

From *E. coli* to plants and mammals...

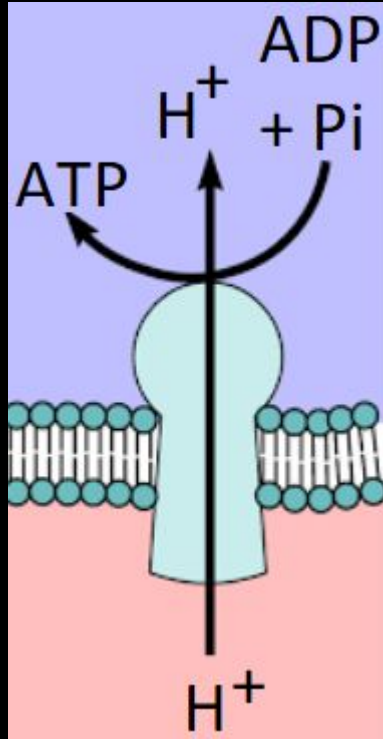


Sara Congost, Júlia Fabà, Clara Sabiote, Ariadna Torres
Structural Biology
(Human Biology, UPF)

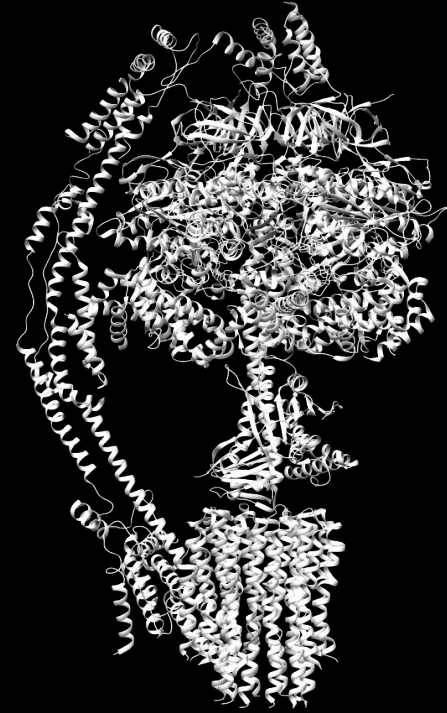


Paul Boyer, 1997

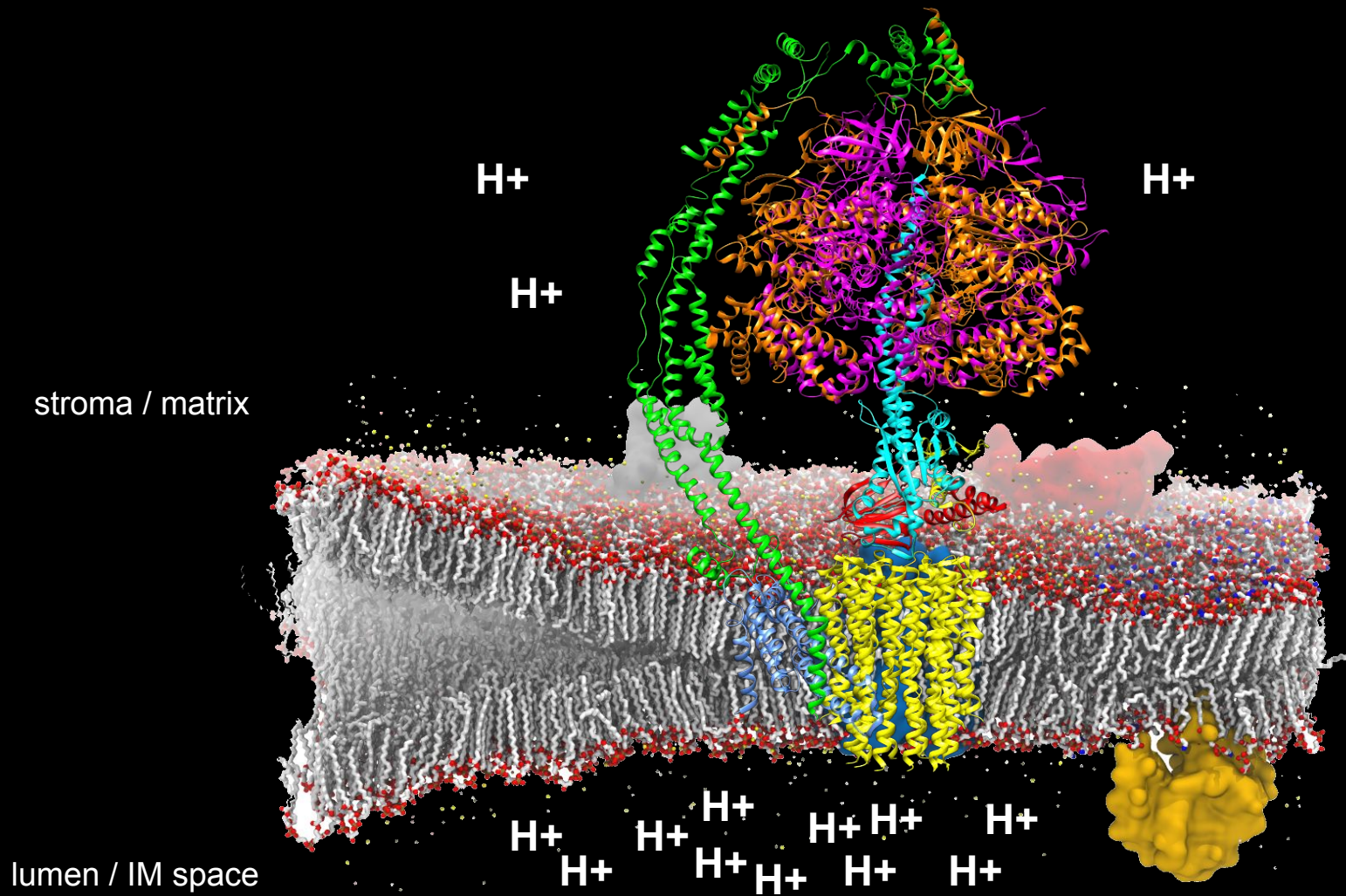
“All enzymes are beautiful,
but ATP synthase is one of
the most beautiful as well
as one of the most unusual
and important”



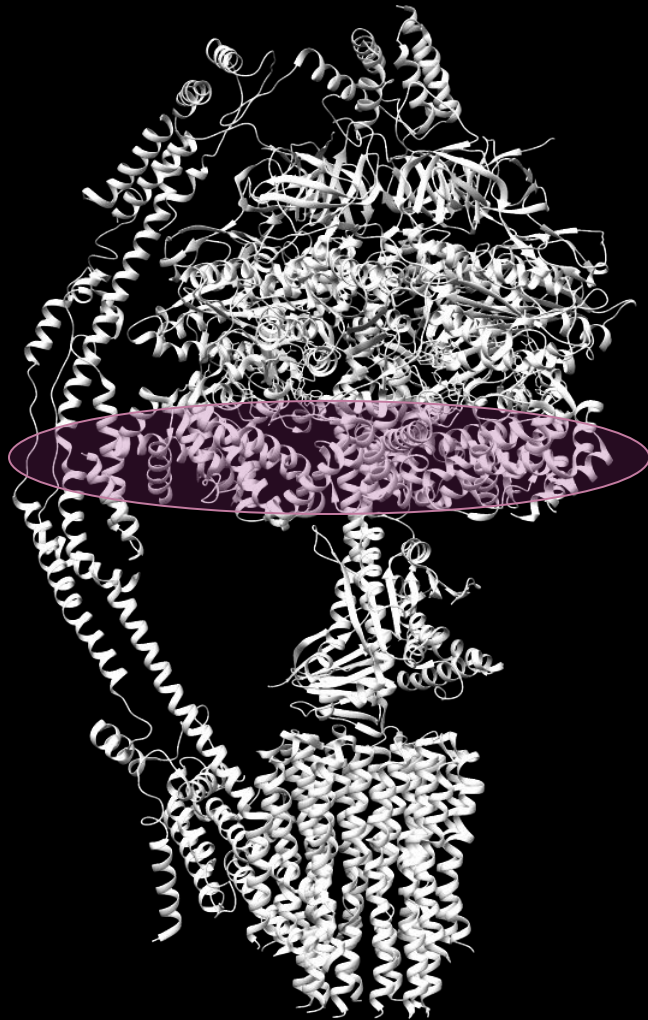
Expectation



Reality



10 nm



20 nm

550 - 1600 kDa

ATP synthase/ase types

In vivo

- F-ATPase: mitochondria, chloroplast and bacterial plasmatic membrane.
- A-ATPase: Archaea and some extremophilic bacteria.
- V-ATPase: vacuoles in eukaryotic cells.
- E-ATPase: cellular surface.
- P-ATPase: bacteria and eukaryotic plasmatic membrane and organelles.

Synthesis

Hydrolysis

All life kingdoms

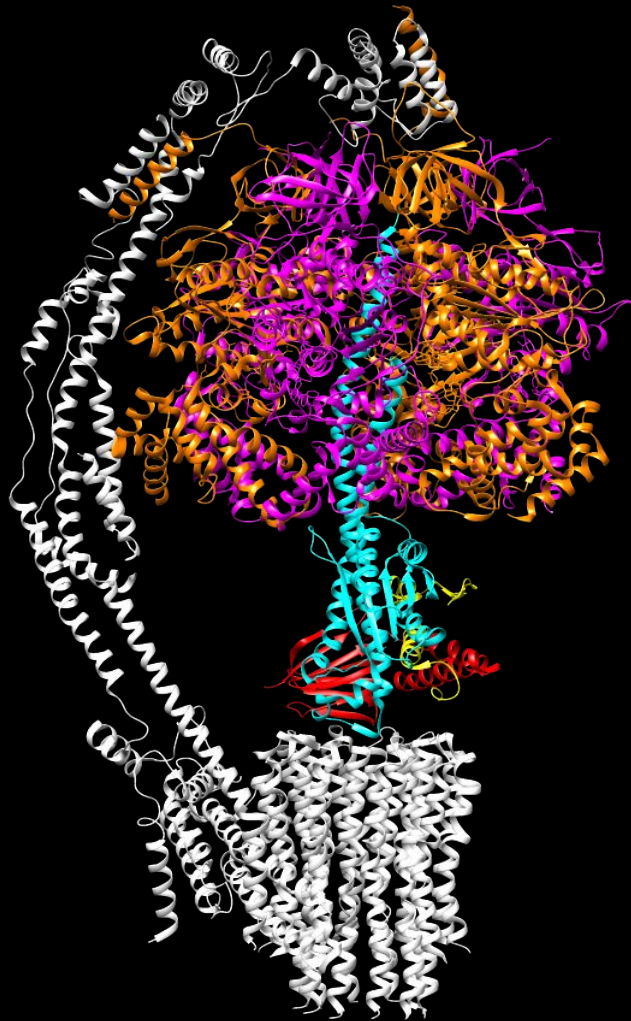
In vitro: reversible

F-type ATP synthase

		Primary function	Bacterial (E. coli)	Chloroplast (Spinach)	Mitochondrial (S. cerevisiae)	Mitochondrial (Bovine)
Fo	Peripheral stalk	Stator F1-Fo link	b	b	b	b
			b'	b'		
		Flexible hinge	δ (not mitochondrial)	δ (not mitochondrial)	OSCP	OSCP
		Structural			d	d
		Structural			H (F6)	H (F6)
	Fo rotor	Stator, proton half channels	a	a	a	a
		Rotor, proton translocation	c	c	c	c
F1	Catalytic head	Structural, catalytic	α	α	α	α
		Catalytic	β	β	β	β
	Central stalk	Torque transmission	γ	γ	γ	γ
		Connection to c-ring			δ	δ
		Connection to c-ring			ϵ	ϵ
Dimer specific subunits	Supernumerary subunits	Dimer stability			e	
		Dimer stability			g	
		Structural			f	
		Structural			j (i, 6.8PL)	
		Dimer stability			k (DAPIT)	
		Structural			8 (A6L)	



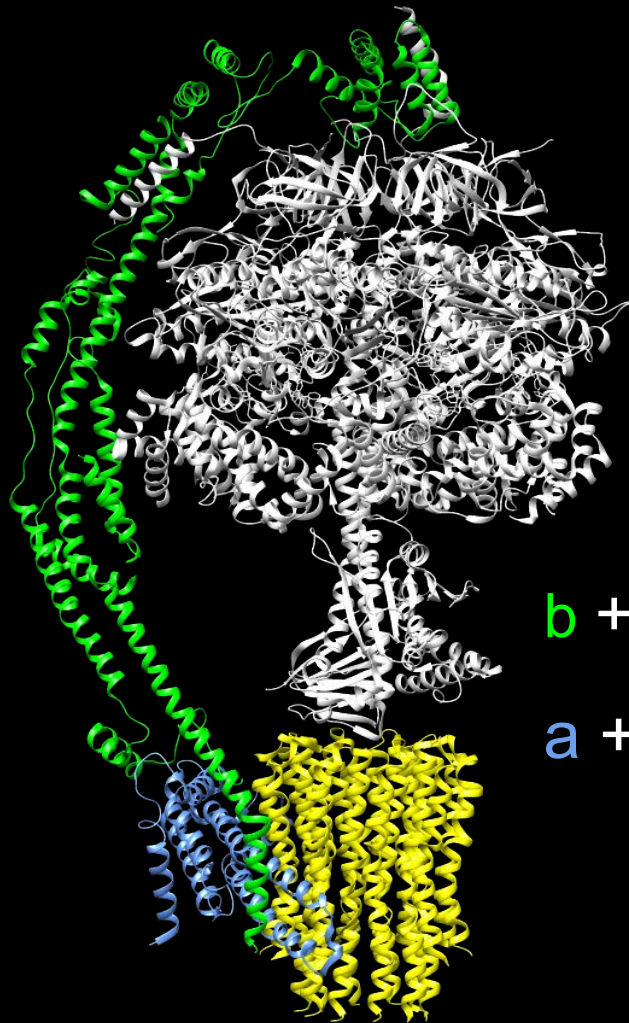
F1



$\alpha + \beta \rightarrow$ CATALYTIC HEAD

$\gamma + \delta + \epsilon \rightarrow$ CENTRAL STALK

F0



$b + \text{OSCP} + d + H \rightarrow \text{PERIPHERAL STALK}$

$a + \text{c-ring} \rightarrow \text{ROTOR}$

Mechanism

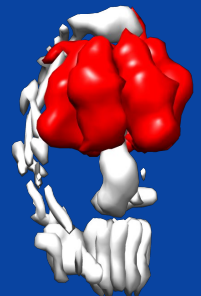
**PROTON
GRADIENT**



ROTATION



TRANSMISSION



**ATP
SYNTHESIS**

I part: motor function



F0 rotor-ATP synthase

Stator,
proton half channels

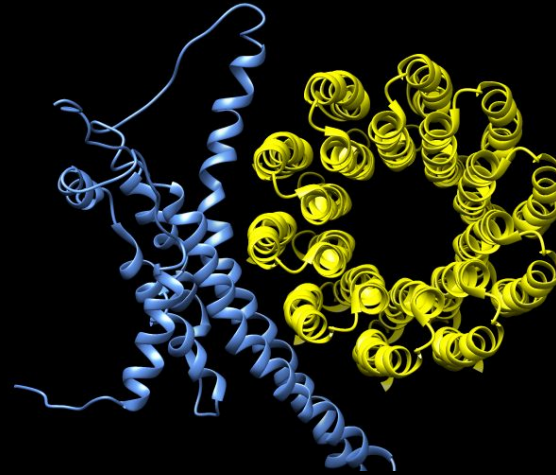


a

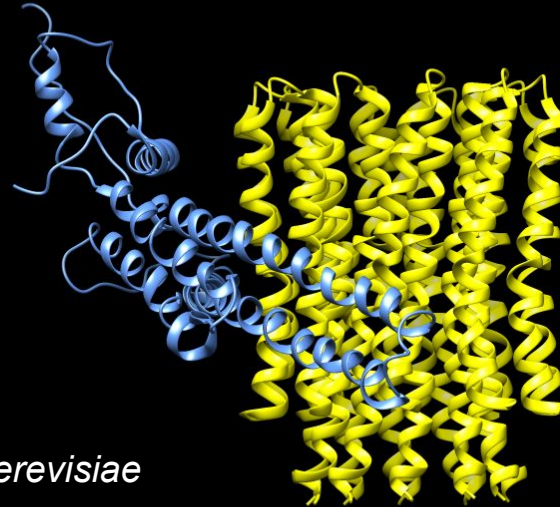
Rotor,
proton translocation



c-ring

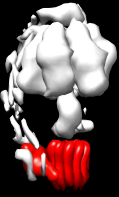


luminal view



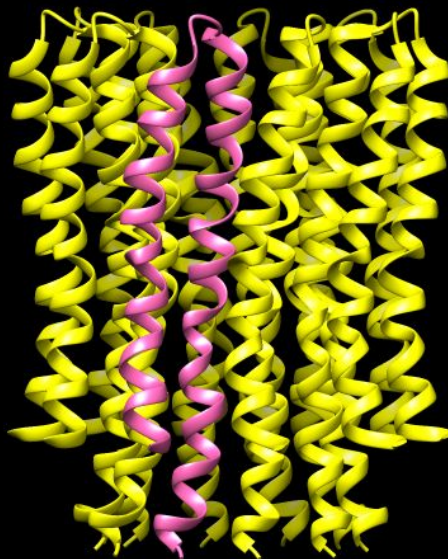
lateral view

S. cerevisiae



C-ring CATH

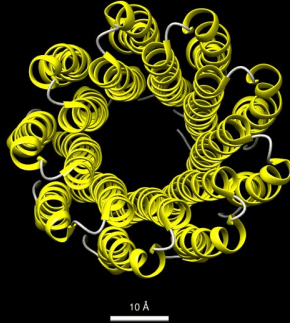
Class	Mainly alpha
Architecture	Up-down bundle
Topology	F1F0 ATP synthase
Homologous Superfamily	F1F0 ATP synthase subunit C



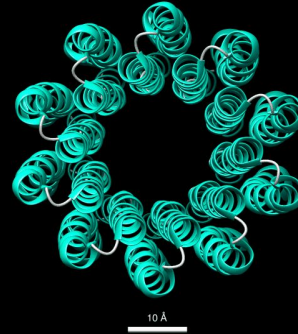
C-ring rotor: monomer number



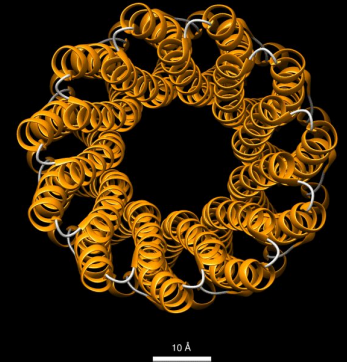
C8 *Bos taurus*



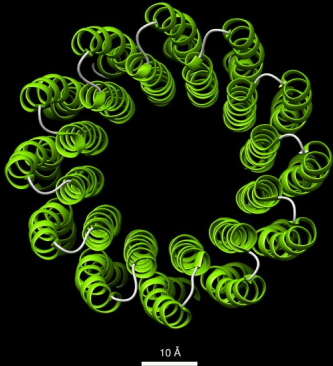
C9 *Mycobacterium phlei*



C10 *S. cerevisiae*



C11 *Iliobacter tartaricus*



C12 *Bacillus pseudofirmus*
OF4 mutant



C13 *B. pseudofirmus* OF4
wildtype



C14 *Pisum sativum*



C15 *Spirulina platensis*

C-ring monomer MSA

	51	61	71	81	91
Consensus	- - - - -	m - p l d a a a k y	i g A g l a t - l a	a i G a g i G i G t	v a G q l i e G i a
Conservation					
Spinacia oleracea	- - - - -	MN P L I A A A S V	I A A G L A V G L A	S I G P G V G Q G T	A A G Q A V E G I A
Pisum sativum	- - - - -	MN P L I A A A S V	I A A G L A V G L A	S I G P G V G Q G T	A A G Q A V E G I A
Trichormus variabilis	- - - - -	MD P L V S A A S V	L A A A L A V G L A	A I G P G I G Q G N	A A G Q A V E G I A
Homo sapiens	A R R E F Q T S V V	S R D I D T A A K F	I G A G A A T - V G	V A G S G A G I G T	V F G S L I I G Y A
Bos taurus	A R R E F Q T S V V	S R D I D T A A K F	I G A G A A T - V G	V A G S G A G I G T	V F G S L I I G Y A
Saccharomyces cerevisiae	V - - - -	- - - - L A A K Y	I G A G I S T - I G	L L G A G I G I A I	V F A A L I N G V S
Polytomella sp.	A Q V R - - - -	S M S V L A A S K M	V G A G C A T - I A	L A G V G A G L G V	M F G S L I N G A A
Paracoccus denitrificans	- - - - -	- - - M E Q M G Q Y	L G A G L A C - I G	M A G A A I G V G N	V A G N Y L S G A L
Escherichia coli	- - - - -	M E N L N M D L L Y	M A A A V M M G L A	A I G A A I G I G I	L G G K F L E G A A
	101	111	121	131	141
Consensus	R n P s a k d q l r	g t a l l g f A l s	E A l g i f c l m V	a l l l L F A v - -	-
Conservation					
Spinacia oleracea	R Q P E A E G K I R	G T L L L S L A F M	E A L T I Y G L V V	A L A L L F A N P F	V
Pisum sativum	R Q P E A E D K I R	G T L L L S L A F M	E A L T I Y G L V V	A L A L L F A N P F	V
Trichormus variabilis	R Q P E A E G K I R	G T L L L S L A F M	E A L T I Y G L V V	A L V L L F A N P F	A
Homo sapiens	R N P S L K Q Q L F	S Y A I L G F A L S	E A M G L F C L M V	A F L I L F A M - -	-
Bos taurus	R N P S L K Q Q L F	S Y A I L G F A L S	E A M G L F C L M V	A F L I L F A M - -	-
Saccharomyces cerevisiae	R N P S I K D T V F	P M A I L G F A L S	E A T G L F C L M V	S F L L L F G V - -	-
Polytomella sp.	R N P N I A K Q L V	G Y A L L G F A L T	E S I A L F S L L V	V F L I L F A - - -	-
Paracoccus denitrificans	R N P S A A A S Q T	A T L F I G M A F A	E A L G I F S F L V	A L L L L F A V - -	-
Escherichia coli	R Q P D L I P L L R	T Q F F I V M G L V	D A I P M I A V G L	G L Y V M F A V A -	-

G 83

G 85

G 87

G 89

R 101

P 103

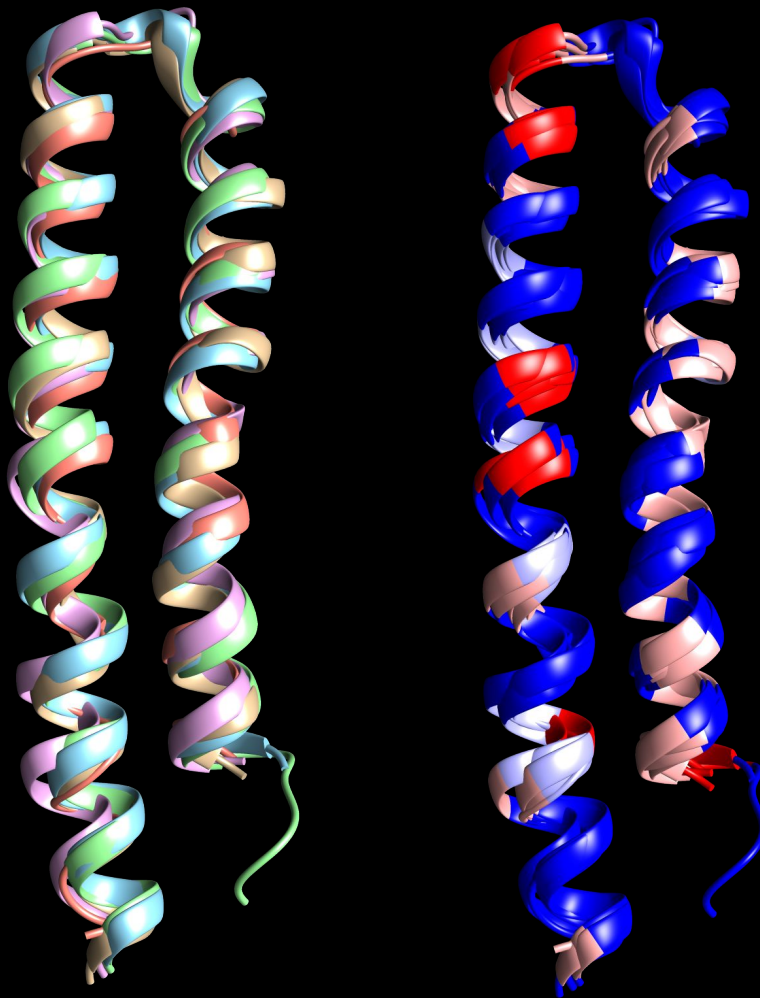
E 121

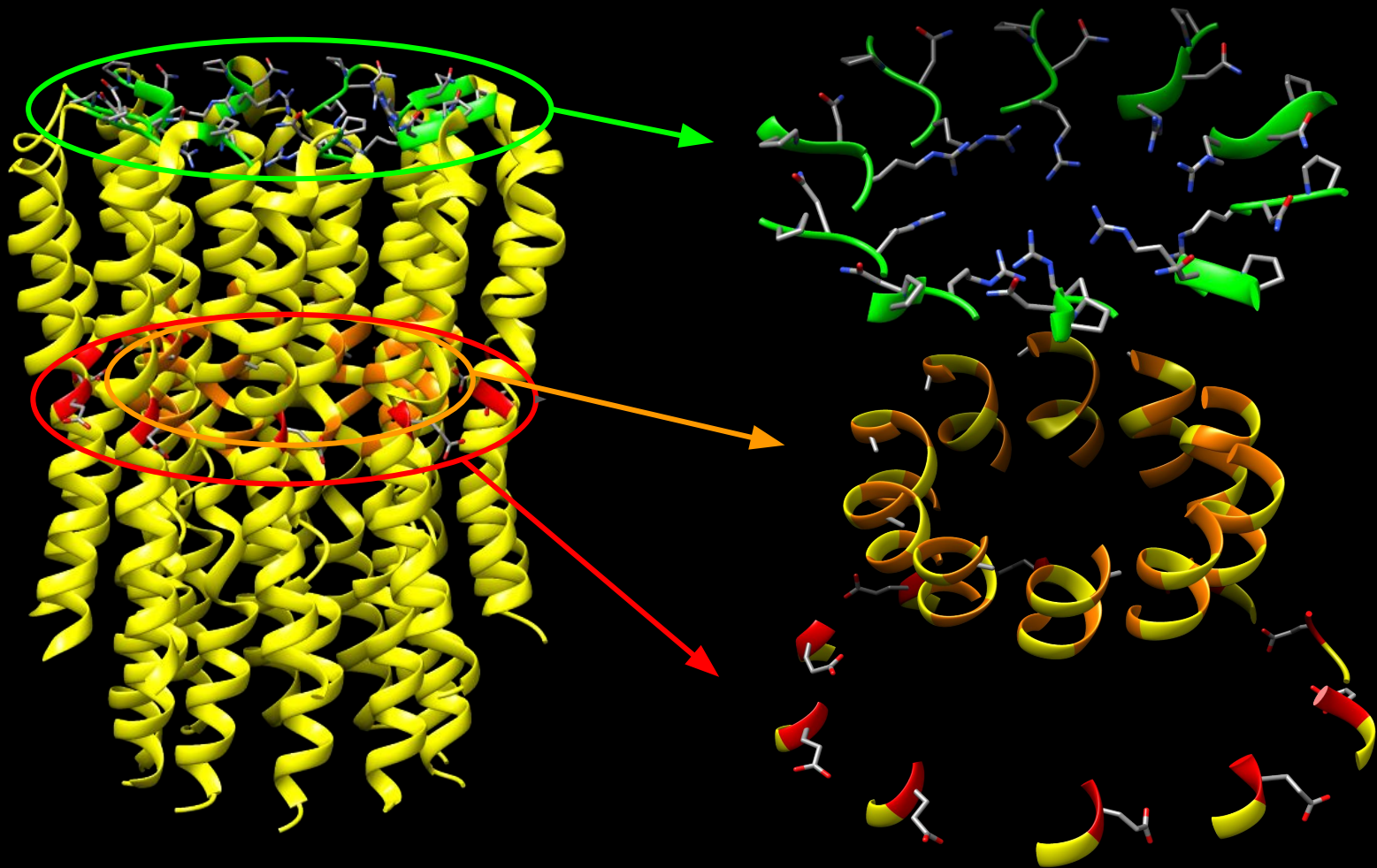
Plant chloroplast
Cyanobacteria chloroplast
Mitochondria
Bacteria

C-ring monomer

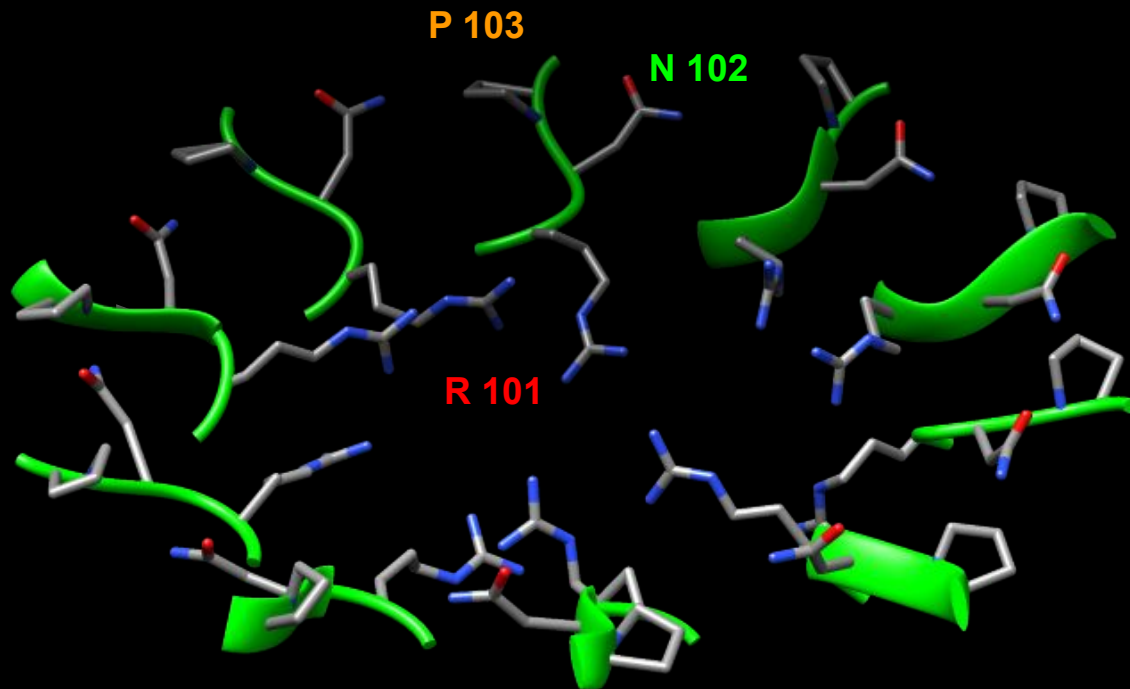
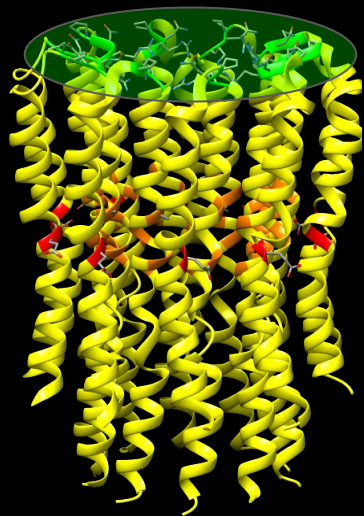
- *S. cerevisiae*
- *E. coli*
- *Polytomella sp.*
- *S. oleracea*
- *B. taurus*

RMSD: 1.086

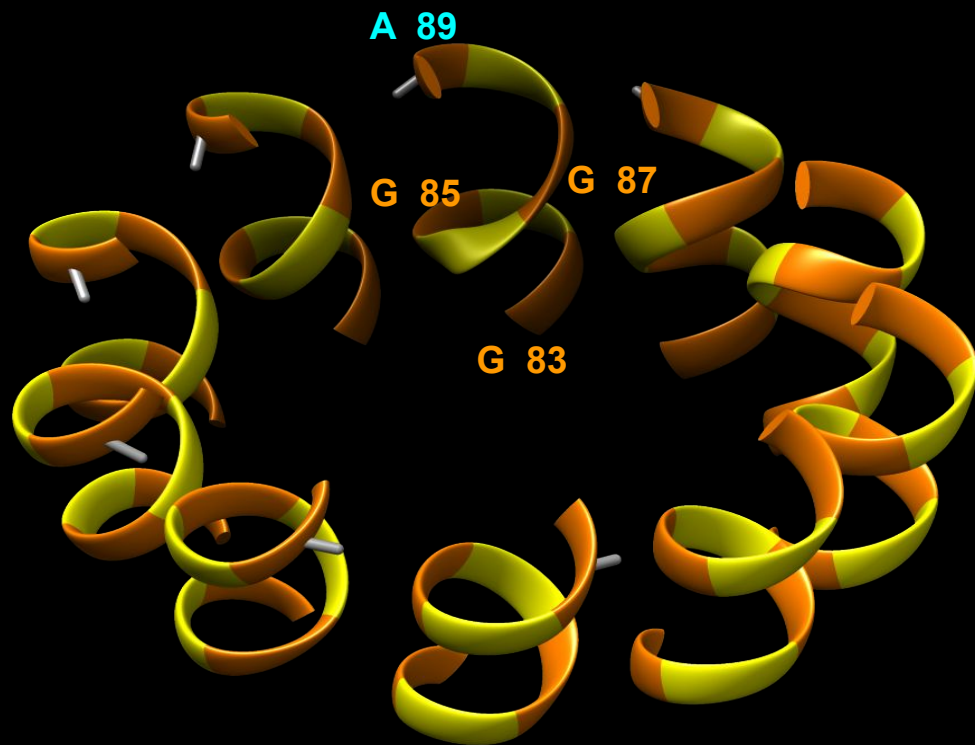
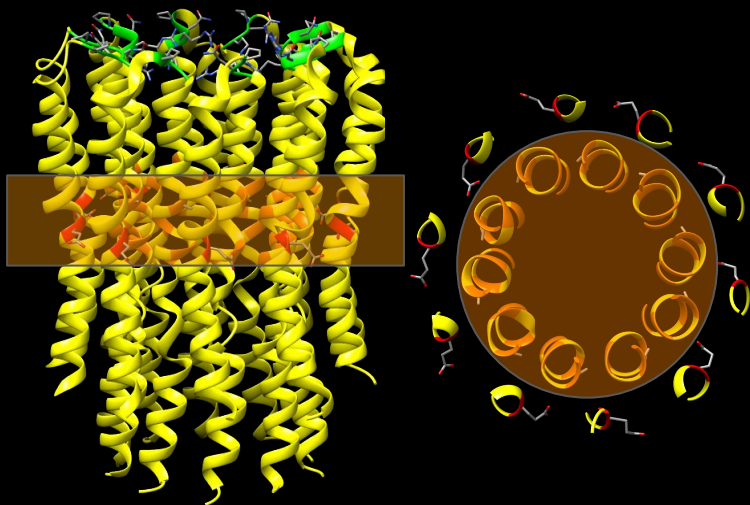




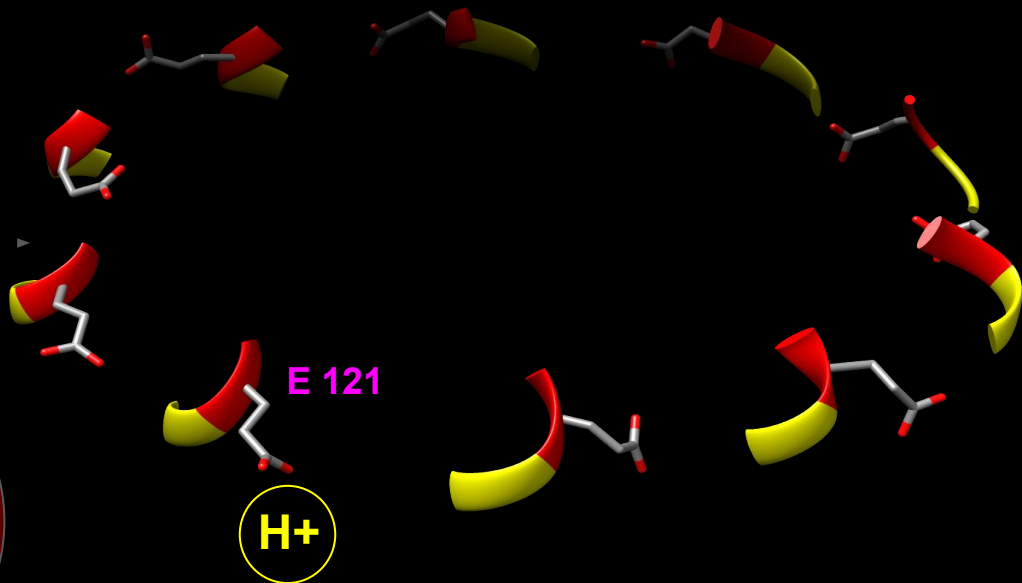
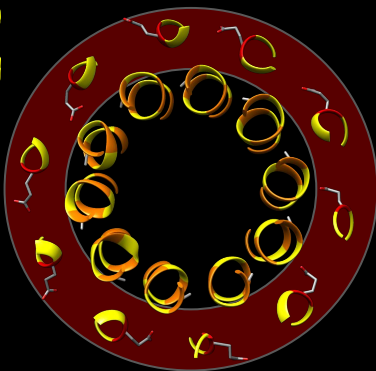
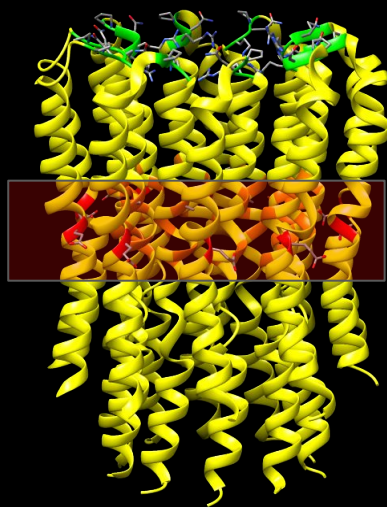
Consensus	R n P
Conservation	
Spinacia oleracea	R Q P
Pisum sativum	R Q P
Trichormus variabilis	R Q P
Homo sapiens	R N P
Bos taurus	R N P
Saccharomyces cerevisiae	R N P
Polytomella sp.	R N P
Paracoccus denitrificans	R N P
Escherichia coli	R Q P



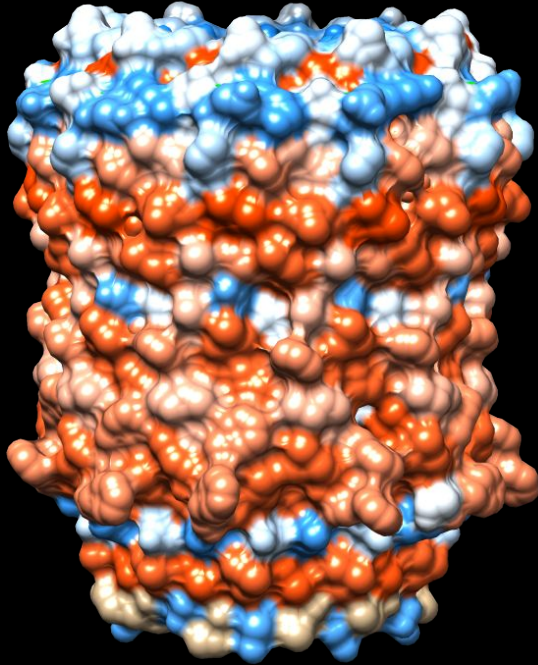
Consensus	G a g i G i G
Conservation	■ ■ ■ ■ ■
<i>Spinacia oleracea</i>	G P G V G Q G
<i>Pisum sativum</i>	G P G V G Q G
<i>Trichormus variabilis</i>	G P G I G Q G
<i>Homo sapiens</i>	G S G A G I G
<i>Bos taurus</i>	G S G A G I G
<i>Saccharomyces cerevisiae</i>	G A G I G I A
<i>Polytomella</i> sp.	G V G A G L G
<i>Paracoccus denitrificans</i>	G A A I G V G
<i>Escherichia coli</i>	G A A I G I G



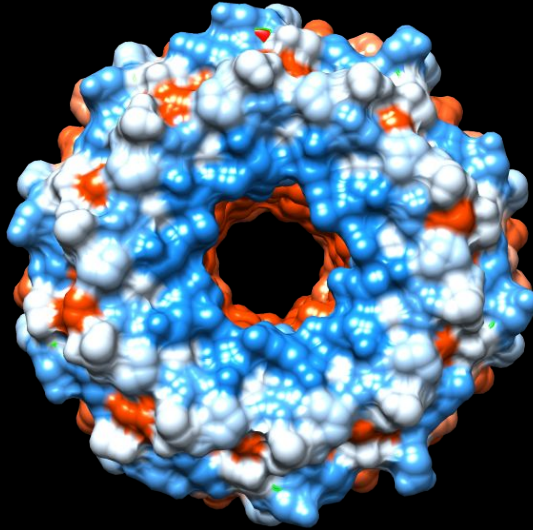
Consensus	E
Conservation	
Spinacia oleracea	E
Pisum sativum	E
Trichormus variabilis	E
Homo sapiens	E
Bos taurus	E
Saccharomyces cerevisiae	E
Polytomella sp.	E
Paracoccus denitrificans	E
Escherichia coli	D



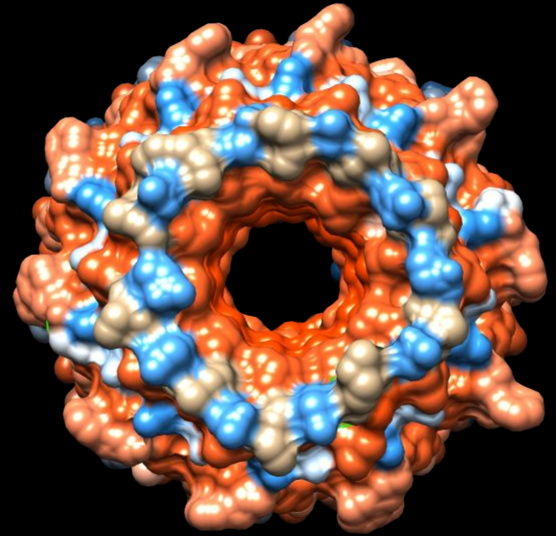
C-ring hydrophobicity



membrane view



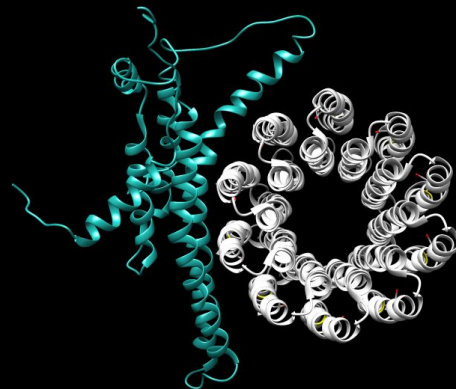
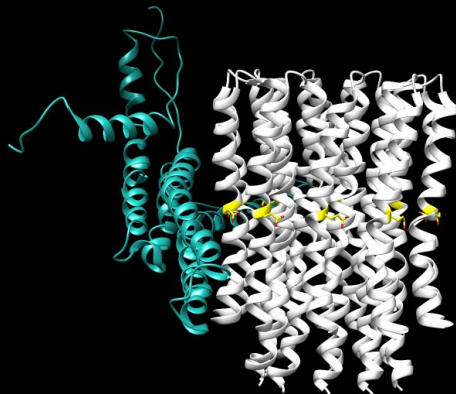
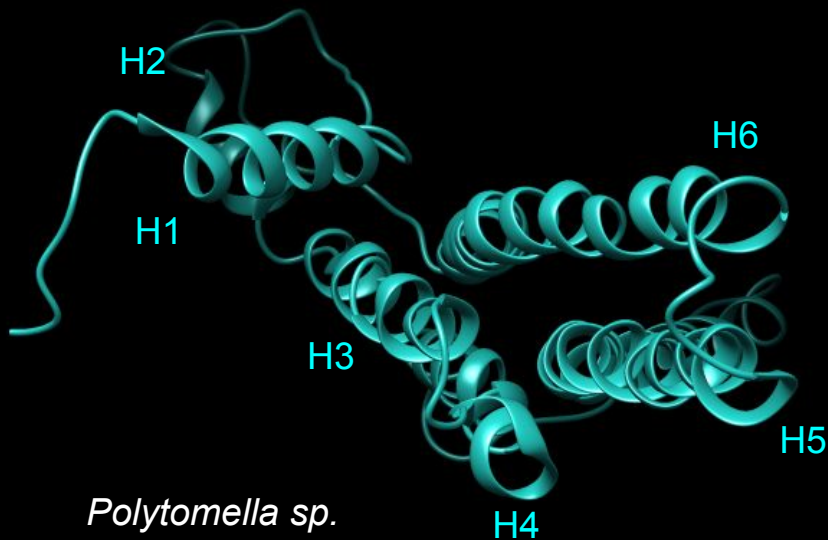
luminal view



matrix view

A subunit CATH

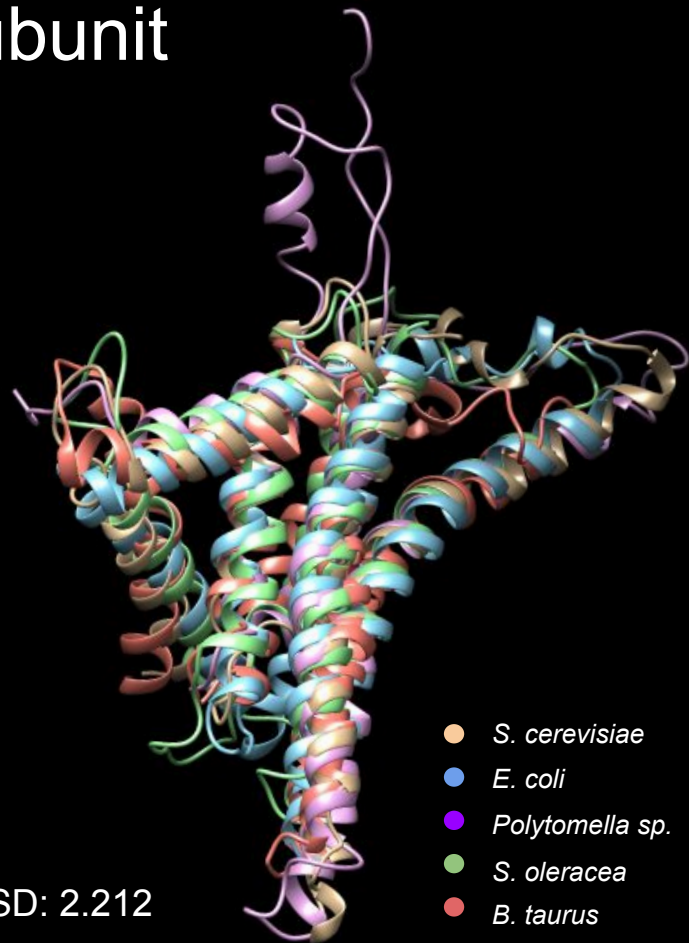
Class	Mainly alpha
Architecture	Up-down bundle
Topology	Four helix bundle
Homologous Superfamily	ATP synthase, F0 complex, subunit A



A subunit MSA

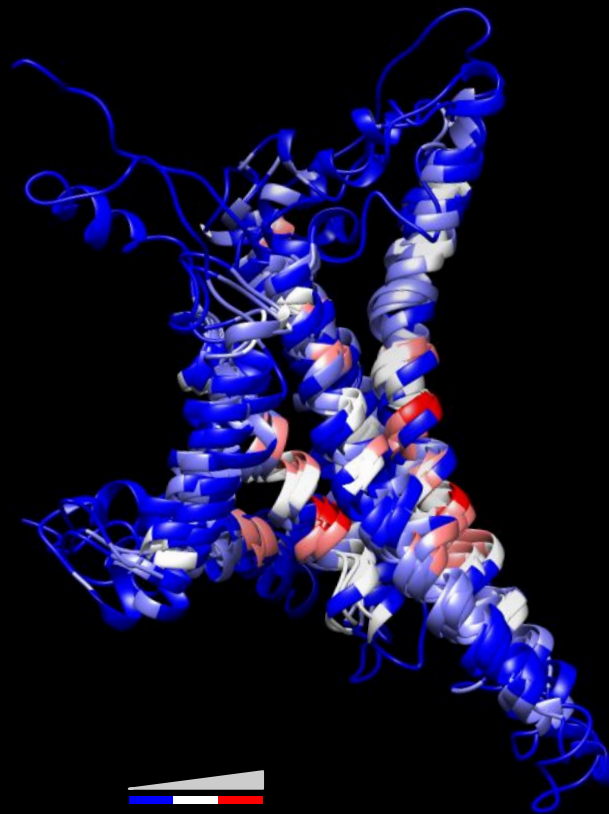
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	1 msvslssvsmsg ----- ----- ----- ----- MSVLSLVSMG -----	11 srigrssllgr ----- ----- ----- ----- SRIGSSLLGR -----	21 ssaymaqcgm ----- ----- ----- ----- SSAYLAQC ^G F ---MASENM	31 spqsylnhyi ----- ----- ----- -MFNLLNTYI STRSNLNG ^S SI TPQDYI ^G HHL	41 nspqsqfqir ----- ----- ----- TS ^P LDQFEIR DTSSSVFQAL NNLQLDLRTF	51 slenlqasfi ----- ----- ----- ----- MNLNLFAS ^F I MNLNLF ^T SFI TLFGLQSS ^F I KIGNLYFS ^T F SSNNENK ^P AA SLVD ^P QNP ^P AA
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	61 t p s i l g L p t m A P T I L G L P A A T P V I L G L P L V D L S C L N L T T F N P S L F M L L T L S P L N V K L P G M T F W T I N I D S M	71 s l i v l i p p l l V L I I L F P P L L T L I V L F P S L L S L Y I L L V L L V S L V I L L L L K T S C S S I L L P H T F F S V V L G L L F	81 i p i a r p f g s q I P - - - - - F P - - - - - I T - - - - - T K K G G - - - S R I A V P F G N Q L V L F R - - S V	91 a t s a t l v n n s - T S K Y L I N N - - T S N R L V S N - - S L Y T L T N N N G N S V N V W Q S T M A M S V R V D A K K A T S G V P G	101 k f i t l l q q w l i R L I T T Q Q W L I R F V T L Q Q W M L N K I I G S R W L I L V E L I Y D F V L K T G S L P T N F L K F Q T A I L V I	111 g l v s k q m m s m K L T S K Q M M T M Q L V S K Q M M S I S Q E A I Y D T I M N L V N E Y I G G L T G V Y R F W R S Q G F V N G S V K D M
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	121 h n t k g q t d p k H N T K G R T - - - H N S K Q T - - - N M T K G I G G K S G N V K Q K - - N P A E K P H D P V Y H G K S K L - -	131 n d r l l p a v v d - N D R L L P A V V D - - - - -	141 a s d k r a s i f p - - - - - W S L - - - - - W T L - - - - - N W G L F F P - - - - - L F F P A S D K R A S I G T - - - - - I A P	151 m i l t l f c f i f M L V S L I I F I A M I F T L F M F I F C L M L V T F T F L L W A T T F F C T I I L A L T I F V W V F	161 s t N L I g l i P y T T N L L G L L P H S T N L L G L L P H I A N L I S M I P Y F R N L Q M I P Y S C N L L G L M P F L M N L M D L L P I	171 s f t p y i a e h v S F T - - - - - S F T - - - - - S F A - - - - - S F T - - - - - N E A - - - - - D L P Y I A E H V
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	181 l g l p a l r v v p - - - - - P - - - - - P - - - - - L - - - - - V - - - - - P L G L P A L R V V P	191 t a q l s m t l g m T T Q L S M N L A M T T Q L S M N L G M S A H L V F I L L G T S H F L I T L G L T S G L G F A T L G S A D V N V T L S M	201 a i p i w a g a t I A I P L W A G T V I A I P L W A G A V I S I V I W L G N T I S F S I F I G I T I G V S V W A T A T I A L G V F I L I L F	211 l g f r k k g k a f M G F R S K I K N A T G F R N K T K A S L G L Y K H G W V F V G F Q R N G L H F L G L S K T G F K F Y S I K M K G I G G	221 l a h f l i p q g p f L A H F L P Q G - - L A H F L P Q G - - F S L F V P A G - - L S F V P A G - - P G H F I P G G - - T K E L T L Q P F	231 t p t p l i p m l v T P T P L I P M L V T P T P L I P M L V T P L P L V P L L V V P L P L A P F L V T W P M A F I V N H W A F I P V N L
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	241 i i E t i S l l i r I I E T I S L L I Q I I E T I S L F I Q I I E T I S Y F A R L L E L I P H C F R P L E T I S Y T F R I L E G V S L L S K	251 a m s L g v R L t a P M A L A V R L T A P M A L A V R L T A A I S L G L R L G S A L S S G I R L F A A V S L G V R L W V P V S L G L R L F G	261 N i t A G H I l m h N I T A G H L L M H N I T A G H L L M H N I L A G H L L M V N M M A G S S V K N M L A G H T L L H N M Y A G E L I F I	271 i i a G a t l a m p L I G S A T L M A L I G G A T L A L - I L A G L T F N F - L S G F A W T M - I L T G M A L A L P L I A G - - - - -	281 m s i n l f s a l i S T I N L P S T L I M S I S T T A L I M L I N L F T L F I L C M N D L L Y F I F S L G F F S M V P - - - - - L L	291 g f t g q l a i l i I F T - - - - I L I T F T - - - - I L I G F V P - L A M I L G D L G P L F I V L A T F G V C C L L S P W W S Q W I L N V
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	301 a l t i L E i a v a L L T I L E I A V A L L T I L F A V A A I M M L E F A I G A L T G L E L G V A A L V G L E L G V A P W A I F H I L I I	311 i i Q a y V F t i L L I Q A Y V F T L L M I Q A Y V F T L L I I Q G Y V W A I L V I L Q A H V F T I L V L S G V F S I L T L Q A F I F M V L	321 t s l Y L h d a t y V S L Y L H N T - V S L Y L H N T - T A S Y L K D A V Y I C I Y V D A I N S T V Y V G E F N H T I V Y L S M A S E	331 l h q i g y a a i i - - - - - - - - - - L H - - - - - L H Q N F Y L F I I D K F I G P A A K I E H - - - - -		

A subunit



RMSD: 2.212

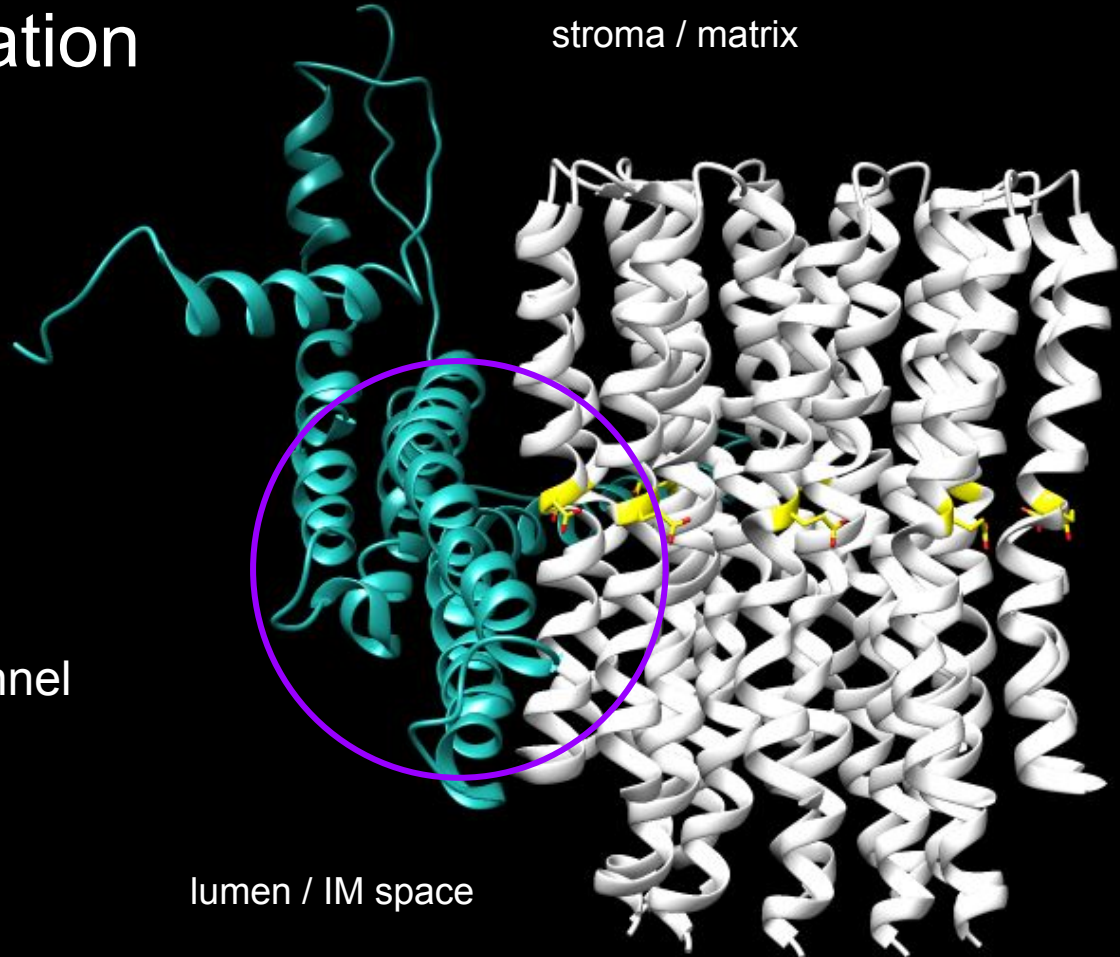
Rendered by conserved residues



Proton translocation

2 hemi-channels:

- Luminal / IM channel
- Matrix channel



GLU 172.M OE2 <-> HIS 248.M NE2: 3.22

Consensus	251	a m s L g v R L t a	261	N i t A G H I l m h
Conservation		■ ■ ■ ■ ■ ■ ■ ■		■ ■ ■ ■ ■ ■ ■ ■
Homo sapiens		P M A L A V R L T A		N I T A G H L L M H
Bos taurus		P M A L A V R L T A		N I T A G H L L I H
Saccharomyces cerevisiae		A I S L G L R L G S		N I L A G H L L M V
Spinacia oleracea		A L S S G I R L F A		N M M A G H S S V K
Polytomella sp.		A V S L G V R L W V		N M L A G H T L L G
Escherichia coli		P V S L G L R L F G		N M Y A G H E L I F I

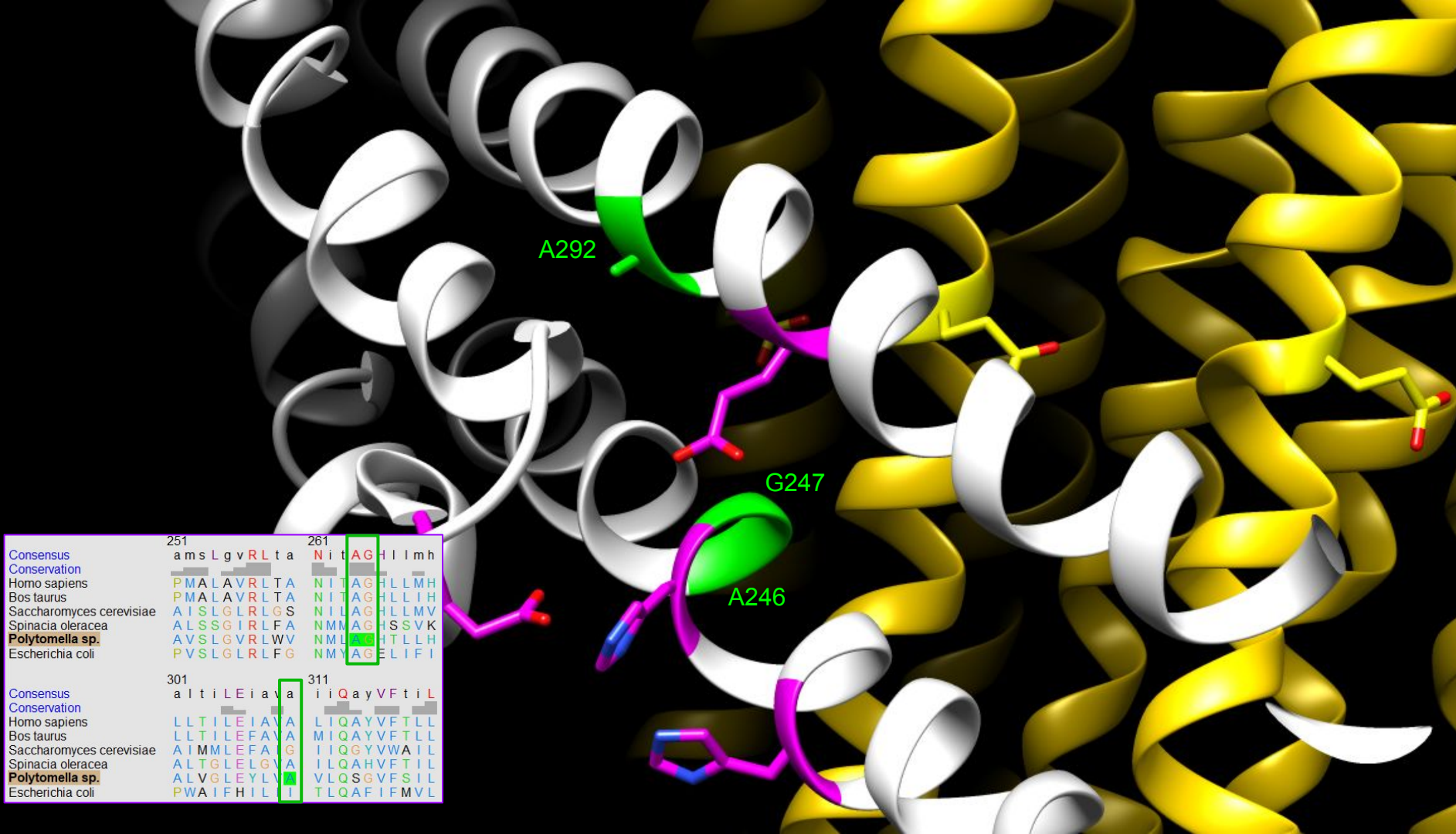
Consensus	301	a l t i L E i a v a	311	i i Q a y V F t i L
Conservation		■ ■ ■ ■ ■ ■ ■ ■		■ ■ ■ ■ ■ ■ ■ ■
Homo sapiens		L L T I L E I A V A		L I Q A Y V F T L L
Bos taurus		L L T I L E I A V A		M I Q A Y V F T L L
Saccharomyces cerevisiae		A I M M L E F A I G		I I Q G Y V W A I L
Spinacia oleracea		A L T G L E L G V A		I L Q A H V F T I L
Polytomella sp.		A L V G L E Y L V A		V L Q S G V F S I L
Escherichia coli		P W A I F H I L I I		T L Q A F I F M V L

E172

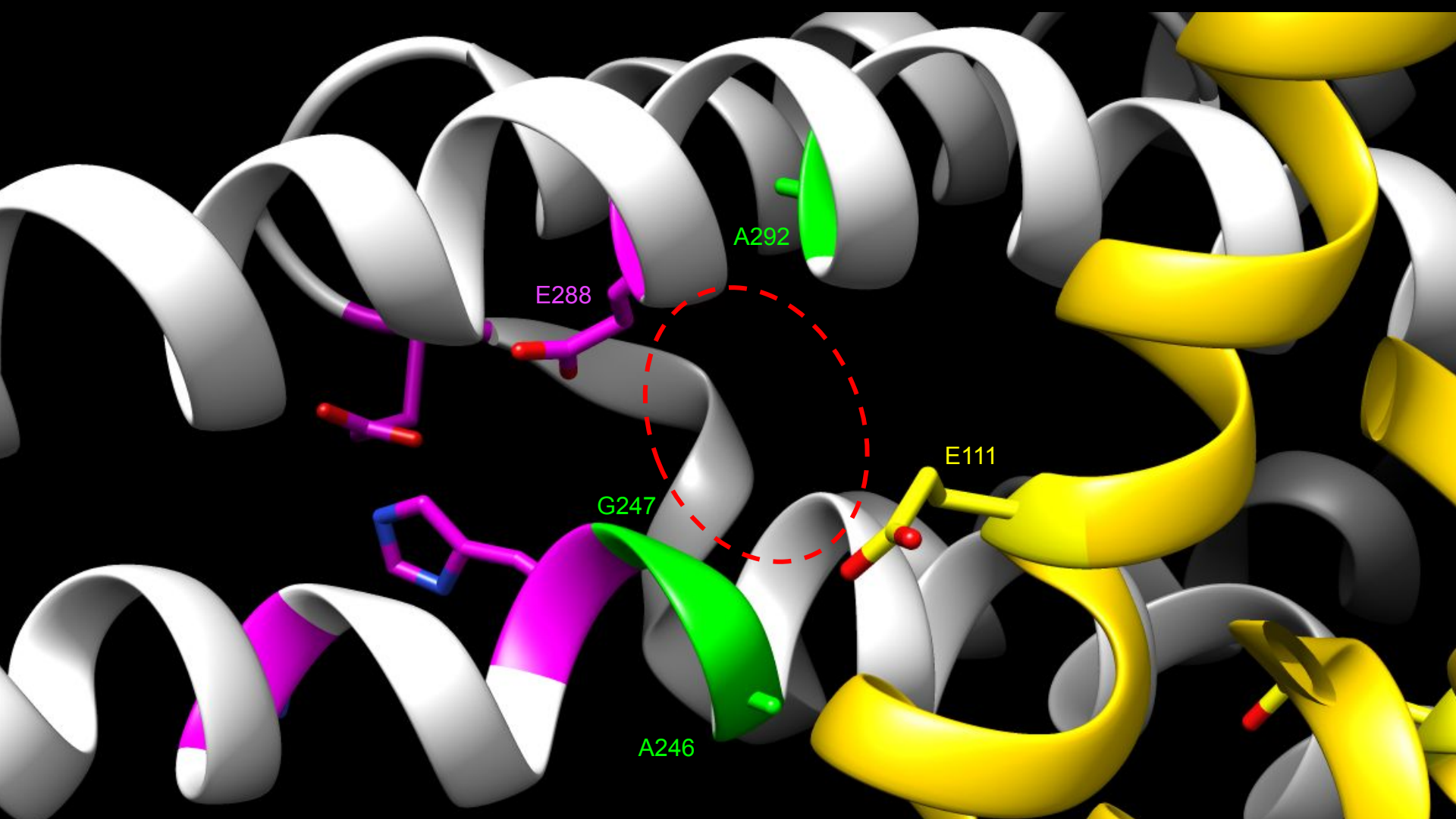
E288

H248

H252



Consensus	251	261
Conservation	amsLgvrLLta	NitAGHllmh
Homo sapiens	PMALAVRLTA	NITAGHLLMH
Bos taurus	PMALAVRLTA	NITAGHLLIH
Saccharomyces cerevisiae	AISLGLRLGS	NITAGHLLMV
Spinacia oleracea	ALSSGIRLFA	NMAGHSSVK
Polytomella sp.	AVSLGVRLWV	NMLGHTLLH
Escherichia coli	PVSLGLRLFG	NMYAGELIFI
Consensus	301	311
Conservation	altiLEiava	iiQayVFtiL
Homo sapiens	LLTILEIAVA	LIQAYVFTELL
Bos taurus	LLTILEFAVA	MIQAYVFTELL
Saccharomyces cerevisiae	AIMMLEFAVA	IIQGYVVAAIL
Spinacia oleracea	ALTGLELGA	LIQAHVFTELL
Polytomella sp.	ALVGLLEYLV	VLQSGVFSEIL
Escherichia coli	PWAIFHILV	TLQAFIFMVL



1 GLN 295 OE1 <-> ASN 243 ND2: 2.60Å

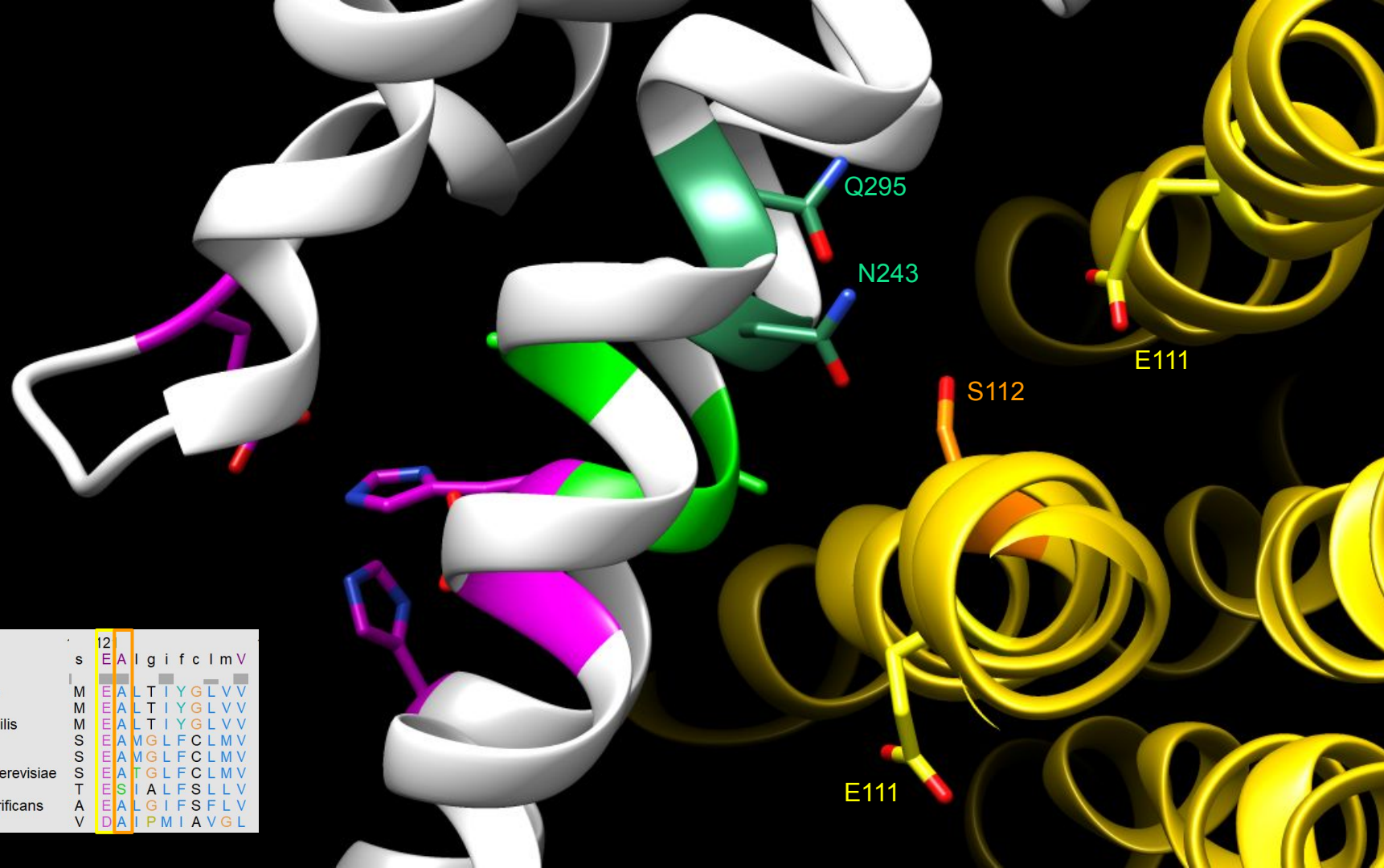
Consensus	281	N	i	t	A	G	H	I	I	m	h
Conservation											
Homo sapiens		N	I	T	A	G	H	L	L	M	H
Bos taurus		N	I	T	A	G	H	L	L	I	H
Saccharomyces cerevisiae		N	I	L	A	G	H	L	L	M	V
Spinacia oleracea		N	M	M	A	G	H	S	S	V	K
Polytomella sp.		N	M	L	A	G	H	T	L	L	H
Escherichia coli		N	M	Y	A	G	E	L	I	F	I

Consensus	311	i	i	Q	a	y	V	F	t	i	L
Conservation											
Homo sapiens		L	I	Q	A	Y	V	F	T	L	L
Bos taurus		M	I	Q	A	Y	V	F	T	L	L
Saccharomyces cerevisiae		I	I	Q	G	Y	V	W	A	I	L
Spinacia oleracea		I	L	Q	A	H	V	F	T	I	L
Polytomella sp.		V	L	S	G	V	F	S	I	L	L
Escherichia coli		T	L	Q	A	F	I	F	M	V	L

Q295

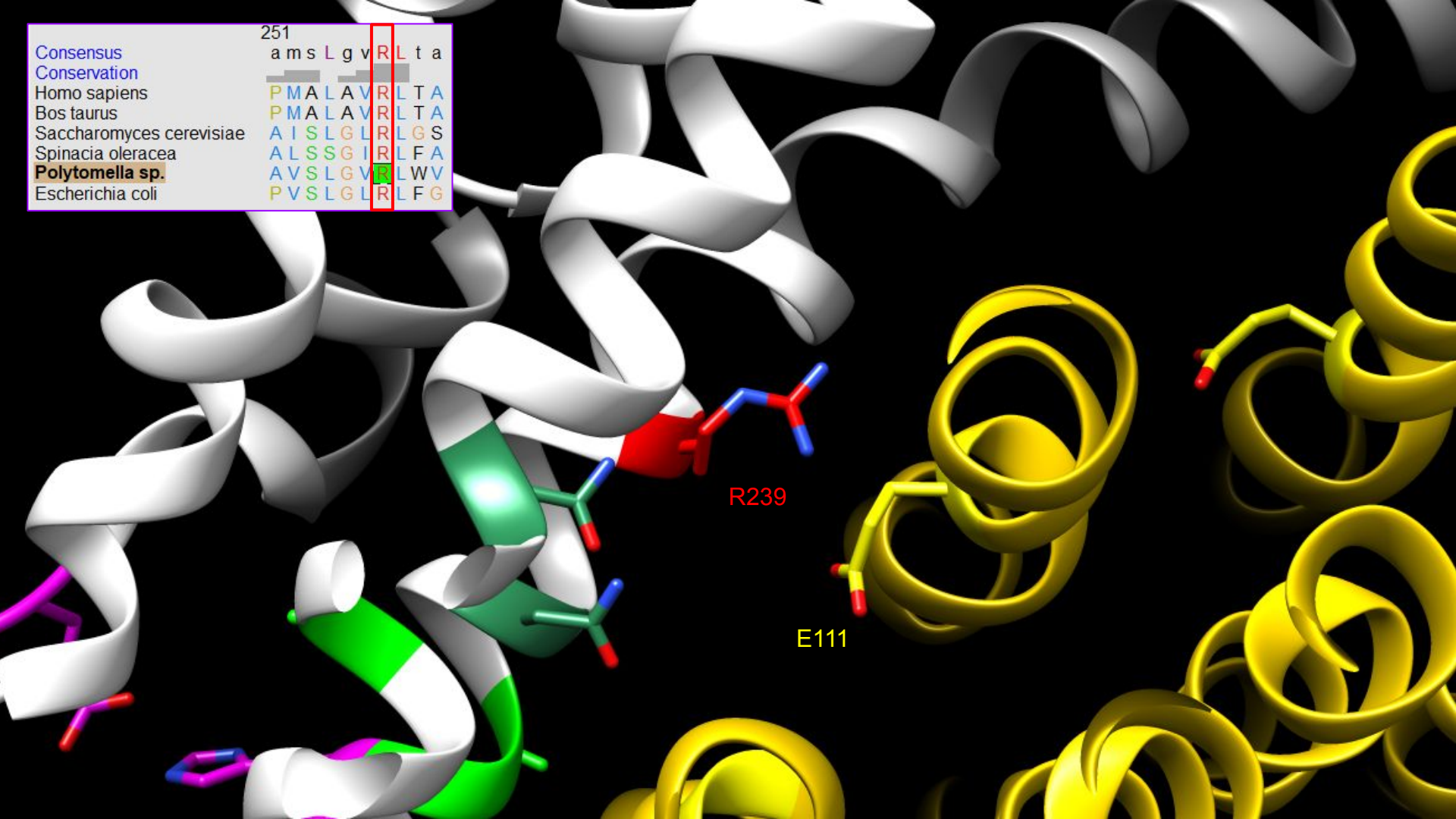
N243

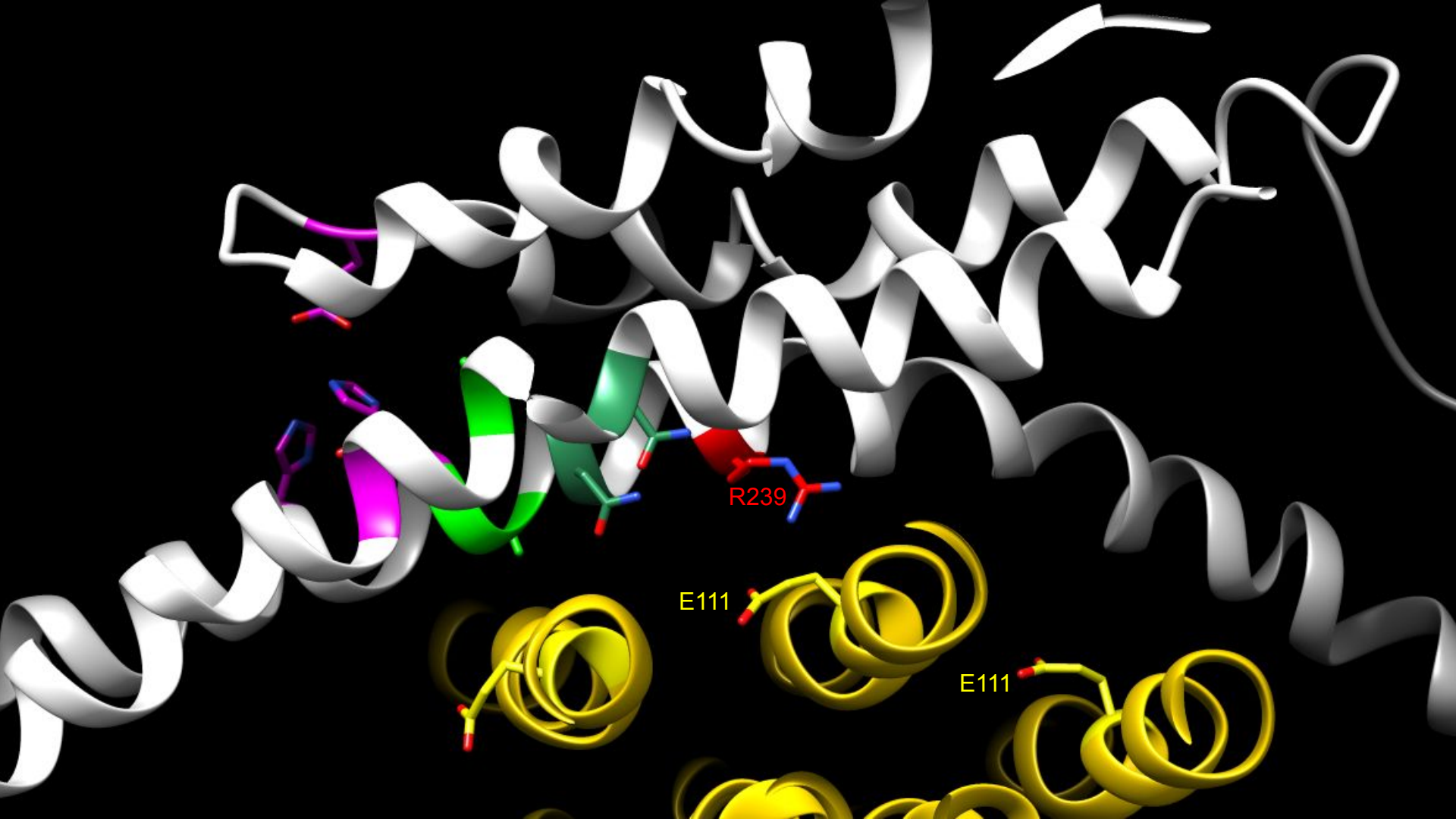
E111

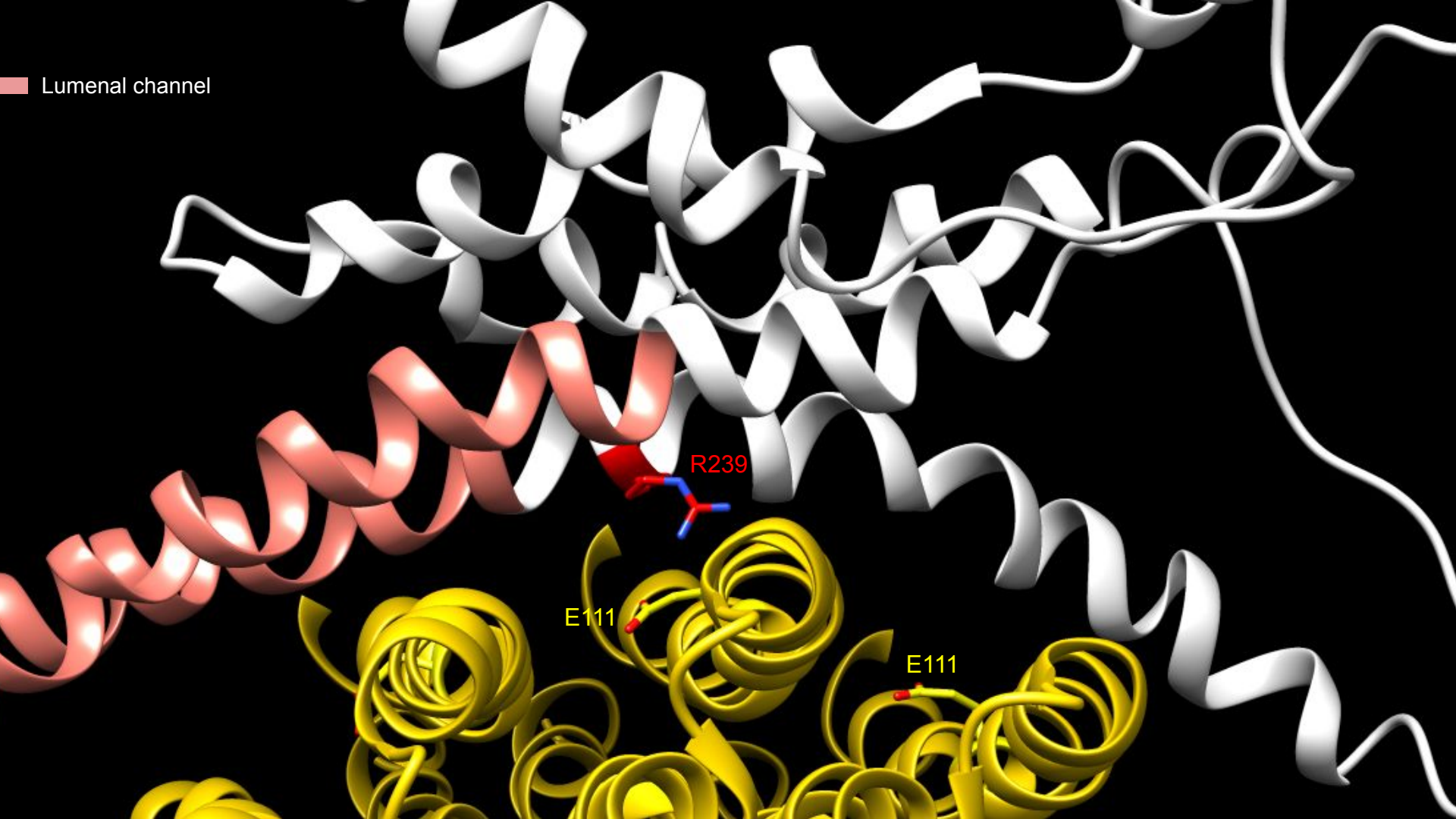


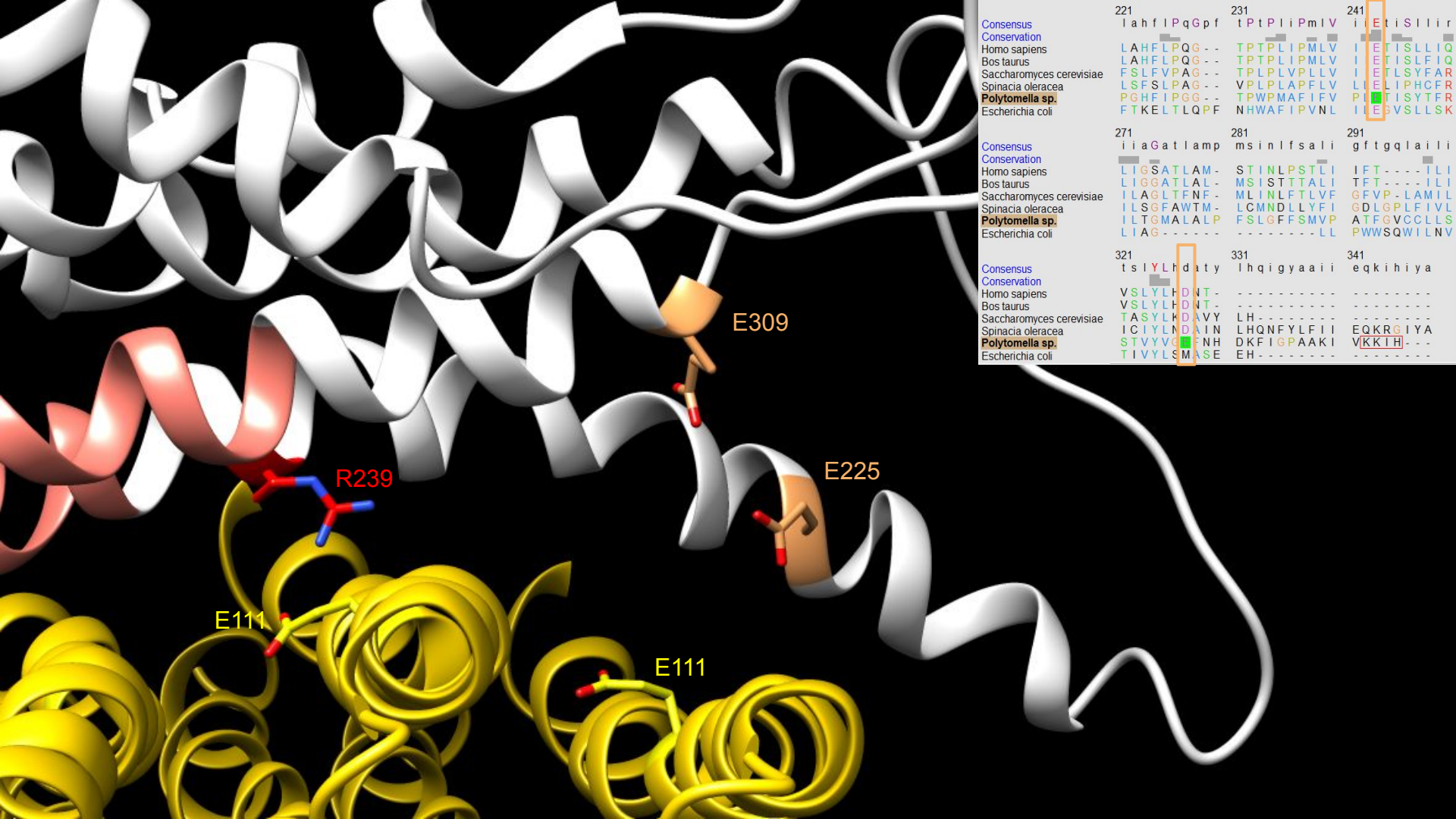
Consensus	s	12	E	A	I	g	i	f	c	l	m	V
Conservation	I											
Spinacia oleracea	M	E	A	L	T	I	Y	G	L	V	V	
Pisum sativum	M	E	A	L	T	I	Y	G	L	V	V	
Trichormus variabilis	M	E	A	L	T	I	Y	G	L	V	V	
Homo sapiens	S	E	A	M	G	L	F	C	L	M	V	
Bos taurus	S	E	A	M	G	L	F	C	L	M	V	
Saccharomyces cerevisiae	S	E	A	T	G	L	F	C	L	M	V	
Polytomella sp.	T	E	S	I	A	L	F	S	L	L	V	
Paracoccus denitrificans	A	E	A	L	G	I	F	S	F	L	V	
Escherichia coli	V	D	A	I	P	M	I	A	V	G	L	

	251
Consensus	a m s L g v R L t a
Conservation	— — — — — — — —
Homo sapiens	P M A L A V R L T A
Bos taurus	P M A L A V R L T A
Saccharomyces cerevisiae	A I S L G L R L G S
Spinacia oleracea	A L S S G I R L F A
Polytomella sp.	A V S L G V R L W V
Escherichia coli	P V S L G L R L F G

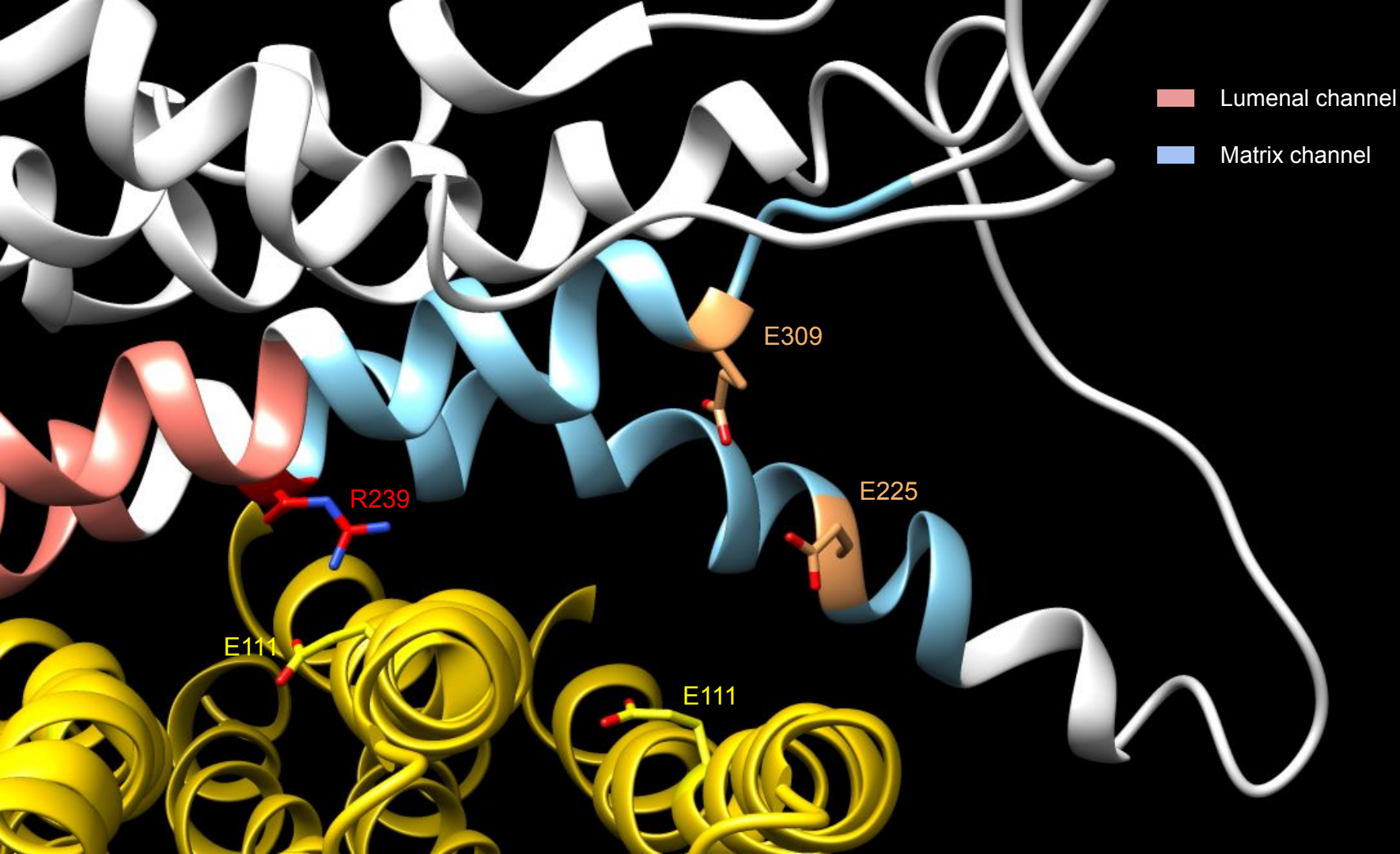








221	l a h f l P q G p f	231	t P t P l i P m l V	241	i E t i s i l i r
Consensus					
Conservation					
Homo sapiens					
Bos taurus					
Saccharomyces cerevisiae					
Spinacia oleracea					
Polytomella sp.					
Escherichia coli					
271	i i a G a t l a m p	281	m s i n l f s a l i	291	g f t g q l a i l
Consensus					
Conservation					
Homo sapiens					
Bos taurus					
Saccharomyces cerevisiae					
Spinacia oleracea					
Polytomella sp.					
Escherichia coli					
321	t s l Y L h d a t y	331	l h q i g y a a i i	341	e q k i h i y a
Consensus					
Conservation					
Homo sapiens					
Bos taurus					
Saccharomyces cerevisiae					
Spinacia oleracea					
Polytomella sp.					
Escherichia coli					



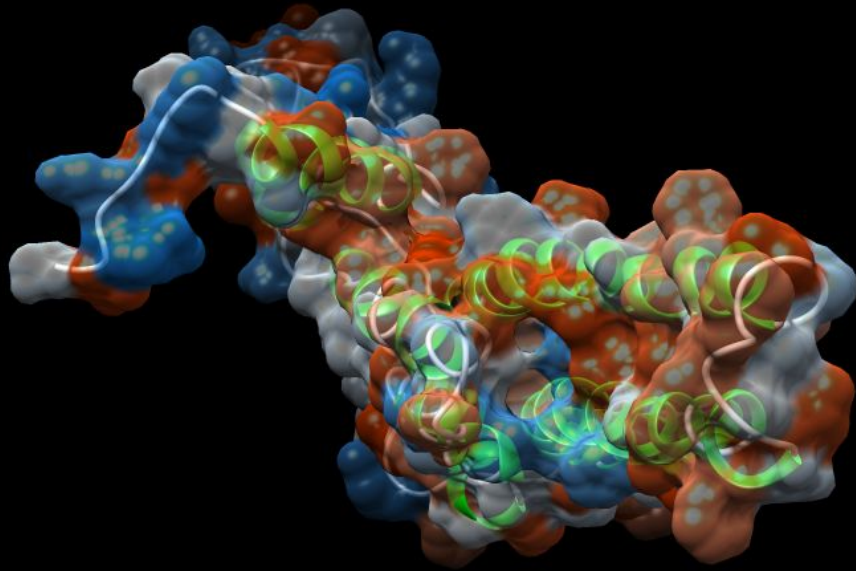
a subunit MSA

Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	1 msv l s s v s m g 11 s r i g s s l l g r 21 s s a y m a q c g m 31 s p q s y l n h y i 41 n s p q s q f q i r 51 s l e n l q a s f i
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	61 t p s i l g l p t m 71 s l i v l l p p l l 81 i p i a r p f g s q 91 a t s a t l v n n s 101 k f i t l q q w l i 111 g l v s k q m m s m
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	121 h n t k g q t d p k 131 n d r l l p a v v d 141 a s d k r a s i f p 151 m i l t l f c f i f 161 s t n l l g l i p y 171 s f t p y i a e h v
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	181 t g l p a l r v v p 191 t a q l s m t l g m 201 a i p i w a g a t l 211 l g f r k k g k a f 221 l a h f l p q g p f 231 t p t p l i p m l v
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	231 t p t p l i p m l v 241 i i e t i s l i l r 251 a m s l g v r l t a 261 n i t a g h l l m h 271 i i a g a t l a m p 281 m s i n i f s a l i
Consensus Conservation Homo sapiens Bos taurus Saccharomyces cerevisiae Spinacia oleracea Polytomella sp. Escherichia coli	291 g f t g q l a i l i 301 a l t i l e i a v a 311 i i q a y v f t i l 321 t s i y l h d a t y 331 l h q i g y a a i i

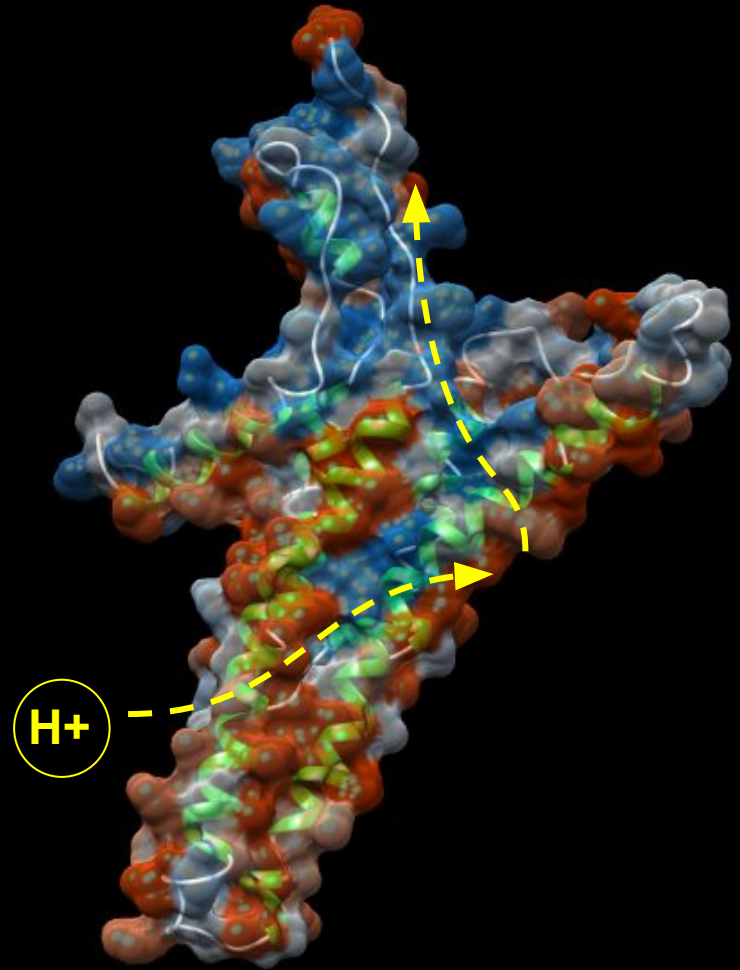
Luminal channel

Matrix channel

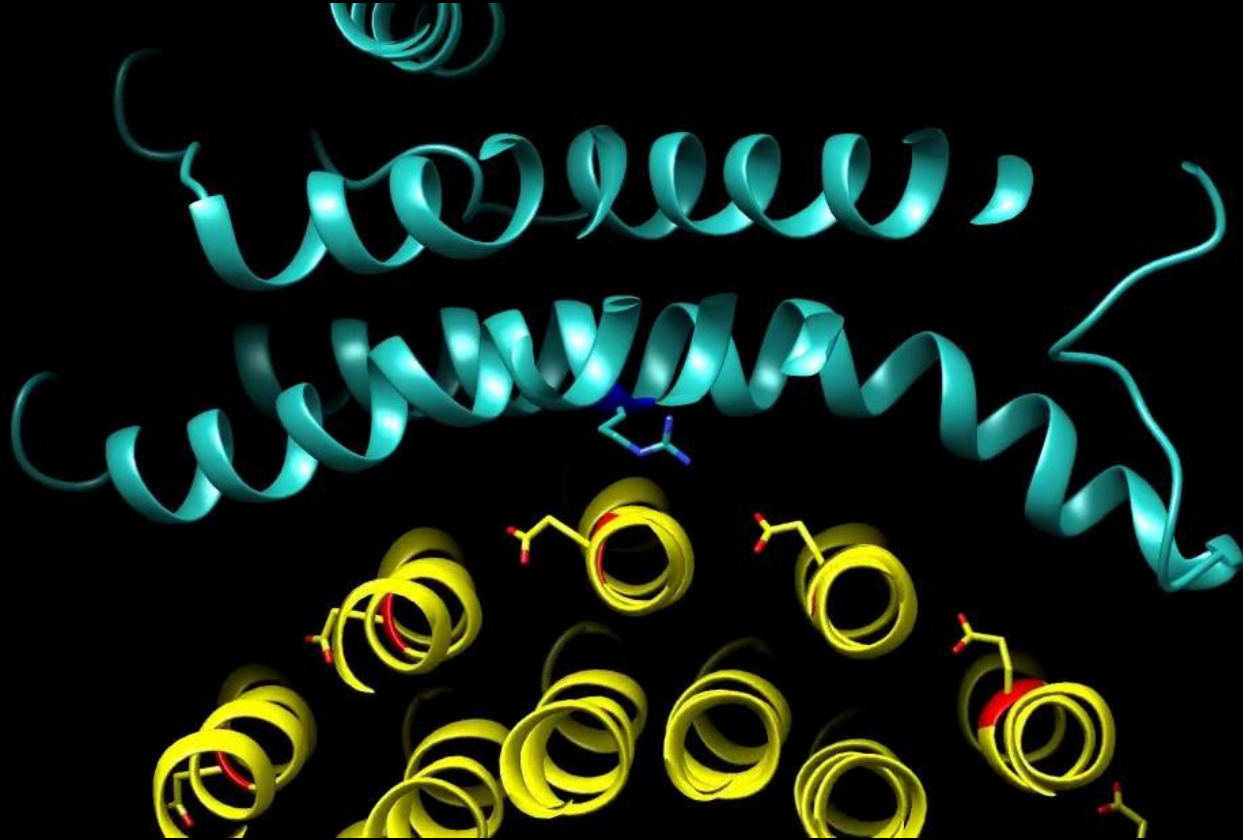
A subunit



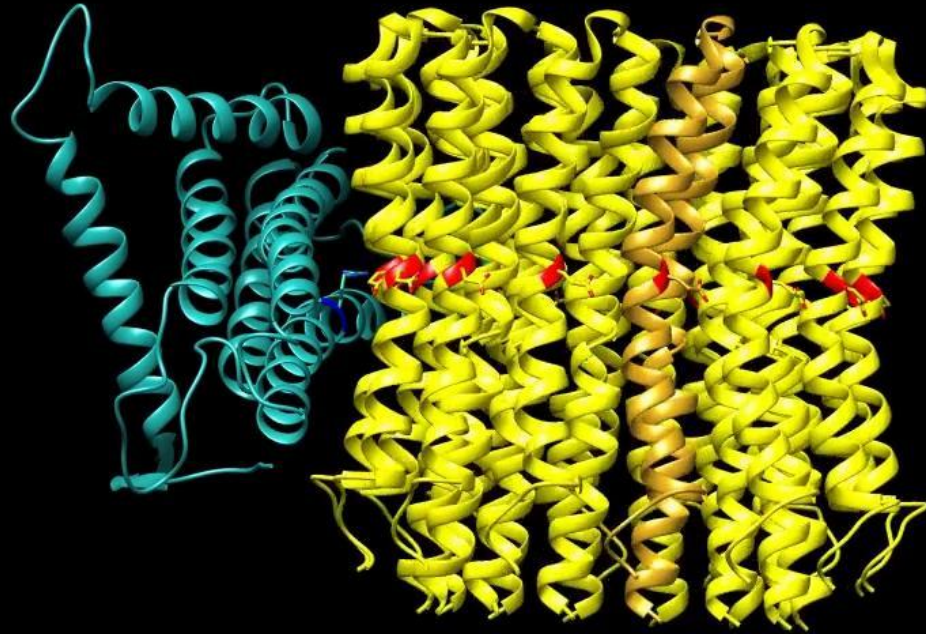
Hydrophobicity surface



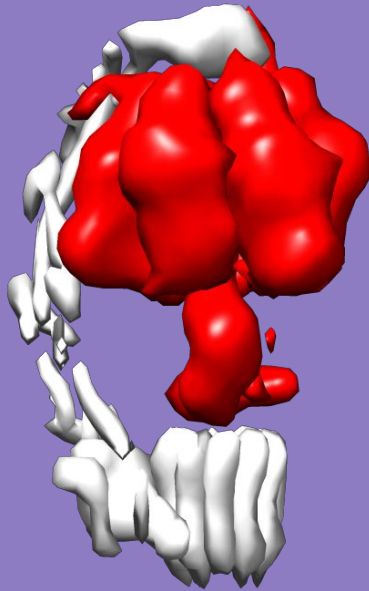
c-ring rotation



c-ring rotation



II part: central stalk + catalytic head



F1-ATP synthase

F1-catalytic
head

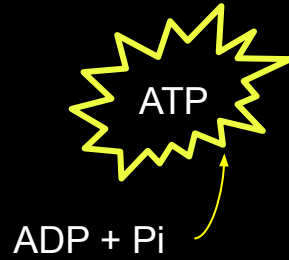


$\alpha_3\beta_3$

Central stalk



$\gamma \epsilon \delta$



β

α

γ

ϵ

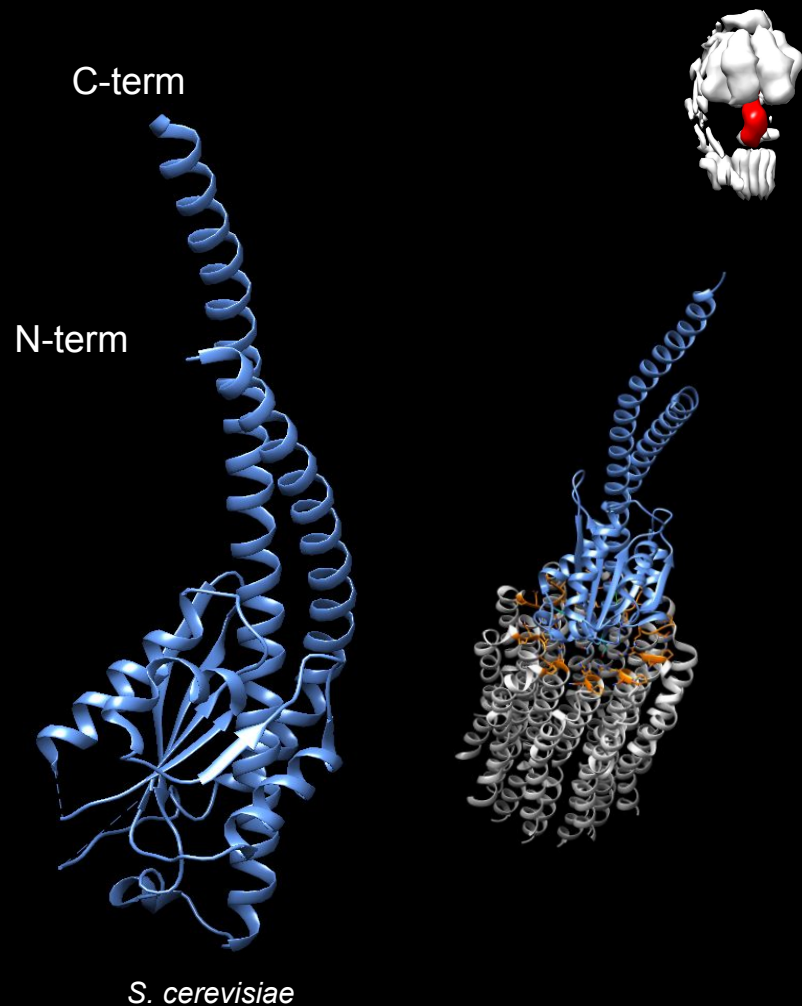
δ

Bos taurus



γ -subunit CATH

Class	Mainly alpha
Architecture	Orthogonal Bundle
Topology	Helix Hairpins
Homologous Superfamily	Helix Hairpins



γ-subunit MSA



Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	1 mamasrilmv --MFSR-- --MFSR-- --MLSR-- --MALRK-- MSSCSNVMFLV MAQSS-- --MPN-- --MAG-- --MPS--	11 sskpslipdas --KKKSHLLI-- --KKKSHLLI-- --KKKSHLLI-- --KKKSHLLI-- SSKPSLIPDAS SSKPSLIPDAS SSKPSLIPDAS SSKPSLIPDAS SSKPSLIPDAS	21 nlstssaaagv --SSSSAAAGV-- --SSSSAAAGV-- --SSSSAAAGV-- --SSSSAAAGV-- NLSFSSAFNP NLSFSSAFNP NLSFSSAFNP NLSFSSAFNP NLSFSSAFNP	31 aglsawtaqp AGLSAWTVQP AGLSAWTVQP AGLSAWTVQP AGLSAWTVQP LQLSQVAAAE LQLSQVAAAE LQLSQVAAAE LQLSQVAAAE LQLSQVAAAE	41 qwppsgaish QWPPSGAISH QWPPSGAISH QWPPSGAISH QWPPSGAISH QWPPSGAISH QWPPSGAISH QWPPSGAISH QWPPSGAISH	51 ptiqvrqayt PTIQVRQAYT PTIQVRQAYT PTIQVRQAYT PTIQVRQAYT PTIQVRQAYT PTIQVRQAYT PTIQVRQAYT PTIQVRQAYT
Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	61 lkdkldrkiks LKDITRRKKS LKDITRRKKS LKDITRRKKS LKDITRRKKS NQAVKQRIRA NQAVKQRIRA NQAVKQRIRA NQAVKQRIRA NQAVKQRIRA	71 vKntqKlITka VKNtqKlITka VKNtqKlITka VKNtqKlITka VKNtqKlITka VKNtqKlITka VKNtqKlITka VKNtqKlITka VKNtqKlITka	81 MkmvAAakvr MKMVAAAKVR MKMVAAAKVR MKMVAAAKVR MKMVAAAKVR MKMVAAAKVR MKMVAAAKVR MKMVAAAKVR MKMVAAAKVR	91 rAqevaiiaar RAQEVAIIAAR RAQEVAIIAAR RAQEVAIIAAR RAQEVAIIAAR RAQEVAIIAAR RAQEVAIIAAR RAQEVAIIAAR RAQEVAIIAAR	101 pyaetlivavy PYAETLIVAVY PYAETLIVAVY PYAETLIVAVY PYAETLIVAVY PYAETLIVAVY PYAETLIVAVY PYAETLIVAVY PYAETLIVAVY	111 ygadiklqte YGADIKLQTE YGADIKLQTE YGADIKLQTE YGADIKLQTE YGADIKLQTE YGADIKLQTE YGADIKLQTE YGADIKLQTE
Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	121 dvdpplikgi --TP----- --TP----- --TP----- --TP----- DIESPLTK-L DIESPLTK-L DIESPLTK-L DIESPLTK-L DIESPLTK-L	131 rdvkkvlliv EDKKKHLLIG EDKKKHLLIG EDKKKHLLIG EDKKKHLLIG RDVKKVLLIV RDVKKVLLIV RDVKKVLLIV RDVKKVLLIV RDVKKVLLIV	141 vtsDrGLCGg VSSDRGLCGG VSSDRGLCGG VSSDRGLCGG VSSDRGLCGG VTSDRGLCGG VTSDRGLCGG VTSDRGLCGG VTSDRGLCGG VTSDRGLCGG	151 inssiakkar IHSSIAKQMK IHSSIAKQMK IHSSIAKQMK IHSSIAKQMK INSSI AKKAR INSSI AKKAR INSSI AKKAR INSSI AKKAR INSSI AKKAR	161 arlaelkaaG SEAAALAAAG SEAAALAAAG SEAAALAAAG SEAAALAAAG ARLAELKAA ARLAELKAA ARLAELKAA ARLAELKAA ARLAELKAA	171 kevtivsiGd KEVTIVSIGD KEVTIVSIGD KEVTIVSIGD KEVTIVSIGD KEVTIVSIGD KEVTIVSIGD KEVTIVSIGD KEVTIVSIGD
Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	181 KgrsqInRrh KIRSLHRRTH KIRSLHRRTH KIRSLHRRTH KIRSLHRRTH KGRSQQLTRIE KGRSQQLTRIE KGRSQQLTRIE KGRSQQLTRIE KGRSQQLTRIE	191 sdpvliafdg SDQFLVTFKE SDQFLVTFKE SDQFLVTFKE SDQFLVTFKE SDPVLIAFDG SDPVLIAFDG SDPVLIAFDG SDPVLIAFDG SDPVLIAFDG	201 vgkppptfge VGRPPPTFGD VGRPPPTFGD VGRPPPTFGD VGRPPPTFGD VGKPPPTFGE VGKPPPTFGE VGKPPPTFGE VGKPPPTFGE VGKPPPTFGE	211 asaladelis ASVALLELLN ASVALLELLN ASVALLELLN ASVALLELLN ASALADELIS ASALADELIS ASALADELIS ASALADELIS ASALADELIS	221 lifdseevdkg LFDSEEVDKG LFDSEEVDKG LFDSEEVDKG LFDSEEVDKG LFDSEEVDKG LFDSEEVDKG LFDSEEVDKG LFDSEEVDKG	231 silynkFvSI SILYNKFVSI SILYNKFVSI SILYNKFVSI SILYNKFVSI SILYNKFVSI SILYNKFVSI SILYNKFVSI SILYNKFVSI
Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	241 isskptikti ISYKTEEKPI ISYKTEEKPI ISYKTEEKPI ISYKTEEKPI LSFSESEKPI LSFSESEKPI LSFSESEKPI LSFSESEKPI LSFSESEKPI	251 lpdltigeic LSLDTIS- LSLDTIS- LSLDTIS- LSLDTIS- LPDLTIGEIC LPDLTIGEIC LPDLTIGEIC LPDLTIGEIC LPDLTIGEIC	261 dingkcvdad DINGKNCVDA DINGKNCVDA DINGKNCVDA DINGKNCVDA DINGKNCVDA DINGKNCVDA DINGKNCVDA DINGKNCVDA	271 edeafsisist --SAESMSIY --SAESMSIY --SAESMSIY --SAESMSIY EDEAFSISIST EDEAFSISIST EDEAFSISIST EDEAFSISIST EDEAFSISIST	281 dgklitverdm DGLKITVERDM DGLKITVERDM DGLKITVERDM DGLKITVERDM DGLKITVERDM DGLKITVERDM DGLKITVERDM DGLKITVERDM	291 iktqtapafsp IKTQTAPAFSP IKTQTAPAFSP IKTQTAPAFSP IKTQTAPAFSP IKTQTAPAFSP IKTQTAPAFSP IKTQTAPAFSP IKTQTAPAFSP
Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	301 ildfeadpnq --DIDAD-- --DIDAD-- --DIDAD-- --DIDAD-- ILDFEADPNQ ILDFEADPNQ ILDFEADPNQ ILDFEADPNQ ILDFEADPNQ	311 lDdlilpyyl VLRLNQEYSL VLRLNQEYSL VLRLNQEYSL VLRLNQEYSL LDLILPYYL LDLILPYYL LDLILPYYL LDLILPYYL LDLILPYYL	321 anqiyratIe ANIIYYSLE ANIIYYSLE ANIIYYSLE ANIIYYSLE ANQIYRAIIE ANQIYRAIIE ANQIYRAIIE ANQIYRAIIE ANQIYRAIIE	331 sIASeqaARM SIASEQAARM SIASEQAARM SIASEQAARM SIASEQAARM SIASEQAARM SIASEQAARM SIASEQAARM SIASEQAARM	341 lAMdnAskNA LAMDNASKNA LAMDNASKNA LAMDNASKNA LAMDNASKNA LAMDNASKNA LAMDNASKNA LAMDNASKNA LAMDNASKNA	351 gemikkLtlv GEMIKKLTLLT GEMIKKLTLLT GEMIKKLTLLT GEMIKKLTLLT GEMIKKLTLLT GEMIKKLTLLT GEMIKKLTLLT GEMIKKLTLLT
Consensus Conservation Bos taurus Homo sapiens Saccharomyces cerevisiae Polytomella sp. Pisum sativum Spinacia oleracea Trichormus variabilis Escherichia coli Paracoccus denitrificans	361 yNraRQAVIT FNRTROAVIT FNRTROAVIT FNRTROAVIT FNRTROAVIT YNRARQAVIT YNRARQAVIT YNRARQAVIT YNRARQAVIT YNRARQAVIT	371 kElIeIIsGA KELIEIISGA KELIEIISGA KELIEIISGA KELIEIISGA KELIEIISGA KELIEIISGA KELIEIISGA KELIEIISGA	381 aaidie AALD- AALD- AALD- AALD- AALD- AALD- AALD- AALD- AALD-			

c-ring - γ interactions

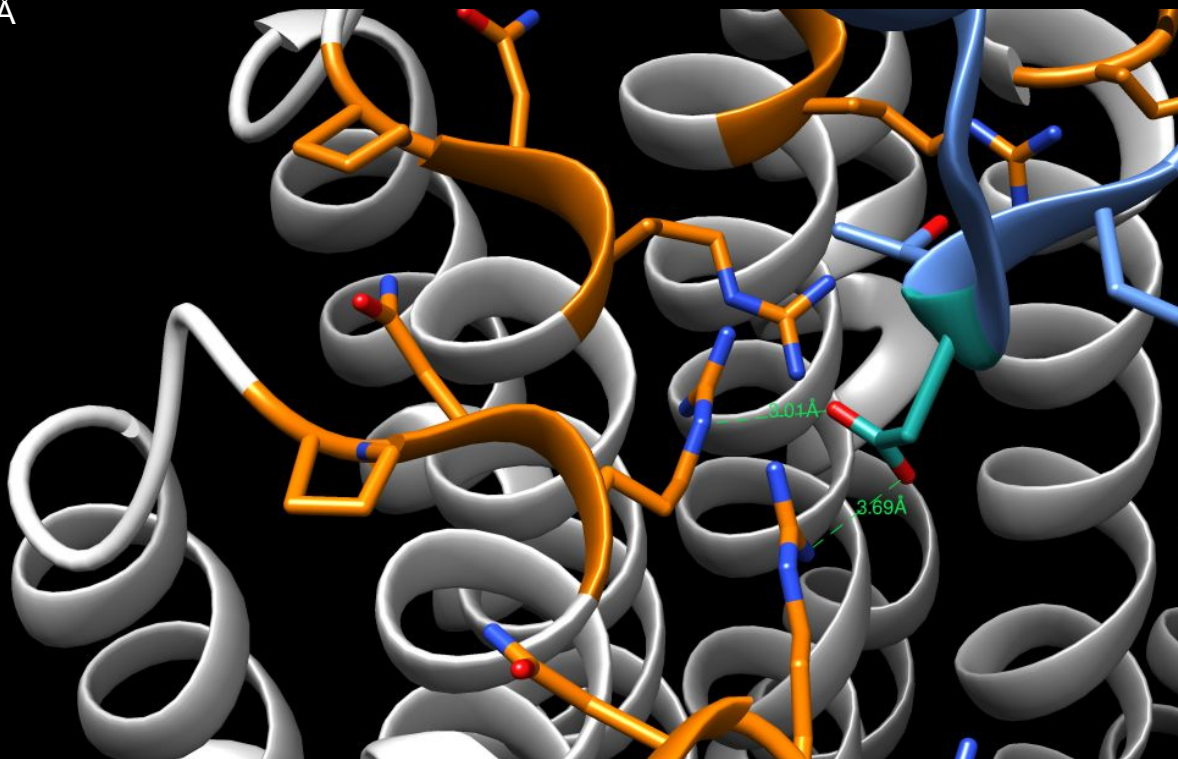
ASP 202.G OD2 $\leftrightarrow$ ARG 39.O NH1: 3.69Å

ASP 202.G OD1 $\leftrightarrow$ ARG 39.P NE: 3.01Å

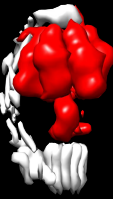
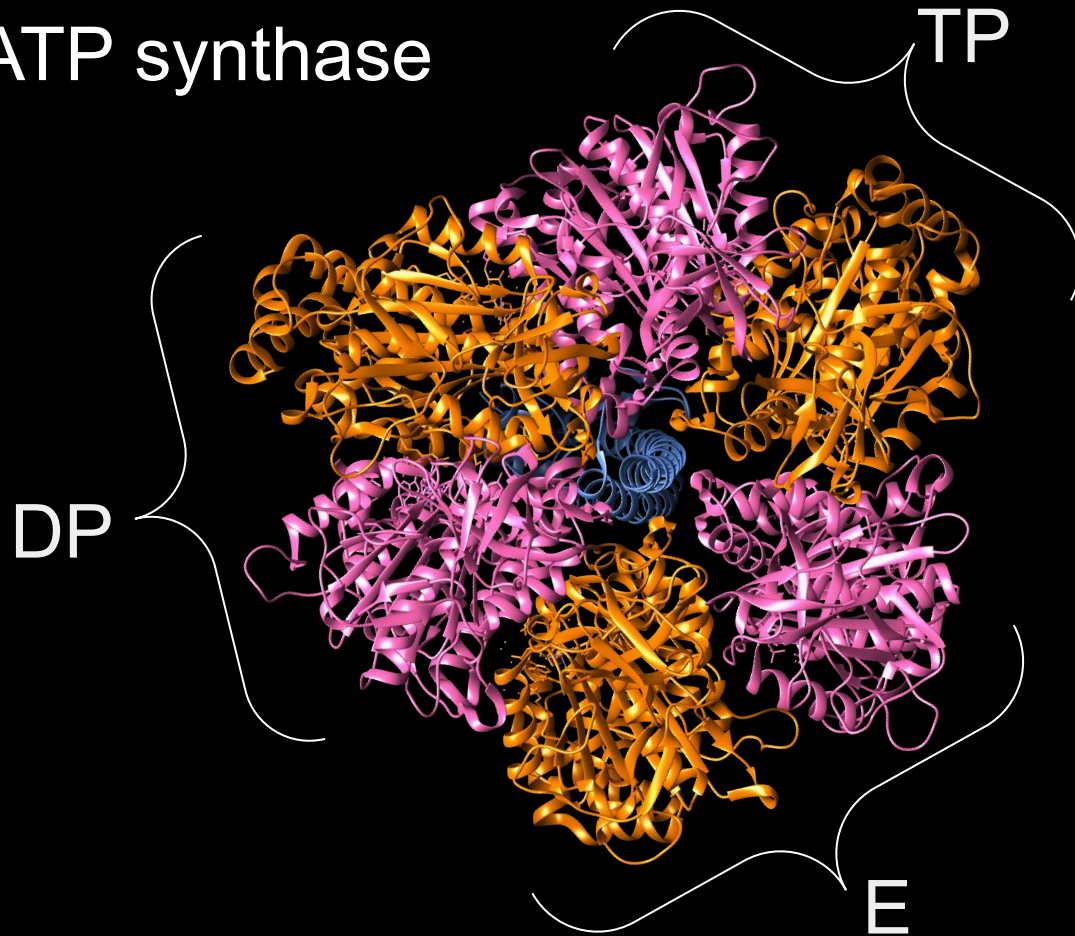
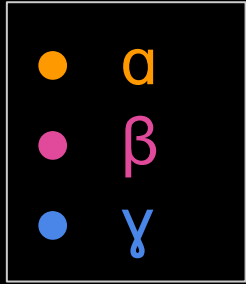
	301	i	l	d	f	e	a	d	p	v	q
Consensus											
Conservation											
Bos taurus	-	-	D	I	D	A	D	-	-	-	-
Homo sapiens	-	-	D	I	D	A	D	-	-	-	-
Saccharomyces cerevisiae	-	-	D	T	D	A	N	-	-	-	-
Polytomella sp.	-	-	E	A	S	H	E	R	S	D	
Pisum sativum	I	L	Q	F	E	Q	D	P	V	Q	
Spinacia oleracea	I	L	E	F	E	Q	D	P	A	Q	
Trichormus variabilis	D	M	I	F	E	Q	D	P	V	Q	
Escherichia coli	-	Y	L	Y	E	P	D	P	K	A	
Paracoccus denitrificans	-	-	-	Y	E	P	D	E	N	A	

c-ring

Consensus	R	n	P
Conservation			
Spinacia oleracea	R	Q	P
Pisum sativum	R	Q	P
Trichormus variabilis	R	Q	P
Homo sapiens	R	N	P
Bos taurus	R	N	P
Saccharomyces cerevisiae	R	N	P
Polytomella sp.	R	N	P
Paracoccus denitrificans	R	N	P
Escherichia coli	R	Q	P



States of F1-ATP synthase

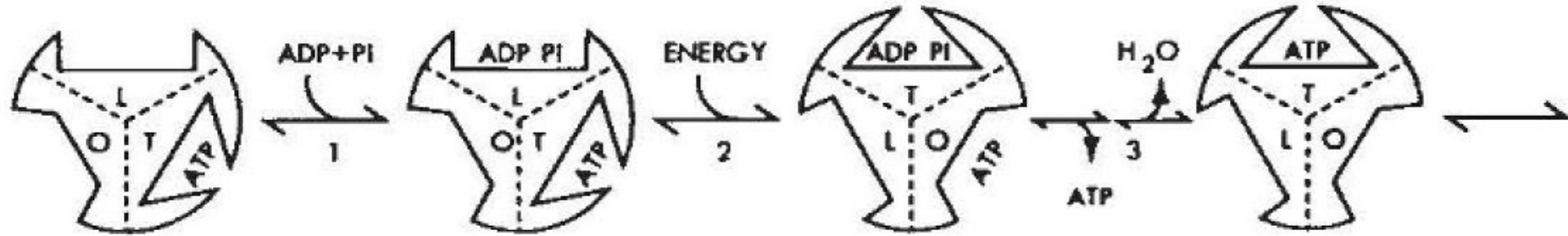


Hexamer $\alpha_3\beta_3$ - Rotational states

O: "open"

L: "loose"

T: "tight"



'Catch residues' in β subunit alignment

	351	361	371	381	391
Consensus	Q E R I T s T k k G	S I T S v Q A v Y V	P A D D L T D P a P	A T T F A H L D A T	T V L S R g i a e l
Conservation					
Homo Sapiens	Q E R I T T T K K G	S I T S V Q A I Y V	P A D D L T D P A P	A T T F A H L D A T	T V L S R A I A E L
Bos taurus	Q E R I T T T K K G	S I T S V Q A I Y V	P A D D L T D P A P	A T T F A H L D A T	T V L S R A I A E L
Paracoccus denitrificans	Q E R I T S T K N G	S I T S I Q A V Y V	P A D D L T D P A P	A T T F A H L D A T	T V L S R A I S E L
S. cerevisiae	Q E R I T T T K K G	S V T S V Q A V Y V	P A D D L T D P A P	A T T F A H L D A T	T V L S R G I S E L
Polytomella sp	Q E R I T T T T K G	S I T S V Q A V Y V	P A D D L T D P G P	A T T F A H L D A T	T V L S R S I A E L
Escherichia coli	Q E R I T S T K T G	S I T S V Q A V Y V	P A D D L T D P S P	A T T F A H L D A T	V V L S R Q I A S L
Spinacia oleracea	Q E R I T S T K E G	S I T S I Q A V Y V	P A D D L T D P A P	A T T F A H L D A T	T V L S R G L A A K
Pisum sativum	Q E R I T S T K E G	S I T S I Q A V Y V	P A D D L T D P A P	A T T F A H L D A T	T V L S R G L A A K
Trichormus variabilis	Q E R I T S T T E G	S I T S I Q A V Y V	P A D D L T D P A P	A T T F A H L D G T	T V L S R G L A A K
	401	411	421	431	441
Consensus	G I Y P A V D P L D	S t S r m l d P n i	V G e E H Y d v a r	g V q k i L Q r Y K	s L Q D I I A I L G
Conservation					
Homo Sapiens	G I Y P A V D P L D	S T S R I M D P N I	V G S E H Y D V A R	G V Q K I L Q D Y K	S L Q D I I A I L G
Bos taurus	G I Y P A V D P L D	S T S R I M D P N I	V G S E H Y D V A R	G V Q K I L Q D Y K	S L Q D I I A I L G
Paracoccus denitrificans	G I Y P A V D P L D	S N S R I L D P A V	V G E E H Y Q V A R	D V Q G I L Q K Y K	S L Q D I I A I L G
S. cerevisiae	G I Y P A V D P L D	S K S R L L D A A V	V G Q E H Y D V A S	K V Q E T L Q T Y K	S L Q D I I A I L G
Polytomella sp	G I Y P A V D P L D	S T S R M R N P N V	I G A E H Y N V A R	G V Q K V L Q D Y K	N L Q D I I A I L G
Escherichia coli	G I Y P A V D P L D	S T S R Q L D P L V	V G Q E H Y D T A R	G V Q S I L Q R Y Q	E L Q D I I A I L G
Spinacia oleracea	G I Y P A V D P L D	S T S T M L Q P R I	V G E E H Y E I A Q	R V K E T L Q R Y K	E L Q D I I A I L G
Pisum sativum	G I Y P A V D P L D	S T S T M L Q P R I	V G E E H Y E T A Q	R V K Q T L Q R Y K	E L Q D M I A I L G
Trichormus variabilis	G I Y P A V D P L G	S T S T M L Q P N I	V G D E H Y N T A R	A V Q S T L Q R Y K	E L Q D I I A I L G
	451	461	471	481	491
Consensus	m D E L S E E D k L	t V a R A R K I q r	F L S Q P F f V A E	V F T G s p G K y V	p L k d T I k g F q
Conservation					
Homo Sapiens	M D E L S E E D K L	T V S R A R K I Q R	F L S Q P F Q V A E	V F T G H M G K L V	P L K E T I K G F Q
Bos taurus	M D E L S E E D K L	T V S R A R K I Q R	F L S Q P F Q V A E	V F T G H L G K L V	P L K E T I K G F Q
Paracoccus denitrificans	M D E L S E E D K L	T V A R A R K I Q R	F L S Q P F D V A K	V F T G S D G V Q V	P L E D T I K S F K
S. cerevisiae	M D E L S E Q D K L	T V E R A R K I Q R	F L S Q P F A V A E	V F T G I P G K L V	R L K D T V A S F K
Polytomella sp	M D E L S E E D K L	T V A R A R K I Q R	F L S Q P F Q V A E	V F T G T P G K Y V	D L A D T I S G F Q
Escherichia coli	M D E L S E E D K L	V V A R A R K I Q R	F L S Q P F F V A E	V F T G S P G K Y V	S L K D T I R G F K
Spinacia oleracea	L D E L S E E D R L	T V A R A R K I E R	F L S Q P F F V A E	V F T G S P G K Y V	G L A E T I R G F Q
Pisum sativum	L D E V S E E D R L	T V A R A R K I E R	F F S Q P F F V A E	V F T G S P G K Y V	G L A E T I R G F Q
Trichormus variabilis	L D E L S E E D R L	I V A R A R K V E R	F L S Q P F F V A E	V F T G S P G K Y V	K L E D T I K G F Q

Asp316, Asp319

γ - α , β interactions

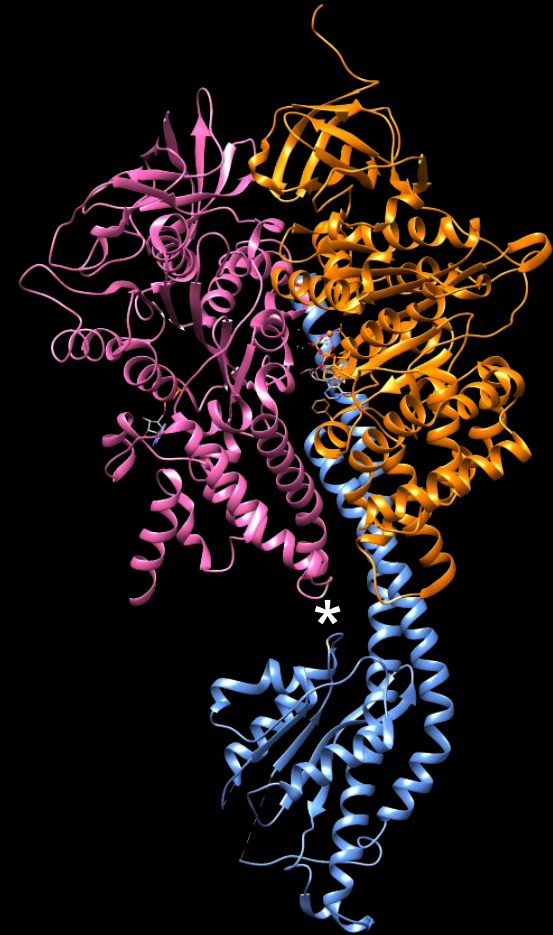
DELSEED loop (β DP) + α E + γ

γ sequence alignment:

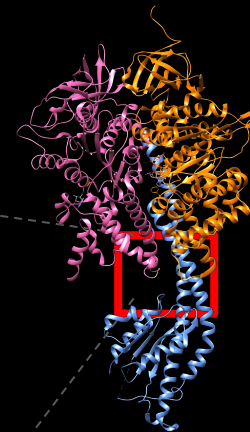
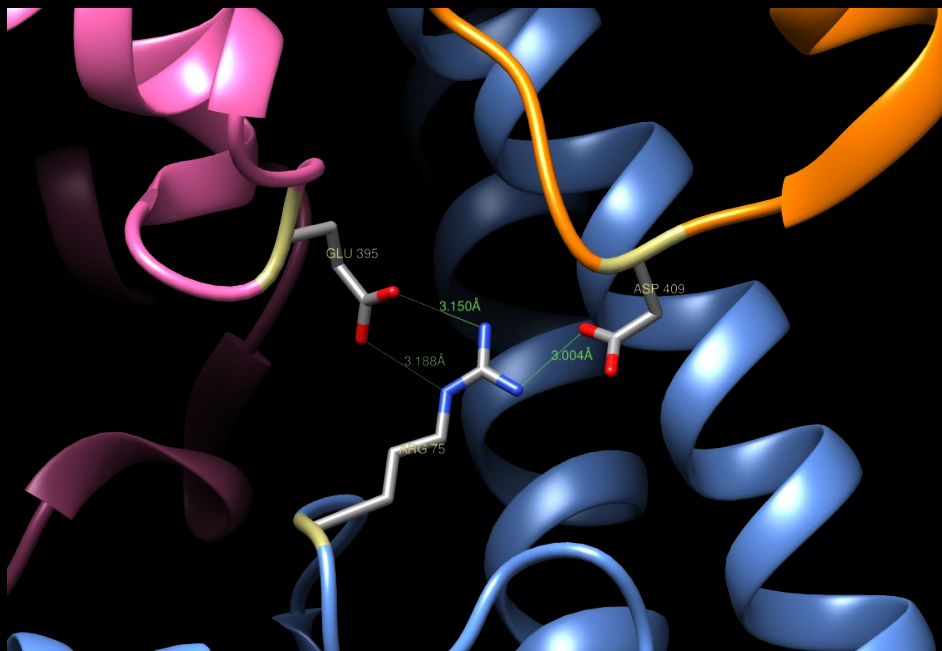
	131	141	151
Consensus	r d v k k v l l v v	v t s D r G L C G g	i n s s i a K k a r
Conservation			
Bos taurus	E D K K K H L I I G	V S S D R G L C G A	I H S S V A K Q M K
Homo sapiens	E D K K K H L L I G	V S S D R G L C G A	I H S S I A K Q M K
Saccharomyces cerevisiae	T G A P K E L I V A	I T S D K G L C G S	I H S Q L A K A V R
Polytomella sp	- - S N K S V V V A	V T S D K G L C G G	L N S N I T K Y T R
Pisum sativum	R P V K K V A L V V	C T G D R G L C G G	F N N A I L K K A E
Spinacia oleracea	R T V K K V A L M V	V T G D R G L C G G	F N M L L K K A E
Trichormus variabilis	R V K S V G L L V	I S G D R G L C G G	Y N T N V I R R A E
Escherichia coli	R V K R V G Y L V	V S T D R G L C G G	L N I N L F K K L L
Paracoccus denitrificans	G E D R R H L L V V	M T S E R G L A G G	F N S S I V K L A R

α sequence alignment:

	471	481	491
Consensus	A F A Q F g S D L D	a A T q q q L a R G	q R L t E L L K Q P
Conservation			
Bos	A F A Q F G S D L D	A A T Q Q L L S R G	V R L T E L L K Q G
Homo	A F A Q F G S D L D	A A T Q Q L L S R G	V R L T E L L K Q G
Saccharomyces	A F A Q F G S D L D	A S T K Q T L V R G	E R L T Q L L K Q N
Paracoccus	A F A Q F G S D L D	A A T Q K L L N R G	A R L T E L M K Q P
Polytomella	A F A Q F G S D L D	A A T Q Y V L E R G	A R L T E M L K Q K
Pisum	A F A Q F A S D L D	K A T Q N Q L A R G	Q R L R E L L K Q S
Spinacia	A F A Q F A S D L D	K A T Q N Q L A R G	Q R L R E L L K Q P
Trichormus	A F A Q F A S D L D	K A T Q D Q L A R G	Q R L R E L L K Q S
Escherichia	A F S Q F A S D L D	D A T R K Q L D H G	Q K V T E L L K Q K



γ - α,β interactions



γ R75- β DpE395

1. NH2(Arg)-OE1(Glu) 3,150Å
2. N(Arg)-OE2(Glu) 3,188Å

γ R75- β D409

1. NH1(Arg)-OD2(Asp) 3,005Å

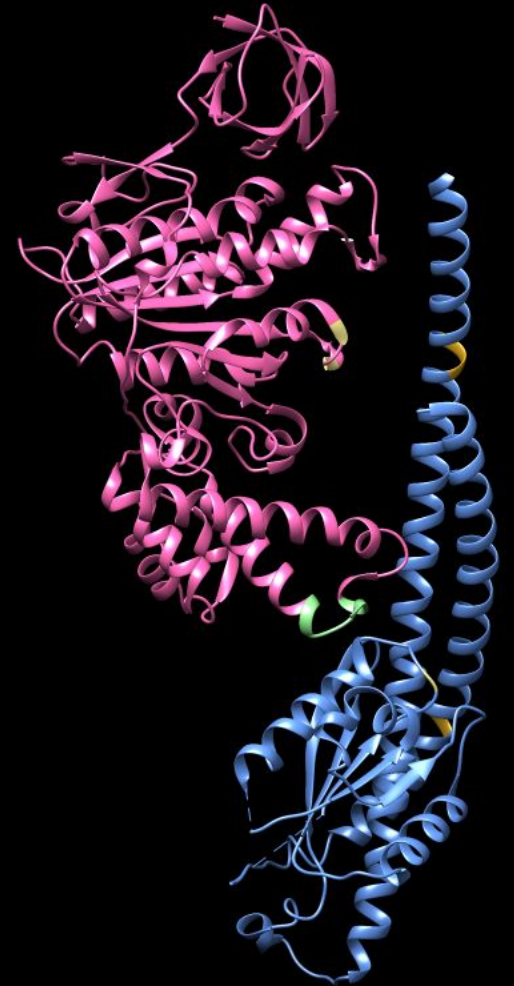
γ - α,β interactions

DELSEED loop (β TP) + γ

γ sequence alignment:

	131		141		151
Consensus	r d v k k v l l v v		v t s D r G L C G g		i n s s i a K k a r
Conservation					
Bos taurus	E D K K K H L I I G		V S S D R G L C G A		I H S S V A K Q M K
Homo sapiens	E D K K K H L L I G		V S S D R G L C G A		I H S S I A K Q M K
Saccharomyces cerevisiae	T G A P K E L I V A		I T S D K G L C G S		I H S Q L A K A V R
Polytomella sp	- - S N K S V V V A		V T S D K G L C G G		L N S N I T K Y T R
Pisum sativum	R P V K K V A L V V		C T G D R G L C G G		F N N A I L K K A E
Spinacia oleracea	R T V K K V A L M V		V T G D R G L C G G		F N N M L L K K A E
Trichormus variabilis	R E V K S V G L L V		I S G D R G L C G G		Y N T N V I R R A E
Escherichia coli	R D V K R V G Y L V		V S T D R G L C G G		L N I N L F K K L L
Paracoccus denitrificans	G E D R R H L L V V		M T S E R G L A G G		F N S S I V K L A E

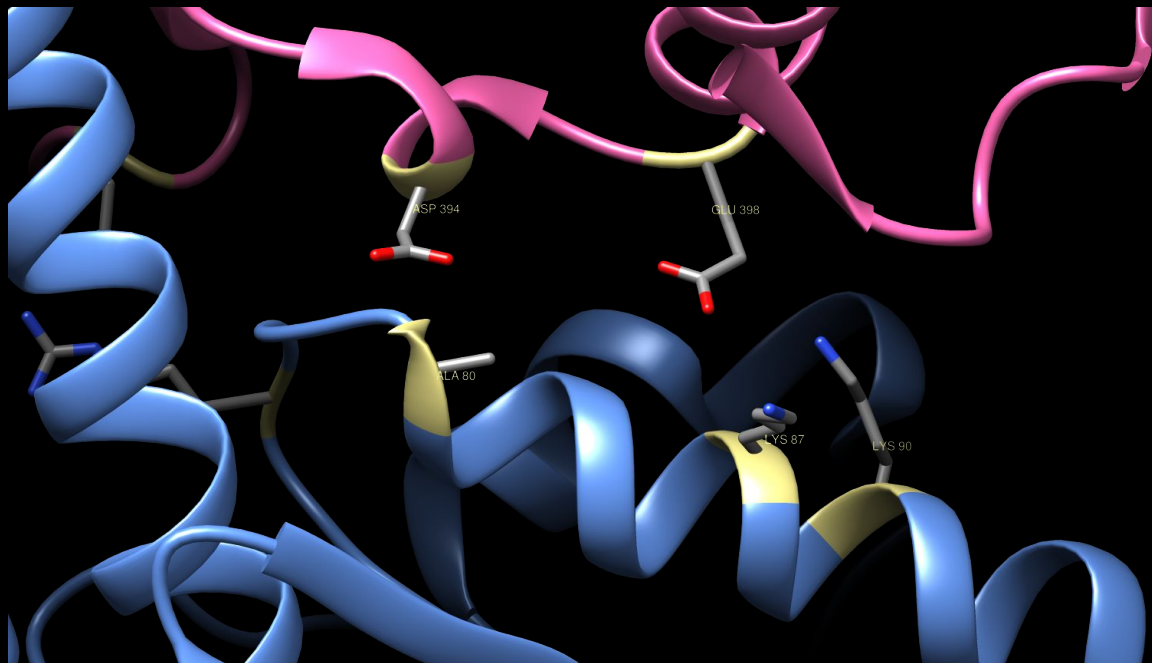
!!!



γ - α,β interactions

γ A80, K87, K90 $\rightarrow$

β_{TP} D394, E398 (DELSEED-loop)

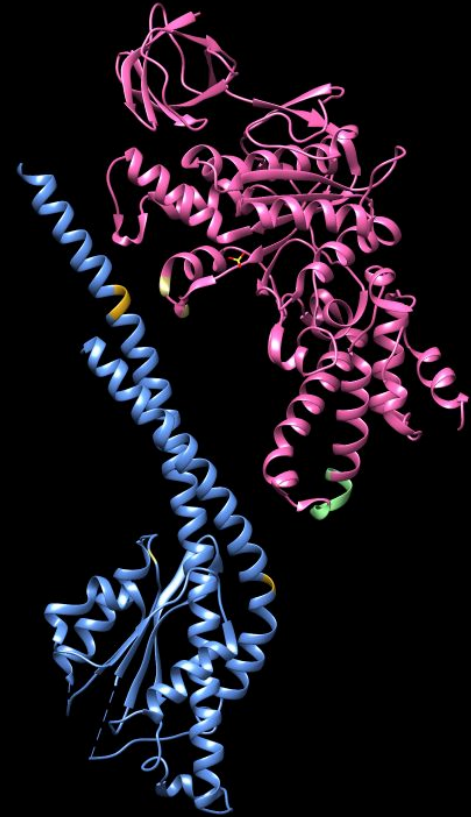


γ - α,β interactions

DELSEED loop (β E) + γ

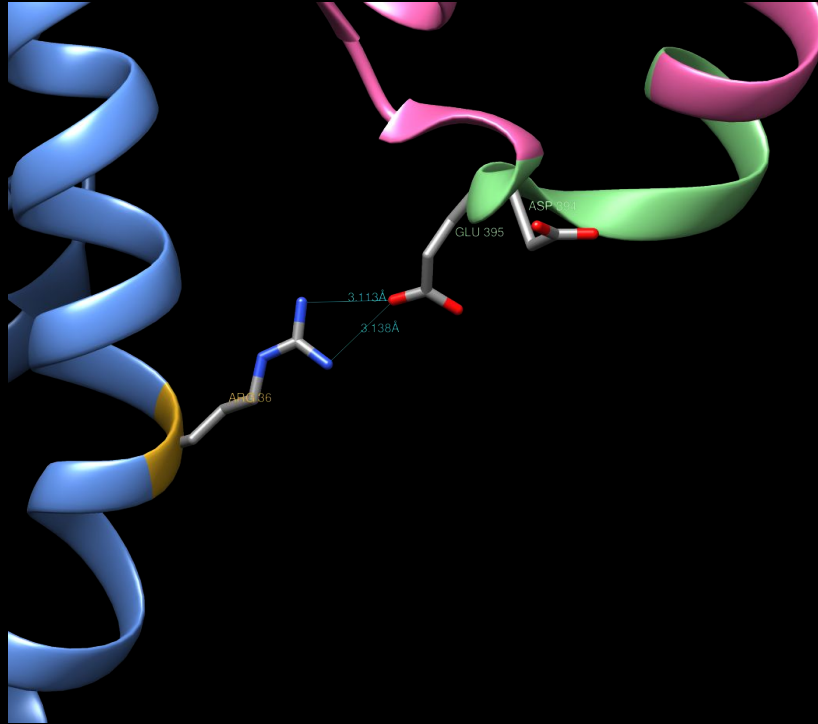
γ sequence alignment:

	131		141		151
Consensus	r d v k k v l l v v		v t s D r G L C G g		i n s s i a K k a r
Conservation					
Bos taurus	E D K K K H L I I G		V S S D R G L C G A		I H S S V A K Q M K
Homo sapiens	E D K K K H L L I G		V S S D R G L C G A		I H S S I A K Q M K
Saccharomyces cerevisiae	T G A P K E L I V A		I T S D K G L C G S		I H S Q L A K A V R
Polytomella sp	- - S N K S V V V A		V T S D K G L C G G		L N S N I T K Y T R
Pisum sativum	R P V K K V A L V V		C T G D R G L C G G		F N N A I L K K A E
Spinacia oleracea	R T V K K V A L M V		V T G D R G L C G G		F N M L L K K A E
Trichormus variabilis	R E V K S V G L L V		I S G D R G L C G G		Y N T N V I R R A E
Escherichia coli	R D V K R V G Y L V		V S T D R G L C G G		L N I N L F K K L L
Paracoccus denitrificans	G E D R R H L L V V		M T S E R G L A G G		F N S S I V K L A R

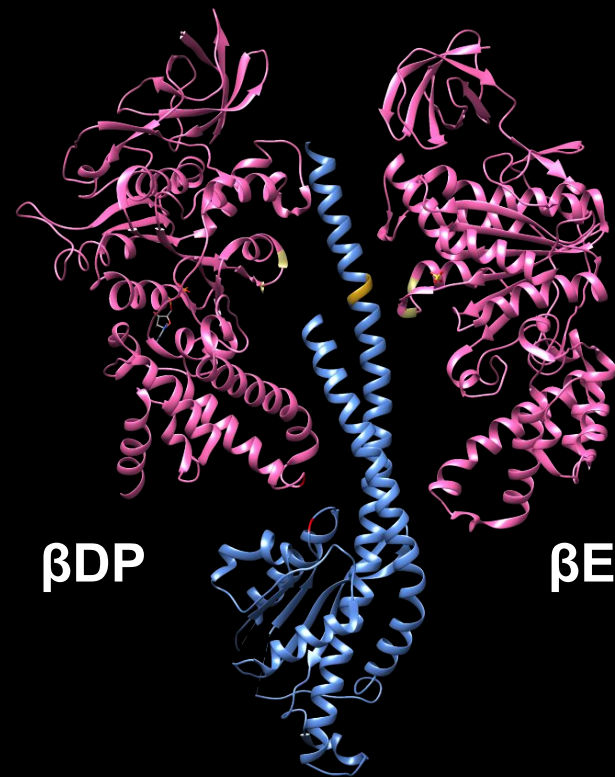
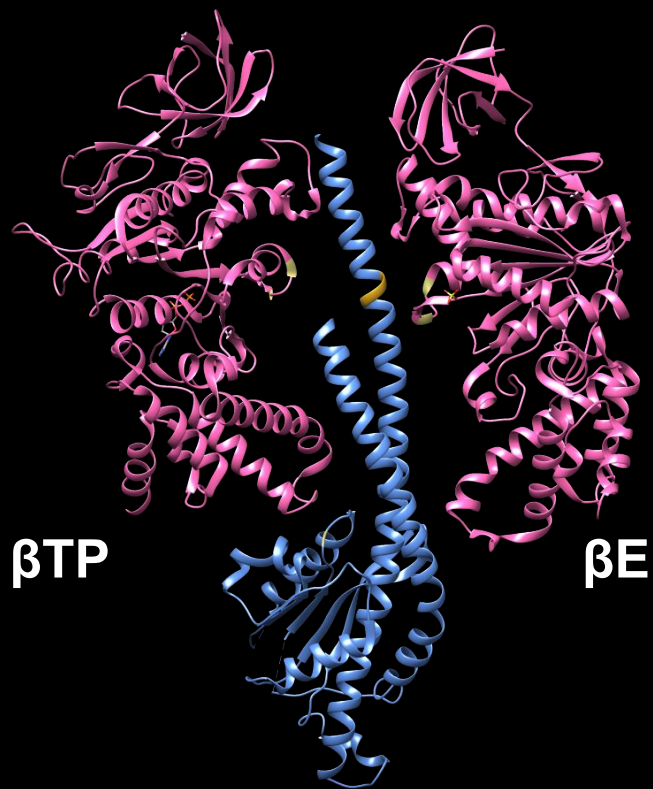


γ - α,β interactions

γ R36 $\rightarrow$ β E395

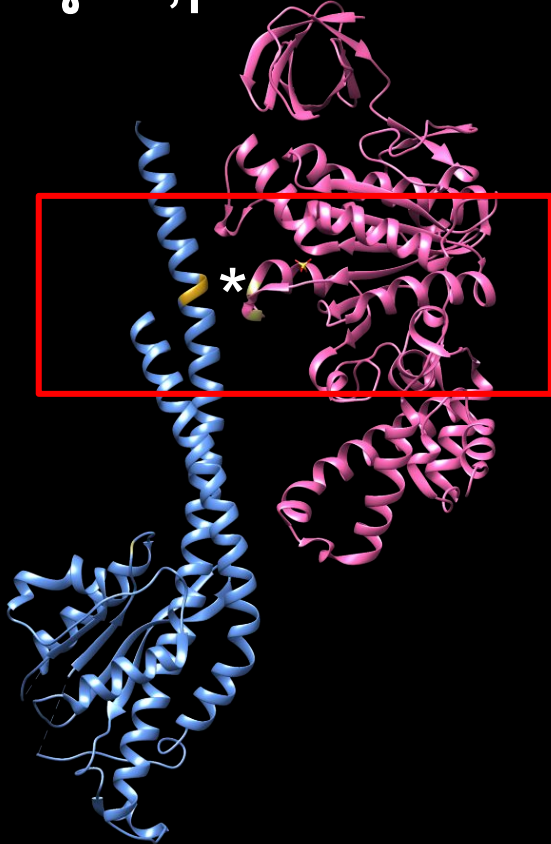


γ - α,β interactions



γ - α,β interactions

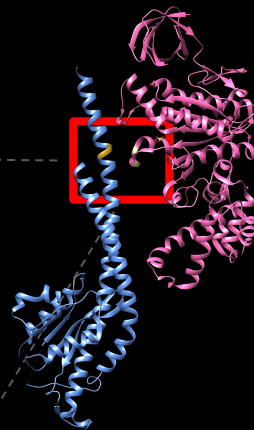
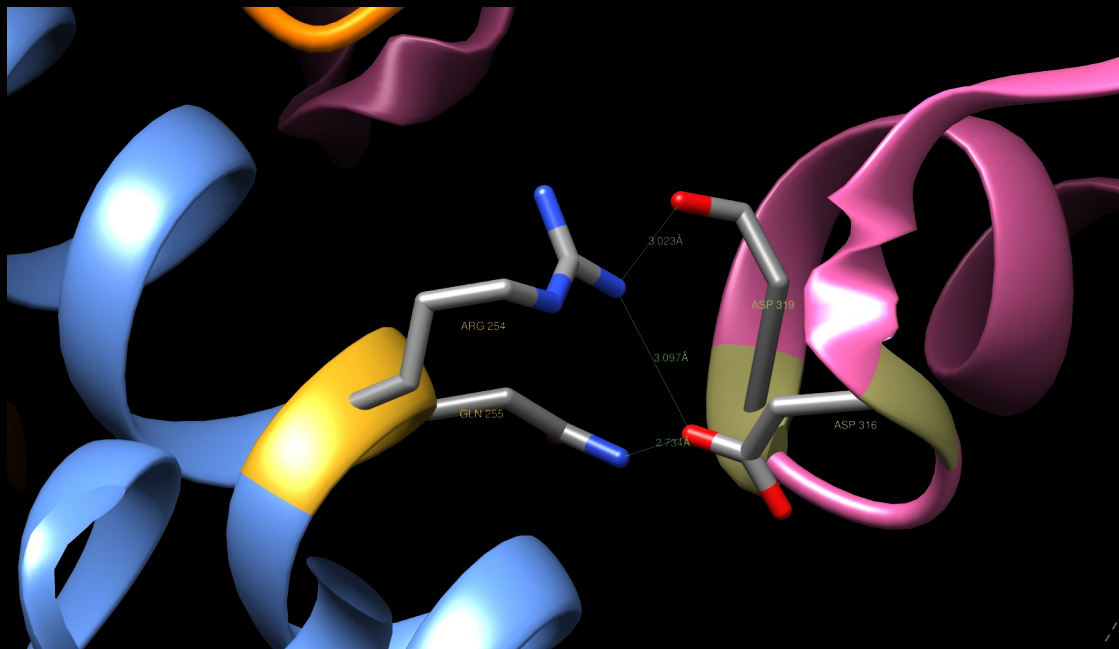
$\gamma \rightarrow$ 'catch' residues (βE)



γ sequence alignment:

	351		361		371		381
Consensus	g e m i k k L t l v		y N r a R Q A v I T		k E l i E i s G A		a a l - - -
Conservation							
Bos taurus	S E M I D K L T L T		F N R T R Q A V I T		K E L I E I I S G A		A A L D - -
Homo sapiens	S E M I D K L T L T		F N R T R Q A V I T		K E L I E I I S G A		A A L D - -
Saccharomyces cerevisiae	G D M I N R Y S I L		Y N R T R Q A V I T		N E L V D I I T G A		S S L G - -
Polytomella sp	G E M L G K L T L D		Y N R K R Q A T I T		T E L I E I I A G A		S A L M D E
Pisum sativum	S E L K T D L T R V		Y N R A T Q A K I T		G E I L E I V A G D		I E C I I W
Spinacia oleracea	N E L K K T L S I N		Y N R A R Q A K I T		G E I L E I V A G A		N A C V - -
Trichormus variabilis	G E L I K S L S L S		Y N K A R Q A A I T		Q E L L E V V G G A		E A L T - -
Escherichia coli	G S L I K E L Q L V		Y N K A R Q A S I T		Q E L T E I V S G A		A A V - - -
Paracoccus denitrificans	G D M I D R L T T V		Y N R S R Q A A I T		K E L I E I I S G A		E A L - - -

γ - α,β interactions

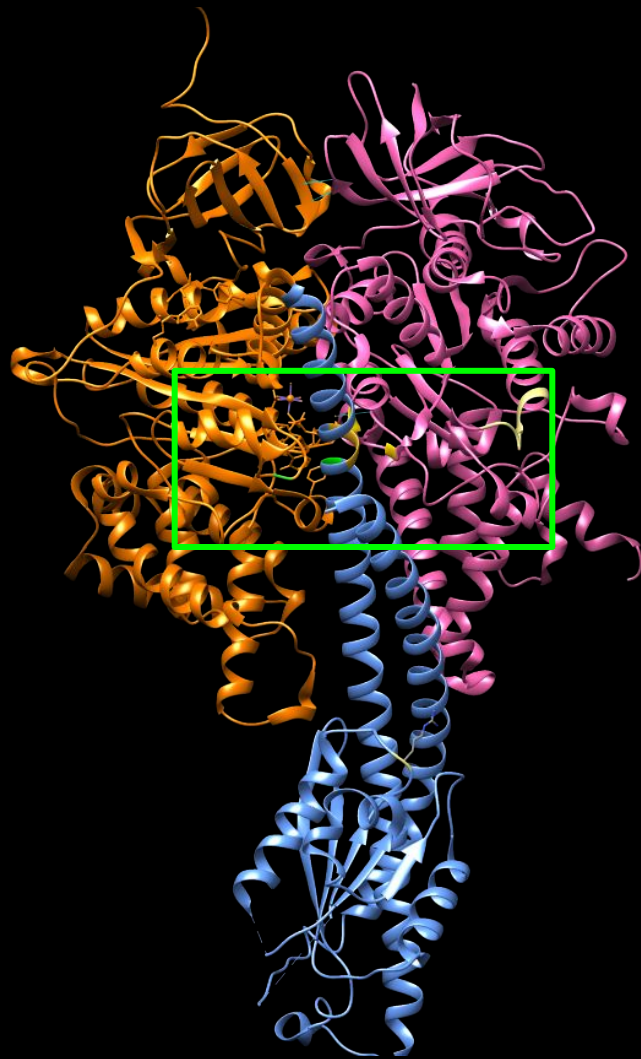


γ R254, γ Q255 - β E316,D319

1. N(Arg254)-OD2(Asp316) 3,097Å
2. N(Arg254)-OD2(Asp319) 3,023Å
3. N(Glu255)-OD2(Asp316) 2,734Å

γ - α,β interactions

$\gamma \rightarrow \alpha E, \beta E$



γ - α,β interactions

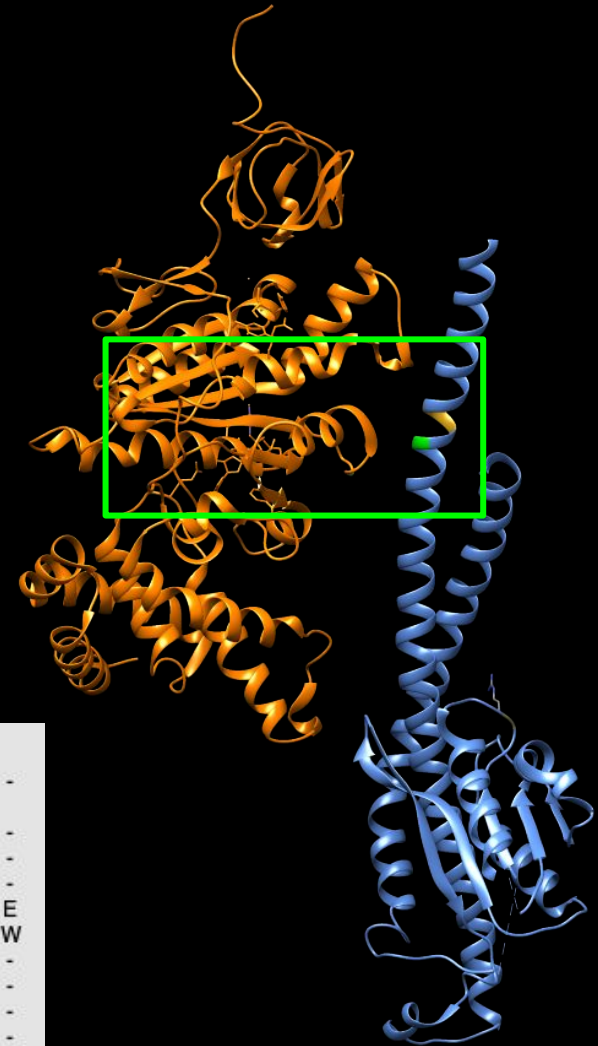
$\gamma \rightarrow \alpha\beta$

γ sequence alignment:

	391	401	411
Consensus	TALP i i ETQ a	GDVSAYIPTN	VISITDGGQIF
Conservation			
Bos	TALPVIETQA	GDVSAYIPTN	VISITDGGQIF
Homo	TALPVIETQA	GDVSAYIPTN	VISITDGGQIF
Saccharomyces	TALPVIETQG	GDVSAYIPTN	VISITDGGQIF
Paracoccus	TALPVIETQA	GDVSAYIPTN	VISITDGGQIF
Polytomella	TAFPVIETQA	GDVSAYIATN	VISITDGGQIF
Pisum	TALPVIETQS	GDVSAYIPTN	VISITDGGQIF
Spinacia	TALPVIETQA	GDVSAYIPTN	VISITDGGQIF
Trichormus	TALPVIETQA	GDVSAYIPTN	VISITDGGQIF
Escherichia	TALPVIETQA	GDVSAFVPTN	VISITDGGQIF

α sequence alignment:

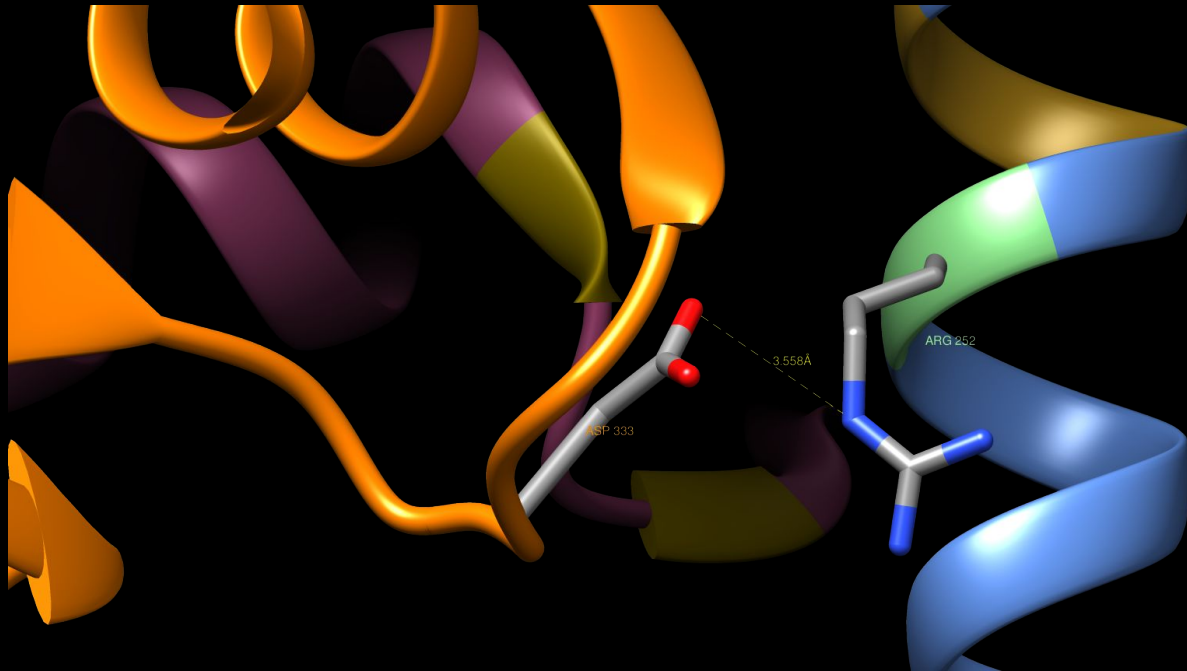
	351	361	371	381
Consensus	gemikkLtlv	yNr aRQAvIT	kEliEiisGA	aaL---
Conservation				
Bos taurus	SEMIDKLTLT	FNRTTRQAVIT	KELIEIISGA	AALD--
Homo sapiens	SEMIDKLTLT	FNRTTRQAVIT	KELIEIISGA	AALD--
Saccharomyces cerevisiae	GDMINRYSIL	YNRTTRQAVIT	NELVDIITGA	SSLG--
Polytomella sp	GEMLGKLTLD	YNRKRAATIT	TELIEIIAGA	SALMDE
Pisum sativum	SELKTDLTRV	YNRAATQAKIT	GEILEIVAGD	IECI IW
Spinacia oleracea	NELKKTLSIN	YNRAARQAKIT	GEILEIVAGA	NACV--
Trichormus variabilis	GELIKSLSL	YNKARQAAIT	QELLEIVVGA	EALT--
Escherichia coli	GSLIKELQLV	YNKARQASIT	QELTEIVSGA	AAV---
Paracoccus denitrificans	GDMIDRLTTV	YNRSRQAAIT	KELIEIISGA	EAL---



γ - α,β interactions

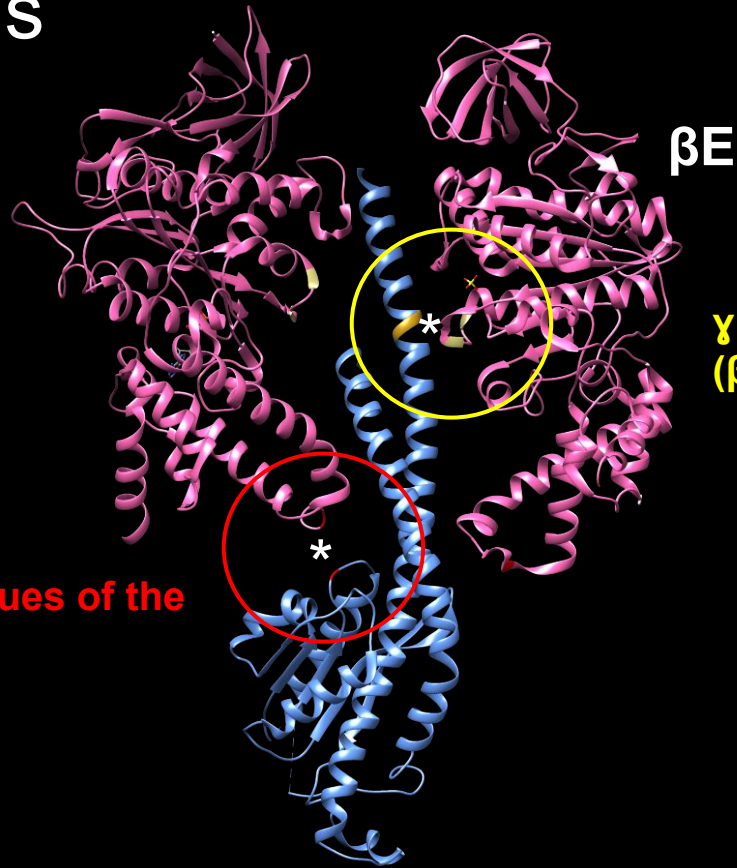
γ R252 - DED333

“salt bridge”



γ - α,β interactions

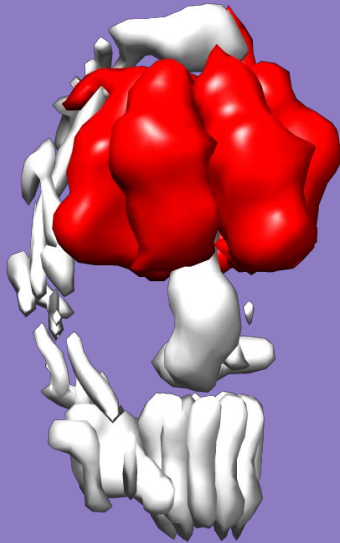
βE , βDP , βTP



$\gamma \rightarrow$ upper 'catch' residues (βE)

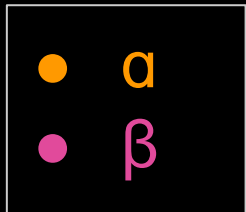
$\gamma \rightarrow$ 'catch' residues of the DELSEED-loop

III part: catalytic function



Catalytic head:

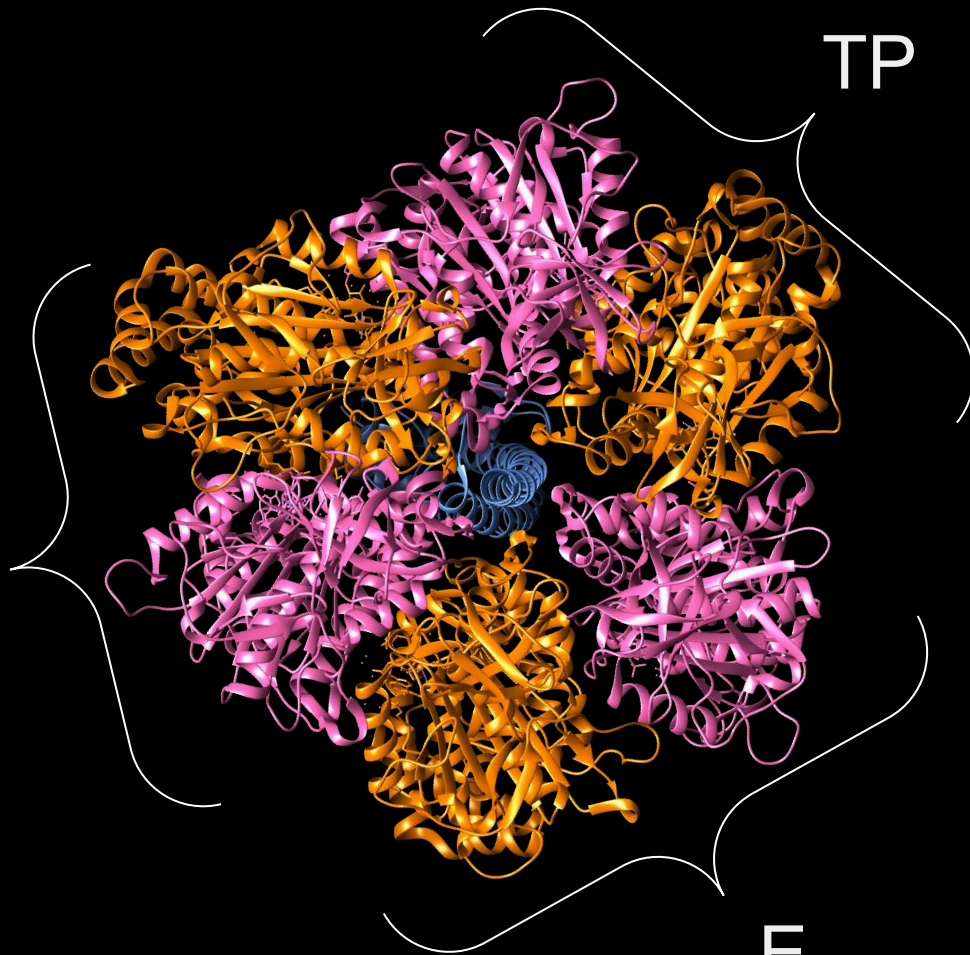
Hexamer $\alpha_3\beta_3$



DP

TP

E





Are they
similar?



α - β superimposition

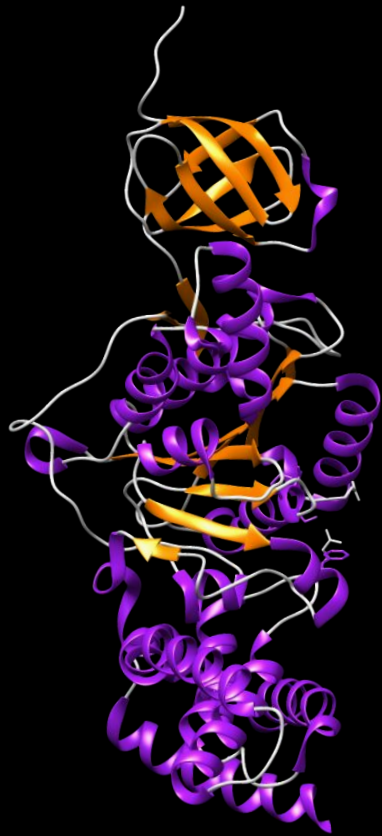
RMSD=1.915



α - β structural alignment

	51	61	71	81	91
Consensus	eealE v q s r .	. . L k l e s a q h	e p e . t v r t i a	m d g d k l i k r G	q i v k r s G A i i
Conservation					
alfa	50 E E M V E F S S G .	. . L K G M S L N L	E P D . N V G V V V	F G N D K L I K E G	D I V K R T G A I V
beta	33 L N A L E V Q G R E	T R L V L E V A Q H	L G E S T V R T I A	M D G T E G L V R G	Q K V L D S G A P I
	101	111	121	131	141
Consensus	r i P V G p E I L G	R i m d a i G e a I	D e k G P I k s K a	r a a i h a k A P e	i i p r i s . q r .
Conservation					
alfa	96 D V P V G E E L L G	R V V D A L G N A I	D G K G P I G S K A	R R R V G L K A P G	I I P R I S . V R E
beta	83 R I P V G P E T L G	R I M N V I G E P I	D E R G P I K T K Q	F A A I H A E A P E	F V E M S V E Q E .
	151	161	171	181	191
Consensus	i m q T G I K a V .	s L . a P i a k G q	k i l i i G d a q t	G K T s i a i e t I	i N . q K a h . . .
Conservation					
alfa	145 P M Q T G I K A V D	S L . V P I G R G Q	R E L I I G D R Q T	G K T S I A I D T I	I N . Q K R F N D G
beta	132 I L V T G I K V V .	D L L A P Y A K G G	K I G L F G G A G V	G K T V L I M E L I	N N V A K A H . . .
	201	211	221	231	241
Consensus	 k l Y c i	y a a i G q k r s e	g a q L y h r m i e	a d a i	k y t i l V y a q a
Conservation					
alfa	193 T D E K K K L Y C I	Y V A I G Q K R S T	V A Q L V K R L T D	A D A M	K Y T I V V S A T A
beta	178 G G Y S V	F A G V G E R T R E	G N D L Y H E M I E	S G V I N L K D A T	S K V A L V Y Q M
	251	261	271	281	291
Consensus	s e a a p a q y r a	a y s G c s m a E Y	F R D q . G q h a L	i i y D d i s k q a	q A y s q m S a L L
Conservation					
alfa	237 S D A A P L Q Y L A	P Y S G C S M G E Y	F R D N . G K H A L	I I Y D D L S K Q A	V A Y R Q M S L L L
beta	223 N E P P G A R A R V	A L T G L T V A E Y	F R D Q E G Q D V L	L F I D N I F R F T	Q A G S E V S A L L
	301	311	321	331	341
Consensus	r R i P s a e a Y q	p d l a y l h s r m	q E R a a k m k . .	k . . G S i T a l q	a i y t q A d D l s
Conservation					
alfa	286 R R P P G R E A Y P	G D V F Y L H S R L	L E R A A K M N D A	F G G G S L T A L P	V I E T Q A G D V S
beta	273 G R I P S A V G Y Q	P T L A T D M G T M	Q E R I T T T K . .	K . . G S I T S V Q	A I Y V P A D D L T

α -subunit

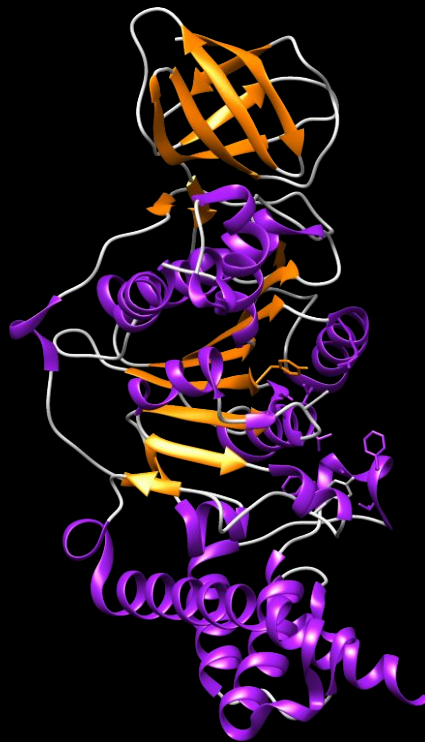


DOMAIN 1

DOMAIN 2

DOMAIN 3

β -subunit



β -subunit CATH

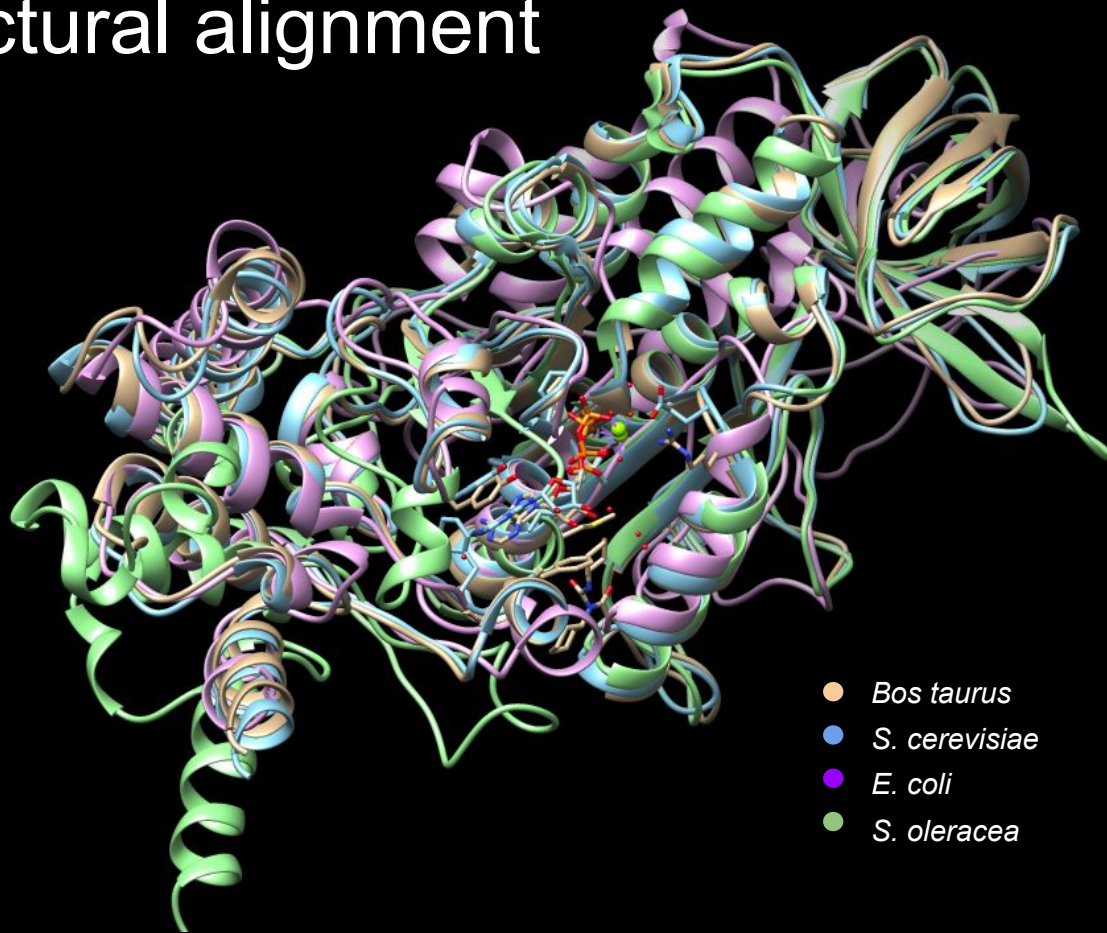
DOMAIN	START	STOP	LENGTH	ARCHITECTURE	TOPOLOGY
1	9	81	72	Beta barrel	Thrombin, subunit H
2	82	357	275	3-Layer(aba) Sandwich	Rossmann fold
3	358	475	117	Orthogonal bundle	Bovine Mitochondrial F1-ATPase, ATP Synthase Beta Chain; Chain D, domain3



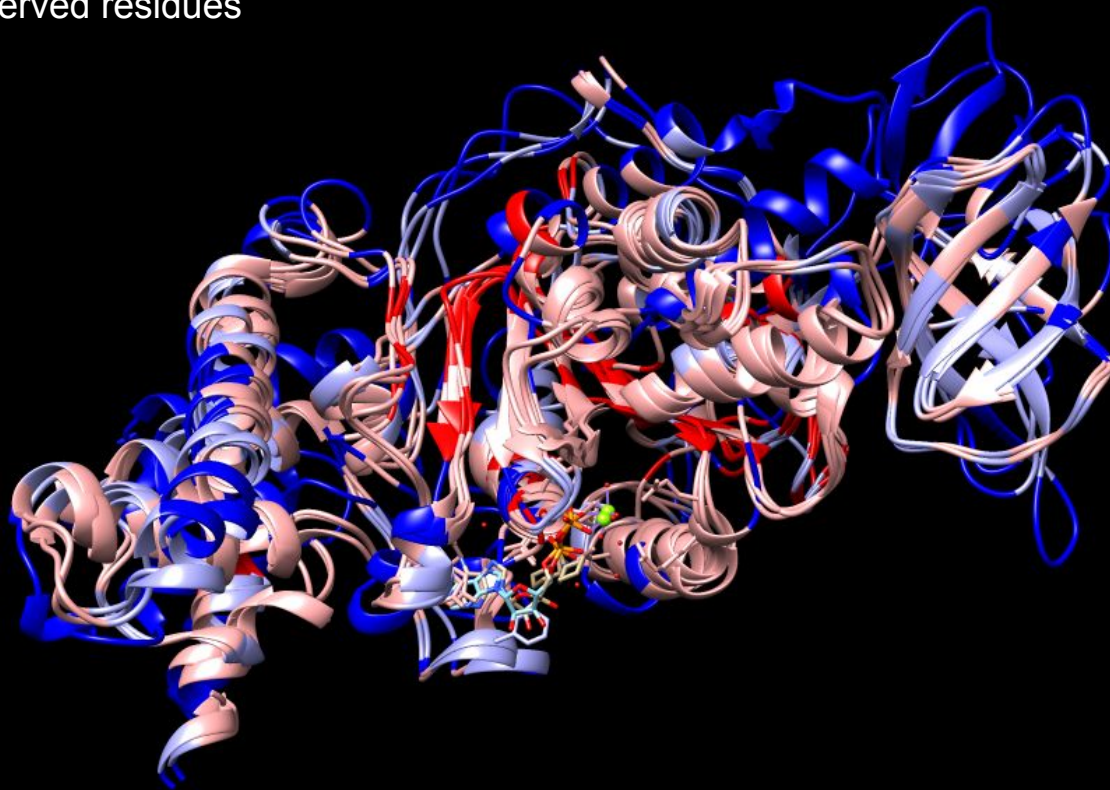
Bos taurus

β -subunit structural alignment

RMSD=2,355



Rendered by conserved residues





α -subunit CATH

DOMAIN	START	STOP	LENGTH	ARCHITECTURE	TOPOLOGY
1	9	81	72	Beta barrel	Elongation Factor Tu (Ef-tu); domain 3
2	82	357	275	3-Layer(aba) Sandwich	Rossmann fold
3	358	475	117	Up-down bundle	Lysin

How conformational changes
become changes in the affinity
of nucleotide-binding?

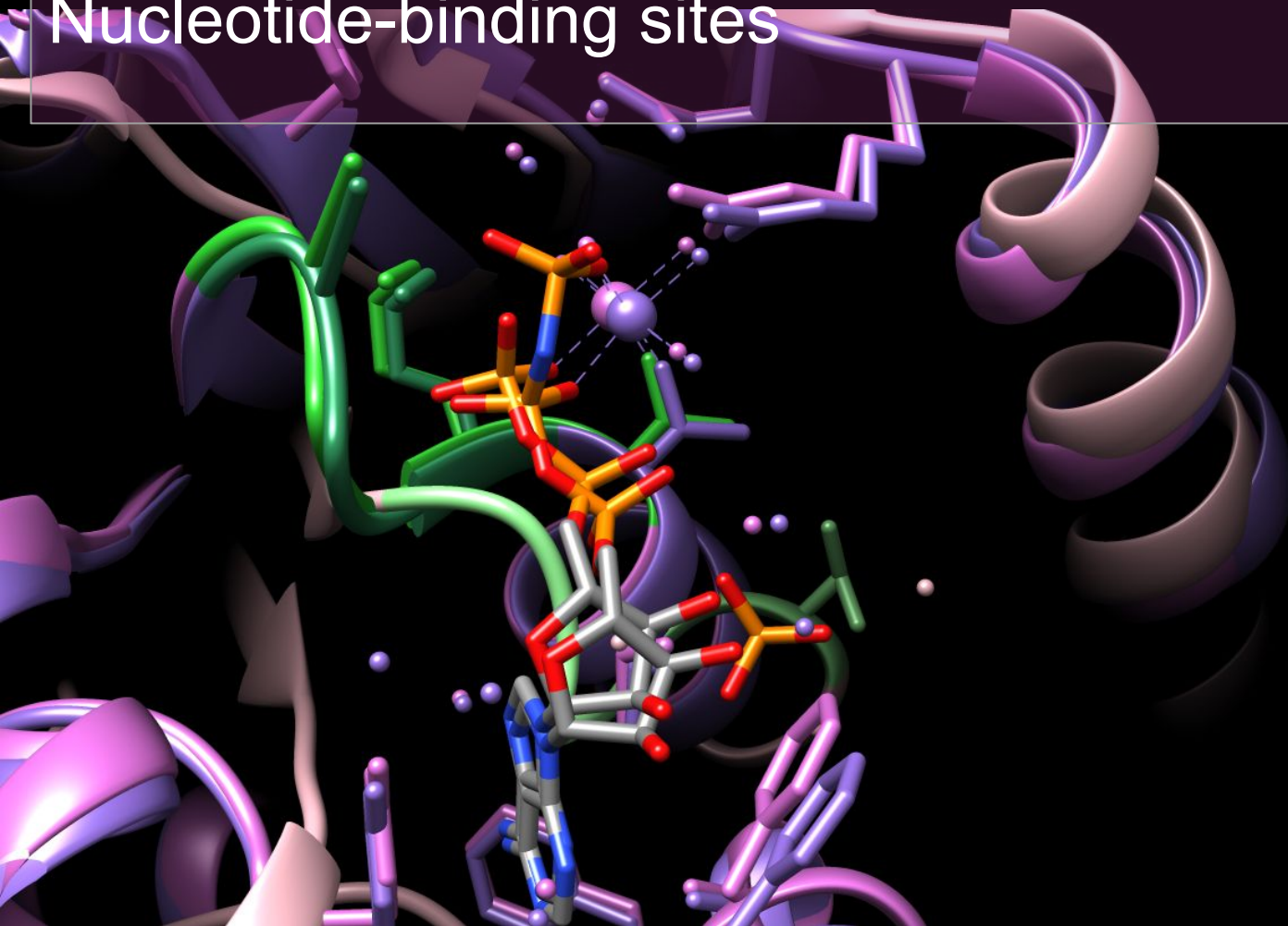
Catalytic site
conformations

β E
 β DP
 β TTP



α E
 α DP
 α TTP

Nucleotide-binding sites



β E (P-loop)
 β DP (P-loop)
 β TP (P-loop)

β-subunit sequence alignment

Consensus	201	211	221	231	241	251	261
Conservation							
L a	PYarGGKIGL	FGGAGVGKTV	l i M E L I N N i A	k a H g G y S V F a	GVGERTREGN	DLYhEMIESg	V i n l k d - - a e
Homo sapiens	LA PYAKGGKIGL	FGGAGVGKTV	LIMELINNVA	KAHGGYSVFA	GVGERTREGN	DLYHEMIESG	VINLKD - - AT
Bos taurus	LA PYAKGGKIGL	FGGAGVGKTV	LIMELINNVA	KAHGGYSVFA	GVGERTREGN	DLYHEMIESG	VINLKD - - AT
Paracoccus denitrificans	LA PYSKGGKIGL	FGGAGVGKTV	LIMELINNVA	KVHS GYSVFA	GVGERTREGN	DLYHEMVESG	VIKPDDL - SK
Saccharomyces cerevisiae	LA PYARGGKIGL	FGGAGVGKTV	FIQELINNIA	KAHGGFSVFT	GVGERTREGN	DLYREMKETG	VINLE - - GE
Polytomella sp	LA PYQRGGKIGL	FGGAGVGKTV	LIMELINNVA	KAHGGFSVFA	GVGERTREGN	DLYREMIESG	VIKLGAERGN
Escherichia coli	MC PFAKGGKVGL	FGGAGVGKTV	NMMELIRNIA	IEHS GYSVFA	GVGERTREGN	DFYHEMTDSN	V I D - - - - -
Spinacia oleracea	LA PYRRGGKIGL	FGGAGVGKTV	LIMELINNVA	KAHGGVSVFG	GVGERTREGN	DLYMEMKESG	VINEQN - IAE
Pisum sativum	LA PYRRGGKIGL	FGGAGVGKTV	LIMELINNVA	KAHGGVSVFG	GVGERTREGN	DLYMEMKESR	VINEKN - IAE
Trichormus variabilis	LT PYRRGGKIGL	FGGAGVGKTV	IMMELINNIA	TQHGGVSVFA	GVGERTREGN	DLYNEMIESG	VINKDN - LNE

p-loop

Glu188, Arg189

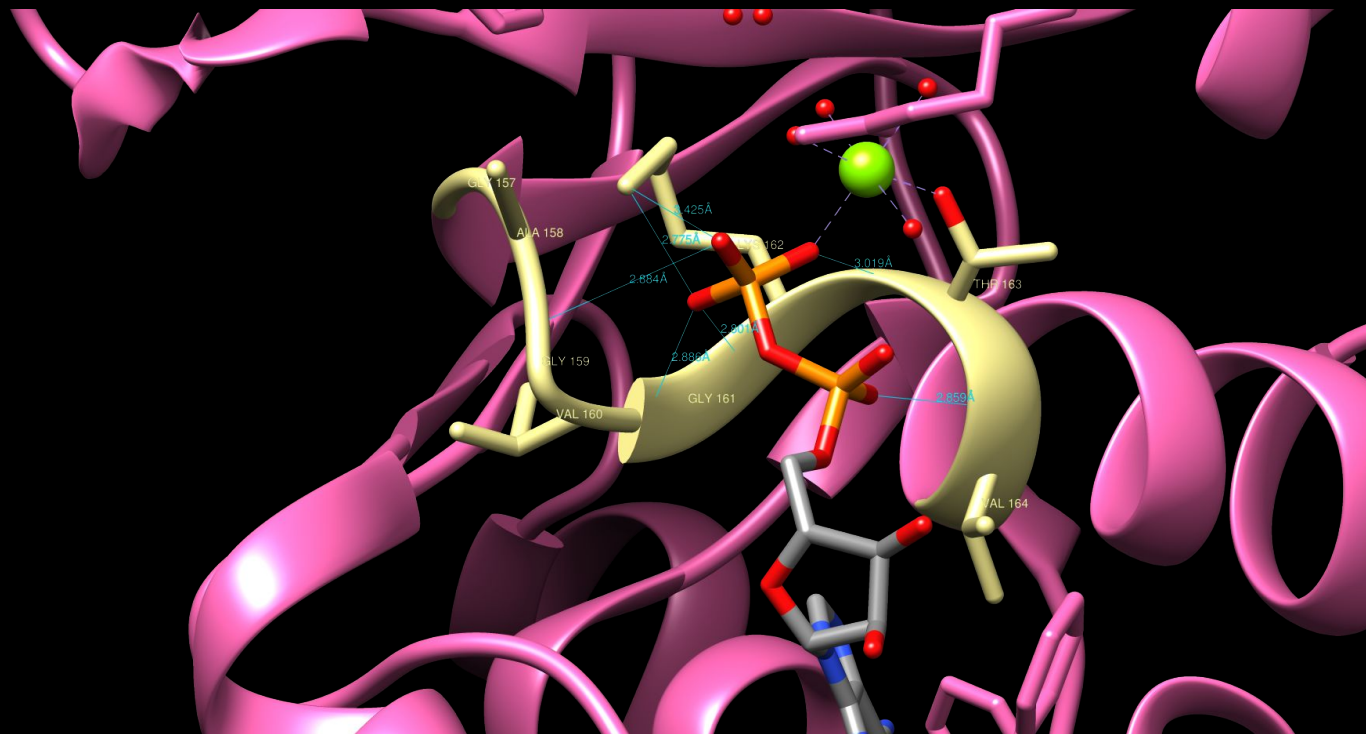
α-subunit sequence alignment

Consensus	401	411	421	431	441	451
Conservation						
i i E T Q a	GDVSAYIPTN	V I S I T D G Q I F	L e t e L F y a G I	R P A i n v G I S V	S R V G S A A Q t k	a M K q V A G k I K
Bos taurus	V I E T Q A	GDVSAYIPTN	V I S I T D G Q I F	R P A I N V G L S V	S R V G S A A Q T R	A M K Q V A G T M K
Homo sapiens	V I E T Q A	GDVSAYIPTN	V I S I T D G Q I F	R P A I N V G L S V	S R V G S A A Q T R	A M K Q V A G T M K
Saccharomyces cerevisiae	V I E T Q G	GDVSAYIPTN	V I S I T D G Q I F	R P A I N V G L S V	S R V G S A A Q V K	A L K Q V A G S L K
Paracoccus denitrificans	I I E T Q A	GDVSAYIPTN	V I S I T D G Q I F	R P A V N T G L S V	S R V G S A A Q T K	A M K S V A G P V K
Polytomella sp	V I E T Q A	GDVSAYIATN	V I S I T D G Q I F	R P A L N V G L S V	S R V G S A A Q F P	G M K Q V A G T L K
Pisum sativum	V I E T Q S	GDVSAYIPTN	V I S I T D G Q I F	R P A I N V G I S V	S R V G S A A Q I K	A M K Q V A G K L K
Spinacia oleracea	I V E T Q A	GDVSAYIPTN	V I S I T D G Q I F	R P A I N V G I S V	S R V G S A A Q I K	A M K K V A G K L K
Trichormus variabilis	I I E T Q A	GDVSAYIPTN	V I S I T D G Q I F	R P A V N P G I S V	S R V G S A A Q T K	A M K K V A G K I K
Escherichia coli	I I E T Q A	GDVS A F V P T N	V I S I T D G Q I F	R P A V N P G I S V	S R V G G A A Q T K	I M K K L S G G I R

Ser372, Arg373

ADP catalytic site (β DP)

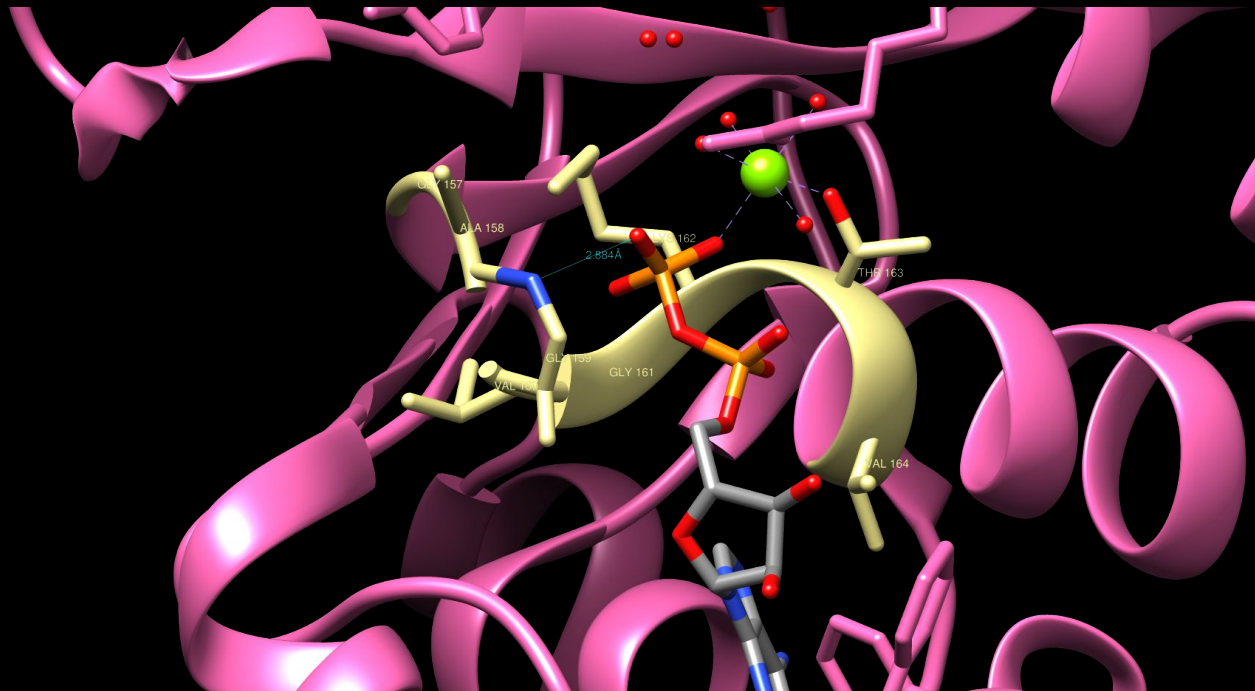
- β
- Gly159
- Gly161
- Lys162
- Thr163
- Val164



ADP catalytic site (β DP)

β (p-loop)

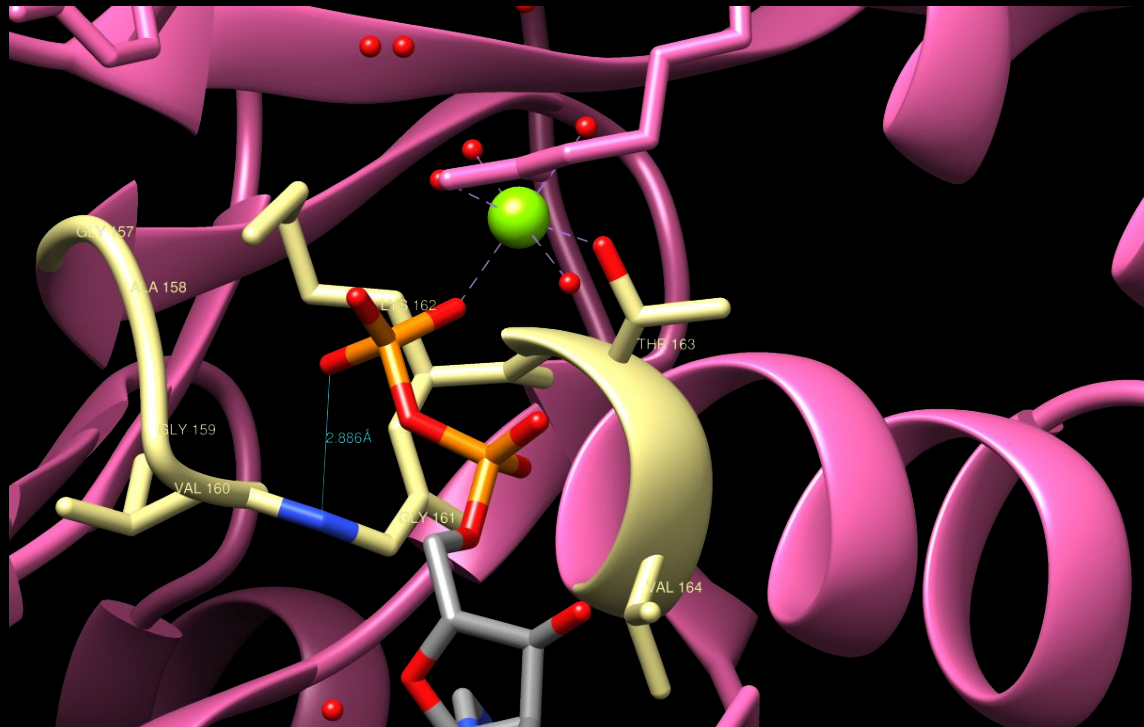
1. N(Gly159)-O3B(ADP) 2,884Å



ADP catalytic site (β DP)

β (p-loop)

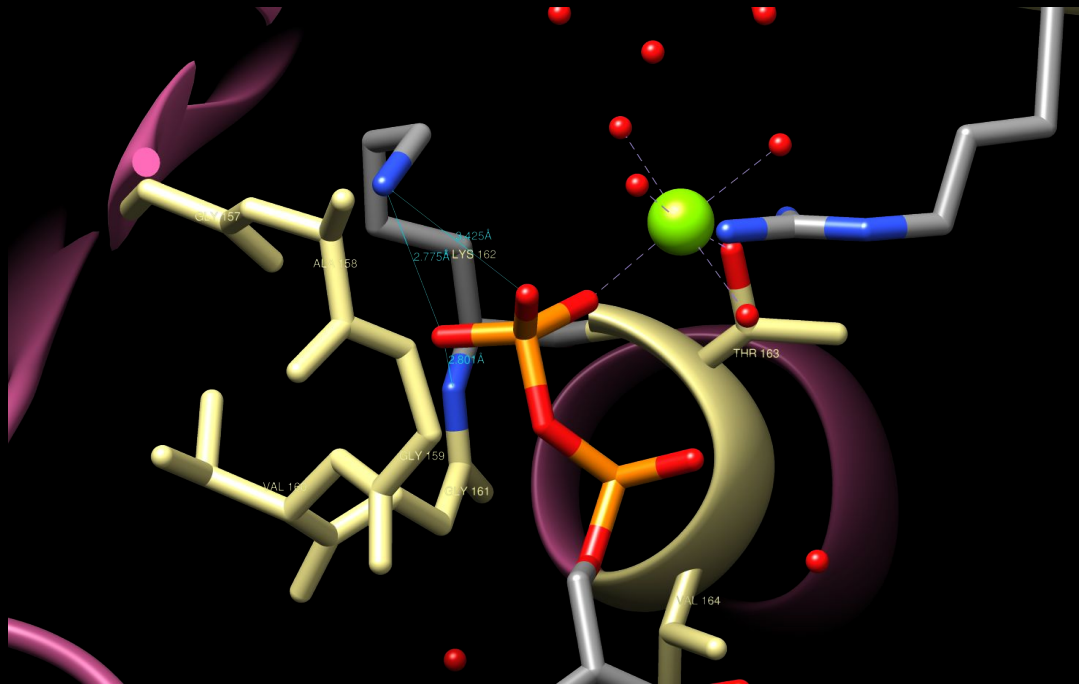
2. N(Gly161)-O1B(ADP) 2,886Å



ADP catalytic site (β DP)

β (p-loop)

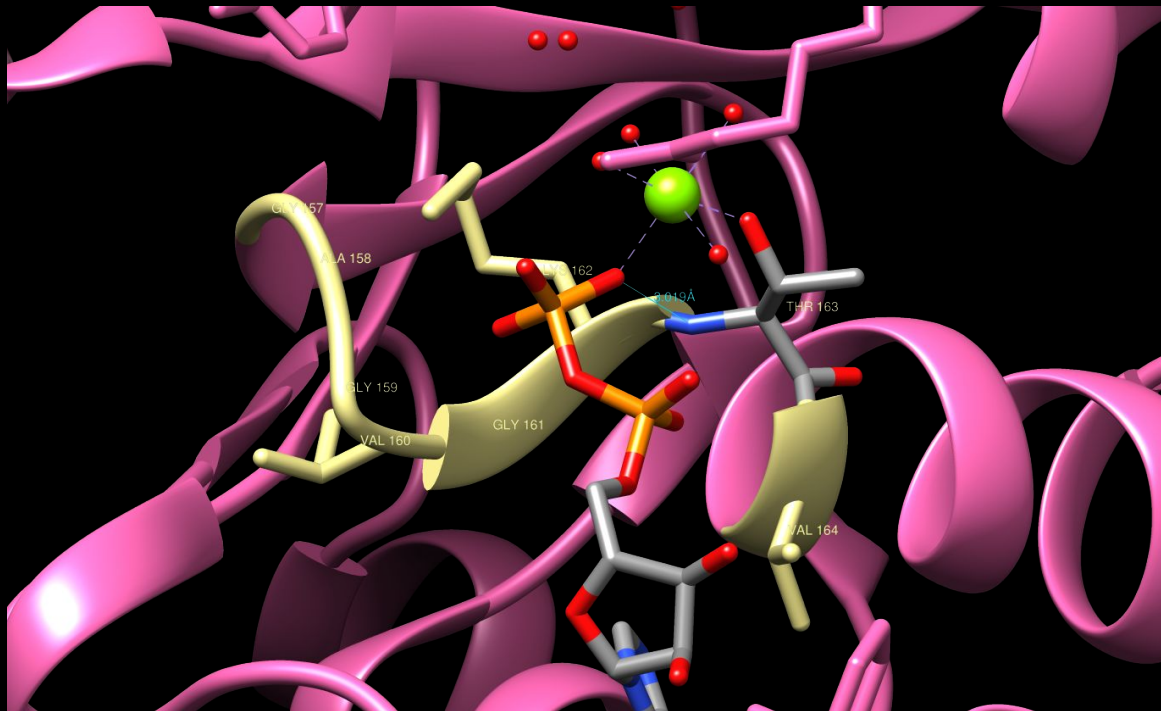
3. N(Lys162)-O1B(ADP) 2,801Å
4. N(Lys162)-O1B(ADP) 2,775Å
5. N(Lys162)-O3B(ADP) 3,425Å



ADP catalytic site (β DP)

β (p-loop)

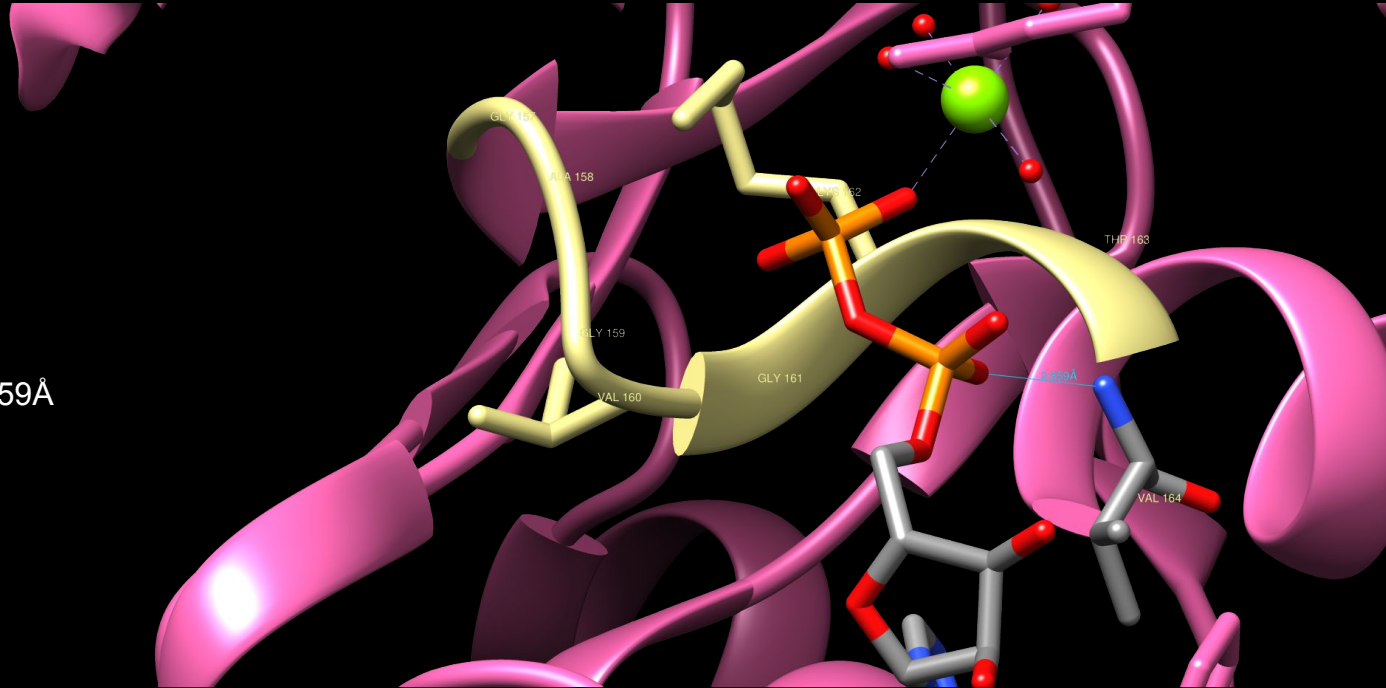
6. N(Thr163)-O2B(ADP) 3,019Å



ADP catalytic site (β DP- α DP)

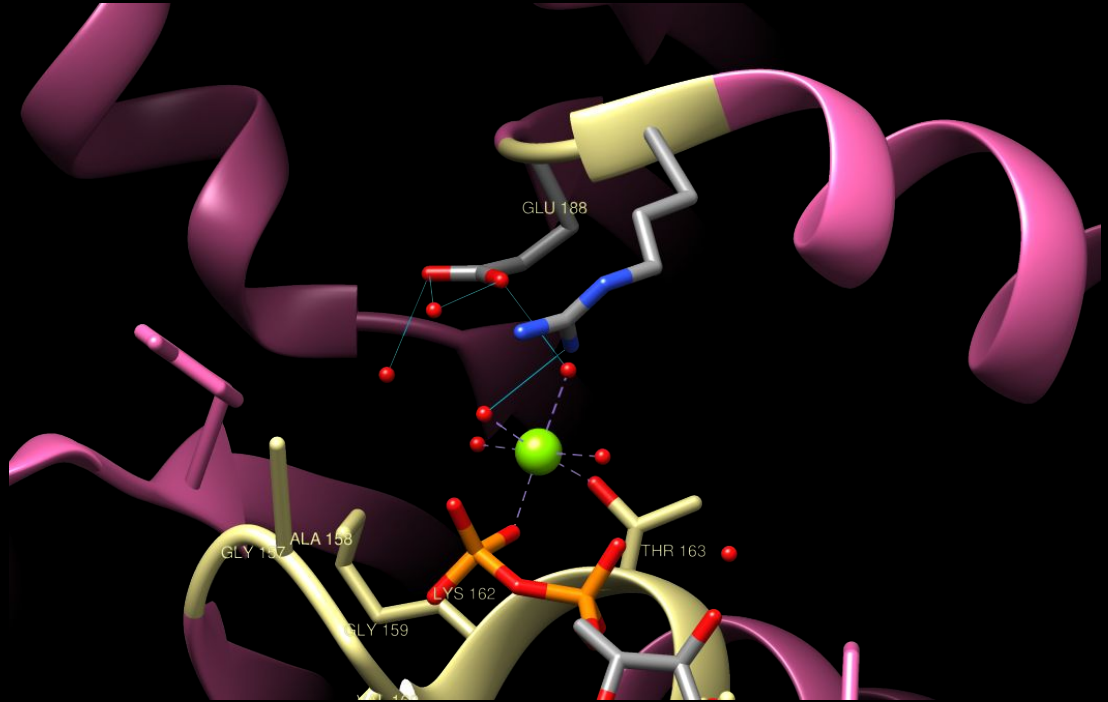
β (p-loop)

7. N(Val164)-O2A(ADP) 2,859Å



ADP catalytic site (β DP- α DP)

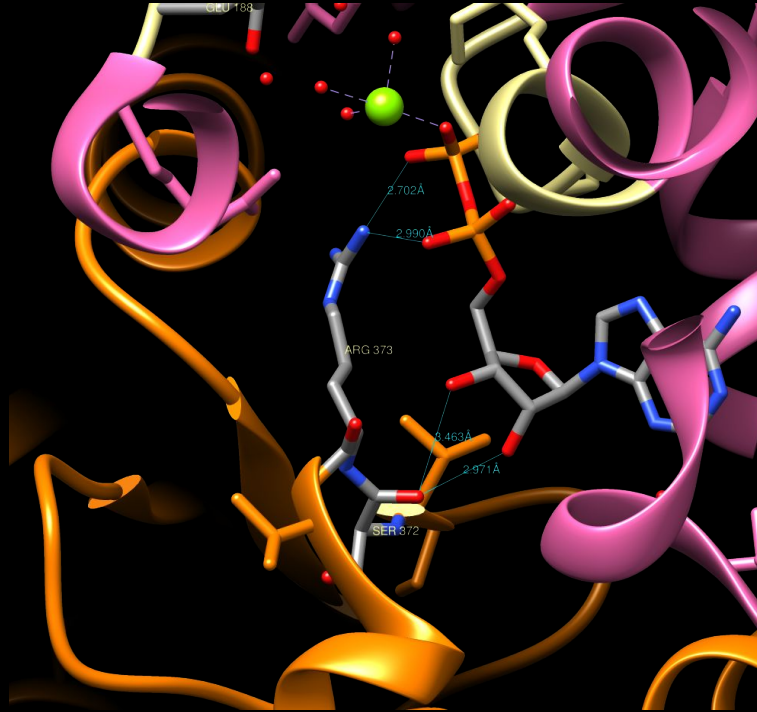
- Glu188
- Arg189



ADP catalytic site (β DP- α DP)

D-subunit

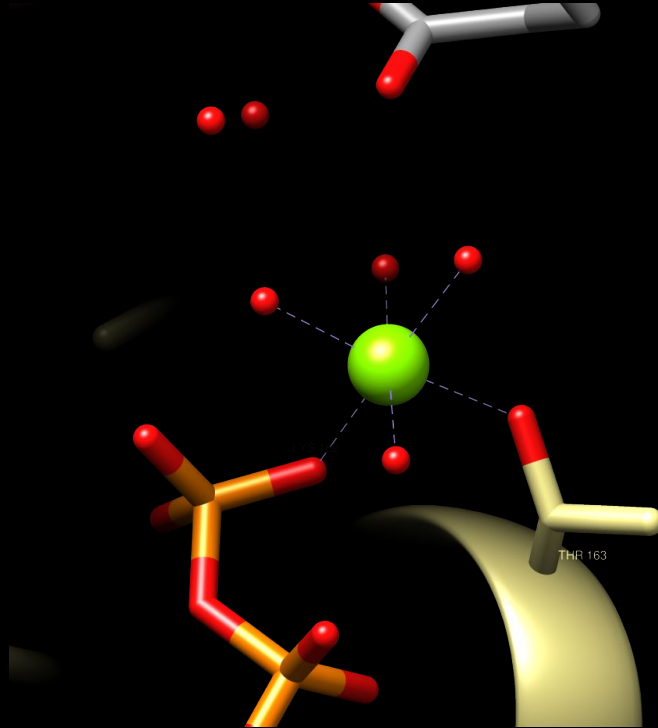
- 8. O(Ser372)-O2(ADP) 2,971Å
- 9. O(Ser372)-O3(ADP) 3,463Å
- 10. N(Arg373)-O1A(ADP) 2,990Å
- 11. N(Arg373)-O3B(ADP) 2,702Å



ADP catalytic site (β DP- α DP)

Mg - β

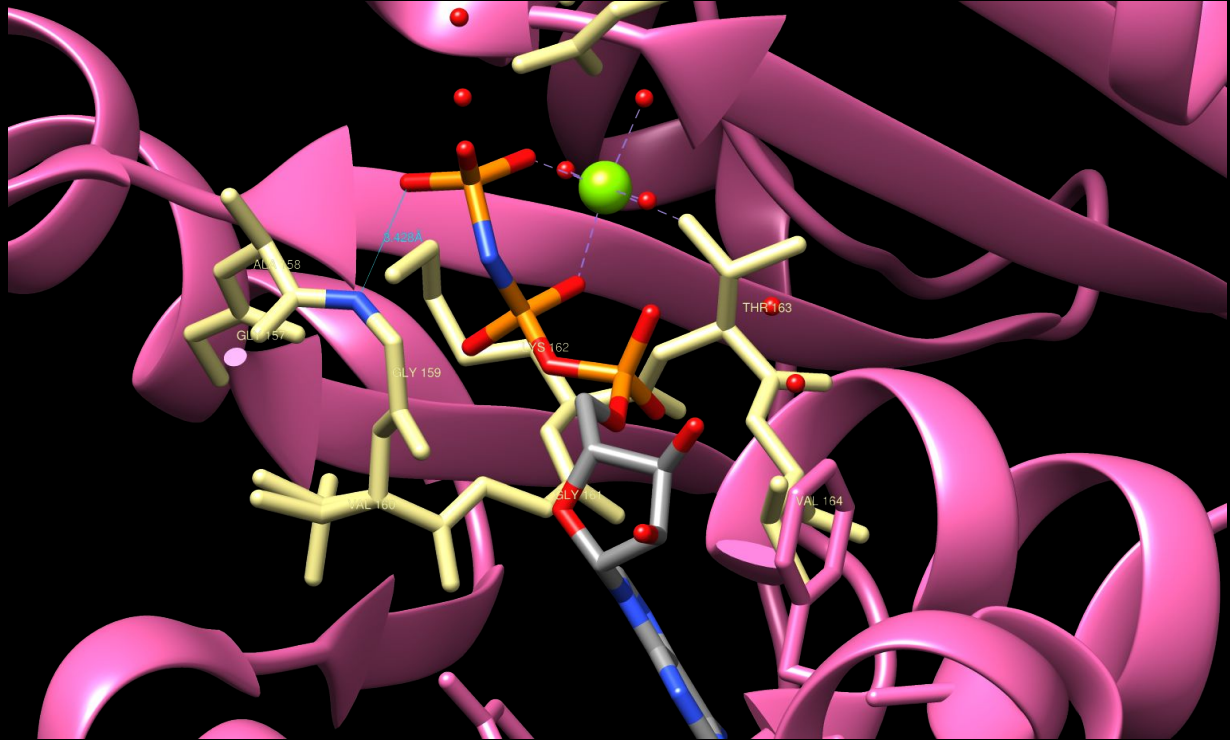
- β OB(ADP)
- OG1(Thr163)
- + H_2O



ATP catalytic site (β TP- α TP)

β (p-loop)

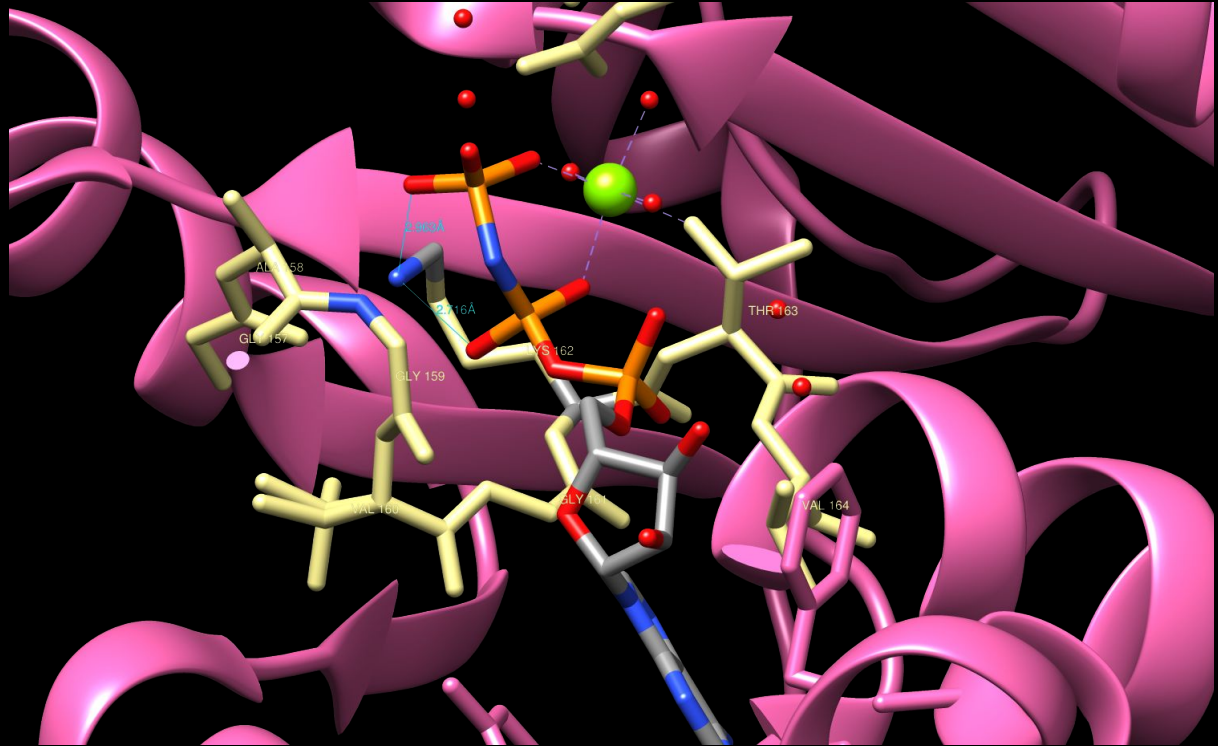
1. N(Gly159)-O3G(ANP) 3,428Å



ATP catalytic site (β TP- α TP)

β (p-loop)

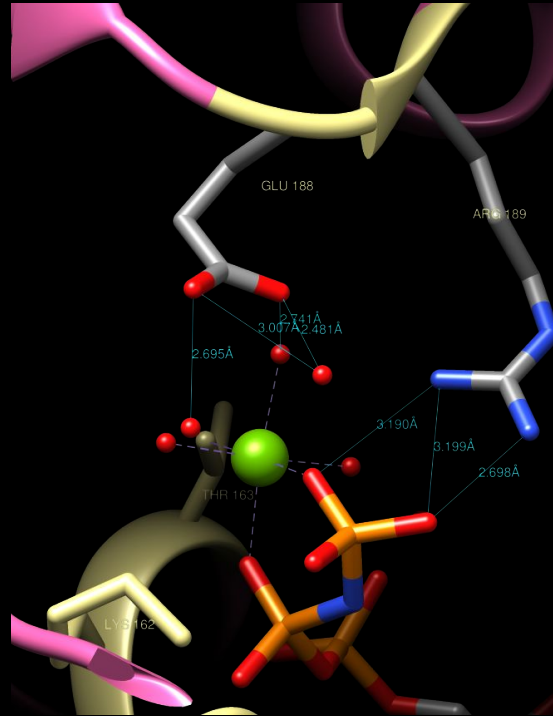
5. N(Lys162)-O3G(ANP) 2,963Å



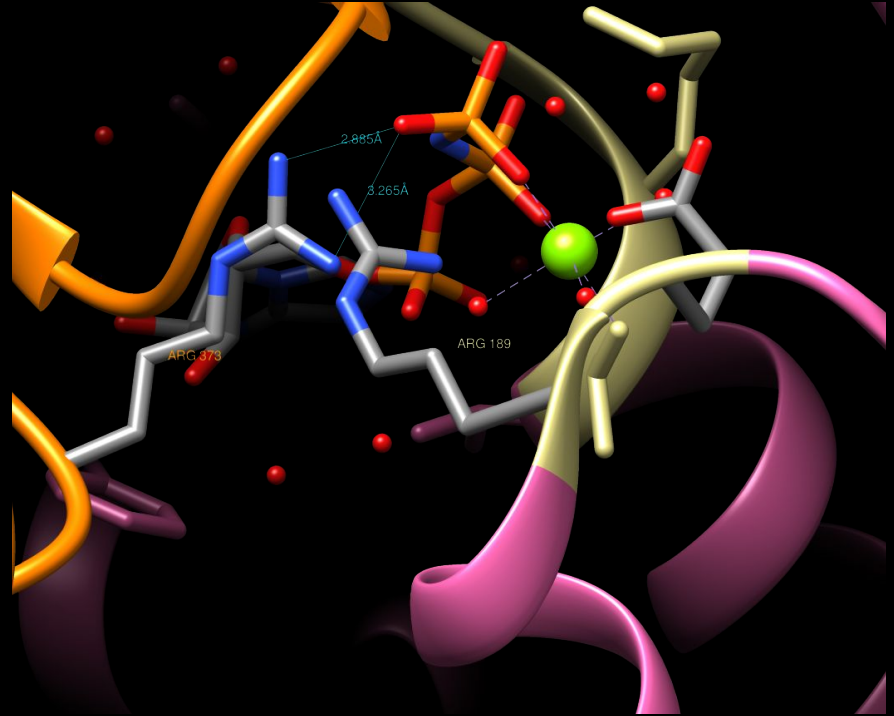
ATP catalytic site (β TP- α TP)

β (catalytic residues)

- 8. O(Glu188)-H₂O
- 9. N(Arg189)-O1G(ANP) 2,698Å
- 10. N(Arg189)-O1G(ANP) 3,199Å
- 11. N(Arg189)-O2G(ANP) 3,190Å



ATP catalytic site (β TP- α TP)

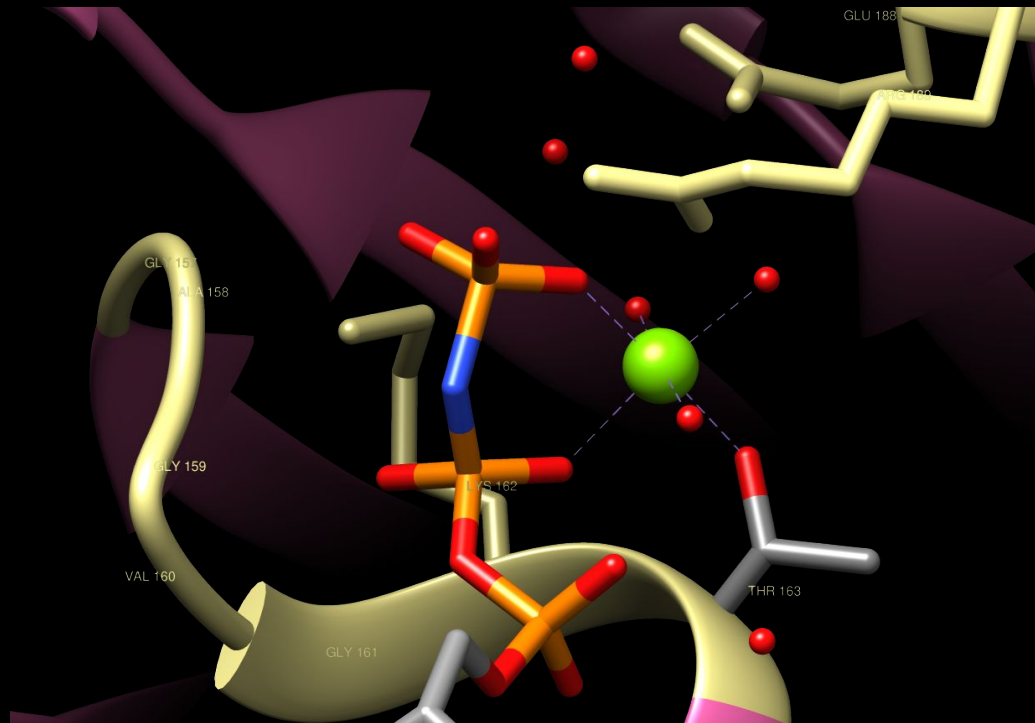


12. N(Arg373)-O1G(ANP) 2,885Å
13. N(Arg373)-O1G(ANP) 3,265Å

ATP catalytic site (β TP- α TP)

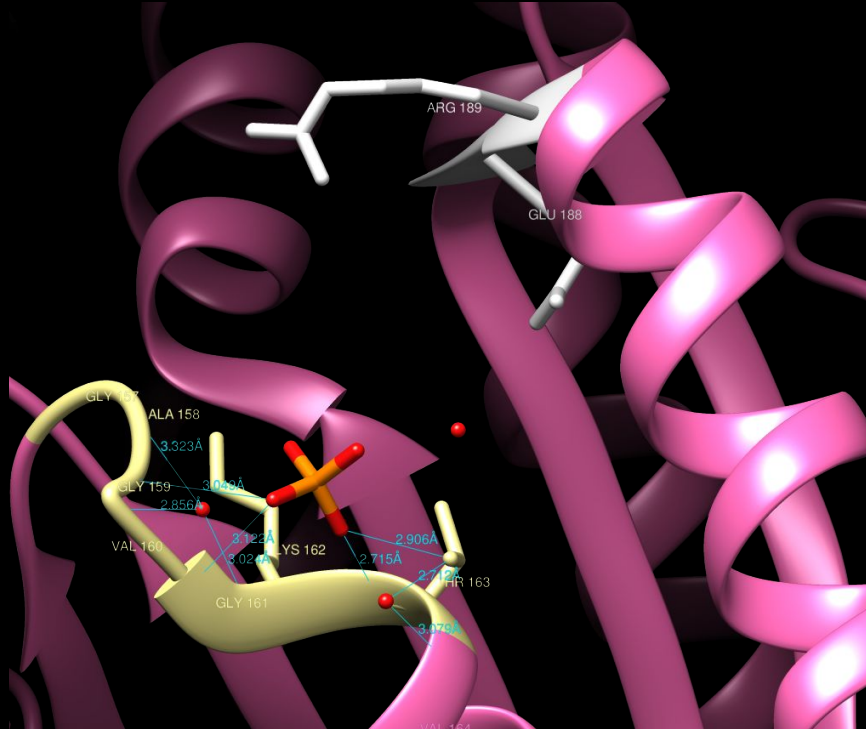
Mg - β

- O2G(PO4)
- OG1(Thr163)
- + H₂O



Catalytic site E (β E- α E)

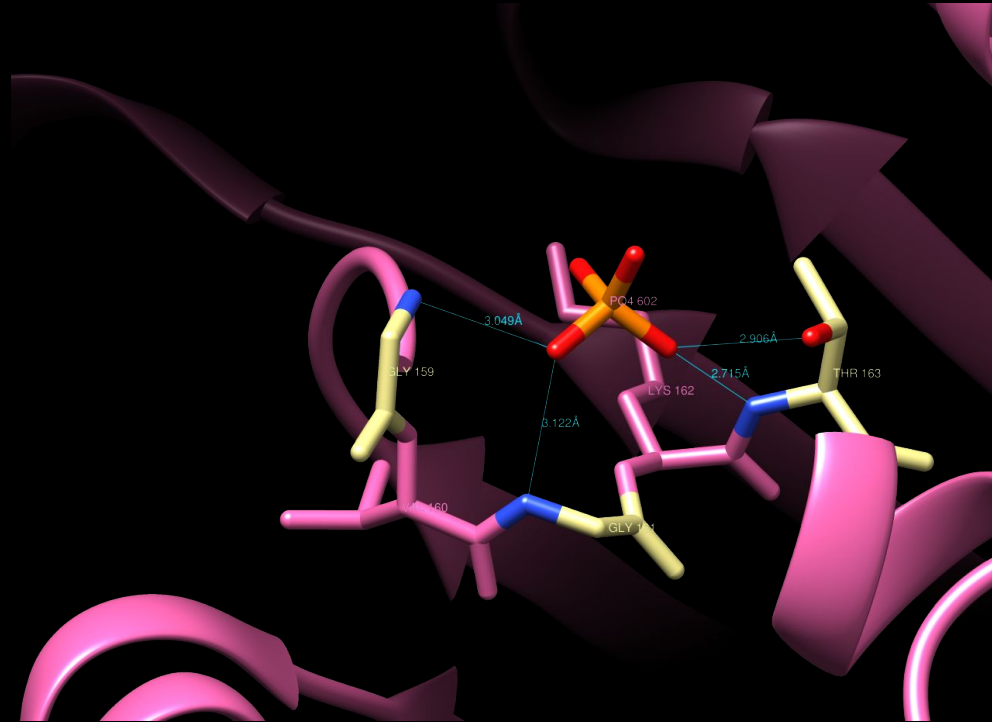
- β
- Gly159
- Gly161
- Lys162
- Thr163



Catalytic site E (β E- α E)

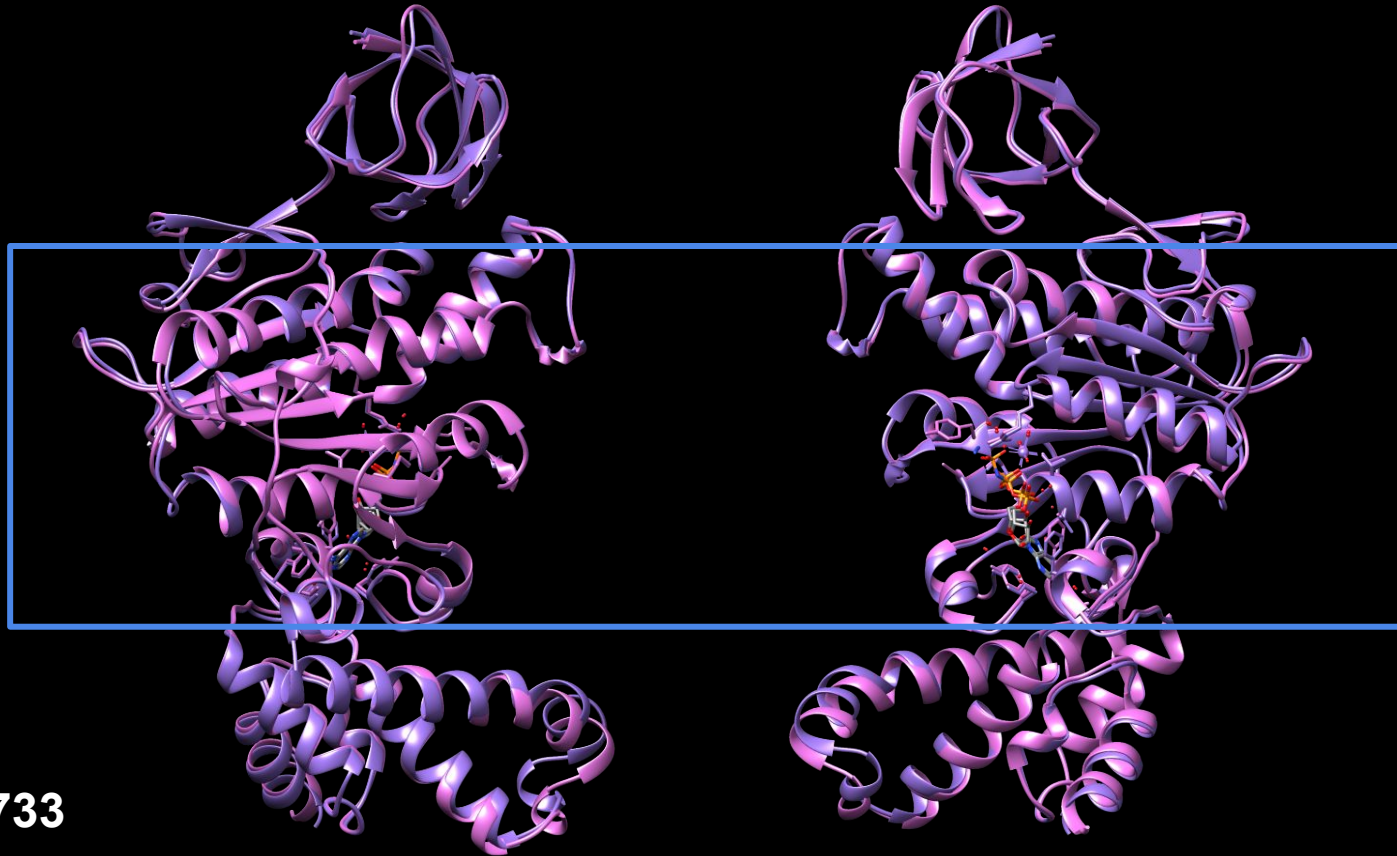
β

1. N(Gly159)-O1(PO4) 3,049Å
2. N(Gly161)-O1(PO4) 3,122Å
3. N(Thr163)-O2(PO4) 2,715Å
4. N(Thr163)-O2(PO4) 2,906Å



**What about chemical energy in
ATP synthesis?**

Superimposition of β DP/ β TP

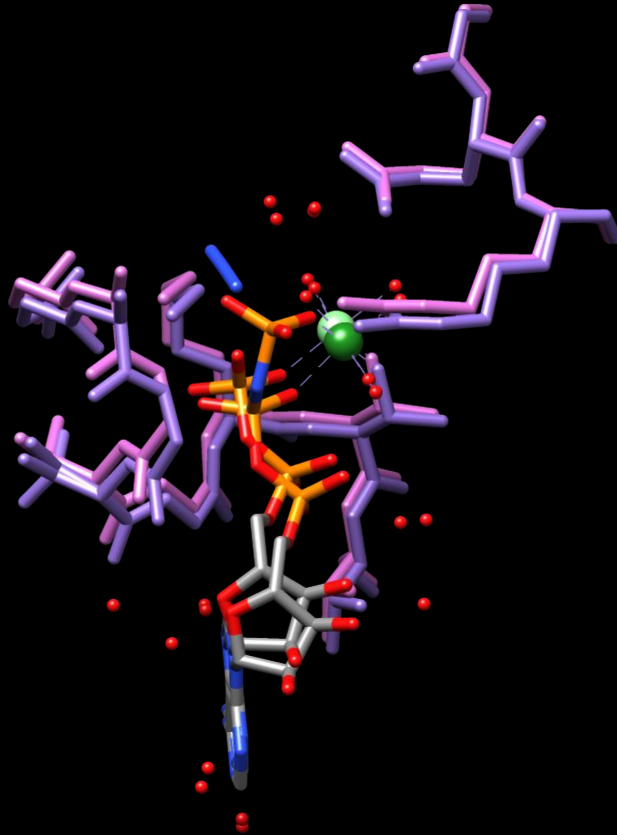


β DP
 β TP

RMSD=0,733

Superimposition of catalytic sites in β DP/ β TTP

β DP
 β TTP



Superimposition of the p-loop

β DP

β TP

DP

1. N(Gly159)-O3B(ADP) 2,884Å
2. N(Gly161)-O1B(ADP) 2,886Å
3. N(Lys162)-O1B(ADP) 2,801Å
4. N(Lys162)-O1B(ADP) 2,775Å
5. N(Lys162)-O3B(ADP) 3,425Å
6. N(Thr163)-O2B(ADP) 3,019Å

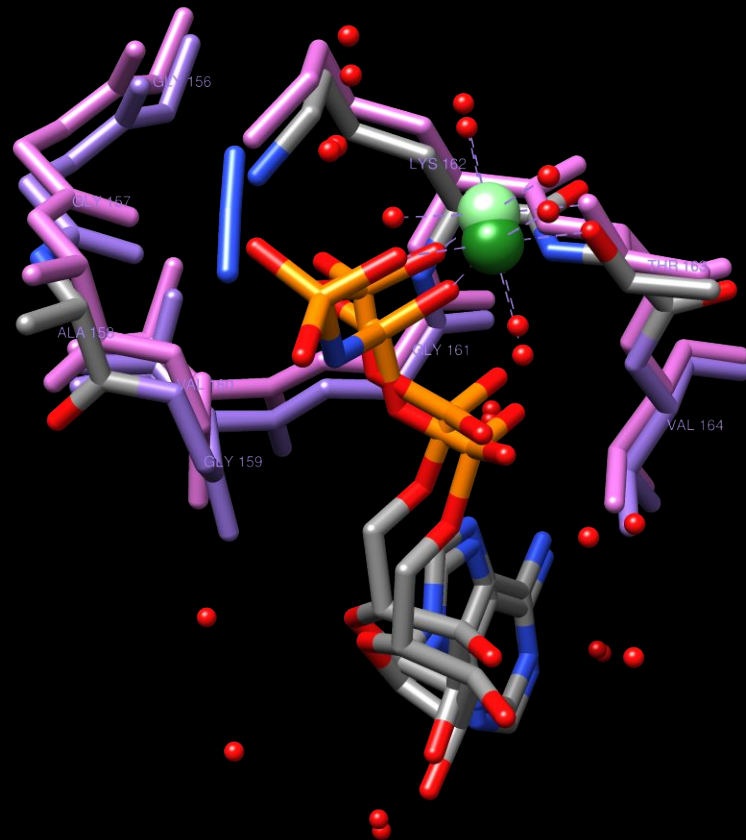
7. N(Val164)-O2A(ADP) 2,859Å

TP

1. N(Gly159)-O3G(ANP) 3,428Å
2. N(Gly161)-O1B(ANP) 3,016Å
3. N(Lys162)-O1B(ANP) 2,915Å
4. N(Lys162)-O1B(ANP) 2,716Å
5. N(Lys162)-O3G(ANP) 2,963Å
6. N(Thr163)-O2B(ANP) 2,900Å

7. N(Val164)-O2A(ANP) 2,600Å

8. N(Arg189)-O1G(ANP) 2,698Å
9. N(Arg189)-O1G(ANP) 3,199Å
10. N(Arg189)-O2G(ANP) 3,190Å

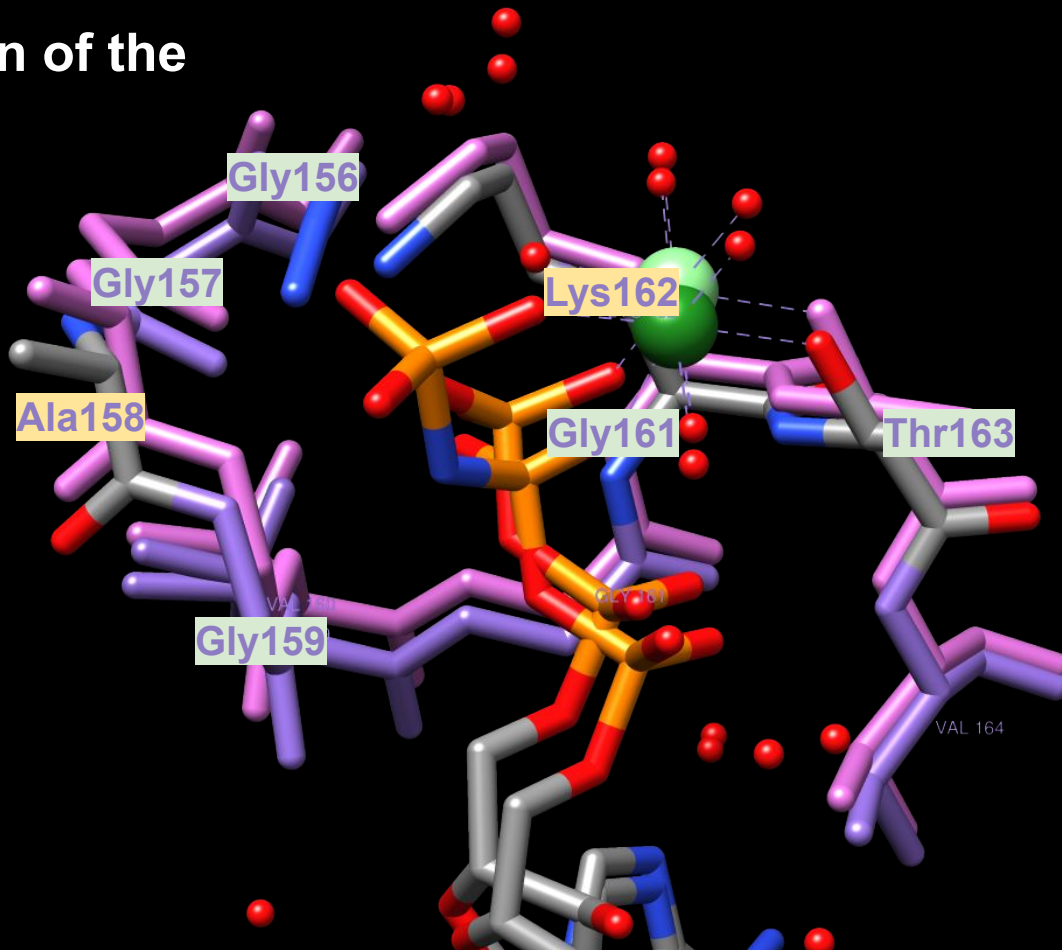


Superimposition of the p-loop

β DP

β TP

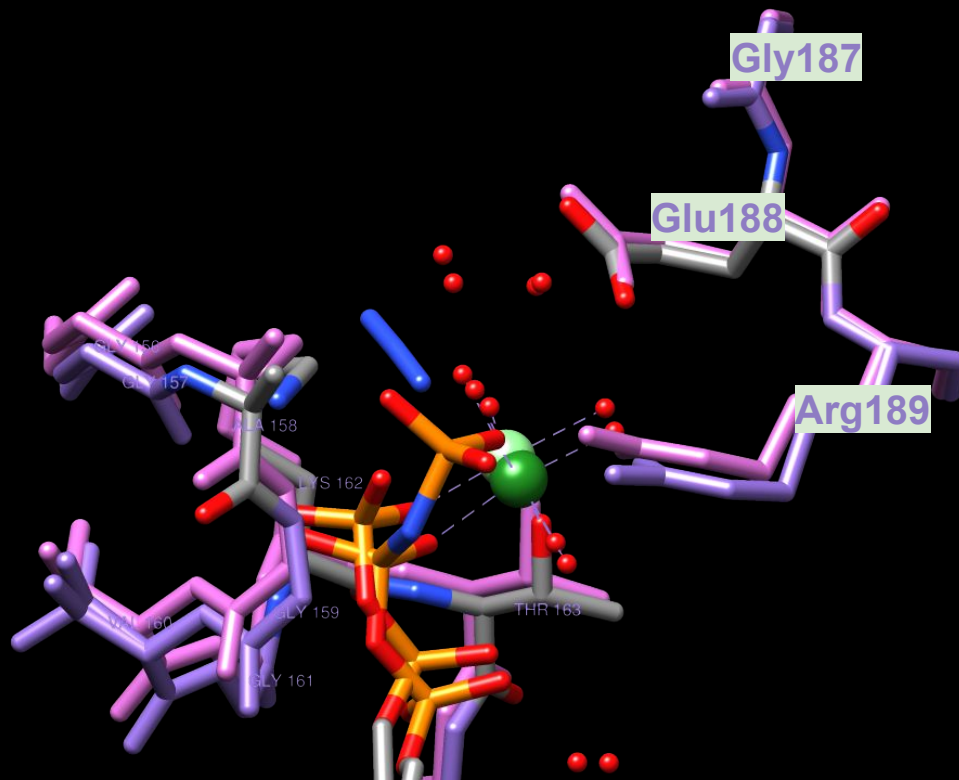
- Glycins
+
- Ala158
- Lys162
- Thr163



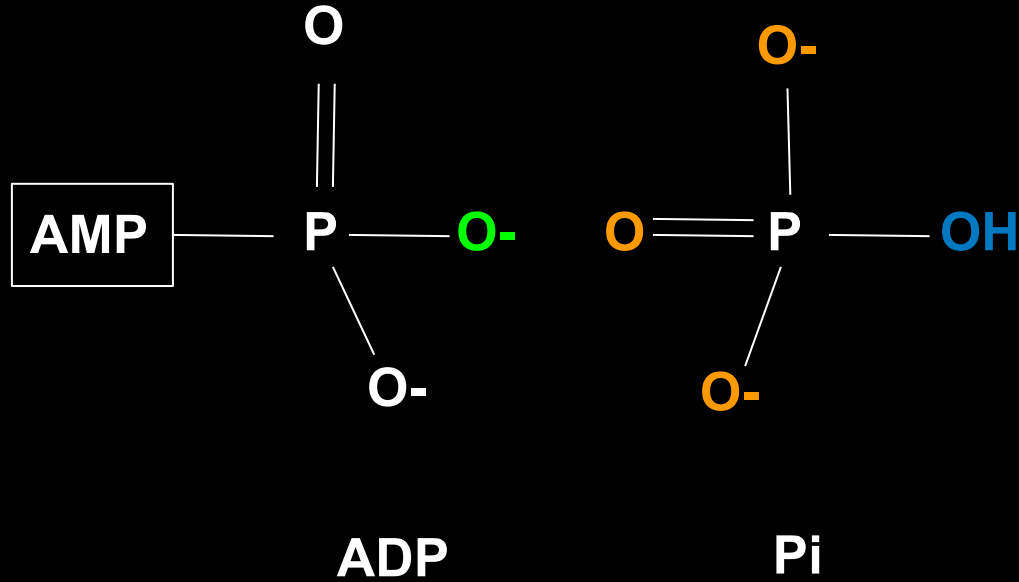
Superimposition of Glu188

β DP

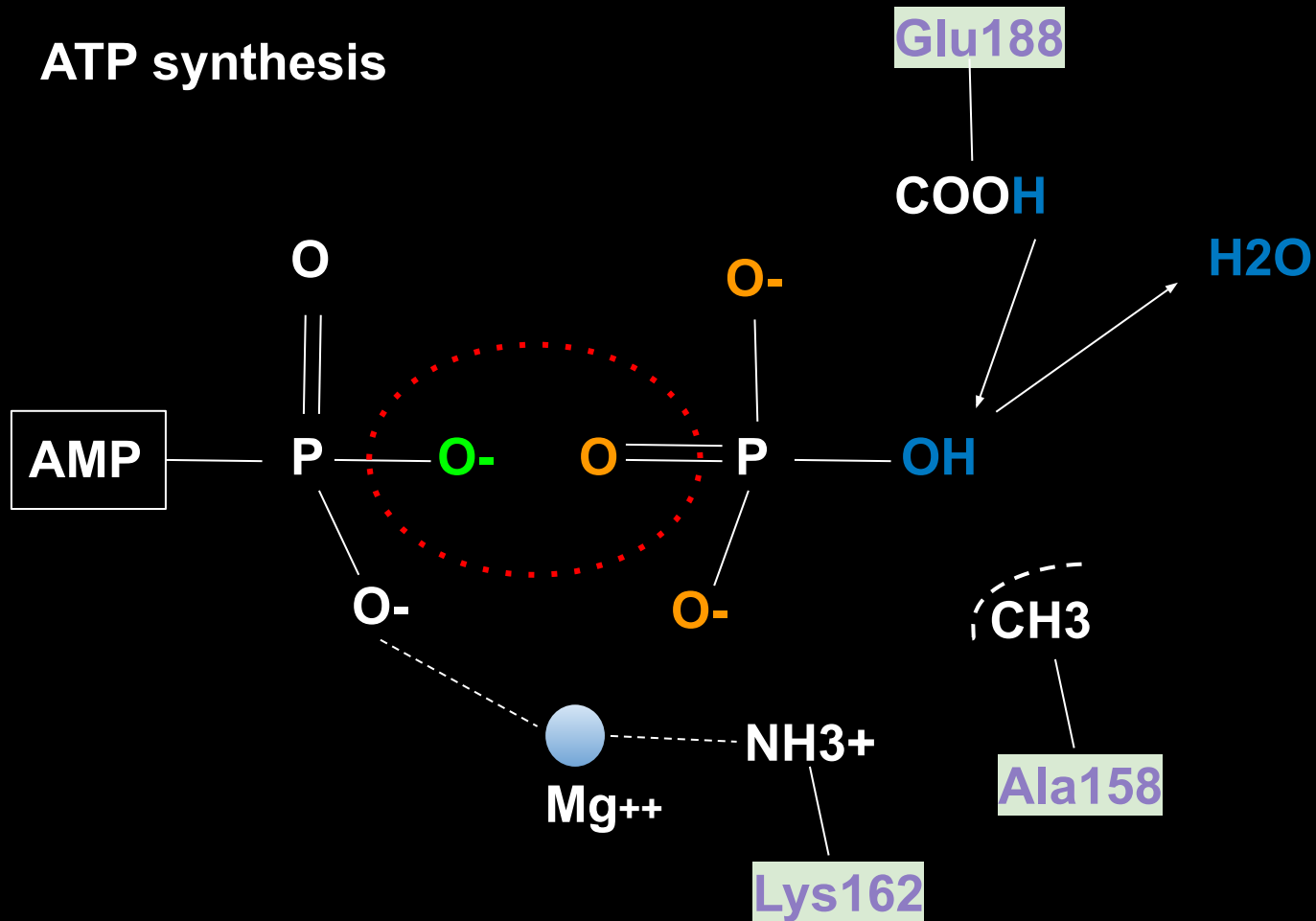
β TTP



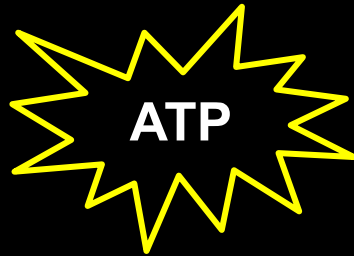
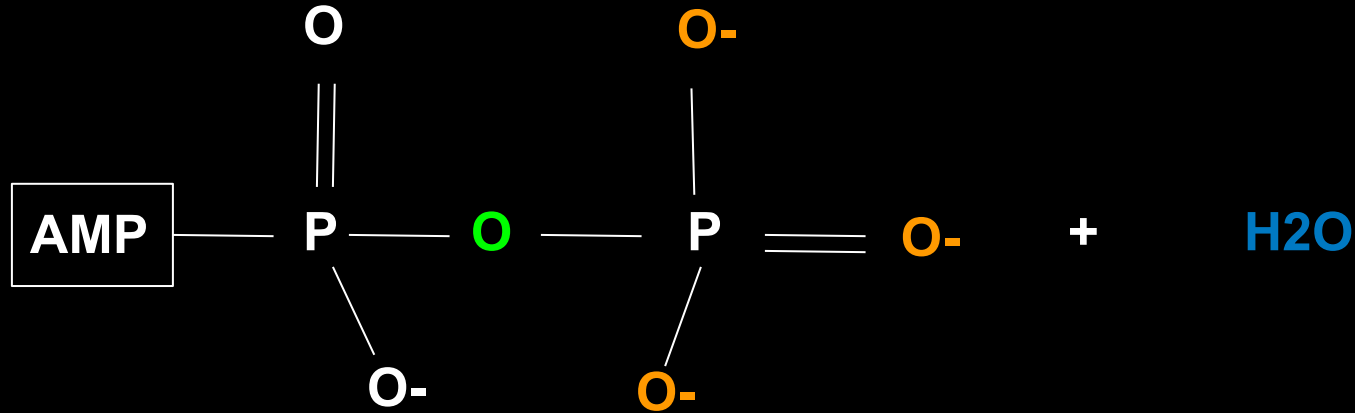
ATP synthesis (substrates)



ATP synthesis



ATP synthesis



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- Gibbons C, Montgomery MG, Leslie AG, Walker JE. The structure of the central stalk in bovine F(1)-ATPase at 2.4 Å resolution. *Nat Struct Biol*. 2000 Nov;7(11):1055-61.
- Mnatsakanyan N, Li Y, Weber J. Identification of two segments of the γ subunit of ATP synthase responsible for the different affinities of the catalytic nucleotide-binding sites. *J Biol Chem*. 2019;294(4):1152–1160.
- Klusch N, Murphy BJ, Mills DJ, Yildiz Ö, Kühlbrandt W. Structural basis of proton translocation and force generation in mitochondrial ATP synthase. *Elife*. 2017;6:1-16.
- Kühlbrandt W. Structure and Mechanisms of F-Type ATP Synthases. *Annu Rev Biochem*. 2019;88(1):515-549.

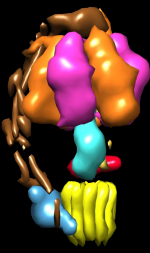
Cross RI, Tab L. Gene duplication as a means for altering H⁺/ATP ratios during the evolution of F₁F₀ ATPases and synthases. Vol. 259. 1990.

Martín-García F, Mendieta-Moreno JI, Marcos-Alcalde Í, Gómez-Puertas P, Mendieta J. Simulation of catalytic water activation in mitochondrial F₁-atpase using a hybrid quantum mechanics/molecular mechanics approach: An alternative role for β-Glu 188. *Biochemistry*. 2013;52(5):959–66.

Walker JE, Saraste M, Runswick MJ, Gay NJ. Distantly related sequences in the a- and f-subunits of ATP synthase, myosin, kinases and other ATP-requiring enzymes and a common nucleotide binding fold. *The EMBO Journal*. 1982.

Zhou A, Rohou A, Schep DG, Bason J V, Montgomery MG, Walker JE, et al. Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM.

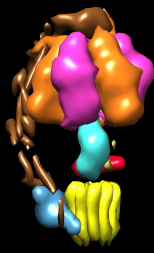
PEM questions



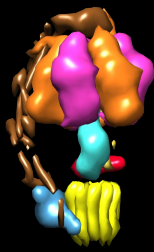
1. ATP synthase:
 - a) Is only present in eukaryotic organisms.
 - b) Is only present in the mitochondria.
 - c) Is only present in *in vivo* conditions.
 - d) Is only present in chloroplasts.
 - e) **Is ubiquitously distributed in all life kingdoms.**

2. Choose the correct answer:
 1. ATP synthase produces three protons from each ATP molecule.
 2. ATP synthase uses physical rotation of its own subunits as a step of catalysis.
 3. The c-ring rotation is generated by catalysis of ATP molecules.
 4. The c-ring rotation is generated by protonation and deprotonation of its conserved glutamates.
 - a) 1, 2 and 3
 - b) 1 and 3
 - c) **2 and 4**
 - d) 4
 - e) 1, 2, 3 and 4

3. The main function of C-ring subunit is:
 - a) Synthesize ATP from ADP and phosphate.
 - b) Hydrolyze ATP to produce ADP and phosphate.
 - c) **Translocate protons to generate physical rotation.**
 - d) Stabilize the "a" subunit across the inner membrane.
 - e) Dimerize ATP synthase between them.



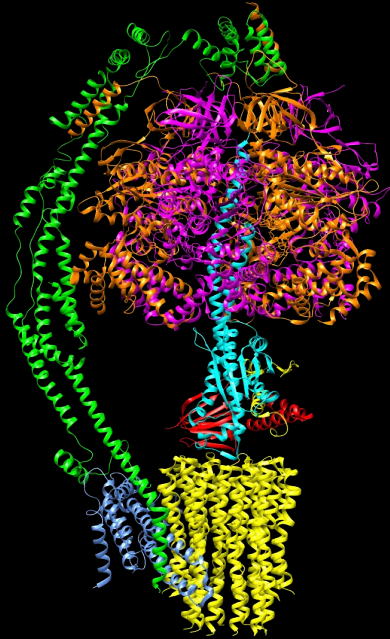
4. Why does beta subunit have catalytic function while alpha doesn't if they share the same conformation?
 - a. Gamma subunit doesn't change alpha conformation
 - b. Alpha subunits contain mutations in the catalytic residues
 - c. Both previous options are correct
 - d. Alpha subunits can't bind ATP
 - e. All options are incorrect
5. Where does ATP synthesis takes place?
 - f. Fo rotor
 - g. Gamma subunit
 - h. Alpha subunit
 - i. Beta and alpha subunit in "open" state
 - j. Beta and alpha subunit in "tight" state
6. Select the correct ones:
 1. ATP synthase can be found in all forms of life
 2. There are more proteins that can transduce a membrane potential directly into biologically useful chemical energy
 3. In vivo, mitochondrial and chloroplast ATP synthase can only act in synthesis mode
 4. In vivo, all ATP synthases are reversible
 - a. 1, 2, 3
 - b. 1, 3
 - c. 2, 4
 - d. 4
 - e. 1, 2, 3, 4



7. Glycins...
 - a. are usually taking part in the nucleotide binding side of a protein.
 - b. are flexible amino acids allowing conformational changes of the protein
 - c. have no side chains
 - d. are the smallest amino acids
 - e. **all**
8. The catalytic head of ATP synthase:
 - a. **have the 3 catalytic sites which are always in a different conformation between each other, but each pass through a cycle of 'open', 'loose' and 'tight' states.**
 - b. consists of an hexamer of three alpha and three beta subunits bounded to delta subunit.
 - c. rotates with the c-ring (rotor).
 - d. is hydrophobic.
 - e. **all**
9. In ATP synthesis...
 - a. **ADP + Pi make a spontaneous reaction at the catalytic site of the F1-ATP synthase.**
 - b. Mg²⁺ make hydrogen bonds with the phosphates of the nucleotide and residues of the catalytic site.
 - c. a and b
 - d. one molecules of ATP is catalyzed within a turn of 360° of the c-ring.
 - e. **all**
10. ATP synthase:
 - a. is a multisubunit assembly that consists of a globular domain F1 and an intrinsic membrane domain Fo linked by the central stalk and the peripheral stalk.
 - b. makes 3 ATP in one rotor movement of 360° of the c-ring.
 - c. the affinity changes of the catalytic sites are determined by the changes in conformation.
 - d. gamma subunit couples the rotation movement to conformational changes in the catalytic domain.
 - e. **all.**

Thank you for your attention

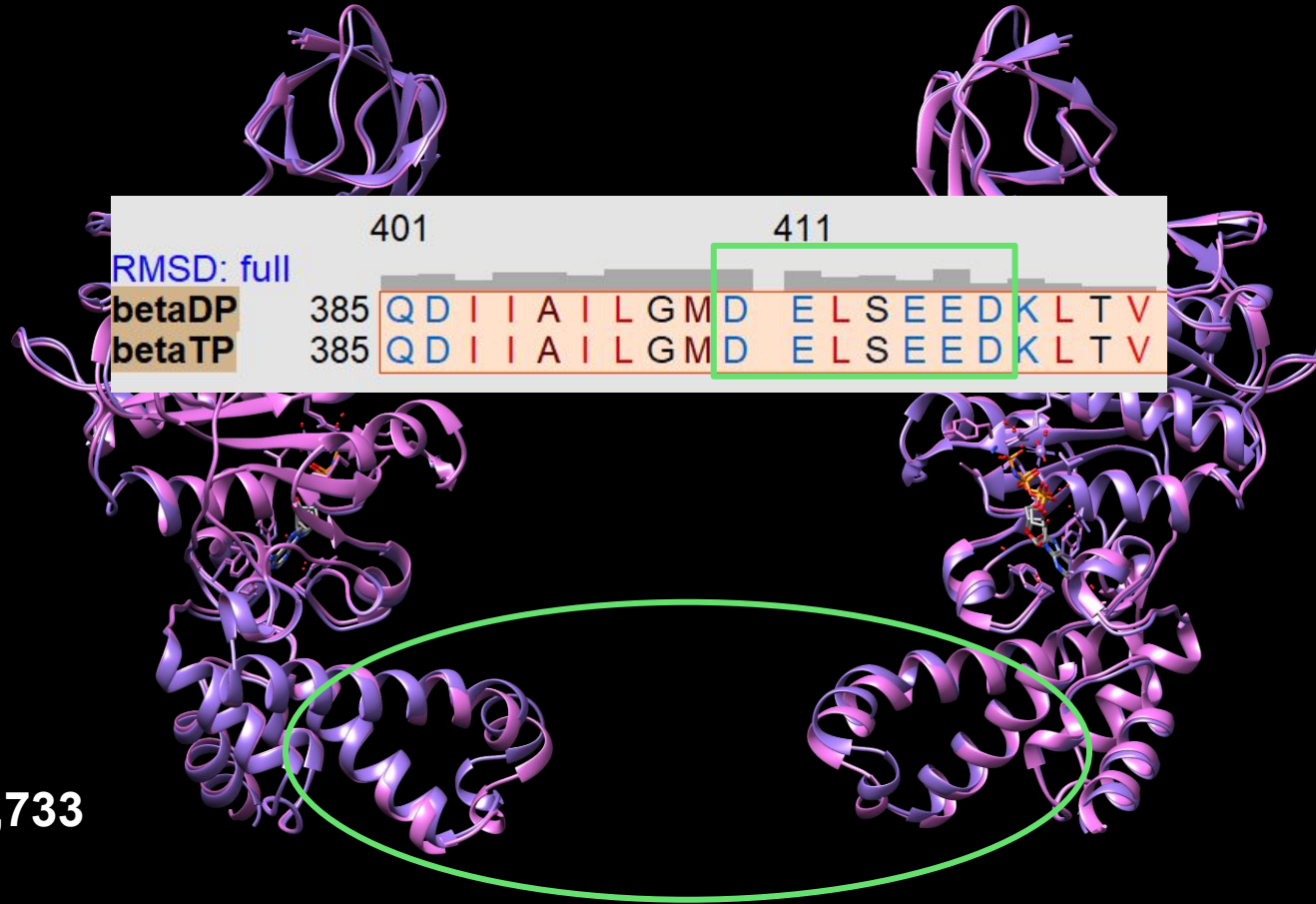
**WHAT A NICE
MACHINERY!!!**



**HOORAY! WE
OBTAINED ATP!!**

EXTRA

What makes the difference?



RMSD=0,733

Ligand interactions

- Nucleotide-binding residues

α	β
Ser372	Gly159
Arg373	Val160
p-loop	Gly161
	Lys162
	Thr163
	Val164
	Glu188
	Arg189

- Mg-binding

β DP	β TP
OG1(Thr163)	O2B(ANP)
O2B(ADP)	O2G(ANP)
O(H ₂ O)	O(H ₂ O)
O(H ₂ O)	O(H ₂ O)

Ligand interactions

- Nucleotide-binding residues

α	β	
Ser372	Gly159	→ β DP, β TP
Arg373	Val160	
p-loop	Gly161	→ β E, β DP, β TP
	Lys162	→ β DP, β TP
	Thr163	→ β E, β DP, β TP
	Val164	→ β DP, β TP
	Glu188	→ β DP, β TP
	Arg189	→ β TP

Comparison between β E- β DP- β TP

E

1. N(Gly159)-O1(PO4) 3,049Å
2. N(Gly161)-O1(PO4) 3,122Å
3. N(Thr163)-O2(PO4) 2,715Å
4. N(Thr163)-O2(PO4) 2,906Å

DP

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2. N(Gly161)-O1B(ADP) 2,886Å
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p-chain

8. O(Ser372)-O2(ADP) 2,971Å
9. O(Ser372)-O3(ADP) 3,463Å
10. N(Arg373)-O1A(ADP) 2,990Å
11. N(Arg373)-O3B(ADP) 2,702Å

TP

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3. N(Lys162)-O1B(ANP) 2,915Å
4. N(Lys162)-O1B(ANP) 2,716Å
5. N(Lys162)-O3G(ANP) 2,963Å
6. N(Thr163)-O2B(ANP) 2,900Å
7. N(Val164)-O2A(ANP) 2,600Å
8. N(Arg189)-O1G(ANP) 2,698Å
9. N(Arg189)-O1G(ANP) 3,199Å
10. N(Arg189)-O2G(ANP) 3,190Å

p-chain

11. N(Arg373)-O1G(ANP) 2,885Å
12. N(Arg373)-O1G(ANP) 3,265Å

S. cerevisiae c-ring monomer

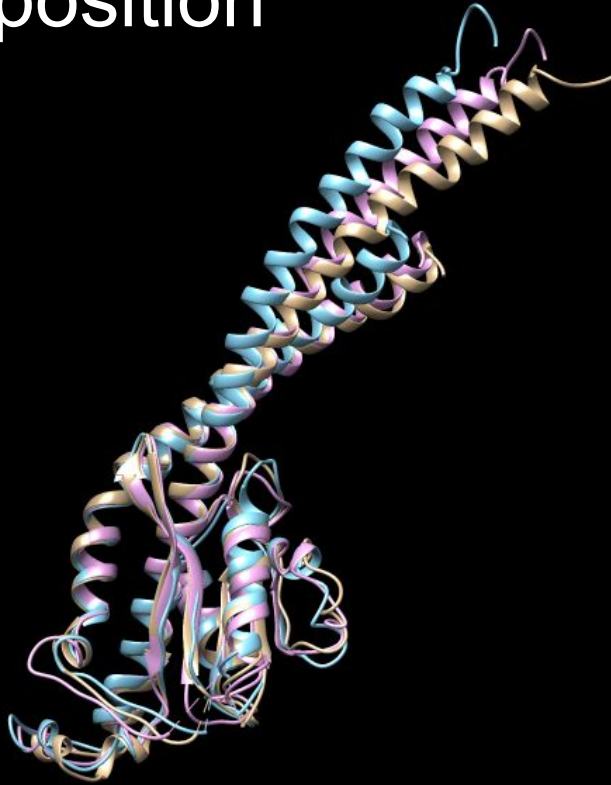
	1	11	21	31	41
Consensus	MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
Conservation					
chain K	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain L	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain M	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain N	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain O	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain P	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain Q	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain R	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain S	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
chain T	1 MQLVLA AKYI	GAGISTIGLL	GAGIGIAIVF	AALINGVSRN	PSIKDTV FPM
	51	61	71	81	91
Consensus	A ILGFAL SEA	TGLFCLMV SF	LLLF		
Conservation					
chain K	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain L	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain M	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain N	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain O	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain P	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain Q	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain R	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain S	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		
chain T	51 A ILGFAL SEA	TGLFCLMV SF	LLLF		

SCOP

	SUBUNIT C
Class	All alpha proteins
Fold	Transmembrane helix hairpin
Superfamily	F1F0 ATP synthase subunit C
Family	F1F0 ATP synthase subunit C

	SUBUNIT A
Class	All alpha proteins
Fold	F1F0 ATP synthase subunit A
Superfamily	F1F0 ATP synthase subunit A
Family	F1F0 ATP synthase subunit A

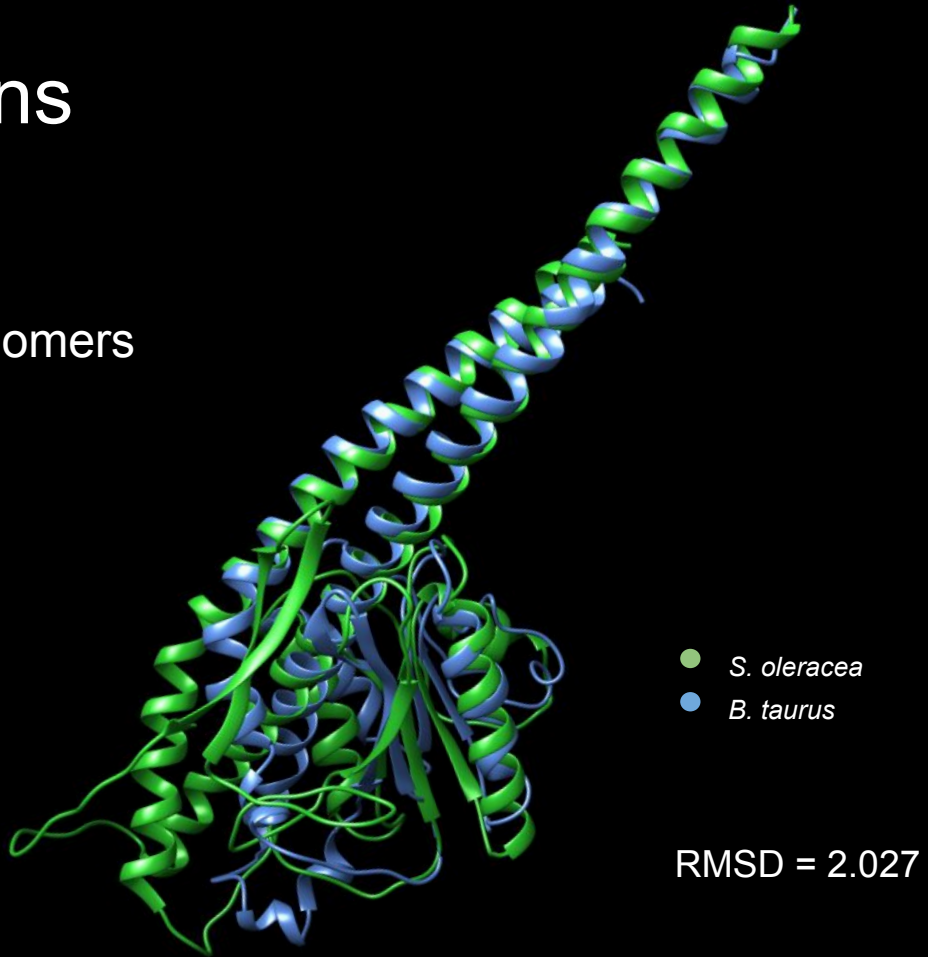
γ states superimposition



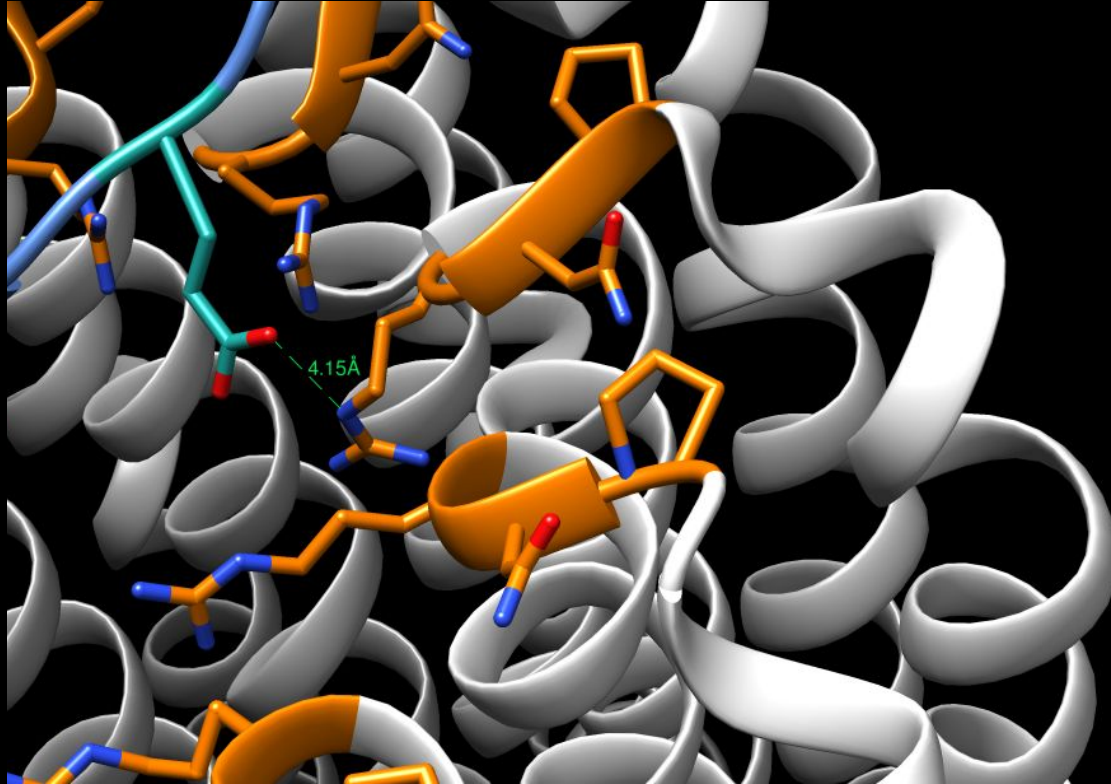
RMSD = 1.613

c-ring - γ interactions

Different number of c-ring monomers
could be the reason why?



c-ring - γ interactions



ARG 39.T NE <-> GLU 198.G OE1: 4.15

	271		281
Consensus	edeafslsty		dgkltverdm
Conservation			
Bos taurus	--SAESMSIY	D	-----
Homo sapiens	--SADSMSIY	D	-----
Saccharomyces cerevisiae	--QSPSFGKF	E	I-----
Polytomella sp.	DVTGNSLDAY	D	I-----
Pisum sativum	EDELFRLLTK	E	GKLTVERDV
Spinacia oleracea	EDELFRLLTK	E	GKLTVERDM
Trichormus variabilis	DDEIFRLTTR	G	QFEVERQT
Escherichia coli	DDDLKHKSW	D	-----
Paracoccus denitrificans	EGEAGASSLY	D	-----

c-ring

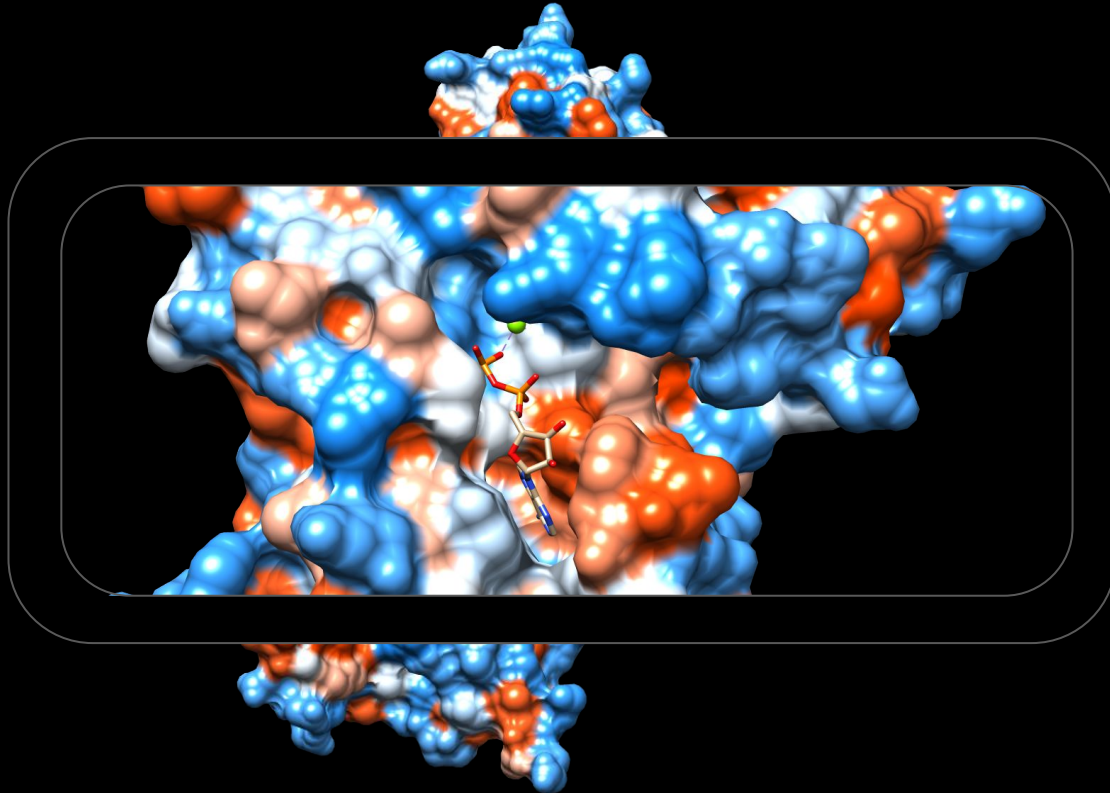
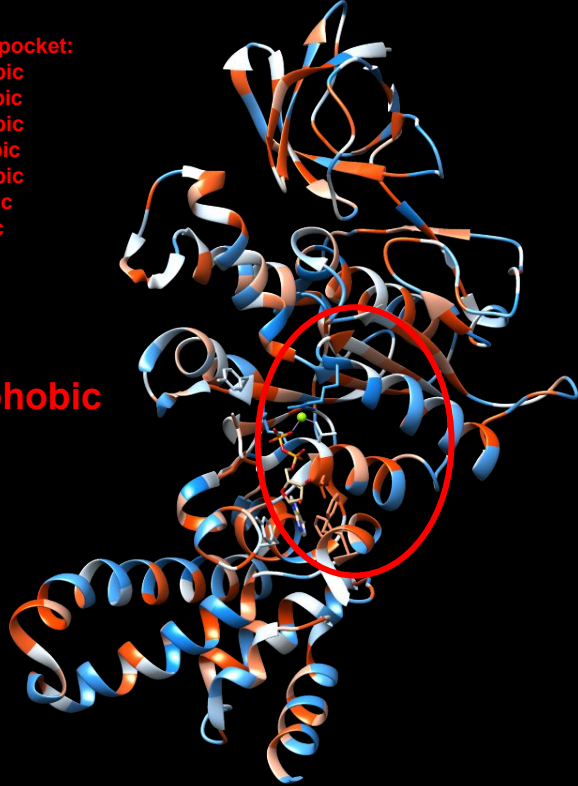
Consensus	R n P
Conservation	
Spinacia oleracea	R Q P
Pisum sativum	R Q P
Trichormus variabilis	R Q P
Homo sapiens	R N P
Bos taurus	R N P
Saccharomyces cerevisiae	R N P
Polytomella sp.	R N P
Paracoccus denitrificans	R N P
Escherichia coli	R Q P

β -subunit hydrophobicity

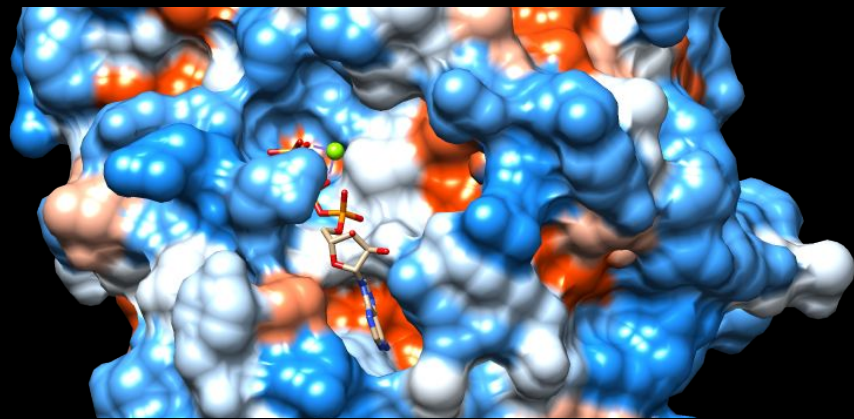
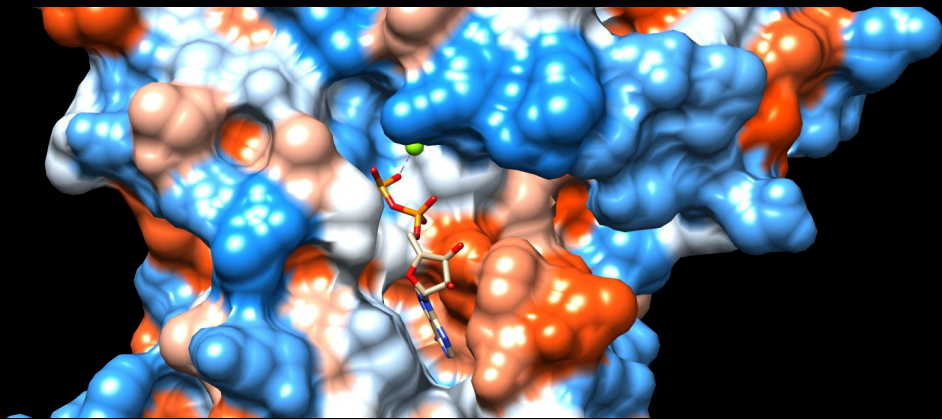
hydrophobic pocket:

G: Hydrophobic
A: Hydrophobic
G: Hydrophobic
V: Hydrophobic
G: Hydrophobic
K: Amphipathic
T: Hydrophilic

hydrophobic
pocket

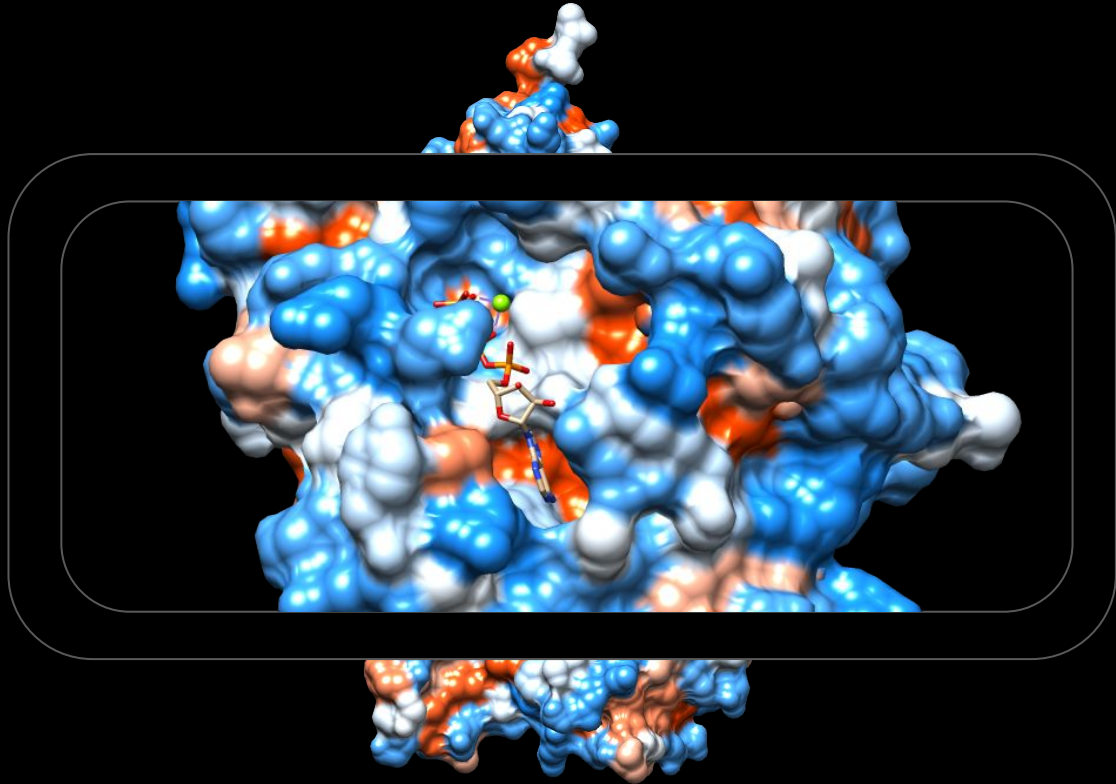
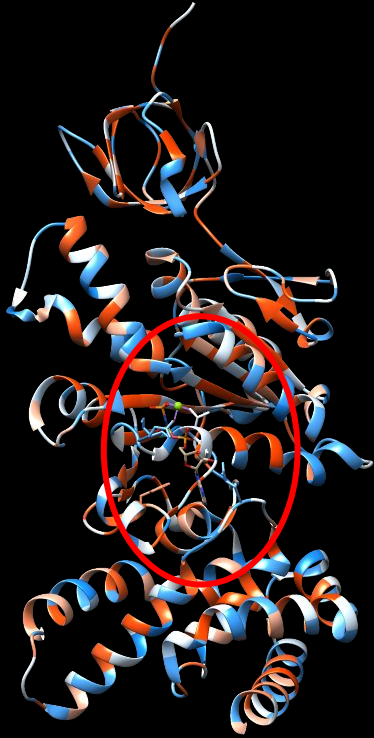


α,β -subunit hydrophobicity



α -subunit hydrophobicity

hydrophobic
pocket

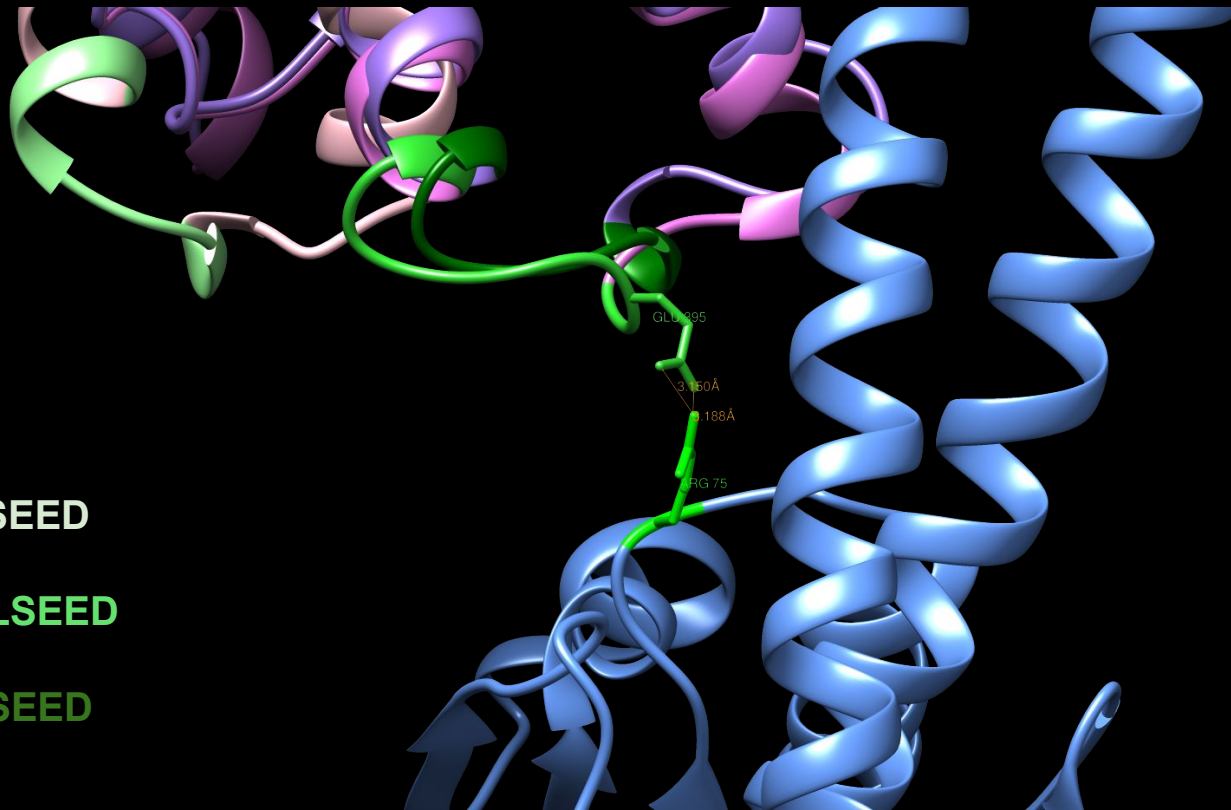


Superimposition of **DELSEED** regions

β E
 β DP
 β TP



Superimposition of DELSEED regions



βE → DELSEED
 βDP → DELSEED
 βTP → DELSEED

Catalytic sites

β TP

β E

β DP

β E

β DP

β TP

