



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 10:56 pm BST

PDB ID : 6L8D
Title : Hexameric structure of the ATPase subunit of magnesium chelatase
Authors : Gao, Y.; Liu, L.
Deposited on : 2019-11-05
Resolution : 2.91 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

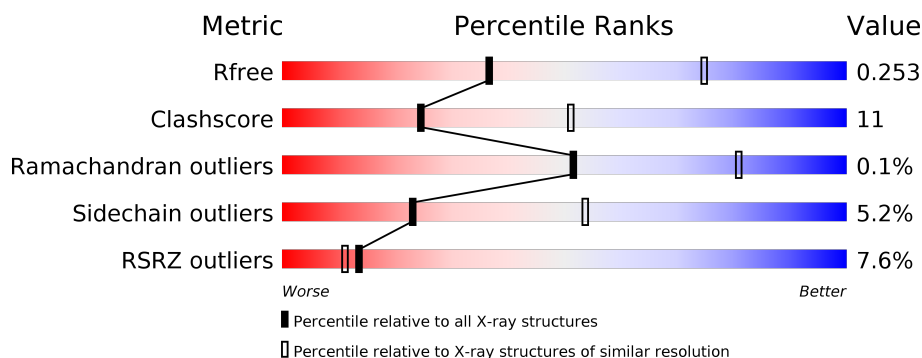
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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 $\leq 5\%$. 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	365	<div> <div>5%</div> <div> <div></div> <div>57%</div> <div>14%</div> <div>•</div> <div>27%</div> </div> </div>
1	B	365	<div> <div>6%</div> <div> <div></div> <div>61%</div> <div>13%</div> <div>•</div> <div>25%</div> </div> </div>
1	C	365	<div> <div>5%</div> <div> <div></div> <div>59%</div> <div>10%</div> <div>•</div> <div>30%</div> </div> </div>
1	D	365	<div> <div>6%</div> <div> <div></div> <div>52%</div> <div>16%</div> <div>•</div> <div>31%</div> </div> </div>
1	E	365	<div> <div>6%</div> <div> <div></div> <div>58%</div> <div>14%</div> <div>•</div> <div>27%</div> </div> </div>
1	F	365	<div> <div>5%</div> <div> <div></div> <div>59%</div> <div>12%</div> <div>•</div> <div>27%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12112 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 Magnesium-chelatase subunit ChlI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2035	1284	349	394	8			
1	B	273	Total	C	N	O	S	0	0	0
			2060	1311	358	383	8			
1	C	256	Total	C	N	O	S	0	0	0
			1943	1229	340	366	8			
1	D	253	Total	C	N	O	S	0	0	0
			1937	1227	339	363	8			
1	E	266	Total	C	N	O	S	0	0	0
			2002	1264	351	379	8			
1	F	267	Total	C	N	O	S	0	0	0
			2023	1277	354	384	8			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	358	LEU	-	expression tag	UNP P51634
A	359	GLU	-	expression tag	UNP P51634
A	360	HIS	-	expression tag	UNP P51634
A	361	HIS	-	expression tag	UNP P51634
A	362	HIS	-	expression tag	UNP P51634
A	363	HIS	-	expression tag	UNP P51634
A	364	HIS	-	expression tag	UNP P51634
A	365	HIS	-	expression tag	UNP P51634
B	358	LEU	-	expression tag	UNP P51634
B	359	GLU	-	expression tag	UNP P51634
B	360	HIS	-	expression tag	UNP P51634
B	361	HIS	-	expression tag	UNP P51634
B	362	HIS	-	expression tag	UNP P51634
B	363	HIS	-	expression tag	UNP P51634
B	364	HIS	-	expression tag	UNP P51634
B	365	HIS	-	expression tag	UNP P51634
C	358	LEU	-	expression tag	UNP P51634

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	359	GLU	-	expression tag	UNP P51634
C	360	HIS	-	expression tag	UNP P51634
C	361	HIS	-	expression tag	UNP P51634
C	362	HIS	-	expression tag	UNP P51634
C	363	HIS	-	expression tag	UNP P51634
C	364	HIS	-	expression tag	UNP P51634
C	365	HIS	-	expression tag	UNP P51634
D	358	LEU	-	expression tag	UNP P51634
D	359	GLU	-	expression tag	UNP P51634
D	360	HIS	-	expression tag	UNP P51634
D	361	HIS	-	expression tag	UNP P51634
D	362	HIS	-	expression tag	UNP P51634
D	363	HIS	-	expression tag	UNP P51634
D	364	HIS	-	expression tag	UNP P51634
D	365	HIS	-	expression tag	UNP P51634
E	358	LEU	-	expression tag	UNP P51634
E	359	GLU	-	expression tag	UNP P51634
E	360	HIS	-	expression tag	UNP P51634
E	361	HIS	-	expression tag	UNP P51634
E	362	HIS	-	expression tag	UNP P51634
E	363	HIS	-	expression tag	UNP P51634
E	364	HIS	-	expression tag	UNP P51634
E	365	HIS	-	expression tag	UNP P51634
F	358	LEU	-	expression tag	UNP P51634
F	359	GLU	-	expression tag	UNP P51634
F	360	HIS	-	expression tag	UNP P51634
F	361	HIS	-	expression tag	UNP P51634
F	362	HIS	-	expression tag	UNP P51634
F	363	HIS	-	expression tag	UNP P51634
F	364	HIS	-	expression tag	UNP P51634
F	365	HIS	-	expression tag	UNP P51634

- Molecule 2 is water.

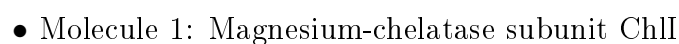
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	20	Total O 20 20	0	0
2	B	22	Total O 22 22	0	0
2	C	19	Total O 19 19	0	0
2	D	19	Total O 19 19	0	0

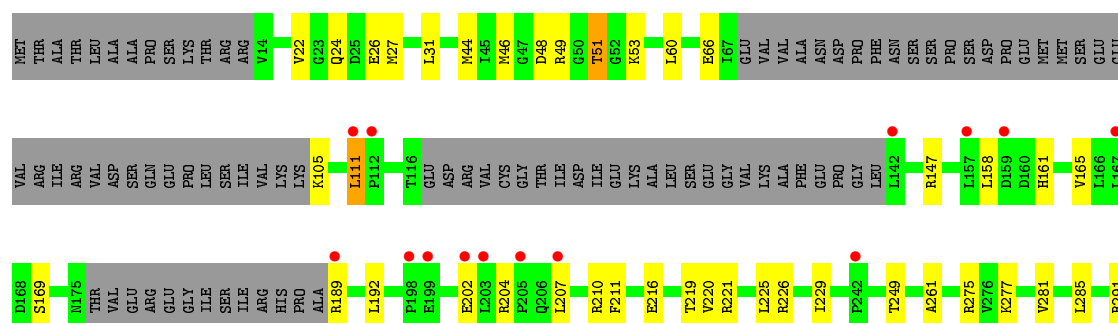
Continued on next page...

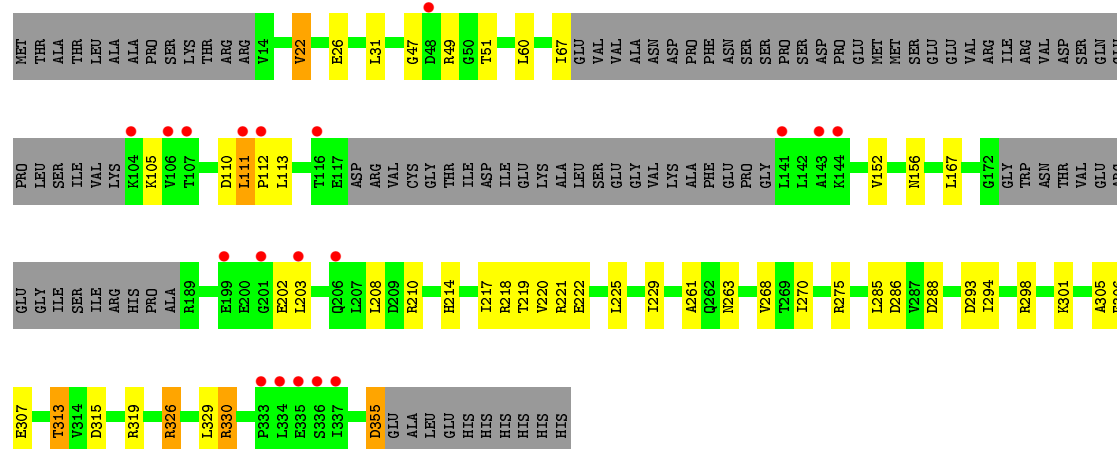
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	14	Total	O	0	0
			14	14		
2	F	18	Total	O	0	0
			18	18		

- Molecule 1: Magnesium-chelatase subunit ChlI







4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	211.03Å 121.15Å 119.42Å 90.00° 99.06° 90.00°	Depositor
Resolution (Å)	49.33 – 2.91 49.33 – 2.90	Depositor EDS
% Data completeness (in resolution range)	80.7 (49.33-2.91) 80.7 (49.33-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.233 , 0.252 0.233 , 0.253	Depositor DCC
R_{free} test set	2725 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	47.0	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	12112	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.31	0/2058	0.52	0/2788
1	B	0.31	0/2085	0.55	1/2826 (0.0%)
1	C	0.35	0/1965	0.54	2/2662 (0.1%)
1	D	0.31	0/1959	0.50	0/2653
1	E	0.32	0/2026	0.52	1/2747 (0.0%)
1	F	0.32	0/2047	0.52	0/2773
All	All	0.32	0/12140	0.53	4/16449 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	188	ALA	CB-CA-C	6.00	119.10	110.10
1	C	66	GLU	N-CA-C	5.46	125.74	111.00
1	C	111	LEU	C-N-CD	5.06	139.02	128.40
1	E	111	LEU	C-N-CD	5.05	139.01	128.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2035	0	2034	47	0
1	B	2060	0	2083	25	0
1	C	1943	0	1943	36	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1937	0	1958	72	0
1	E	2002	0	1992	32	0
1	F	2023	0	2025	57	0
2	A	20	0	0	1	0
2	B	22	0	0	2	0
2	C	19	0	0	2	0
2	D	19	0	0	2	0
2	E	14	0	0	1	0
2	F	18	0	0	0	0
All	All	12112	0	12035	262	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 11.

The worst 5 of 262 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:F:111:LEU:HD13	1:F:152:VAL:CG2	1.58	1.33
1:A:51:THR:HG21	1:A:217:ILE:CG2	1.69	1.23
1:F:111:LEU:CD1	1:F:152:VAL:HG22	1.73	1.15
1:C:106:VAL:HG12	1:C:107:THR:N	1.56	1.15
1:D:169:SER:HB3	1:D:190:PHE:HE2	1.07	1.13

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	259/365 (71%)	243 (94%)	16 (6%)	0	100	100
1	B	263/365 (72%)	252 (96%)	11 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	246/365 (67%)	235 (96%)	11 (4%)	0	100	100
1	D	243/365 (67%)	230 (95%)	13 (5%)	0	100	100
1	E	258/365 (71%)	246 (95%)	12 (5%)	0	100	100
1	F	259/365 (71%)	242 (93%)	16 (6%)	1 (0%)	34	65
All	All	1528/2190 (70%)	1448 (95%)	79 (5%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	111	LEU

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	219/315 (70%)	205 (94%)	14 (6%)	17	44
1	B	218/315 (69%)	204 (94%)	14 (6%)	17	44
1	C	206/315 (65%)	198 (96%)	8 (4%)	32	64
1	D	209/315 (66%)	199 (95%)	10 (5%)	25	57
1	E	210/315 (67%)	202 (96%)	8 (4%)	33	65
1	F	215/315 (68%)	203 (94%)	12 (6%)	21	50
All	All	1277/1890 (68%)	1211 (95%)	66 (5%)	23	54

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	49	ARG
1	D	22	VAL
1	F	263	ASN
1	C	108	MET
1	C	189	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	255	GLN
1	D	206	GLN
1	E	24	GLN
1	F	255	GLN

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	267/365 (73%)	0.27	17 (6%) 19 16	17, 37, 85, 92	0
1	B	273/365 (74%)	0.22	21 (7%) 13 11	22, 41, 83, 93	0
1	C	256/365 (70%)	0.30	20 (7%) 13 10	24, 44, 87, 95	0
1	D	253/365 (69%)	0.29	22 (8%) 10 8	22, 43, 81, 91	0
1	E	266/365 (72%)	0.27	21 (7%) 12 10	25, 48, 86, 100	0
1	F	267/365 (73%)	0.21	19 (7%) 16 13	19, 43, 85, 97	0
All	All	1582/2190 (72%)	0.26	120 (7%) 13 11	17, 43, 85, 100	0

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	203	LEU	7.6
1	B	334	LEU	7.4
1	A	104	LYS	6.7
1	C	199	GLU	6.1
1	E	334	LEU	5.8

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.