



wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 04:50 pm BST

PDB ID : 4MJN
Title : Structure of the c ring of the CF1FO ATP synthases.
Authors : Balakrishna, A.M.; Gruber, G.
Deposited on : 2013-09-04
Resolution : 6.00 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

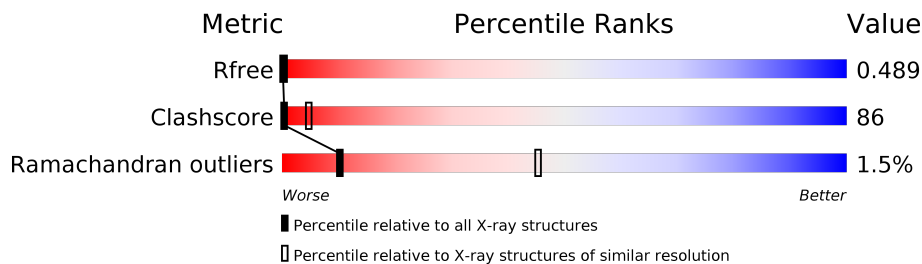
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.00 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}	130704	1000 (8.00-3.88)
Clashscore	141614	1049 (8.00-3.90)
Ramachandran outliers	138981	1016 (8.00-3.86)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	81	52% 38% 9%
1	B	81	41% 41% 9% 9%
1	C	81	74% 17% 9%
1	D	81	63% 27% 9%
1	E	81	51% 41% 9%
1	F	81	83% 9% 9%
1	G	81	62% 26% 9%
1	H	81	68% 23% 9%
1	I	81	68% 23% 9%

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Mol	Chain	Length	Quality of chain
1	J	81	 44% 47% 9%
1	K	81	 74% 15% 9%
1	L	81	 65% 25% 9%
1	M	81	 53% 37% 9%
1	N	81	 63% 25% 9%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 5026 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 c, chloroplastic.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	74	359	211	74	74	0	0	0
1	B	74	359	211	74	74	0	0	0
1	C	74	359	211	74	74	0	0	0
1	D	74	359	211	74	74	0	0	0
1	E	74	359	211	74	74	0	0	0
1	F	74	359	211	74	74	0	0	0
1	G	74	359	211	74	74	0	0	0
1	H	74	359	211	74	74	0	0	0
1	I	74	359	211	74	74	0	0	0
1	J	74	359	211	74	74	0	0	0
1	K	74	359	211	74	74	0	0	0
1	L	74	359	211	74	74	0	0	0
1	M	74	359	211	74	74	0	0	0
1	N	74	359	211	74	74	0	0	0

3 Residue-property plots [i](#)

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. 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. 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.

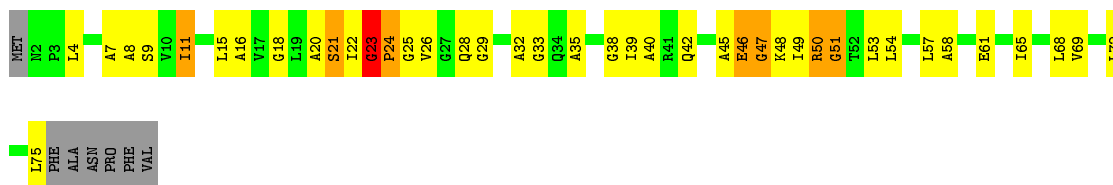
- Molecule 1: ATP synthase subunit c, chloroplastic

Chain A: 



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain B: 



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain C: 



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain D: 




- Molecule 1: ATP synthase subunit c, chloroplastic

Chain E: 



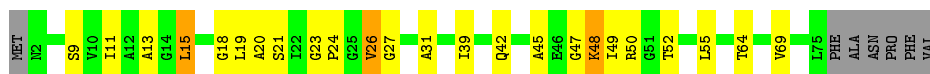
- Molecule 1: ATP synthase subunit c, chloroplastic

Chain F:  83% 9% 9%



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain G:  62% 26% 9%



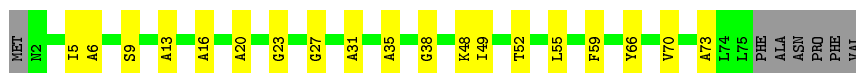
- Molecule 1: ATP synthase subunit c, chloroplastic

Chain H:  68% 23% 9%



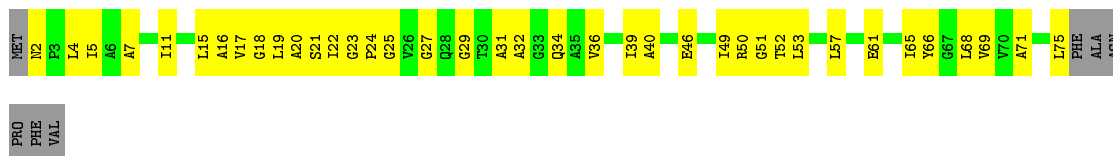
- Molecule 1: ATP synthase subunit c, chloroplastic

Chain I:  68% 23% 9%



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain J:  44% 47% 9%



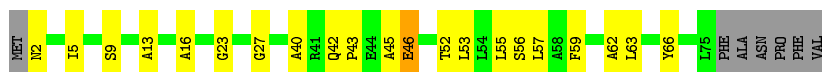
- Molecule 1: ATP synthase subunit c, chloroplastic

Chain K:  74% 15% 9%



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain L:  65% 25% 9%



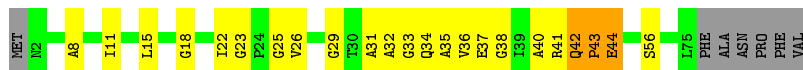
- Molecule 1: ATP synthase subunit c, chloroplastic

Chain M:  53% 37% 9%



- Molecule 1: ATP synthase subunit c, chloroplastic

Chain N:  63% 25% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.42Å 99.30Å 123.51Å 90.00° 104.34° 90.00°	Depositor
Resolution (Å)	19.76 – 6.00 19.76 – 6.00	Depositor EDS
% Data completeness (in resolution range)	93.8 (19.76-6.00) 96.7 (19.76-6.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.95 (at 5.92Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.358 , 0.378 0.415 , 0.489	Depositor DCC
R_{free} test set	204 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	313.4	Xtrriage
Anisotropy	0.455	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.53 , 463.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.56$, $\langle L^2 \rangle = 0.40$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	5026	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8040e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	1.06	1/358 (0.3%)	1.16	2/493 (0.4%)
1	B	1.08	1/358 (0.3%)	1.39	6/493 (1.2%)
1	C	0.84	0/358	0.99	1/493 (0.2%)
1	D	0.87	0/358	0.99	0/493
1	E	0.82	0/358	0.97	0/493
1	F	0.70	0/358	0.82	0/493
1	G	1.13	1/358 (0.3%)	1.18	2/493 (0.4%)
1	H	1.10	2/358 (0.6%)	1.04	2/493 (0.4%)
1	I	0.79	0/358	0.92	0/493
1	J	1.16	0/358	1.33	2/493 (0.4%)
1	K	0.95	0/358	0.97	0/493
1	L	0.91	0/358	0.92	0/493
1	M	0.93	0/358	1.03	0/493
1	N	0.91	0/358	0.94	0/493
All	All	0.96	5/5012 (0.1%)	1.06	15/6902 (0.2%)

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	B	0	3
1	D	0	1
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	75	LEU	N-CA	10.52	1.67	1.46
1	A	11	ILE	N-CA	7.12	1.60	1.46
1	G	15	LEU	N-CA	6.29	1.58	1.46
1	B	9	SER	N-CA	5.62	1.57	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	74	LEU	CA-C	5.20	1.66	1.52

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	23	GLY	N-CA-C	-8.97	90.69	113.10
1	A	17	VAL	CB-CA-C	8.45	127.45	111.40
1	B	50	ARG	N-CA-C	-7.51	90.72	111.00
1	B	47	GLY	N-CA-C	7.18	131.06	113.10
1	H	74	LEU	C-N-CA	6.95	139.08	121.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	23	GLY	Peptide
1	B	46	GLU	Mainchain
1	B	51	GLY	Peptide
1	D	16	ALA	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	359	0	203	171	0
1	B	359	0	202	230	0
1	C	359	0	203	20	0
1	D	359	0	203	62	0
1	E	359	0	203	69	0
1	F	359	0	203	8	0
1	G	359	0	203	71	0
1	H	359	0	203	64	0
1	I	359	0	203	49	0
1	J	359	0	203	110	0
1	K	359	0	203	75	0
1	L	359	0	203	60	0
1	M	359	0	203	145	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	359	0	203	87	0
All	All	5026	0	2841	679	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 86.

The worst 5 of 679 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:G:23:GLY:H	1:H:22:ILE:CB	1.10	1.64
1:A:23:GLY:HA3	1:B:22:ILE:CB	1.11	1.59
1:A:59:PHE:CB	1:B:58:ALA:CB	1.74	1.57
1:A:59:PHE:CB	1:B:58:ALA:CA	1.78	1.57
1:A:23:GLY:CA	1:B:22:ILE:CB	1.78	1.55

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	72/81 (89%)	66 (92%)	5 (7%)	1 (1%)	11	46
1	B	72/81 (89%)	69 (96%)	2 (3%)	1 (1%)	11	46
1	C	72/81 (89%)	69 (96%)	2 (3%)	1 (1%)	11	46
1	D	72/81 (89%)	70 (97%)	1 (1%)	1 (1%)	11	46
1	E	72/81 (89%)	68 (94%)	4 (6%)	0	100	100
1	F	72/81 (89%)	69 (96%)	2 (3%)	1 (1%)	11	46
1	G	72/81 (89%)	68 (94%)	2 (3%)	2 (3%)	5	30
1	H	72/81 (89%)	70 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	72/81 (89%)	69 (96%)	3 (4%)	0	100	100
1	J	72/81 (89%)	66 (92%)	6 (8%)	0	100	100
1	K	72/81 (89%)	68 (94%)	2 (3%)	2 (3%)	5	30
1	L	72/81 (89%)	68 (94%)	2 (3%)	2 (3%)	5	30
1	M	72/81 (89%)	71 (99%)	0	1 (1%)	11	46
1	N	72/81 (89%)	67 (93%)	2 (3%)	3 (4%)	3	22
All	All	1008/1134 (89%)	958 (95%)	35 (4%)	15 (2%)	10	45

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	24	PRO
1	D	43	PRO
1	G	48	LYS
1	K	42	GLN
1	N	42	GLN

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

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](#)

There are no ligands in this entry.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.