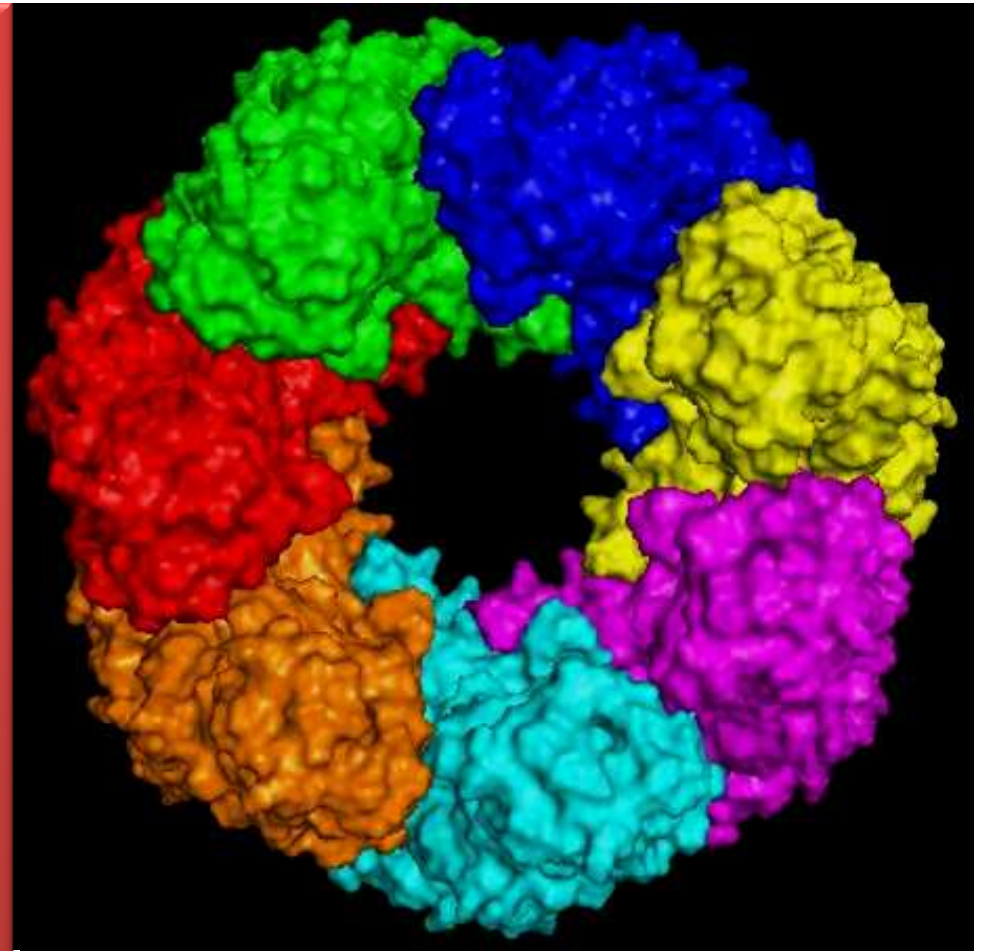


MOLECULAR CHAPERONES

Chaperonins



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Laura Luque i Rebeca Reus**

4rt del Grau en Biologia Humana
UPF

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1. Introduction

2. Molecular chaperones

3. Chaperonins

a) Group I – GroEL/GroES

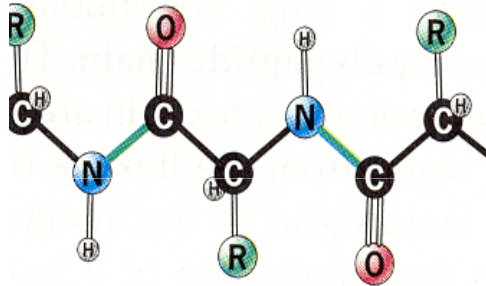
- Main characteristics
- Sequence and structure conservation
- General structure
- Interactions
- Folding cycle

b) Group II – MmCpn

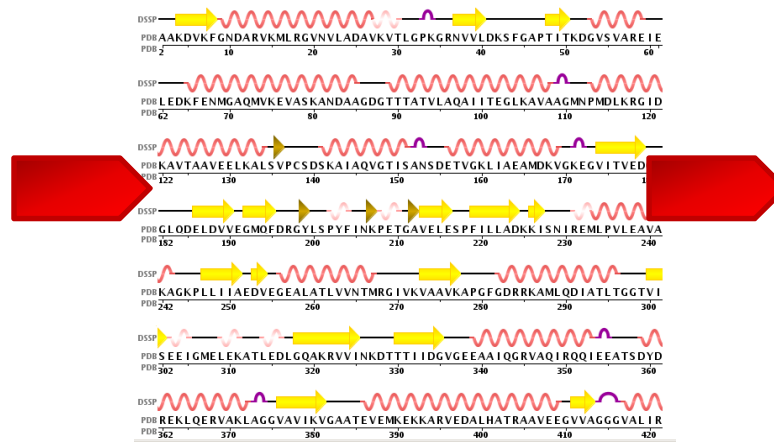
- Main characteristics
- Sequence and structure conservation
- Folding cycle

Introduction > Protein folding

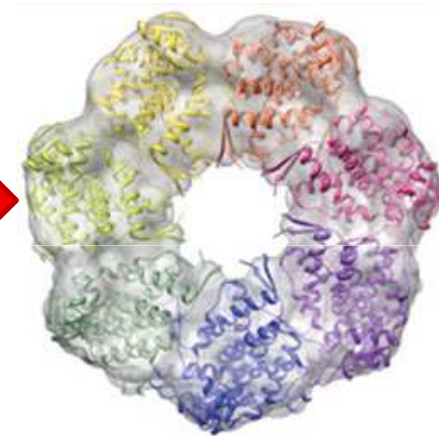
How is tertiary structure determined in a protein?



PRIMARY STRUCTURE



SECONDARY STRUCTURE



TERTIARY STRUCTURE

Introduction > Molecular chaperones

Chaperone: protein that interacts, stabilizes or helps non-native proteins to acquire their native conformation.

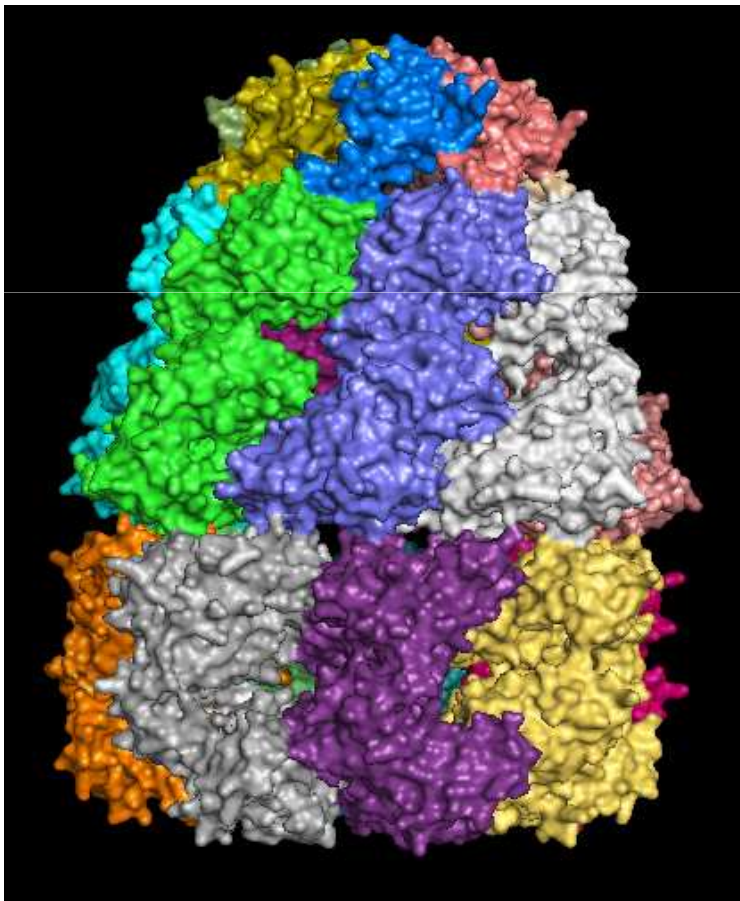


Fig1. GroEL/GroES chaperone complex (1AON)

Not present in the final functional structure.

Functions:

- *De novo* folding.
- Refolding of denatured species.
- Disruption of unspecific aggregations.

Introduction > Protein aggregation

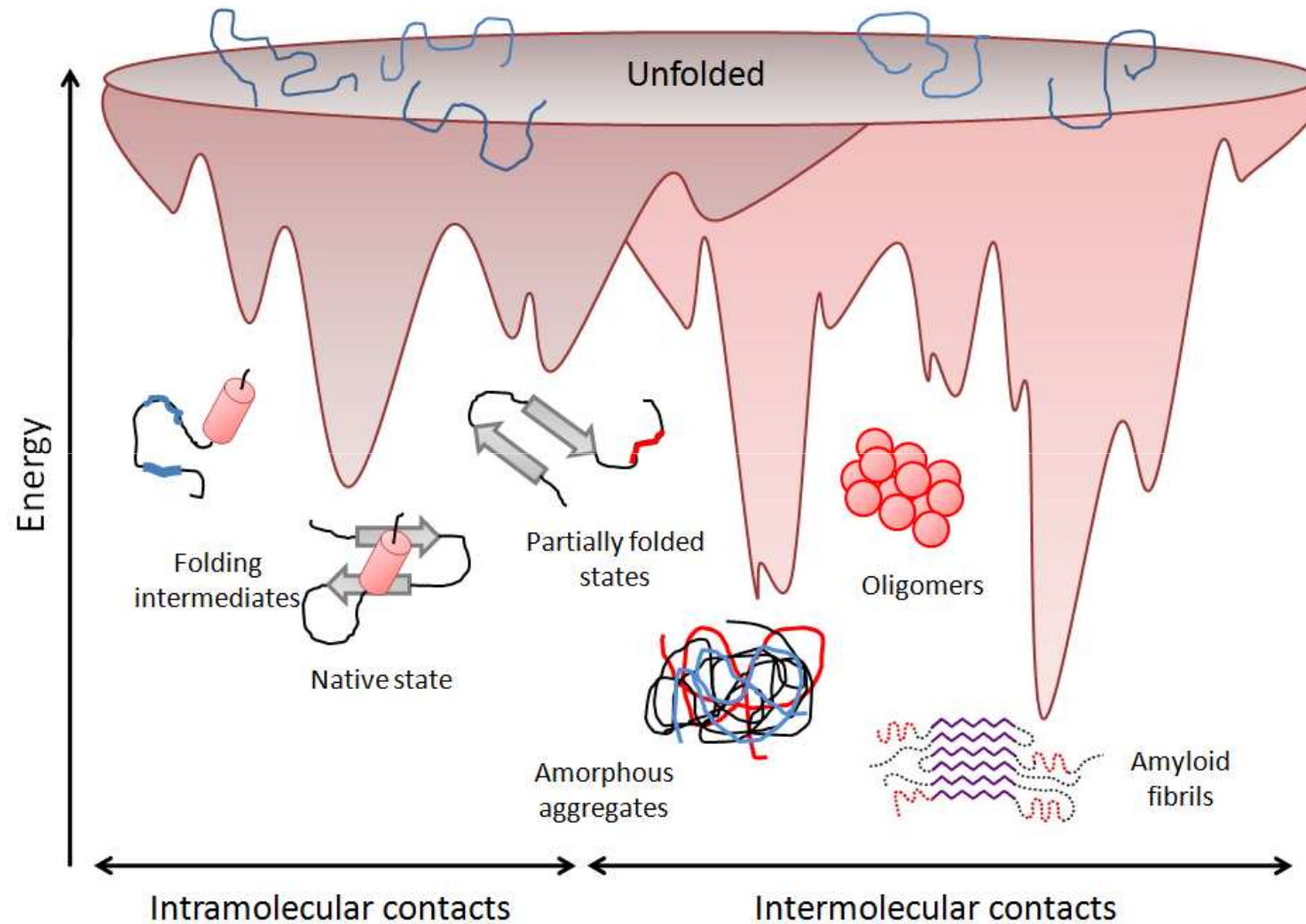


Fig2. Energy landscape scheme of protein folding and aggregation

Molecular chaperones > General features

- Recognition of exposed hydrophobic groups.
- ATP-regulated cycle.
- Unrelated, heterogeneous proteins.
- Network organization.

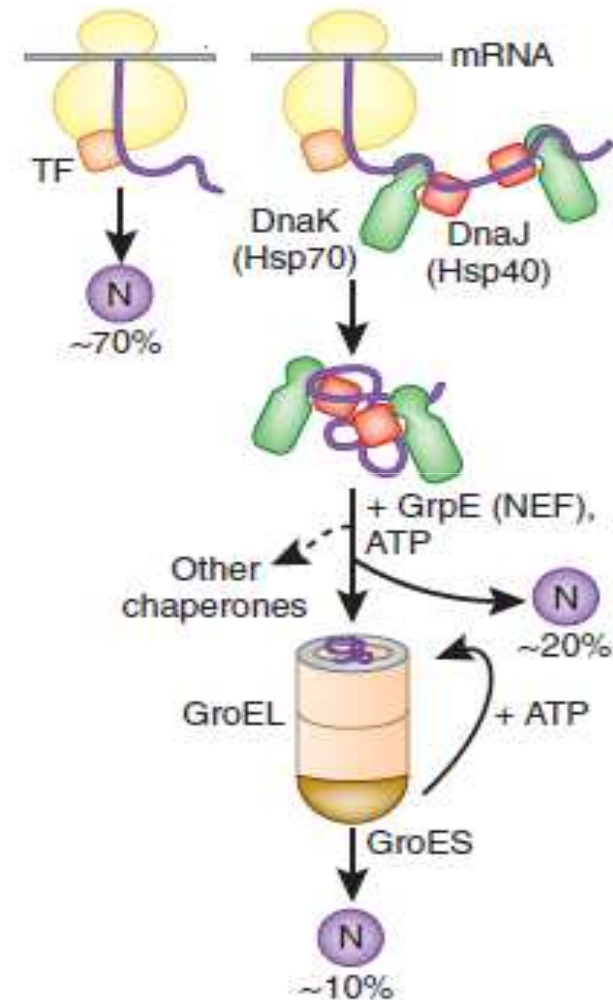


Fig3. Protein folding in the bacterial cytosol, extracted from:
Hartl FU, Hayer-Hartl M. Converging concepts of protein folding in vitro and in vivo. Nat Struct Mol Biol. 2009; 16(6): 574-81.

Chaperone groups > **Trigger factor**

- **Prokaryotic**
- **Ribosome-associated**
- **Not ATP binding**
- **Channel-shaped**

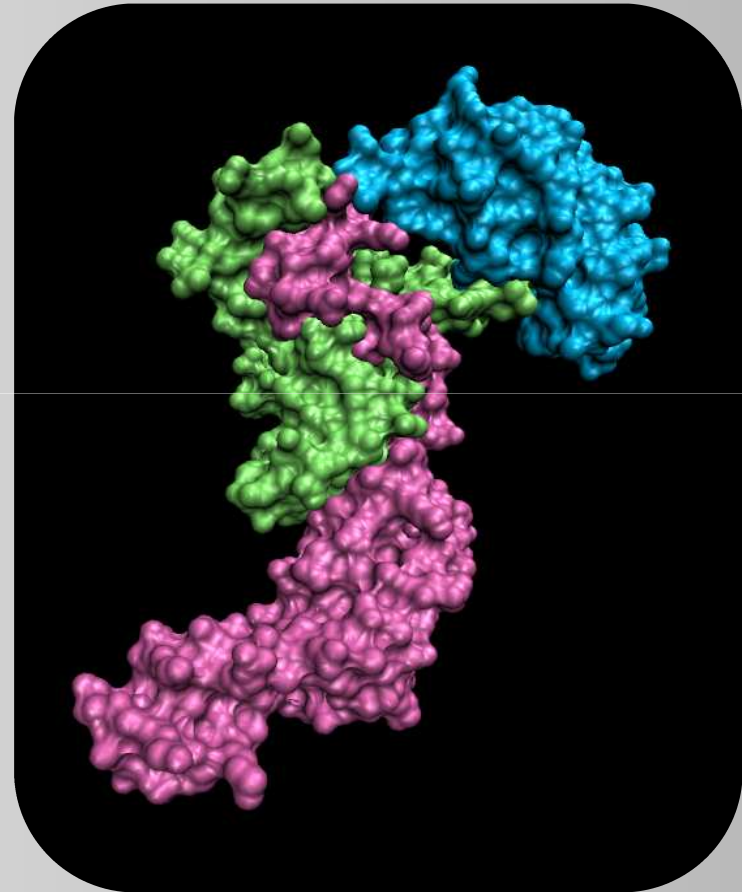


Fig4. Trigger factor of *V. Cholerae* (1T11)

Chaperone groups > **Hsp70**

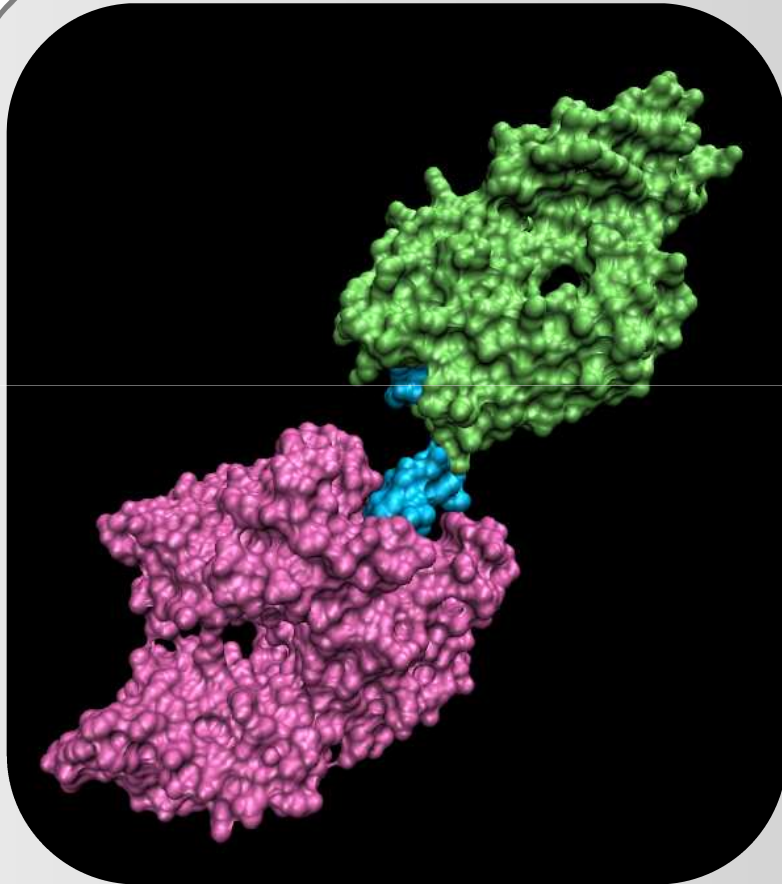


Fig5. DnaK of *E. Coli* (2KHO)

- Prokaryotes and eukaryotes
- ATP-driven cycle
- Central organizer of the chaperone network

Chaperone groups > **Hsp90**

- Eukaryotes and bacteria
- ATP-driven cycle
- Homodimer with 3 domains per subunit

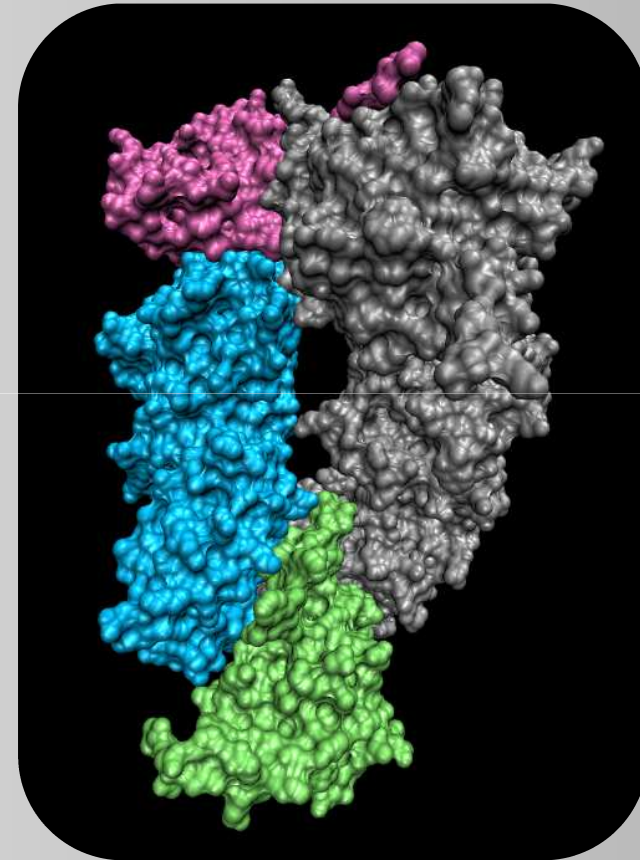
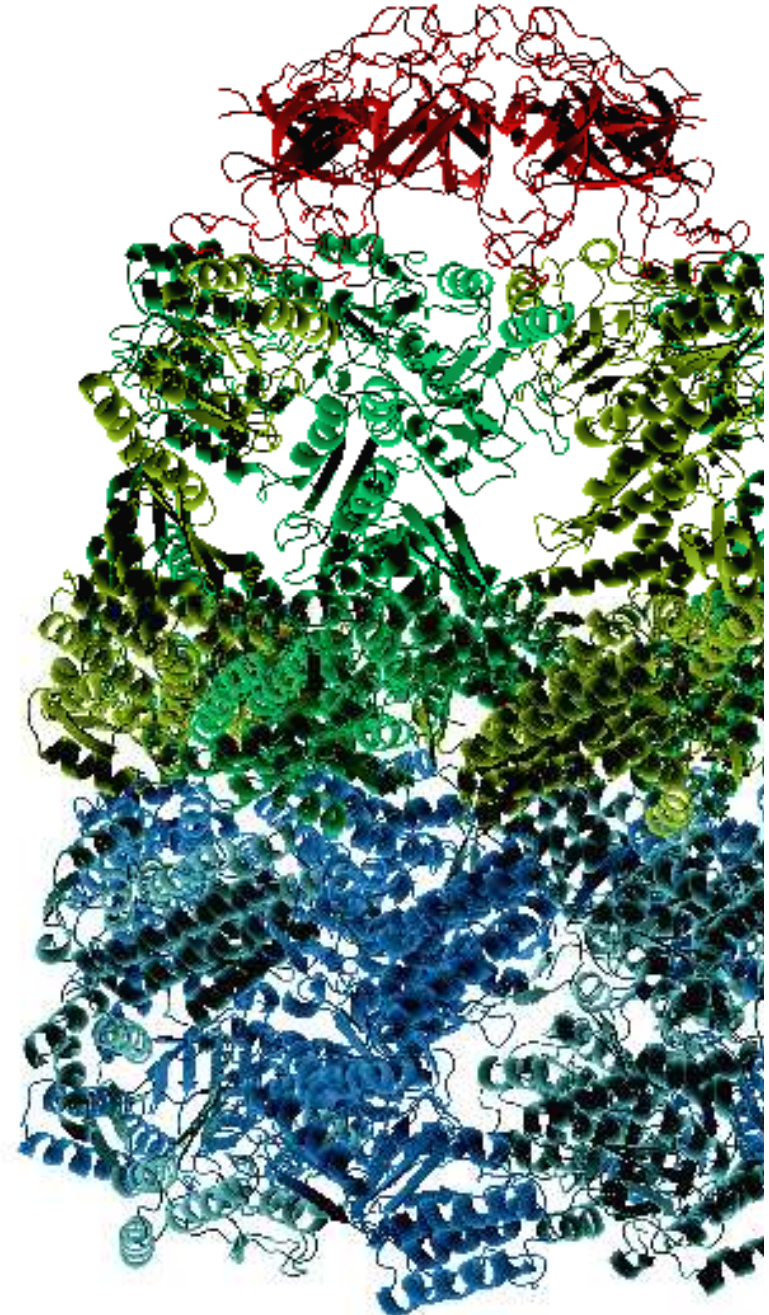


Fig6. Hsp90 of *S. cerevisiae* (2CG9)

Chaperone groups > Chaperonins

- Large, cage-like cylindrical complexes
- Eukaryotes and prokaryotes
- ATP-driven cycle
- 3 domains
- Organization in rings

Fig7. GroEL/GroES complex of *E. coli*
(1AON)



Chaperone groups > Chaperonins

GroEL apical domain-like superfamily

SCOP classification

Root: [SCOP hierarchy in SUPERFAMILY \[SCOP_0\]](#) (11)

Class: [Alpha and beta proteins \(a/b\) \[SCOP_51349\]](#) (147)

Fold: [The "swivelling" beta/beta/alpha domain \[SCOP_52008\]](#) (10)

Superfamily: [GroEL apical domain-like \[SCOP_52029\]](#) (2)

Families: [GroEL-like chaperone, apical domain \[SCOP_52030\]](#)

[Group II chaperonin \(CCT, TRIC\), apical domain \[SCOP_52034\]](#)

GroEL-intermediate domain like superfamily

SCOP classification

Root: [SCOP hierarchy in SUPERFAMILY \[SCOP_0\]](#) (11)

Class: [Alpha and beta proteins \(a+b\) \[SCOP_53931\]](#) (376)

Fold: [GroEL-intermediate domain like \[SCOP_54848\]](#)

Superfamily: [GroEL-intermediate domain like \[SCOP_54849\]](#) (2)

Families: [GroEL-like chaperone, intermediate domain \[SCOP_54850\]](#)

[Group II chaperonin \(CCT, TRIC\), intermediate domain \[SCOP_54853\]](#)

GroEL equatorial domain-like superfamily

SCOP classification

Root: [SCOP hierarchy in SUPERFAMILY \[SCOP_0\]](#) (11)

Class: [All alpha proteins \[SCOP_46456\]](#) (284)

Fold: [GroEL equatorial domain-like \[SCOP_48591\]](#)

Superfamily: [GroEL equatorial domain-like \[SCOP_48592\]](#) (2)

Families: [GroEL chaperone, ATPase domain \[SCOP_48593\]](#)

[Group II chaperonin \(CCT, TRIC\), ATPase domain \[SCOP_48596\]](#)

GroES-like superfamily

SCOP classification

Root: [SCOP hierarchy in SUPERFAMILY \[SCOP_0\]](#) (11)

Class: [All beta proteins \[SCOP_48724\]](#) (174)

Fold: [GroES-like \[SCOP_50128\]](#) (2)

Superfamily: [GroES-like \[SCOP_50129\]](#) (2)

Families: [GroES \[SCOP_50130\]](#) (2)

Chaperone groups > Chaperonins

<i>Thermosoma_TAI/1-545</i>	1 MMTG - QVPILVLKEGTQREQGKNAQRNNIEAAKAIADAVRTTLGPKGMDKMLVDSIGDIIISNDGATILKEMDVE - - - - HPTAKMIVEV84	
<i>Cpn-ts_MMV/1-543</i>	1 MSQQ - - - - PGVLPENMKRYMGDAQRMNILAGRIIAETVRSTLGPKGMDKMLVDDLDGVVVTNDGVTILREMSVE - - - - HPAAKMLIEV81	
<i>ChaperoninII_TKS-1/1-548</i>	1 MAQLSGQPVVILPEGTQRYVGRDAQRLNILAARIIAETVRTTLGPKGMDKMLVDSLGDIVVTNDGATILDKIDLQ - - - - HPAAKMMVEV85	
<i>GroEL_EC/1-525</i>	1 AAK - - - - DVKF - - - - - GNDAGVKMLRGVNVLDADVKTTLGPKGRNVVLDKSFQAPTITKDGVSVAEIELEDKFENMGAGMVKEV76	
<i>Cpn60_TT/1-543</i>	1 MAK - - - - ILVF - - - - - DEARRALERGVNAVAVAVKVTLGPGRNVVLEKKFGSPTITKDGVTVAKEVELEHLENIGQQLLKEV76	
<i>Thermosoma_TAI/1-545</i>	85 SKAQDTAVGDDGTTTAVVLSGELLKQAEETLLDQGVHPTVISNQRRLAVNEARKIIDEIAEK - - - - STDDATLRKIALTALSQKNTGLSNDFL171	
<i>Cpn-ts_MMV/1-543</i>	82 AKTQEKEVGDDGTTTAVVAGELLRKAEELLDDQNVHPTIVVKYQAAQKAEELLKTIACEVGAQDKIELTKIAMTSITGKGAEKAKEKL170	
<i>ChaperoninII_TKS-1/1-548</i>	86 AKTQDKEAGDDGTTTAVVIAAGELLRKAEELLDDQNIHPSIIIKQYALAAEKAEILDEIAIRVDPDDDEETLLKIAATSITGKNAESHKELL174	
<i>GroEL_EC/1-525</i>	77 ASKANDAAAGDDGTTTATVLAQAIITEGLKAVAAAGMNPMDLKRQIDKAVTVAVEELKALSVP - - - - CSKSAIAQVGTISA - - - - - NSDETIV157	
<i>Cpn60_TT/1-543</i>	77 ASKTNDVAGDDGTTTATVLAQAIIVREGLKNVAAAGANPLALKRQIEKAVEAAVEKIKALAIIP - - - - VEDRKAIEEVATISA - - - - - NDP - EV156	
<i>Thermosoma_TAI/1-545</i>	172 ADLVVKAVNAVAVAEVRDQKTIIVDTANIKVDKKNQGSVNDTQFISQIVIDKEKVHSKMPDVVKNKAKIALIDSALEIKKTEIEAKVQISDPS260	
<i>Cpn-ts_MMV/1-543</i>	171 AEIIVEAVSAVVD - DEQK - - - - VDKDLIKIEKKSGASIDDTTELKGVLVVDKERVSAQMPKKVTDKIALLNCAIEIKETETDAEIRITDPA256	
<i>ChaperoninII_TKS-1/1-548</i>	175 AKLAVEAVKQVAEKDKQKYVVDLDNLIKFEKKAGEGVEESELVRGVVIDKEVVHPRMPKRVENAKIALINEALEVKKTTETDAKINITSPTD263	
<i>GroEL_EC/1-525</i>	158 GKLIAEAMDKVG - - - - KEQ - - - - - VITVEDGTG - LQDELVDVEGMQFDRGYLSPYFINKPETGAVELESFFILLADK - - - - - KISNIR230	
<i>Cpn60_TT/1-543</i>	157 GKLIAADAMEKVG - - - - KEQ - - - - - IITVEESKS - LETELKFVEGQYQFDKGYISPYFVTNPETMEAVLEDAFILIVEK - - - - - KVSNNVR229	
<i>Thermosoma_TAI/1-545</i>	261 KIQDFLNQETNTFKQMVKEIKKSGANVVLCCQKIGDDVAQHYLAK - - - - EGIIYAVRRV - - - - - KKSDEMEKLAKATGAKIVTD - - - - - L333	
<i>Cpn-ts_MMV/1-543</i>	257 KLMEFIEQEEKMLKDMVAEIKASGANVLFCCQKIGDDLQAHYLAK - - - - EGIIYAVRRV - - - - - KKSDEMEKLAKATGANVIAA - - - - - I329	
<i>ChaperoninII_TKS-1/1-548</i>	264 QLMSFLEQEEKMLKDMVDHIAQTGANVVFVQKIGDDLQAHYLAK - - - - YGIMAVRRV - - - - - KKSDEMEKLAKATGAKIVTN - - - - - V336	
<i>GroEL_EC/1-525</i>	231 EMLP - - - - - - - - - - VLEAVAKAGKPLLIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLDQIATLTGGTIVISEEIGMEL308	
<i>Cpn60_TT/1-543</i>	230 ELLP - - - - - - - - - - ILEQVAQTGKPLLIIAEDVEGEALATLVVNKLRTLSVAAVKAPGFGDRRKEMLKDIAAVTGGTIVISEELGFKL307	
<i>Thermosoma_TAI/1-545</i>	334 DDLTPSVLGEAETVEERKIGDDRMFTVMQCKNPKAVS - - - - - ILIRGGTDHVVSSEVERA387	
<i>Cpn-ts_MMV/1-543</i>	330 AALSAQDLGDAGLVEERKISGDSMIFVEECKHPKAVT - - - - - MLIRGTTTEHVIEEVARA383	
<i>ChaperoninII_TKS-1/1-548</i>	337 KDLTPEDLGYAEVVEERKLAGENMIFVEQCKNPKAVT - - - - - ILIRGGTEHVIEEVARA390	
<i>GroEL_EC/1-525</i>	309 EKATLEDLQAKRV - - - - - VINKDTTTTIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKAR394	
<i>Cpn60_TT/1-543</i>	308 ENATLSMLGRAERV - - - - - RITKDETTIVGQKGGKEDIARINGIKKELETTDSEYAREKLQERLAKLAGGVAVIRVGAATETELKEKKHR393	
<i>Thermosoma_TAI/1-545</i>	388 LNDAIRVVAITKEDGKFLWGGGAVEAEELAMRLAKYANSVGGREQLAIEAFAKALEIIPRTLAENAGIDPINTLIKLLKADDEK - GRISVG475	
<i>Cpn-ts_MMV/1-543</i>	384 VDDAVGVVGCTIEDGRIVSGGGSTEVELSMKLREYAEGISGREQLAVRAFADALEVIRPTLAENAGLDAIEILVKVRAAHASNGNKCAG472	
<i>ChaperoninII_TKS-1/1-548</i>	391 LEDAVKVVVDVMDGAVLPAGGAPEIELAIRLDEYAKQVGGKEALAIENFADALKIIPKTLAENAGLDTVEMLVKVISEHKN - RGLGIG478	
<i>GroEL_EC/1-525</i>	395 VEDALHATRAAAVEG - VVAGGGVALIRVASKLADLRGQ - NEDQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANTVKGGD - - - - - GNYG476	
<i>Cpn60_TT/1-543</i>	394 FEDALNATRAAAVEG - IVPGGGVTLTLRAISAVEELIKKLEGDEATGAKIVRRALAEAPARQIAENAGYEGSVIVQQILAEETKN - - - - - PRYG478	
<i>Thermosoma_TAI/1-545</i>	476 VDLDNNGVGDMAKAGVVDPLRVKTHALESAVEVATMILRIDDVIAASKKST - - - - PPSQGGGQGGQMPG - - - - - GMP - EY545	
<i>Cpn-ts_MMV/1-543</i>	473 LNVFTGAVEDMCENGVEPLRVKTDQAIQSAAESTEMLLRIDDVIAAEKLRGAPDMGD - - - - - MGGMPG - MGGMPGMM543	
<i>ChaperoninII_TKS-1/1-548</i>	479 IDVFEGKPADMLEKGIIEPLRVKKQAIKSASEAAIMILRIDDVIAAKATK - - - - - PEGGQ - - - - - GGGMPGGMGGMDMGM548	
<i>GroEL_EC/1-525</i>	477 YNAATEEYGNMIDMGILDPKTVTRSAALQYASVAGLMITTECMVTD - LPK525	
<i>Cpn60_TT/1-543</i>	479 FNAATGEFVDMVEAGIVDPAKVTRSAALQNAASIGALILITTEAVVAEKPEK - - - - - KES - PASAGAGDMDF543	

Fig8. Sequence alignment between members of both group I and II of chaperonins

Chaperone groups > Chaperonins

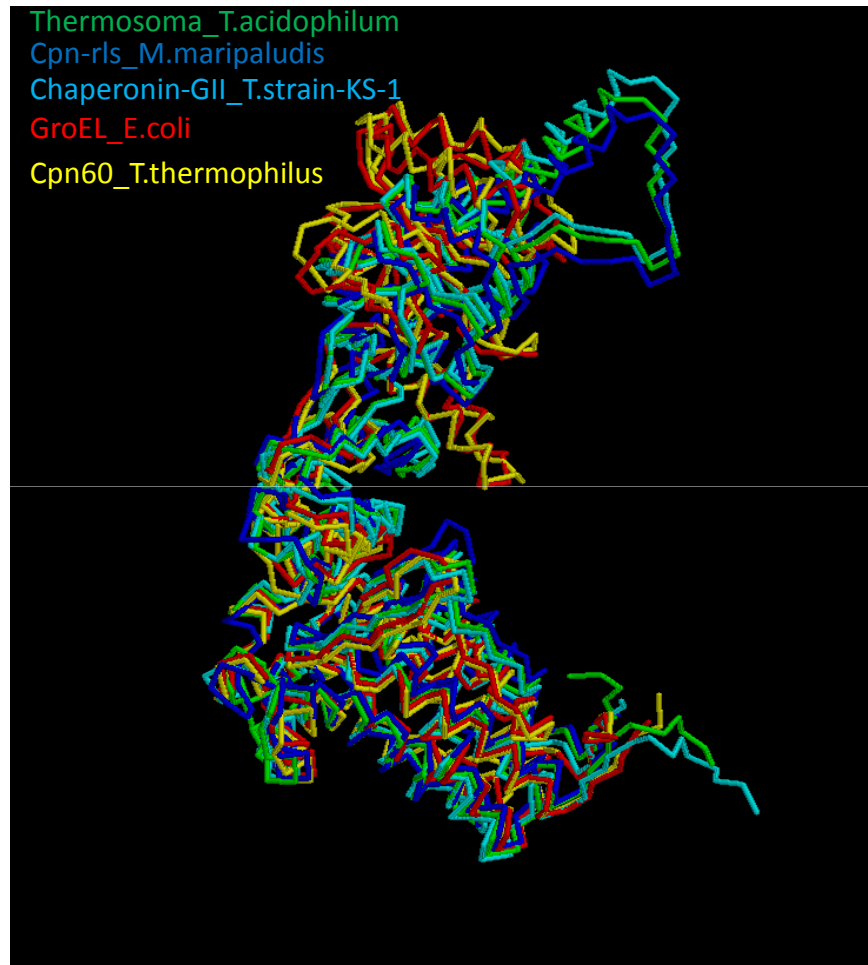


Fig9. Chaperonin
whole-subunit
structural alignment

RMSD 2.58
Sc 6.88

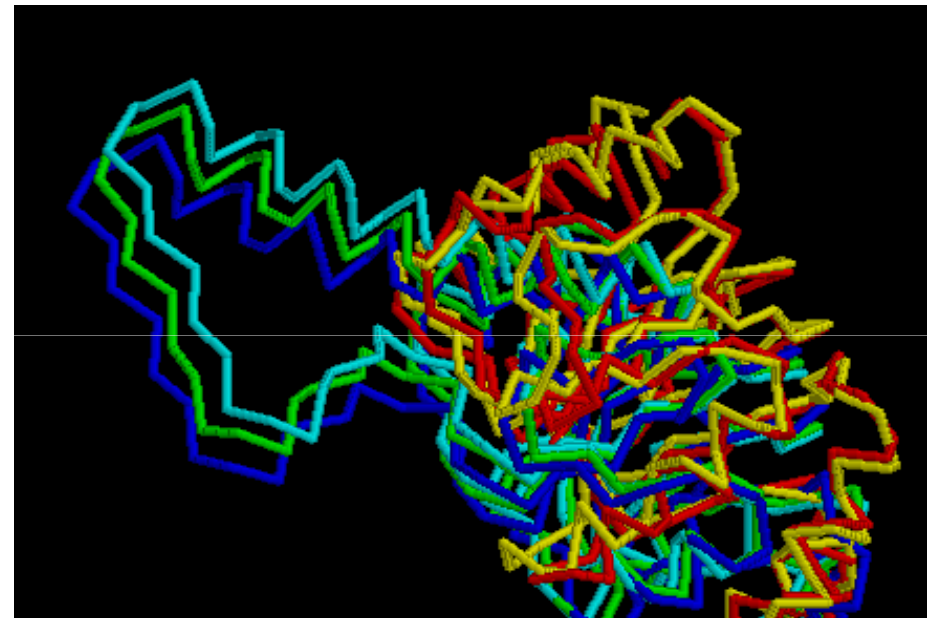


Fig10. Chaperonin apical domain structural alignment

Introduction

Molecular chaperones

Chaperonins group I

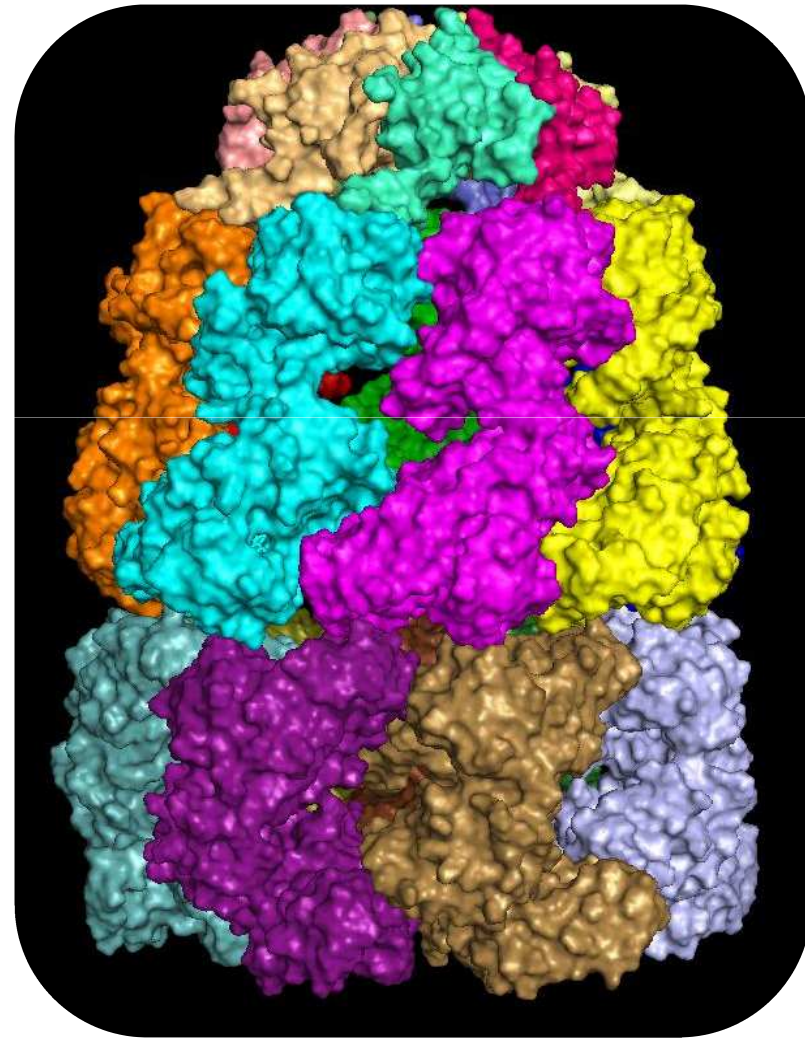
Chaperonins group II

GROUP I CHAPERONINS

Chaperonins group I > Main characteristics

- Eubacteria, mitochondria and chloroplasts
- Cochaperonin-dependent
- GroEL-GroES from *E. coli*

Fig11. GroEL complex with the cochaperonin GroES of *E. coli* (1AON)



GroEL/GroES > General structure

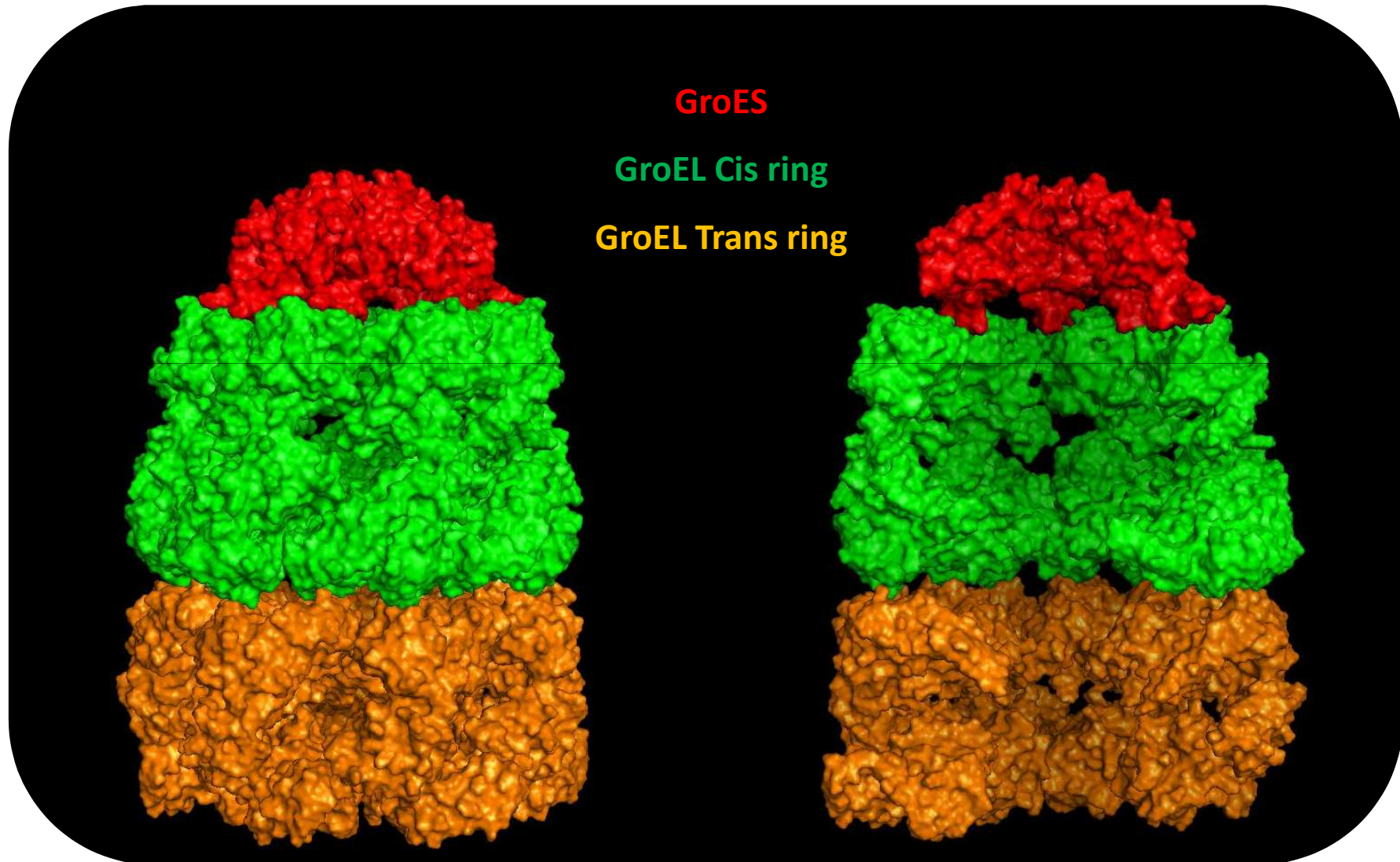


Fig13. GroEL/GroES surface (1AON)

Fig14. GroEL/GroES internal cavity (1AON)

GroEL/GroES > General structure

GroES → 7 subunits

GroEL Cis ring → 7 subunit

GroEL Trans ring → 7 subunit

119,553 atoms

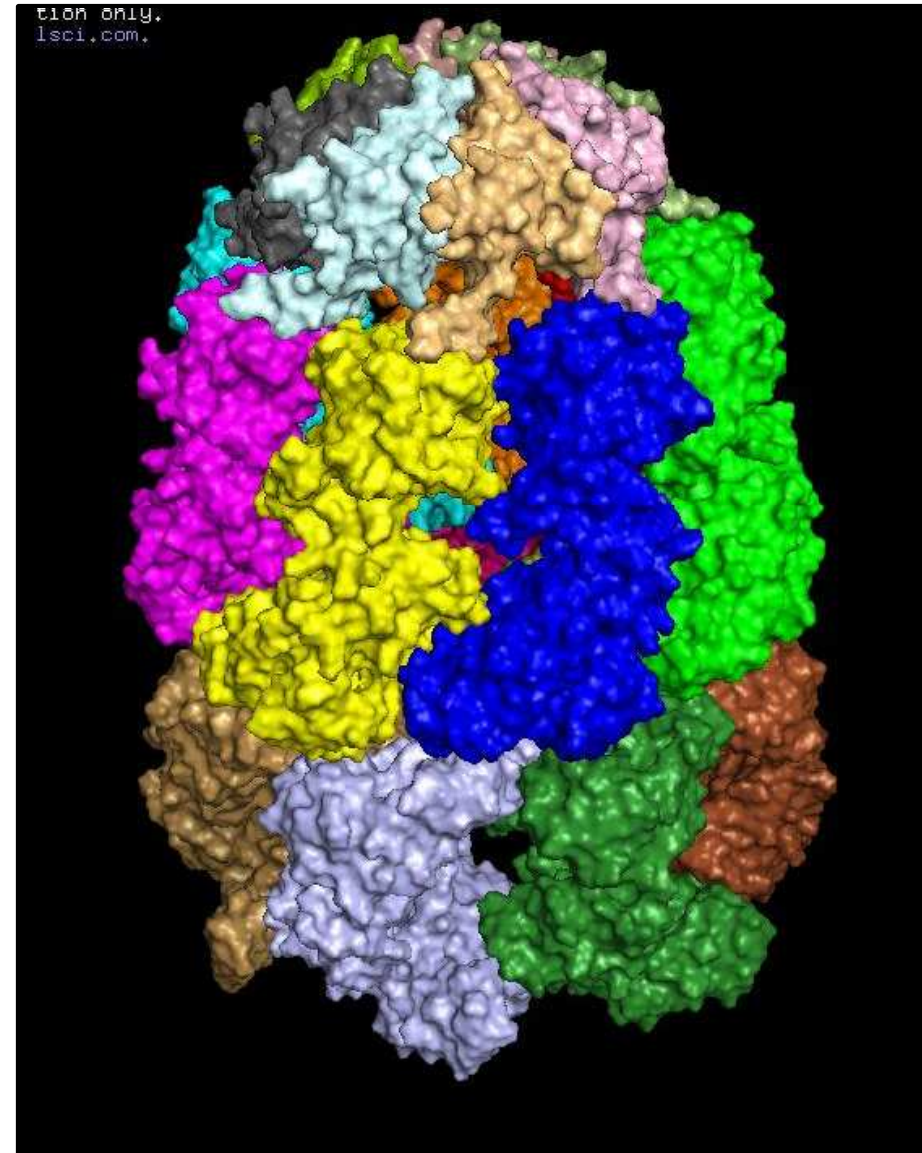
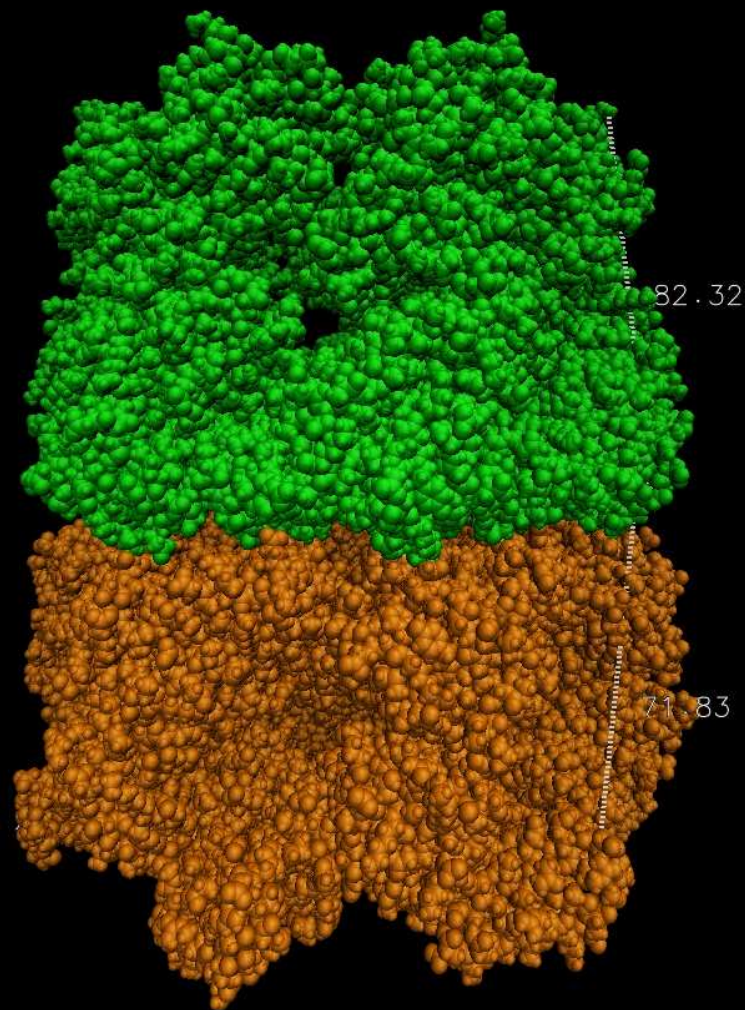


Fig15. GroEL/GroES subunit reconstruction (1AON)

GroEL/GroES> General structure GroEL



Cis ring

Volume: 175,000 Å³

Trans ring

Volume: 85,000 Å³

Fig16. GroEL cis and trans rings (1AON)

GroEL/GroES> General structure GroEL

The cis ring has the internal cavity **polar** to promote producing folding

The trans ring has the internal cavity **hydrophobic**

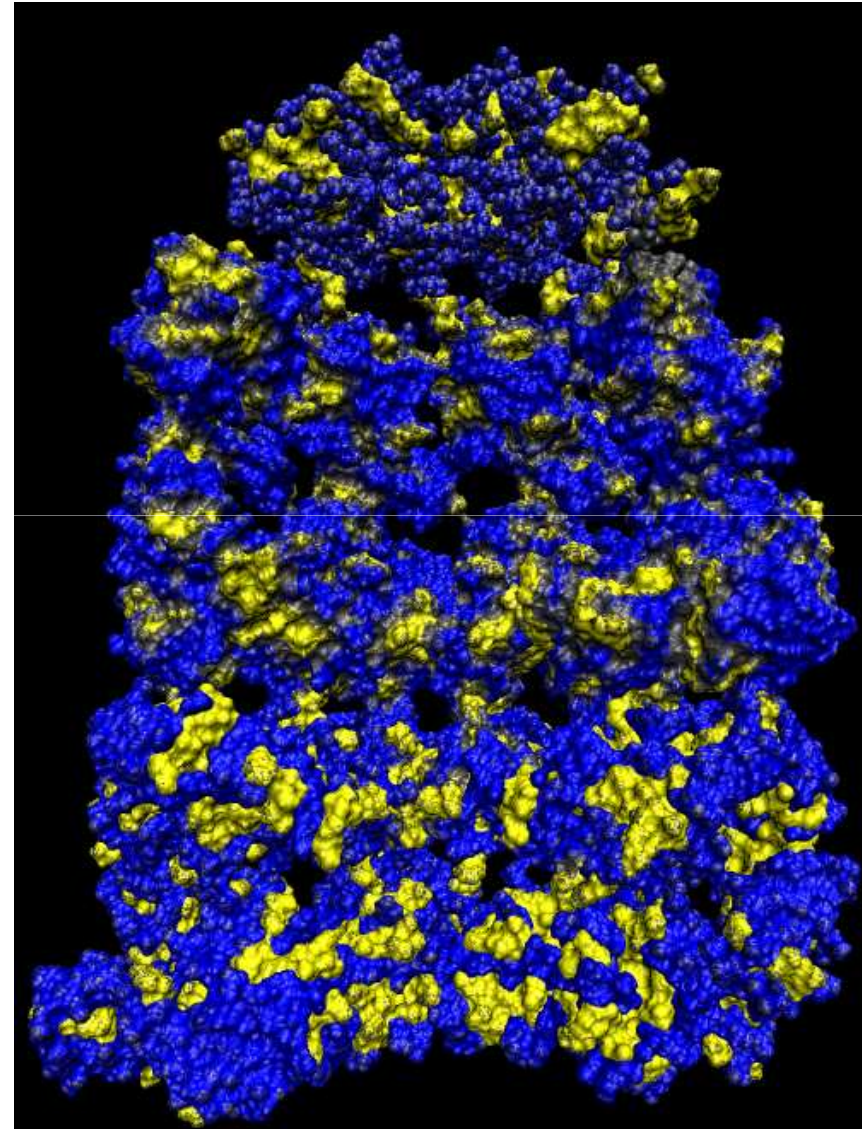


Fig17. GroEL/GroES internal cavity (1AON)

GroEL/GroES> General structure GroEL

Subunits of 548 aa

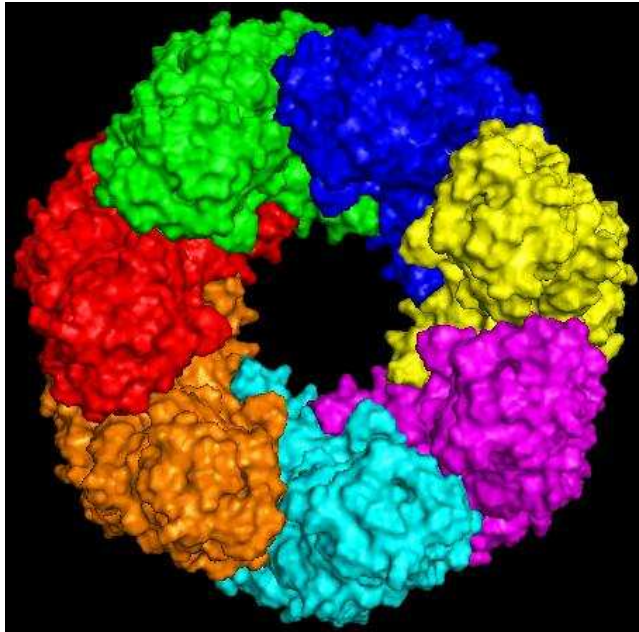


Fig18. GroEL cis ring subunits (1AON)

Domains: **apical**
intermediate
equatorial

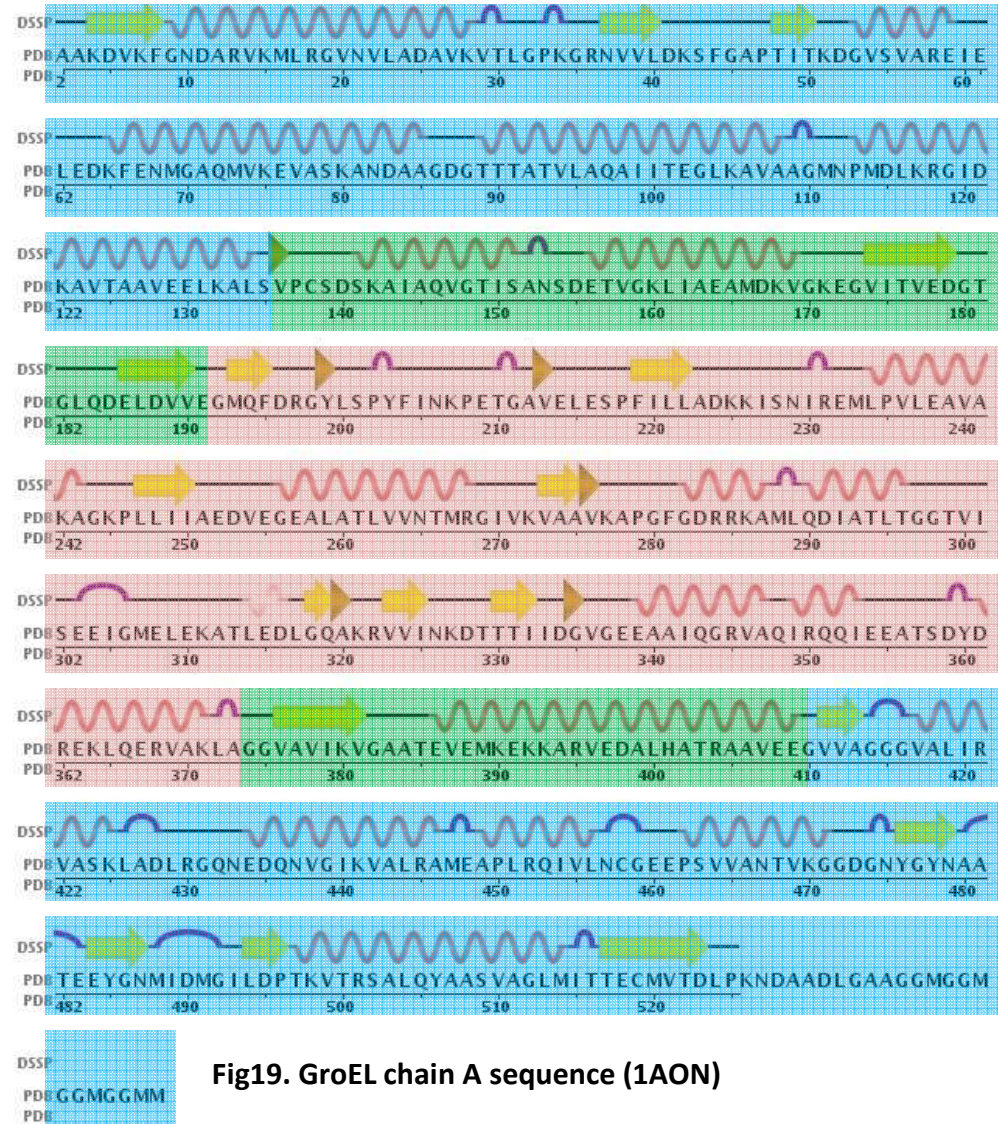


Fig19. GroEL chain A sequence (1AON)

GroEL/GroES> Subunit structure

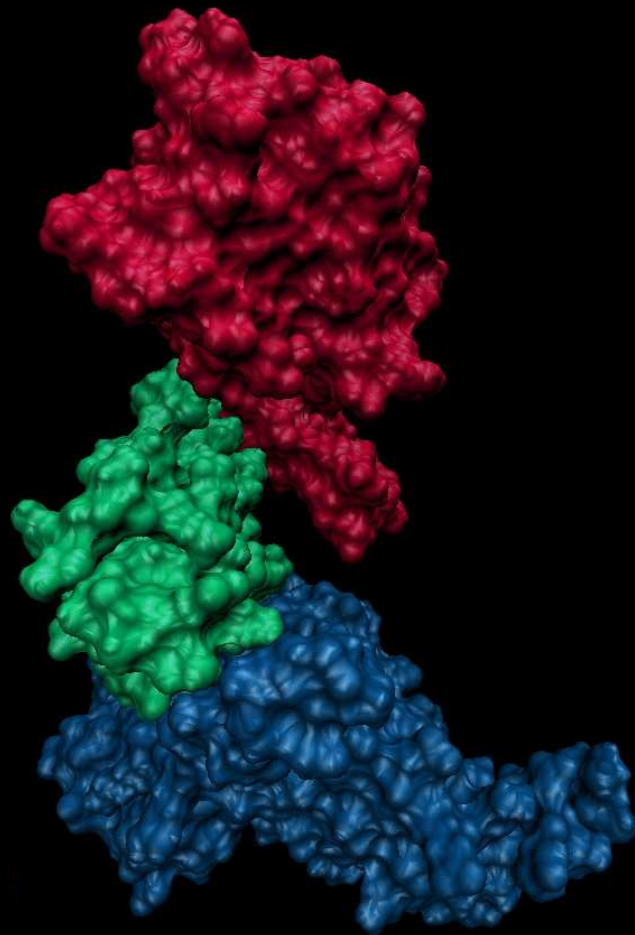


Fig20. GroEL chain A domains (1AON)

Apical
Intermediate
Equatorial

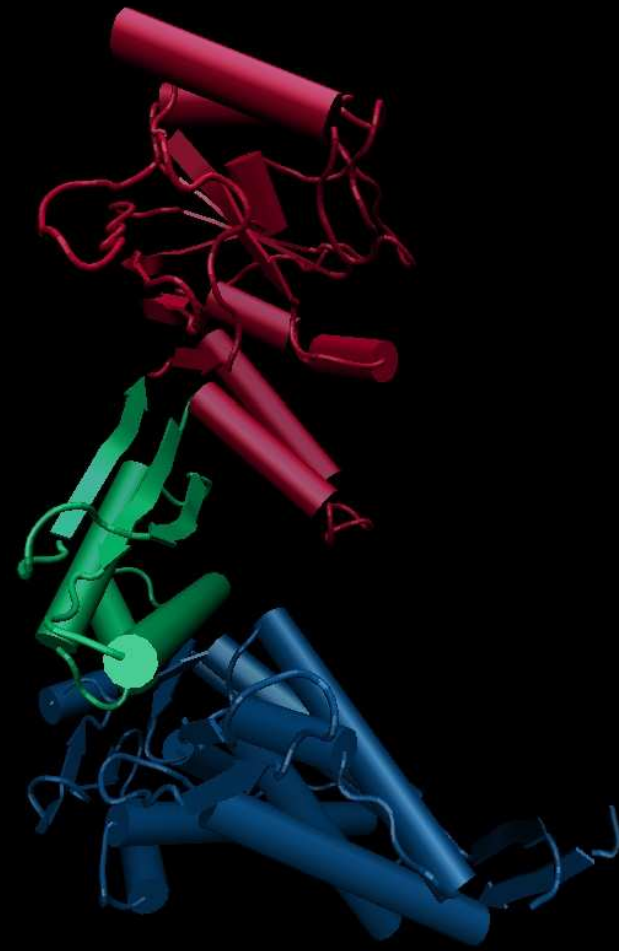


Fig21. GroEL chain A domains (1AON)

GroEL/GroES> Inter-ring interactions

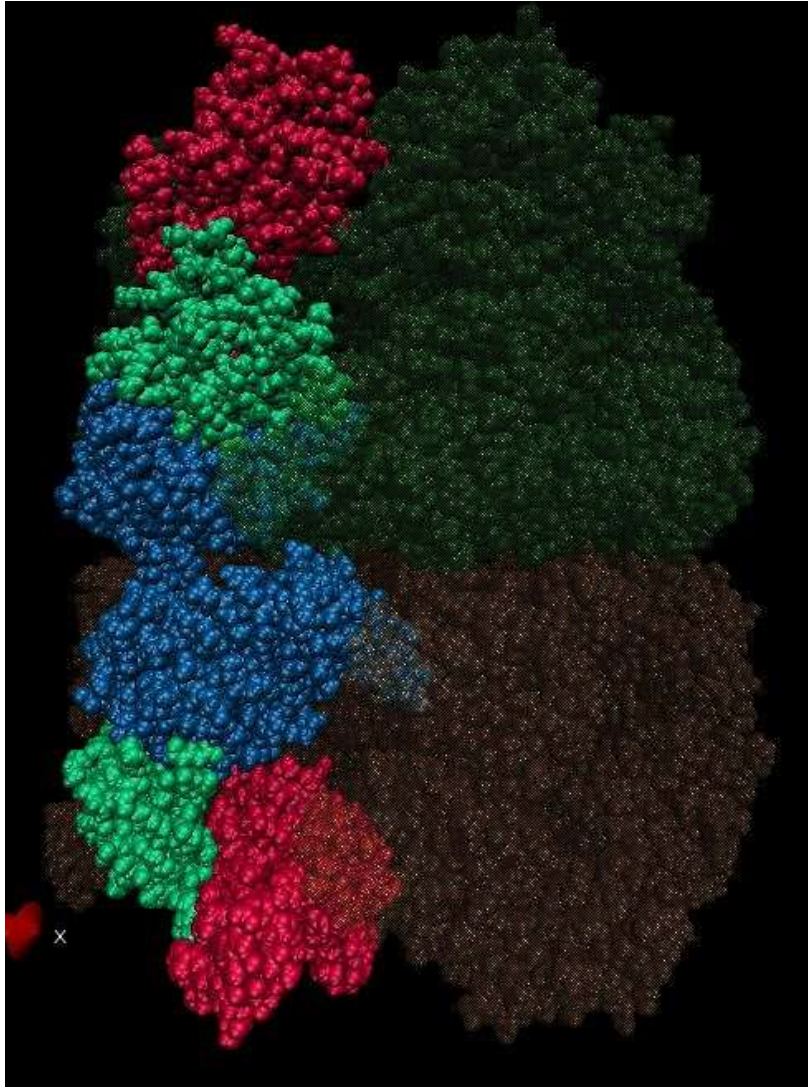


Fig22. GroEL chain A and H (1AON)

LEFT SITE: interaction between adjacent subunits



Fig23. GroEL equatorial domains chain A and H (1AON)

GroEL/GroES> Inter-ring interactions

LEFT SITE

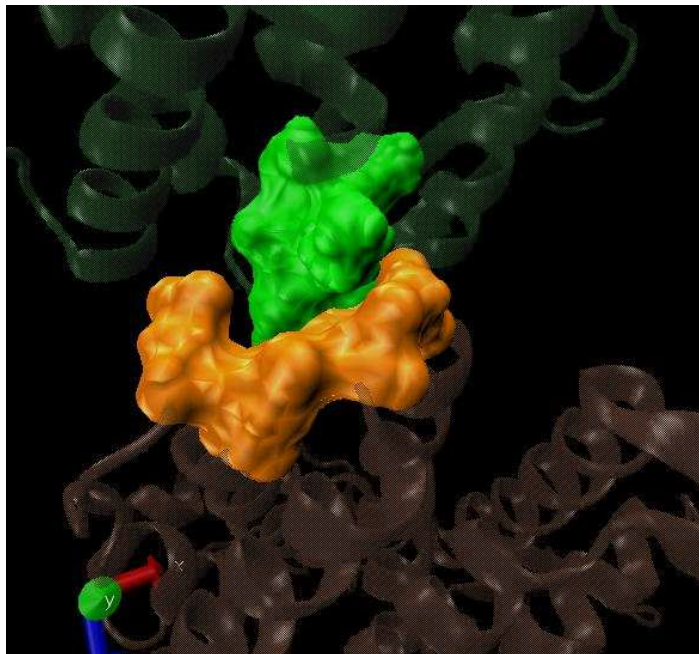


Fig24. Inter-ring interaction residues, surface (1AON)

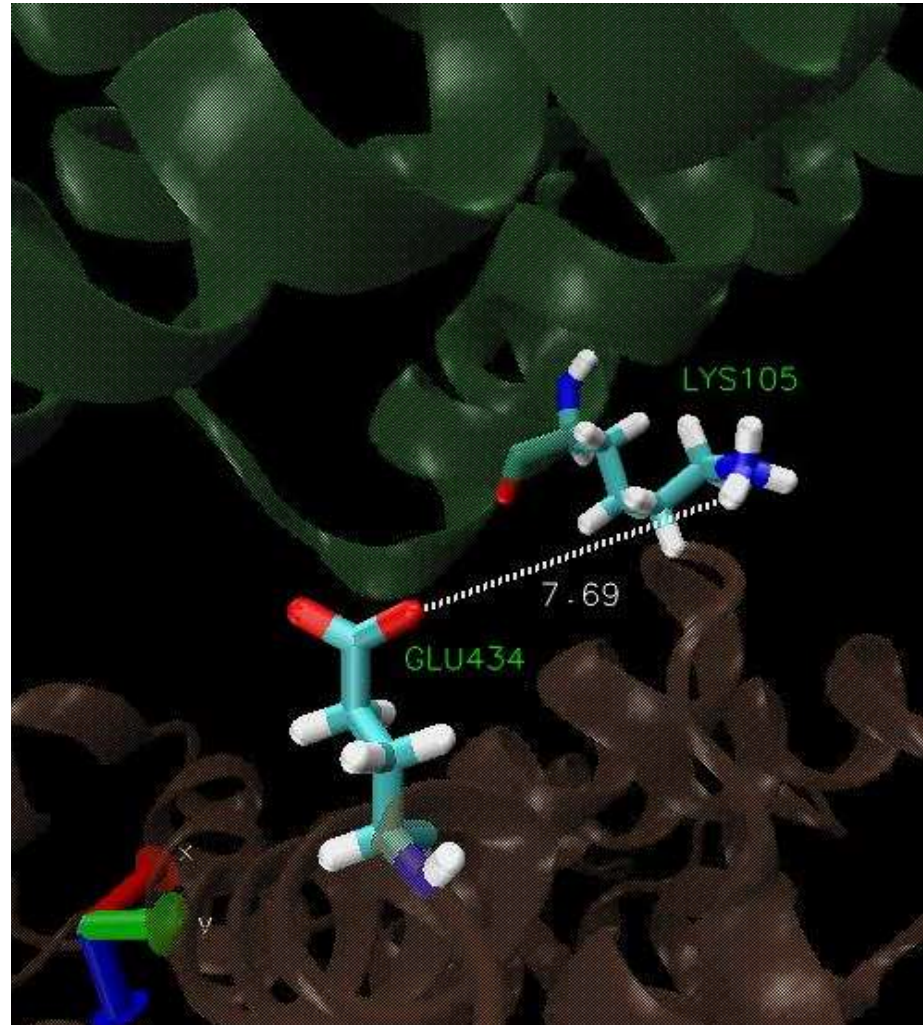


Fig25. Inter-ring interaction residues, salt bridge (1AON)

GroEL/GroES> Inter-ring interactions

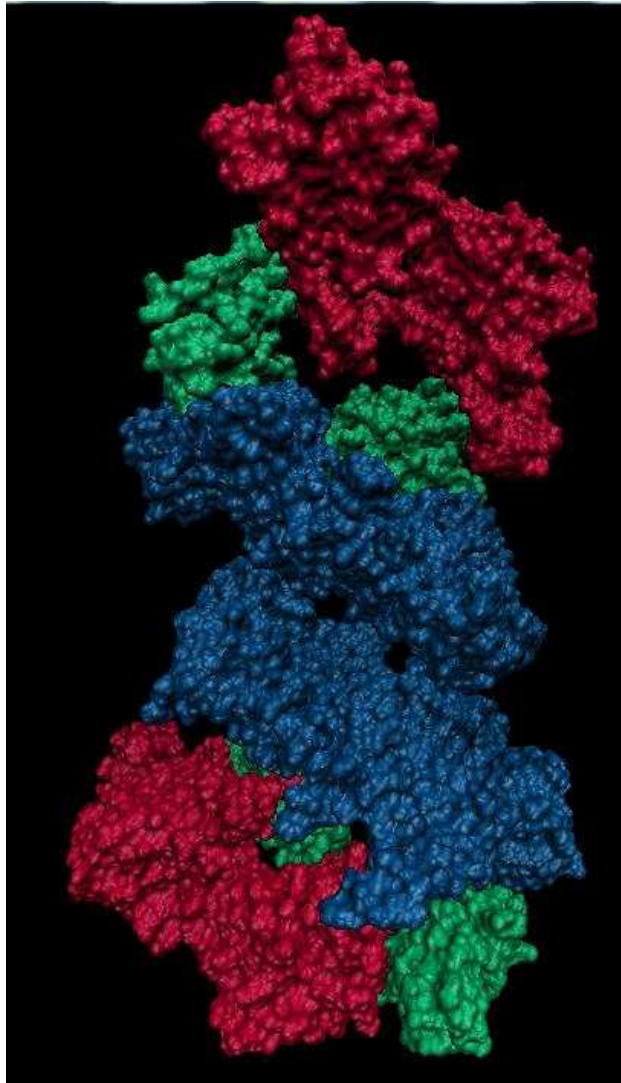


Fig26. GroEL chains A-B (cis) and H-I (trans) (1AON)

RIGHT SITE: interaction between one cis subunit and the left subunit from the trans ring

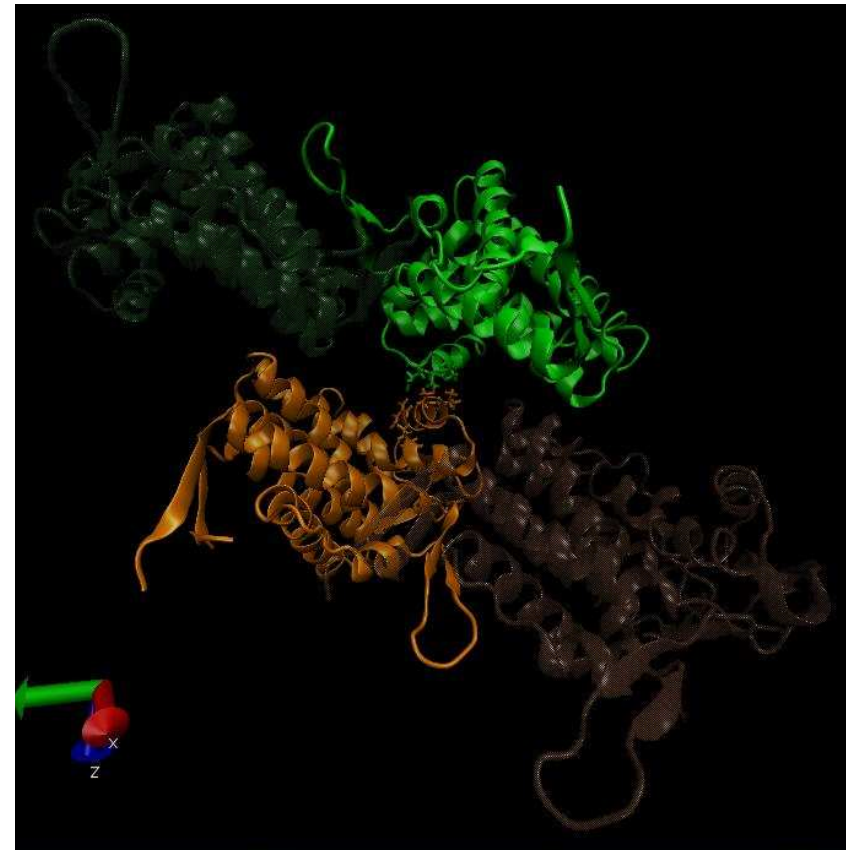


Fig27. GroEL chains B and H, equatorial domains (1AON)

GroEL/GroES> Inter-ring interactions

RIGHT SITE

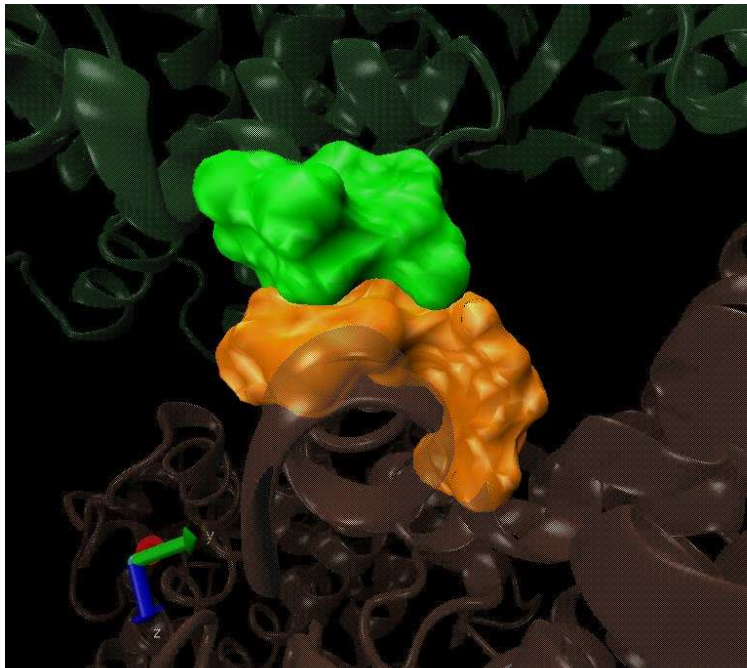


Fig28. Inter-ring interaction residues, surface (1AON)

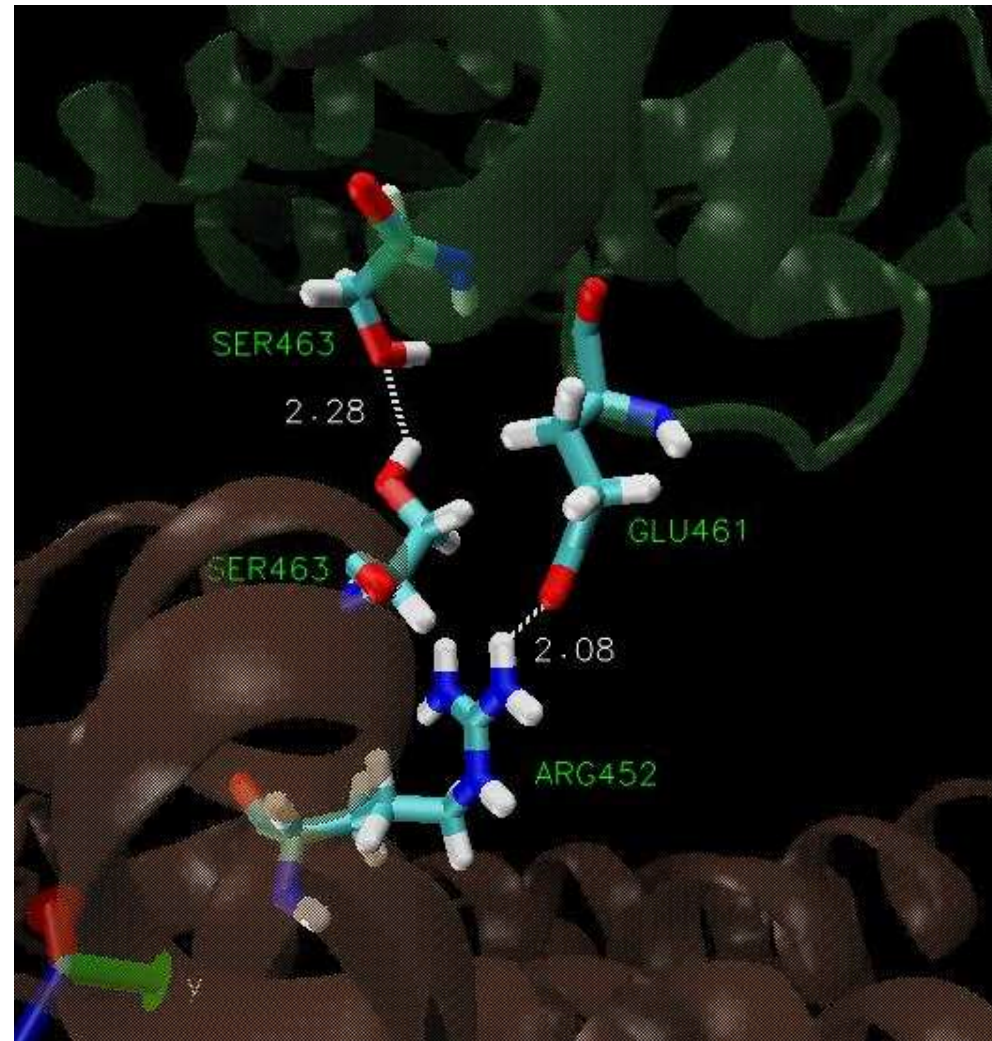


Fig29. Inter-ring interaction residues, salt bridge and Hbond (1AON)

GroEL/GroES> Intra-ring interactions

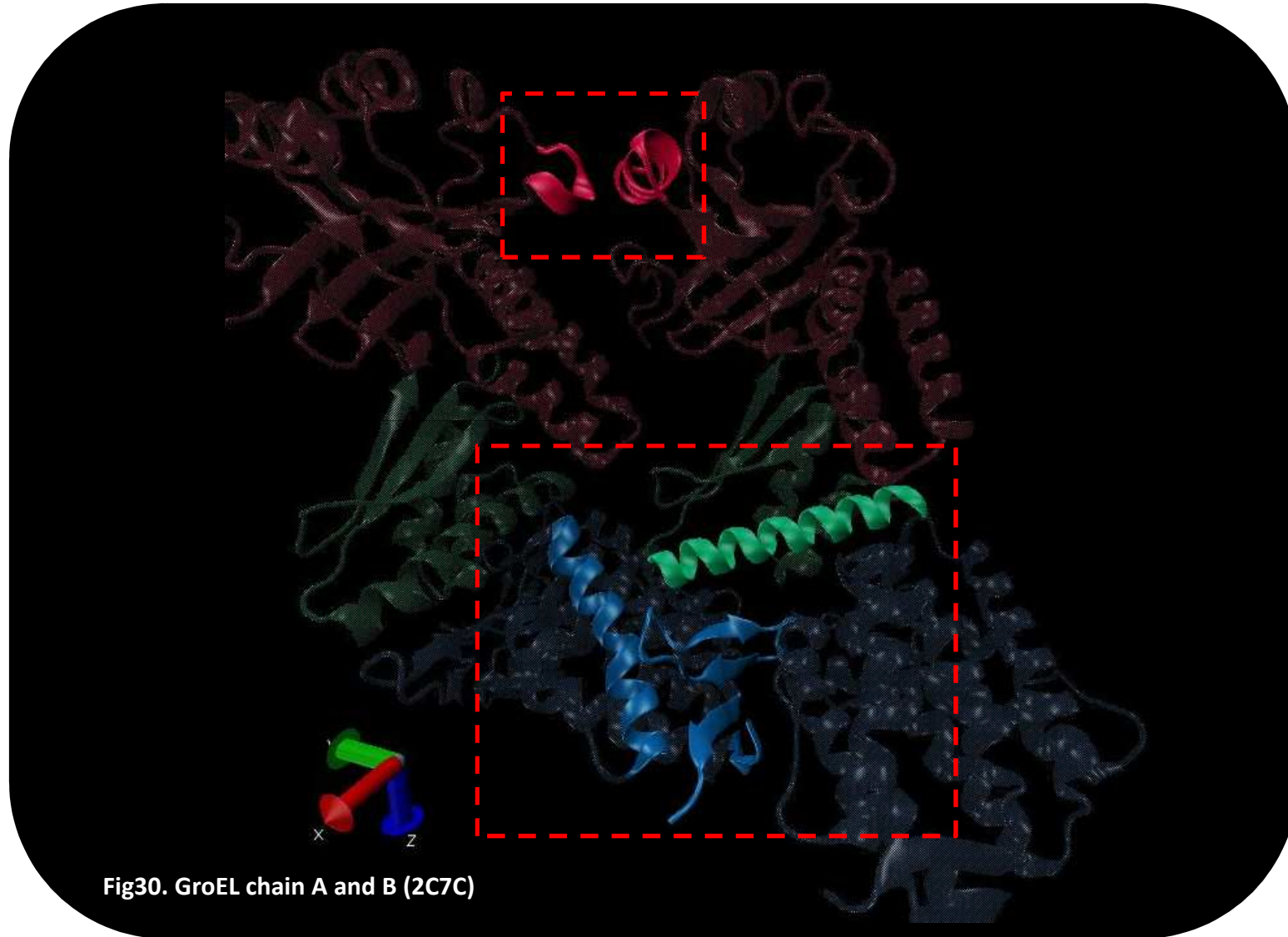


Fig30. GroEL chain A and B (2C7C)

GroEL/GroES> Intra-ring interactions

Hydrophobic interactions between apical domains

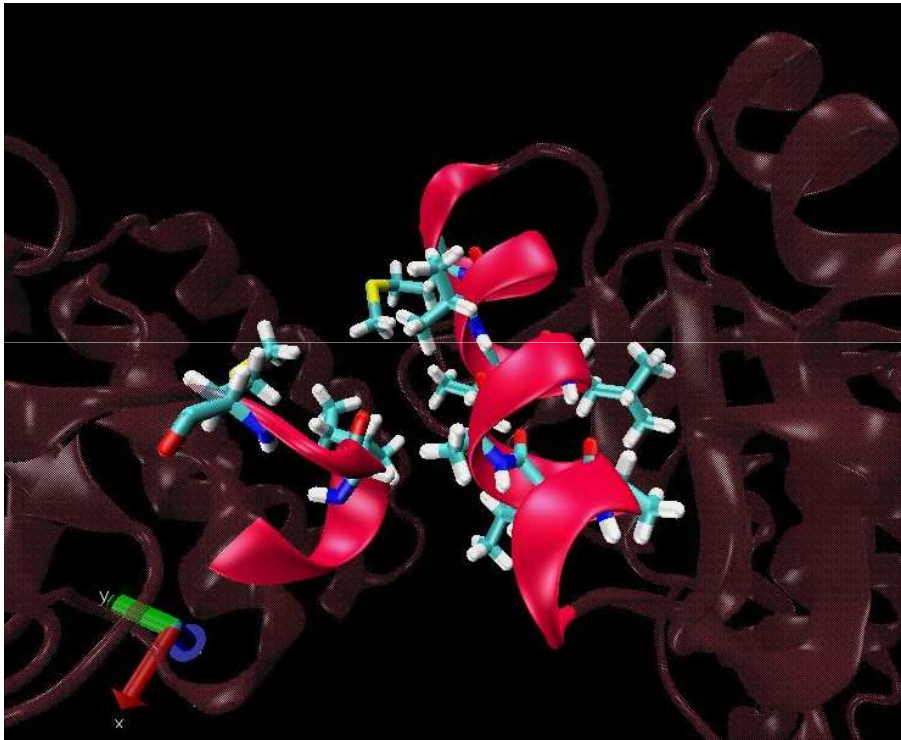


Fig31. GroEL chain A and B, hydrophobic apical interactions (2C7C)

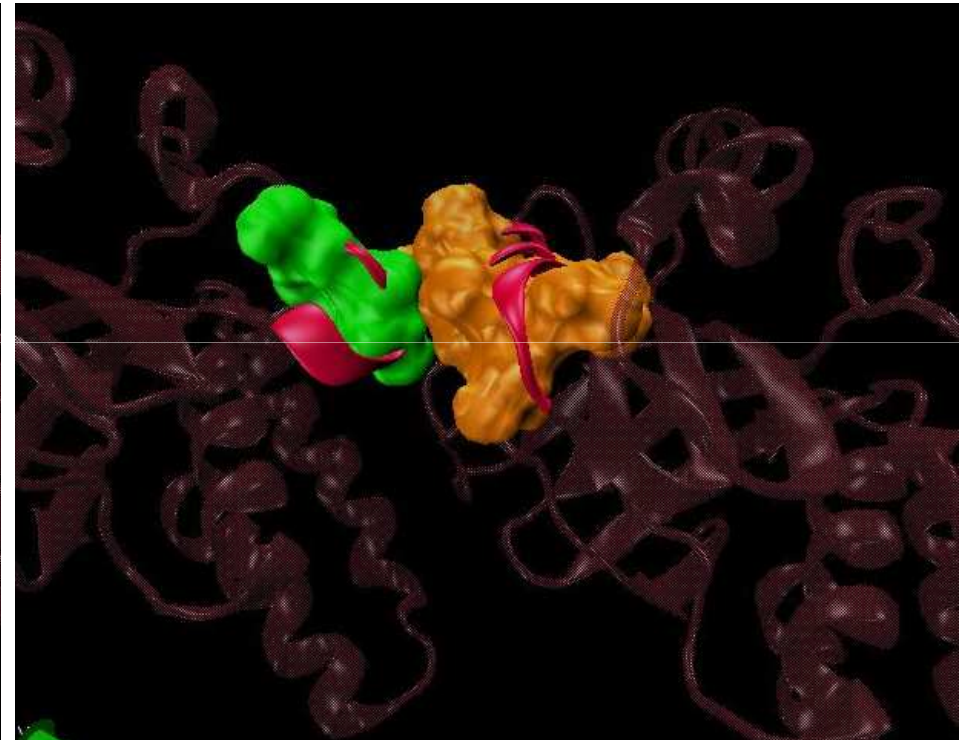


Fig32. GroEL chain A and B, surface hydrophobic apical interactions (2C7C)

GroEL/GroES> Intra-ring interactions

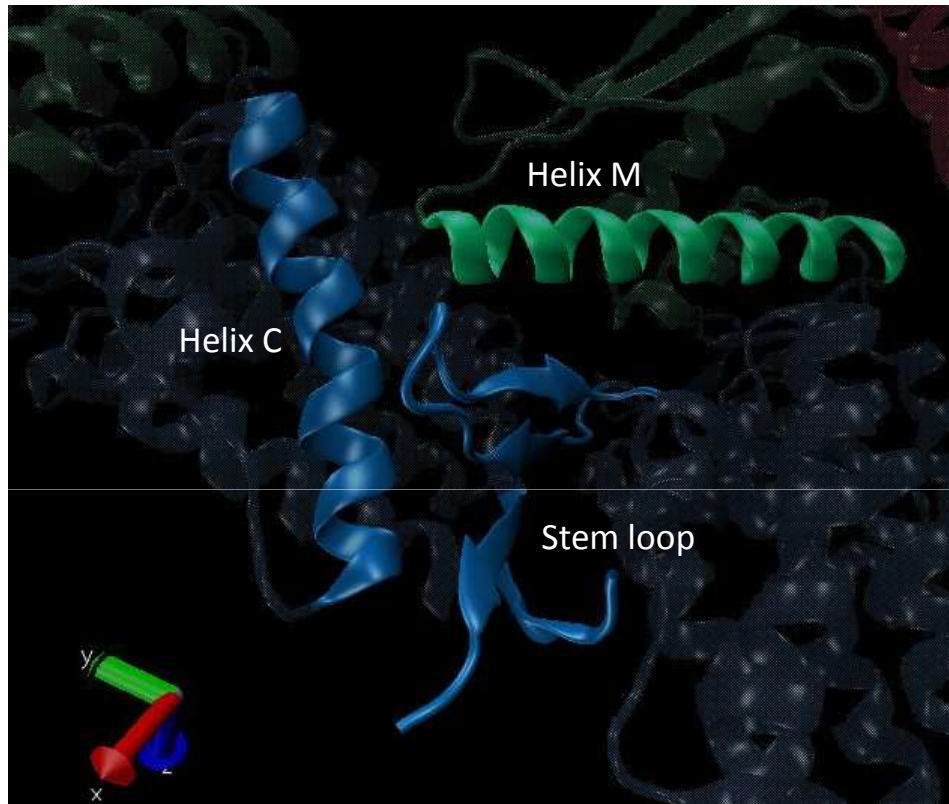


Fig33. GroEL chain A and B, intermediate and equatorial interactions (2C7C)

B-sheet inner contacts and hydrogen bonds between intermediate and equatorial domains

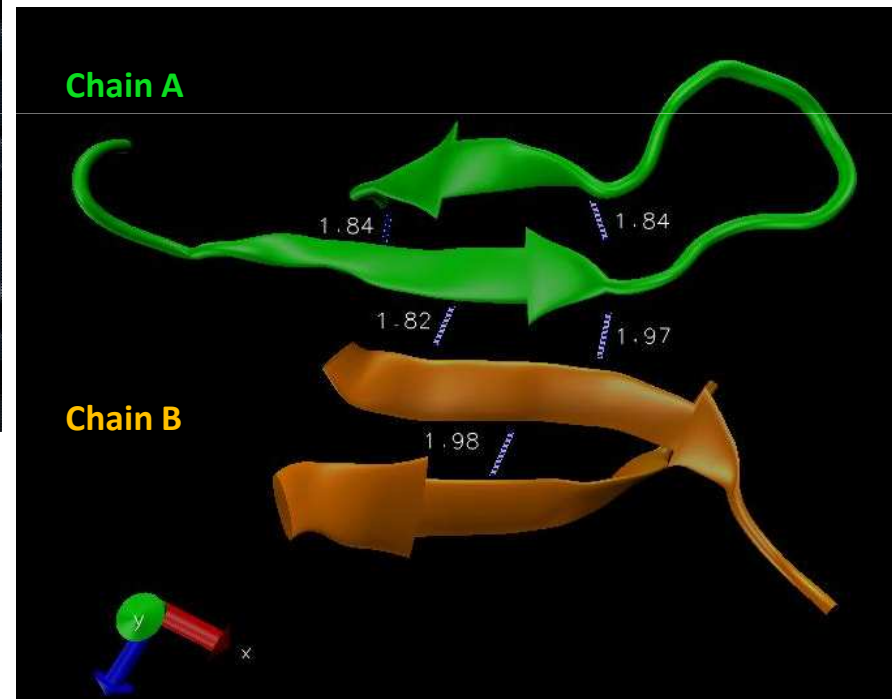


Fig34. β -sheet inner contacts (2C7C)

GroEL/GroES> Intra-ring interactions

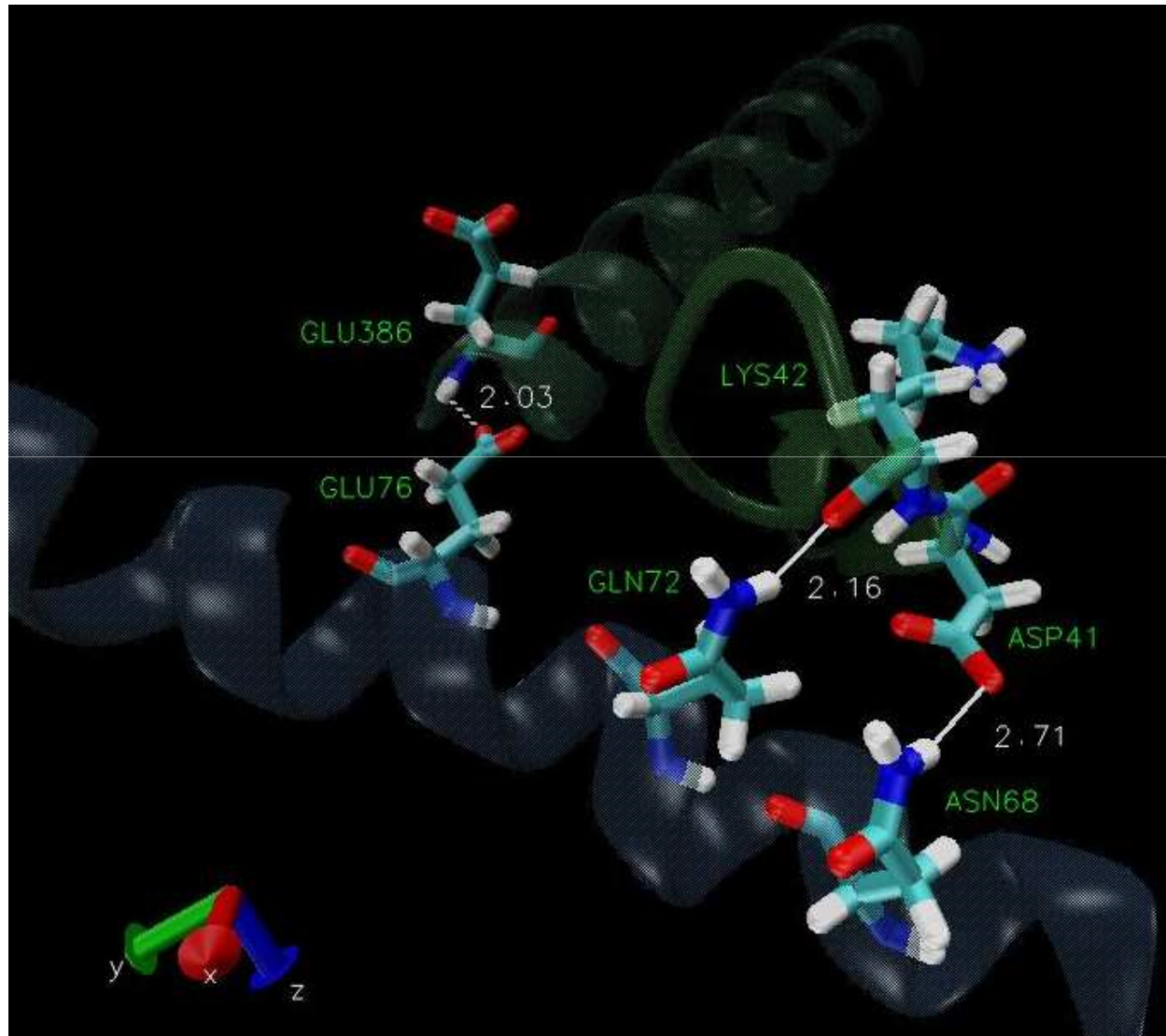


Fig35. Intra-ring interactions, Hbonds (2C7C)

GroEL/GroES> General structure GroES

Subunits of 97 aa

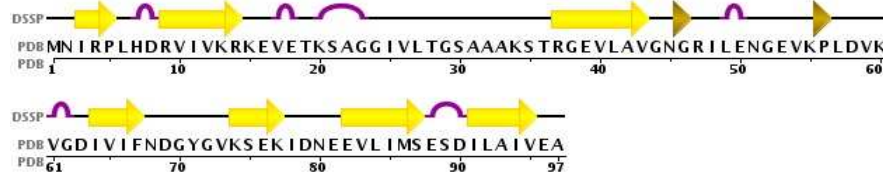


Fig36. GroES chain O sequence (1AON)

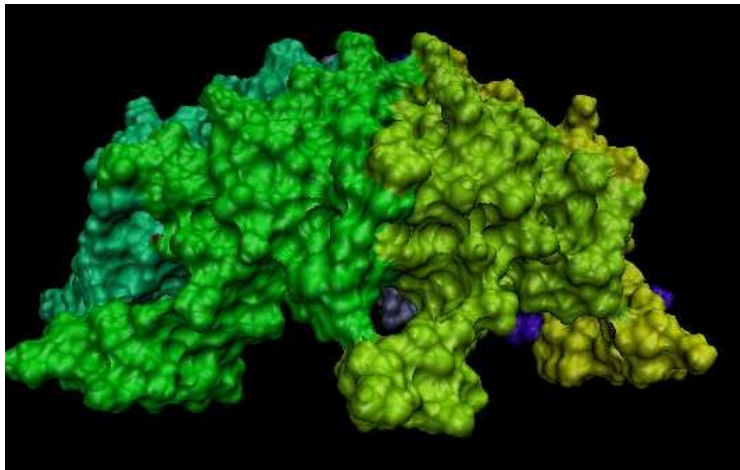


Fig37. GroES subunits, lateral view (1AON)

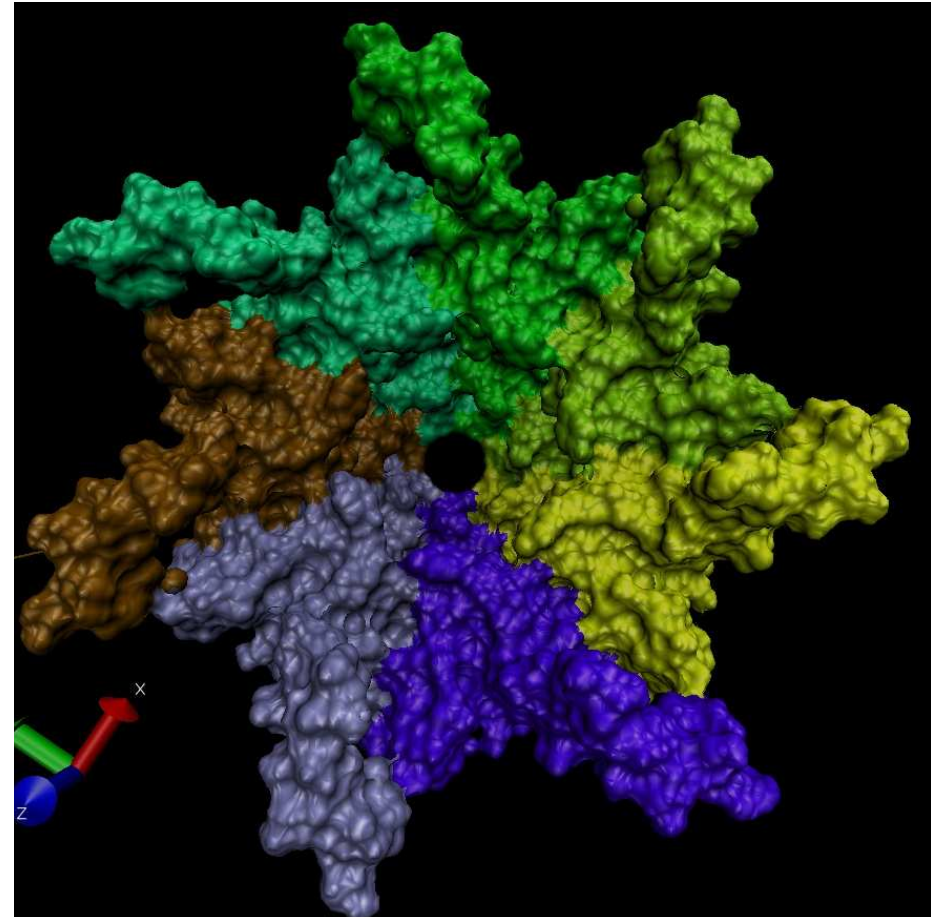
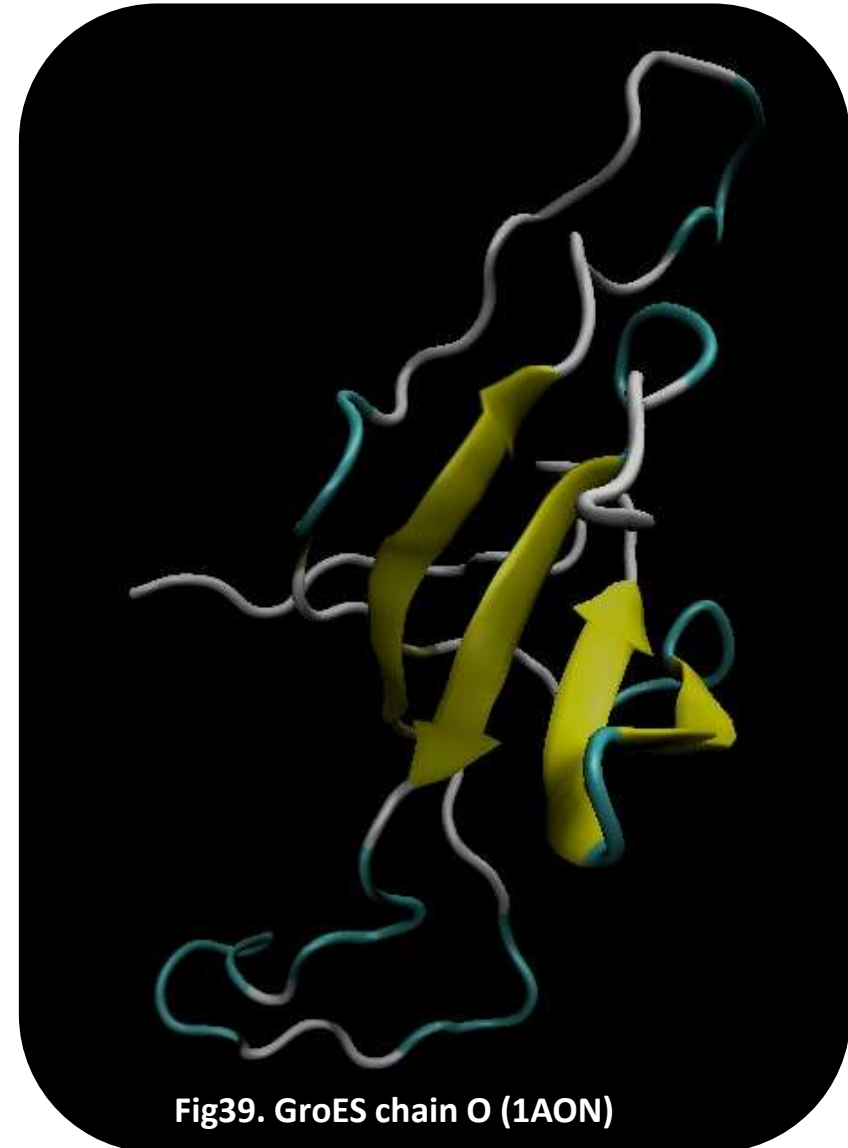


Fig38. GroES subunits, internal view(1AON)

GroEL/GroES > **General structure GroES**

One domain; β -barrel in the core
and 2 β -hairpins loops



GroEL/GroES> General structure GroES

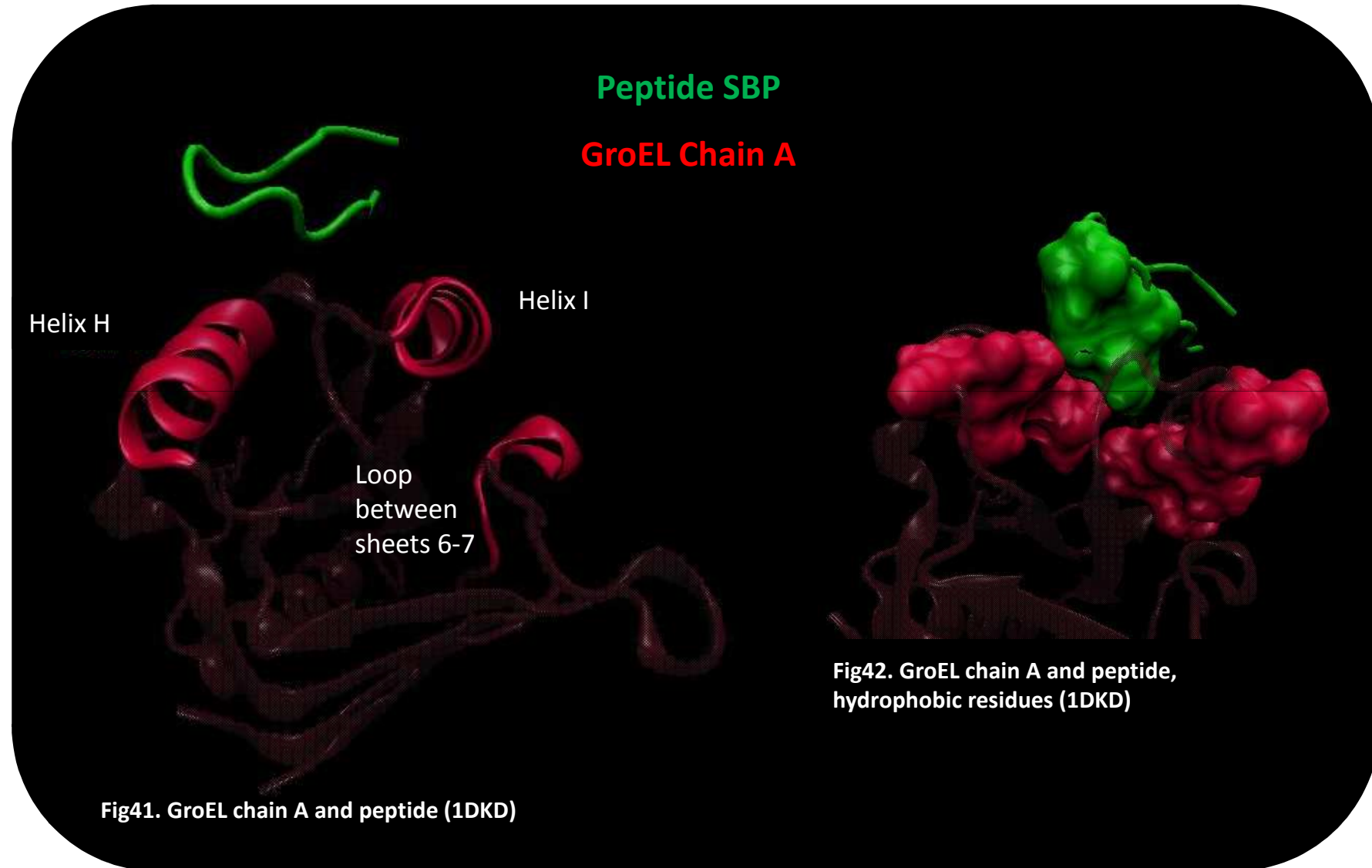
One domain; β -barrel in the core and 2 β -hairpins loops

GroES structure free and bound to GroEL is very similar. Only changes de mobile loop residues (16-32)



Fig40. GroES mobile loop (1AON)

GroEL/GroES> GroEL – polypeptide interaction



GroEL/GroES> GroEL – polypeptide interaction

Hydrophobic interactions

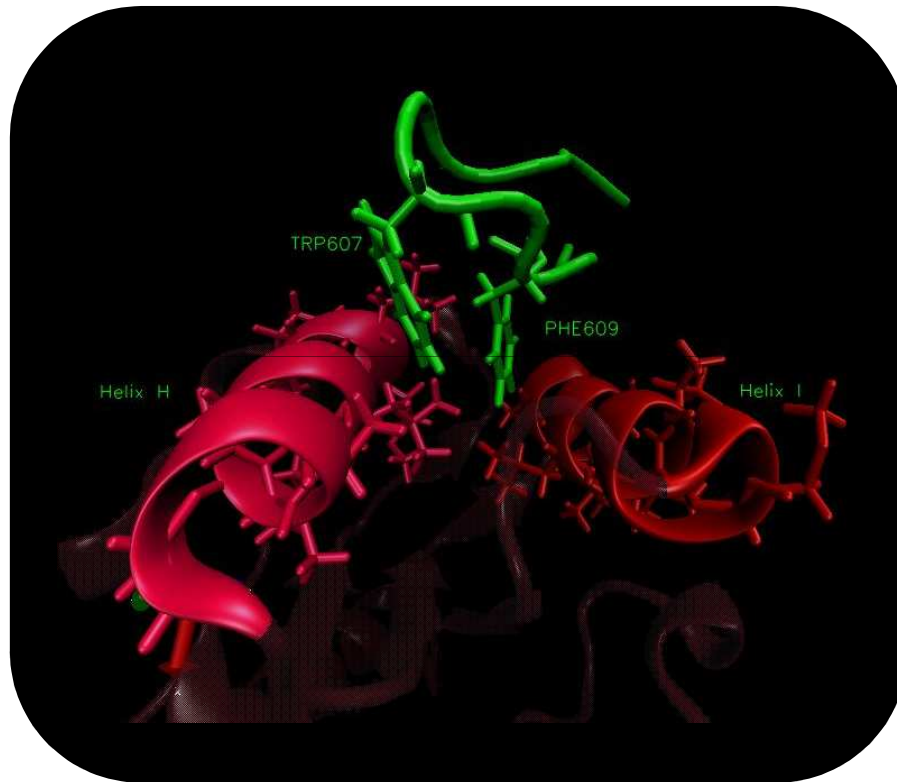


Fig43. GroEL - polypeptide interface, hydrophobic pocket (1DKD)

Hydrogen bonds

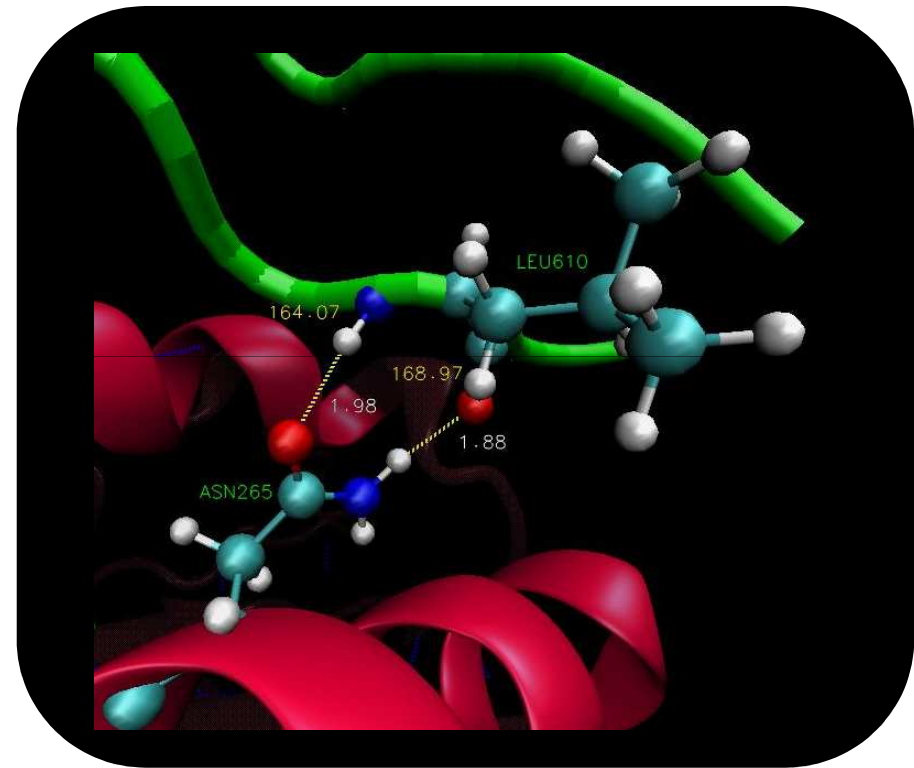


Fig44. GroEL – polypeptide interface, H bonds (1DKD)

GroEL/GroES> **GroEL – polypeptide interaction**

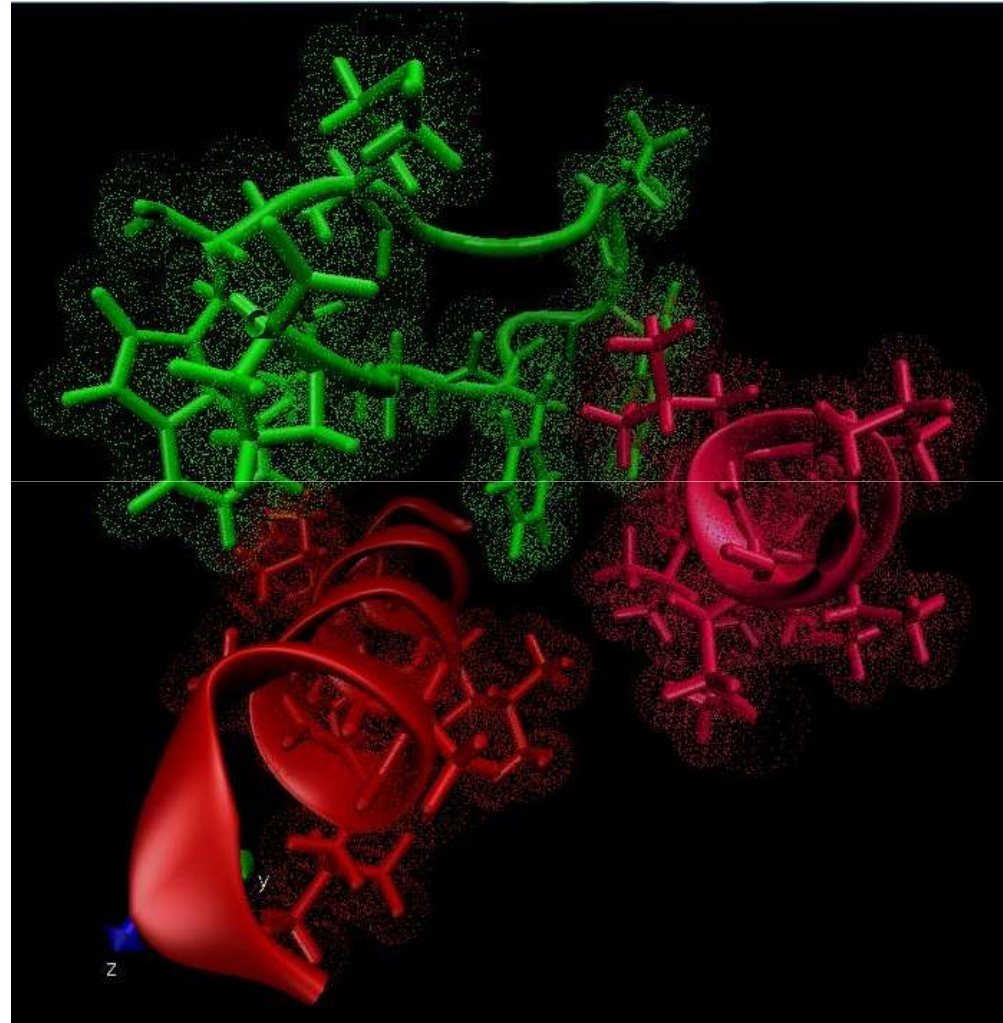
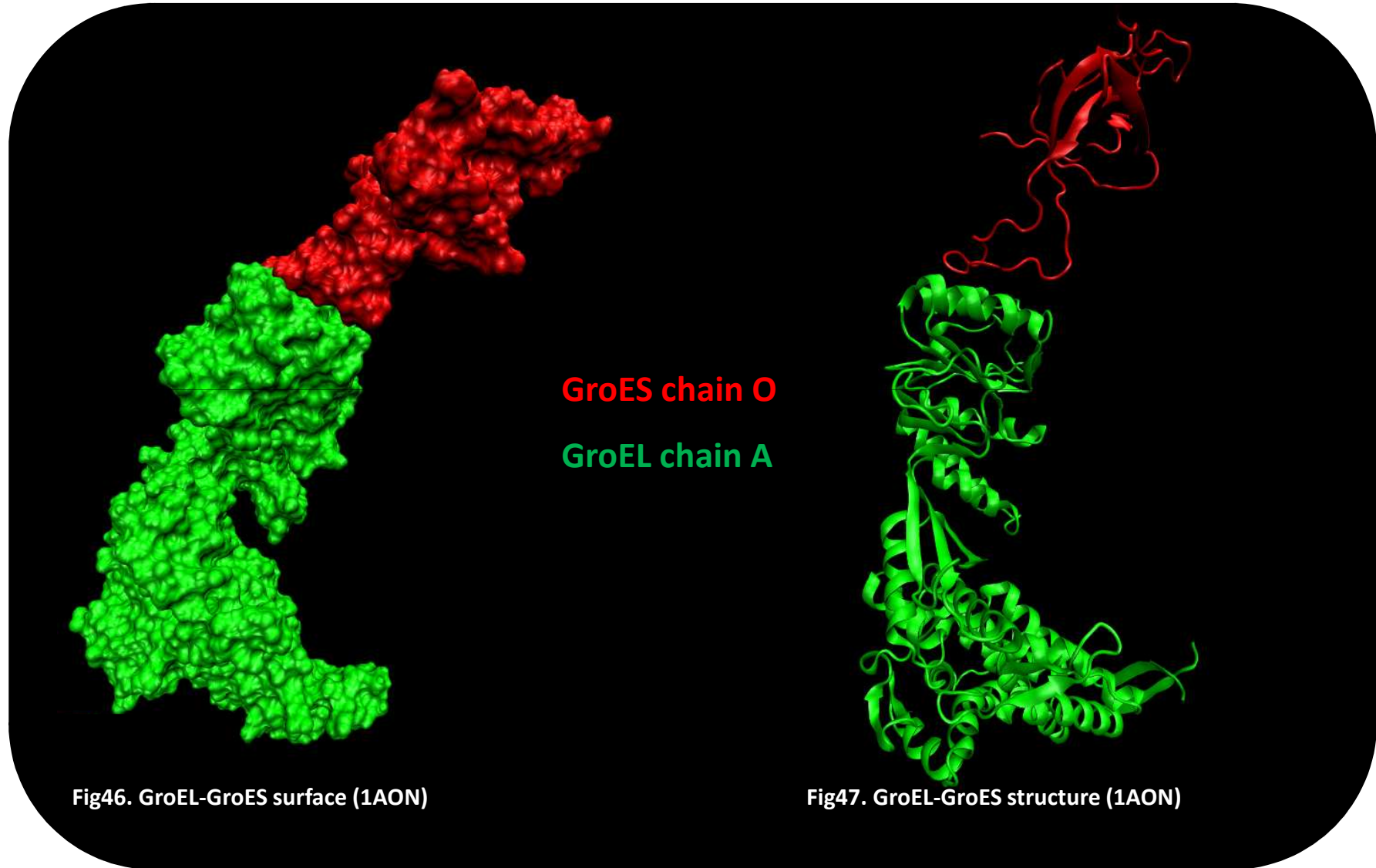


Fig45. GroEL – polypeptide interface, hydrophobic residues (1DKD)

GroEL/GroES> GroEL – GroES interaction



GroEL/GroES> **GroEL – GroES interaction**

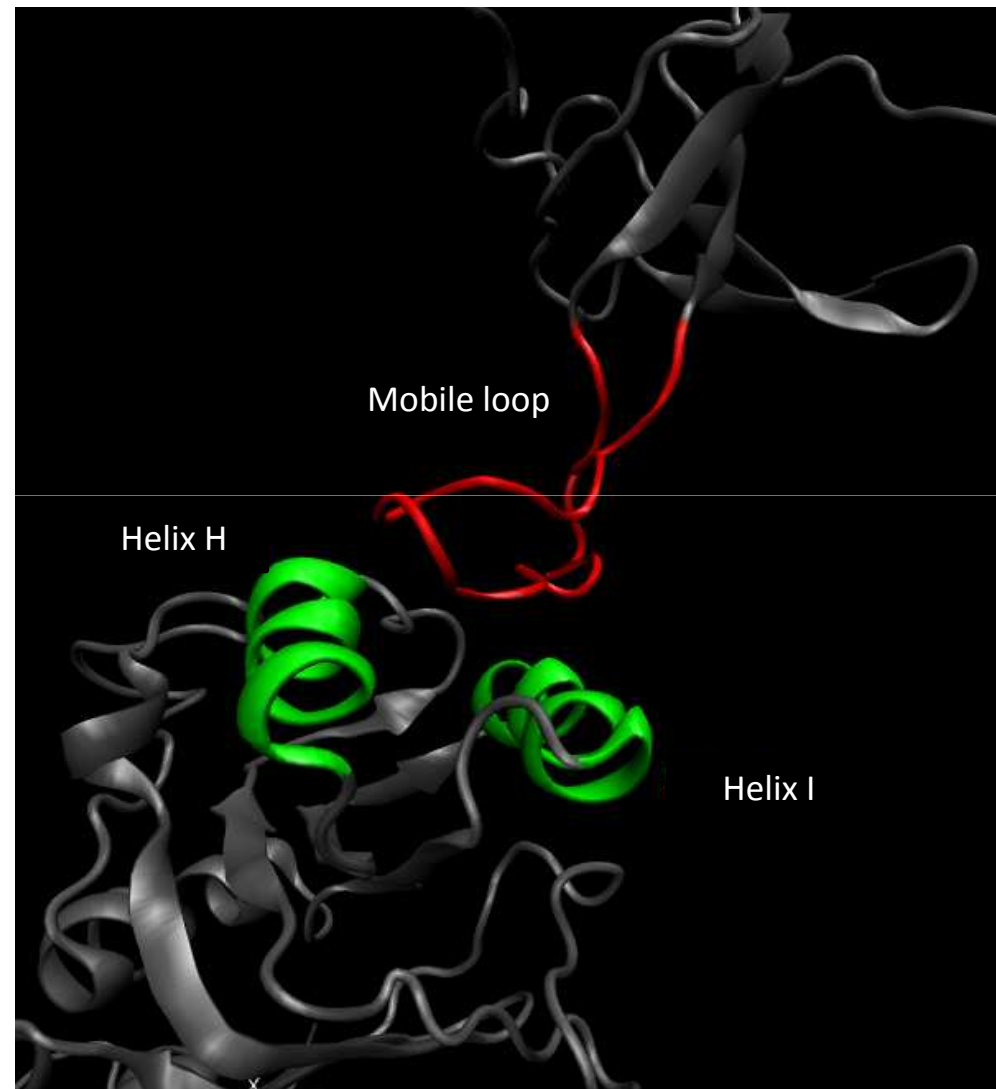


Fig48. GroEL-GroES chain A and O, interface zoom (1AON)

GroEL/GroES > GroEL – GroES interaction

Hydrophobic interactions

GroEL	Leu 234	Leu 237	Val 264
GroES	Val26	Ile25	Leu 27

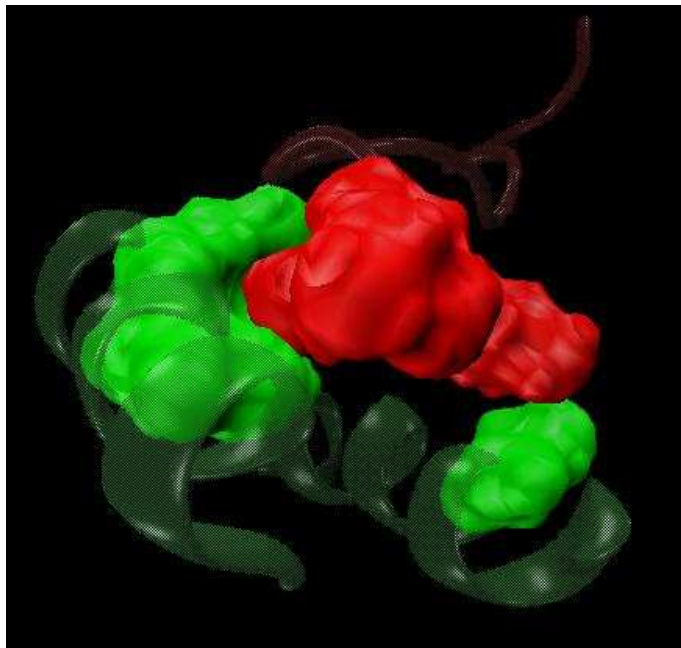


Fig49. GroEL-GroES interface, hydrophobic residues surface (1AON)

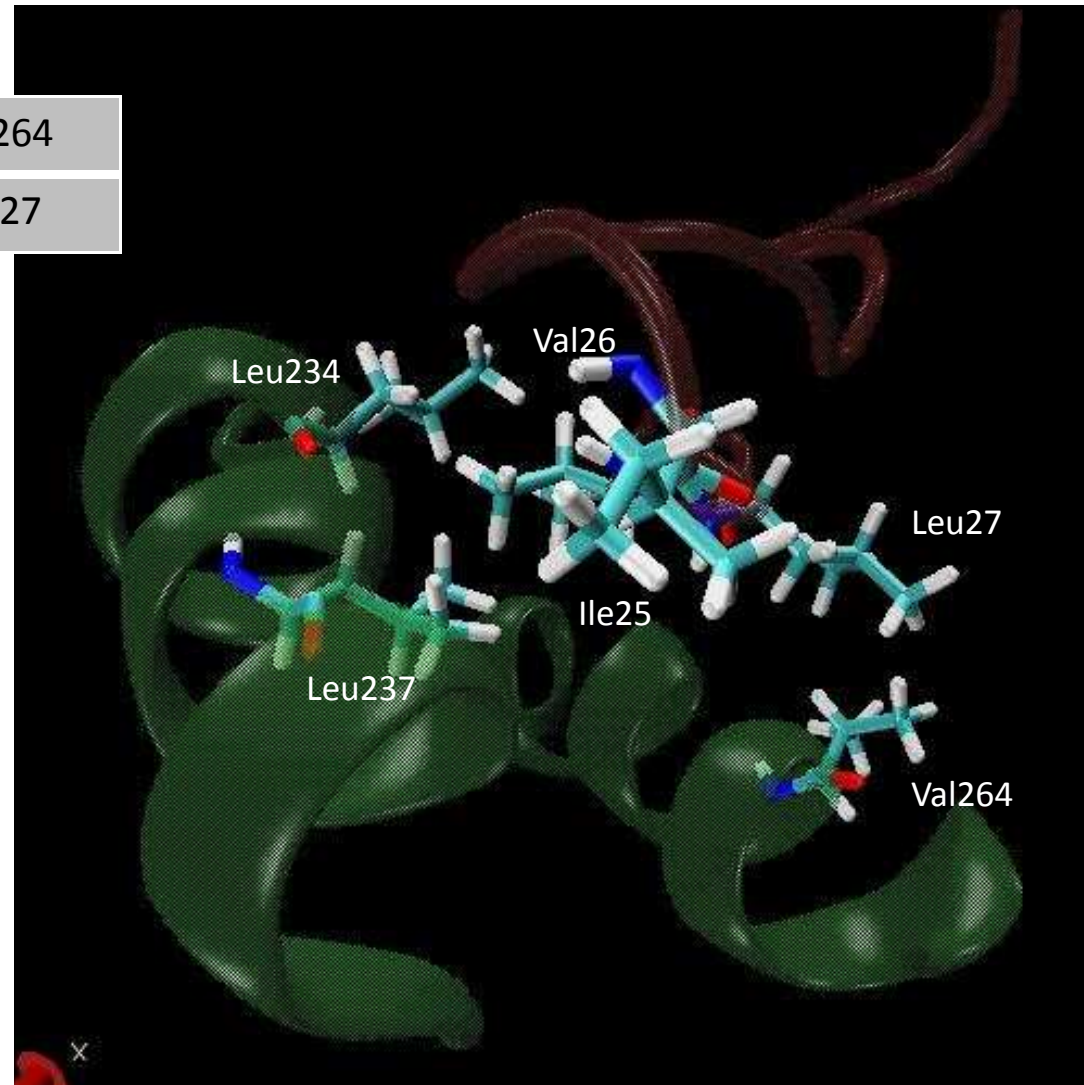


Fig50. GroEL-GroES interface, hydrophobic residues (1AON)

GroEL/GroES > GroEL – nucleotide interaction



Cis ring

Trans ring

Fig51. GroEL rings and ADP bound to the cis ring (1AON)

GroEL/GroES> GroEL – nucleotide interaction

NUCLEOTIDE BINDING SITE:

equatorial domain, but

intermediate domain acts as a lid

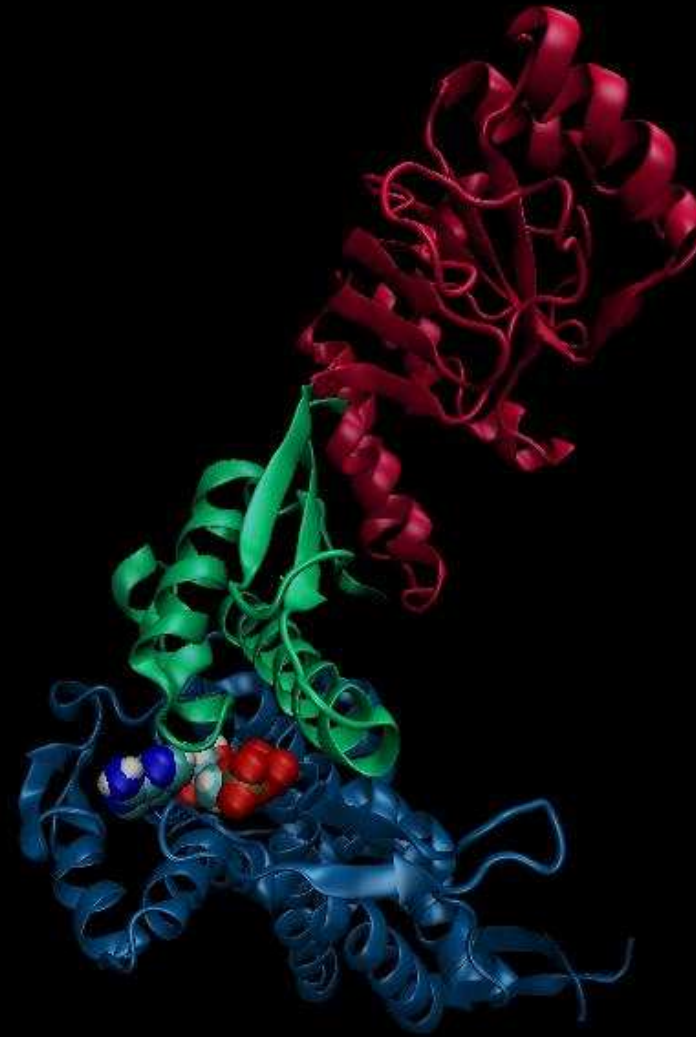


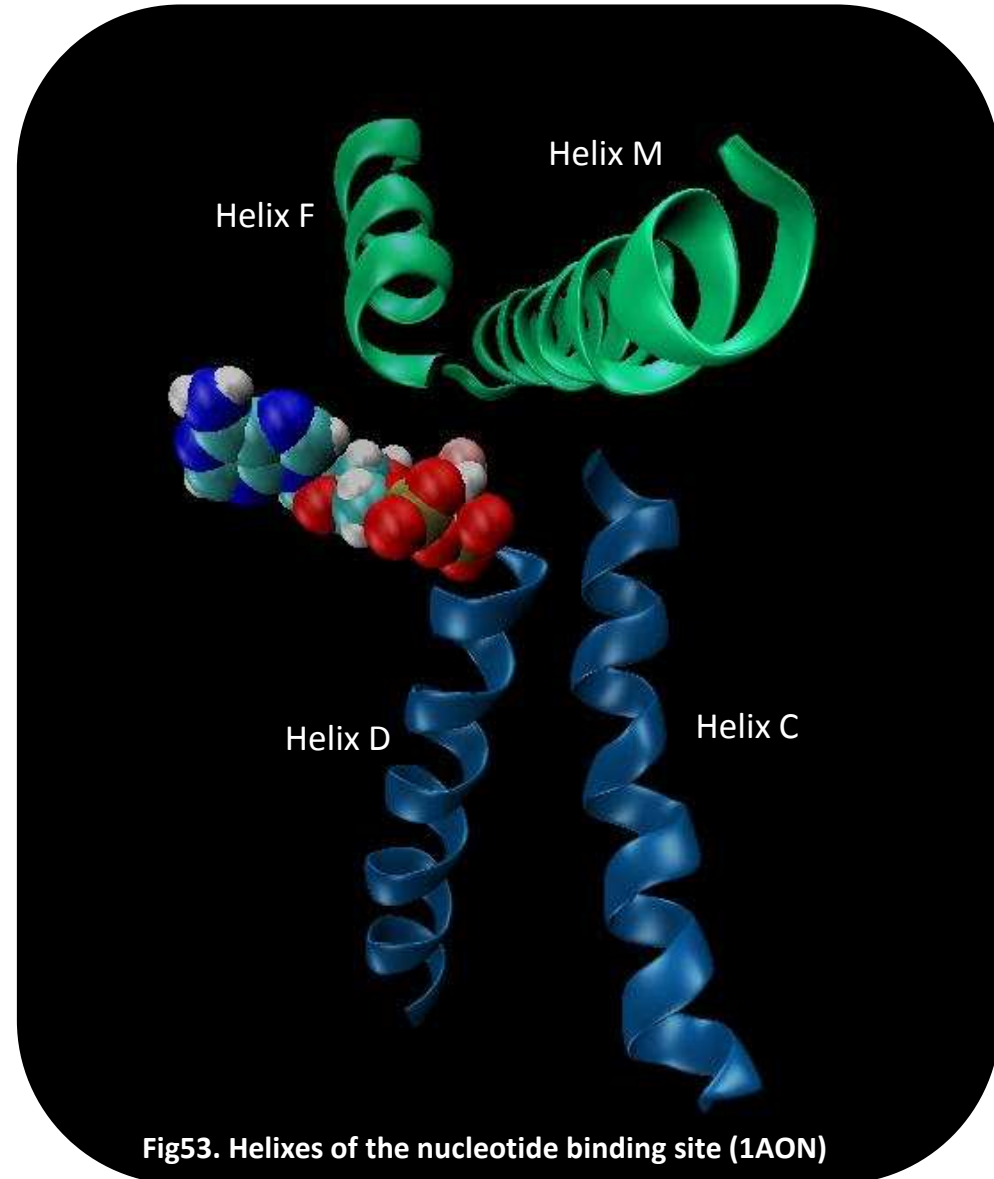
Fig52. GroEL chain A and ADP (1AON)

GroEL/GroES> GroEL – nucleotide interaction

NUCLEOTIDE BINDING SITE:

equatorial domain, but

intermediate domain acts as a lid



GroEL/GroES> GroEL – nucleotide interaction

Phosphate binding loop
(DGT TT) conserved in all
chaperonin

```

1 MSQQ - - - PGVLPENMKRYMGRDAQRMN
1 MAQLSGQPVVILPEGTQRYVGRDAQRRLN
1 AAK - - - - DVKF - - - - GNDAGVKM
1 MAK - - - - ILVF - - - - DEAARRAL

5 SKAQDTAVGGDGT TTAVVLSGELLKQAET
2 AKTQEKEVGGDGT TTAVVLAGELLRKAAE
3 AKTQDKEAGDGT TTAVVLAGELLRKAAE
7 ASKANDAGDGT TTATVLAQAIITEGLK
7 ASKTNDVAGDGT TTATVLAQAIIVREGLK

2 ADLVVKAVNAVAEVRD SKTIVDTANIKV
1 AEIIVEAVSAVVD - DECK - - VDKDLIKI
5 AKLAVEAVKQVAEKKDGKYVVDLDNIKF
3 GKLIAEAMDKVG - - KEG - - - - - VITV
7 GKLIADEMEKVG - - KEG - - - - - IITV

1 KIQDFLNQETNTFKQMVEKIKKSGANVV
7 KLMEFIEQEEKMLKDMVAEIKASGANVL
1 QLMSEIEQEEKMLKDMVAEIKASGANVV
  
```

Fig54. Sequence alignment between members of both group I and II of chaperonins, conserved region.

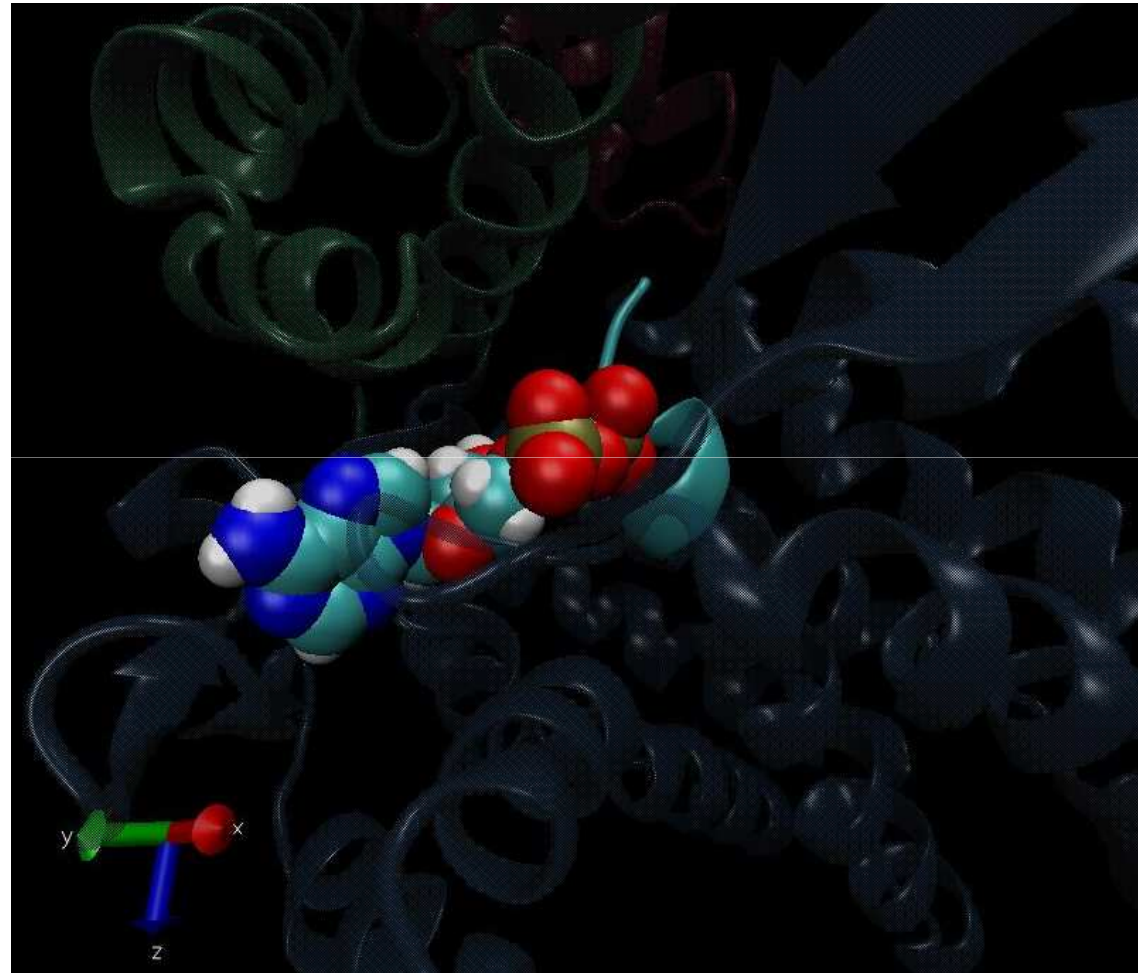


Fig55. Zoom nucleotide binding site (1AON)

GroEL/GroES> GroEL – nucleotide interaction

PHOSPHATE BINDING LOOP

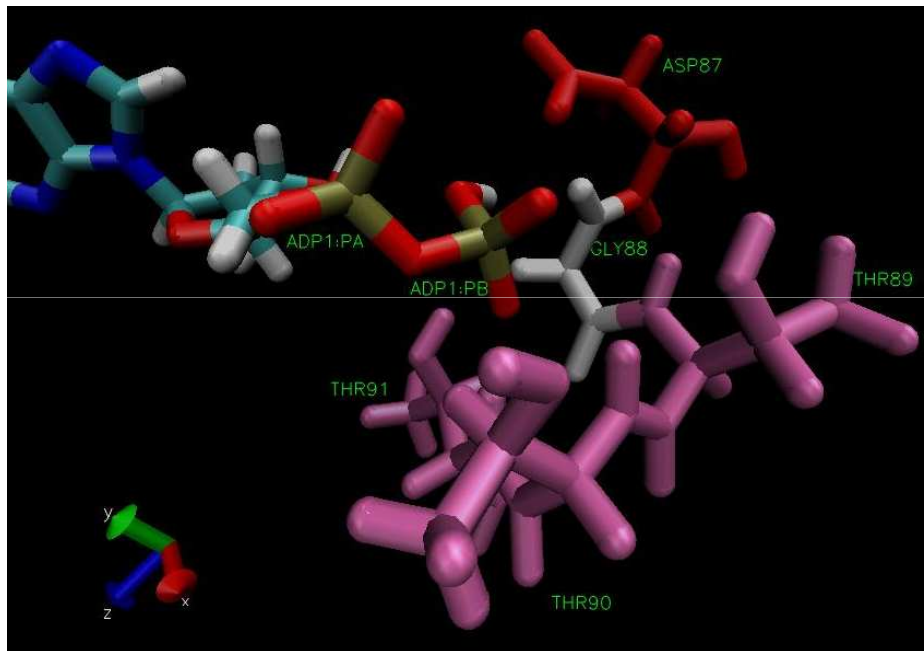


Fig56. Phosphate binding loop and ADP (1AON)

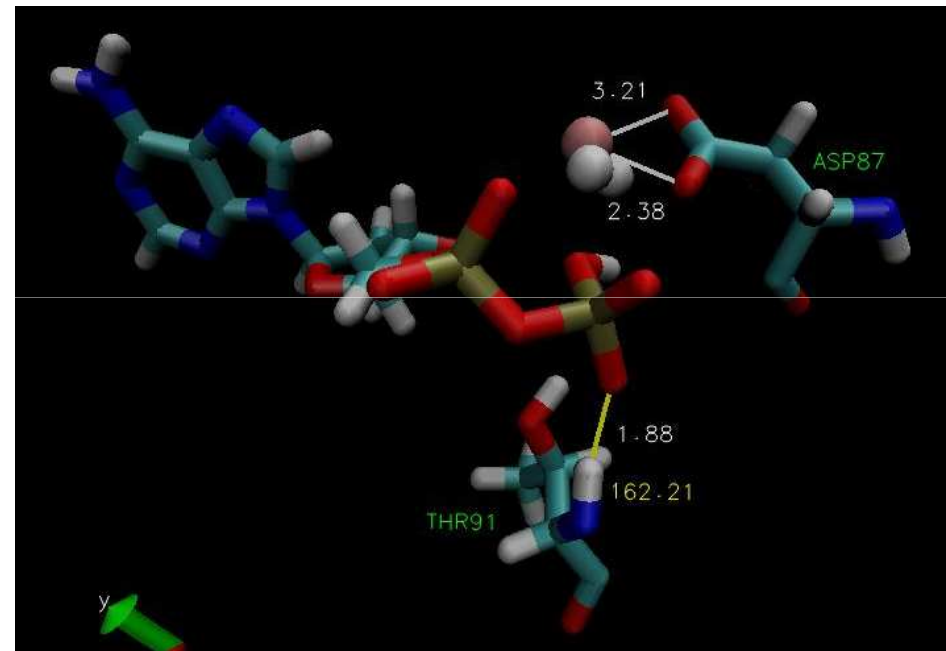


Fig57. Phosphate binding loop and ADP interactions (1AON)

GroEL/GroES > GroEL – nucleotide interaction

Hydrogen bonds

Magnesium coordinations

van der Waals contacts

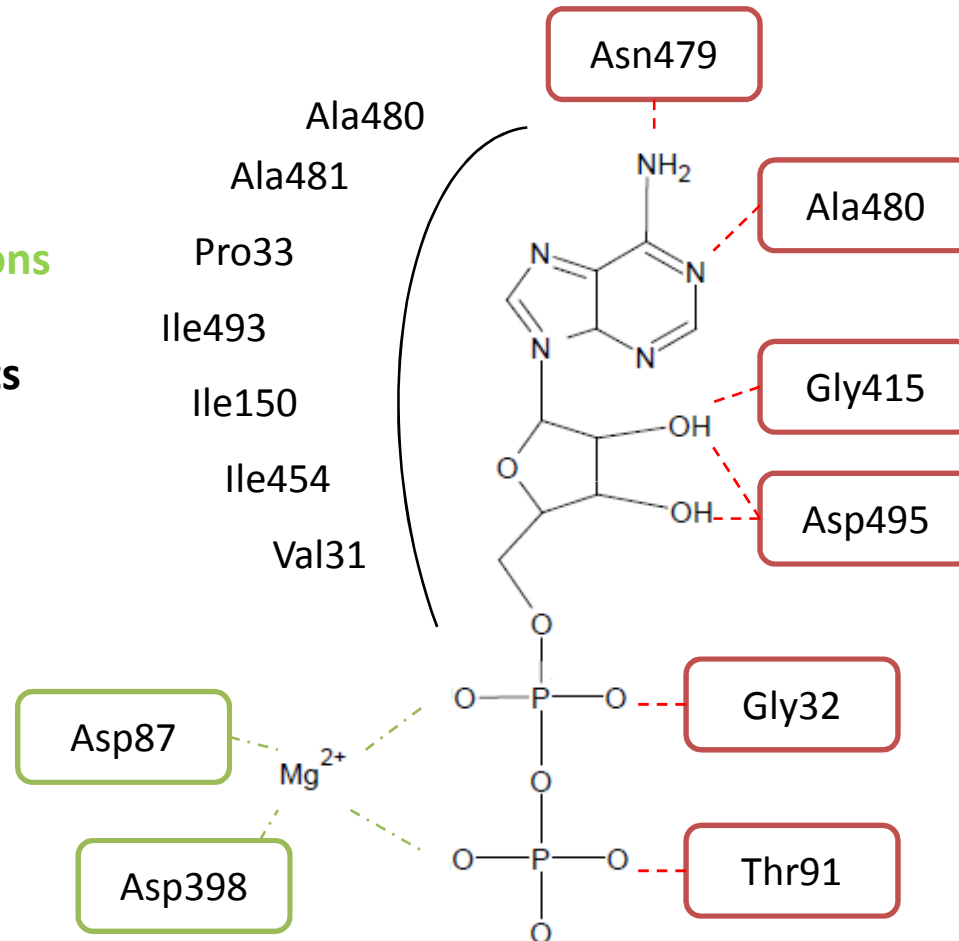


Fig58. Interactions between ADP, Mg²⁺ and GroEL residues (ChemSketch)

GroEL/GroES> GroEL – nucleotide interaction

Magnesium coordinates

Hbonds

VDW

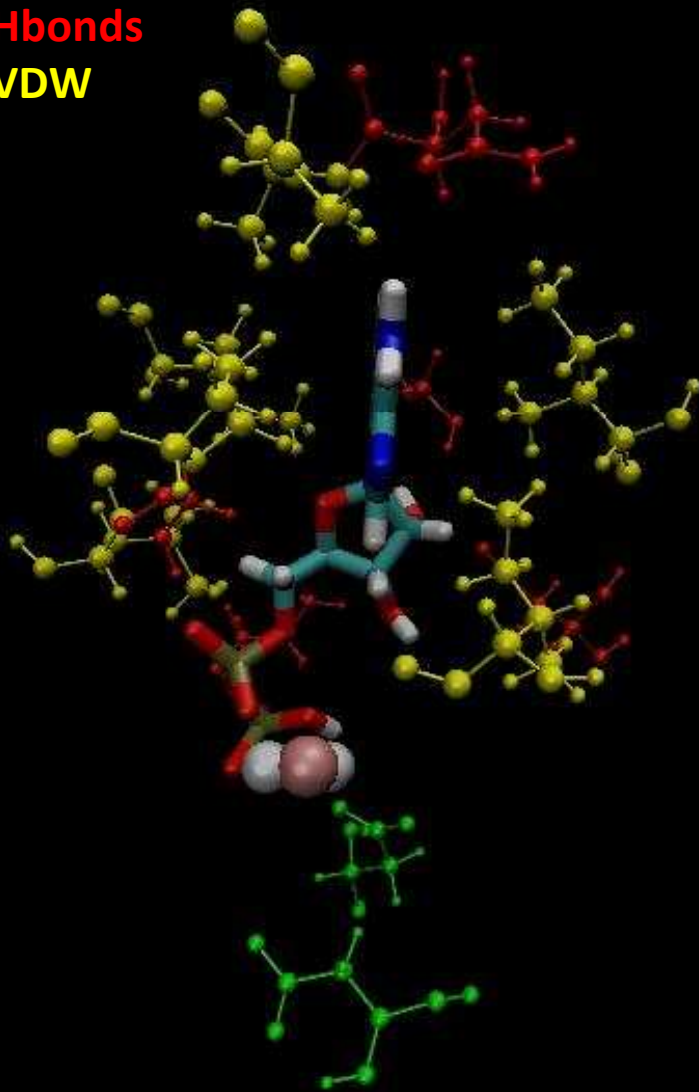


Fig59. Interactions between ADP, Mg²⁺ and GroEL residues (1AON)

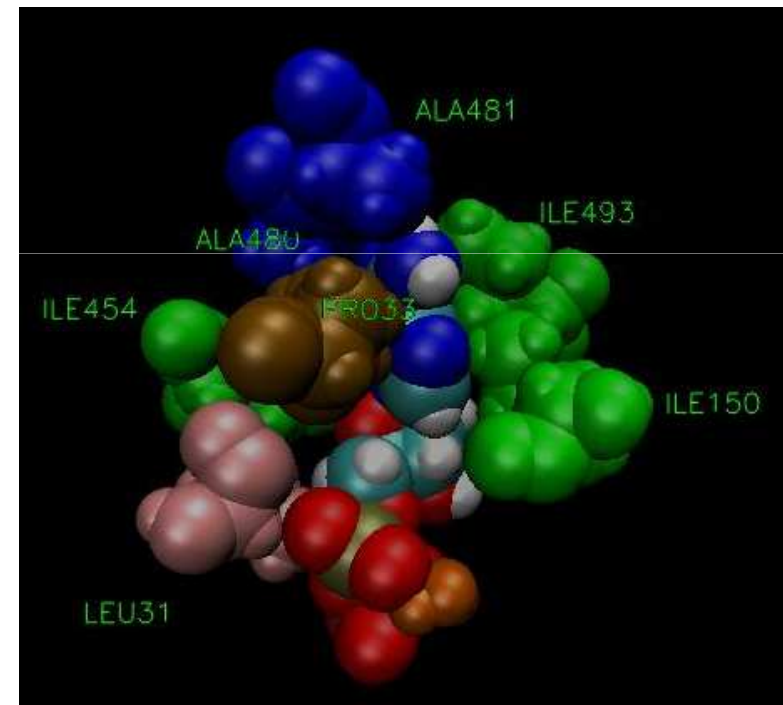


Fig60. Van der Waals interactions between GroEL and ADP (1AON)

GroEL/GroES > GroEL – nucleotide interaction

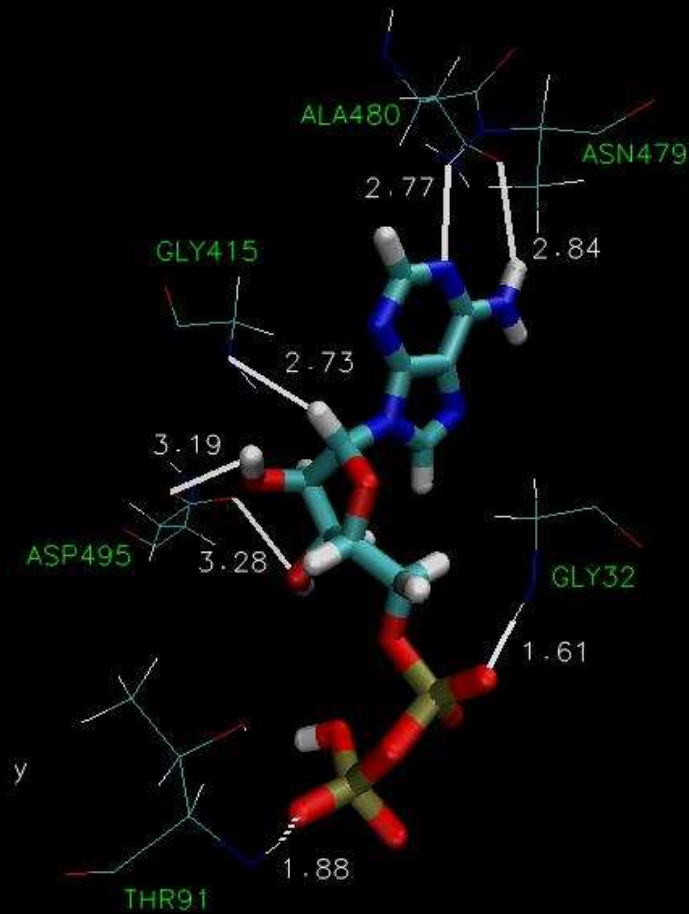


Fig61. Interactions between ADP and GroEL residues, Hbonds (1AON)

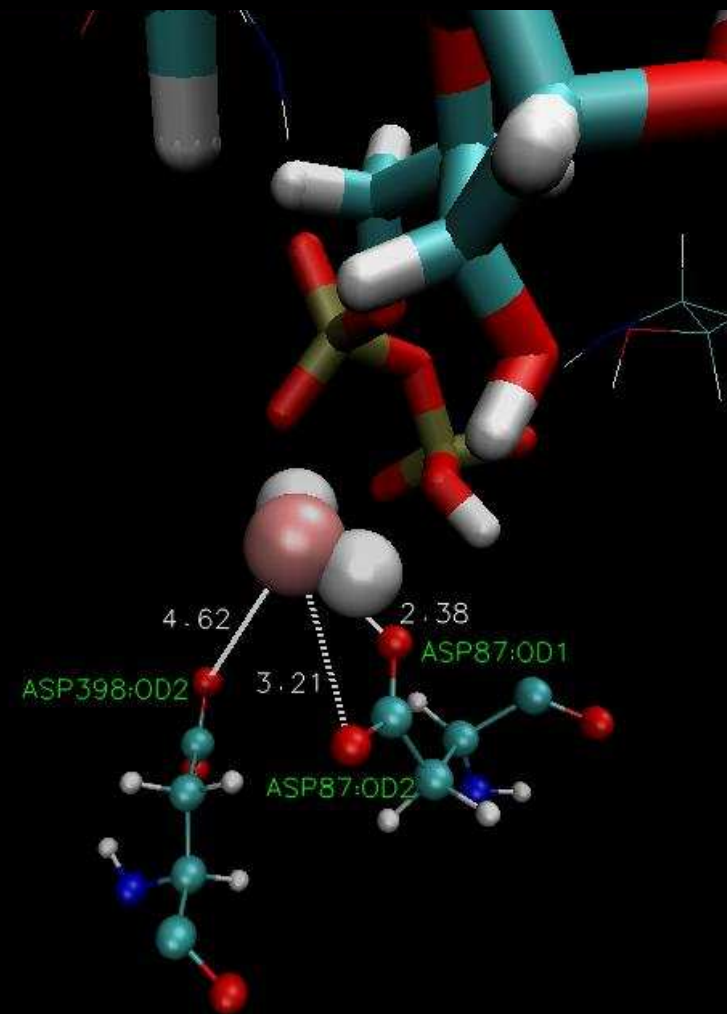


Fig62. Interactions between Mg^{2+} and GroEL residues, magnesium coordinations (1AON)

GroEL/GroES> GroEL – nucleotide interaction

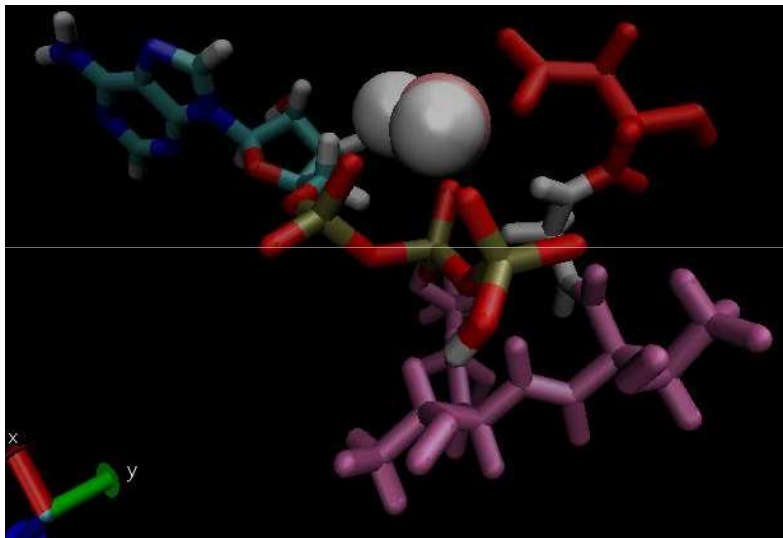


Fig63. Interactions between ATP and GroEL residues (1SX3)

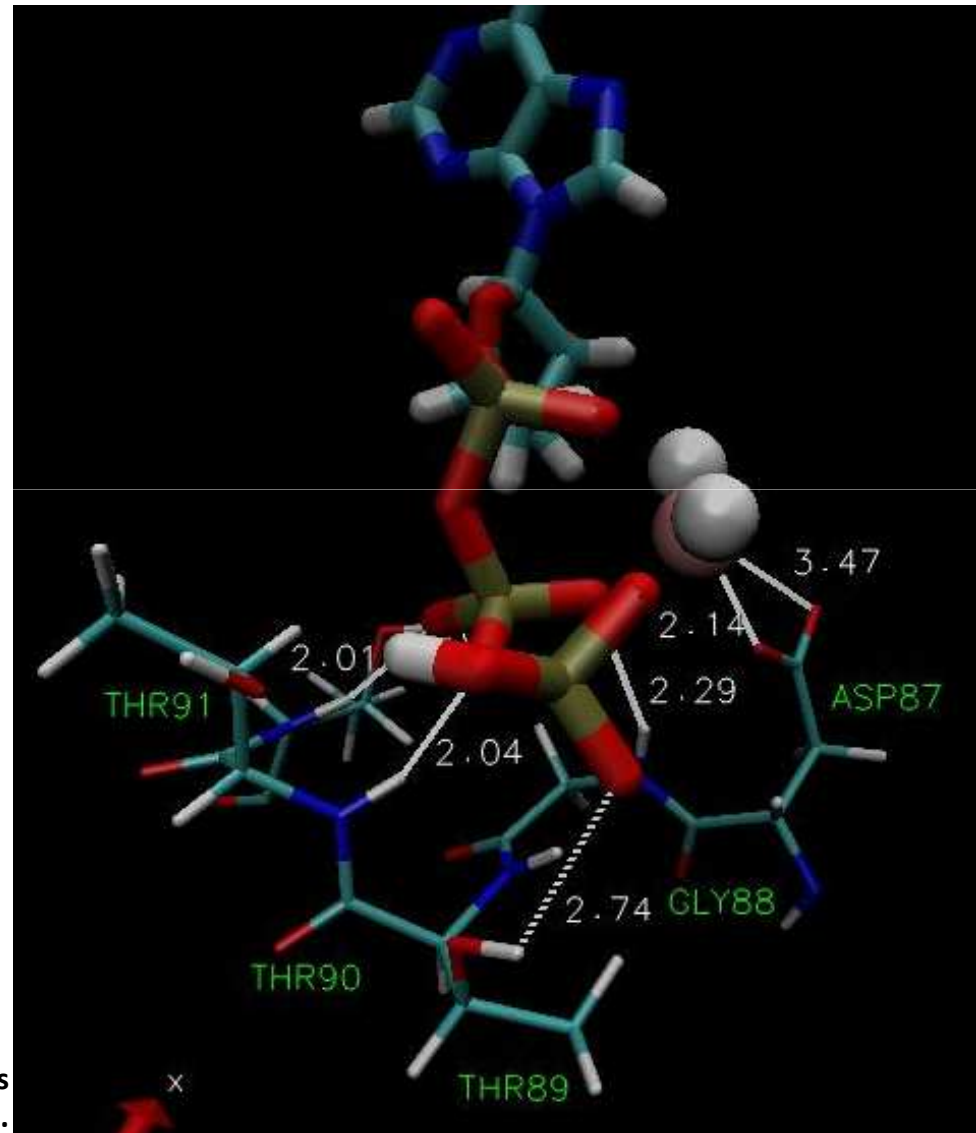
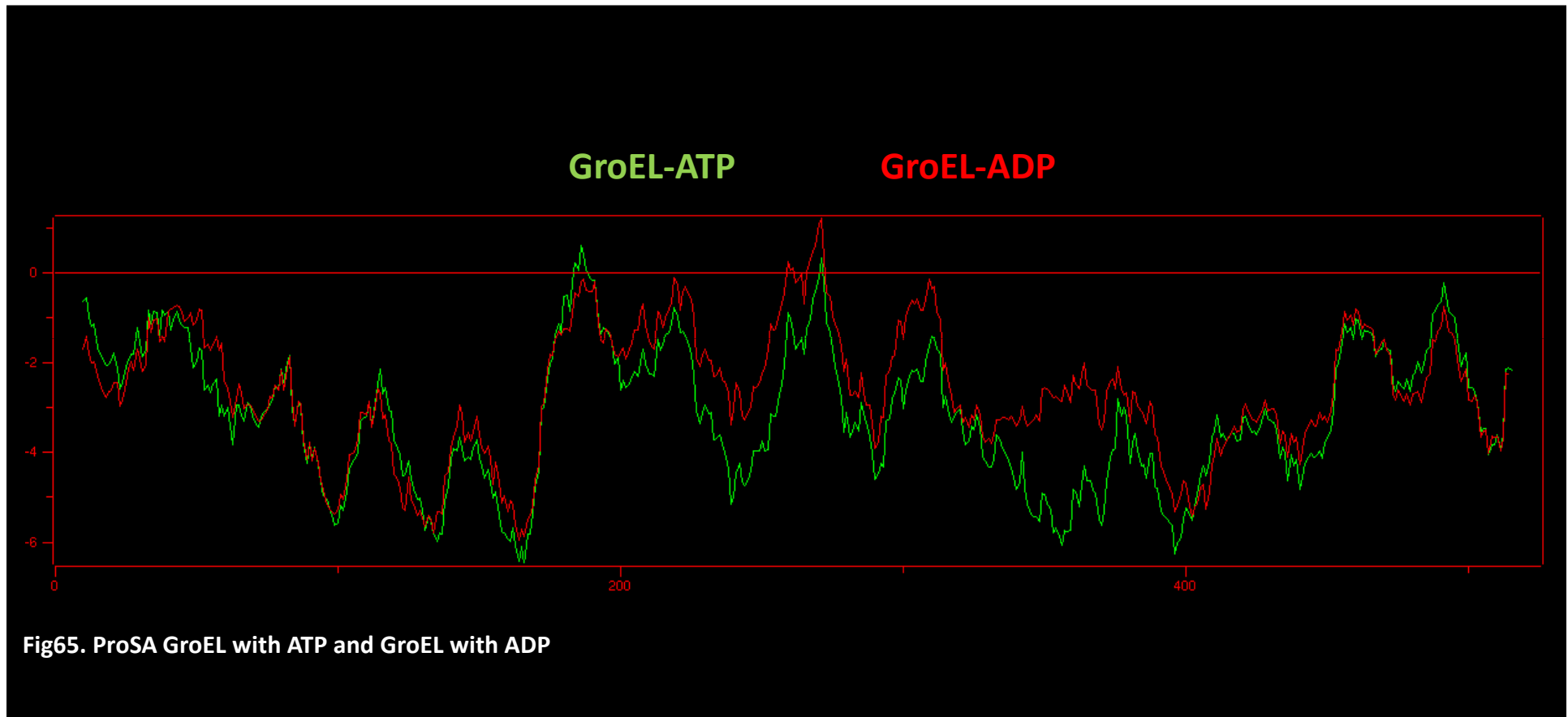


Fig64. Interactions between ATP and GroEL residues (1SX3).

GroEL/GroES> GroEL – nucleotide interaction



GroEL/GroES> **Folding cycle overview**

This reaction cycle can be divided into four phases:

- I. Polypeptide Binding
- II. Nucleotide and GroES Binding
- III. Polypeptide Release and Folding
- IV. Protein Folding and Release of Ligands

GroEL/GroES > Folding cycle overview

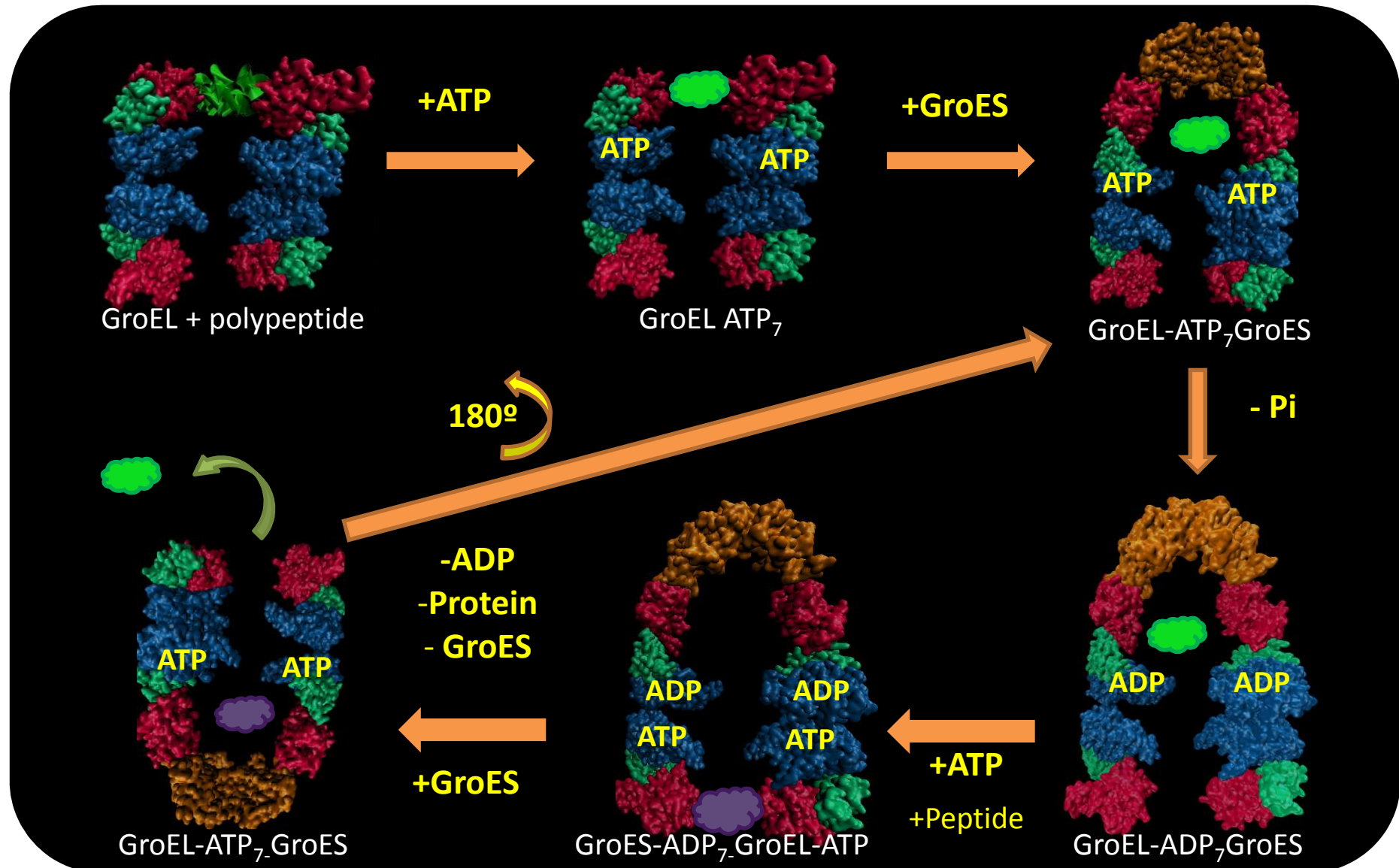


Fig55. GroEL-GroES cycle overview (1MNF, 1SX3, 1SVT, 1SX4, 1GRU)

GroEL/GroES > **Folding cycle** > Phase I

Polypeptide Binding

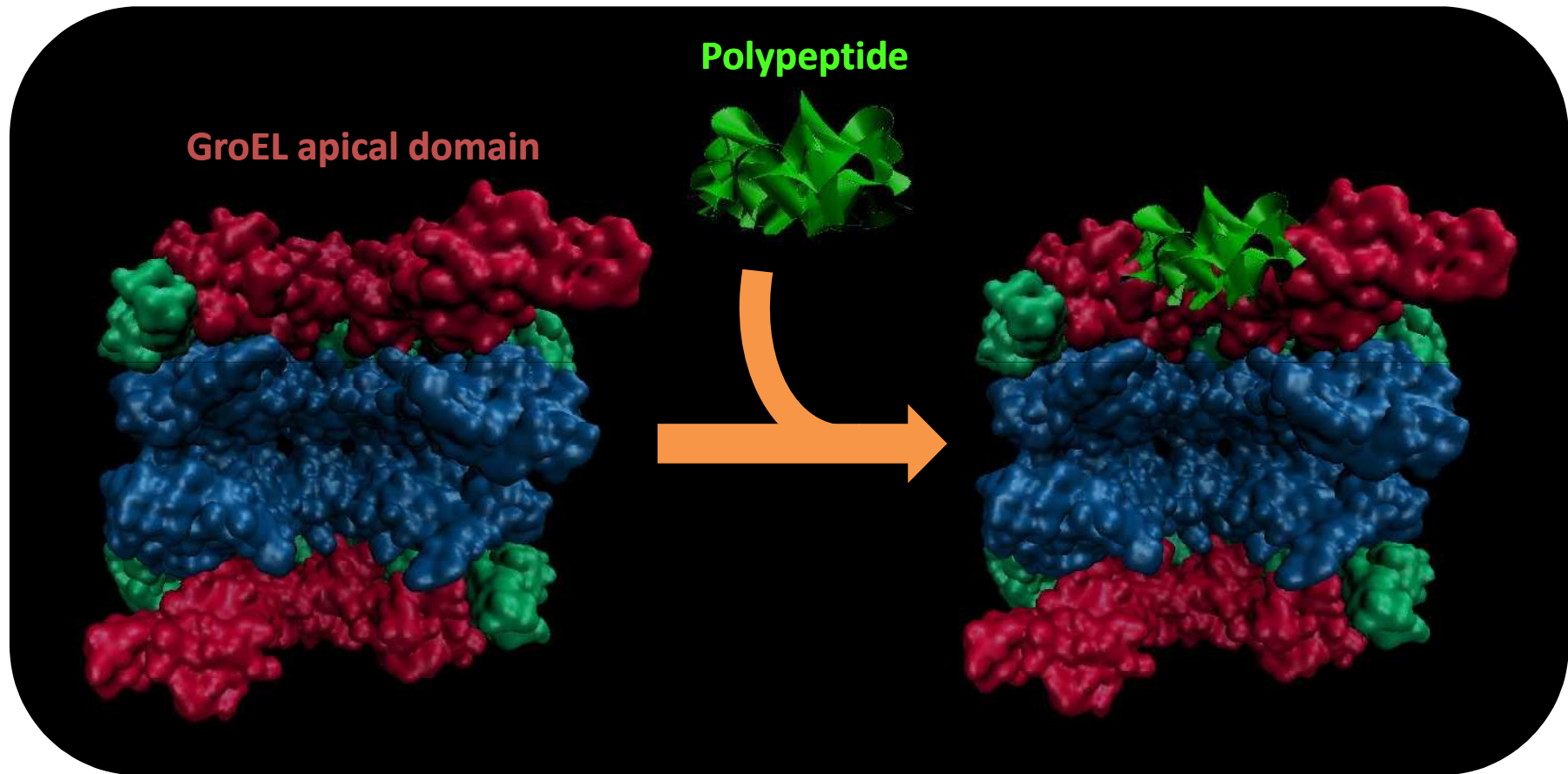


Fig67. Polypeptide binding (1MNF)

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding



Fig68. GroEL (1SS8), chain A

+ ATP

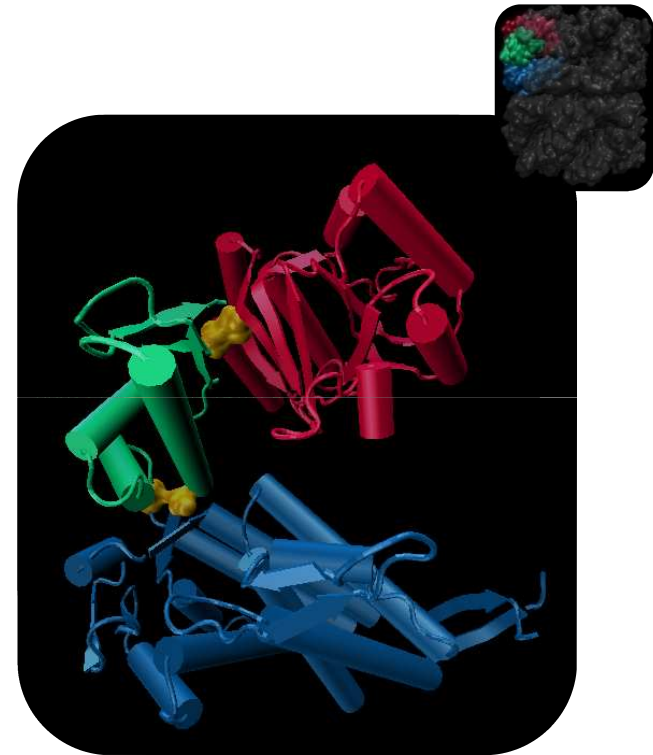


Fig69. GroEL ATP₇ (1SX3), chain A

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding



Fig70. GroEL ATP₇ (1SX3), chain A

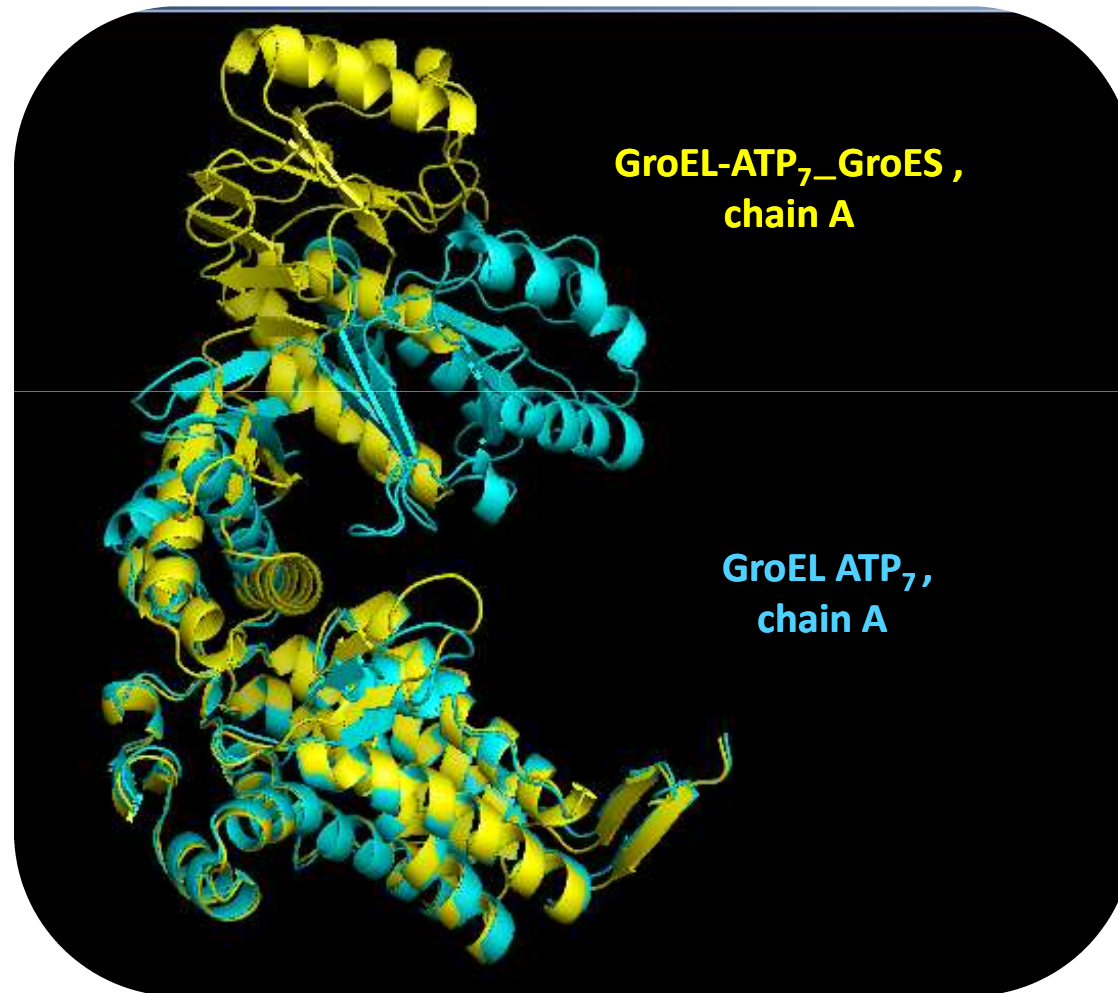
+ GroES



Fig71. GroEL-ATP₇-GroES (1SVT), chain A

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding



RMSD 1.12
Sc 3.91

Fig72. STAMP GroEL ATP₇ (1SX3), chain A vs GroEL-ATP₇-GroES (1SVT), chain A

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

GroEL ATP₇, GroEL-ATP₇-GroES

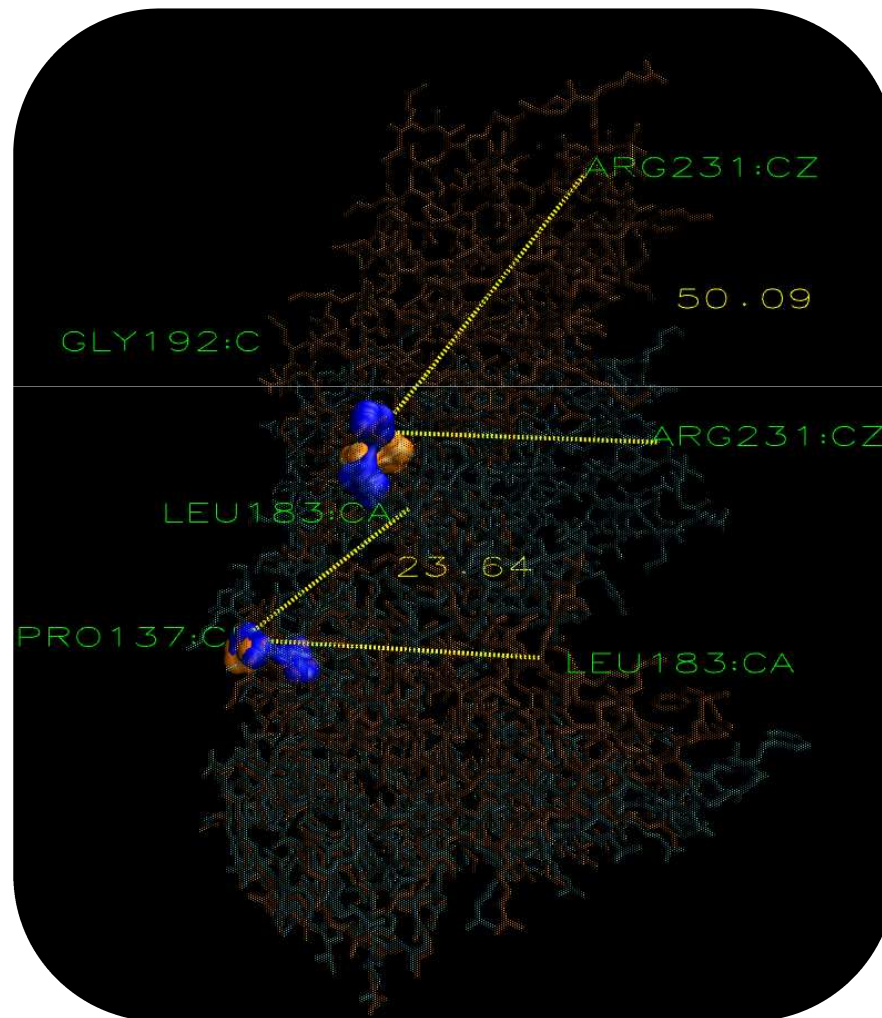
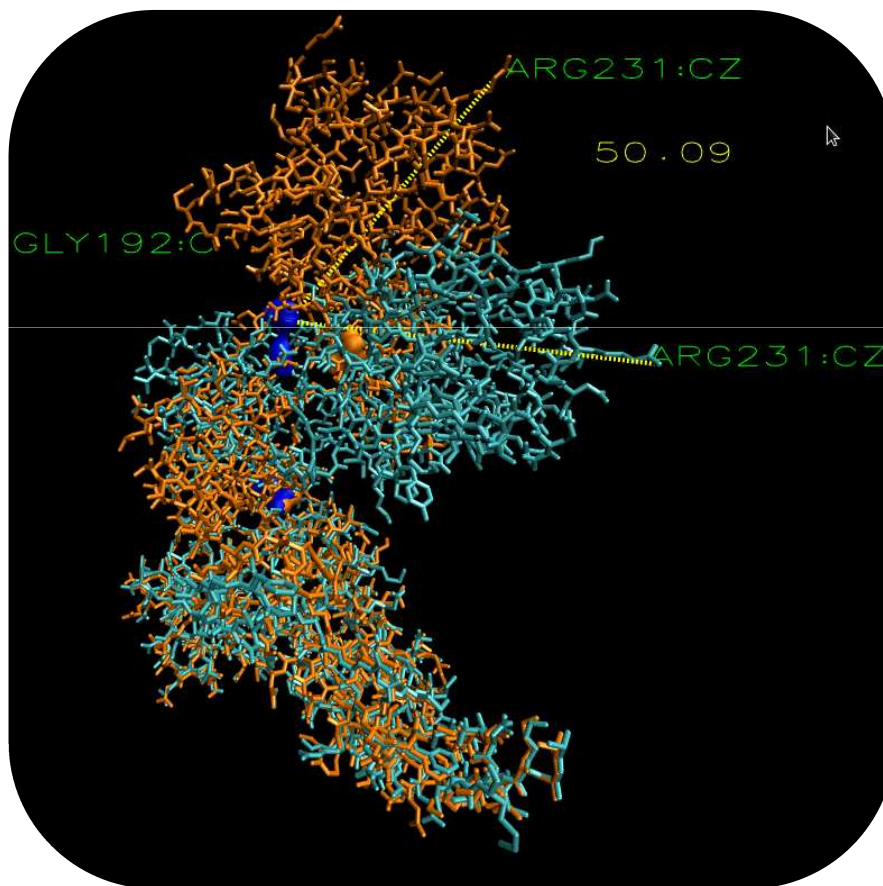


Fig73. STAMP GroEL ATP₇ (1SX3), GroEL-ATP₇-GroES (1SVT).

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

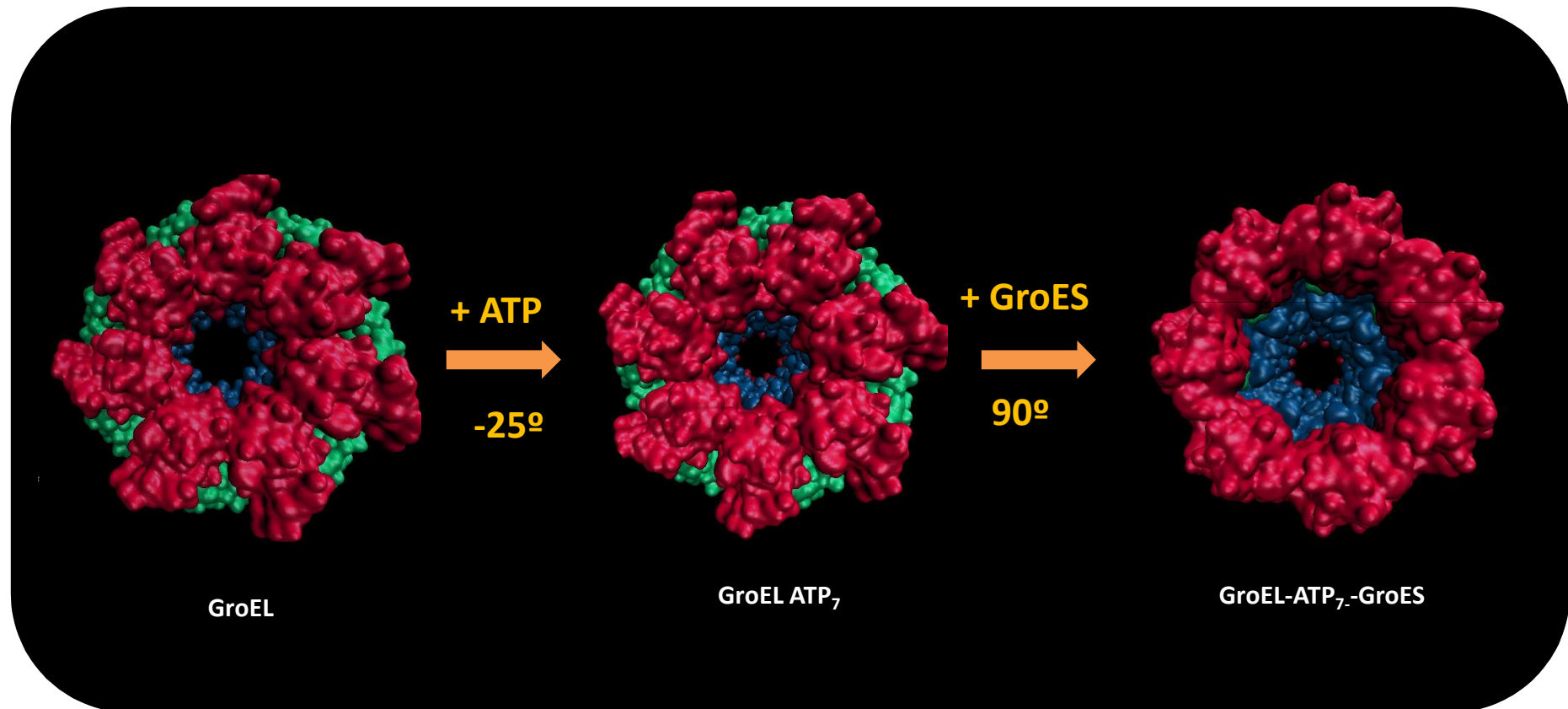


Fig 74. Twist of the apical domains (1SS8, 1SX3, 1SVT)

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

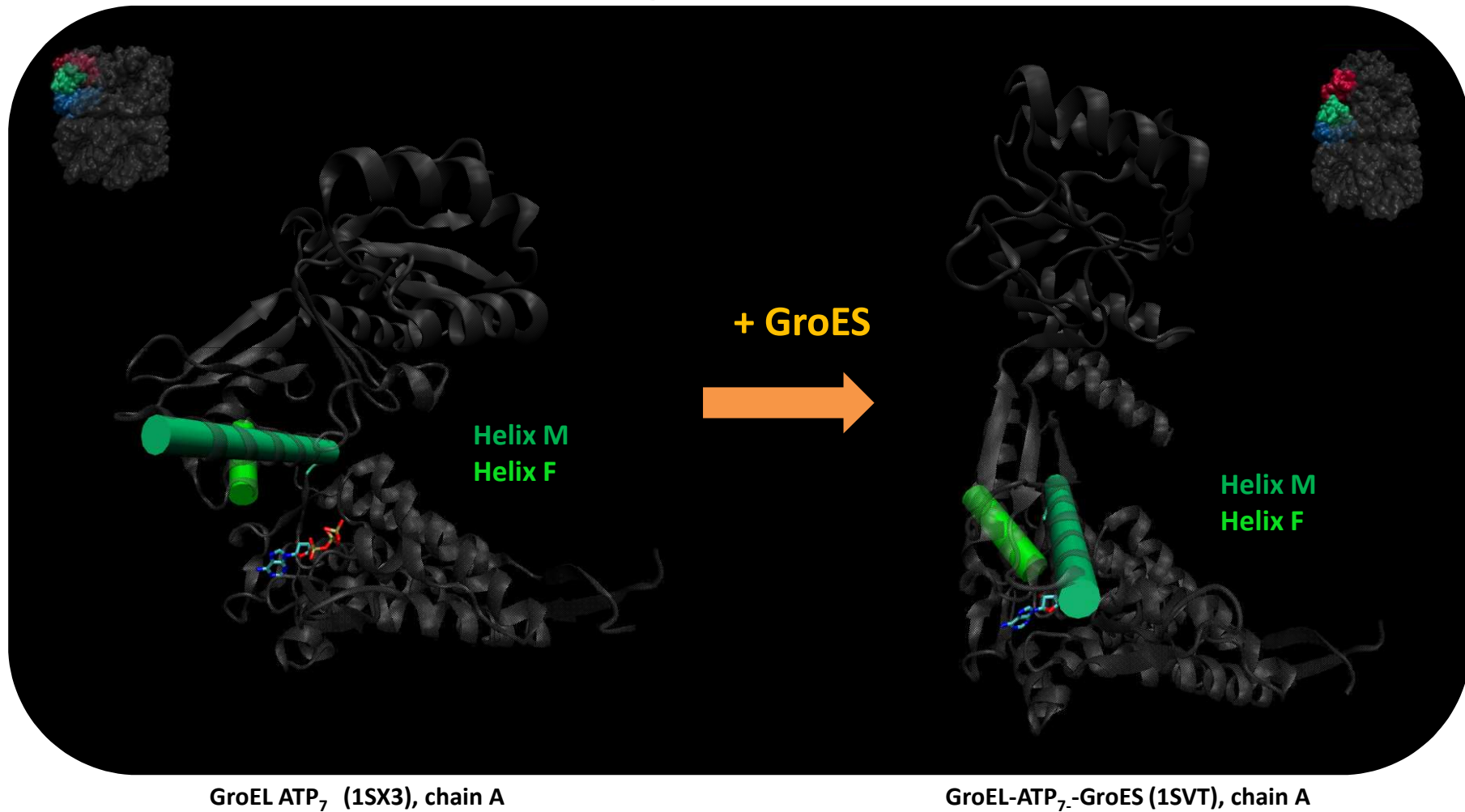


Fig75. Closing the nucleotide binding site

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

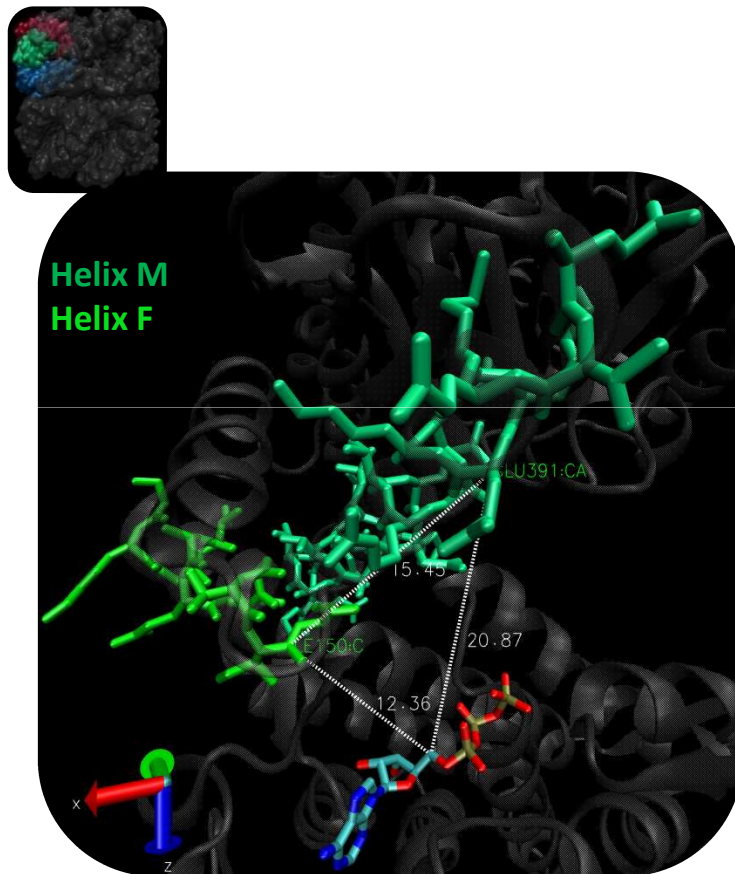


Fig76. GroEL (1SX3)

+ GroES

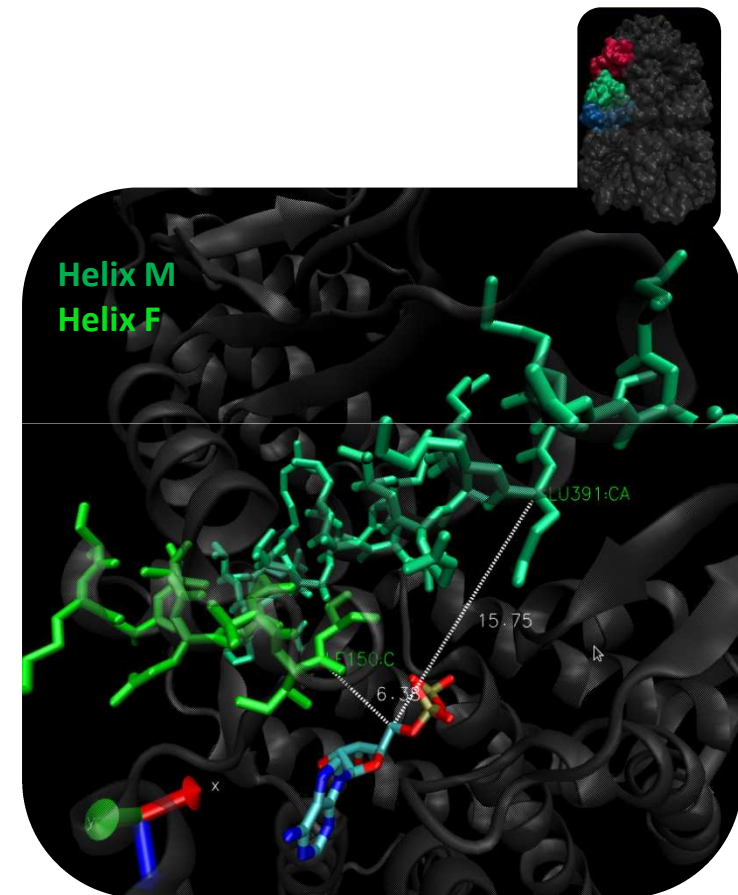


Fig77. GroEL-GroES (1SVT)

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

GroEL ATP₇, GroEL-ATP₇-GroES

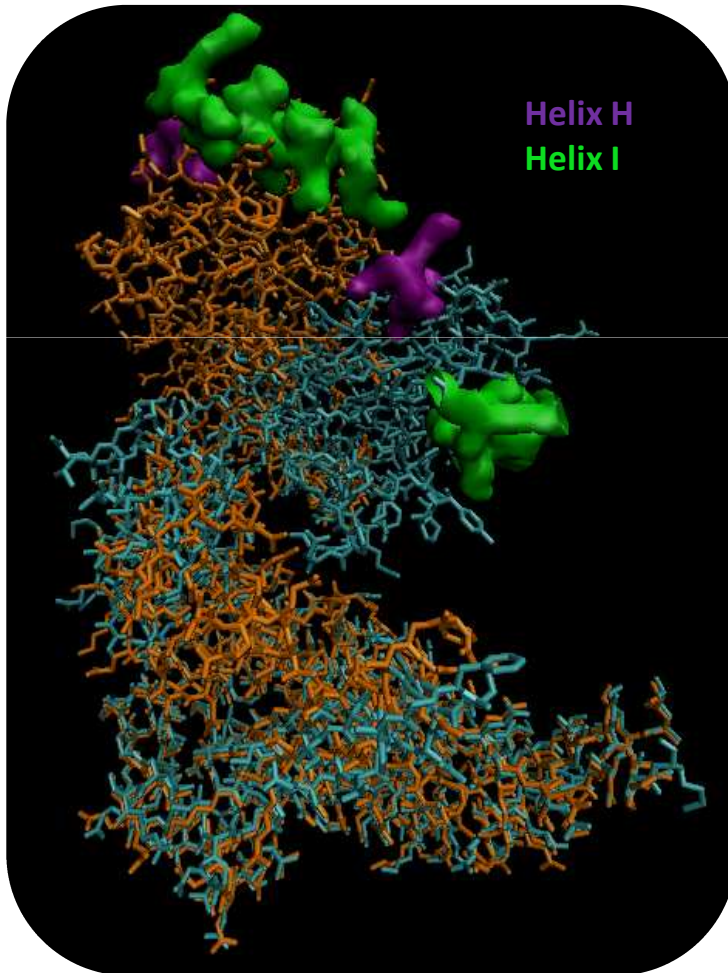


Fig78. STAMP GroEL ATP₇ (1SX3), GroEL-ATP₇-GroES (1SVT).

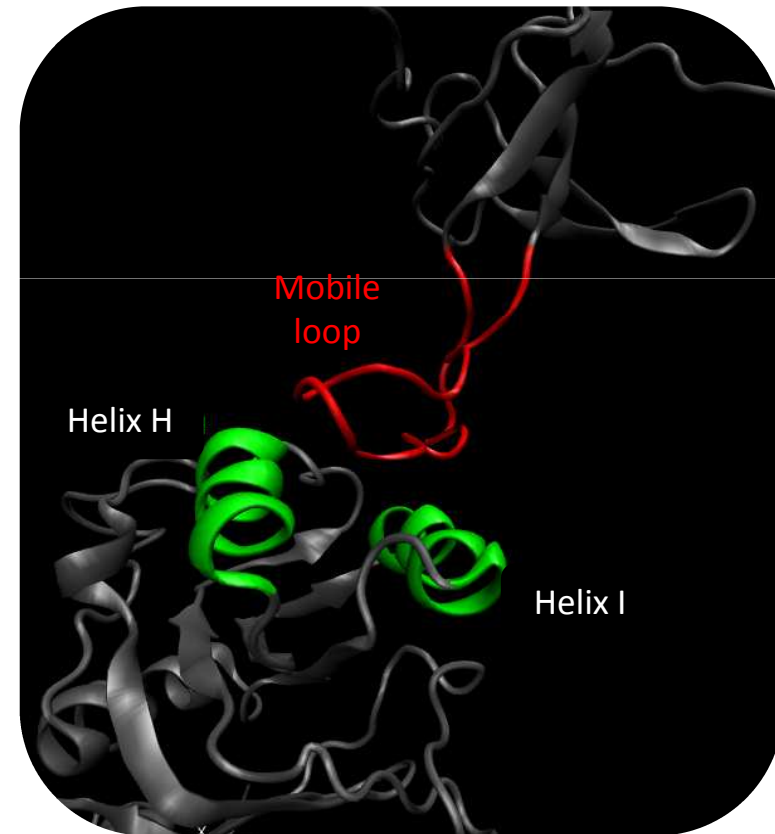


Fig79. GroEL-GroES chain A and O, interface zoom (1AON)

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

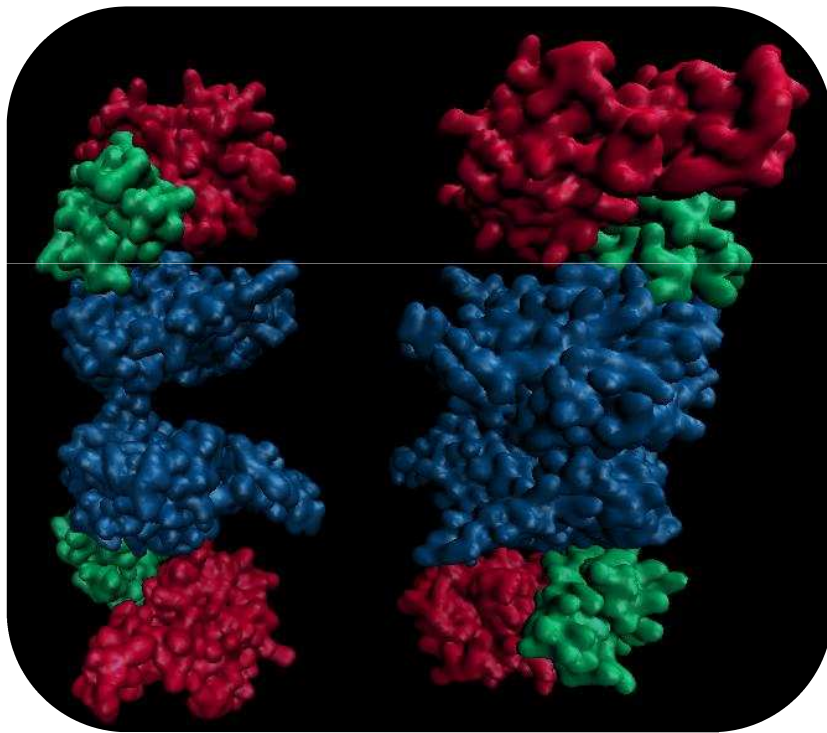


Fig80. GroEL ATP₇ (1SX3)

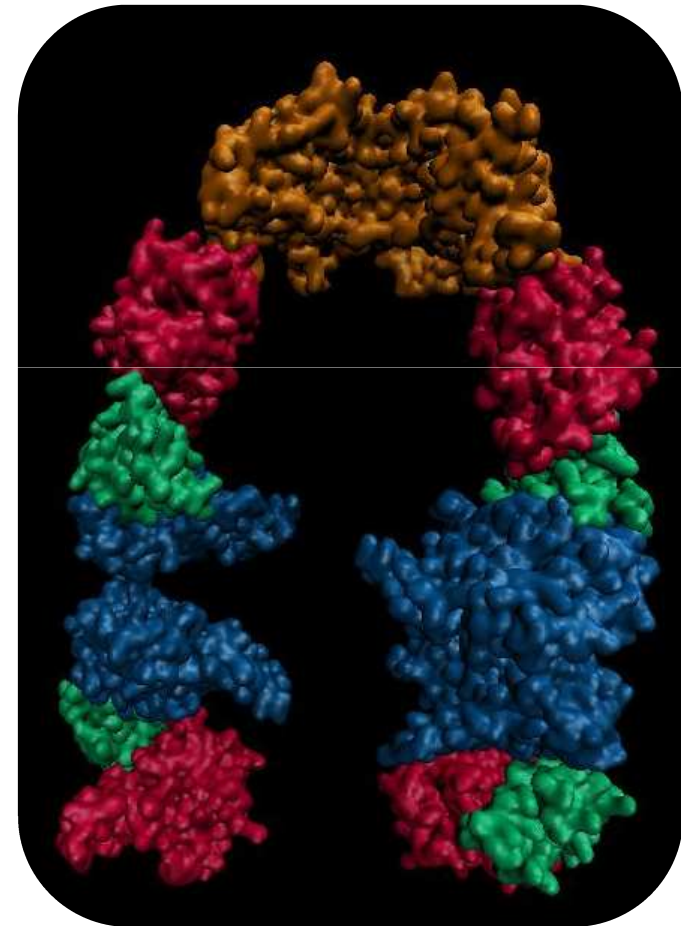
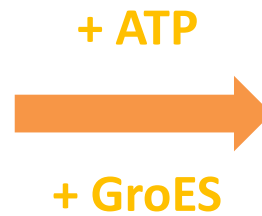


Fig81. GroEL-ATP₇-GroES (1SVT)

GroEL/GroES > **Folding cycle** > Phase II

Nucleotide and GroES Binding

STAMP

GroEL ATP₇ (1SX3) vs
GroEL-ATP₇-GroES (1SVT)

RMSD 3.03

Sc 1.21

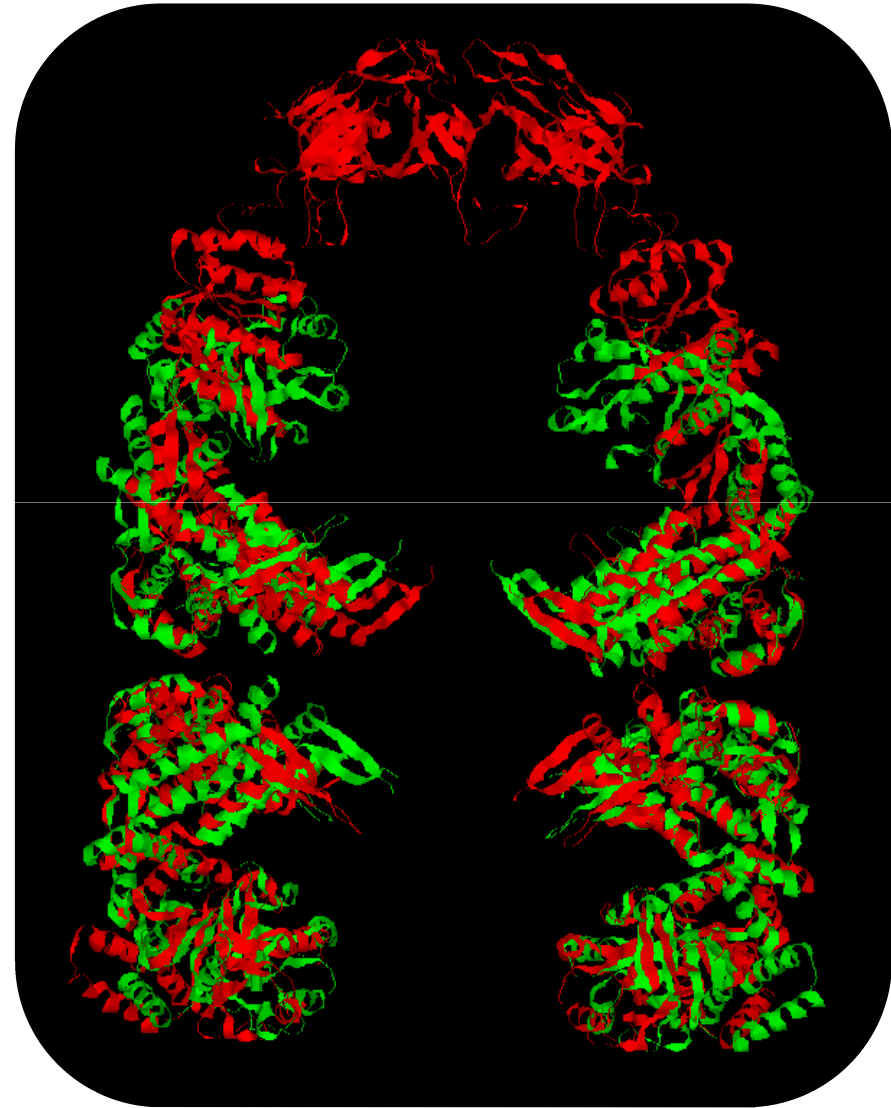


Fig82. STAMP GroEL ATP₇ (1SX3) vs GroEL-ATP₇-GroES (1SVT)

GroEL/GroES > **Folding cycle** > Phase III

Polypeptide Release and Folding

Hydrophobic residues
Polar residues

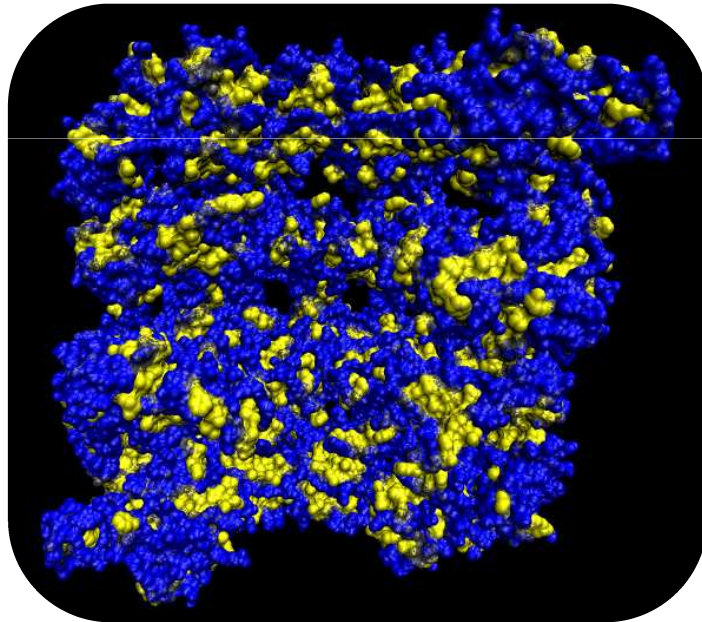


Fig83. GroEL cavities (1MNF)

+ GroEL
→

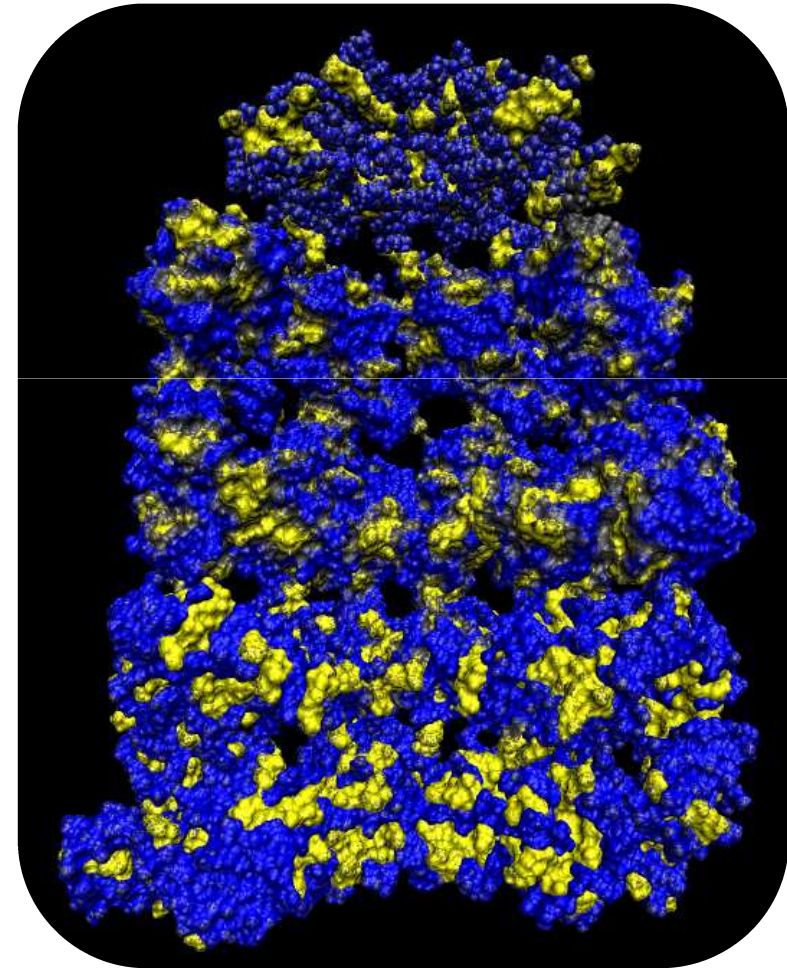


Fig84. GroEL-GroES cavities (1AON)

GroEL/GroES > **Folding cycle** > Phase IV

Protein Folding and Release of Ligands

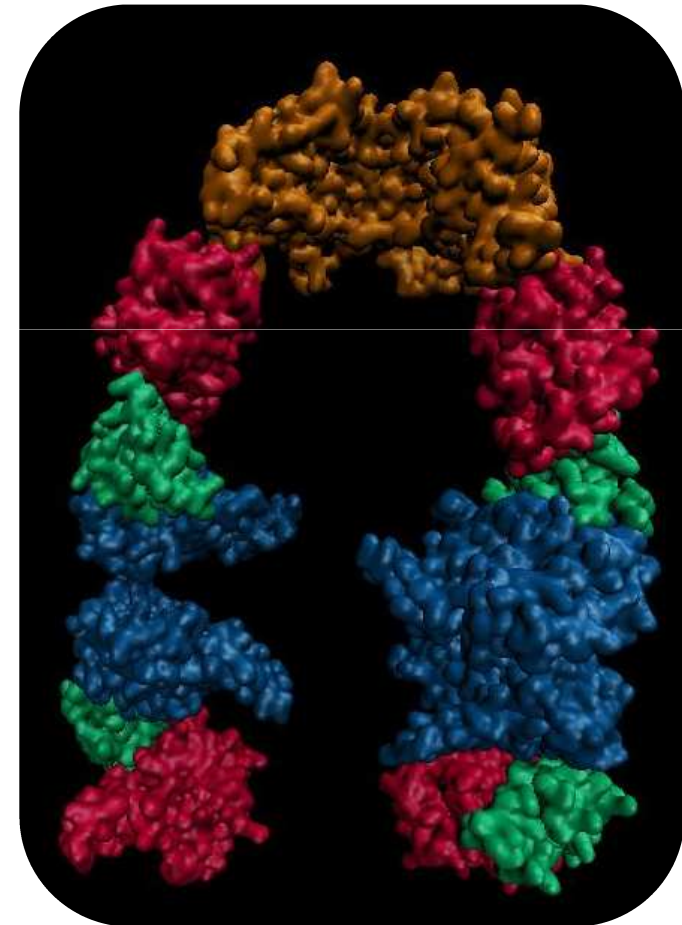
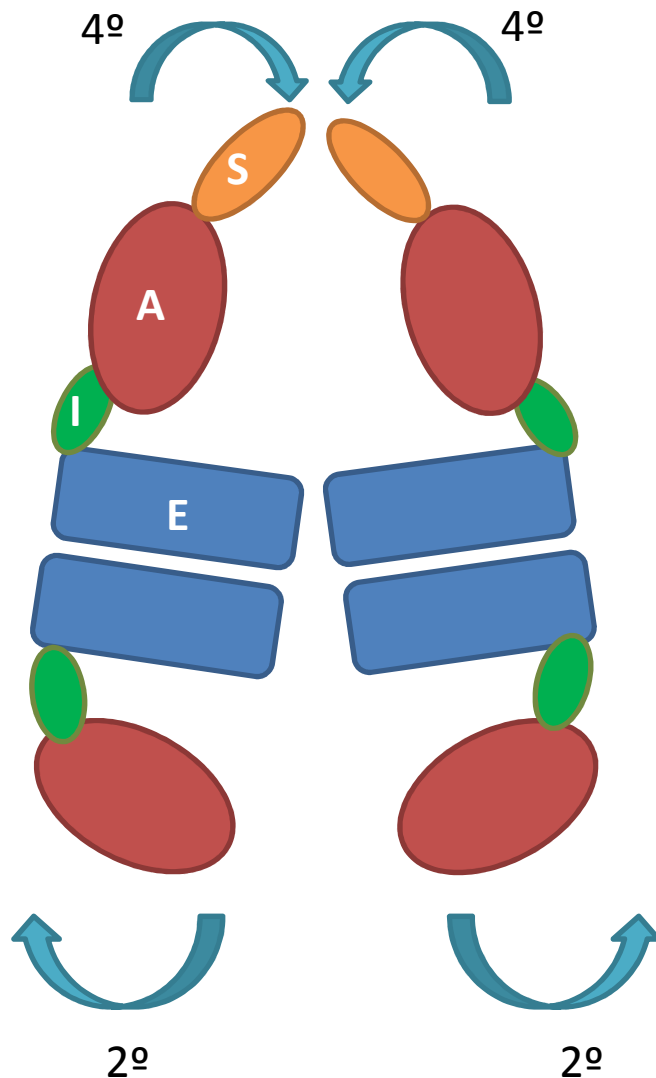


Fig85.GroEL-ATP₇-GroES (1SVT)

GroEL/GroES > **Folding cycle** > Phase IV

Protein Folding and Release of Ligands

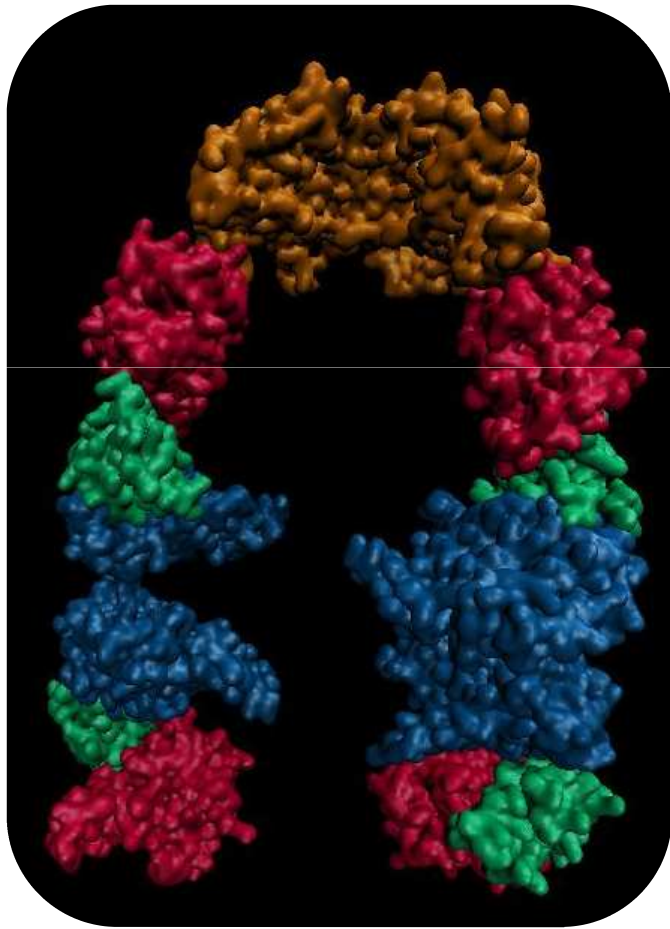


Fig86. GroEL-ATP₇-GroES (1SVT)

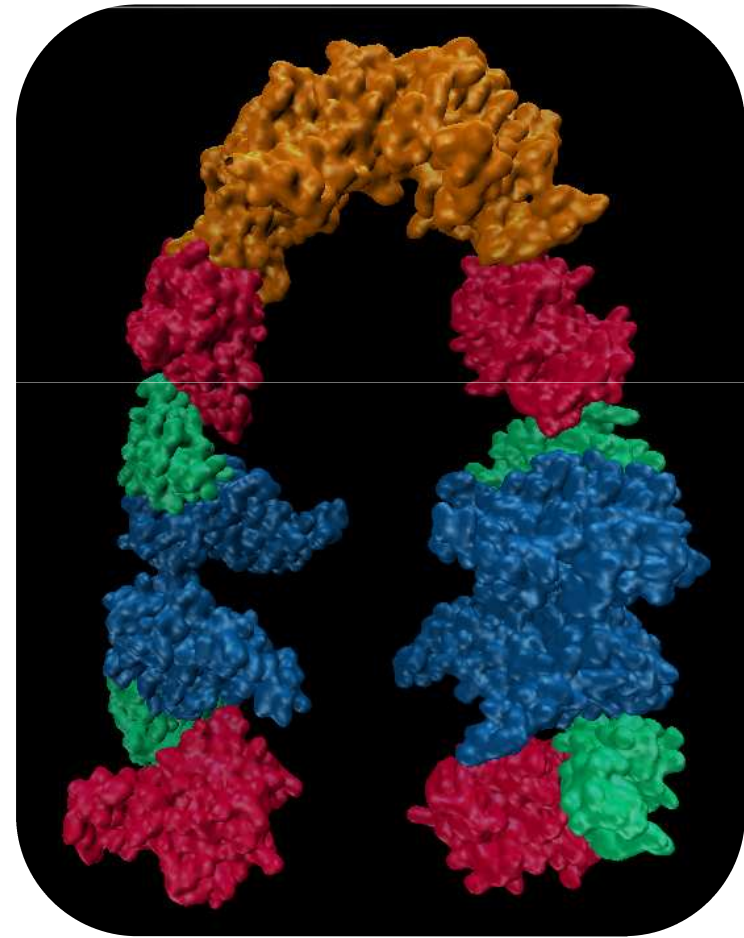


Fig87. GroEL-ADP₇-GroES (1SX4)

GroEL/GroES > **Folding cycle** > Phase IV

Protein Folding and Release of Ligands

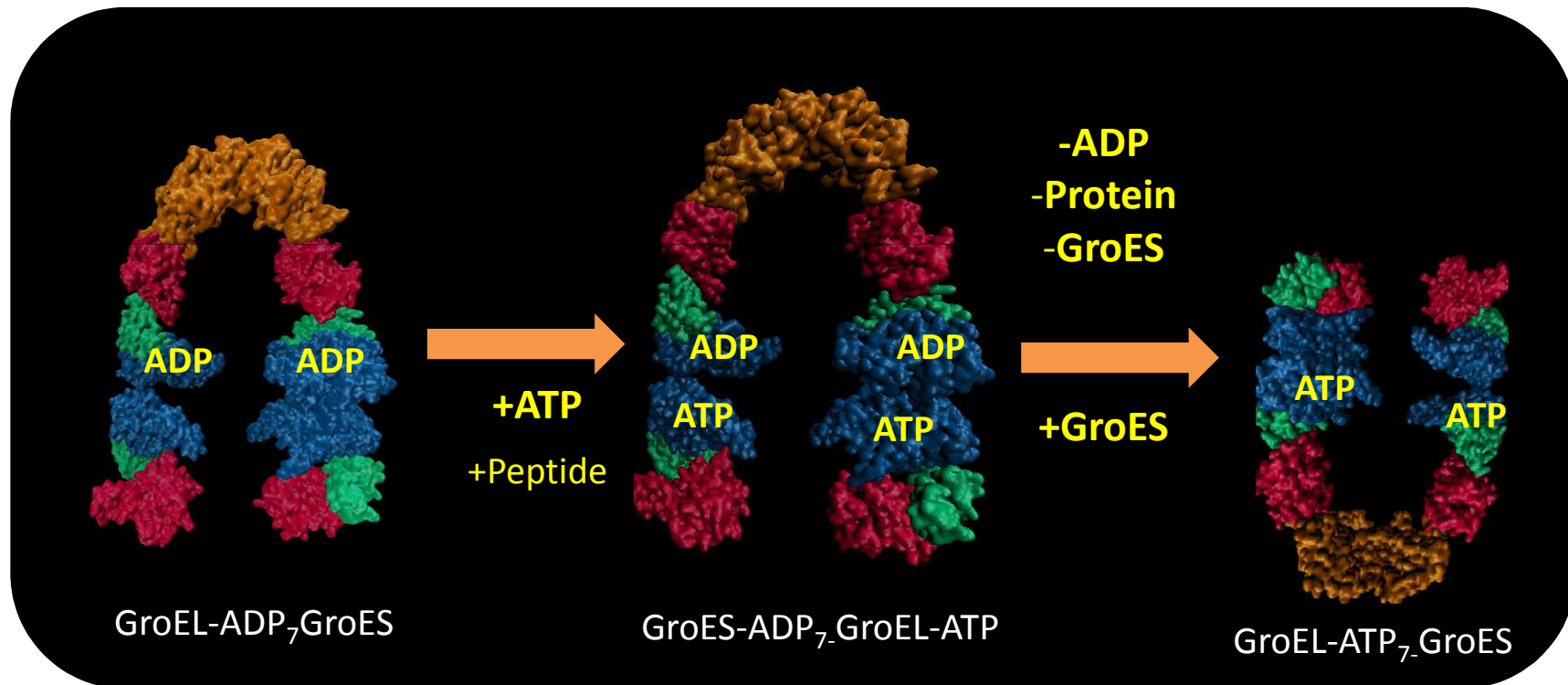


Fig88. Release of Ligands (1SX4, 1GRU, 1SVT)

Introduction

Molecular chaperones

Chaperonins group I

Chaperonins group II

GROUP II CHAPERONINS

Group II > Main characteristics

Archaea (Thermosome) and Eukaryotes (TRiC/CCT)

Two hetero or homo rings with 8 to 9 subunits

Major structural difference: “Build-in lid”

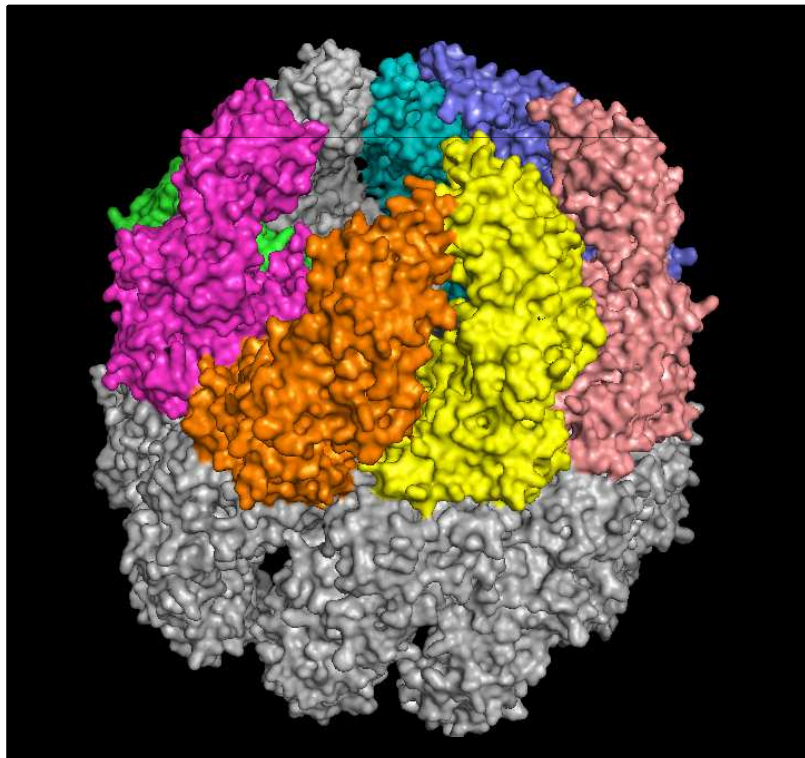


Fig89. TRiC/CCT, eukaryote chaperonin (4A0O)

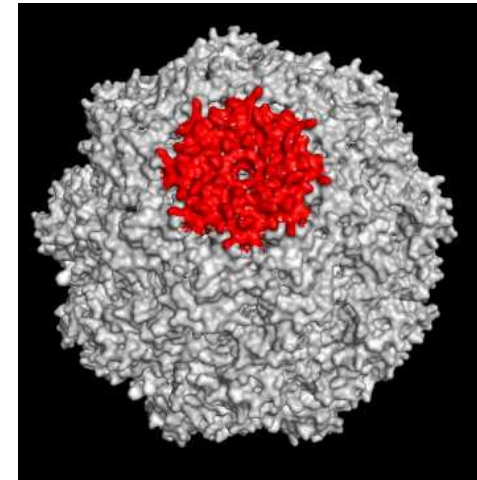


Fig90. Lids closing the chamber (3LOS)

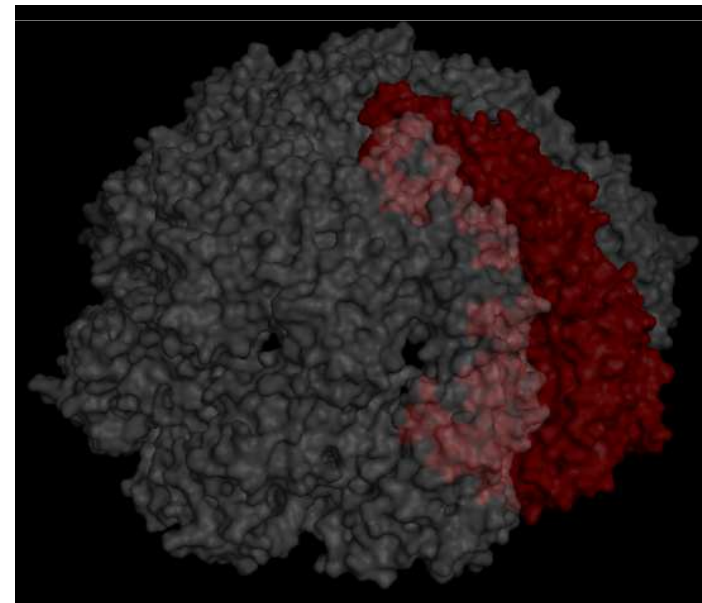


Fig91. Single subunit of MmCpn (3LOS)

Group II > Sequence alignment

<i>Mm Cpn1-1-543</i>	1 MSQQPG.....VLPENMKRYMGRDAQRNMLLAGRIIAETVRSITLGPCKGMDKMLVDDLGGVV...VTNDGVTILREMSVEHPAAKMLIEVAKTDEKEVGDDTTAVVVAGELLRKAEELLDQNVHRTIVVKGYQAAQKAEELDKTIACE....VGAQDKEILTK 152
<i>KS-1_alpha/1-548</i>	1 MAQLSGQPVVILPEGTQRYVGRDAQRNMLLAGRIIAETVRTTLGPCKGMDKMLVDSLGDIV...VTNDGATILDKIDLOHPAAKMMVEVAKTDEKEAGDGTAVVIVAGELLRKAEELLDQNIHPSIIKGYALAAEKAEELDEIAIR....VDPDDEETLTK 158
<i>Themosome_alpha/1-545</i>	1...MMTGQVPILVLKEGTQREGGKNAQRNIEAAKAIADAVRTTLGPCKGMDKMLVDSIGDI...ISNDGATILKEMDVEHPTAKMIEVSKAODTAVGDDTTAVVVLGSELLKQAEELLDQGVHPTVINSGYRLAVNEARKIDEIAEK....S...TDDATLRK 153
<i>Themosome_beta/1-543</i>	1...MIAQG...PIFILKEGTQRESGKDKAMKENIEAAIAISNSVRSSLGPRGMDKMLVDSLGDIV...ITNDGVTILKEMDVEHPAAKMMVEVSKTQDSFVGDDTTAVIIAGGLLQQAQGLINQNVHPTVISEGYRMASEEAKRVIDEISTK....IGADEKALLLK 154
<i>CCT_gamma/1-515</i>	1.....NTKRESGRKVSQGNINAAKTJADIIRTCGLPKSMMKMLDPMGGIV...MTNDGNAIILREIQVHPAAKSMIEISRTDDEEVGDDTTSVIIILAGEMLSVAEHLEQQMHPTVVSAYRKALDDMIITLKKISIP....VDTSNRDTMLN 142
<i>CCT_delta/1-518</i>	1.....SAYQDRDKPAQIRFSNISAAKAVADARTSLGPKGMDKMIQDDGKDDVT...ITNDGATILKQMQVLHPAARMVLVLSKAODIEAGDGTTSVVIILAGSLDSTCKLQKGIHPTIISSEFQKALEKGIELTDMSR...P...VELSDRETILN 144
<i>CCT_epsilon/1-515</i>	1.....DRKSLRMGLEALKSHIMAAKAVANTMKTSLGPNGLDKMMVDKDDVT...VTNDGATILSMMDVDHQAIAKMLVLSKSDDEIDGDDTTGVVVLAGALLEAEQQLDRGIHPIRADGYEQAAARIAIEHLDKISDSVL...VDMKNTETLIQ 145
<i>CCT_alpha/1-529</i>	1.....VFQDRTGAEARISQNMMAASIANIVKSSSLGPGVGLDKMLVDDIGDVT...ITNDGATILKLLVEHPAAKVLCELADLDQKEVGDDTTSVVIILAEELKNADELVKQKIHTPSVISGYRLACKEAVRYISENLIIN...TDELG...RDCLIN 144
<i>CCT_beta/1-513</i>	1.....AGADEERAETARLSSFIGAIIAGDLVKSTLGPCKGMDKMLSSGRDASLMVINDGATILKNIQVNDPAKVLVDMRSVDDDEVGDDTTSVTVLAEELREAESLIAKKIHPTIAGWREATKAARQALLNSAVDHG...SDEVKFRDDLMN 148
<i>CCT_eta/1-515</i>	1.....KEGTDSSQGIPQLVSNISACQVIAEAVRTTLGPRGMDKLIVDGRKAT...ISNDGATILKLLDVHPAAKTLVDIAKSDDAEVGDGTTSVTLIAEELKQVKPYVEEGLHPQIIIRAFRTATQLAVNKIKEIAVTVKKEDKVEQRKLEK 148
<i>CCT_zeta/1-517</i>	1.....PKAEVARAQALAVNISARGLQDLVRLNLPCKGTMKMLVSGAGDIK...LTGDNVLLHEMQIQHTASLIAKVATAODITGDDTTSNVLIIIGELLKQADLYISEGLHRIITEGFEAAKEKALQLEQVKVSK....EMDRETILID 142
<i>CCT_theta/1-512</i>	1.....EGAKHFSGLEEAAYRNIOACKELAQTTRTAYSPNMGKMKVINHLEKLF...VTNDAAATILRELEVHPAAKMIIMASHMQEVEGDDTNFVFGALGALLEAEELRLGLSVSEVIEGYEIACKKAHEILPDLVCCS...AKNLRDDEVSS 148
<i>Mm Cpn1-1-543</i>	153 IAMTSITGKGAKEAKEKLAEIIEAVSAVDD...EGK...VDKDLIK...IEKSSGASIDDTLEIKGLVD...KERVSAQMPKKVTDAKTALLNCAIEIKETE...TDAEIRITDPAKLMFIEQEKMLKDMVAEKASG.....ANVLFQCKG.....IDD 292
<i>KS-1_alpha/1-548</i>	157 IAAITSITGKNAESHKELLAKLAVEAVKQVAEKKGKYYVVDLNDIK...FEKKAGEGVESSELVRGVVID...KEVVHPRMPKRVENAKIALINEALEVKKTE...TDAKINITSPDQLMSFLEQEKMLKDMVDHIAQTG.....ANVVFQCKG.....IDD 299
<i>Themosome_alpha/1-545</i>	154 IALTALSGKNTGLSNDFLADLVKKAVNAEVRDGTIVDTANIK...VDKKNSSGVNDTQFISGIVID...KEKVHSPMPQVVKNAKIALIDSALEIKKTE...IEAKVQISDPSKIQDFLNQETNTFKQMVKKIKKSG.....ANVVFQCKG.....IDD 296
<i>Themosome_beta/1-543</i>	155 MAQTSLNSKSSASVAKDKLAEISYEAVKSVAEALRDGKYYVDFDNIIQ...VVKKQGGAIIDDTQLINGIIVD...KEKVHSPMPQVVKNAKIALLDAPLEIKKPE...FTNLRIEDPSMIQKFLACEENMLREMYDKIKSVG.....ANVVFQCKG.....IDD 297
<i>CCT_gamma/1-515</i>	143 IINSSITTKVIRSWSSLAACIALDAVKTQVFEENGRIEIDIKKYARVEKIPGGIIEDSCVLRGVMIN...KDVTHPRMRRYIKNPRVLLDSSLEYKKGE...SQTDIEITREEDFTRILQMEEYIQQLCEDIQLK.....PDVVITEKG.....ISD 288
<i>CCT_delta/1-518</i>	145 SAATSLNSKVVSYSSLLSPMSVDVAMKVIDP...ATATSVDLRDIK...IVKKLGGTIDDCLEVEGLVLT...QKVANSGITR...VEKAKIGLIQFCLSAKTD...MDNQIVVSDYVQMDRVLREERAYILNLVKQKKTG.....CNVLLIQKSLRLDALSD 290
<i>CCT_epsilon/1-515</i>	146 TAKTTLGSKVVNSCHRMMAEIAVNAVLTVD...MQRRDVFELIK...VEGVKGGLEDTKLIGVIVD...KDFSHQMPKQVEDAKIAILTCFPEPPKPK...TKHKLDVTSVEDFKALQKYEKEFEEMIROIKETG.....ANLAVCQWG.....FDD 286
<i>CCT_alpha/1-529</i>	145 AAKTSMSSKVIIGINGDFFANLVVDVAIAIKYTDIRQGPYPVNSINVLKAHRSQMESMLINGYALN...CVVGSGQMPKRIVNAKIALCLDFSLQTKMK...LGVQVVIIDPEKLDQIRQRESIDTKERIQKILATG.....ANVILTTGG.....IDD 288
<i>CCT_beta/1-513</i>	140 IAGTTLSKLLTHHKDHFTKLAVEAYRLKGGSN...LEAIHWIKLGGSLADYDEGLLD...KKIGVN...QPKRIENAKILLIANTGMOTDKIKIFGSRVVDSTAKVAIEHAIEKMKKEKERLKKH.....INCFINRL.....LYN 295
<i>CCT_eta/1-515</i>	149 CAMTALSSKLIISQKAFKAKMVVDVAMMLDQLLQ.....LKMIGIKVQGGALEESQLVAGVAFKKTFSYAGFEMOPKKYHNPM...ALLNVELELKAIE...DNAEIRVHTVEDYQAIVDAEWNIYDKLEKIHHS.....AKVVLKSLP.....IGD 288
<i>CCT_zeta/1-517</i>	143 VARTSLRTKHAELADVLTEAVVDSILAIAKKQDEP...IDLFMVEIMEMKHKSETDLSIRGLVLD...HGARHPDKKRVEDAYILTCNVSLEYKTE...VNSGFFYKSAEEREKLVKAEKRFIEDRKKIIEELKKVCGSDKGFVVINQKG.....IDP 291
<i>CCT_theta/1-512</i>	147 LHTSVMSKQYG...NEVFLAKLIAQCVSIFPDSGFHN...VDNIRVCKILSGVHSSSVLHGMVFK...KETEGGDVTSGYKDAIAYVSCFPDGMITE...TKGTVLIKSAEELMNFSGKENLMDAQVKAADTG.....ANVVTGGR.....VAD 283
<i>Mm Cpn1-1-543</i>	293 LAQHYLAKEGIVAAARRVKKSDMEKLAKATGANVITNIKDS.....AQDLGD...AGLVEERKISGD...SMIFVEECKHP...KAVTMLIRGTEHVIIEVARAVDDAVGVGCTIEDGRIISGSGSTEVELSMKLEAYE6ISQREQLAVRAFADALEVIRTL 444
<i>KS-1_alpha/1-548</i>	300 LAQHYLAKEGIMAVRRVKKSDMEKLAKATGAKIVTNVKDLT.....PEDLGY...AEVVEERKLAGE...NMIFVEGCKNP...KAVTILIRGTEHVIDEVERALEDAVKKVVDKMDGDAVLPAGGAPEIELAIRLDEYAKQVGGKEALAIENFADALKIIPKT 451
<i>Themosome_alpha/1-545</i>	297 VAQHYLAKEGIVAVRRVKKSDMEKLAKATGAKIVTDLDDLT.....PSVLGE...AETVEERKISGD...RMTFVMOCKNP...KAVSILIRGTDHVVSEVERALNDARVVAITKEDGKFLWGGGAEEALAMRLAKYANSVGGREQLAIEAFKAKALEIIPRT 448
<i>Themosome_beta/1-543</i>	298 MAQHYLSRAGIYAVRRVKKSDMDKLAKATGASIVSTIDEIS.....SSDLGT...AERVEQVKGED...YMTFTVTOCKNP...KAVSILVRGTEHVVDEMERISITDSLHVVASALEDDGAYAGGATAAEIAFRLRSYAKQIGGRQDLAIEKFADEIEEIPRAL 440
<i>CCT_gamma/1-515</i>	287 LAQHYLMRANITAIRRVKTDNNRIARACGARIVSRPEELR.....EEDVGTGAGLLEIKKIGDE...YFTFITECKDP...KACTILLRGAASKEILSEVERNLDQAMQVCRNVLLDQPLVPGGGAEMAVAHALTEKSKAMTQVEQWPRYAVAAQALEVIRTL 439
<i>CCT_delta/1-518</i>	291 LALHFLNKMKIMVVKDIEREDIEFICKTIGTPKPAHVDDQFT.....ADM LGS...AELAEVSLNGS...GKLKIKITGASPGKTVTVVVRGSKNLVIEEAERSIHDAICVIRCLVKKRALIAGGGAPEIELALRLTEYSRTLSGMESYGIRAFADAMEVIRPSTL 444
<i>CCT_epsilon/1-515</i>	287 EANHLLQNDLPVRRVGGPEIELIAIATGGRIVPRFSELT.....AEKLG...AGLVKEISFGTTDKDKMLVIEQCKNS...RAVTIFIRGNGKMIIEEAERSLHDAICVIRNLIRDRNVVYGGGAEEISCALAVSQEADKCPTEQYAMRAFADALEVIRPMA 440
<i>CCT_alpha/1-529</i>	289 MCLKYFVEAGAMAVRRVLKRLDKRIKASAGATVLTSLTANLEGEETFEASMLQG...AEELVQERICDD...ELILIKNTKAR...TSASVILRGANDFMDDEMERSLHDAICVVKRVLESKSVVPGGGAEEAALSYLENYATSMGSRQDLAIEAFARSLVLIRPNTL 446
<i>CCT_beta/1-513</i>	286 YPEQLFGAAGVMAIEHADFGVERLALVTGGEIASTFDHP.....ELVKLG...CKLIEEVMIQED...KLHFSGVALG...EACTIVLRGATQQLIDEAERSLHDAICVLAQTVKDSRTVYGGGCEMLMAHAVTQLASRTPKAEAVAMESYAKALRMLPTII 437
<i>CCT_eta/1-515</i>	289 VATQYFADGDMFCAGRVPEEDLKRTMMACGSGIOTSVNAL.....SSDVLGR...CQVFEETQIGGE...RYNFFTGCPKA...KTCTIILRGGAEQFMEETERSLHDAIMIYVRAIKNDSVVAAGGAIEEMELSKYLRDYSRTIPGKQQLLIGAYAKALEIIPRL 440
<i>CCT_zeta/1-517</i>	292 FSLDALAKEGIIALRRAKRRNMERLTACGGIALNSLDDLN.....PDCLLG...HAGVVEYTLGEE...KFTFIEKCNPP...RSVTLLIKSPNKHTLTQIKDAIRDLGRVAKNAIDGGCVVPGGAEEAVAMAEALVKYKPSVKGRALQGVQAFADALLIPKV 443
<i>CCT_theta/1-512</i>	284 MALHYANKYINMLVRLNSKWDLRLRLCKTVGATALPRNLPPV.....LEEMGH...CDSVYSEVGDT...QVVVFHKEKEDGAISTIVLRGSTDNLMDDIERAVDDGVNTFKVLTRKRLVPGGGAETELAKQITSYGETCPGLEQYAIKKFAEAEFAIPRAL 436
<i>Mm Cpn1-1-543</i>	445 AENAGLDAIEILVKVRAAHASNGK.....CAGLNVPFGAEDMCENGVEEPLRVKTAQISAAESTEMLLRIDVIAAEKLRGAPDMDGMDGMPG...MGMPGMM 543
<i>KS-1_alpha/1-548</i>	452 AENAGLDTVEMLVKVIIEKKNRG...L.....GIGIDVFEKGPADMLEKGIIEPLRVKKQAIKSASAAIMILRIDDVIAAKATK...PEGGGGGMPGMMGMDMGM 548
<i>Themosome_alpha/1-545</i>	449 AENAGIDPNTILIKLKADEKGR...I.....SVGVDLNDNGVGMKAKGVDDPRVKTALHSAVEAVTAMILRIDVIAKSKST...PPSGGGGGGQMPGMMGMPY 545
<i>Themosome_beta/1-543</i>	450 AENAGLDPIDILLKRAEAKGN...K.....TYGINVFTIEEDMVKNQVIEPIRVGKQAIESTATEAAIMILRIDDVIAATKSS...SSSNPPKSGSSSESSED... 543
<i>CCT_gamma/1-515</i>	440 IQNCGASTIRLLTSRAKHTQENCE.....TWGVNGETGLVDMKELGIEWEPLAVKLQTYKTAVETAVLLLRIDDIVSGHK..... 515
<i>CCT_delta/1-518</i>	445 AENAGLNPISVTVELRNRHAQGEK.....TTGINVRKGGISNILEELVVOPLLVSALTATETVRSILKIDDVNTR..... 518
<i>CCT_epsilon/1-515</i>	441 AENSQMNPIDMTVEVRAQVKEVNP.....ALGIDCLCHKGTNDMKHQHVIETLIGKKQISLATQVMRMILKIDDIRKPG... 515
<i>CCT_alpha/1-529</i>	447 AYNAADDSTDLVAKLRAFNEAQVNPERKNLKWIGLDLVNKKPRDNKQAGVFERTIVVKVSKLFATEAAITILRIDDLIKLHP... 520
<i>CCT_beta/1-513</i>	438 ADNAGYSADLVLAQRAAHSEKKT.....AGLDMKEGTIGDMSVLGITESFQVKRQVLLSAAEAAEVLIRVDNIKAAPR... 513
<i>CCT_eta/1-515</i>	441 CDNAGFDATNLLNKLRAHAQGGMW.....YGVDFINTEDIANDFEAWEPAMVRINALTAASEAACLIVSDETIKNPR... 515
<i>CCT_zeta/1-517</i>	444 AONSQFLQETLVKVAEHSSEGL.....VGVDLNTEPMVAAEAIWQNYCVKKQLLHSCVTIATNILLVDEIMRAG... 517
<i>CCT_theta/1-512</i>	437 AENSVKANEVISKLYAVMOENKN.....VGDLIEAEVPAVKDMLAEGLDITYLGYWAIKLAATNAAVTVLRVDQIIIMAK... 512

Fig92. Sequence alignment between members of the group II chaperonins

Group II > Structural alignment

The structure is much more conserved than the sequence

Sc 8,17
RMSD 1,56

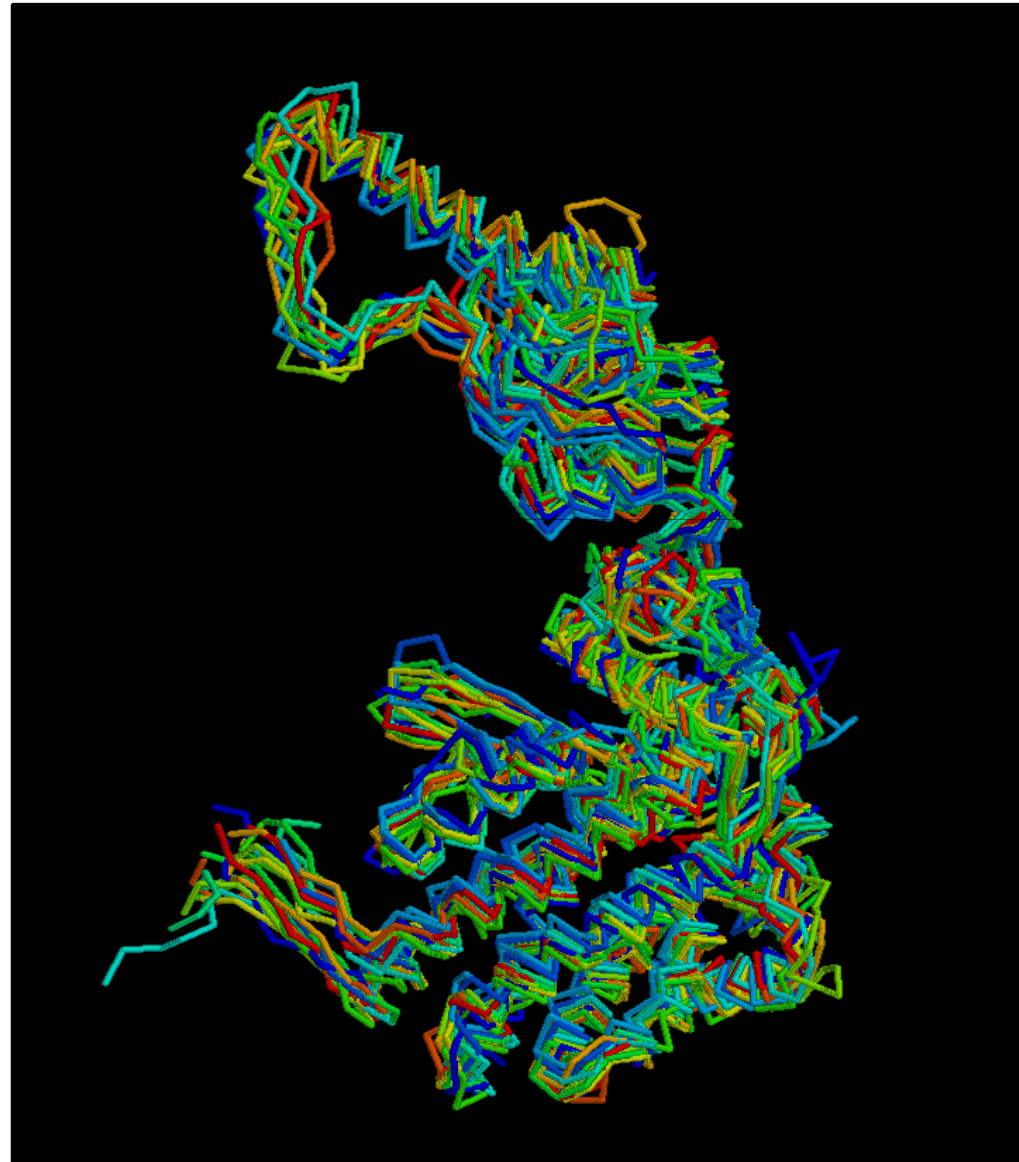


Fig93. Structural alignment between members of the group II chaperonins

MmCpn > General structure

Archaea: *Methanococcus maripaludis*

Homo- octameric ring

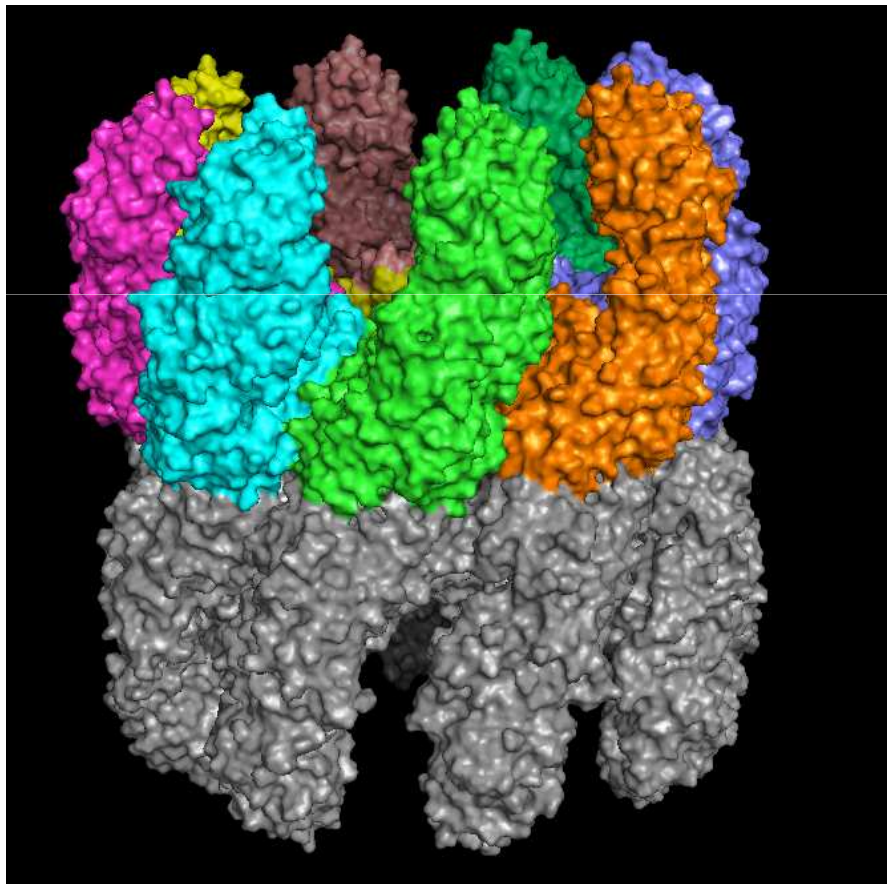


Fig94. Lateral view of MmCpn in open conformation (3IYF)

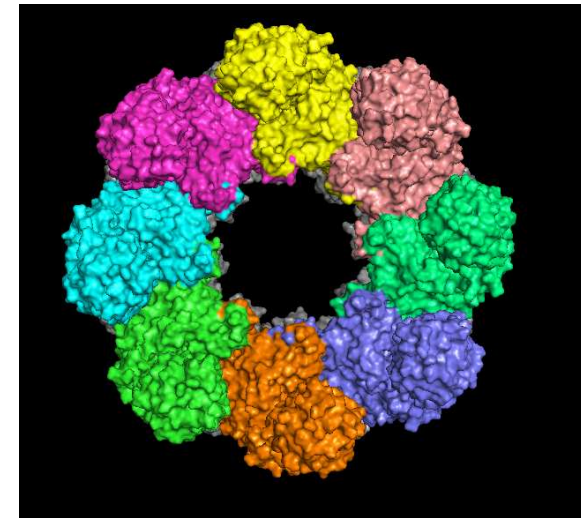


Fig95. Top view of MmCpn in open conformation (3IYF)

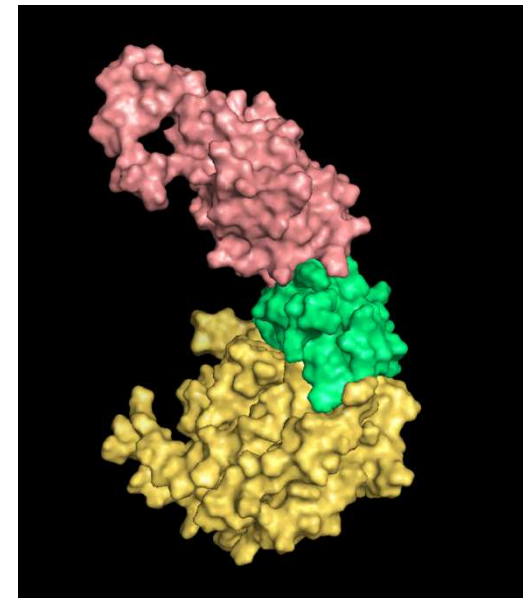


Fig96. Subunit architecture (3KFB)

MmCpn > Cycle overview

ATP-dependent protein folding cycle

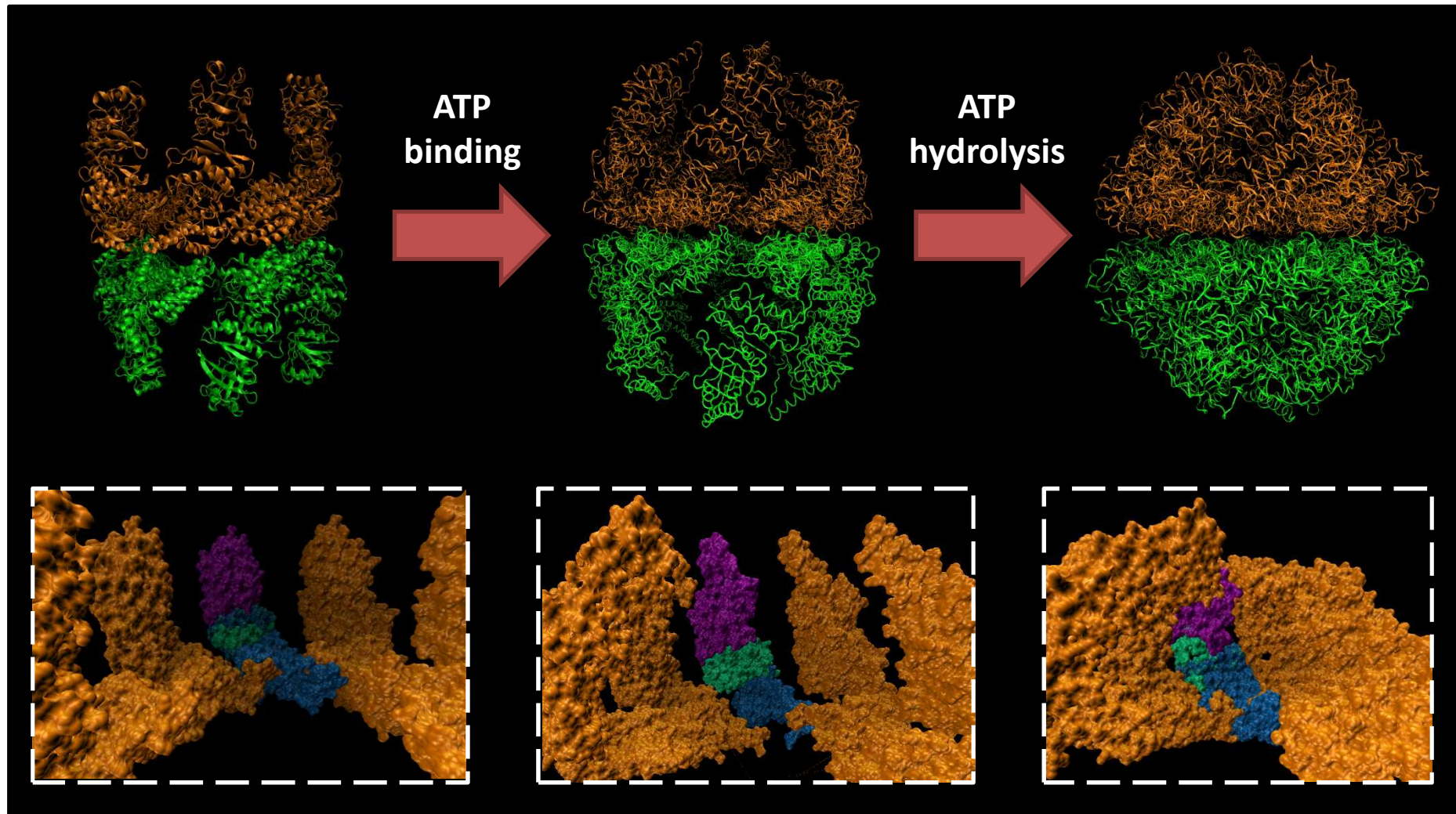


Fig97. Cycle overview (3IYF, 3IZH, 3LOS)

MmCpn > Open state

Contacts

Inter-ring

Intra-ring

Substrate binding site

Nucleotide binding site

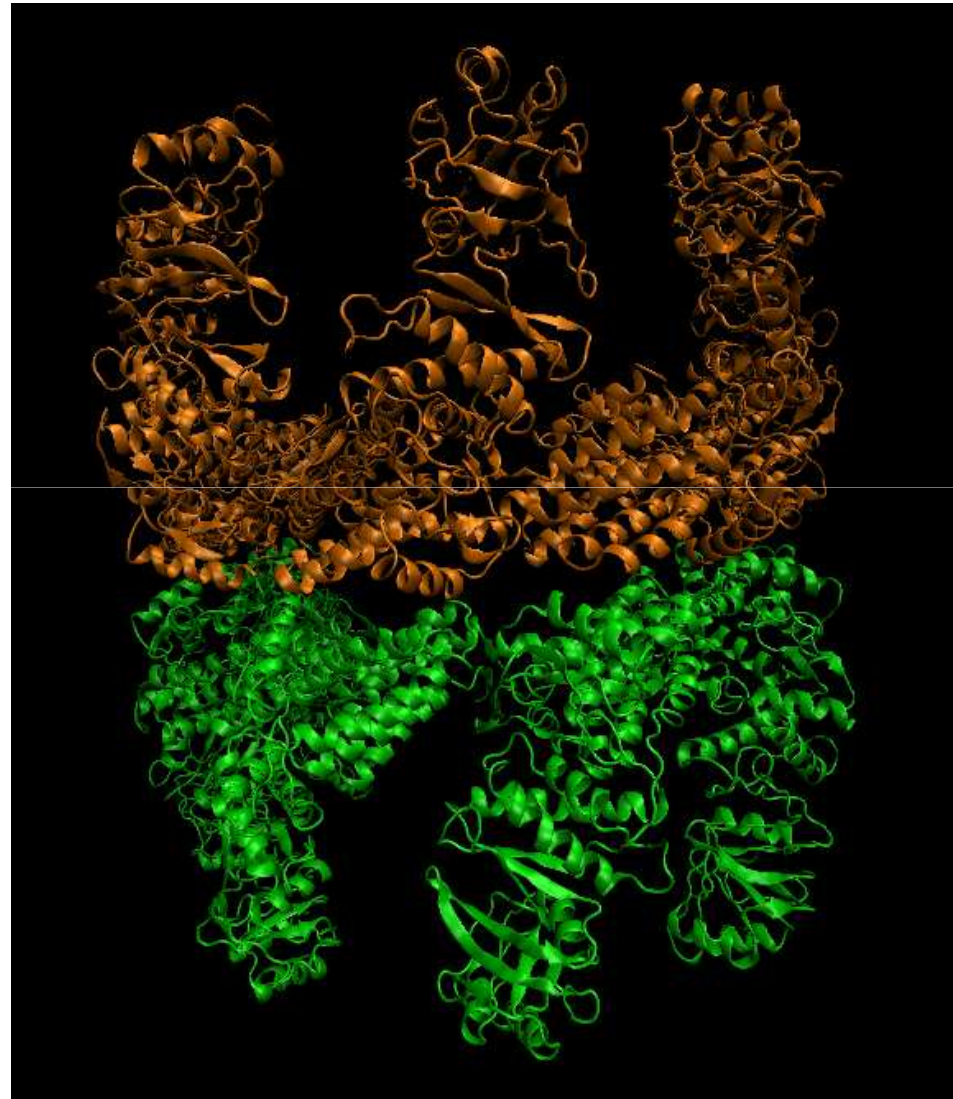


Fig98. MmCpn in open conformation (3IYF)

MmCpn > **Open state** > Inter-ring interactions

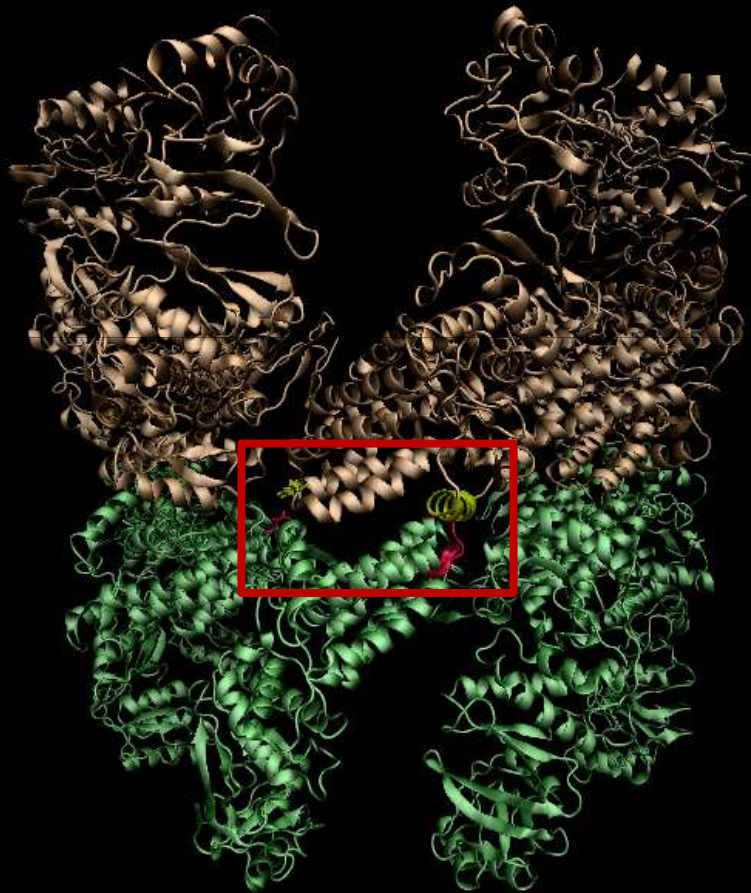


Fig99. Inter-ring contacts in open conformation (3IYF)

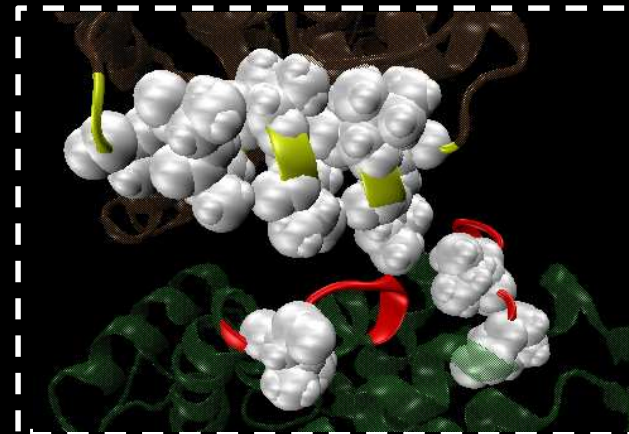


Fig100. Hydrophobic interactions between rings (3IYF)

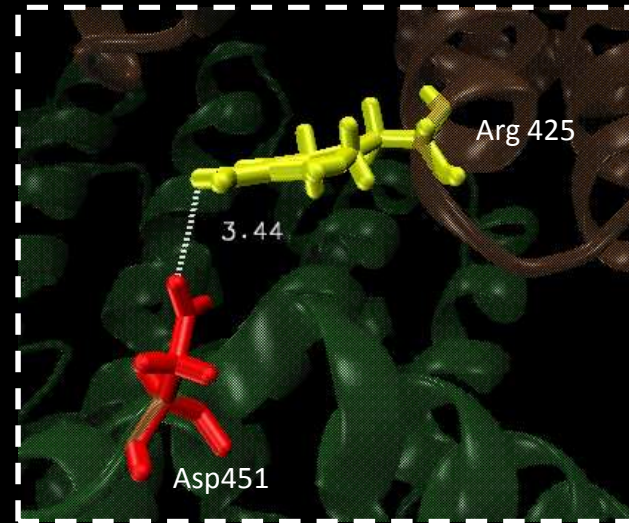


Fig101. Salt bridge contact between rings (3IYF)

MmCpn > **Open state** > Intra-ring interactions



Fig102. Intra-ring contacts in open conformation (3IYF)

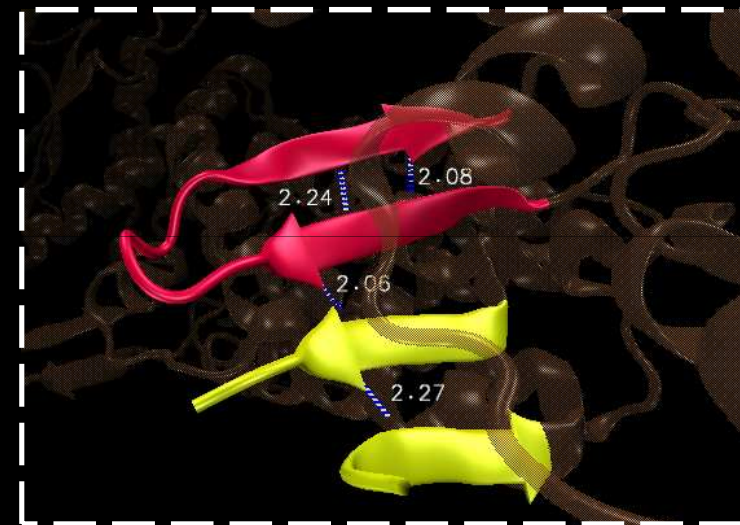


Fig103. B-sheet inner contact (3IYF)

MmCpn > **Open state** > Substrate binding site

Hydrophobic patch in
the apical domain

Interface between
helices H10 and H11

Fig104. Hydrophobic patch
between H10 and H11 (3IYF)

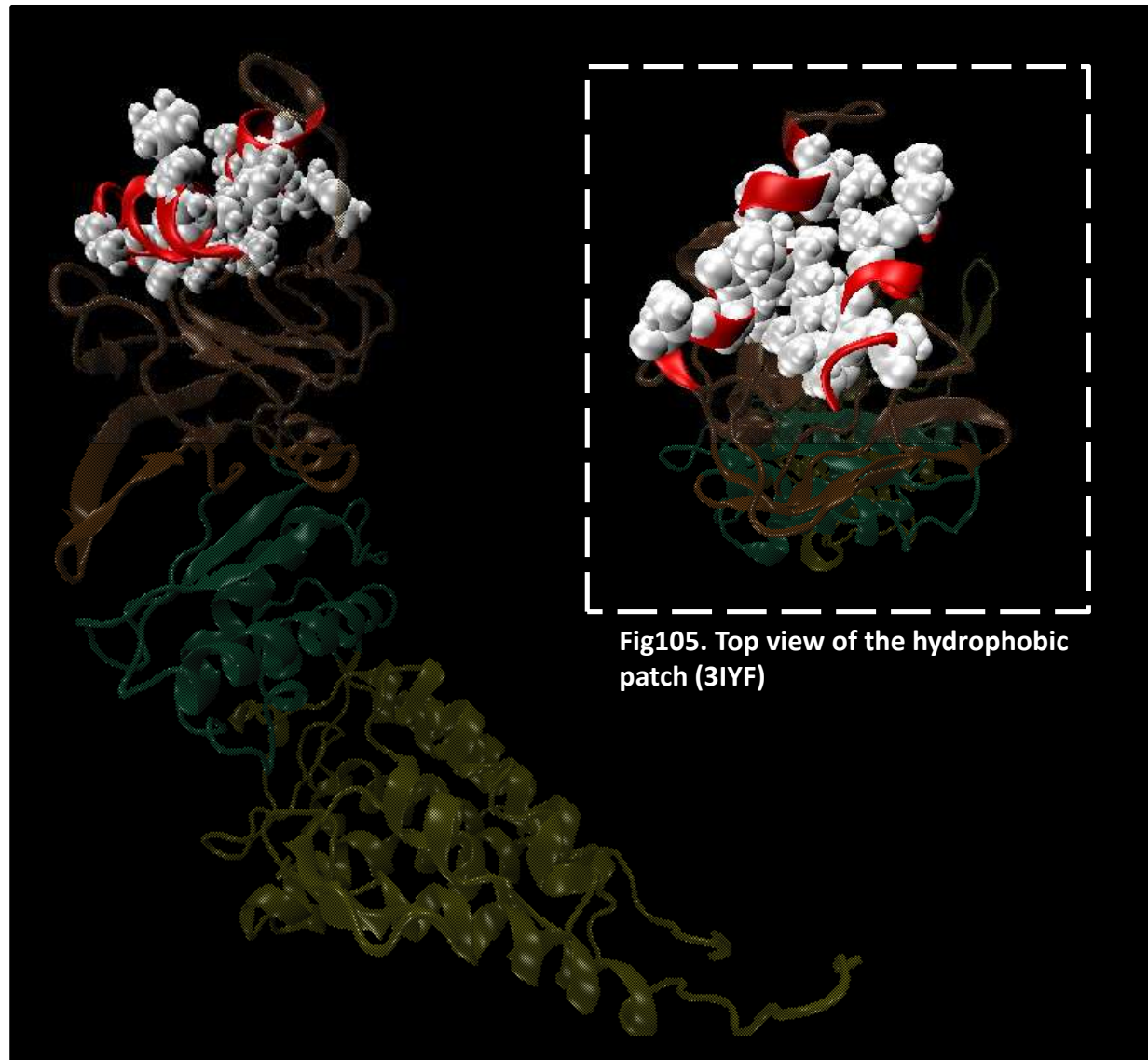


Fig105. Top view of the hydrophobic
patch (3IYF)

MmCpn > **Open state** > Nucleotide binding site



Fig108. Important residues in the Nucleotide binding site (3IYF)

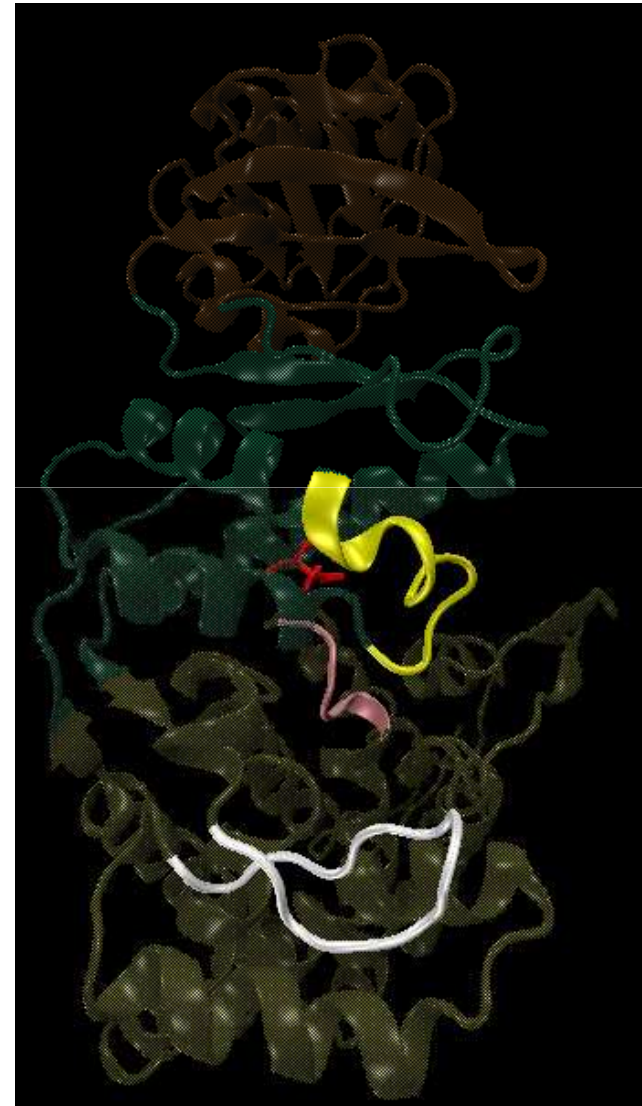


Fig109. Rear view of the Nucleotide binding site (3IYF)

MmCpn > Prehydrolysis state

ATP binds to the nucleotide binding site.

Large *en bloc* movement of the domains in each subunit:

- Apical
- Intermediate



Fig110. MmCpn in Prehydrolysis conformation (3IZH)

MmCpn > **Prehydrolysis state** > General movement

Apical and intermediate domains tilt toward the equatorial domain

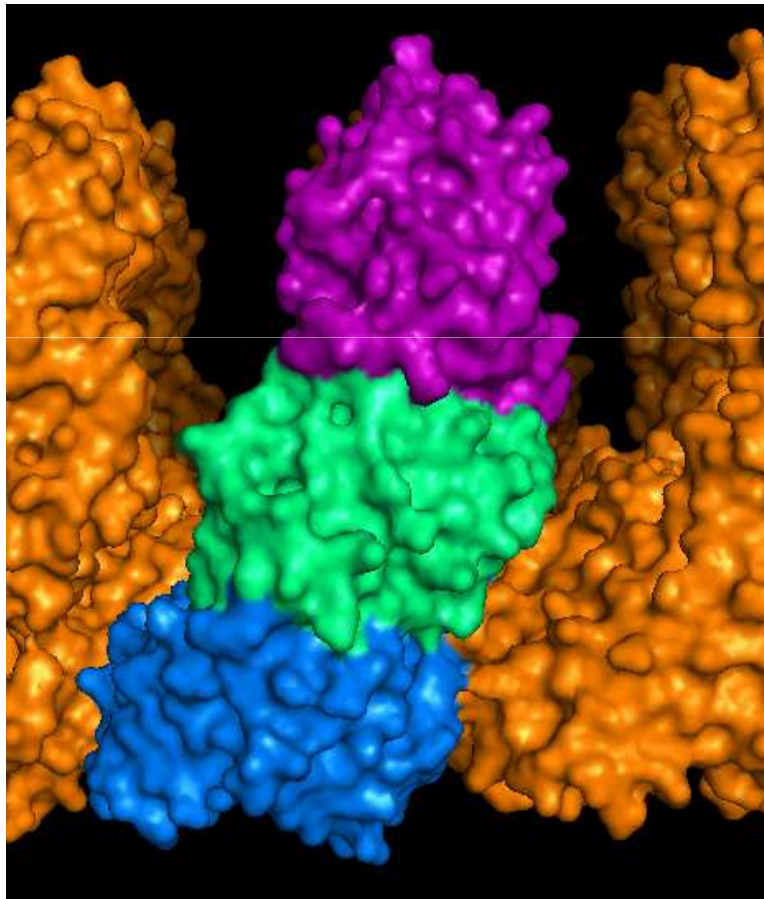


Fig111. Single subunit in open conformation (3IYF)

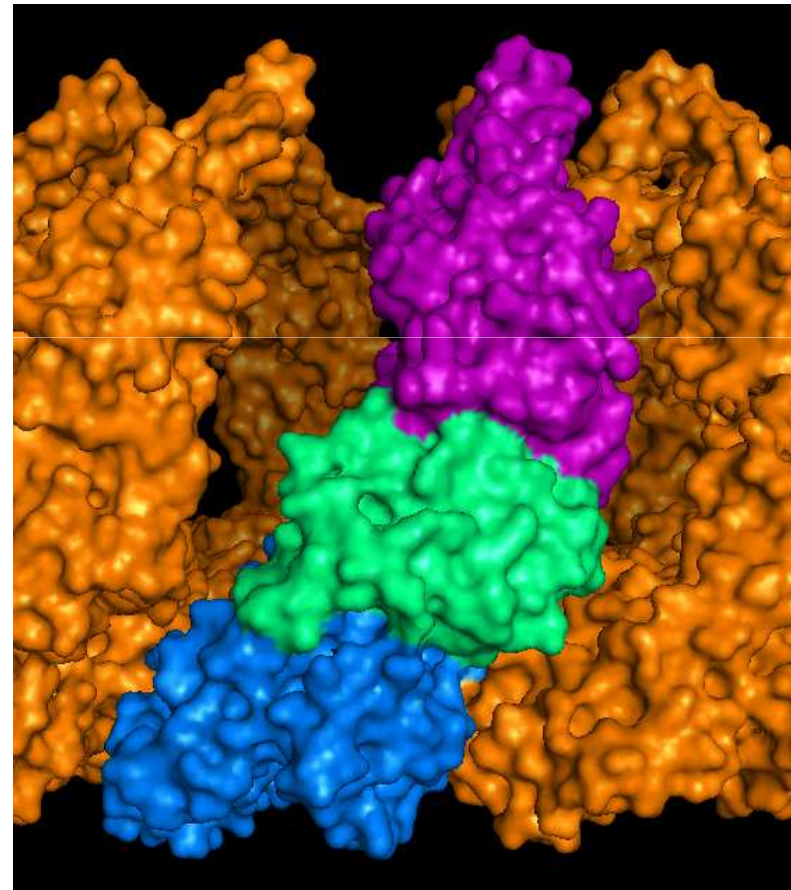


Fig112. Single subunit in Prehydrolysis conformation (3IZH)

MmCpn > Prehydrolysis state > Apical movement

Counter-clockwise rotation of the apical domains

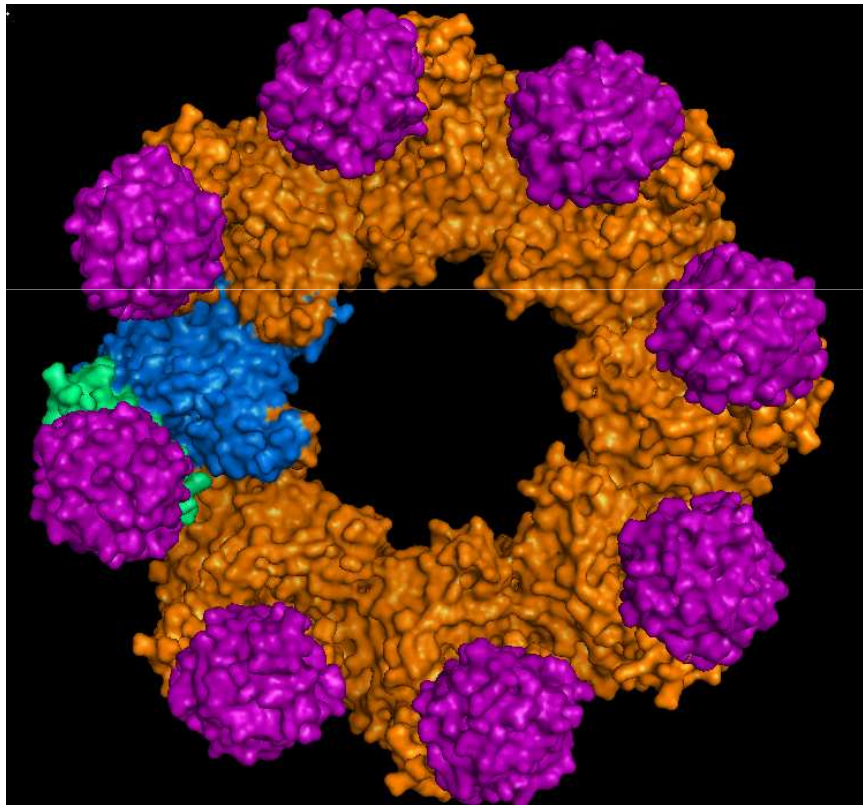


Fig113. Apical domains in open conformation (3IYF)

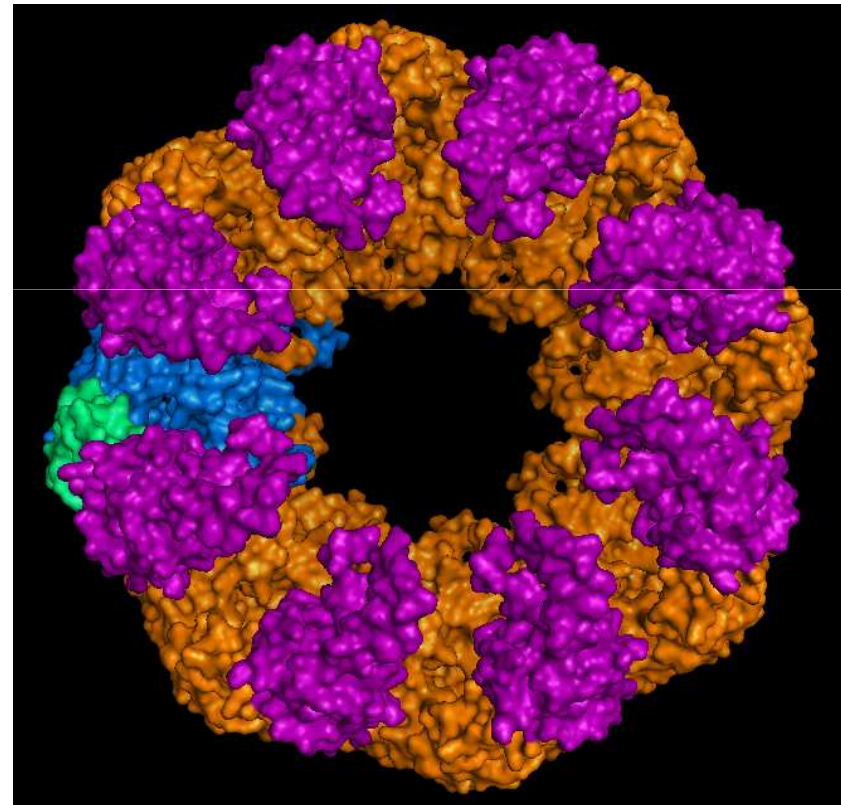


Fig114. Apical domains in Prehydrolysis conformation (3IZH)

MmCpn > **Prehydrolysis state** > Intermediate movement

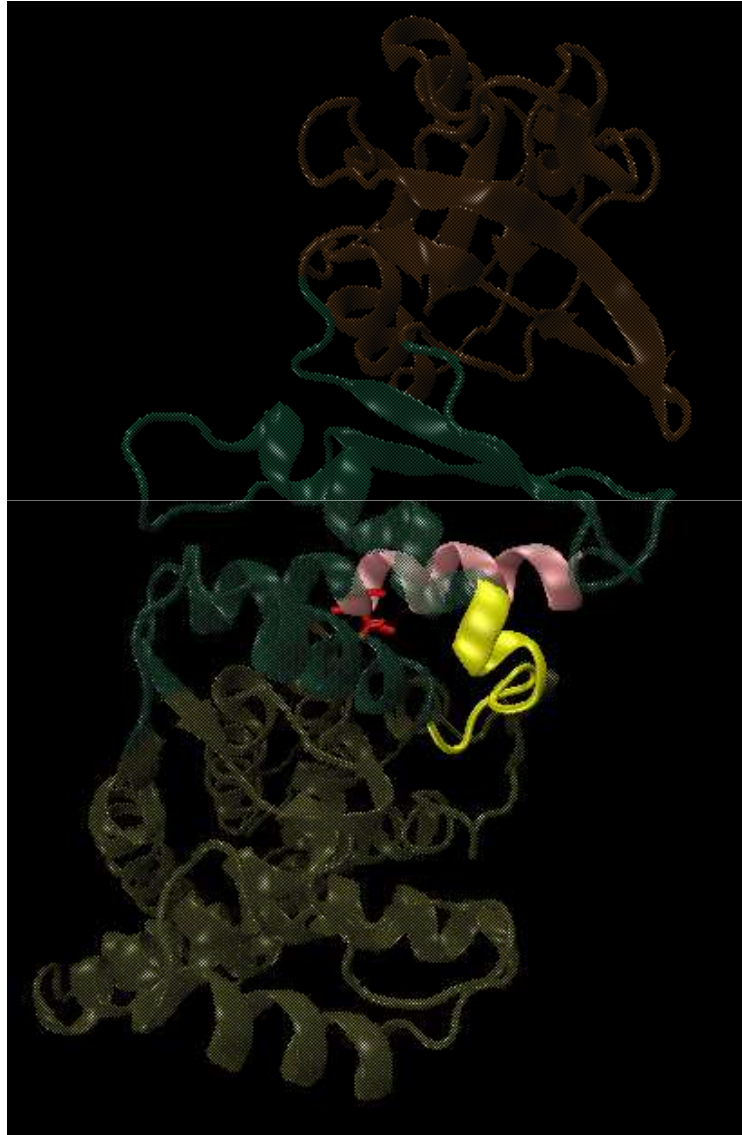


Fig115. NSL and Asp386 in open state (3IYF)

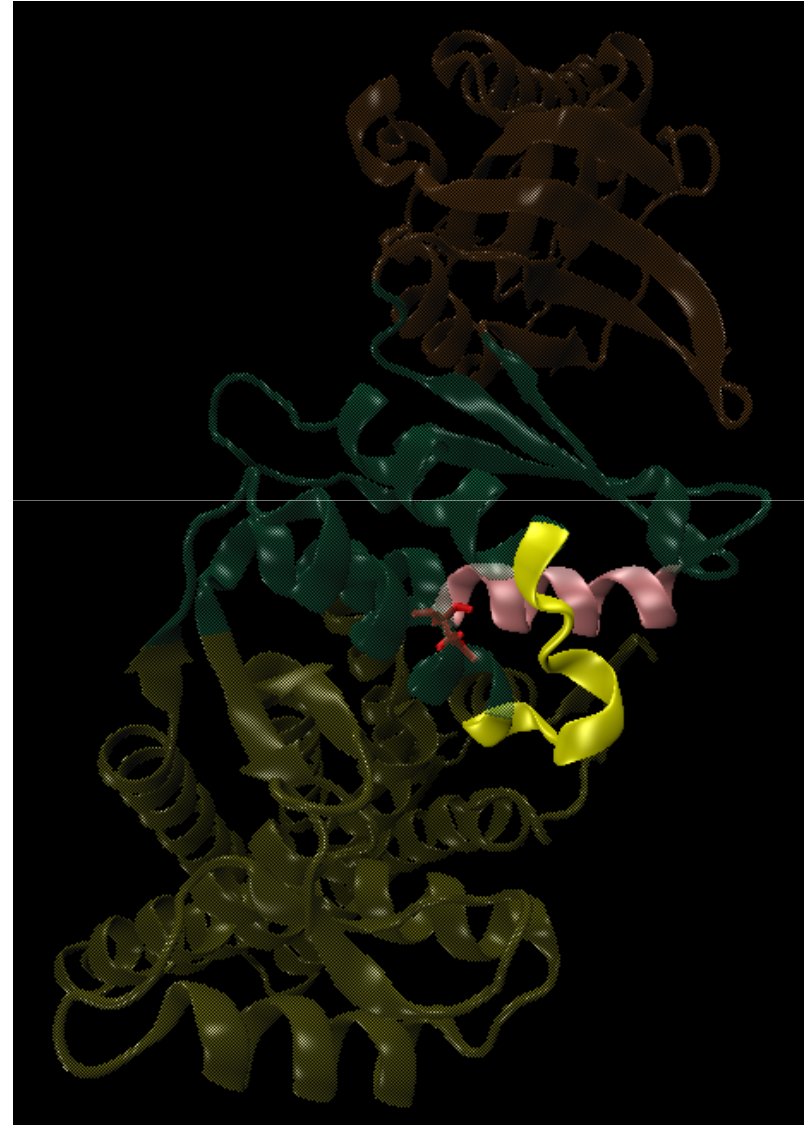
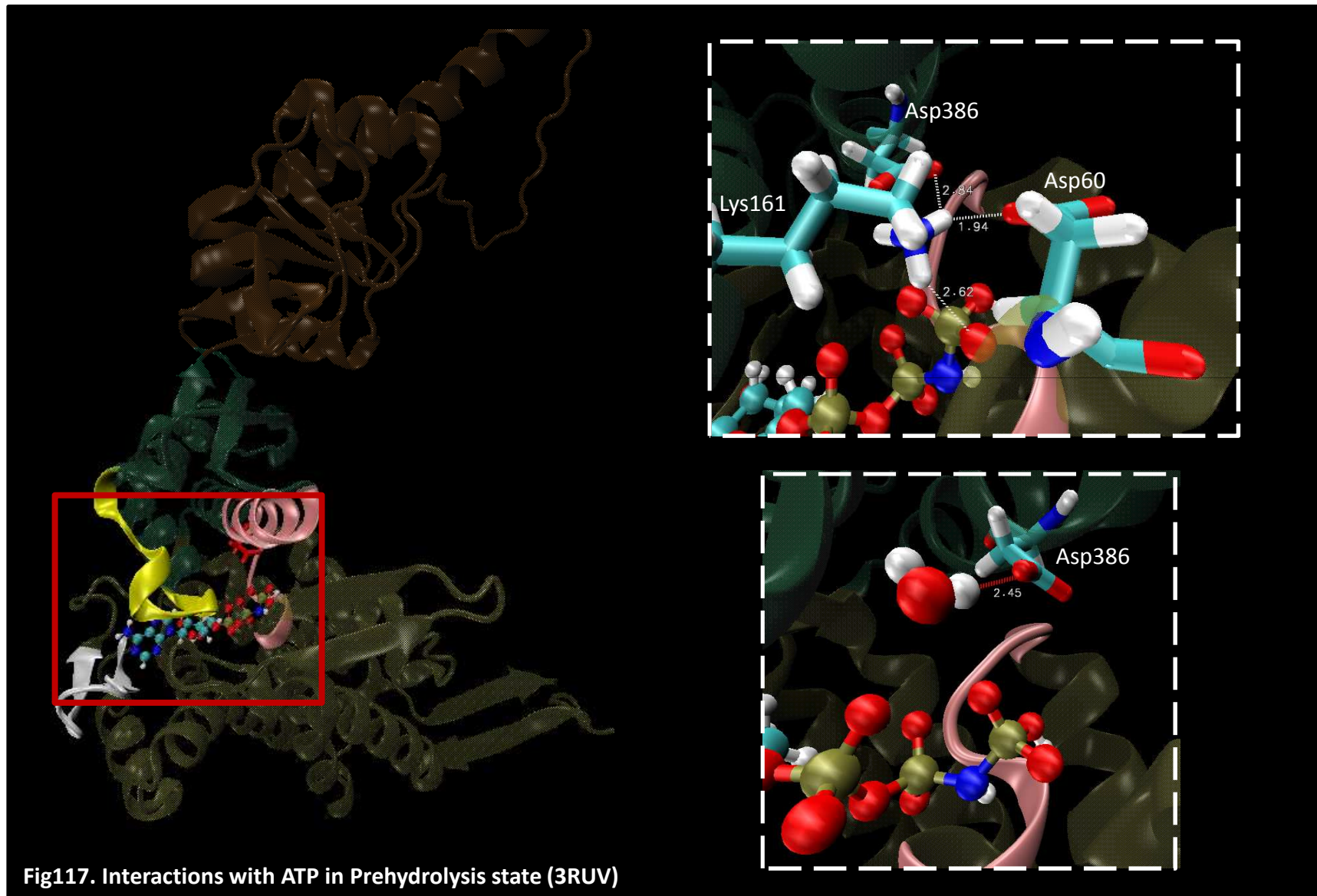
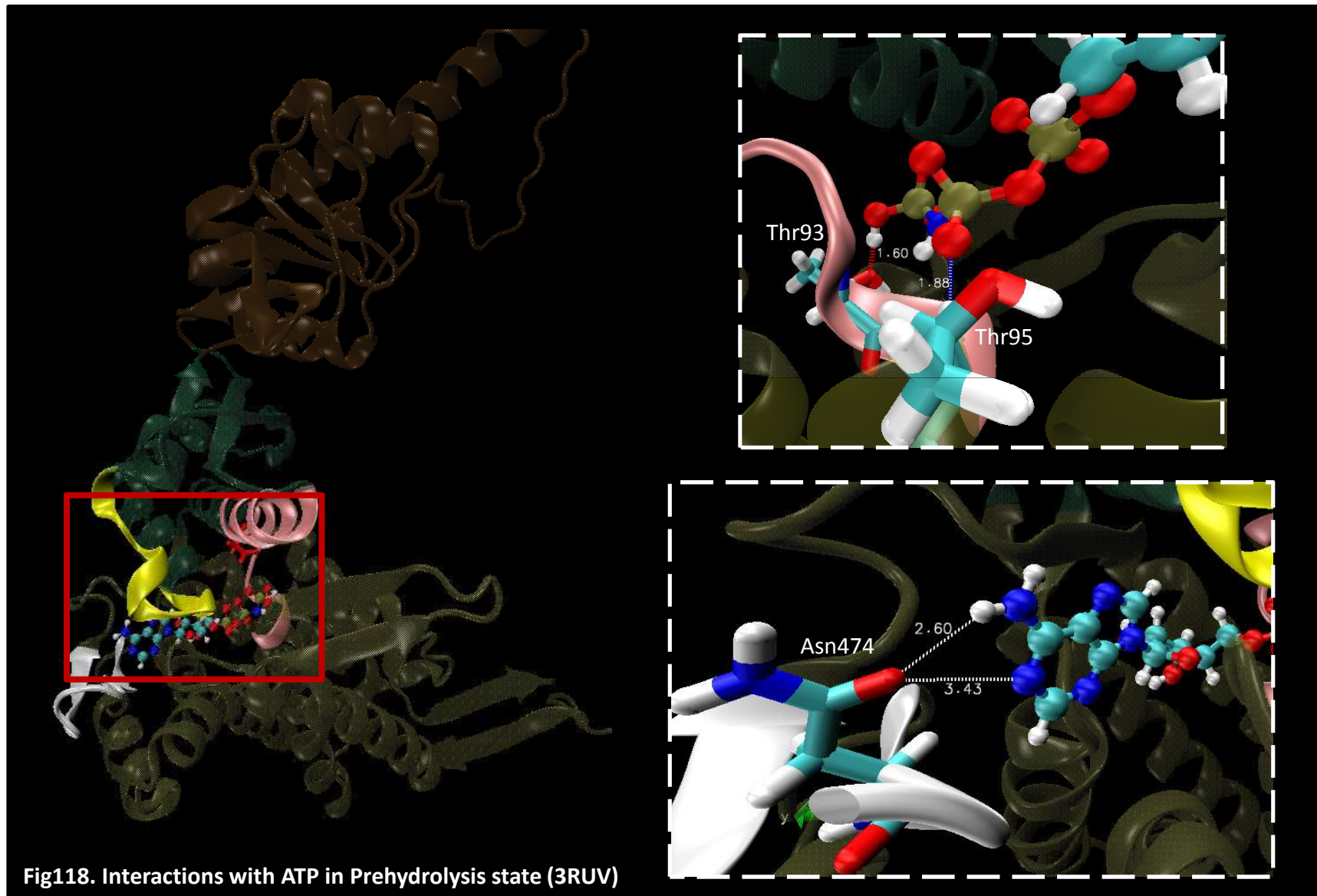


Fig116. NSL and Asp386 in Prehydrolysis state (3RUV)

MmCpn > Prehydrolysis state > Nucleotide binding site



MmCpn > Prehydrolysis state > Nucleotide binding site



MmCpn > **Prehydrolysis state** > Nucleotide binding site

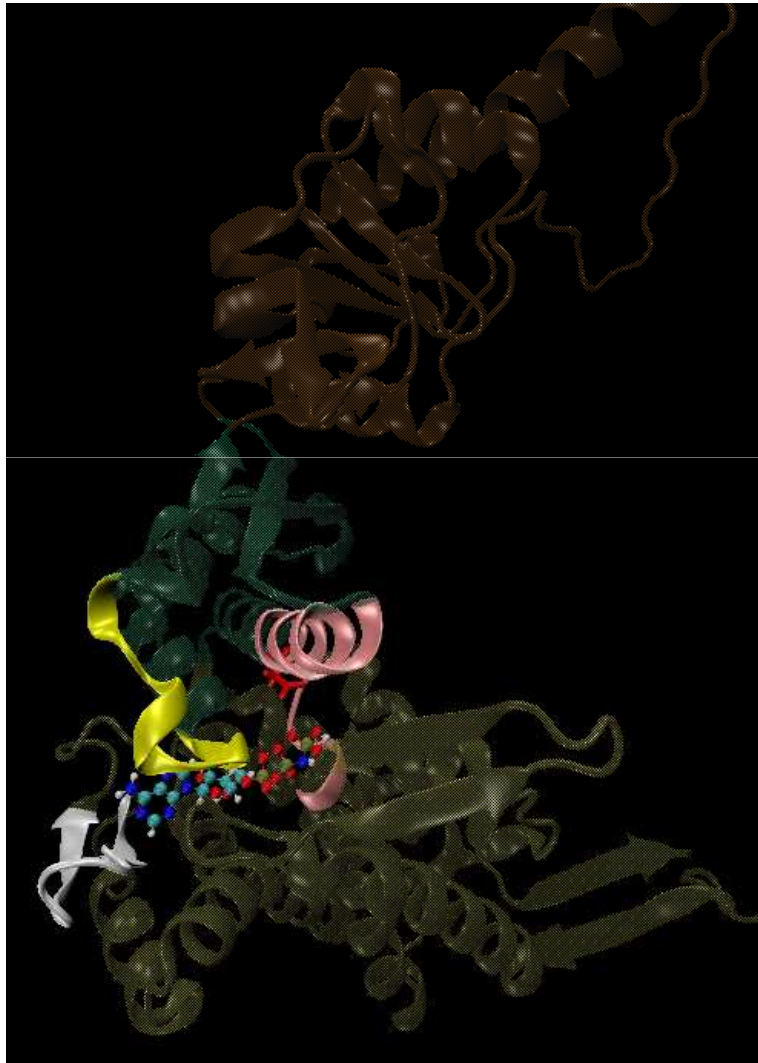


Fig119. Lateral view of the nucleotide binding pocket (3RUV)



Fig120. Rear view of the nucleotide binding pocket (3RUV)

MmCpn > Closed state

ATP is hydrolyzed in the nucleotide binding site

All the three domains suffer a large rocking motion to completely close the chamber

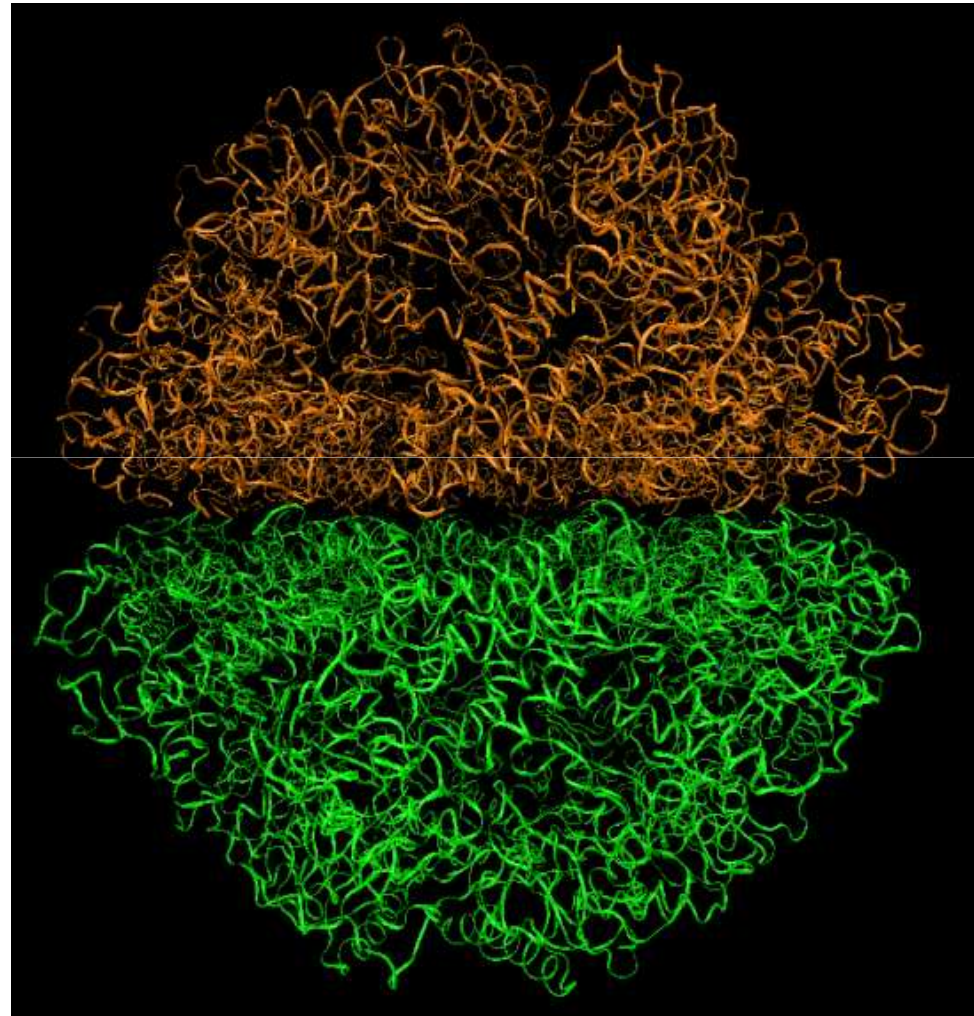


Fig121. MmCpn in Closed conformation (3LOS)

MmCpn > Closed state

Equatorial domains suffers a significant outward and lateral rotation

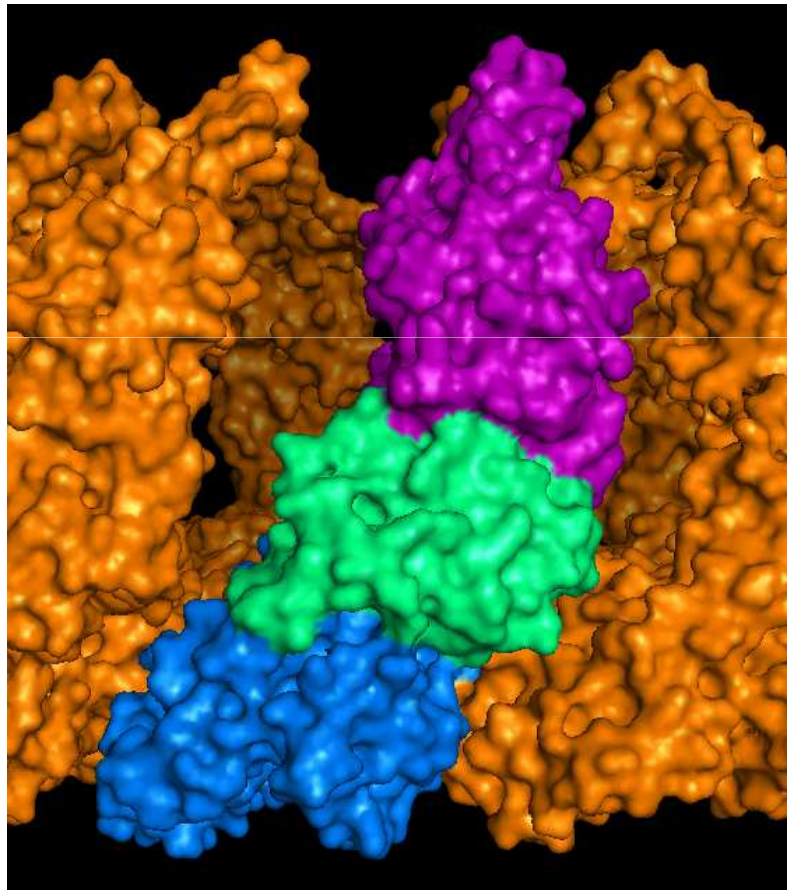


Fig122. Single subunit in Prehydrolysis conformation (3IZH)

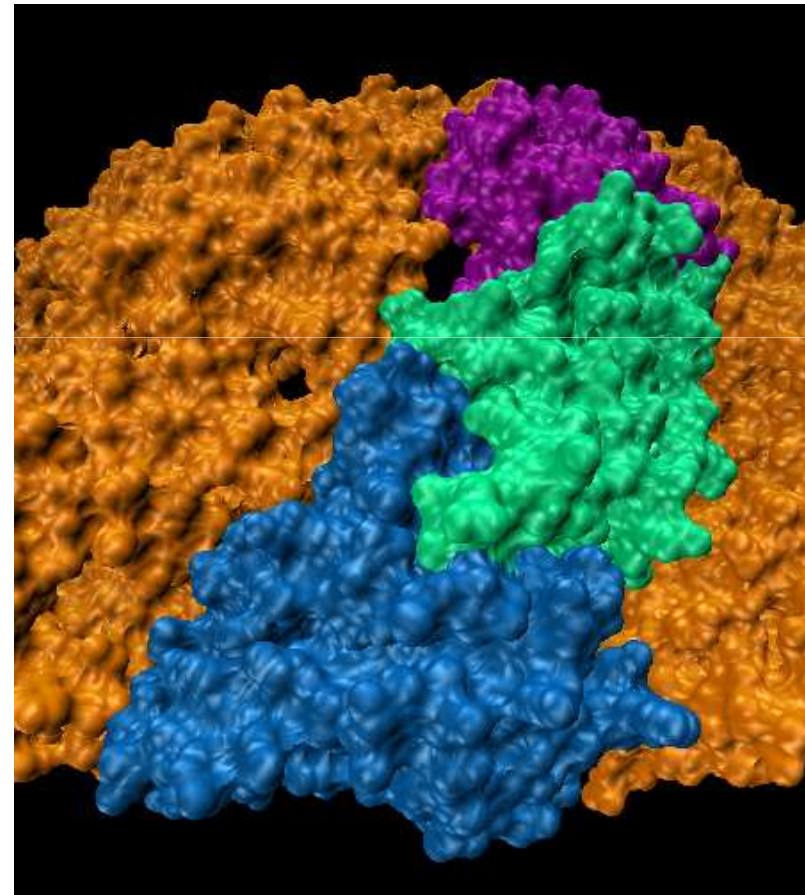


Fig123. Single subunit in Closed conformation (3LOS)

MmCpn > Closed state > Closing the chamber

ATP hydrolysis has a dual function: { Chamber closure
Substrate release

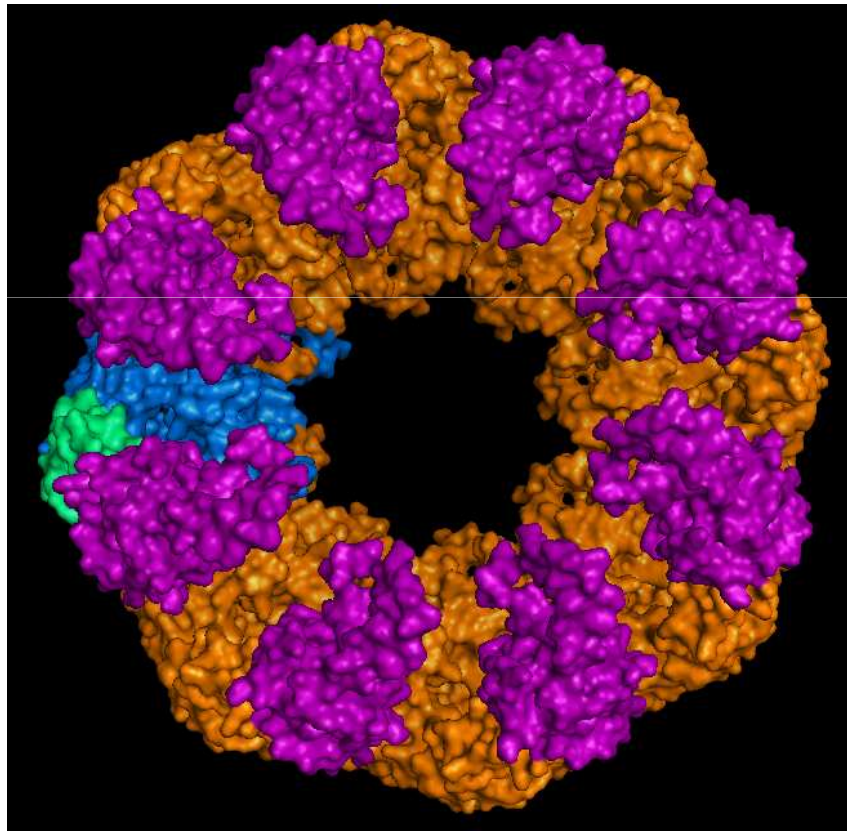


Fig124. Apical domains in Prehydrolysis conformation (3IZH)

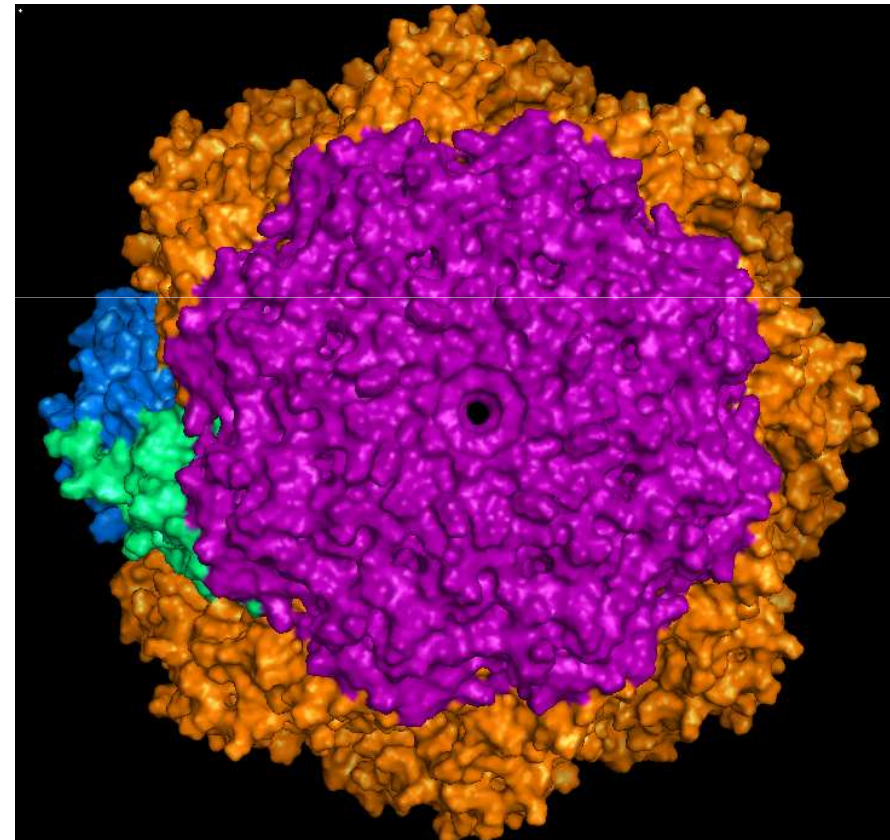
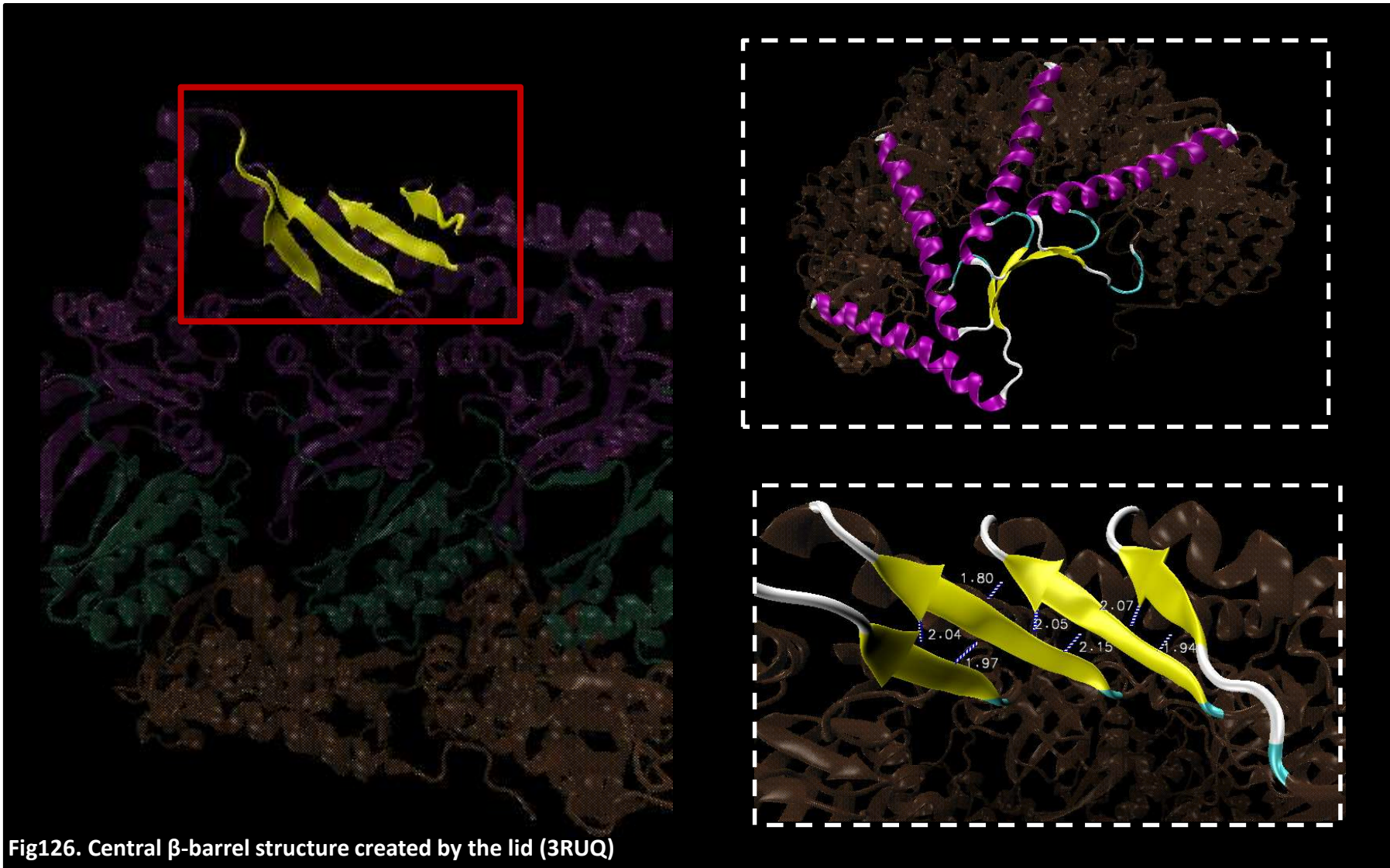


Fig125. Apical domains in Closed conformation (3LOS)

MmCpn > **Closed state** > Closing the chamber



MmCpn > **Closed state** > Closing the chamber

Hydrophilic residues exposed
inside the closed chamber

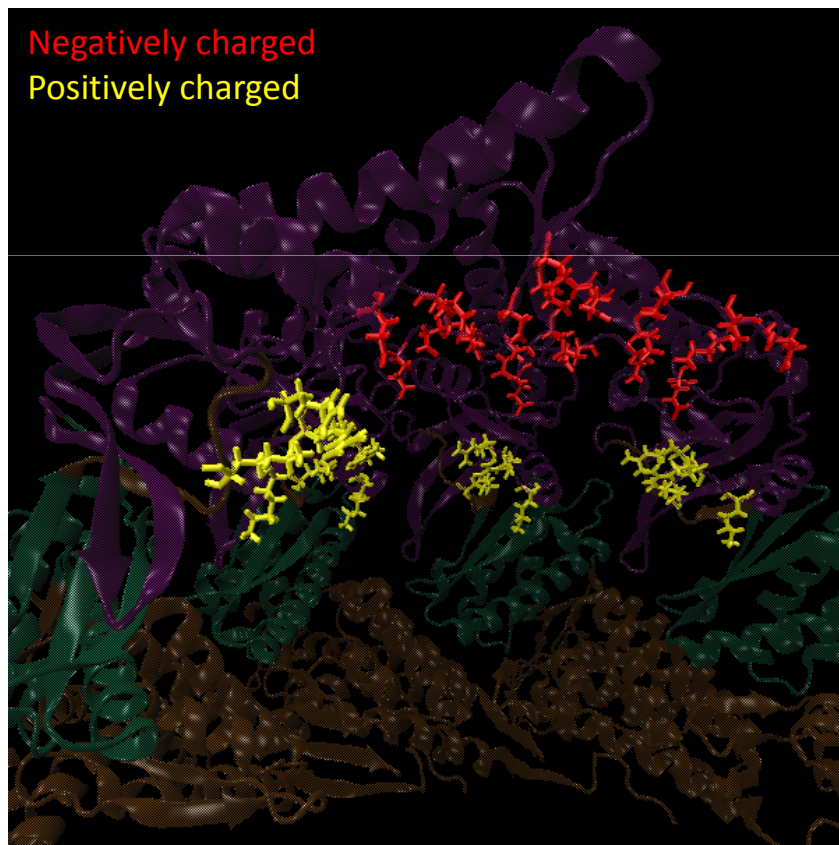


Fig127. Polar residues inside the closed chamber (3RUQ)

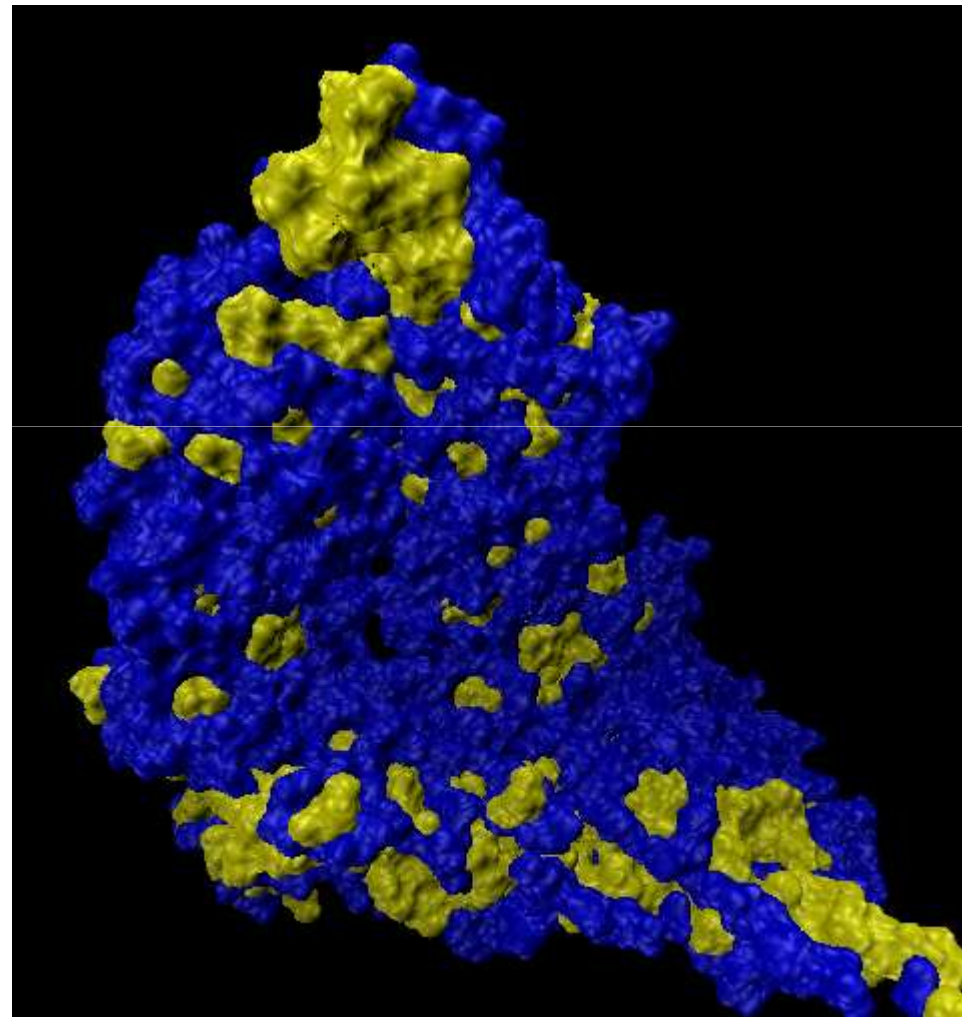
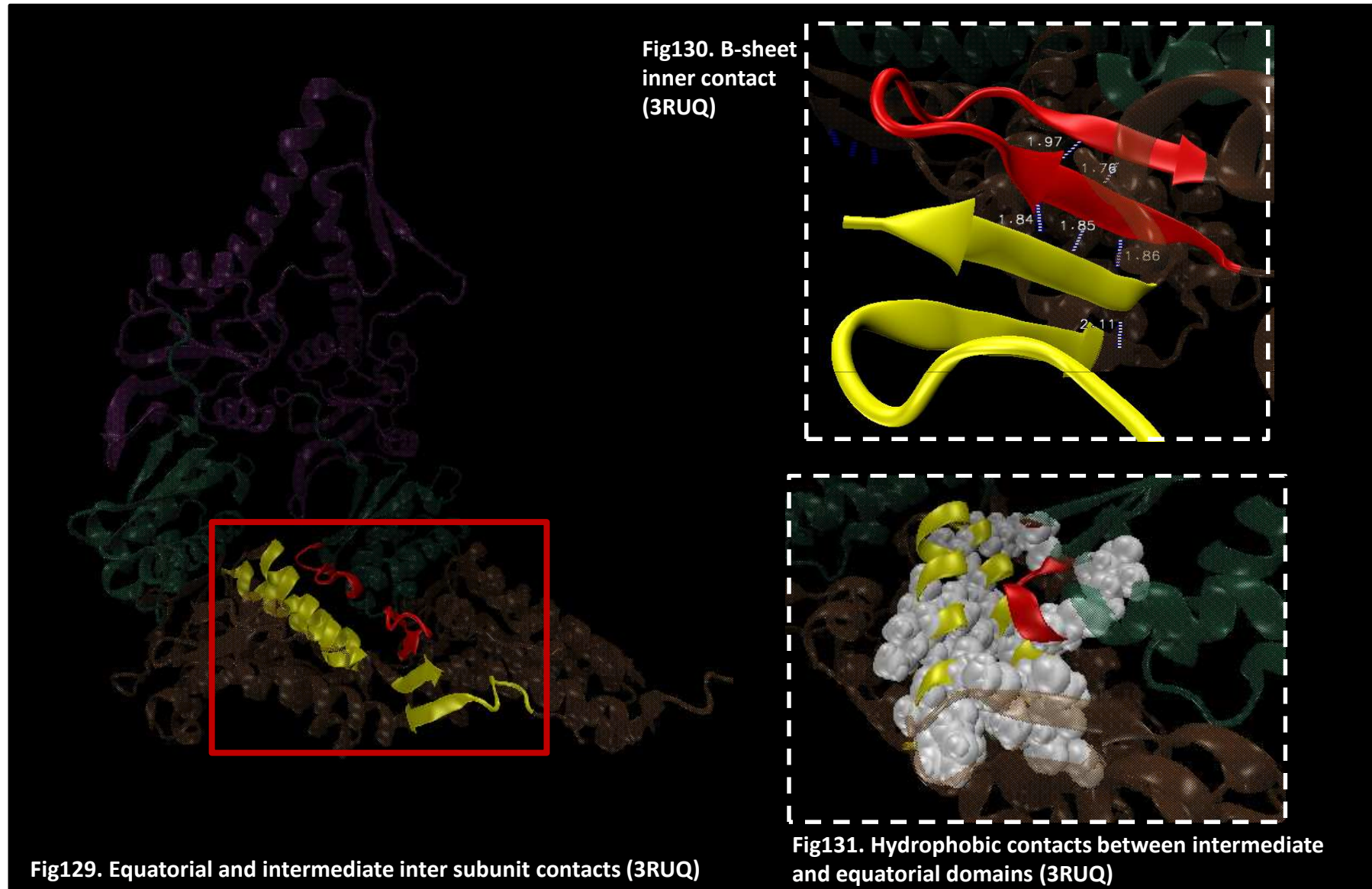
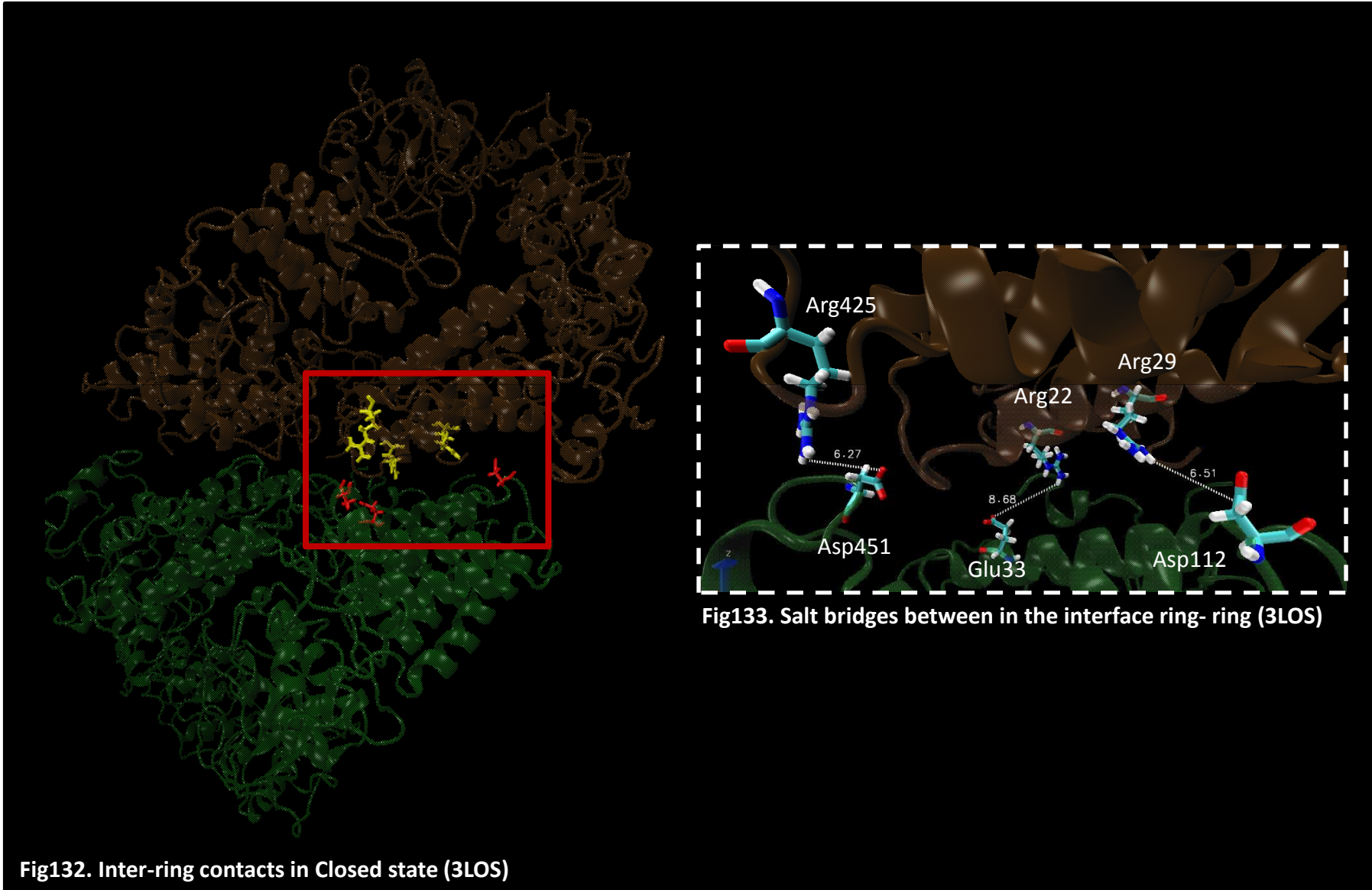


Fig128. Hydrophilic inner surface of the closed chamber (3RUQ)

MmCpn > Closed state > Intra-ring interactions



MmCpn > Closed state > Inter-ring



MmCpn > **Closed state** > Nucleotide binding site

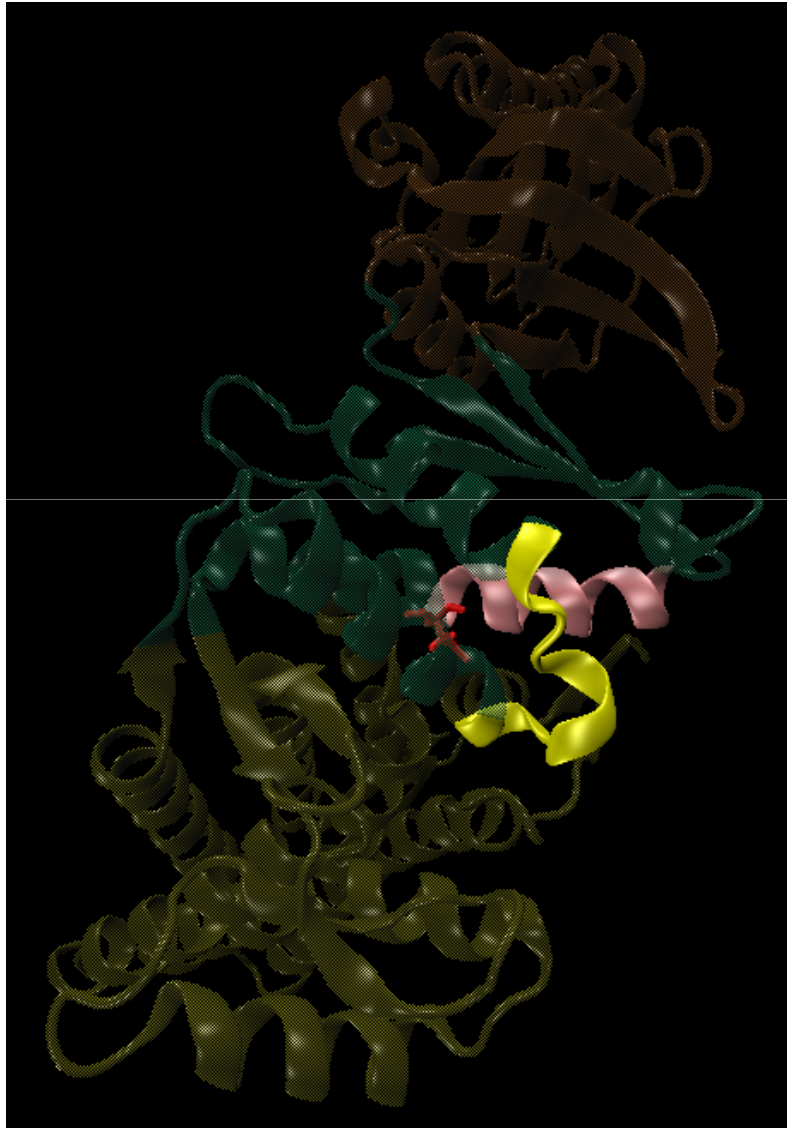


Fig134. NSL and Asp386 in Prehydrolysis state (3RUV)

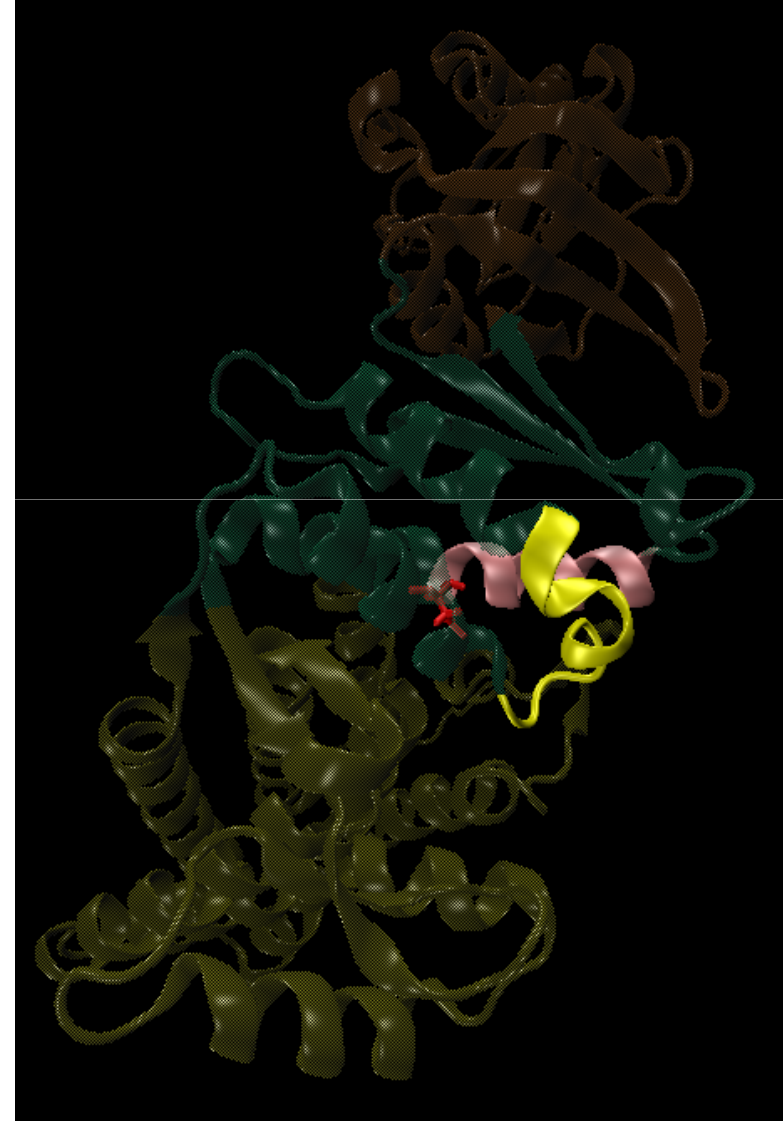
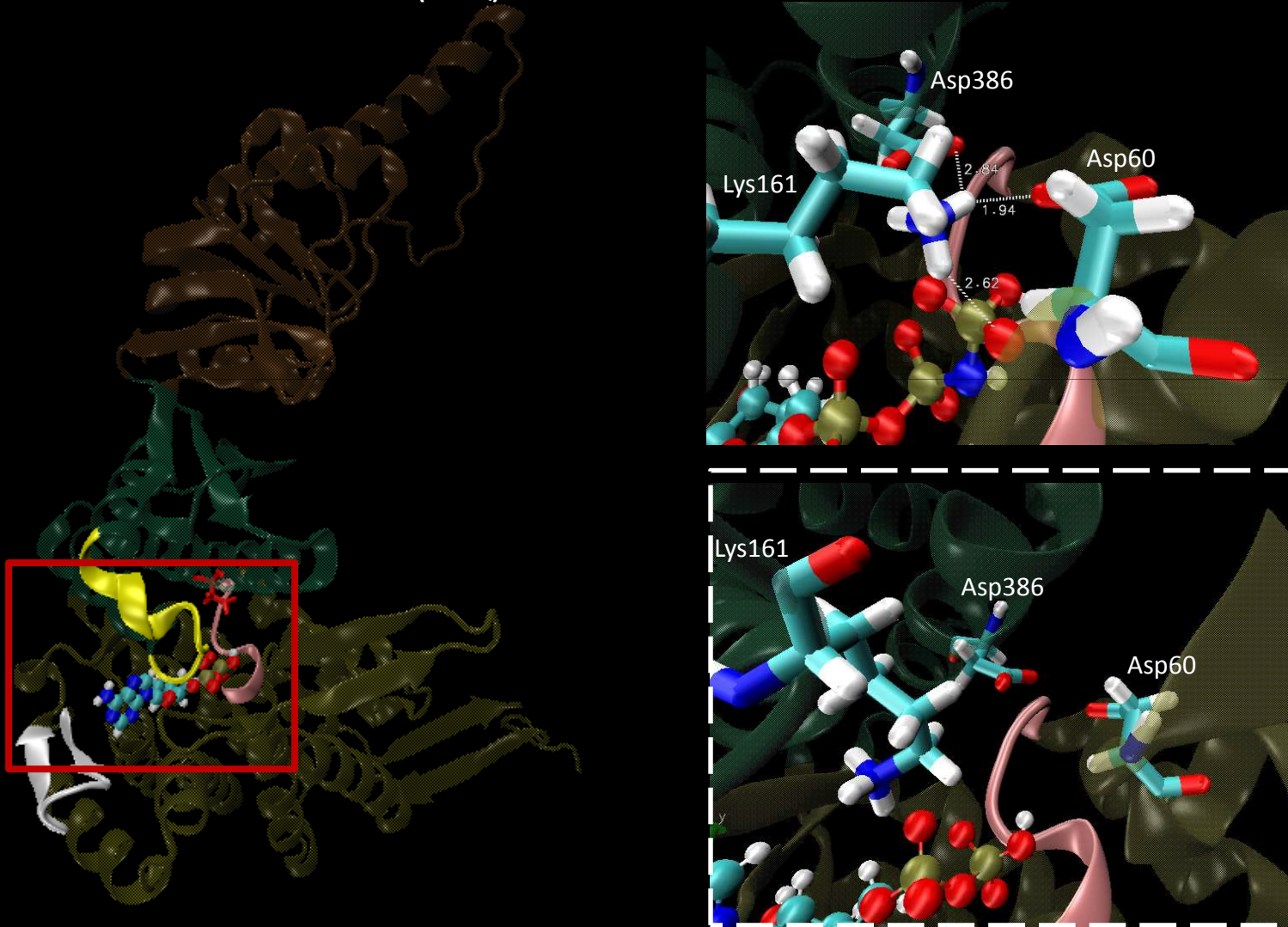


Fig135. NSL and Asp386 in Closed state (3RUQ)

MmCpn > **Closed state** > Nucleotide binding site

Fig136. Interactions with ADP in the Closed state (3RUQ)



MmCpn > Closed state > Nucleotide binding site

PREHYDROLYSIS STATE

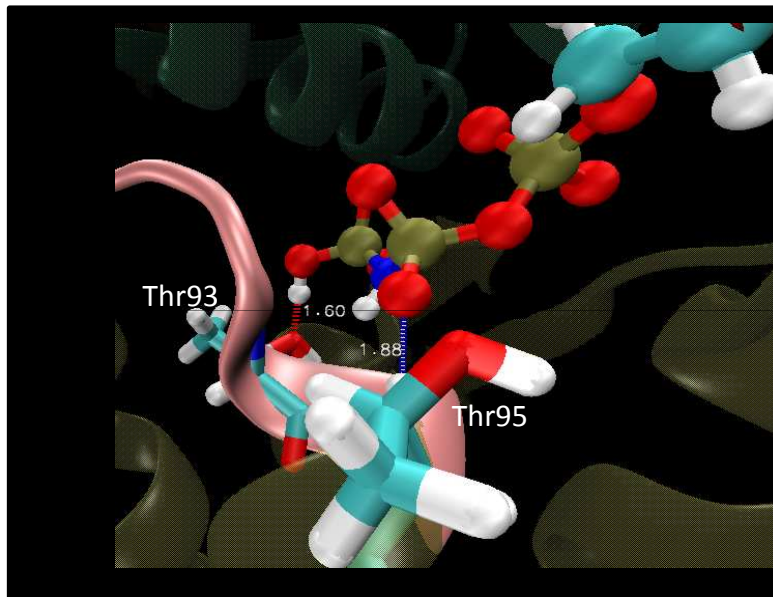


Fig137. P-loop interaction with the gamma and beta phosphate in Prehydrolysis state (3RUV)

CLOSED STATE

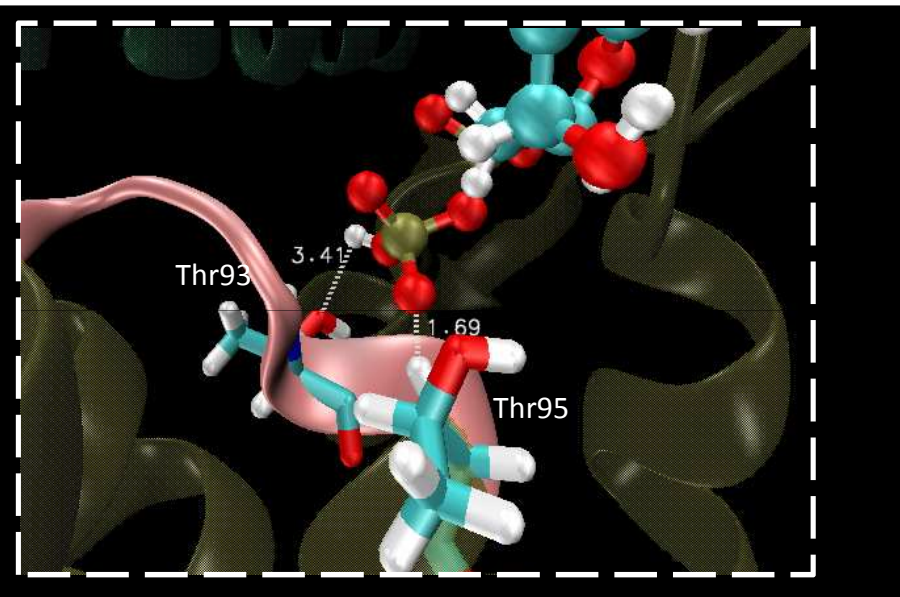


Fig138. P-loop interaction with the beta phosphate in Closed state (3RUQ)

MmCpn > Closed state > Nucleotide binding site

PREHYDROLYSIS STATE

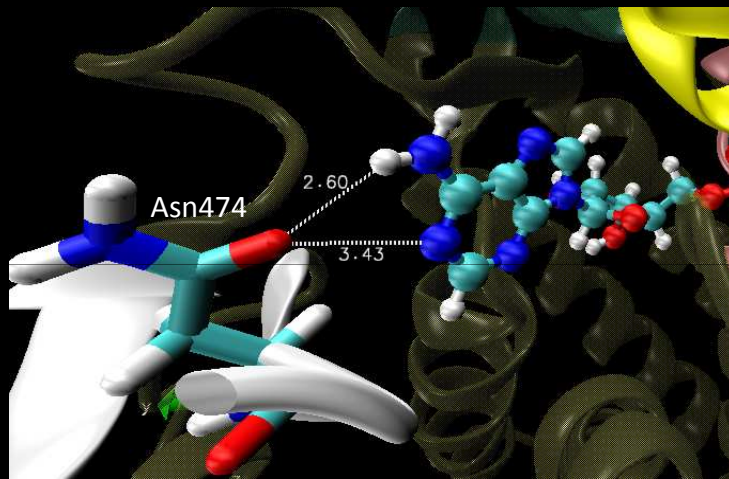


Fig139. Asn474 interaction with the adenine base of ATP (3RUV)

CLOSED STATE

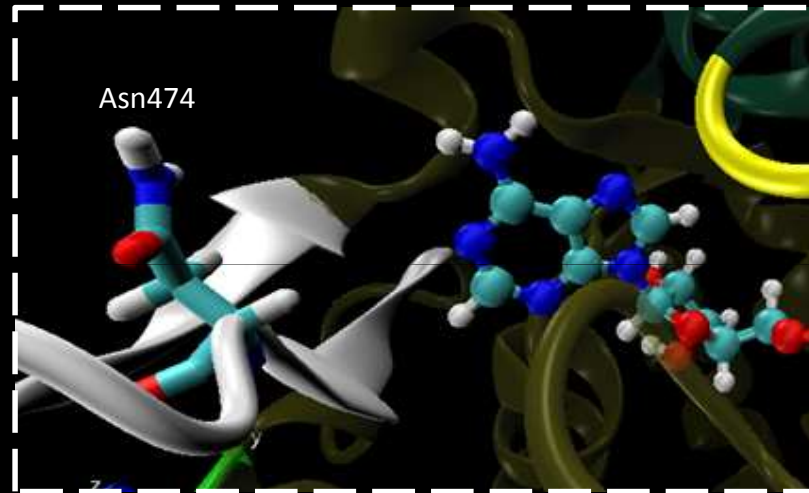


Fig140. Asn474 disposition in Closed state (3RUQ)

MmCpn > **Closed state** > Nucleotide binding site

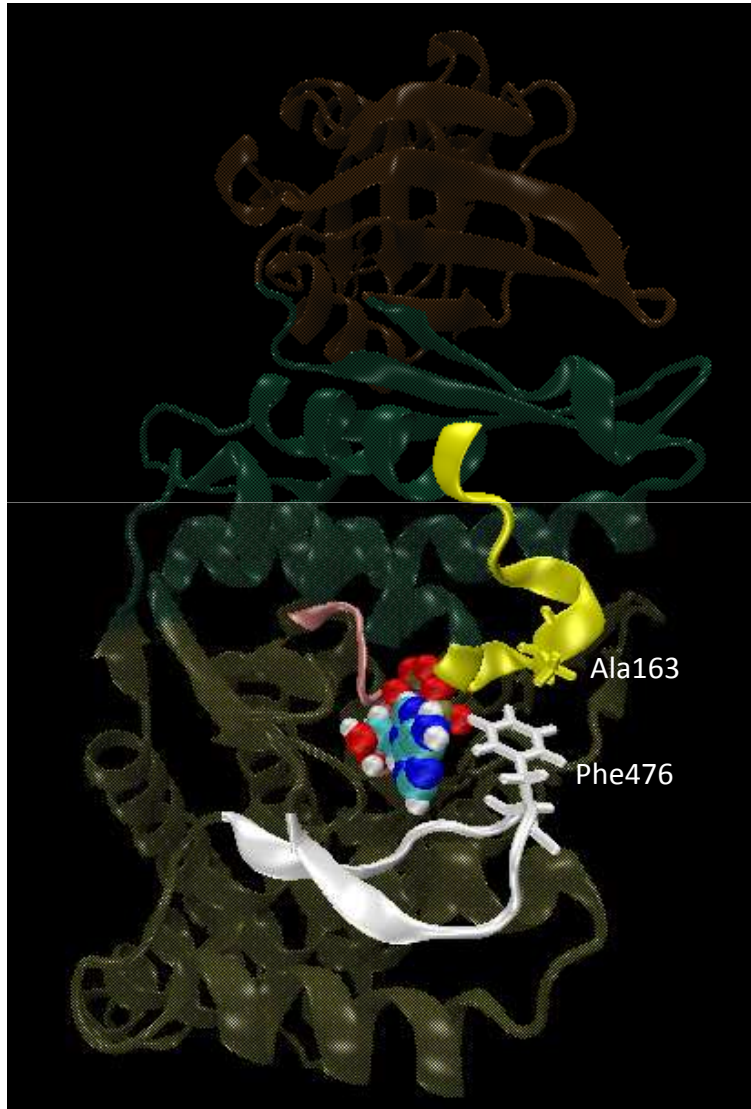


Fig141. Rear view of the nucleotide binding pocket in Prehydrolysis state (3RUV)

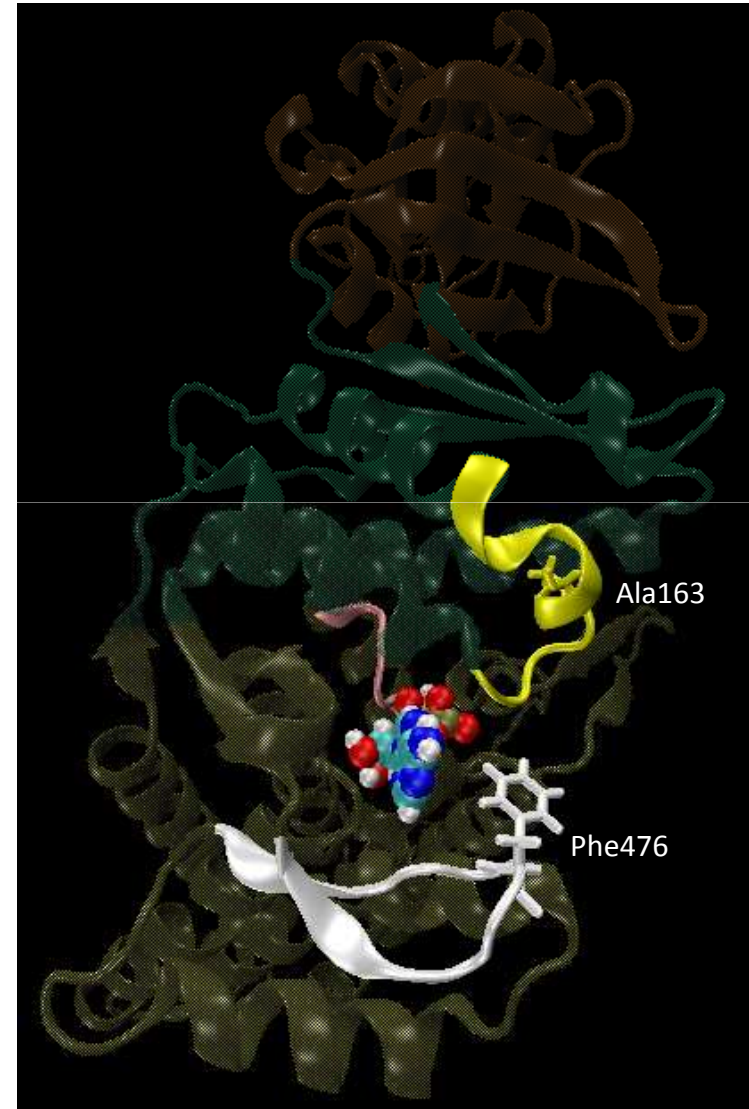


Fig142. Rear view of the nucleotide binding pocket in Closed state (3RUQ)

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USED PROGRAMMES

PDBs:

- 1AON
- 1DKD
- 1GRU
- 1MNF
- 1SS8
- 1SVT
- 1SX3
- 1SX4
- 2C7C
- 3IYF
- 3A0O
- 3KFB
- 3IZH
- 3RUV
- 3RUQ

PROGRAMMES:

- VMD
- PYMOL
- ChemScketch
- ProSA
- Jalview
- Rasmol
- STAMP