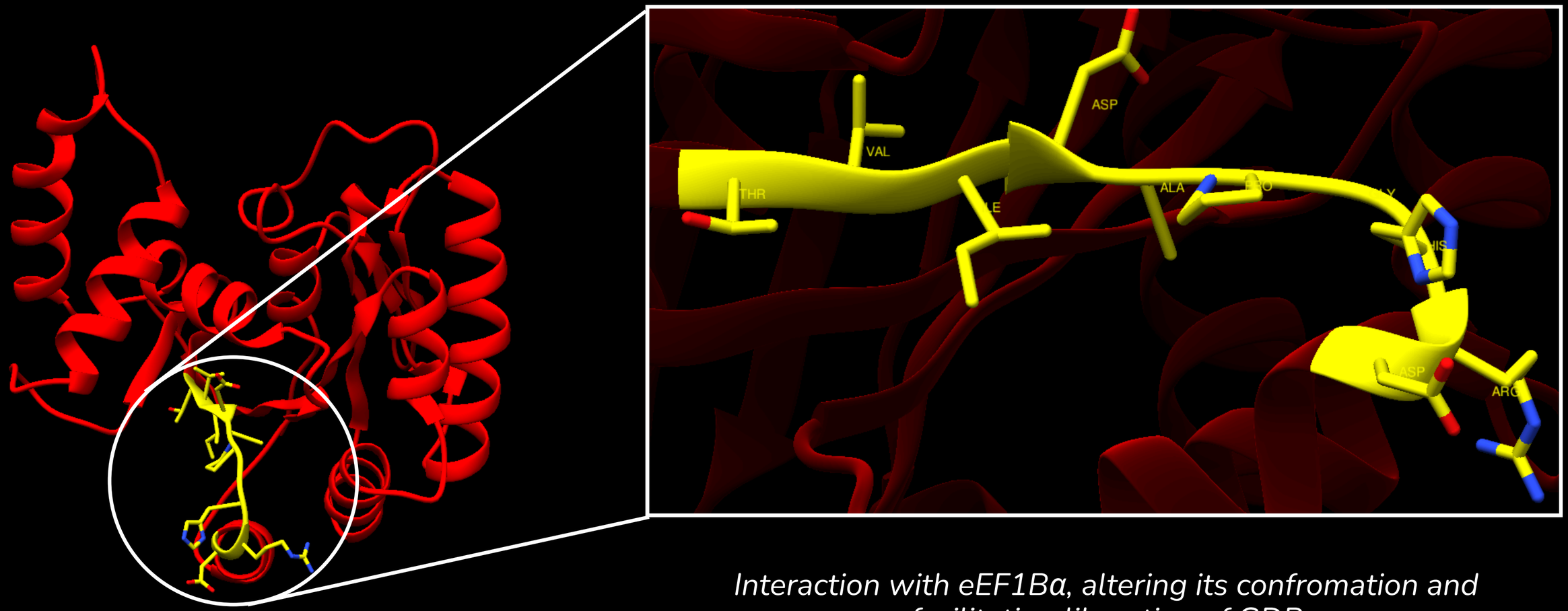


70-GITIDIAL-77 motif
A76->S76 in vertebrates (no functional change)

*e*EF1A DOMAIN 1- SWITCH-II

(Residues 88-97)

DXXG motif



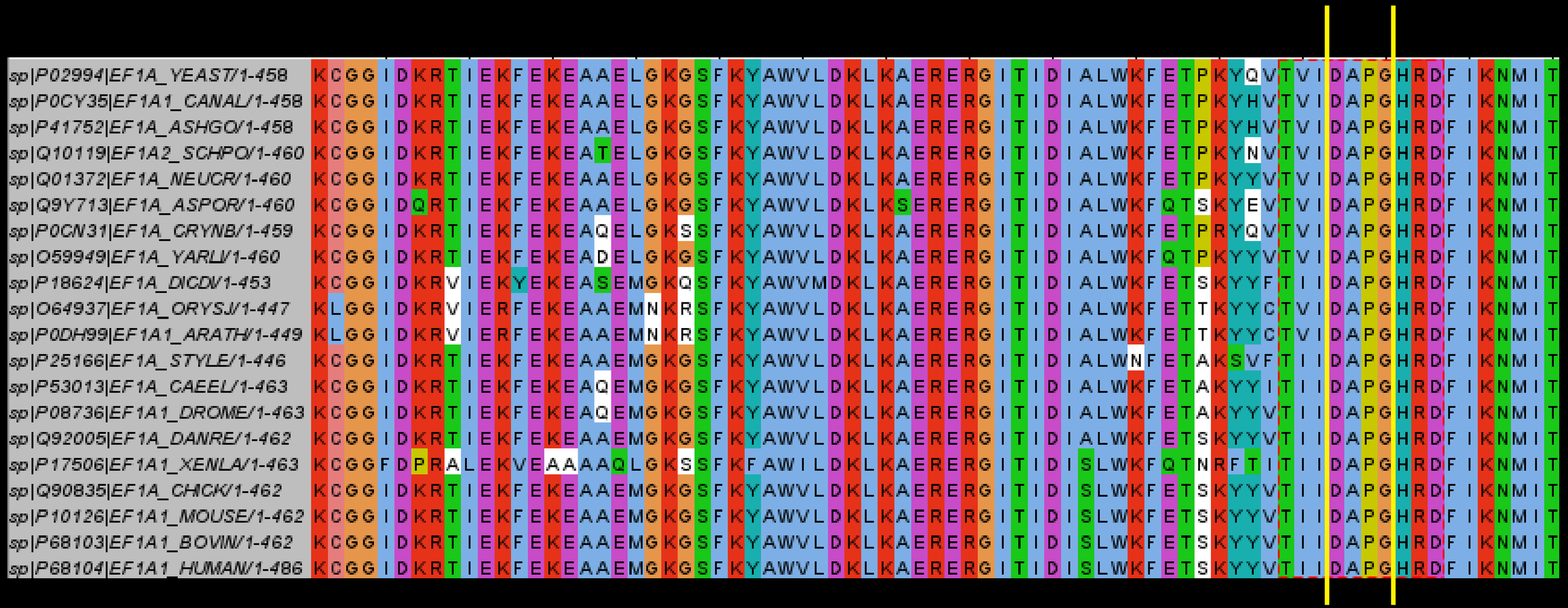
PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

Interaction with eEF1Bα, altering its confromation and facilitating liberation of GDP

Binding to Sarcin-Ricin loop from the ribosome to hydrolize GTP

eEF1A DOMAIN 1- SWITCH-II



Motif DXXG
Asp91-Gly94

Asp is highly conserved
Gly is highly conserved

*e*EF1A DOMAIN 2

(Central, residues 241–336)

-Is primarily responsible for recognizing and binding to the aminoacyl end of aminoacyl-tRNA.

-Ensures the fidelity of protein translation by transporting only correctly charged tRNAs to the ribosome.

-Organized into two β sheets that form a β barrel



PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

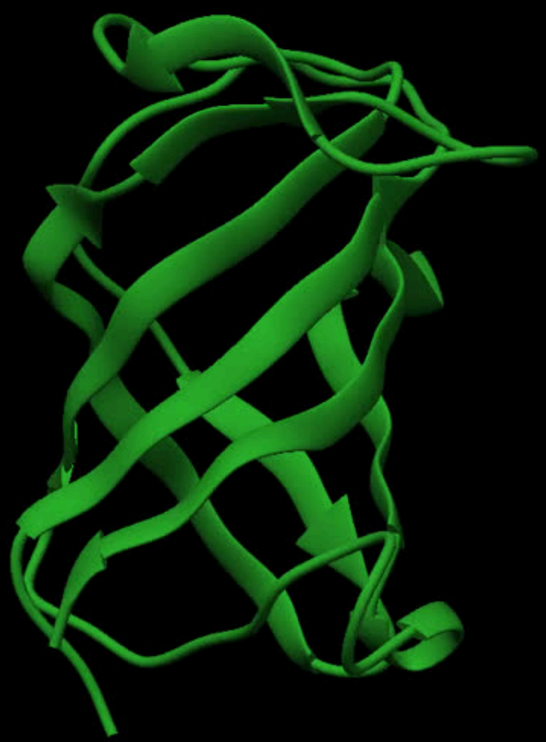
*e*EF1A DOMAIN 3

(C-terminal, residues 337–458)

-Plays a key role as an anchoring module and conformational sensor during tRNA delivery to the ribosome.

-Works with domain I to trigger GTP hydrolysis.

-This domain is key to the change to the extended conformation that allows eEF1A to release tRNA.



PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

GLOBAL STRUCTURE - *eEF1Bα*

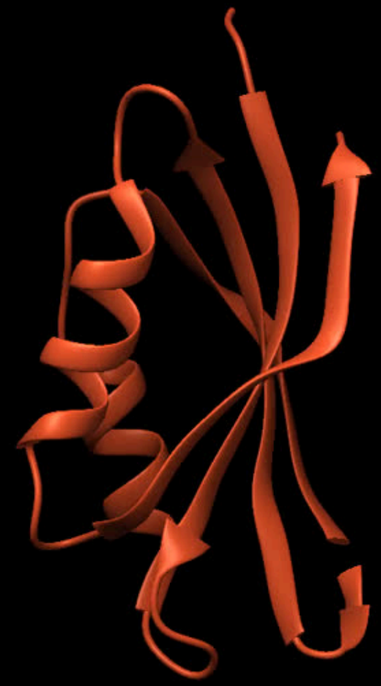
(Residues: 117 - 206)

- Is the catalytic subunit of the eukaryotic guanine nucleotide exchange factor (GEF), called the eEF1B complex

-The primary function of eEF1Bα is to accelerate the release of GDP from eEF1A so that a new GTP can bind.

-The end of eEF1Bα buries itself between switch regions 1 and 2 of domain 1 of eEF1A

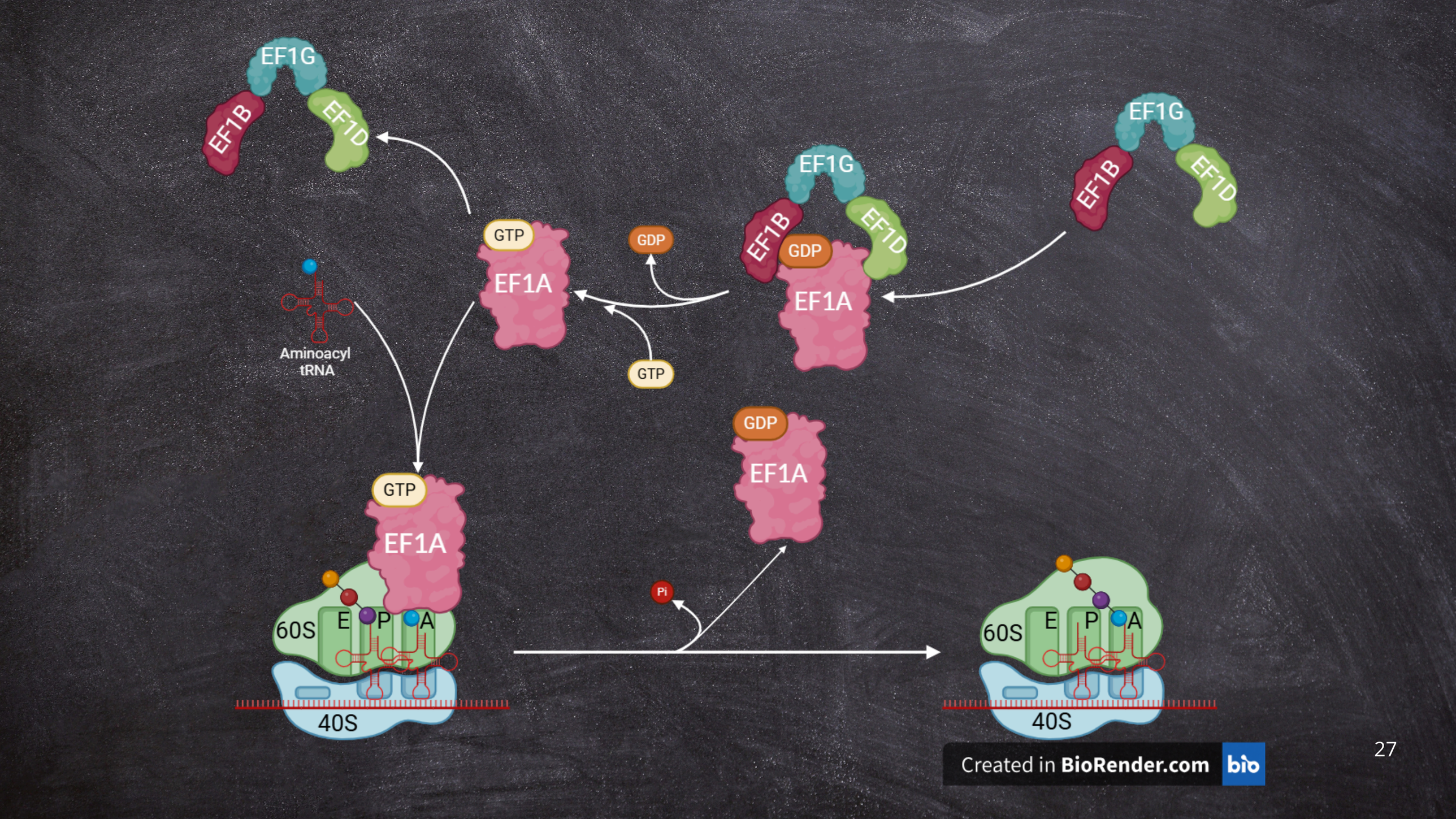
-At the same time, buries into domain 2 occupying exactly the same place where the aminoacyl end of tRNA should bind.

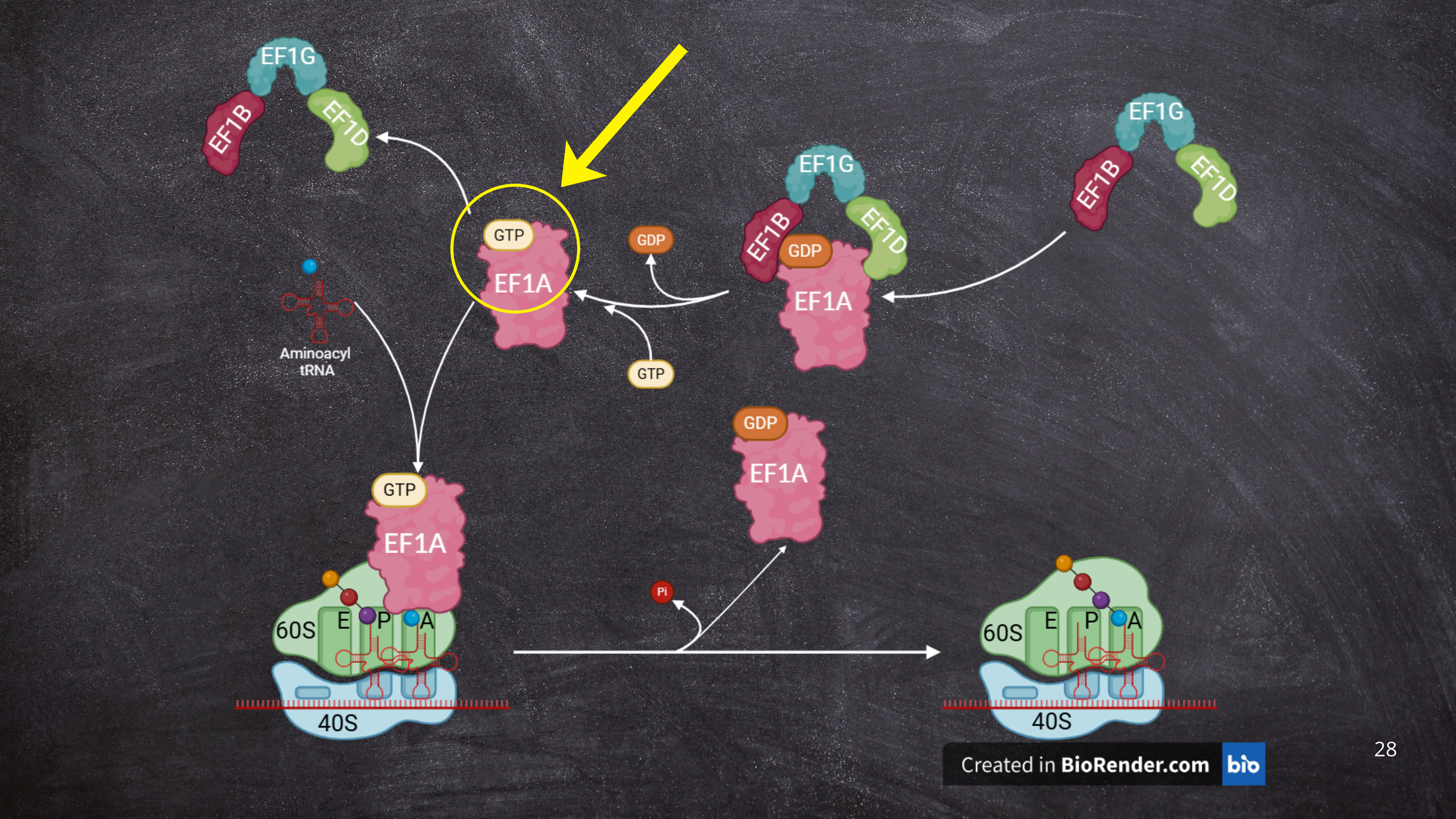


PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

3. INTERACTIONS

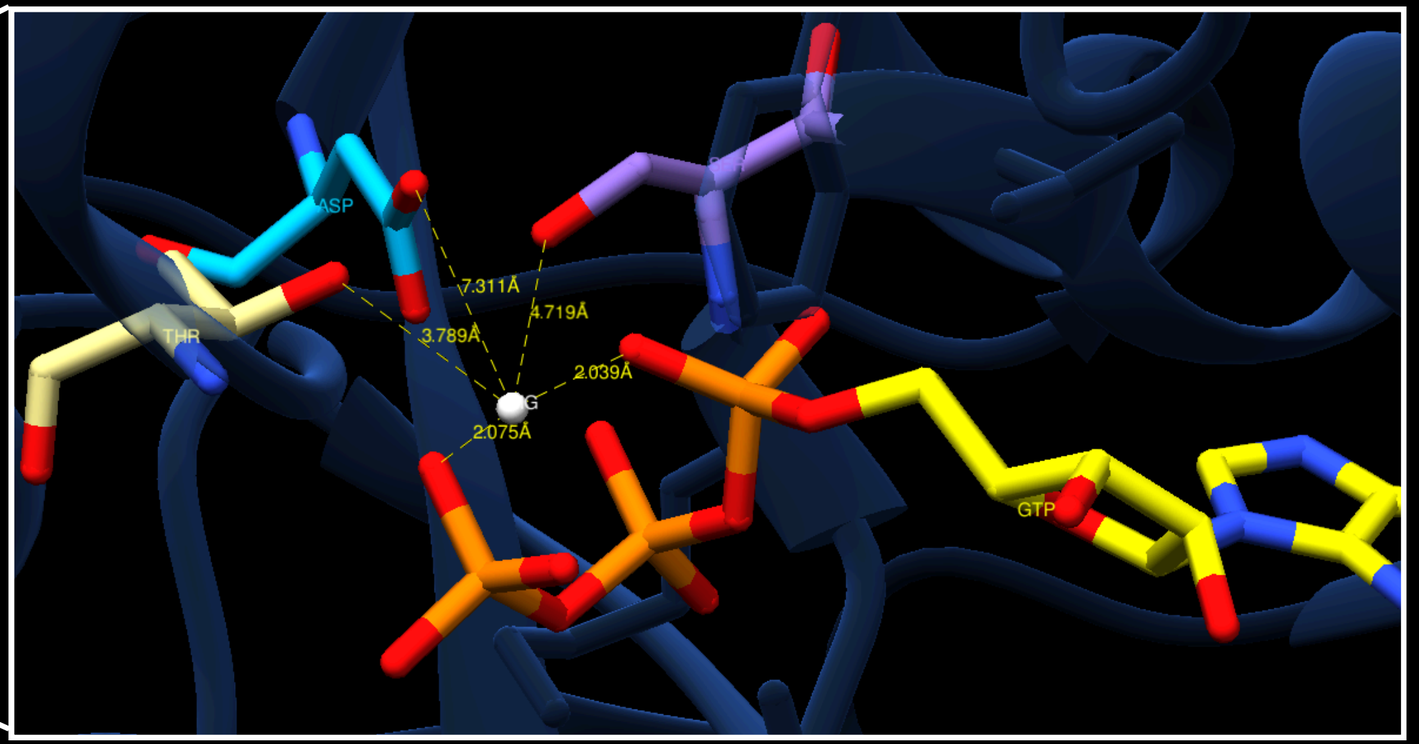

EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
P
A
40S
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bio


EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
GDP
EF1A
Pi
60S
E
P
A
40S
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INTERMOLECULAR INTERACTIONS:
*e*EF1A - GTP - Mg2+

Mg2+ coordination.



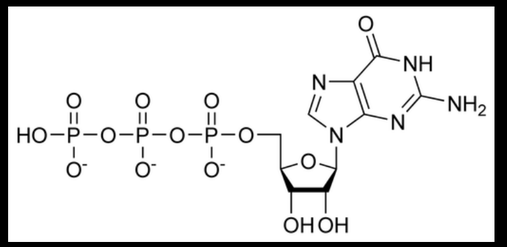


PDB | ID: 8VVQ | *Oryctolagus cuniculus*

2.7 Å

Mg2+

- **γ/α-phosphate** (GTP)
- **Ser21** (eEF1A)
- **Thr72** (eEF1A)
- **Asp91** (eEF1A)

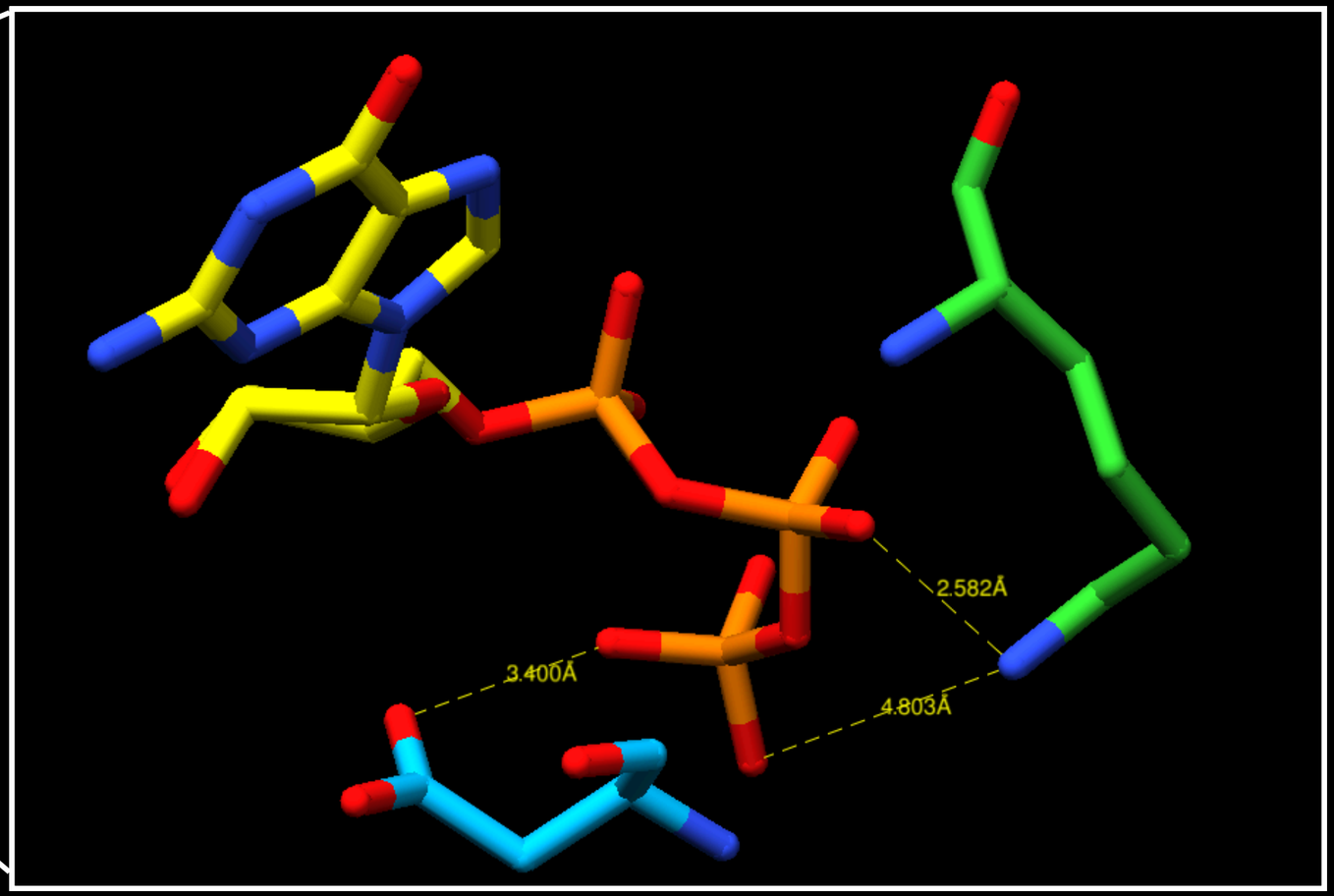

HO
O
O
O

INTERMOLECULAR INTERACTIONS:

eEF1A - GTP - Mg2+

Binding to the phosphates of GTP.





PDB | ID: 8VVQ | *Oryctolagus cuniculus*

2.7 Å

γ/β -phosphate (GTP) — **Asp17** (eEF1A)

γ/β -phosphate (GTP) — **Lys20** (eEF1A)

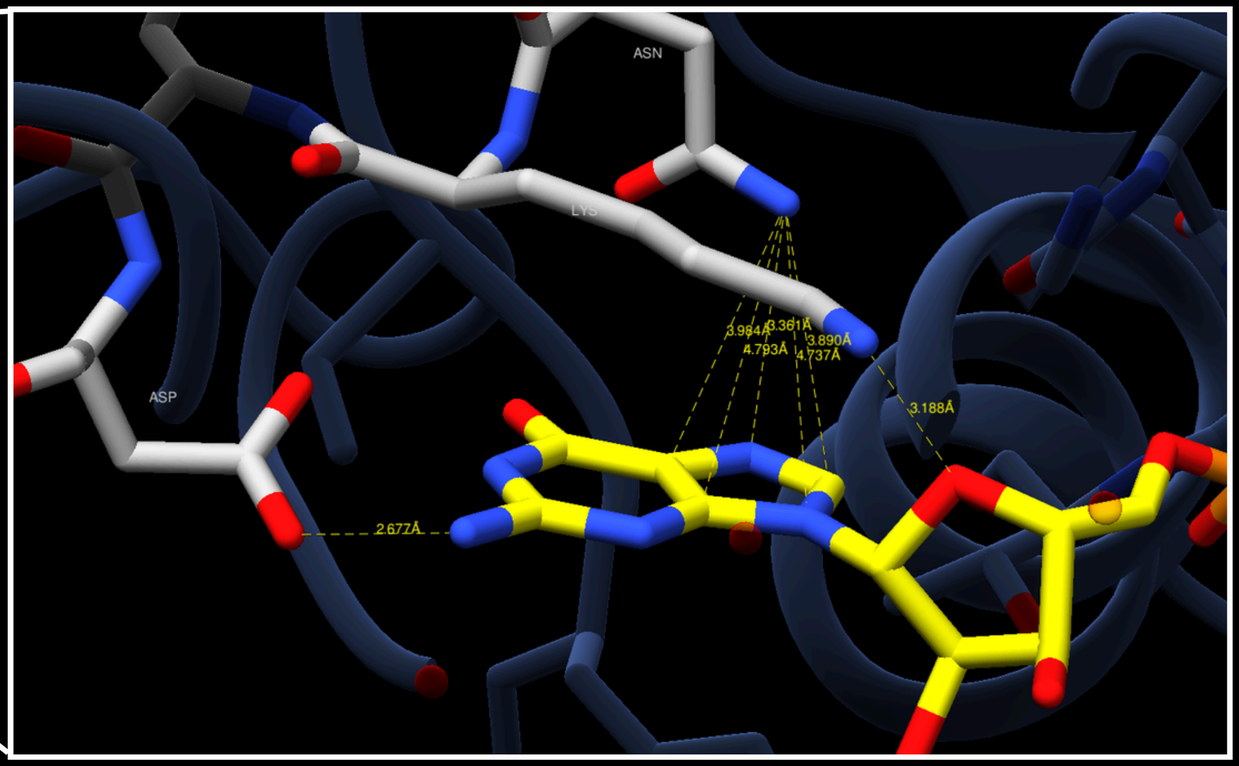
INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+

Asn153-NKMD-Asp156 motif



PDB | ID: 1G7C | *Saccharomyces cerevisiae*

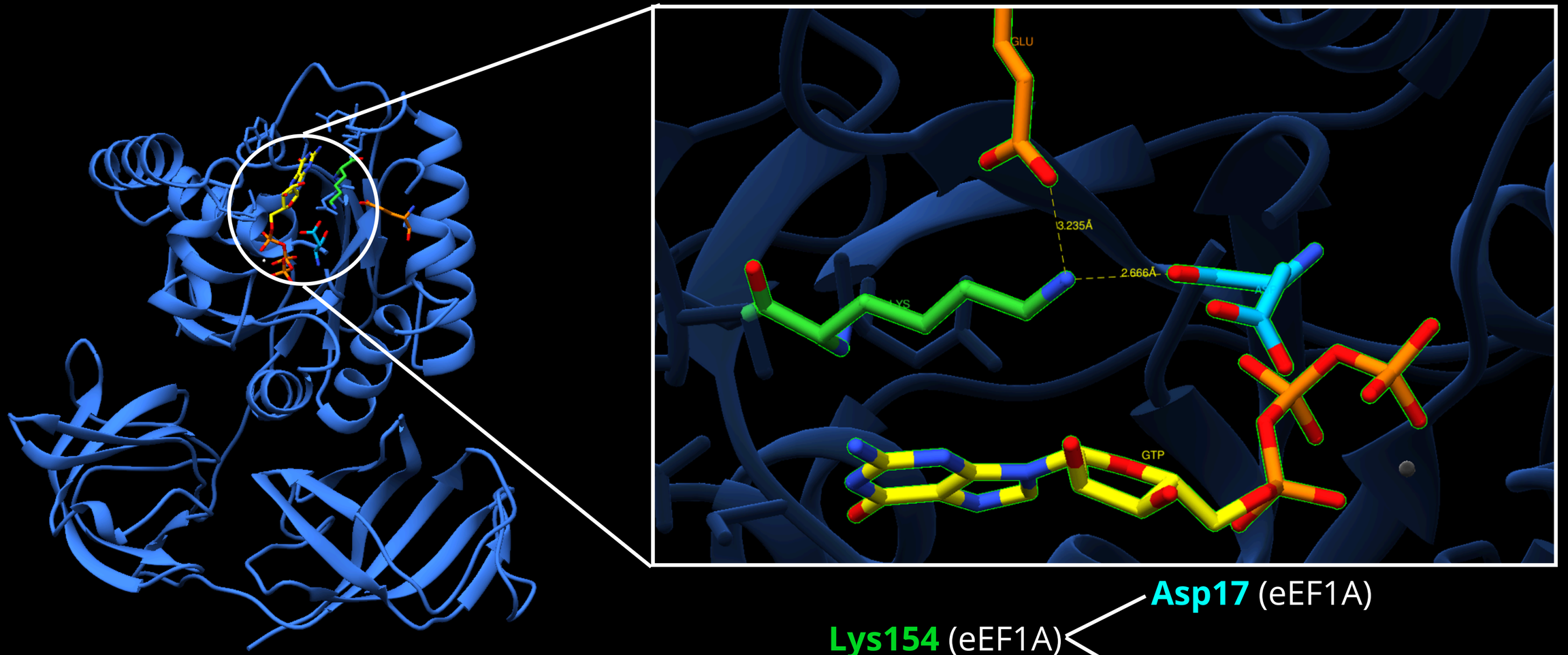
2.05 Å



Asp 156 - Guanine(GTP) | Lys154 - Ribose(GTP)
Asn153 - Guanine(GTP)

INTRAMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+

Asn153-NKMD-Asp156 motif



Asp17 (eEF1A)

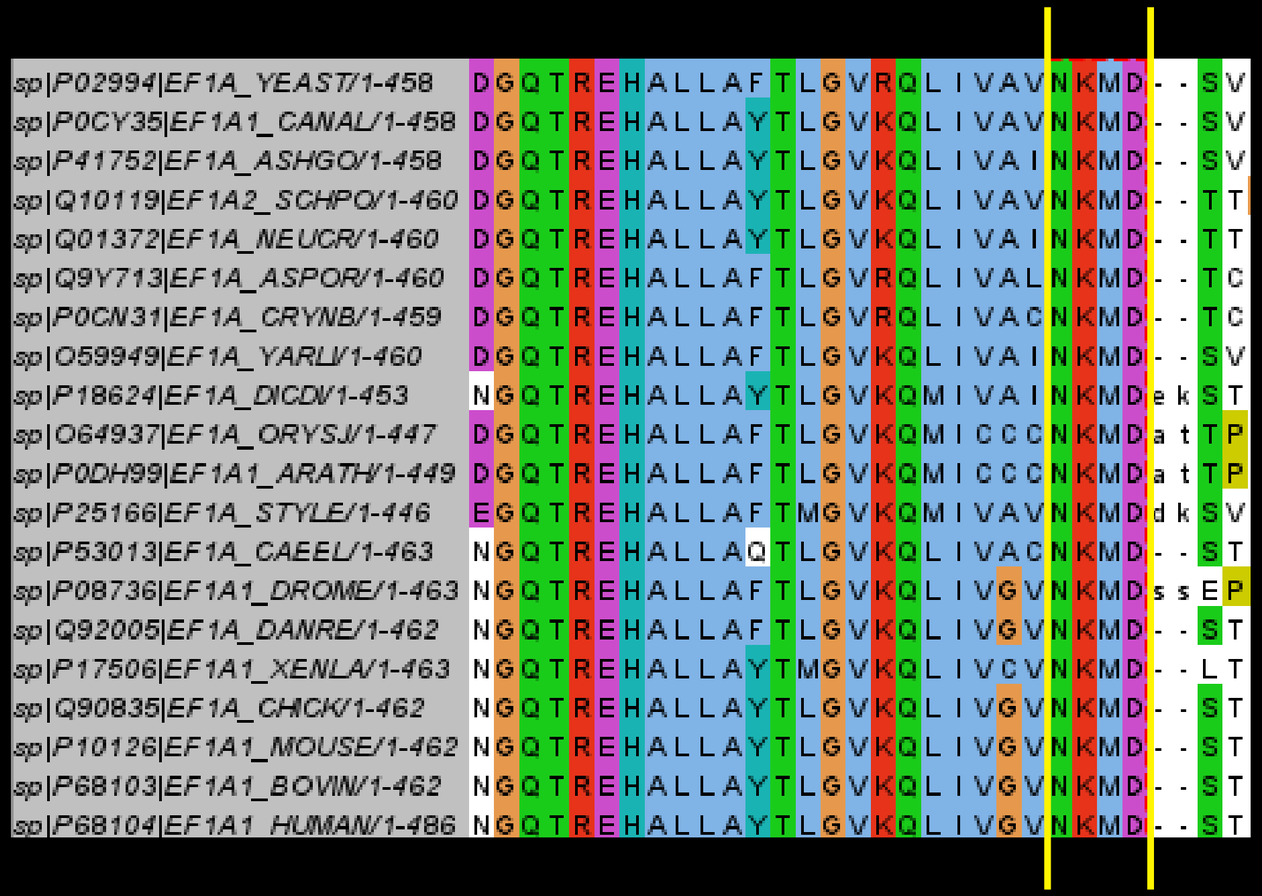
Lys154 (eEF1A)

Glu122 (eEF1A)

PDB | ID: 8VVQ | *Oryctolagus cuniculus*

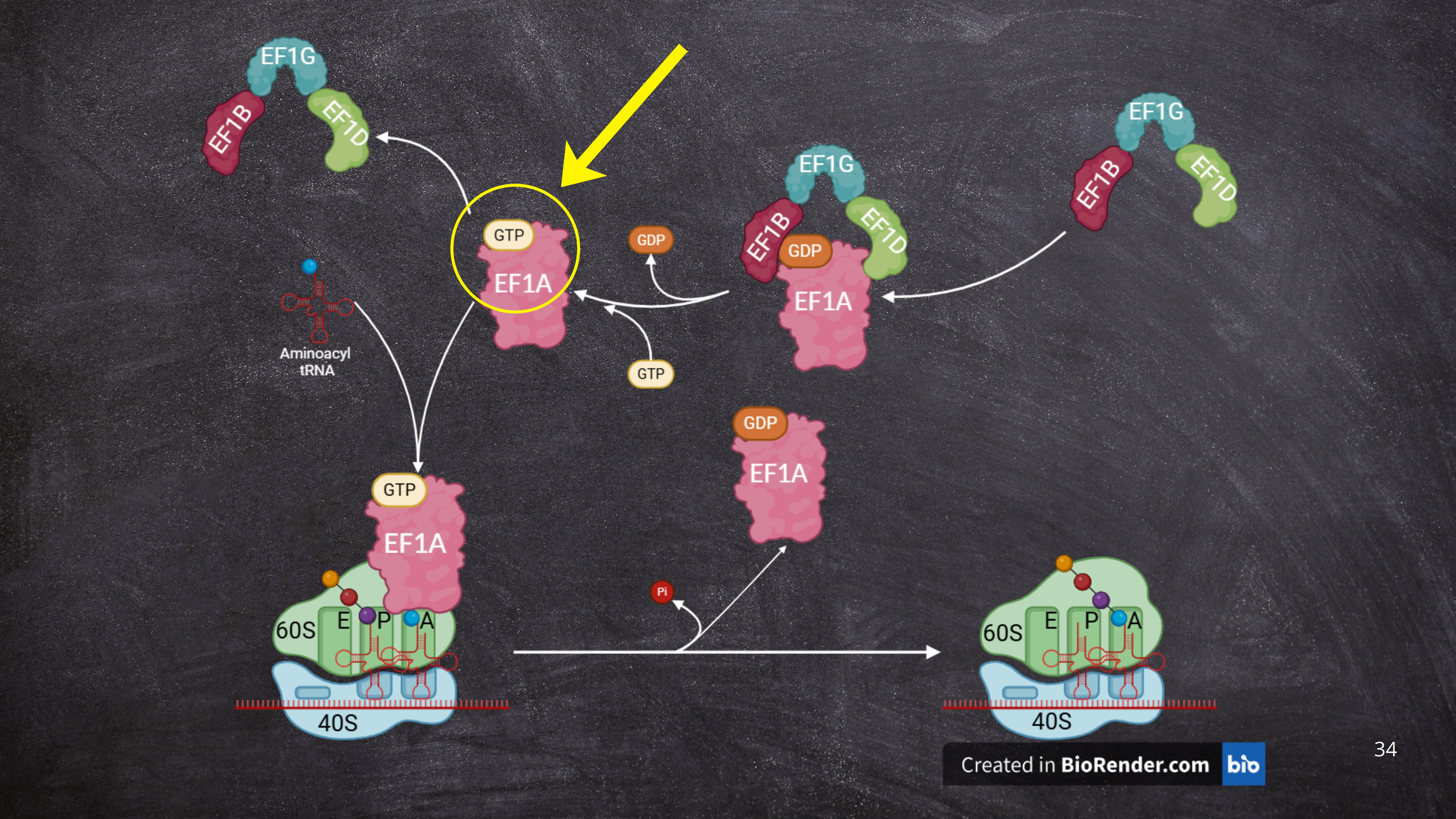
2.7 Å

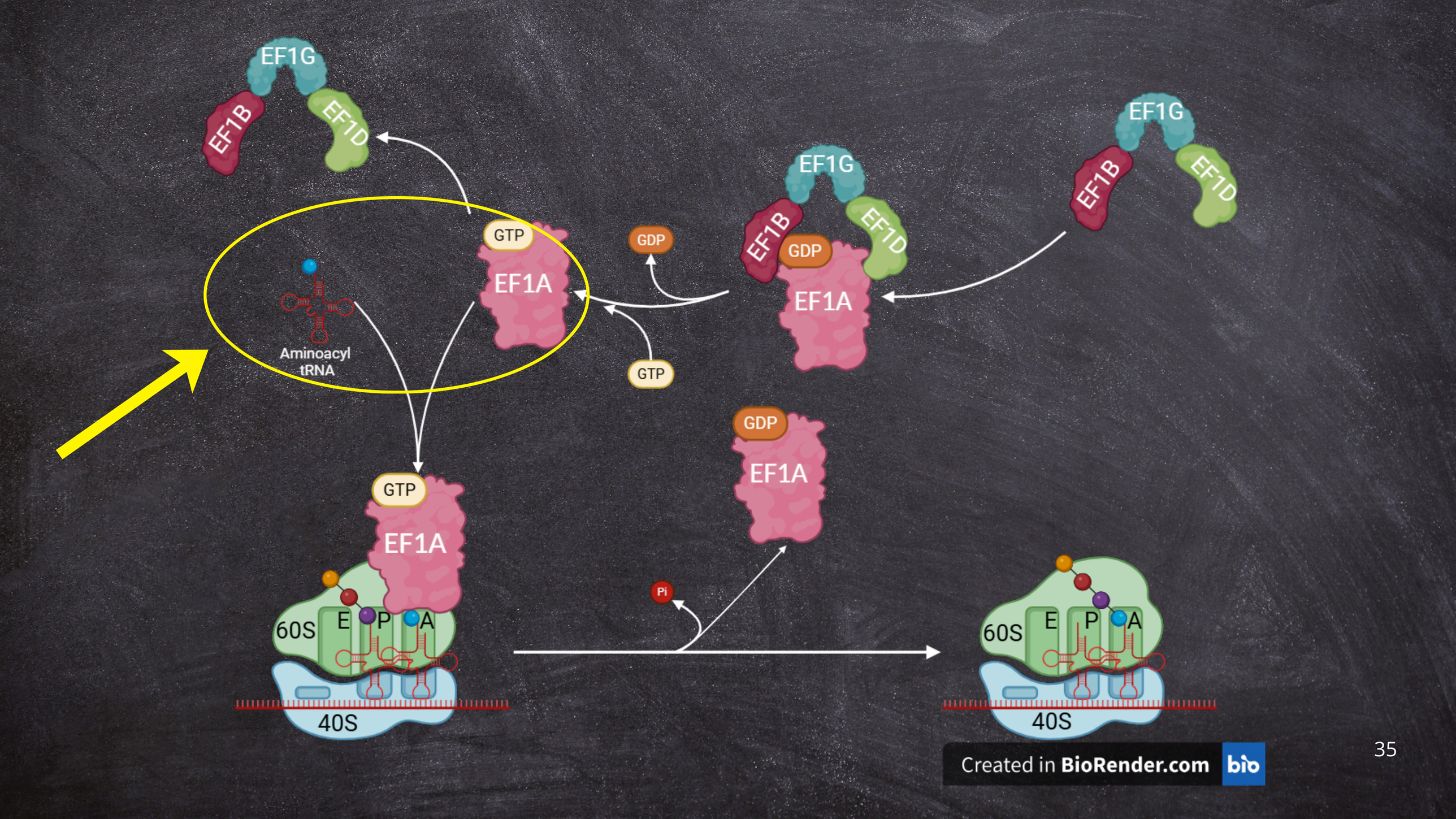
INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+



NKMD motif

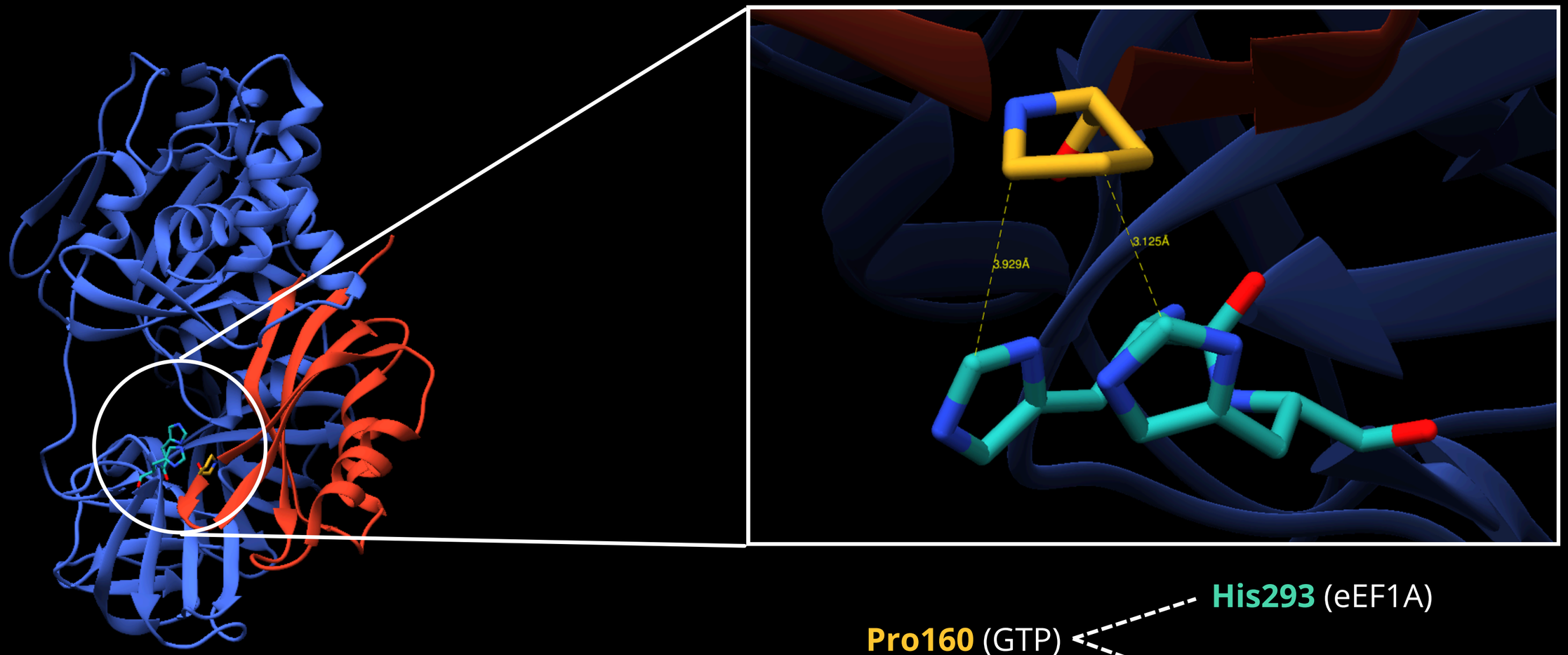
Highly conserved among all **Eukaryotes**


EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
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40S
Created in BioRender.com
bio


EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
P
A
40S
Created in BioRender.com
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INTERMOLECULAR INTERACTIONS:

eEF1A:eEF1Bα - GTP



PDB | ID: 1F60 | *S. cerevisiae*

1.67 Å

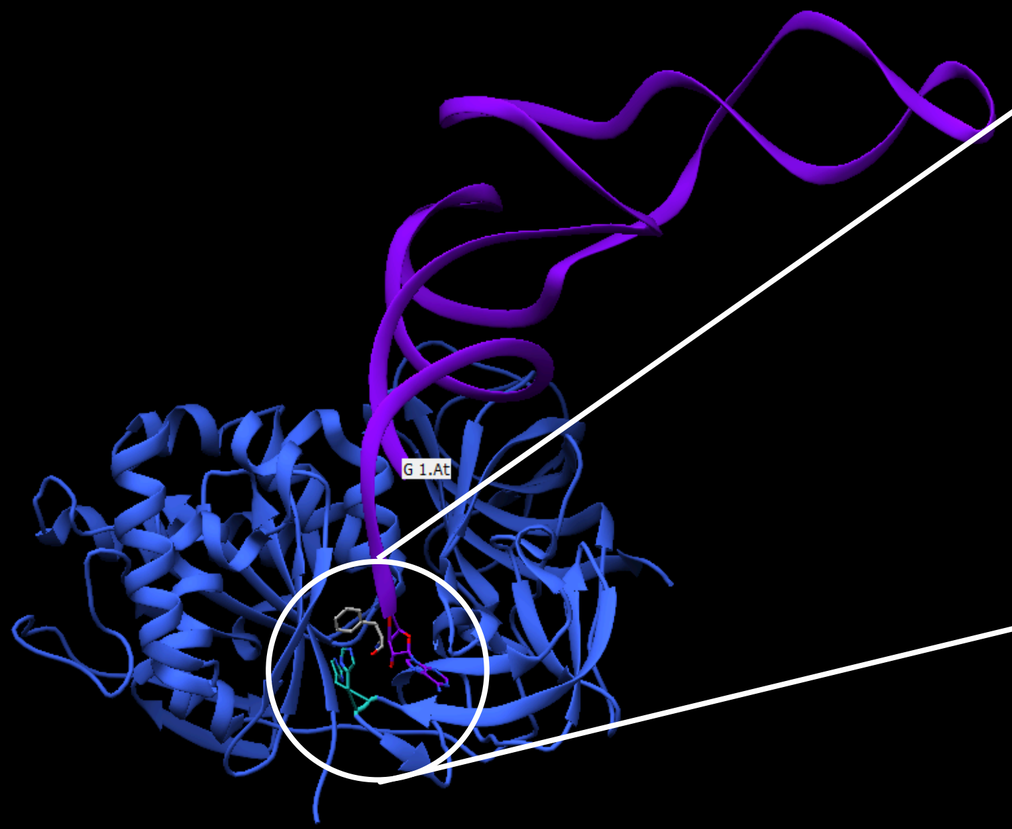
Pro160 (GTP) --- **His293** (eEF1A)

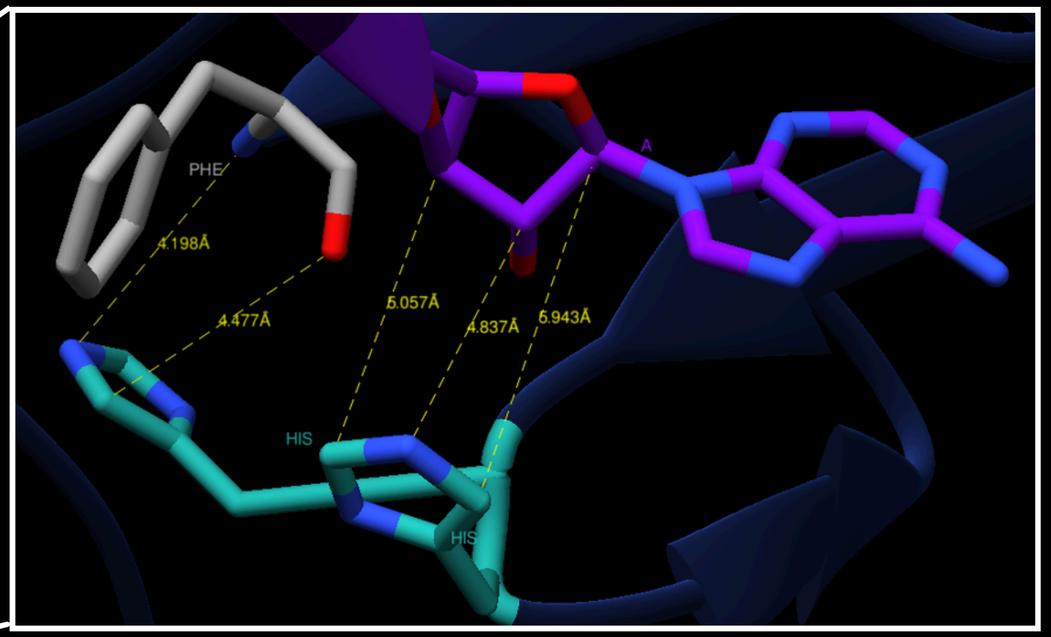
Pro160 (GTP) --- **His294** (eEF1A)

*The nature of the interactions is not fully described because the electron density is weak in this crystallization.

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA

tRNA binding





PDB | ID: 8G60 | *Homo sapiens*

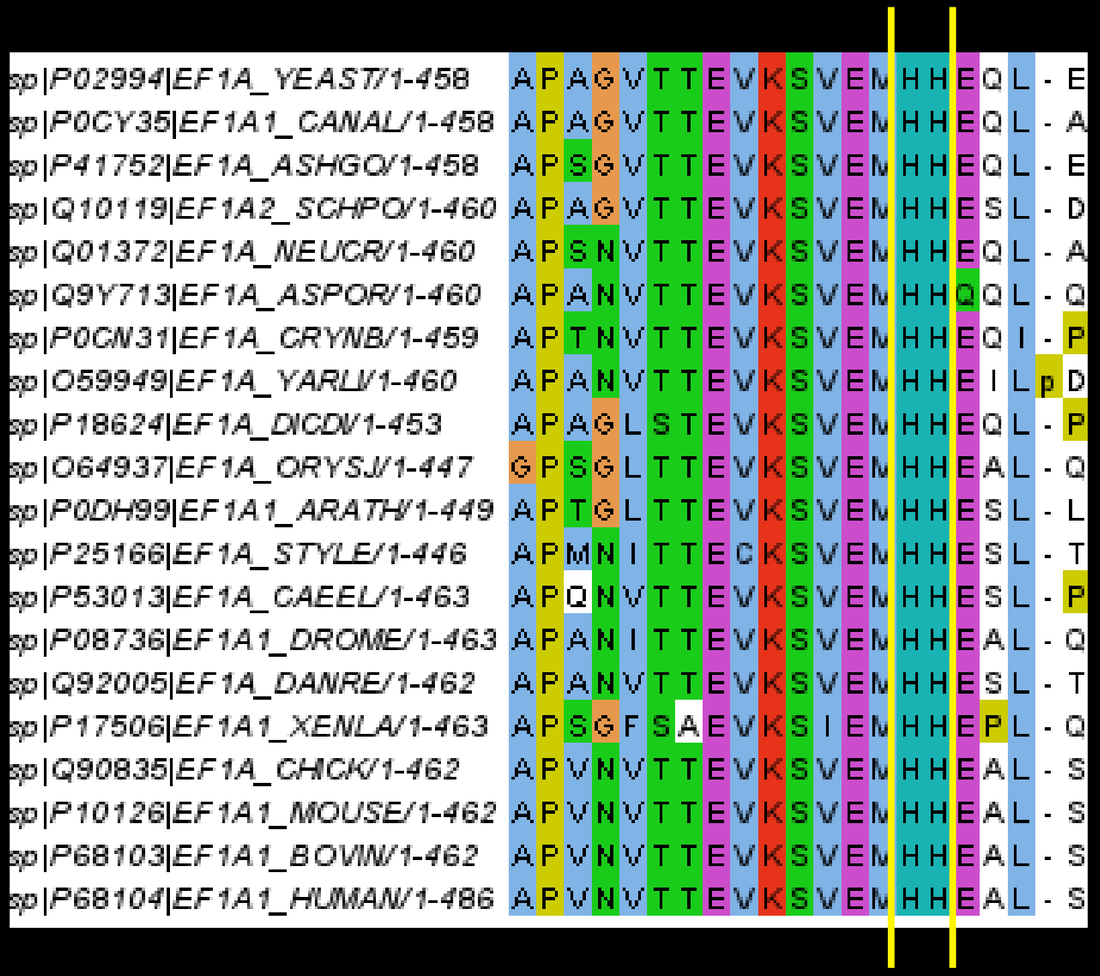
2.54 Å

His293 (eEF1A) - **Phe** (aa tRNA)

His294 (eEF1A) - **A76** (aa tRNA)

INTERMOLECULAR INTERACTIONS:

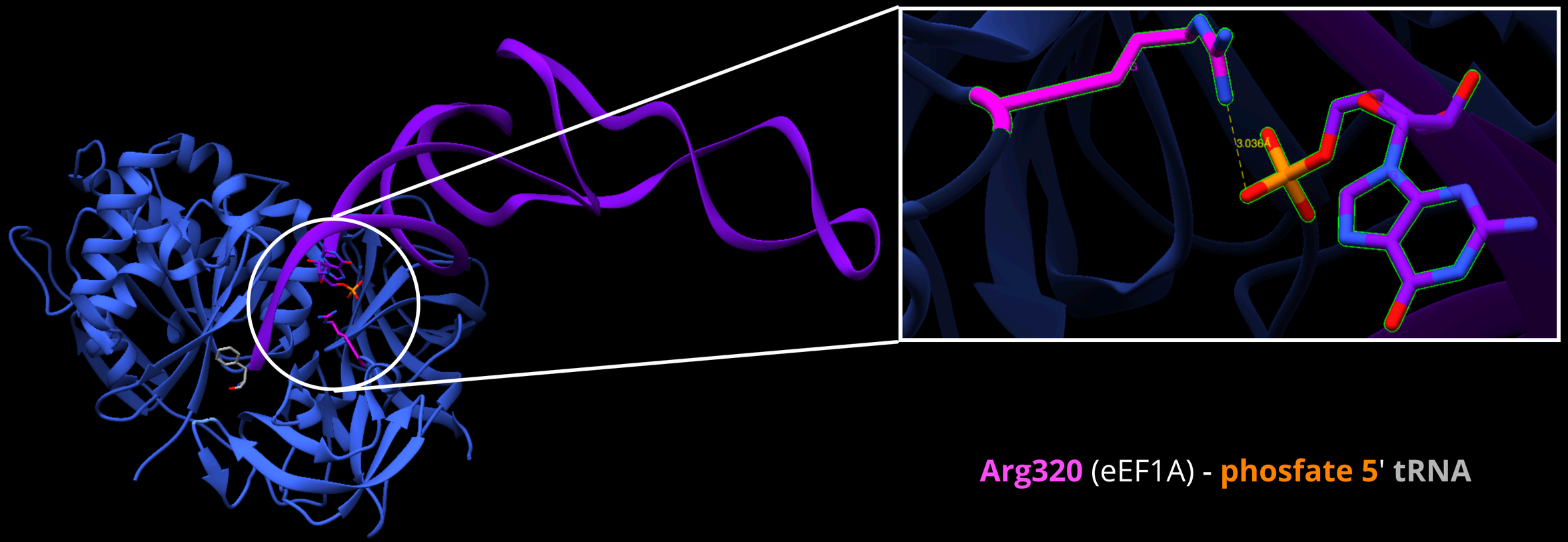
eEF1A - GTP - Mg2+ - tRNA



His293 and **His294** **(eEF1A)**

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA

tRNA binding



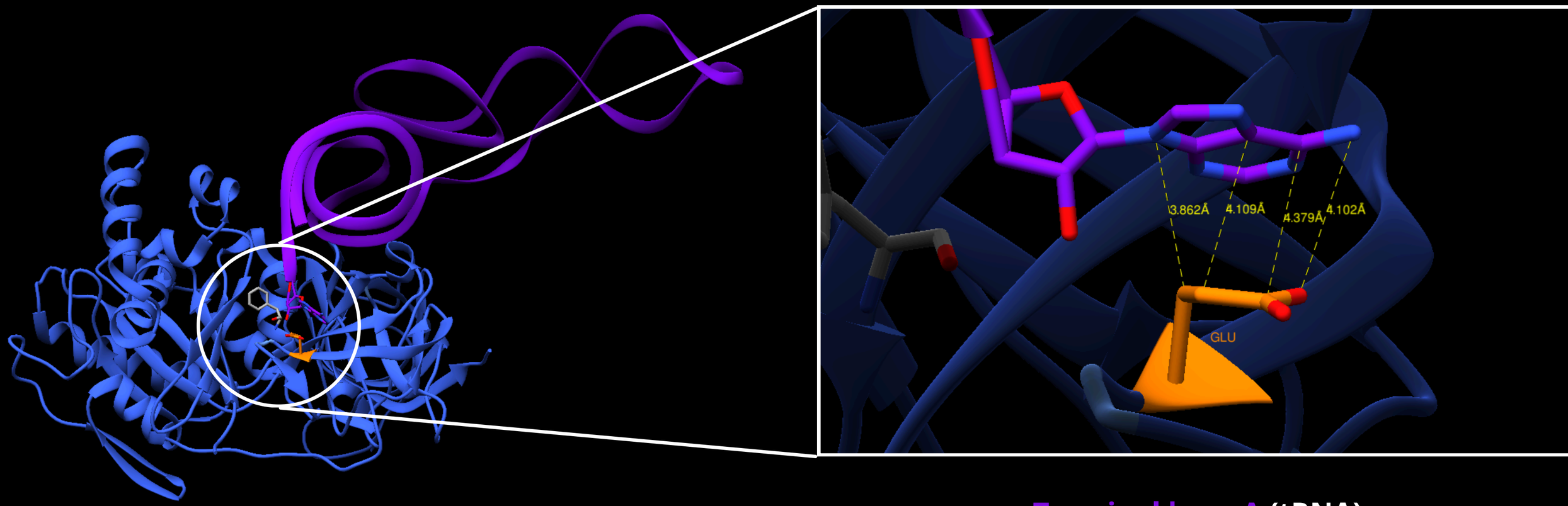
Arg320 (eEF1A) - **phosfate 5' tRNA**

PDB | ID: 8G60 | *Homo sapiens*

2.54 Å

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA

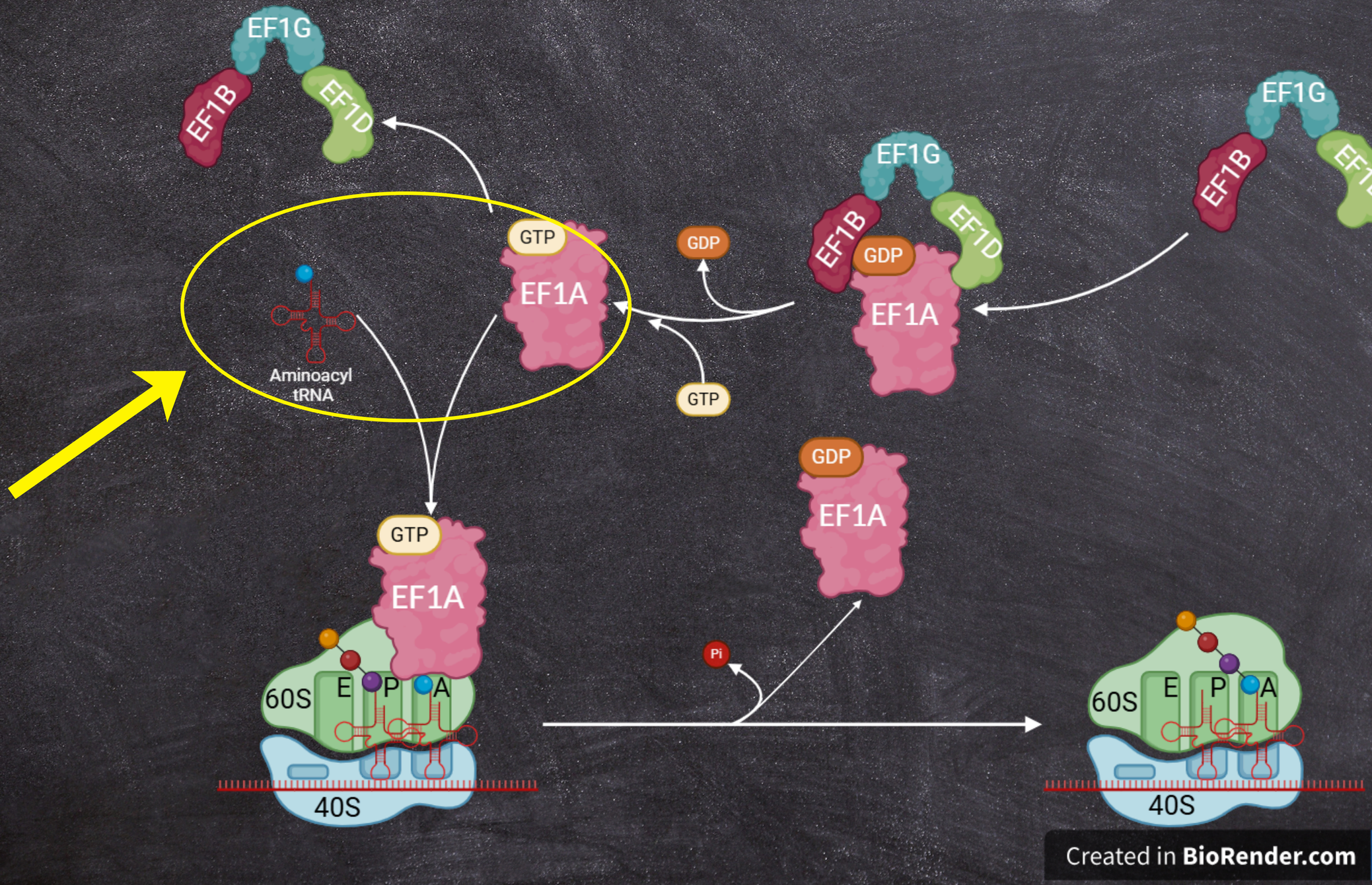
tRNA binding

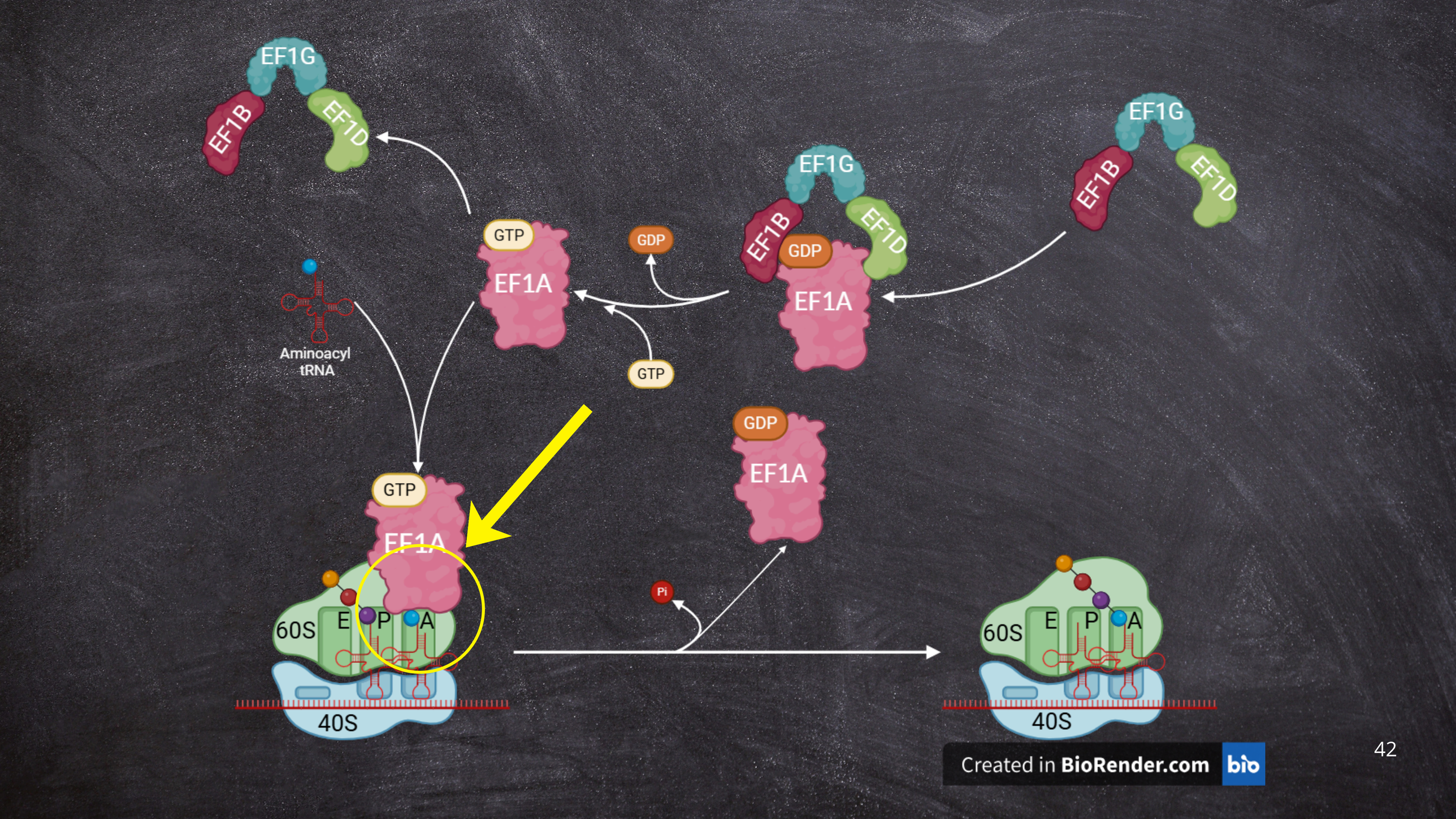


Terminal base A (tRNA)
Glu291 (eEF1A)

PDB | ID: 8G60 | *Homo sapiens*

2.54 Å

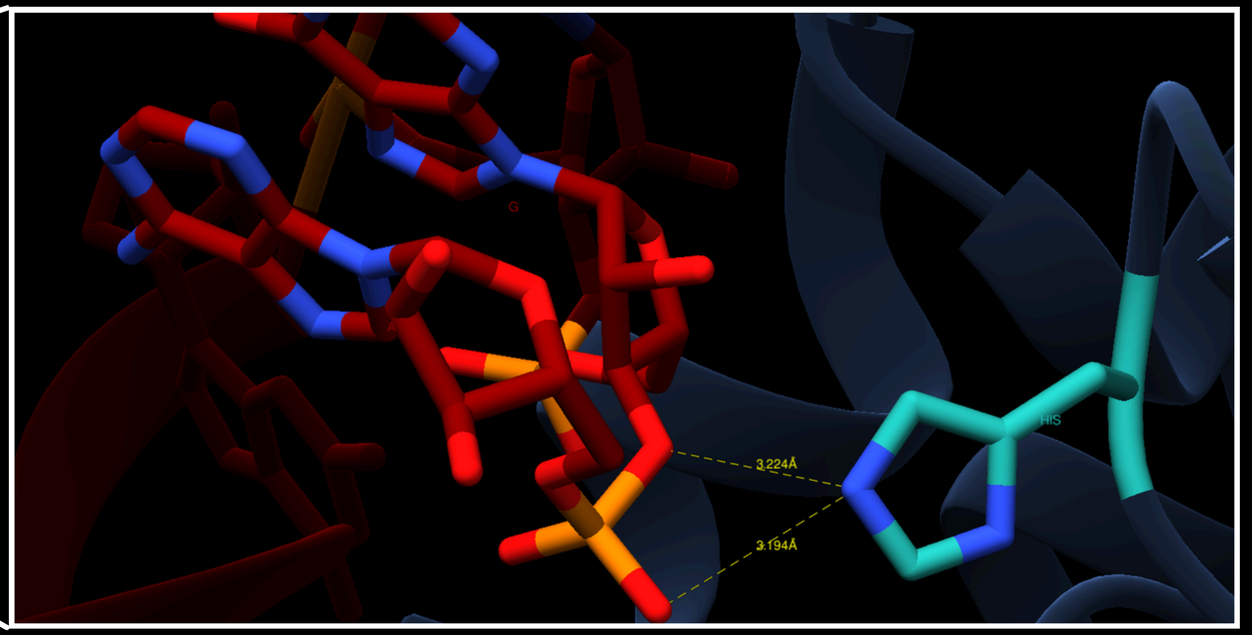

EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
P
A
40S
Created in BioRender.com
bio


EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
60S
E
P
A
40S
Pi
Created in BioRender.com
bio

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

Ribosome-Dom 1 interactions



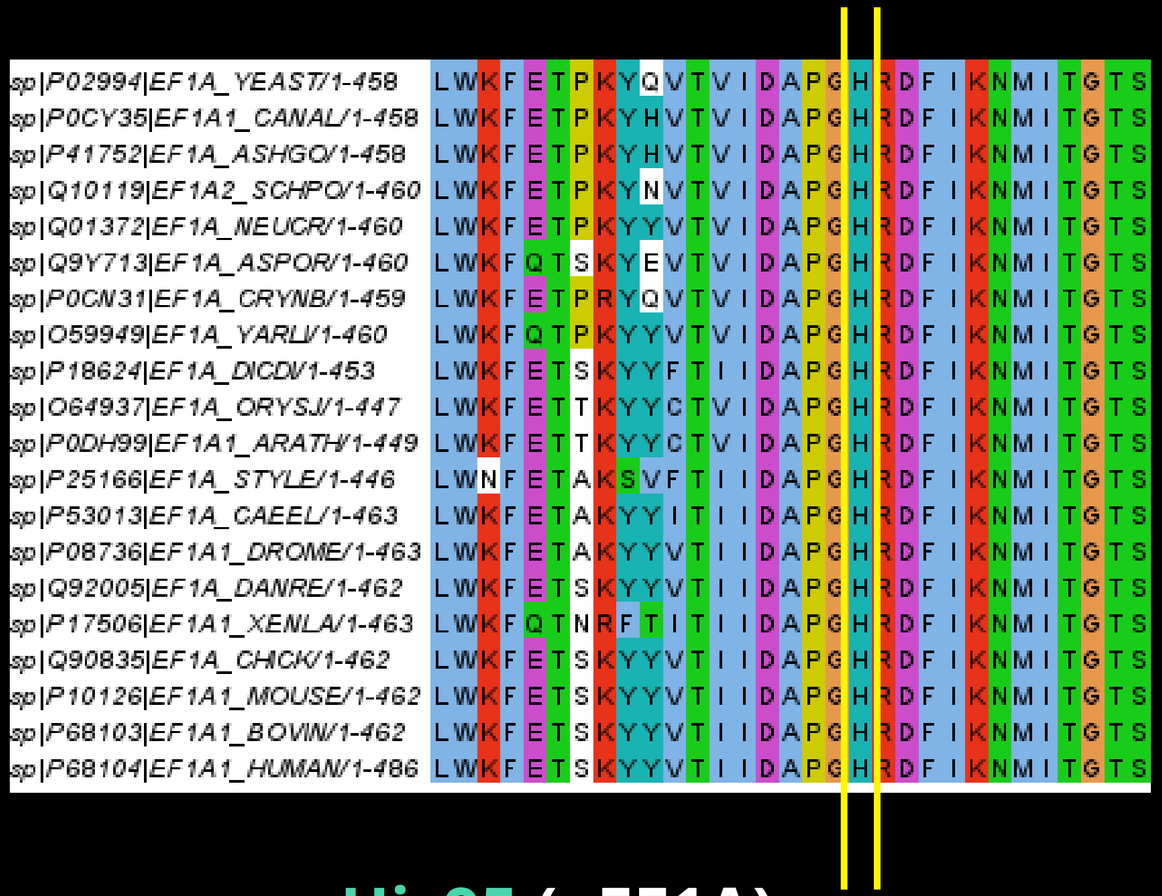


PDB | ID: 8G5Z | *Homo sapiens*

2.64 Å

G4606-A4607 (SRL) - His95 (eEF1A)

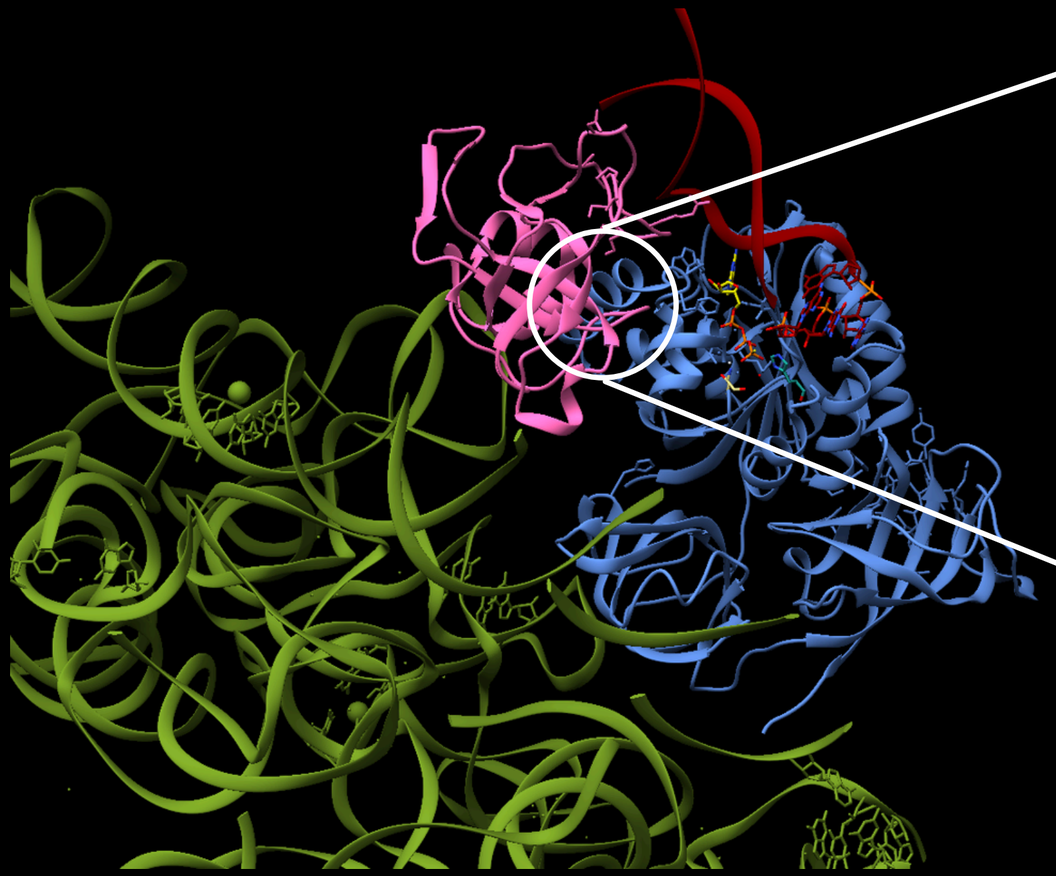
INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

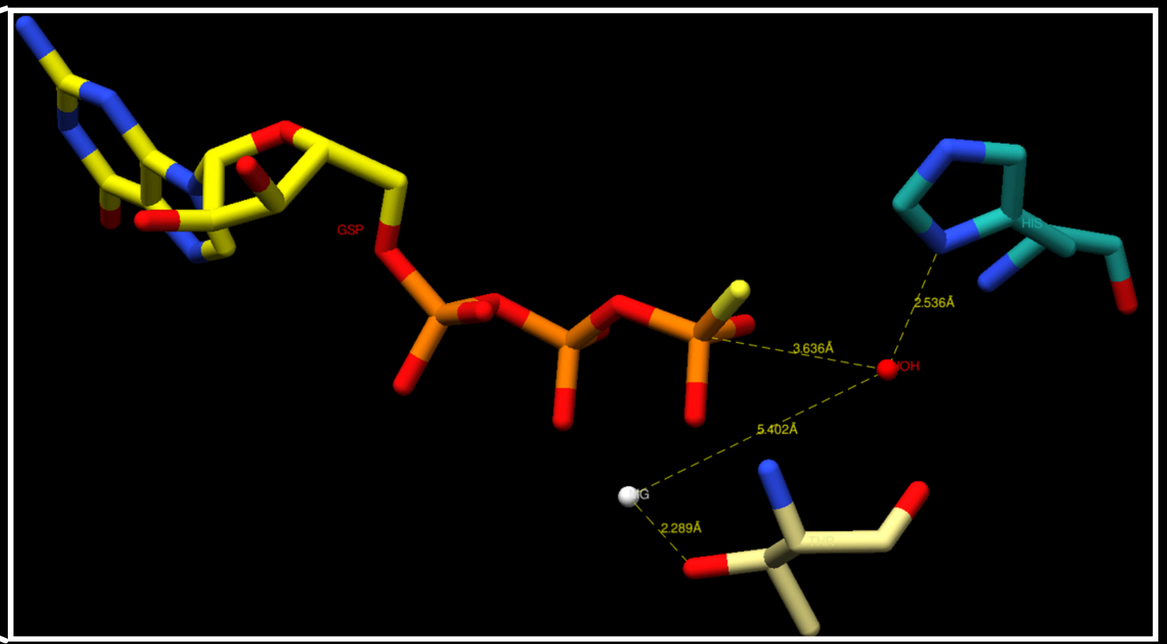


His95 (eEF1A)

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

Nucleophilic attack





PDB | ID: 8G5Z | *Homo sapiens*

2.64 Å

His95

Thr72 + Mg^{2+}

H_2O → **γ-phosphate (GTP)**

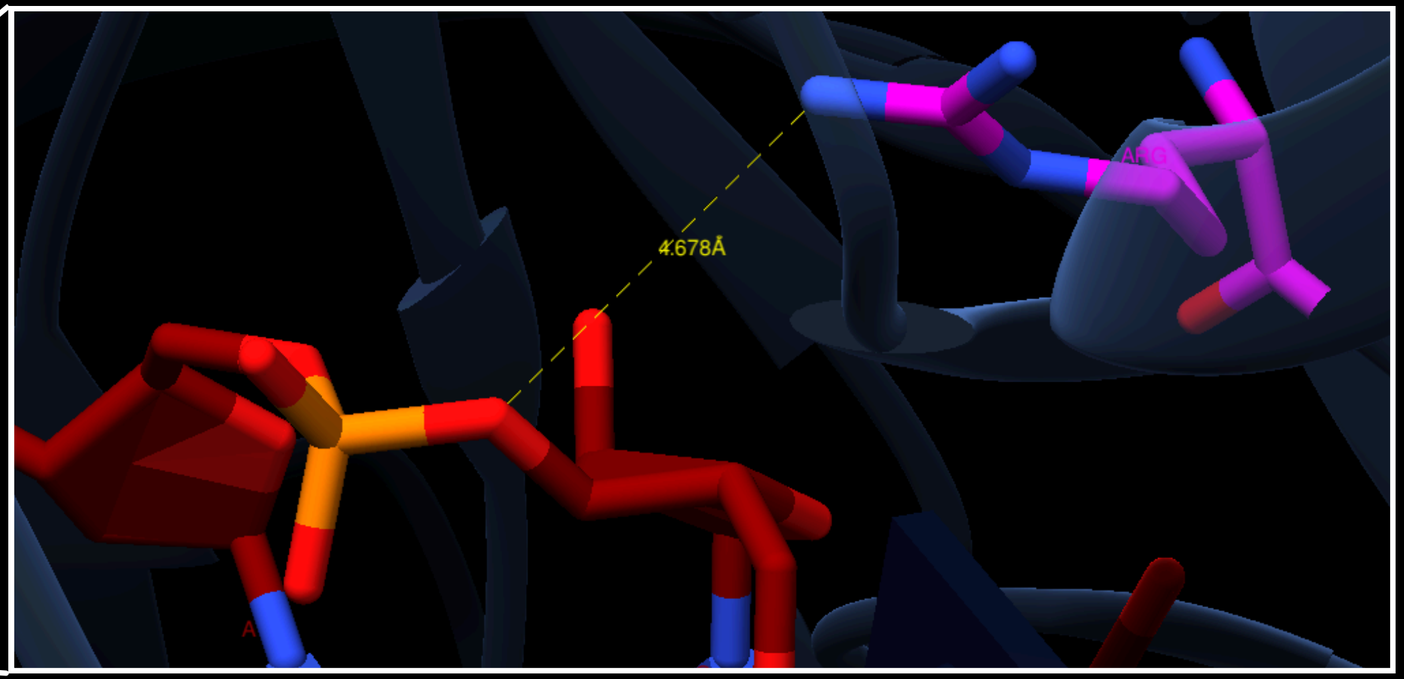
INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

Ribosome-Dom 3 interactions



PDB | ID: 8G5Z | *Homo sapiens*

2.9 Å

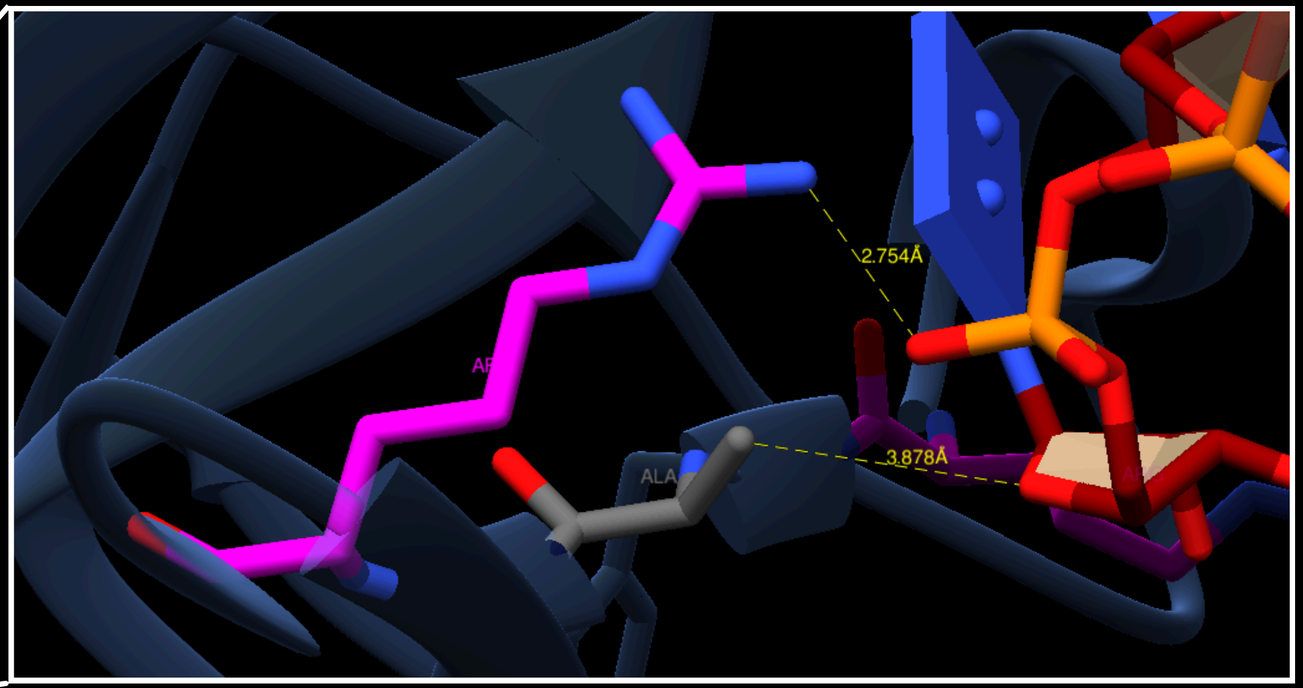


G4606 (SRL) - Arg423 (eEF1A)

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

Ribosome-Dom 3 interactions





PDB | ID: 8G5Z | *Homo sapiens*

2.9 Å

Arg427 (eEF1A)

Ala425 (eEF1A)

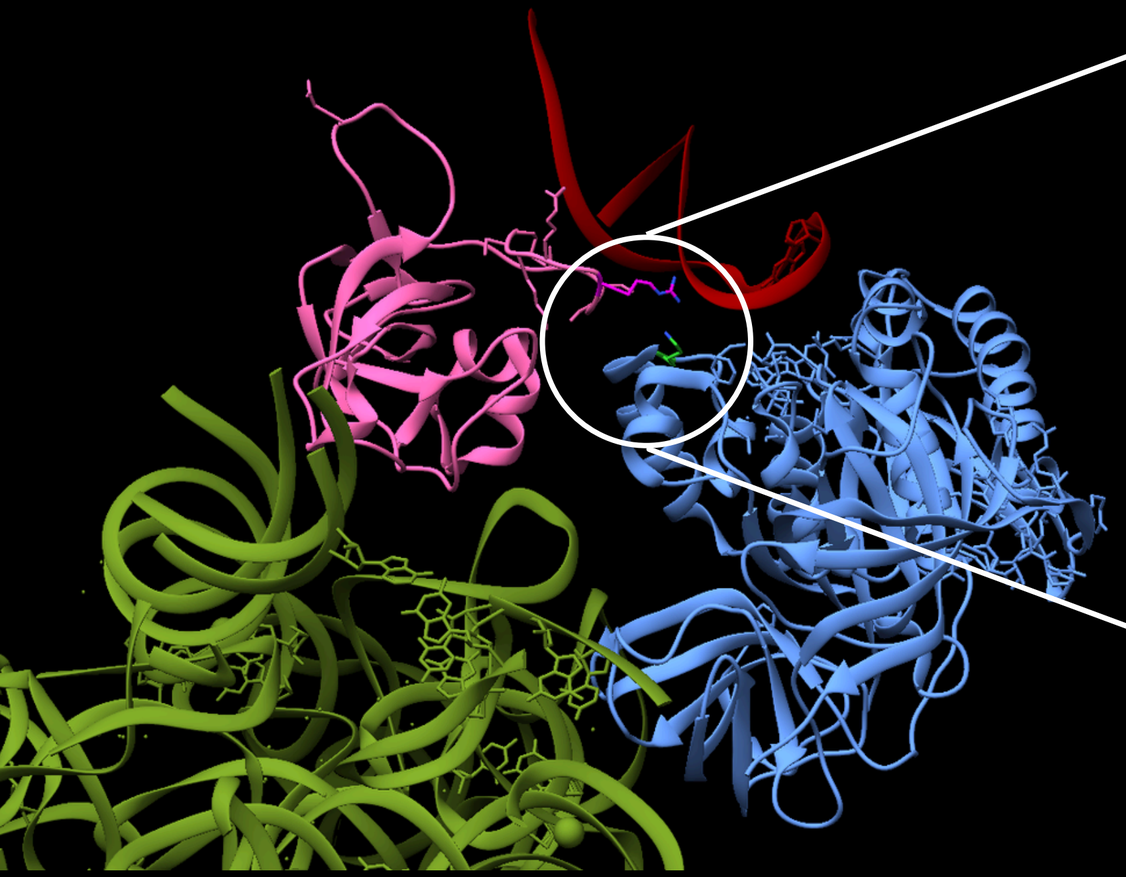
G4606 **(SRL)**

INTERMOLECULAR INTERACTIONS:
alpha-2 + uL14 (60S) + h14 (40S)

INTERSUBUNITARY TEMPORAL BRIDGE (B8)

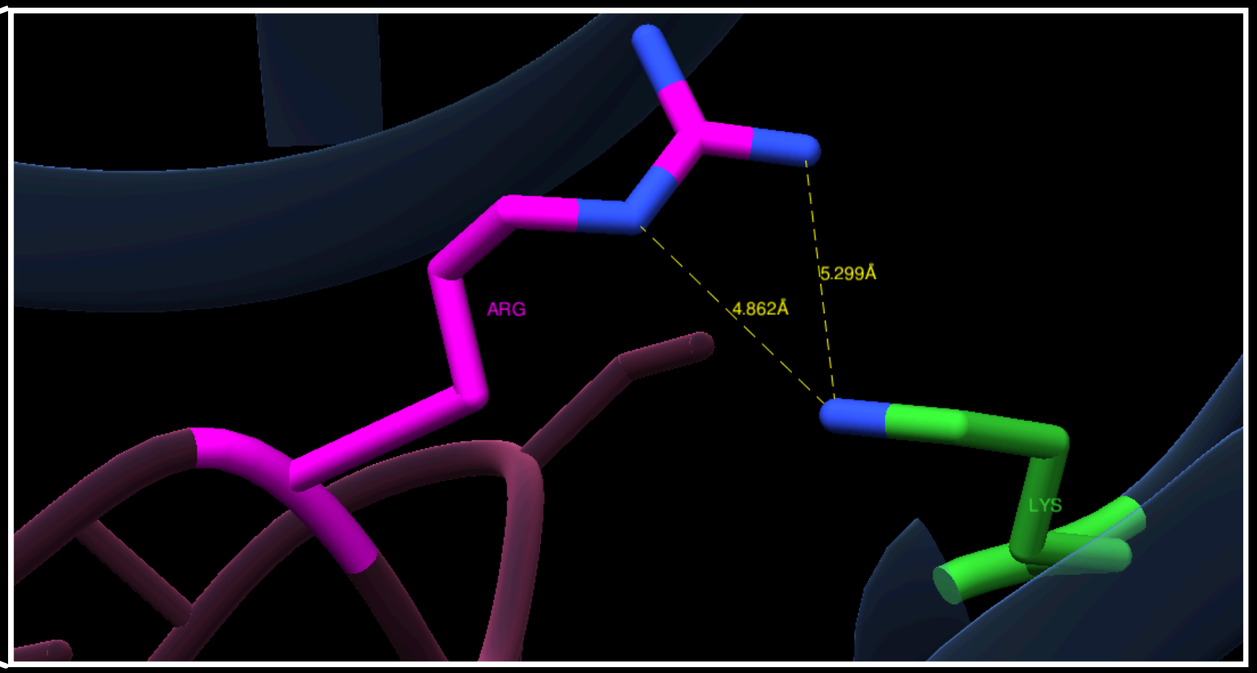
INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

Ribosome-Dom 1 interactions



PDB | ID: 8G5Z | *Homo sapiens*

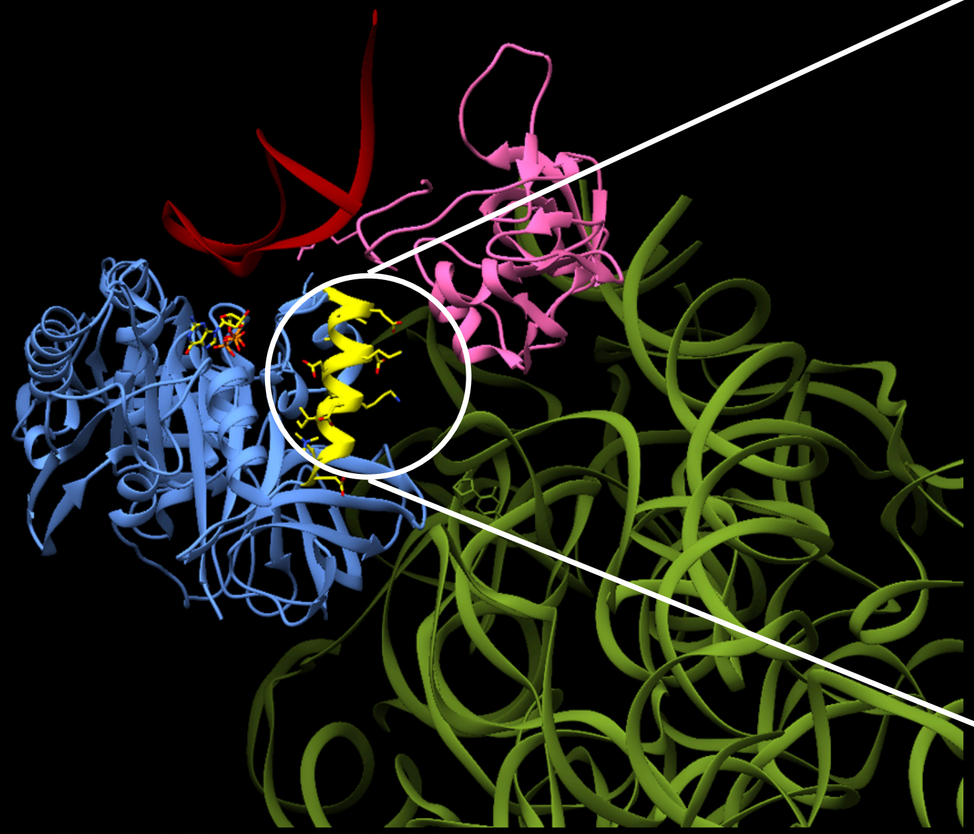
2.64 Å



Arg6 (uL14) - Lys51 (eEF1A)

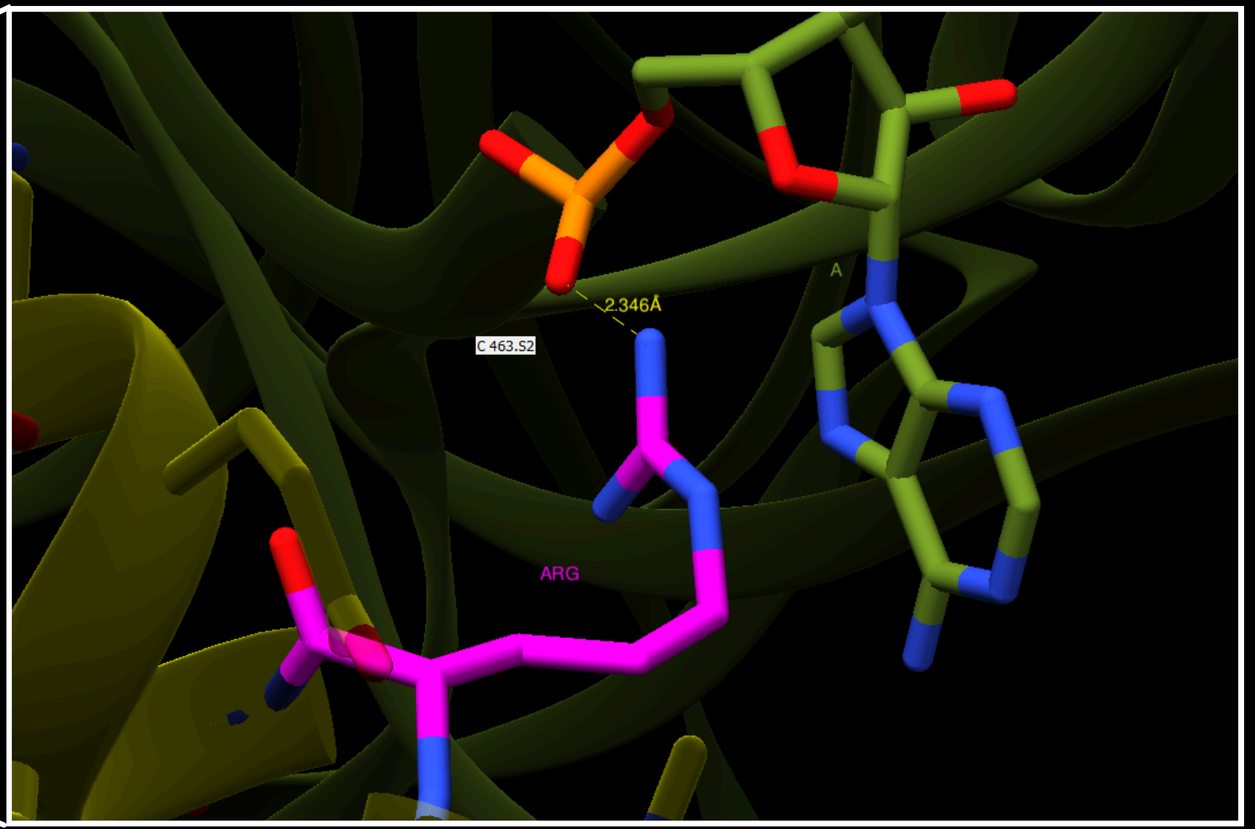
INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome

Ribosome-Dom 3 interactions



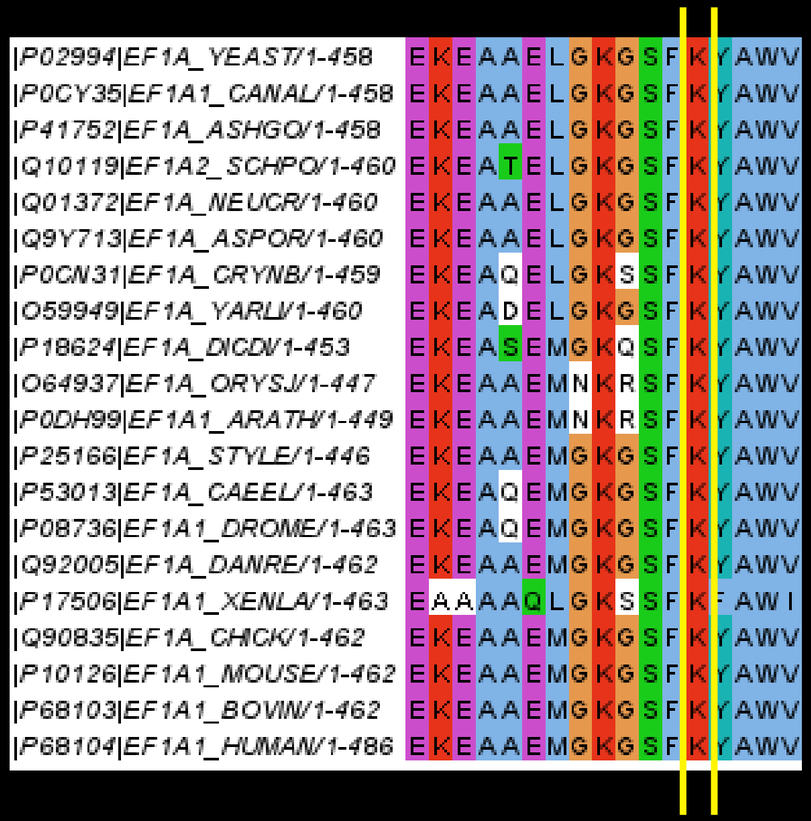
PDB | ID: 8G5Z | *Homo sapiens*

2.9 Å

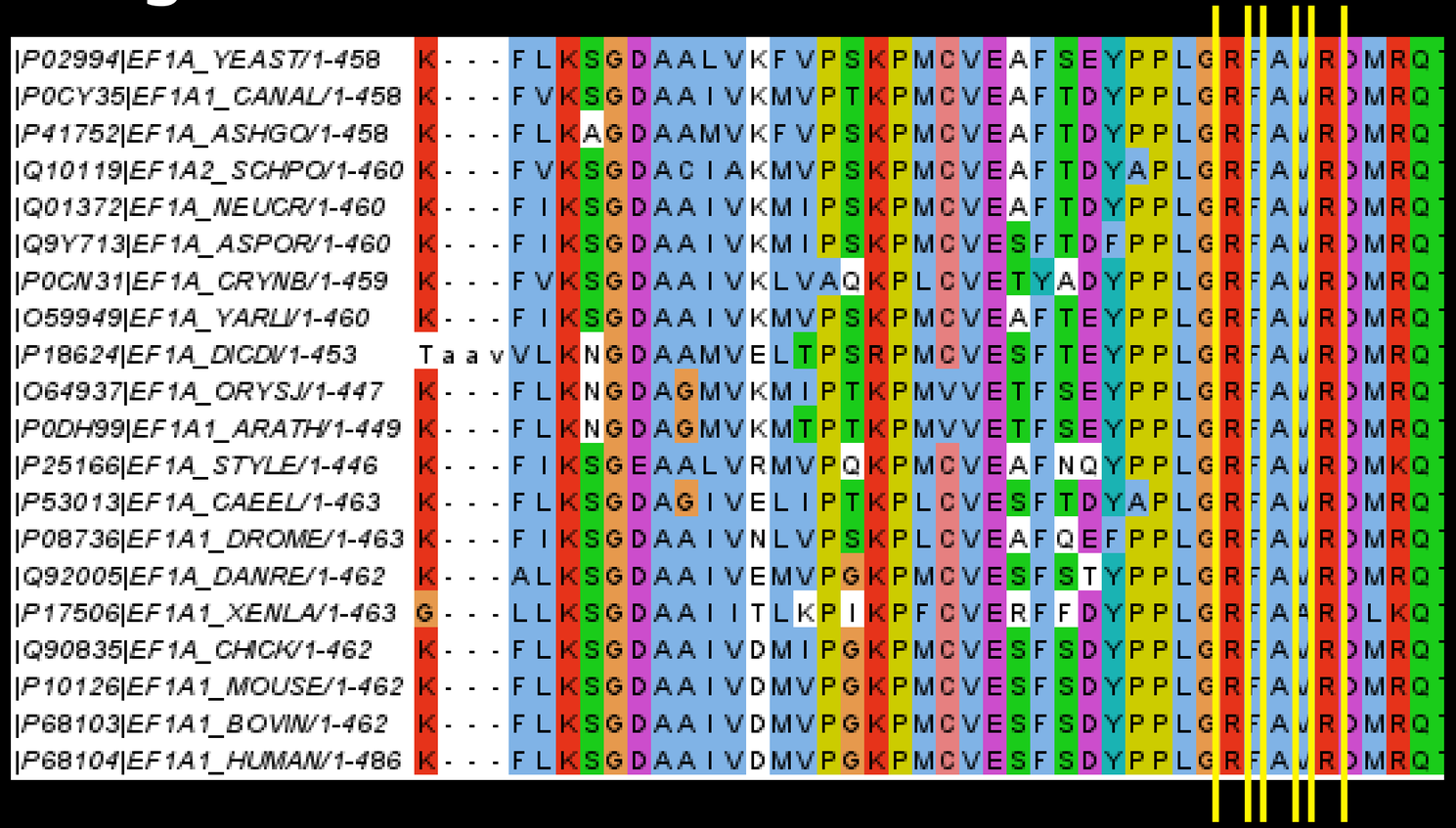


Arg37 (eEF1A) - A464 (h14)

INTERMOLECULAR INTERACTIONS:
eEF1A - GTP - Mg2+ - tRNA - Ribosome



Lys51 (eEF1A)



Arg423 + **Ala425** + **Arg427**
(eEF1A)

LIBERATION FASE:

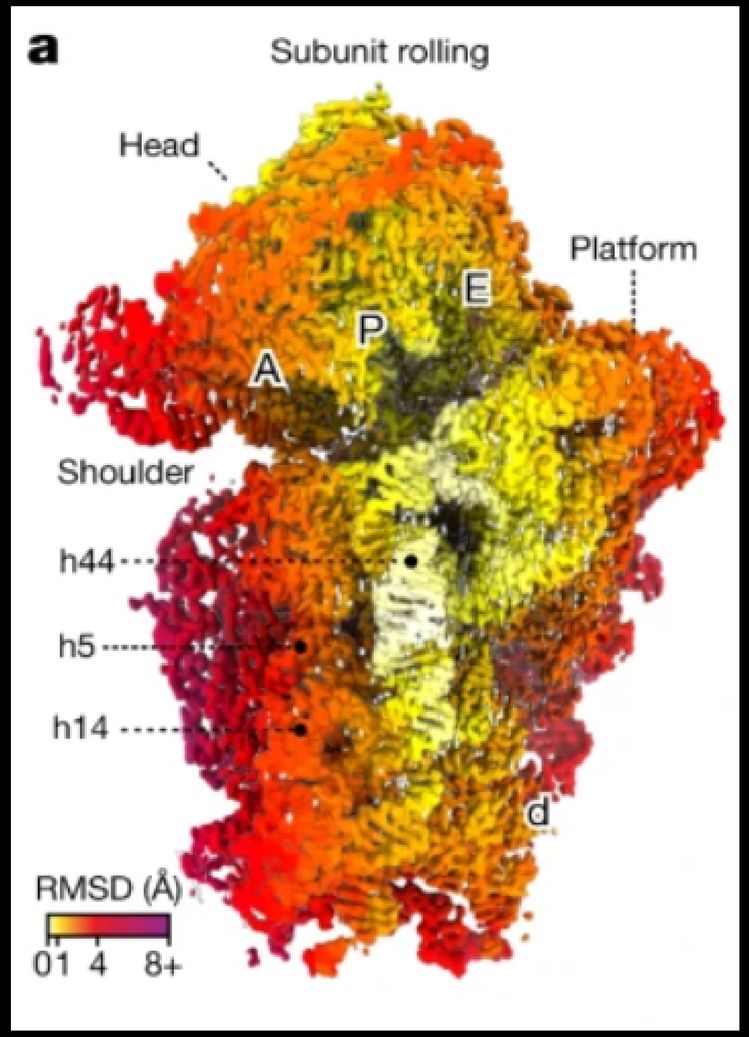


Fig 4.A Holm et al.

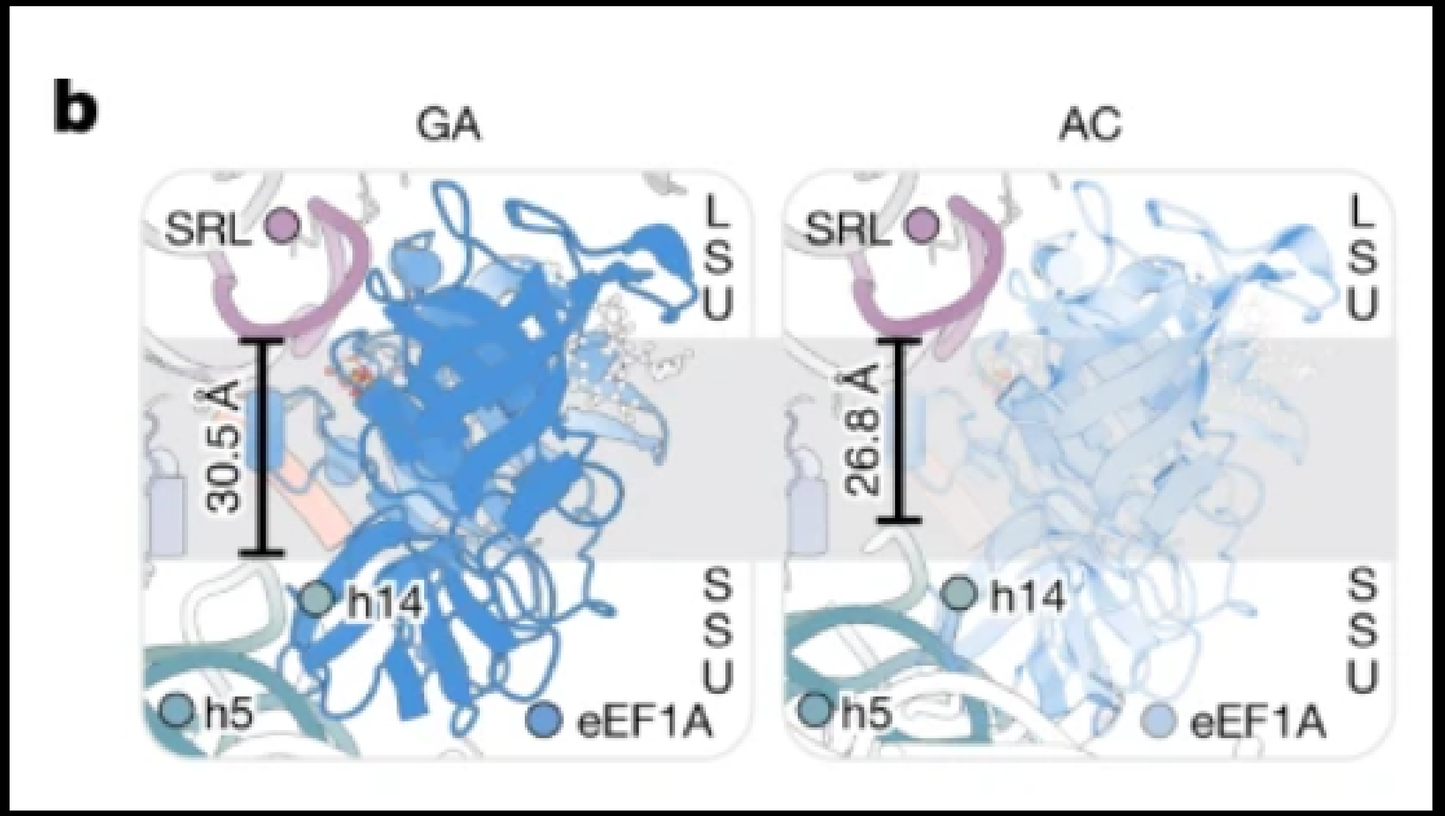
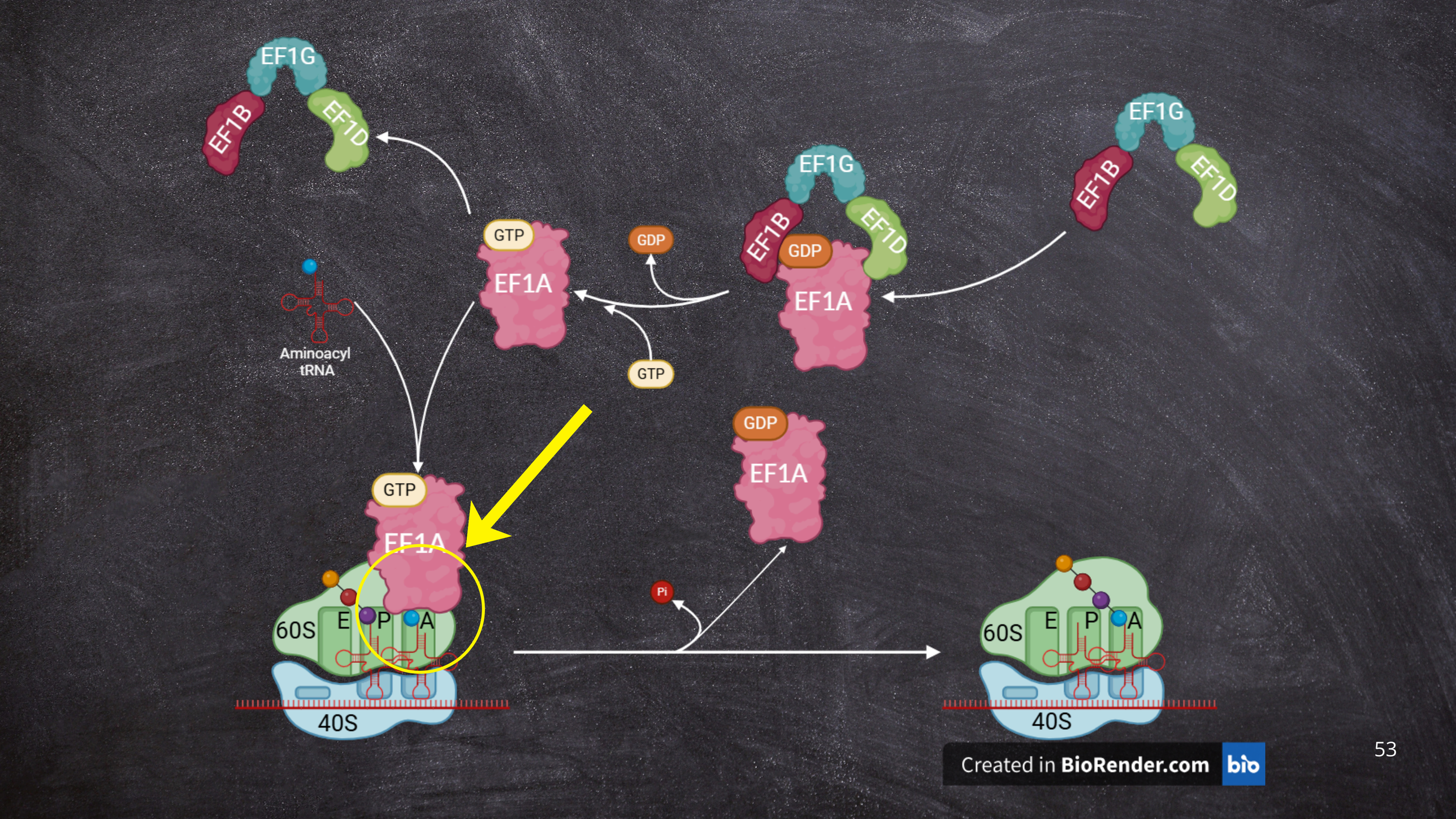
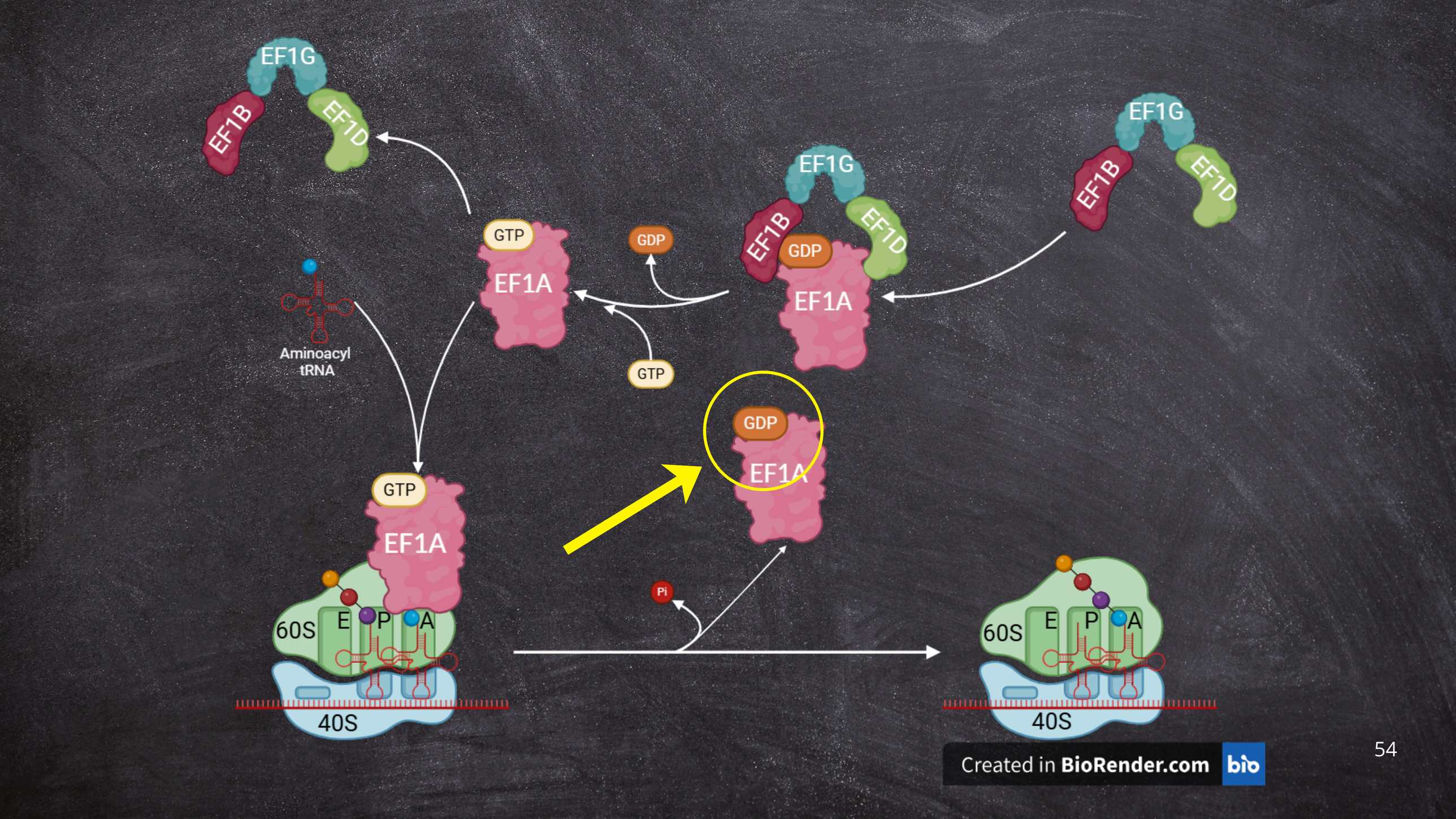


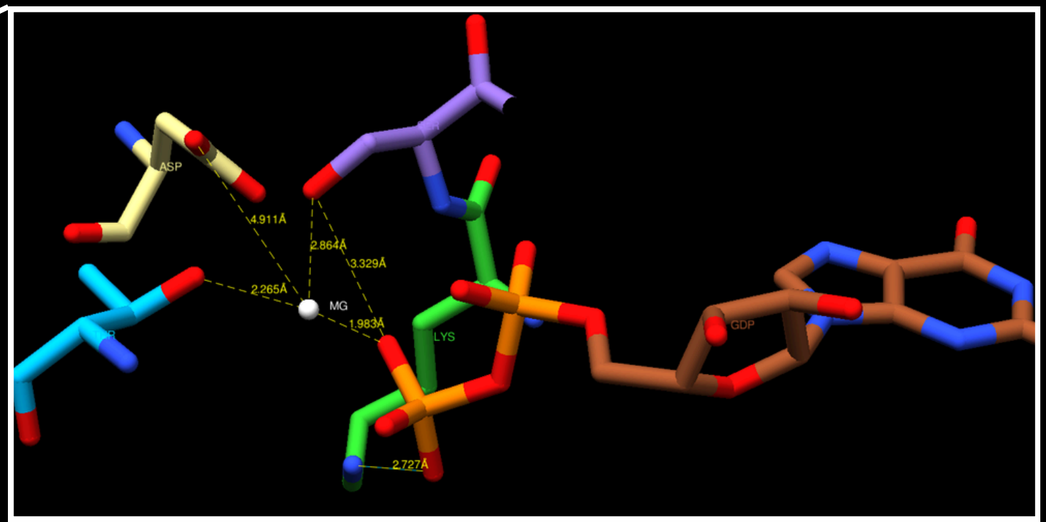
Fig 4.B Holm et al.

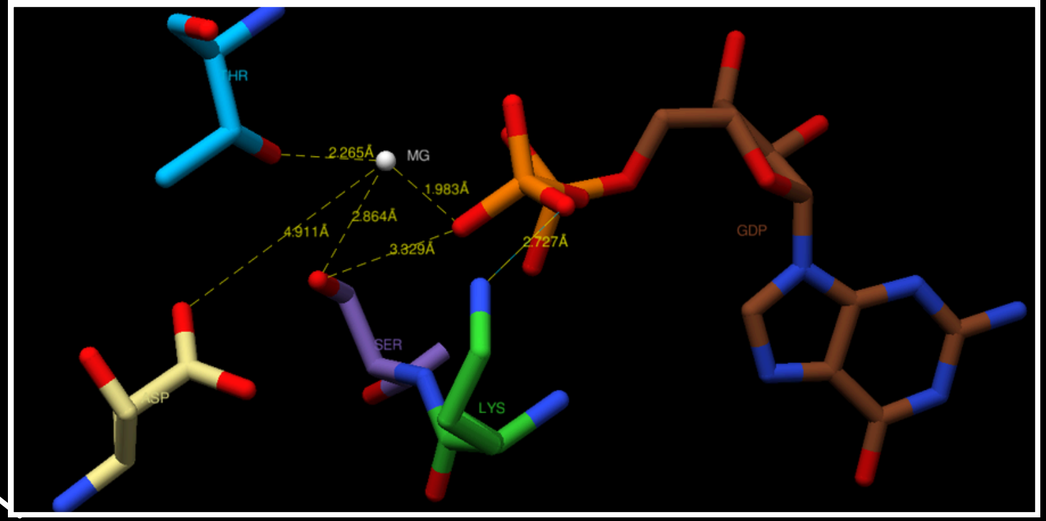

EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
P
A
40S
Created in BioRender.com
bio


EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
Pi
60S
E
P
A
40S
Created in BioRender.com
bio

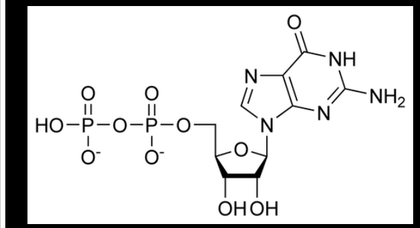
INTERMOLECULAR INTERACTIONS:
eEF1A - GDP - Mg2+







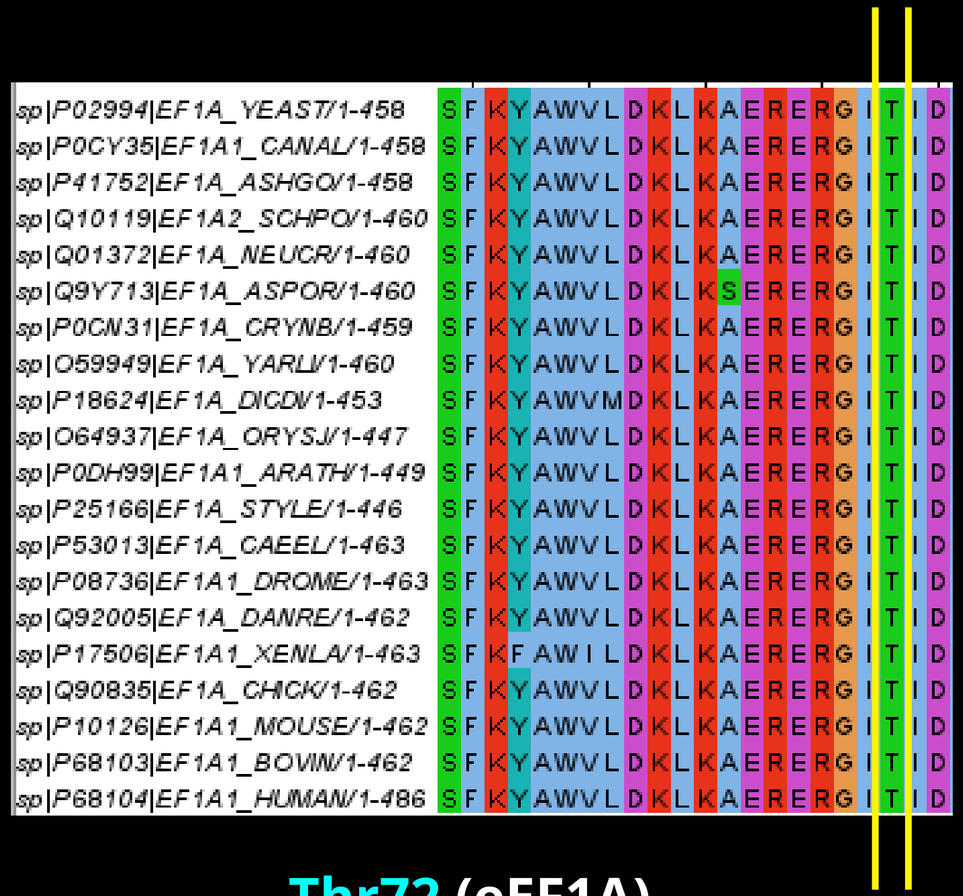
β -fosfate (GDP)
- **Ser21** (eEF1A)
- **Lys20** (eEF1A)
- **Asp91** (eEF1A)
- **Thr72** (eEF1A)



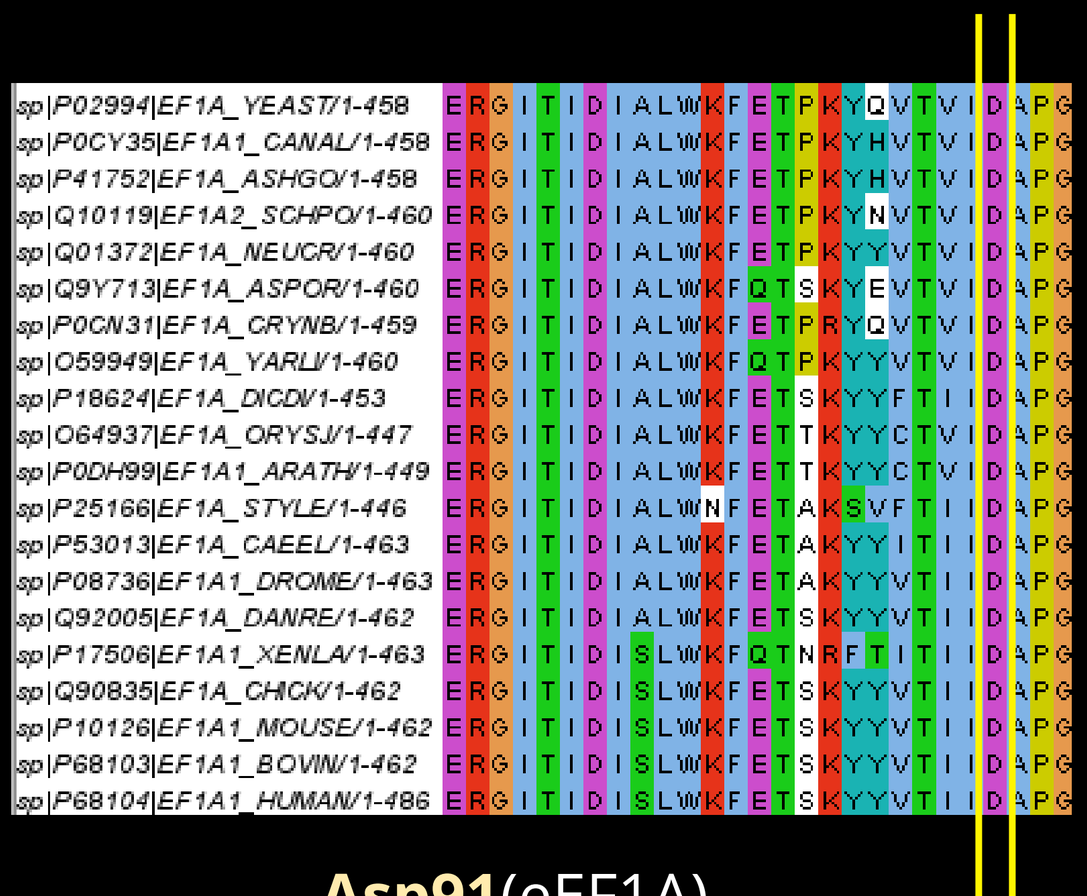
PDB | ID: 5LZS | *Oryctolagus cuniculus*

3.31Å

INTERMOLECULAR INTERACTIONS:
eEF1A - GDP - Mg2+



Thr72 (eEF1A)

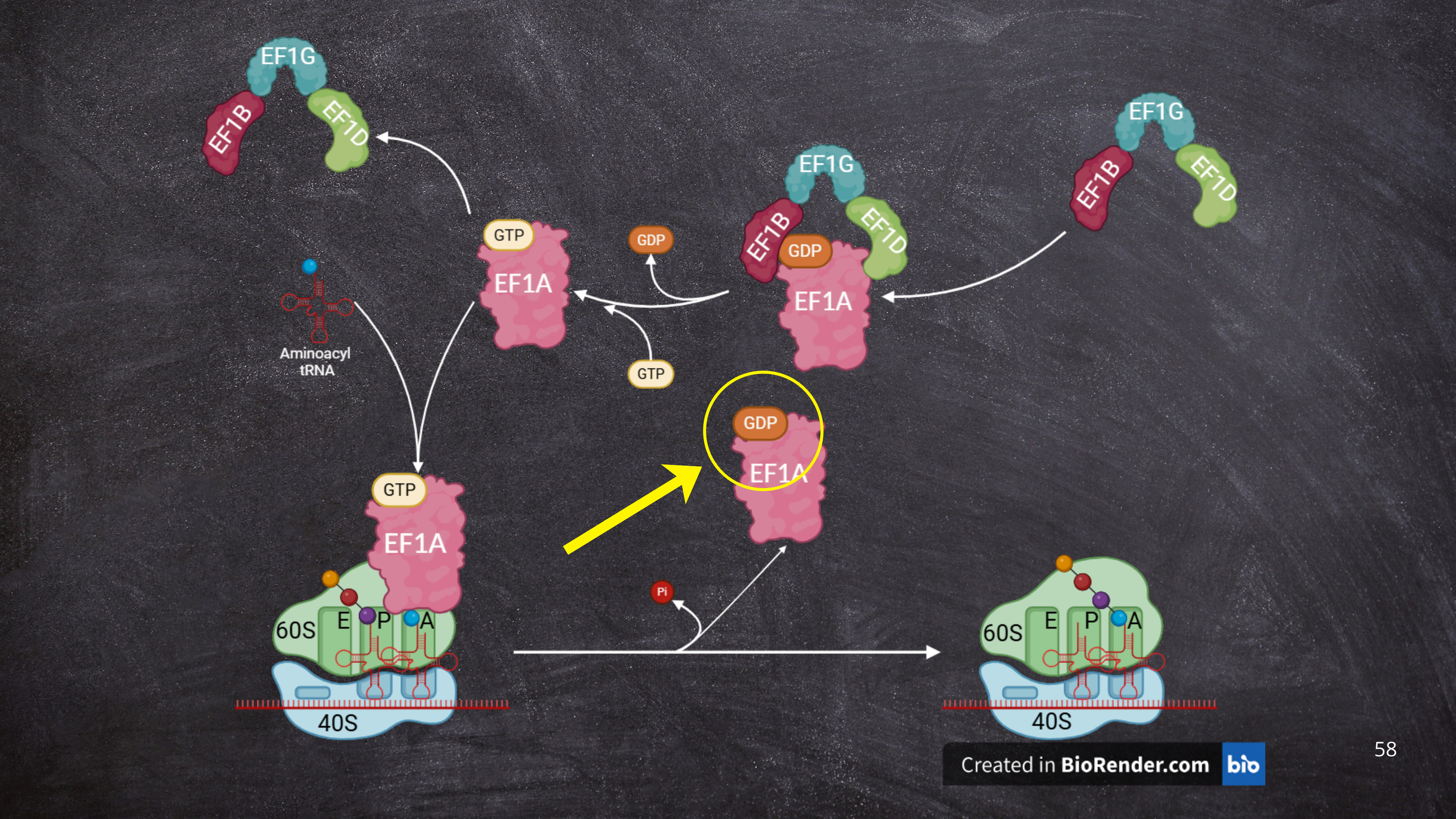


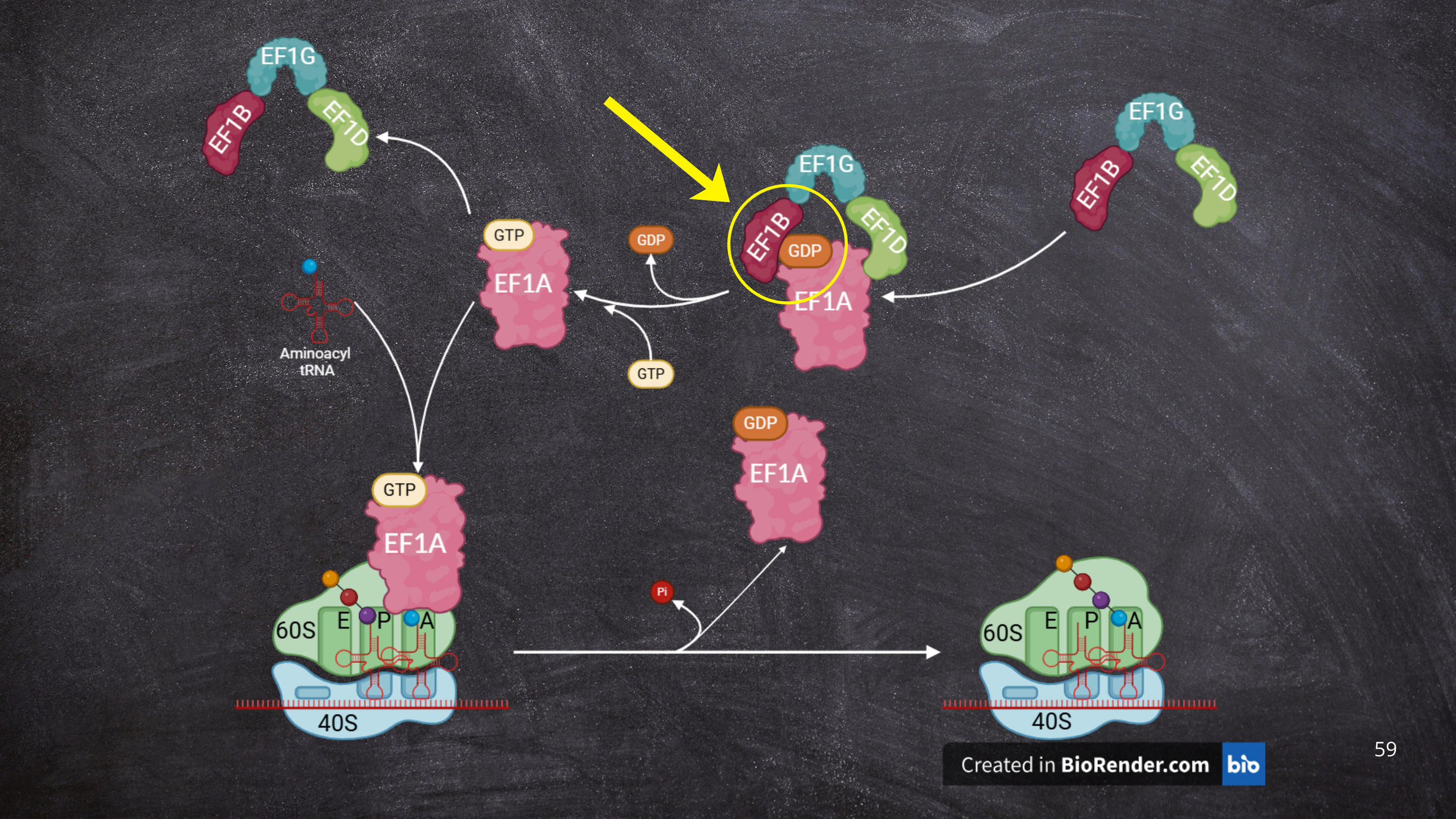
Asp91(eEF1A)

STAMP: eEF1A: eEF1Bα - GDP vs eEF1A - GTP



RMSD = 6.296 Å

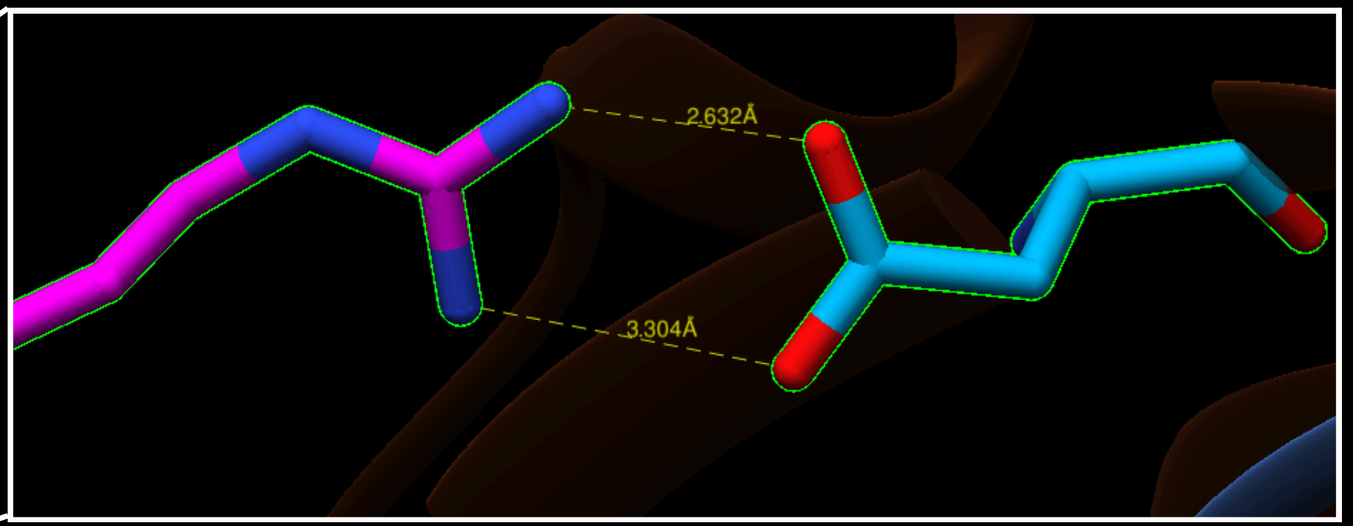

EF1G
EF1B
EF1D
GTP
EF1A
GDP
Aminoacyl tRNA
GTP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
P
A
40S
Created in BioRender.com
bio


EF1G
EF1B
EF1D
GTP
EF1A
GDP
EF1G
EF1B
GDP
EF1D
EF1A
EF1G
EF1B
EF1D
Aminoacyl
tRNA
GTP
GDP
EF1A
GTP
EF1A
Pi
60S
E
P
A
40S
60S
E
P
A
40S
Created in BioRender.com
bio

INTERMOLECULAR INTERACTIONS:
eEF1A:eEF1Bα - GDP - Mg2+

Initial anchor



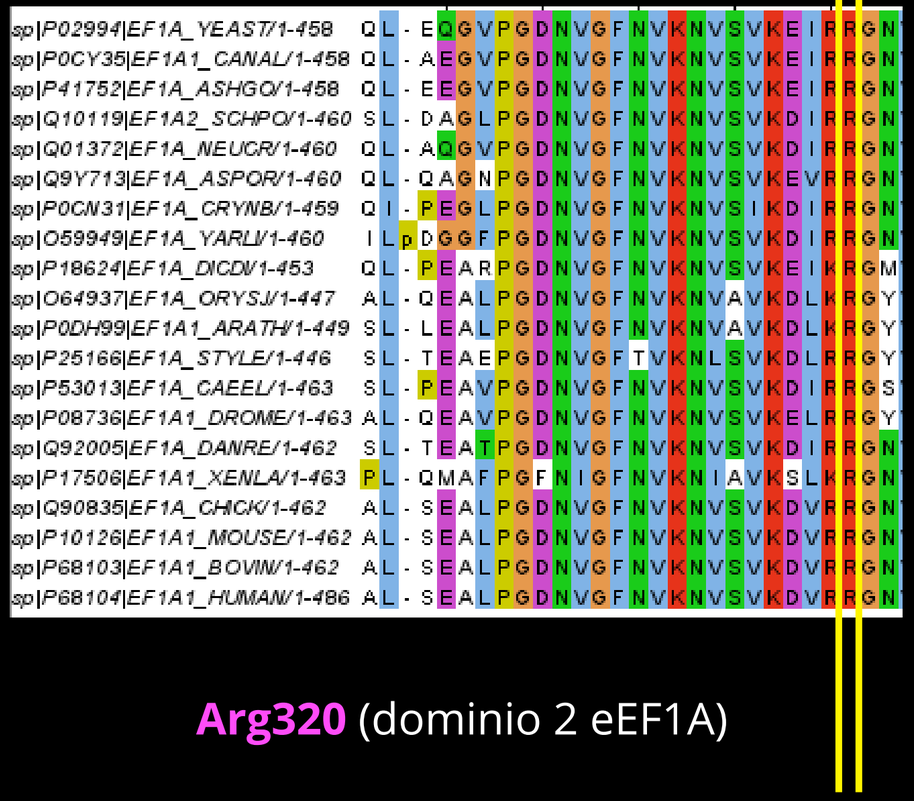


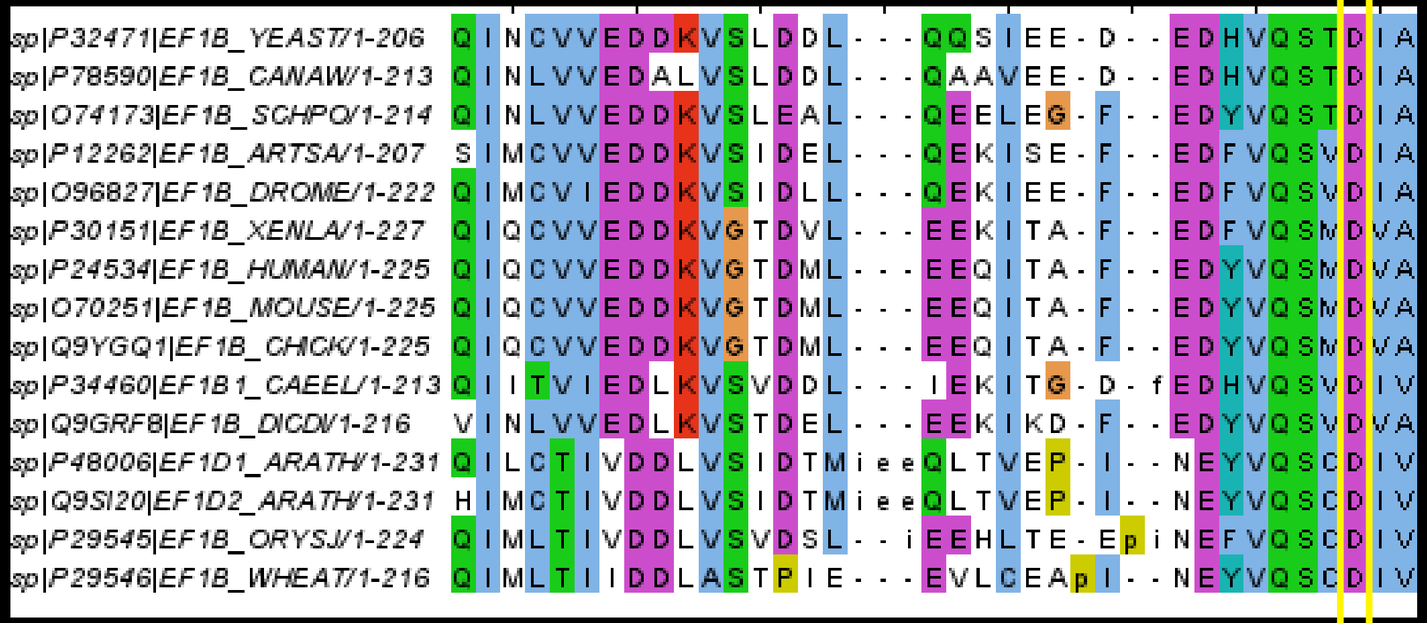
Arg320 (dominio 2 eEF1A) - **Asp-199** (eEF1Bα)

PDB | ID: 2B7B | *Saccharomyces cerevisiae*

2.6 Å

INTERMOLECULAR INTERACTIONS:
*e*EF1A:*e*EF1Bα - GDP - Mg2+



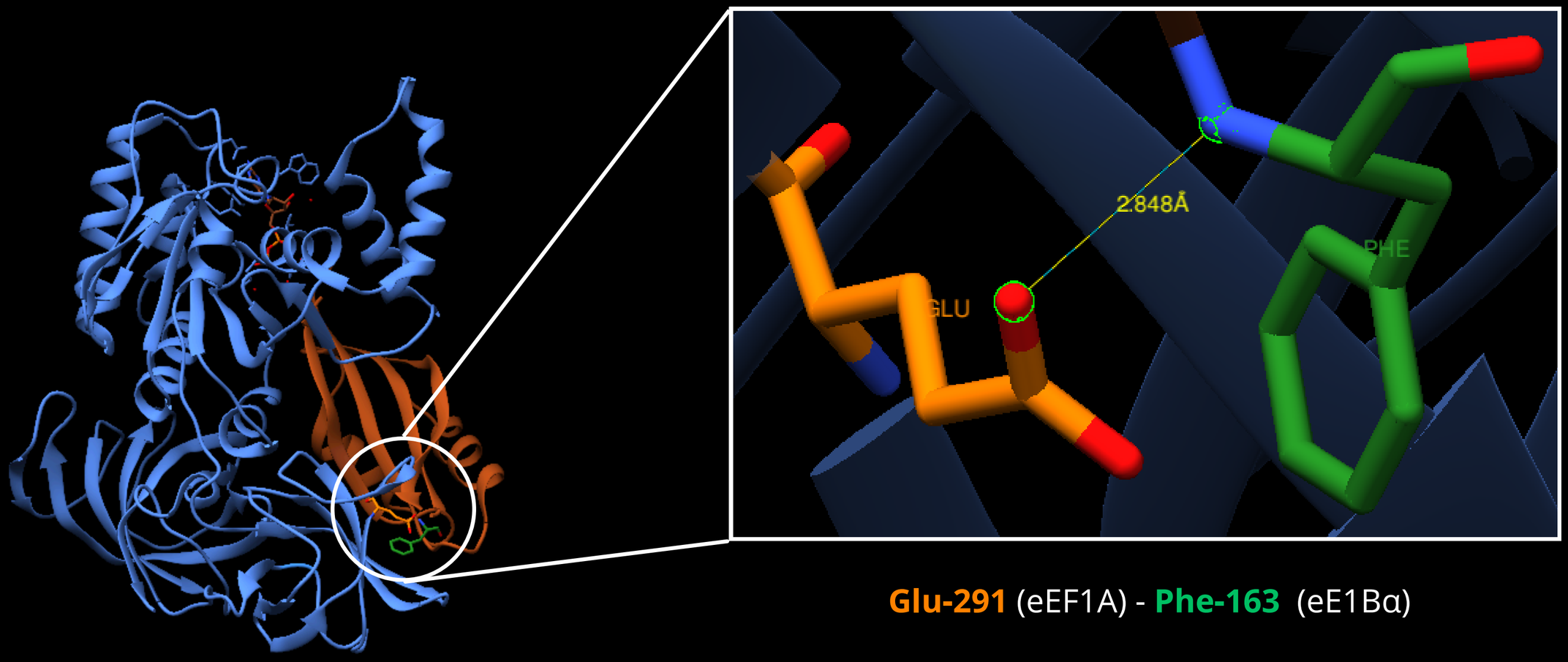


Arg320 (dominio 2 eEF1A)

Asp-199 (eEF1Bα)

INTERMOLECULAR INTERACTIONS:
eEF1A:eEF1Bα - GDP - Mg2+

Region stabilization

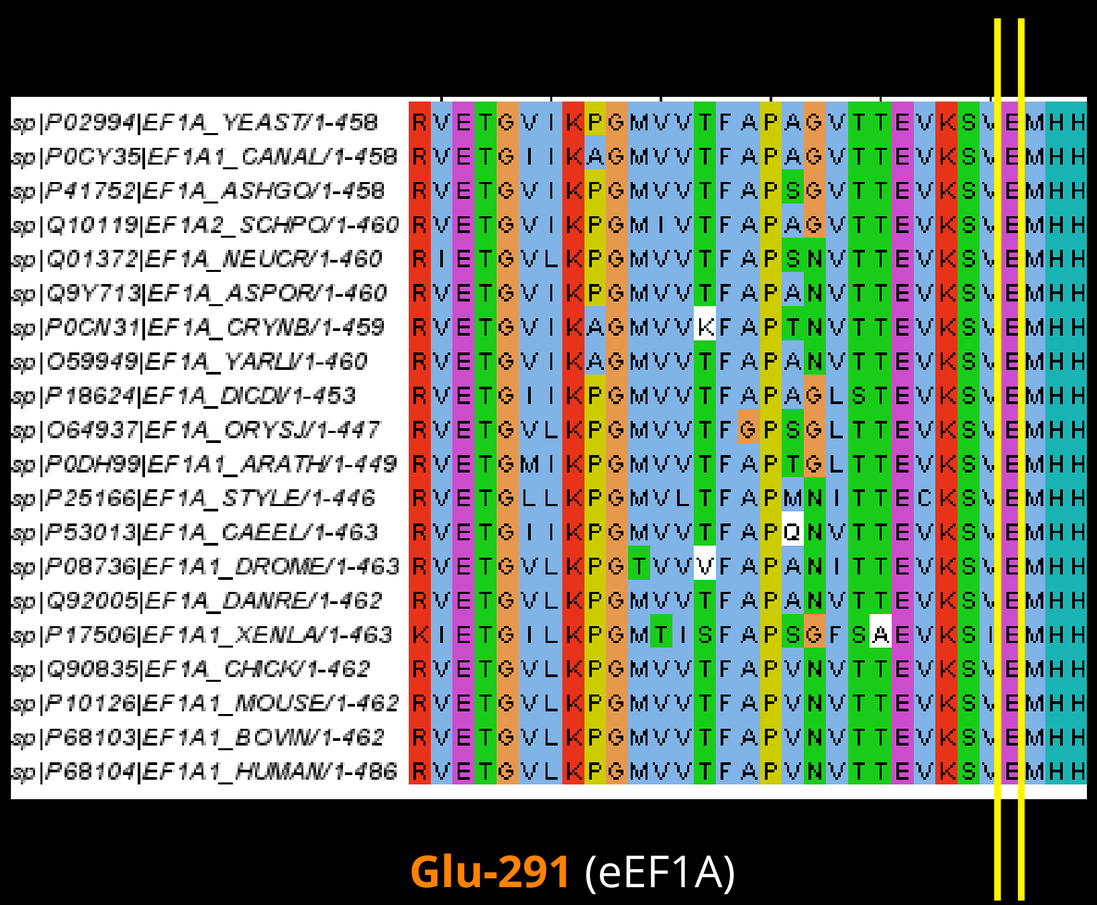


Glu-291 (eEF1A) - **Phe-163** (eE1Bα)

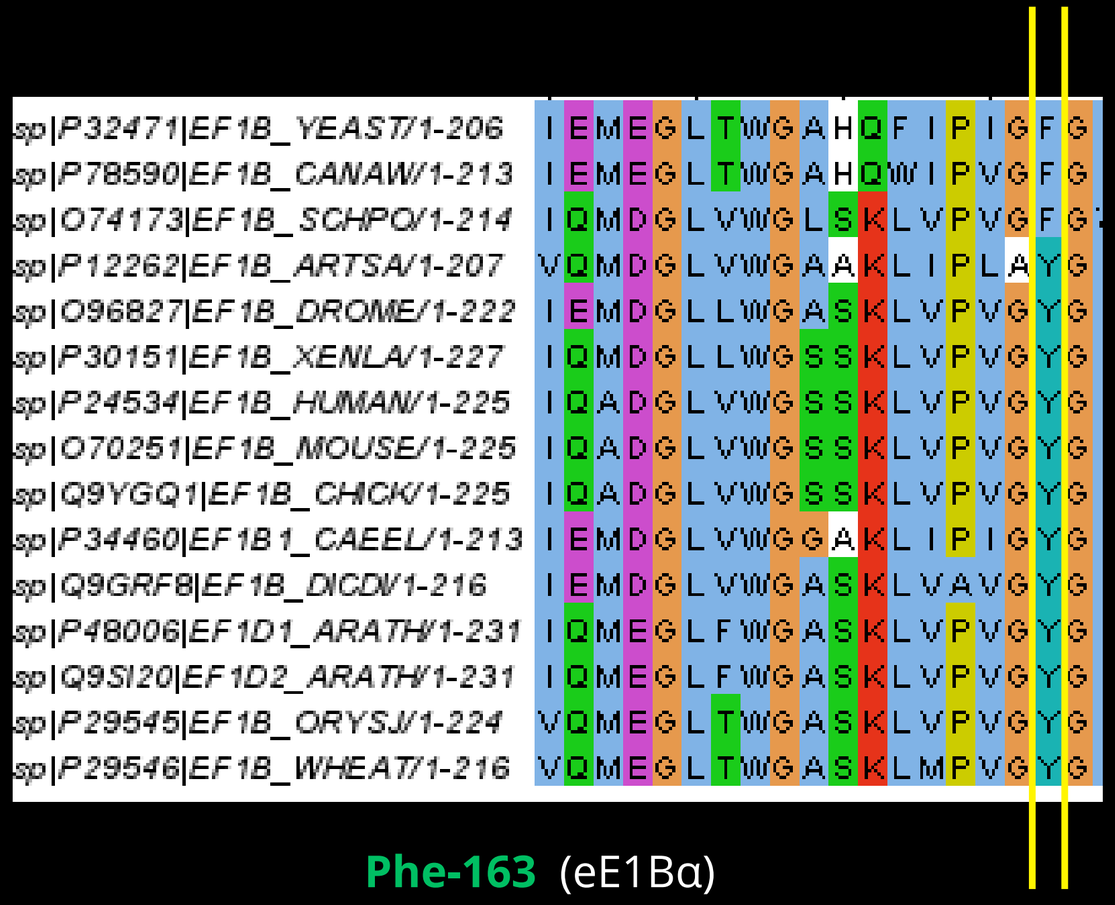
PDB | ID: 2B7B | *Saccharomyces cerevisiae*

2.6 Å

INTERMOLECULAR INTERACTIONS:
eEF1A:eEF1Bα - GDP - Mg2+



Glu-291 (eEF1A)

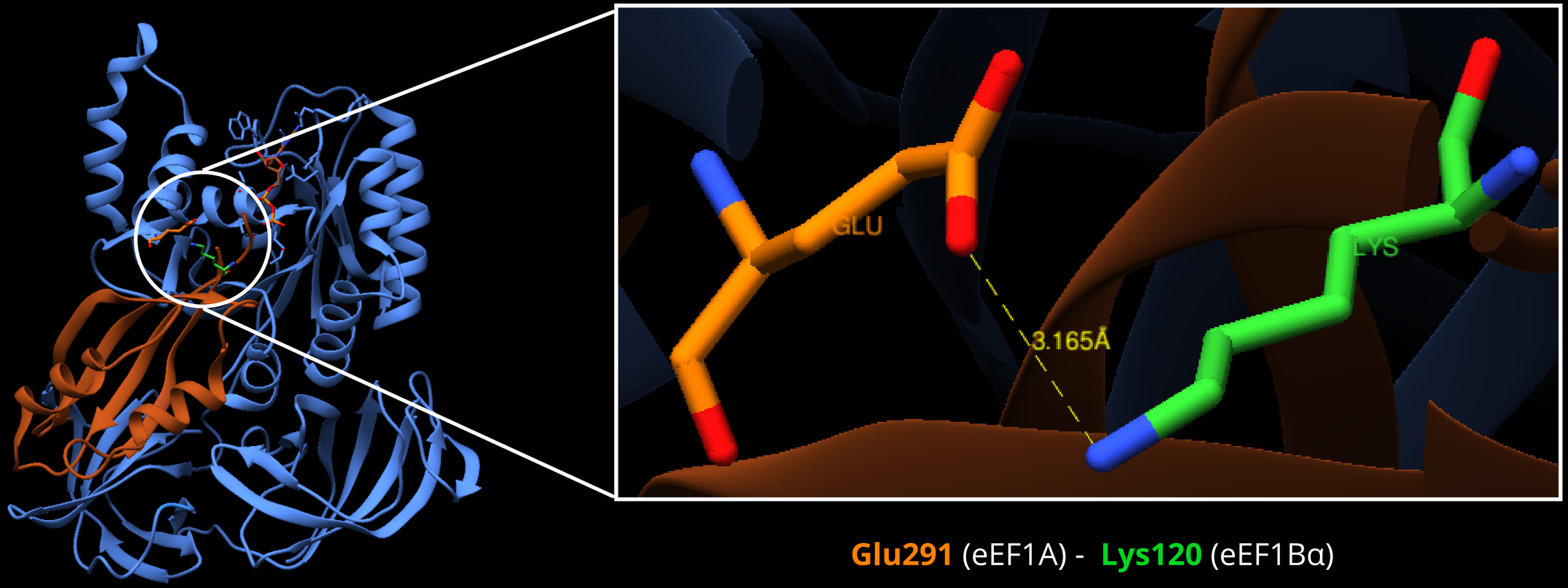


Phe-163 (eE1Bα)

INTERMOLECULAR INTERACTIONS:

eEF1A:eEF1Bα - GDP - Mg2+

Region stabilization

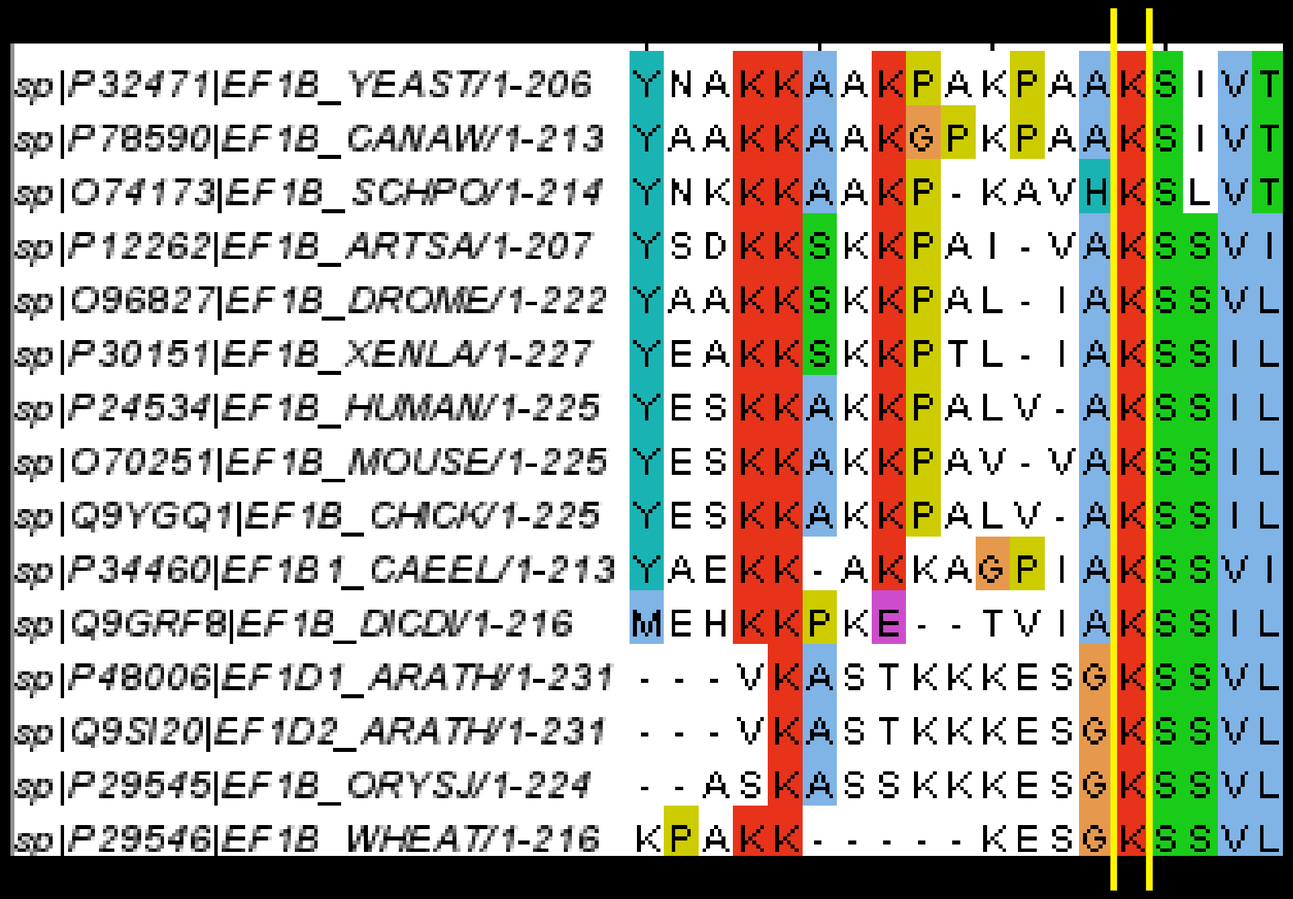


Glu291 (eEF1A) - **Lys120** (eEF1Bα)

PDB | ID: 2B7B | *Saccharomyces cerevisiae*

2.6 Å

INTERMOLECULAR INTERACTIONS:
eEF1A:eEF1Bα - GDP - Mg2+



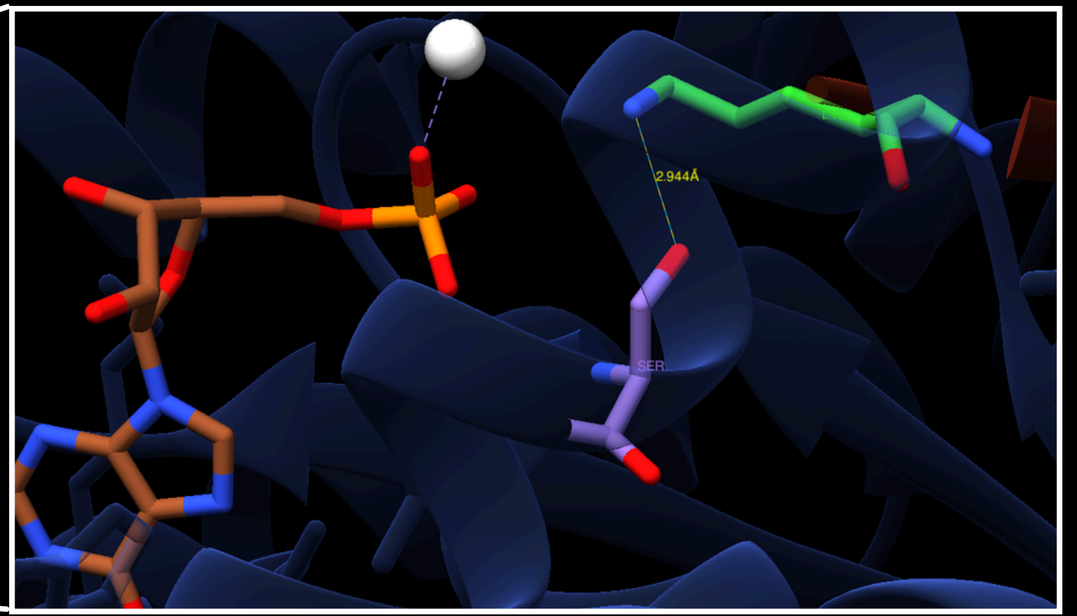
Lys120 (eEF1Bα)

INTERMOLECULAR INTERACTIONS:

eEF1A:eEF1Bα - GDP - Mg2+

Mg^{2+} displacement





α-fosfate (GDP) ← **Lys205** (eEF1Bα) - **Ser21** (eEF1A)



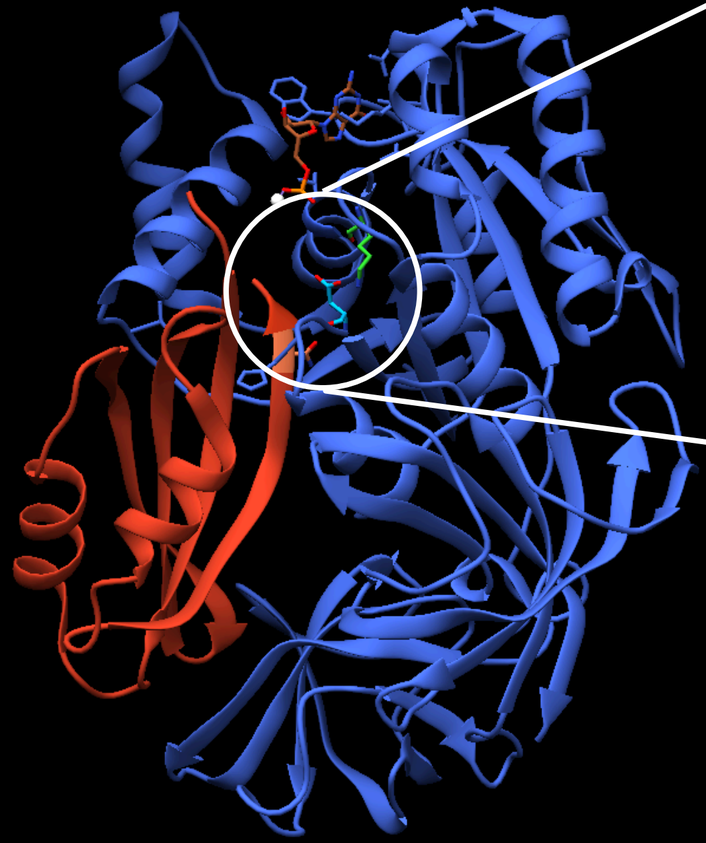
PDB | ID: 1IJF | *Saccharomyces cerevisiae*

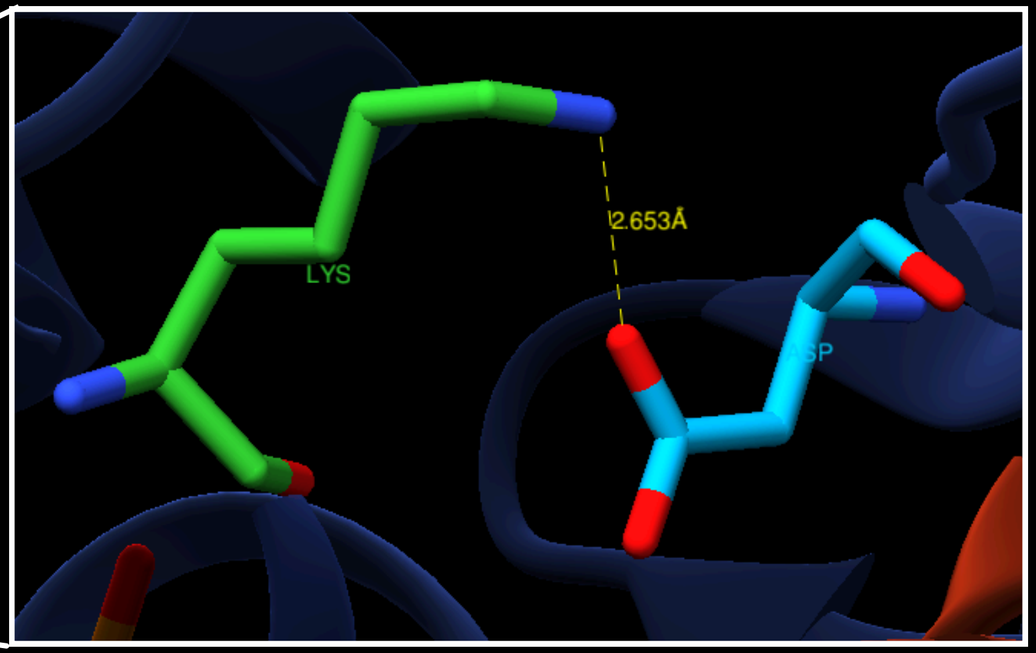
3 Å

INTERMOLECULAR INTERACTIONS:

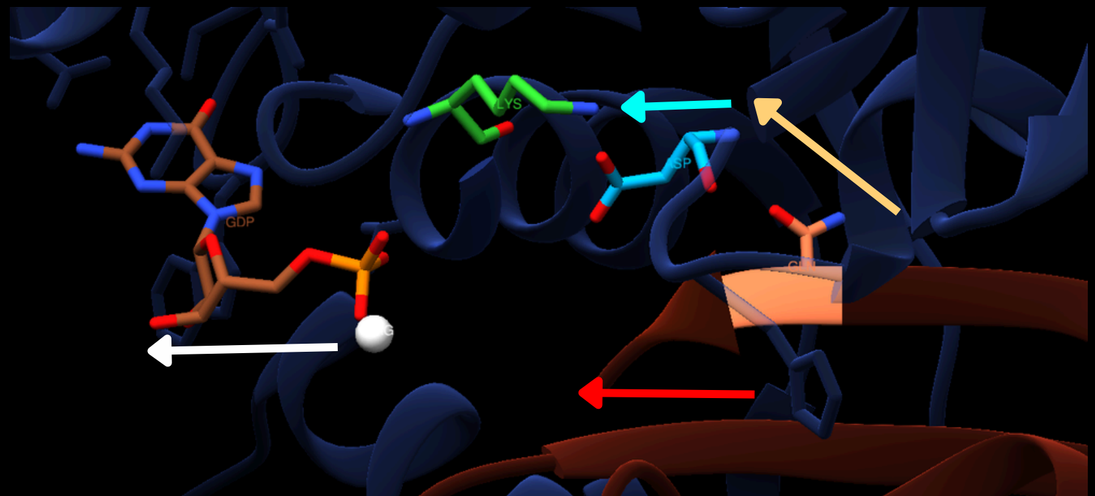
eEF1A:eEF1Bα - GDP - Mg2+

Mg^{2+} displacement





(Lys-20 - Asp91) eEF1A ← **Gln204** (eEF1Bα)

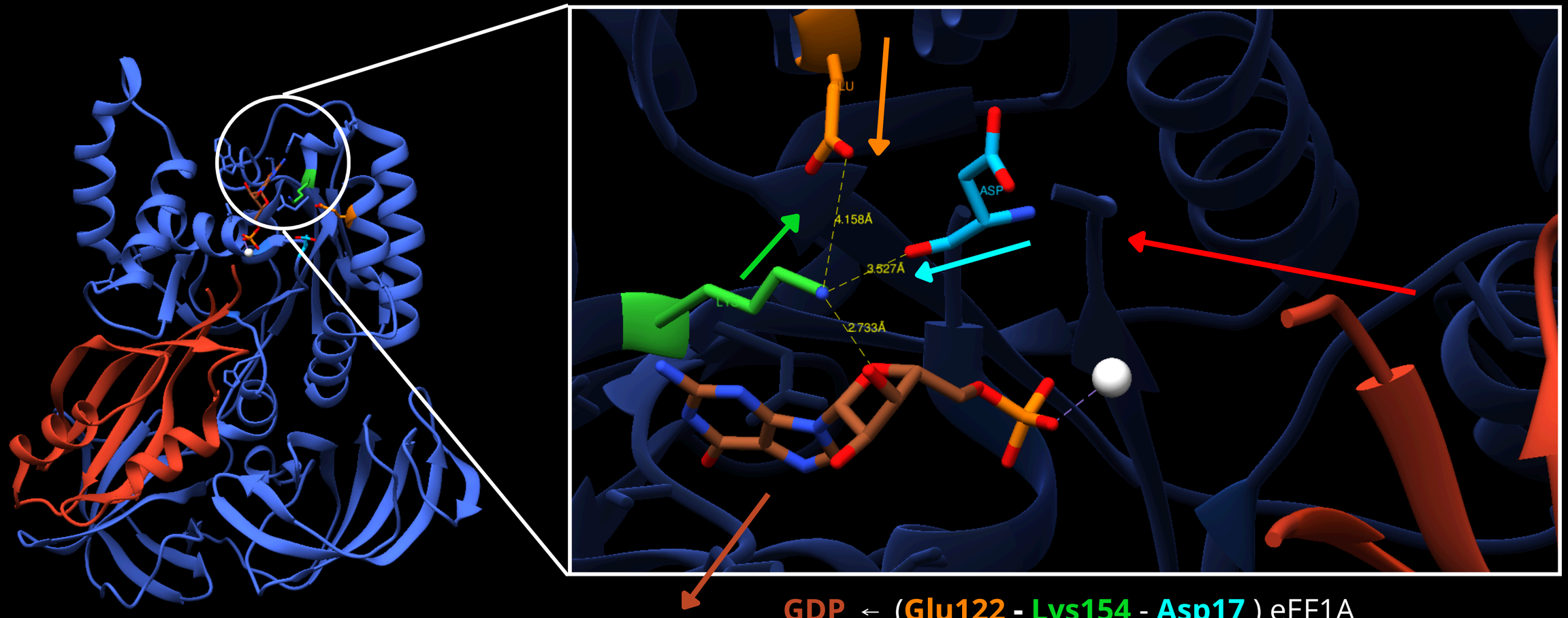


PDB | ID: 1IJF | *Saccharomyces cerevisiae*

3 Å

INTERMOLECULAR INTERACTIONS:
eEF1A:eEF1Bα - GDP - Mg2+

Reorganization of the P-loop

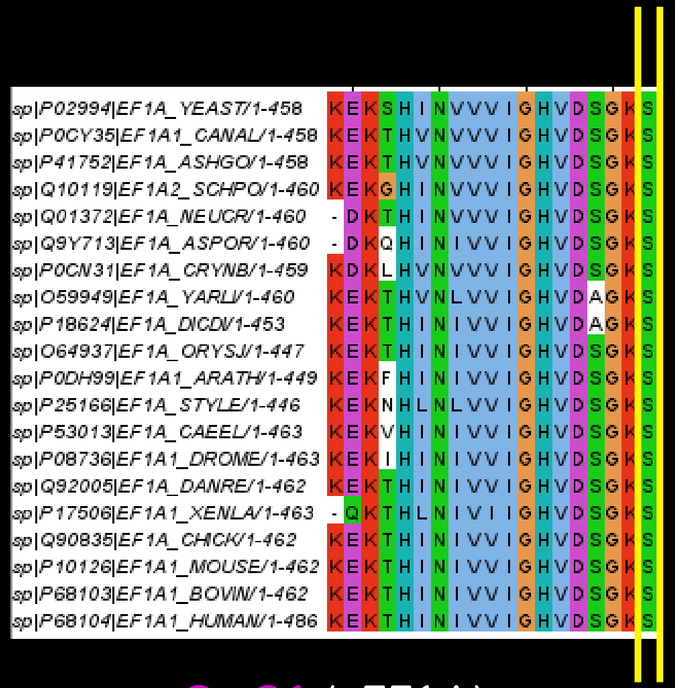


GDP ← (Glu122 - Lys154 - Asp17) eEF1A

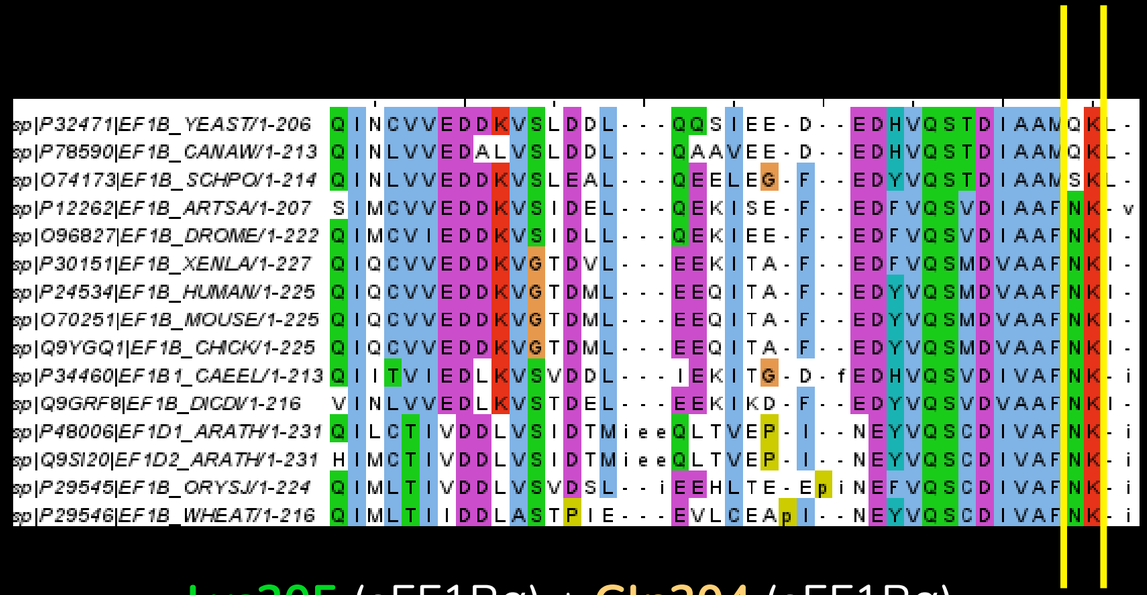
PDB | ID: 1IJF | *Saccharomyces cerevisiae*

3 Å

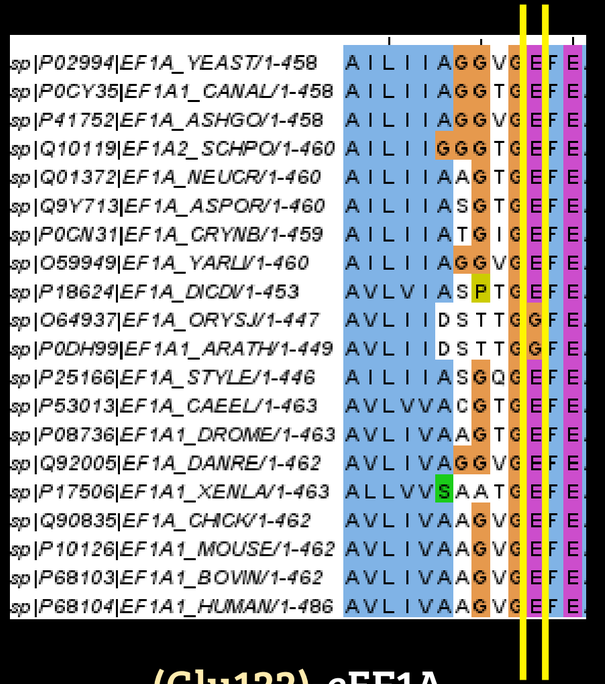
INTERMOLECULAR INTERACTIONS:
eEF1A:eEF1Bα - GDP - Mg2+



Ser21 (eEF1A)



Lys205 (eEF1Bα) + **Gln204** (eEF1Bα)



(Glu122)-eEF1A

TAKE HOME MESSAGE

The eukaryotic elongation factor eEF1A operates through a sophisticated mechanical and allosteric network defined by:

-An active dismantling of the nucleotide site by eEF1Bα for recycling

-A high-fidelity "rolling" mechanism in the ribosome that discriminates between correct and incorrect tRNAs

-A system that ensures high efficiency by preventing the loss of translational components to the cytoplasm



THANK YOU!

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PEM QUESTIONS: correct awnsers are underlined

1. What is the primary function of the eEF1A protein in the eukaryotic elongation cycle?

A) Catalyzing peptide bond formation at the P-site.
B) Recycling GDP to GTP through its own intrinsic activity.
C) Delivering aminoacyl-tRNA (aa-tRNA) to the ribosomal A-site.
D) Acting as a termination factor to release the polypeptide chain.
E) Translocating the mRNA exactly three nucleotides forward.

2. During nucleotide exchange, what specific interaction occurs in Switch 2 following the insertion of eEF1Bα?

A) Switch 2 is stabilized by a water molecule binding to Mg^{2+}.
B) Asp-91a is displaced and forms a salt bridge with Lys-20a of the P-loop.
C) Helix B moves to seal the nucleotide-binding pocket.
D) Switch 2 interacts directly with the adenine base of ATP.
E) Lys-205b forms a covalent bond with the γ-phosphate.

PEM QUESTIONS: correct awnsers are underlined

3. Which domain(s) interact with the Sarcin/Ricin Loop “SRP” of the ribosome?

A) Domains 1 and 3
B) Domains 2 and 3
C) Domain 2
D) Domains 1, 2, and 3
E) Domains 1 and 2

4. The "NKMD" motif in eEF1A is a specific set of amino acids that recognizes which part of the nucleotide?

A) The adenine base
B) The guanine base
C) The phosphate tail only
D) The water molecules
E) The ribosome backbone

PEM QUESTIONS: correct awnsers are underlined

5. Which structural element of eEF1A helps coordinate the decoding process?
A) The P-loop.
B) The *α*2 helix, which interacts with intersubunit bridge B8.
C) A and B are correct.
D) The *β*-strands of the Domain 2 barrel.
E) All above are correct .

6. What phenomenon explains the competition between eEF1Ba and tRNA?

A) pH changes
B) Interaction with ribosomes
C) Overlap of their binding sites on eEF1A
D) Degradation of tRNA
E) None of the above is correct

PEM QUESTIONS: correct awnsers are underlined

7. What is the role of subunit "rolling" in the eukaryotic ribosome?

A) It is a rotary movement that permanently expels eEF1A.
B) It is the process by which the ribosome detaches from the ER membrane.
C) A and B are true.
D) It serves to move the A-site tRNA to the E-site without passing through the P-site.
E) None of the above is correct.

8. The competition for Domain 2 is biologically significant because it ensures that:

A) eEF1Bα only leaves eEF1A when a new aa-tRNA is ready to be loaded.
B) GTP is never used by the elongation factor.
C) The ribosome can only bind one tRNA at a time.
D) The G-domain is always in an inactive GDP state.
E) Amino acids are only attached to the 5’ end of the tRNA.

PEM QUESTIONS: correct awnsers are underlined

9. According to structural analysis of the eEF1A:eEF1Bα complex, what is the role of Gln-204b?

A) It forms a salt bridge with the γ-phosphate of GTP.
B) It acts as a "wedge" by inserting between two antiparallel β-strands connecting Switch 1 and Switch 2.
C) It coordinates the Mg2+ion in the inactive state.
D) It stabilizes the binding of the tRNA CCA-end.
E) C and D are correct.

10. To which site of the ribosome is the aminoacyl-tRNA (aa-tRNA) delivered when it is carried by EEF1A?

A) The P site (Peptidyl site).
B) The E site (Exit site).
C) The A site (Aminoacyl site).
D) The Z site (Noncanonical site).
E) The Sarcin-Ricin Loop (SRL).