



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 10, 2017 – 01:18 PM EDT

PDB ID : 4XD7  
Title : Structure of thermophilic F1-ATPase inhibited by epsilon subunit  
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Deposited on : 2014-12-19  
Resolution : 3.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029077  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029077

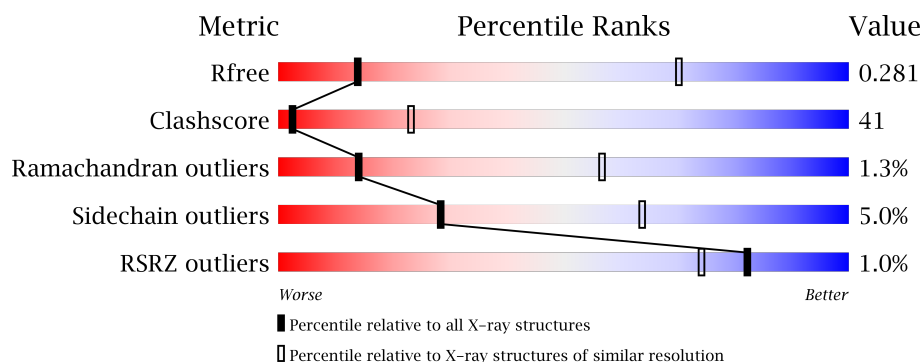
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	1007 (4.20-3.60)
Clashscore	112137	1103 (4.20-3.60)
Ramachandran outliers	110173	1062 (4.20-3.60)
Sidechain outliers	110143	1053 (4.20-3.60)
RSRZ outliers	101464	1020 (4.20-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	502	
1	B	502	
1	C	502	
2	D	483	
2	E	483	

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Mol	Chain	Length	Quality of chain
2	F	483	
3	G	285	
4	H	133	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SO4	A	700	-	-	X	X
5	SO4	E	700	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22656 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	Se	0	0	0
			3462	2189	606	658	9			
1	B	423	Total	C	N	O	Se	0	0	0
			2833	1786	484	554	9			
1	C	475	Total	C	N	O	Se	1	0	0
			3329	2109	577	634	9			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	193	SER	CYS	conflict	UNP Q5KUJ1
A	254	LYS	GLN	conflict	UNP Q5KUJ1
A	463	PHE	TRP	conflict	UNP Q5KUJ1
B	193	SER	CYS	conflict	UNP Q5KUJ1
B	254	LYS	GLN	conflict	UNP Q5KUJ1
B	463	PHE	TRP	conflict	UNP Q5KUJ1
C	193	SER	CYS	conflict	UNP Q5KUJ1
C	254	LYS	GLN	conflict	UNP Q5KUJ1
C	463	PHE	TRP	conflict	UNP Q5KUJ1

- Molecule 2 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	470	Total	C	N	O	Se	1	0	0
			3480	2199	599	669	13			
2	E	469	Total	C	N	O	Se	0	0	0
			3484	2198	598	676	12			
2	F	464	Total	C	N	O	Se	4	0	0
			3334	2097	580	644	13			

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	MSE	-	initiating methionine	UNP Q5KUJ3
D	-8	HIS	-	expression tag	UNP Q5KUJ3
D	-7	HIS	-	expression tag	UNP Q5KUJ3
D	-6	HIS	-	expression tag	UNP Q5KUJ3
D	-5	HIS	-	expression tag	UNP Q5KUJ3
D	-4	HIS	-	expression tag	UNP Q5KUJ3
D	-3	HIS	-	expression tag	UNP Q5KUJ3
D	-2	HIS	-	expression tag	UNP Q5KUJ3
D	-1	HIS	-	expression tag	UNP Q5KUJ3
D	0	HIS	-	expression tag	UNP Q5KUJ3
D	1	HIS	-	expression tag	UNP Q5KUJ3
E	-9	MSE	-	initiating methionine	UNP Q5KUJ3
E	-8	HIS	-	expression tag	UNP Q5KUJ3
E	-7	HIS	-	expression tag	UNP Q5KUJ3
E	-6	HIS	-	expression tag	UNP Q5KUJ3
E	-5	HIS	-	expression tag	UNP Q5KUJ3
E	-4	HIS	-	expression tag	UNP Q5KUJ3
E	-3	HIS	-	expression tag	UNP Q5KUJ3
E	-2	HIS	-	expression tag	UNP Q5KUJ3
E	-1	HIS	-	expression tag	UNP Q5KUJ3
E	0	HIS	-	expression tag	UNP Q5KUJ3
E	1	HIS	-	expression tag	UNP Q5KUJ3
F	-9	MSE	-	initiating methionine	UNP Q5KUJ3
F	-8	HIS	-	expression tag	UNP Q5KUJ3
F	-7	HIS	-	expression tag	UNP Q5KUJ3
F	-6	HIS	-	expression tag	UNP Q5KUJ3
F	-5	HIS	-	expression tag	UNP Q5KUJ3
F	-4	HIS	-	expression tag	UNP Q5KUJ3
F	-3	HIS	-	expression tag	UNP Q5KUJ3
F	-2	HIS	-	expression tag	UNP Q5KUJ3
F	-1	HIS	-	expression tag	UNP Q5KUJ3
F	0	HIS	-	expression tag	UNP Q5KUJ3
F	1	HIS	-	expression tag	UNP Q5KUJ3

- Molecule 3 is a protein called ATP synthase gamma chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	G	254	Total	C	N	O	S	Se	0	0	0
			1797	1142	308	339	1	7			

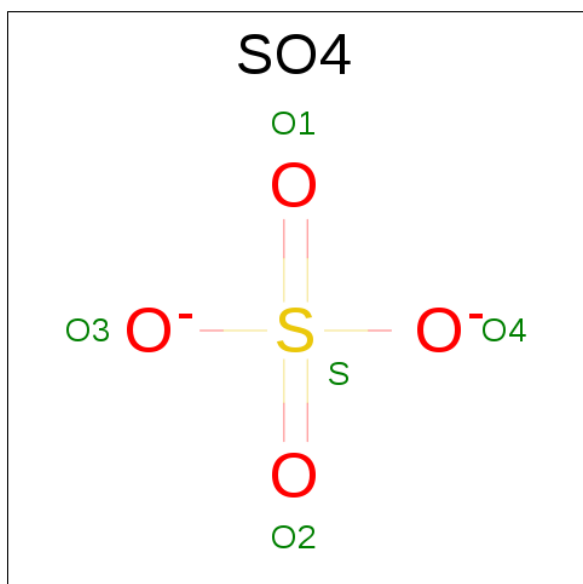
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	109	CYS	SER	conflict	UNP Q5KUJ2

- Molecule 4 is a protein called ATP synthase epsilon chain.

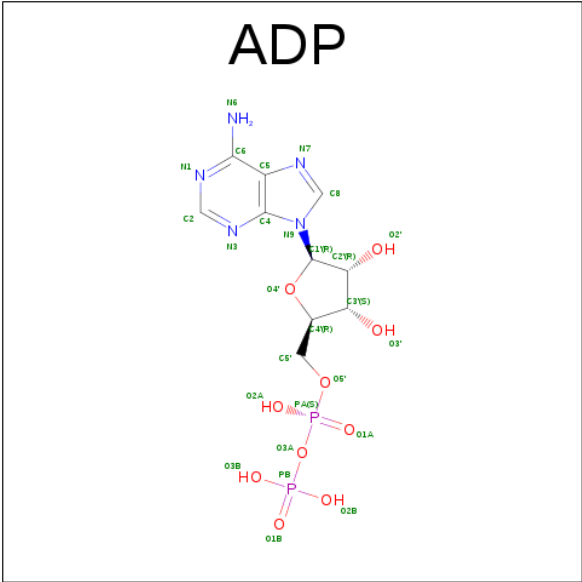
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	129	Total	C	N	O	Se	0	0	0
			890	563	148	175	4			

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).

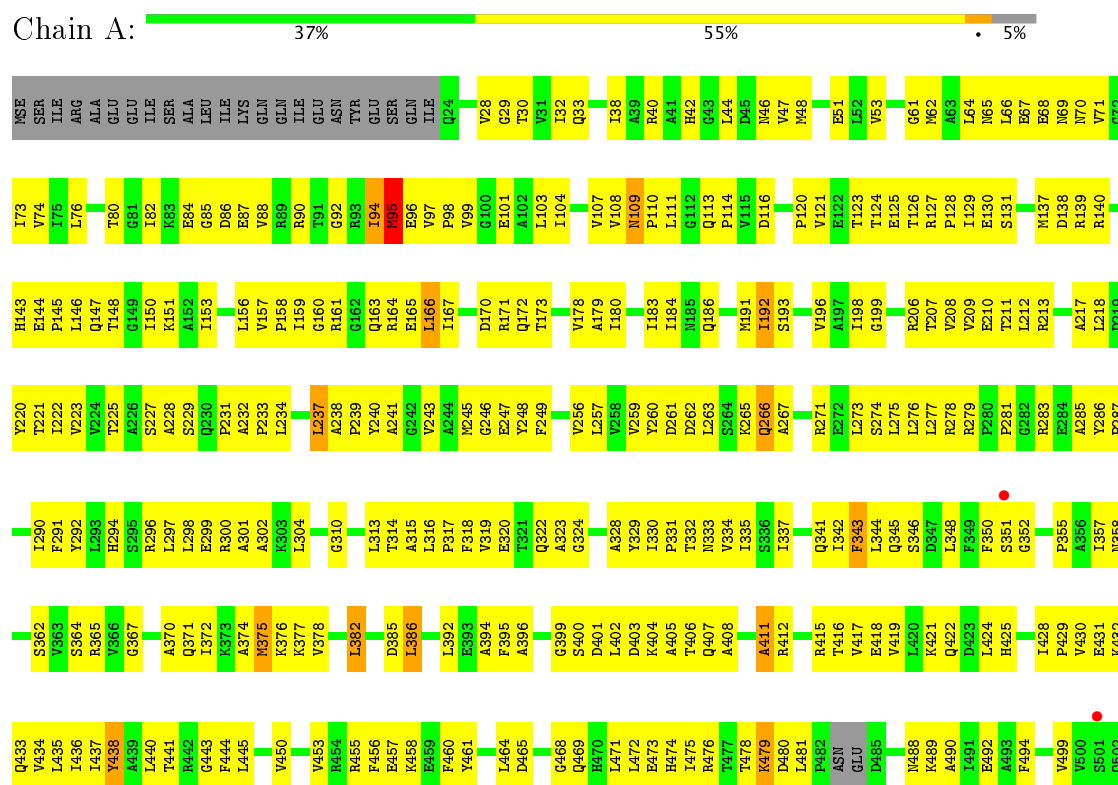


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

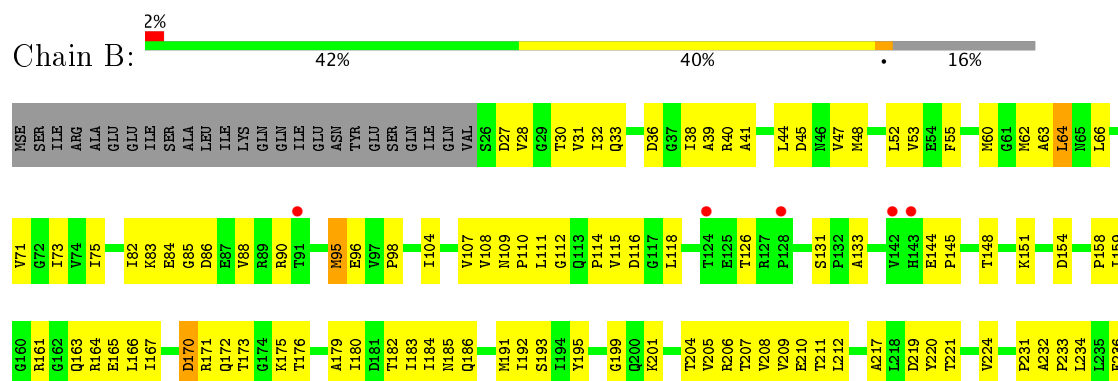
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

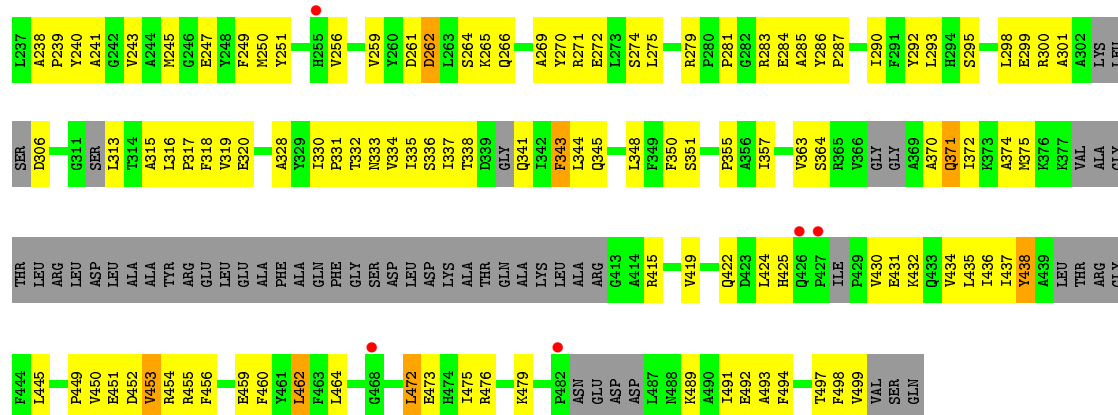
#### • Molecule 1: ATP synthase subunit alpha



#### • Molecule 1: ATP synthase subunit alpha

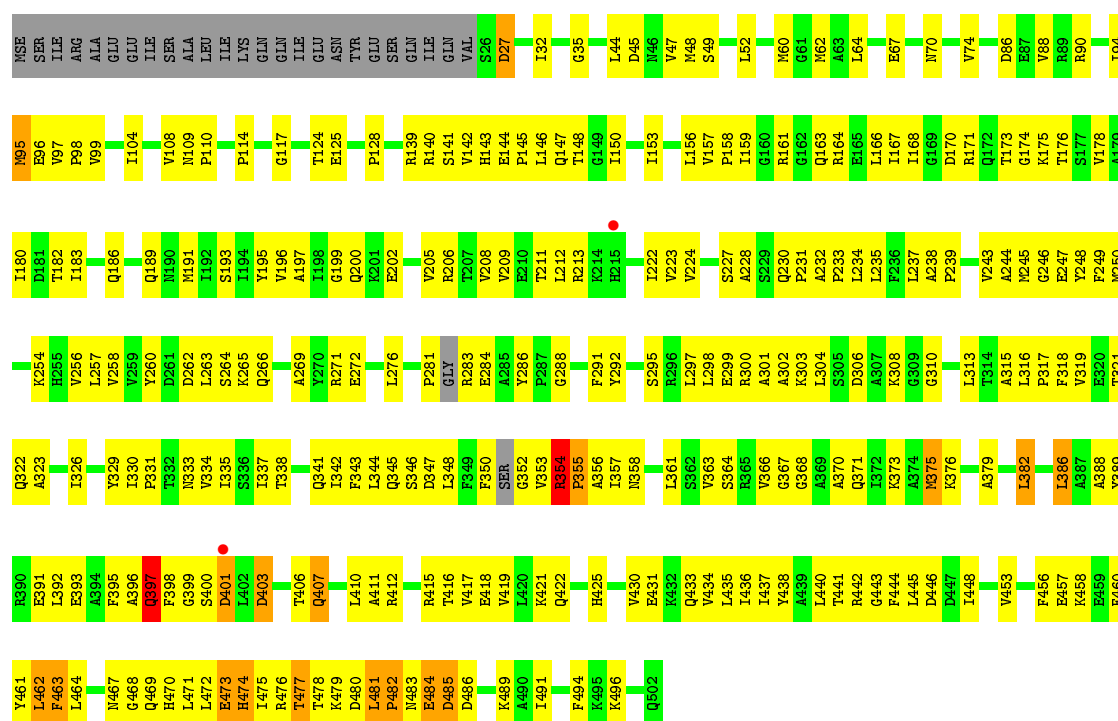






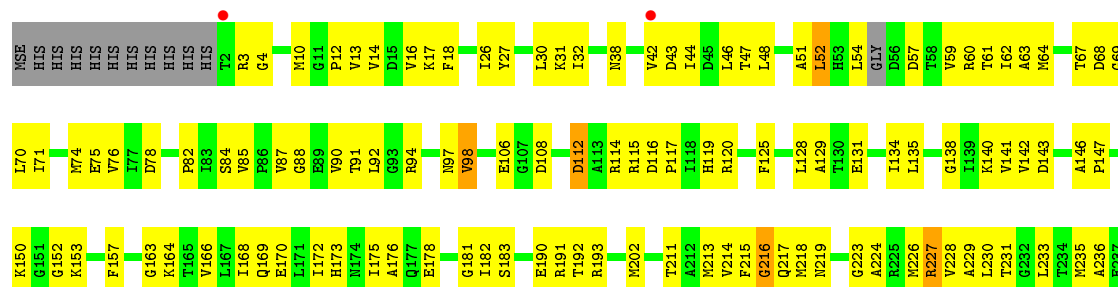
• Molecule 1: ATP synthase subunit alpha

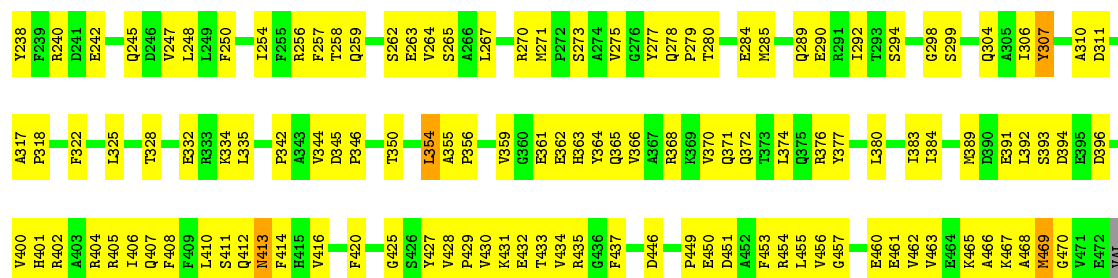
Chain C: 43% 48% 5%



• Molecule 2: ATP synthase subunit beta

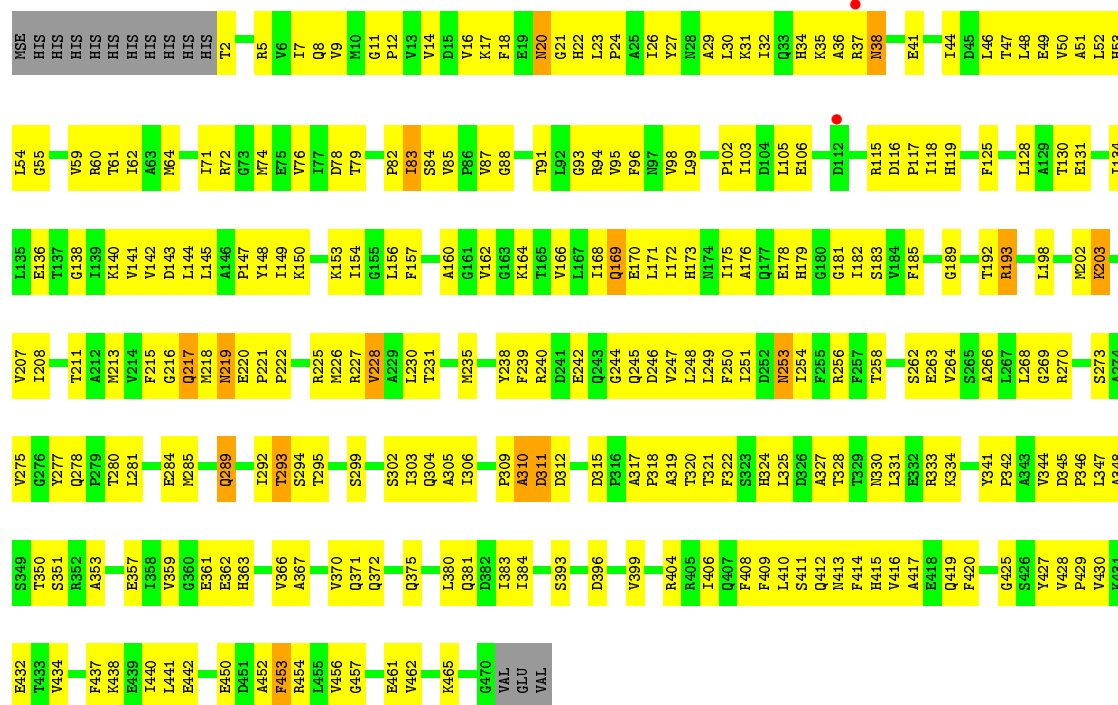
Chain D: 48% 47%





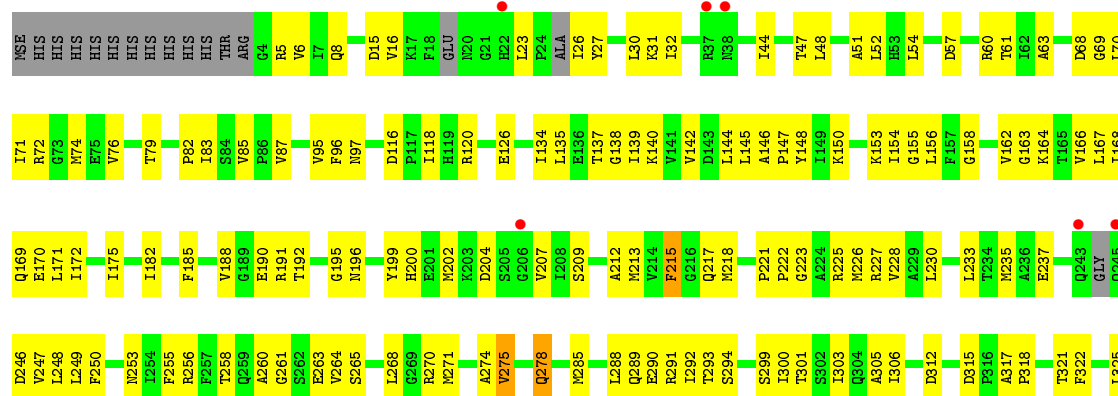
• Molecule 2: ATP synthase subunit beta

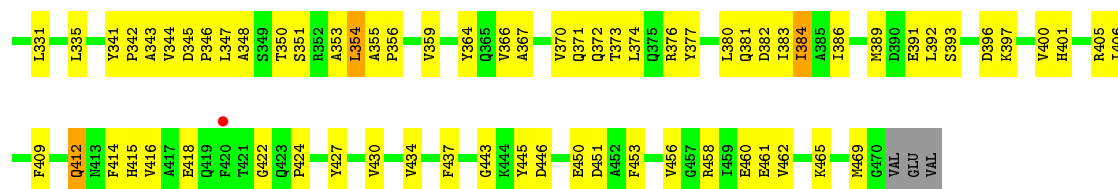
Chain E: 43% 51%



• Molecule 2: ATP synthase subunit beta

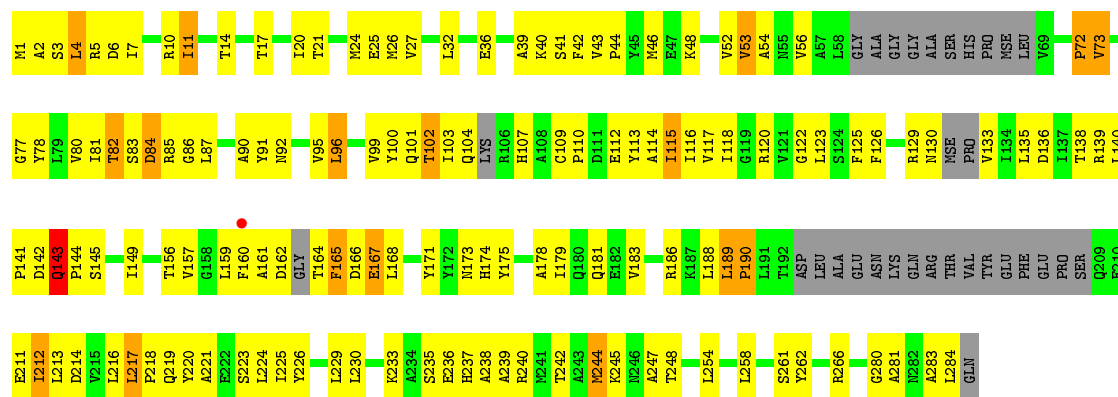
Chain F: 53% 42%





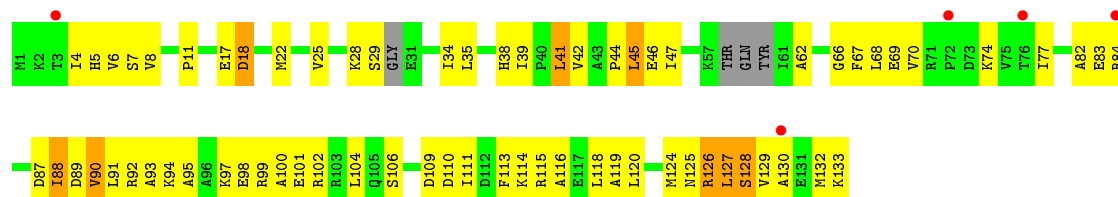
• Molecule 3: ATP synthase gamma chain

Chain G: 39% 44% 6% 11%



• Molecule 4: ATP synthase epsilon chain

Chain H: 4% 45% 46% 6%



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	233.40 Å   233.40 Å   303.96 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	19.99 – 3.90 19.99 – 3.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (19.99-3.90) 99.7 (19.99-3.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 3.71 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.250 , 0.282 0.244 , 0.281	Depositor DCC
$R_{free}$ test set	1910 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	123.5	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 86.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	22656	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	122.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.89% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ADP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.55	0/3496	0.75	0/4711
1	B	0.46	0/2853	0.70	0/3840
1	C	0.49	0/3367	0.74	3/4526 (0.1%)
2	D	0.50	0/3519	0.70	0/4735
2	E	0.54	0/3524	0.74	0/4751
2	F	0.45	0/3362	0.69	0/4504
3	G	0.54	0/1808	0.83	3/2435 (0.1%)
4	H	0.56	0/895	0.80	0/1202
All	All	0.51	0/22824	0.74	6/30704 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2
2	D	0	2
2	F	0	1
3	G	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	484	GLU	N-CA-C	-6.31	93.97	111.00
3	G	217	LEU	CA-CB-CG	5.65	128.28	115.30
1	C	397	GLN	N-CA-C	-5.60	95.87	111.00
3	G	186	ARG	N-CA-C	-5.60	95.89	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	115	ILE	N-CA-C	5.53	125.93	111.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	354	ARG	Peptide
1	C	401	ASP	Peptide
2	D	216	GLY	Peptide
2	D	391	GLU	Peptide
2	F	215	PHE	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3462	0	3344	321	0
1	B	2833	0	2533	243	0
1	C	3329	0	3032	283	0
2	D	3480	0	3309	272	0
2	E	3484	0	3345	268	0
2	F	3334	0	3069	202	0
3	G	1797	0	1665	192	0
4	H	890	0	833	87	0
5	A	5	0	0	3	0
5	B	5	0	0	1	0
5	D	5	0	0	0	0
5	E	5	0	0	0	0
6	F	27	0	12	1	0
All	All	22656	0	21142	1787	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 41.

The worst 5 of 1787 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:262:ASP:H	1:C:318:PHE:HB2	1.05	1.13
1:A:404:LYS:HG3	1:A:405:ALA:H	1.06	1.11
4:H:129:VAL:HG13	4:H:132:MSE:HA	1.33	1.09
2:F:139:ILE:HA	2:F:412:GLN:NE2	1.69	1.07
1:A:32:ILE:HG22	1:A:33:GLN:HG3	1.40	1.04

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	473/502 (94%)	429 (91%)	42 (9%)	2 (0%)	38	76
1	B	403/502 (80%)	357 (89%)	42 (10%)	4 (1%)	18	61
1	C	469/502 (93%)	411 (88%)	51 (11%)	7 (2%)	12	54
2	D	466/483 (96%)	414 (89%)	50 (11%)	2 (0%)	38	76
2	E	463/483 (96%)	418 (90%)	39 (8%)	6 (1%)	14	57
2	F	456/483 (94%)	406 (89%)	46 (10%)	4 (1%)	20	63
3	G	242/285 (85%)	193 (80%)	38 (16%)	11 (4%)	3	31
4	H	123/133 (92%)	108 (88%)	12 (10%)	3 (2%)	7	45
All	All	3095/3373 (92%)	2736 (88%)	320 (10%)	39 (1%)	14	57

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	371	GLN
1	C	354	ARG
2	D	393	SER
2	E	311	ASP
3	G	143	GLN

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	332/402 (83%)	309 (93%)	23 (7%)	18	55
1	B	242/402 (60%)	232 (96%)	10 (4%)	35	69
1	C	291/402 (72%)	274 (94%)	17 (6%)	23	60
2	D	333/385 (86%)	318 (96%)	15 (4%)	32	67
2	E	349/385 (91%)	334 (96%)	15 (4%)	33	68
2	F	309/385 (80%)	301 (97%)	8 (3%)	51	78
3	G	157/231 (68%)	148 (94%)	9 (6%)	24	61
4	H	78/104 (75%)	71 (91%)	7 (9%)	11	44
All	All	2091/2696 (78%)	1987 (95%)	104 (5%)	28	64

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	471	LEU
2	D	242	GLU
3	G	244	MSE
1	C	474	HIS
2	D	98	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	289	GLN
2	D	304	GLN
2	E	304	GLN
1	C	433	GLN
1	C	474	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.



## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	SO4	A	700	-	4,4,4	0.18	0	6,6,6	0.31	0
5	SO4	B	700	-	4,4,4	0.19	0	6,6,6	0.19	0
5	SO4	D	700	-	4,4,4	0.18	0	6,6,6	0.17	0
5	SO4	E	700	-	4,4,4	0.21	0	6,6,6	0.19	0
6	ADP	F	600	-	25,29,29	1.07	1 (4%)	24,45,45	1.64	3 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SO4	A	700	-	-	0/0/0/0	0/0/0/0
5	SO4	B	700	-	-	0/0/0/0	0/0/0/0
5	SO4	D	700	-	-	0/0/0/0	0/0/0/0
5	SO4	E	700	-	-	0/0/0/0	0/0/0/0
6	ADP	F	600	-	-	0/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	600	ADP	C5-C4	3.27	1.47	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	600	ADP	N3-C2-N1	-5.89	123.72	128.86
6	F	600	ADP	C4-C5-N7	-2.25	107.24	109.41
6	F	600	ADP	C4'-O4'-C1'	2.08	111.98	109.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	700	SO4	3	0
5	B	700	SO4	1	0
6	F	600	ADP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	468/502 (93%)	-0.55	2 (0%) 92 88	63, 97, 156, 240	0
1	B	414/502 (82%)	-0.21	10 (2%) 59 49	92, 129, 236, 263	0
1	C	466/502 (92%)	-0.39	2 (0%) 92 88	86, 124, 177, 215	0
2	D	457/483 (94%)	-0.35	2 (0%) 92 88	70, 107, 165, 212	0
2	E	456/483 (94%)	-0.39	2 (0%) 92 88	71, 103, 155, 210	0
2	F	451/483 (93%)	-0.22	7 (1%) 72 63	95, 137, 164, 211	0
3	G	247/285 (86%)	-0.25	1 (0%) 92 88	80, 134, 182, 199	0
4	H	125/133 (93%)	0.05	5 (4%) 39 30	114, 143, 168, 191	0
All	All	3084/3373 (91%)	-0.33	31 (1%) 82 74	63, 119, 180, 263	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	243	GLN	5.9
2	D	2	THR	4.0
4	H	76	THR	4.0
2	F	420	PHE	3.9
1	B	142	VAL	3.5

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	SO4	A	700	5/5	0.80	0.51	4.16	184,186,190,192	0
5	SO4	E	700	5/5	0.76	0.34	2.09	185,189,190,191	0
5	SO4	B	700	5/5	0.57	0.38	1.18	187,190,191,194	0
6	ADP	F	600	27/27	0.79	0.34	0.55	173,198,203,203	0
5	SO4	D	700	5/5	0.84	0.25	-0.16	190,192,193,194	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.