

Mar 10, 2022 – 07:06 pm GMT

PDB ID	:	7P3N
EMDB ID	:	EMD-13181
Title	:	F1Fo-ATP synthase from Acinetobacter baumannii (state 2)
Authors	:	Demmer, J.K.; Phillips, B.P.; Uhrig, O.L.; Filloux, A.; Allsopp, L.P.; Bublitz,
		M.; Meier, T.
Deposited on	:	2021-07-08
Resolution	:	4.60 Å(reported)
This is	s a l	Full wwPDB EM Validation 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/EMValidationReportHelp with specific help available everywhere you see the (i) symbol.

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

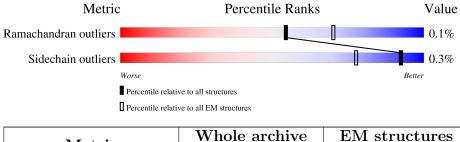
EMDB validation analysis	:	$0.0.0.{ m dev}97$
Mogul	:	1.8.4, CSD as 541 be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 4.60 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	$egin{array}{c} { m Whole \ archive}\ (\#{ m Entries}) \end{array}$	${f EM} {f structures} \ (\#{f Entries})$		
Ramachandran outliers	154571	4023		
Sidechain outliers	154315	3826		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	А	514	99%
1	В	514	100%
1	С	514	98% •
2	D	464	100%
2	Е	464	99%
2	F	464	99%
3	G	81	5% 98% ·
3	Н	81	9 9% •
3	J	81	99%



Mol	Chain	Length	Quality of chain	
3	K	81	5%	·
3	L	81	98%	·
3	О	81	<u>6%</u> 99%	
3	Р	81	99%	•
3	Q	81	99%	•
3	R	81	99%	·
3	S	81	98%	·
4	a	291	6% 95%	5%
5	b	156	92%	• 7%
5	р	156	99%	•
6	d	178	97%	••
7	е	139	9%	
8	g	289	• 99%	



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 37114 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

Mol	Chain	Residues		At		AltConf	Trace		
1	А	512	$\begin{array}{c} \text{Total} \\ 3875 \end{array}$	C 2438		O 757	S 15	0	0
1	В	514	Total 3892	C 2448	N 668	O 760	S 16	0	0
1	С	506	Total 3821	C 2405	N 656	0 745	S 15	0	0

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

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

Mol	Chain	Residues		At	oms		AltConf	Trace	
2	D	464	Total 3533	C 2228	N 603	O 688	S 14	0	0
2	Е	463	Total 3525	C 2223	N 602	O 687	S 13	0	0
2	F	463	Total 3525	C 2223	N 602	O 687	S 13	0	0

• Molecule 3 is a protein called ATP synthase subunit c.

Mol	Chain	Residues		Atc	\mathbf{ms}			AltConf	Trace	
3	G	79	Total	С	Ν	Ο	S	0	0	
0	G	19	577	388	92	95	2	0	0	
3	Н	80	Total	С	Ν	Ο	S	0	0	
0	11	80	585	393	93	96	3	0	0	
3	J	80	Total	С	Ν	Ο	S	0	0	
0	0 0	80	585	393	93	96	3	0	0	
3	3 K	79	Total	С	Ν	Ο	S	0	0	
0	П		577	388	92	95	2		0	
3	L	79	Total	С	Ν	Ο	S	0	0	
0	L	19	577	388	92	95	2	0	0	
3	0	80	Total	С	Ν	Ο	S	0	0	
0	3 0	80	585	393	93	96	3	0	0	
3	Р	80	Total	С	Ν	Ο	S	0	0	
5	1		585	393	93	96	3	0	0	



Mol	Chain	Residues		Ato	\mathbf{ms}		AltConf	Trace	
2	3 Q	80	Total	С	Ν	Ο	S	0	0
3 Q	80	585	393	93	96	3	0	0	
2	3 R	80	Total	С	Ν	Ο	S	0	0
0			585	393	93	96	3		
3	C	79	Total	С	Ν	Ο	S	0	0
0	S	19	577	388	92	95	2		U

• Molecule 4 is a protein called ATP synthase subunit a.

Mol	Chain	Residues		At		AltConf	Trace		
4	a	277	Total 2104	C 1405	N 336	O 350	S 13	0	0

• Molecule 5 is a protein called ATP synthase subunit b.

Mol	Chain	Residues		At	oms		AltConf	Trace	
F	h	145	Total	С	Ν	0	S	0	0
a a	140	1112	688	207	214	3	0	0	
5	n	155	Total	С	Ν	0	S	0	0
0	o p	100	1185	734	220	228	3		U

• Molecule 6 is a protein called ATP synthase subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	174	Total 1347	C 849	N 227	0 270	S 1	0	0

• Molecule 7 is a protein called ATP synthase epsilon chain.

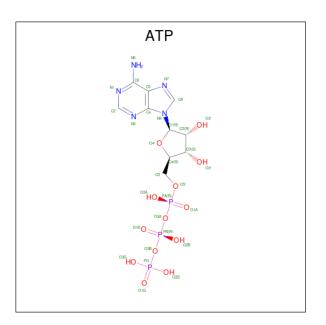
Mol	Chain	Residues	Atoms				AltConf	Trace	
7	е	138	Total 1010	C 631	N 175	0 201	${ m S} { m 3}$	0	0

• Molecule 8 is a protein called ATP synthase gamma chain.

Mol	Chain	Residues	Atoms			AltConf	Trace		
8	g	288	Total 2243	C 1411	N 400	O 420	S 12	0	0

• Molecule 9 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).





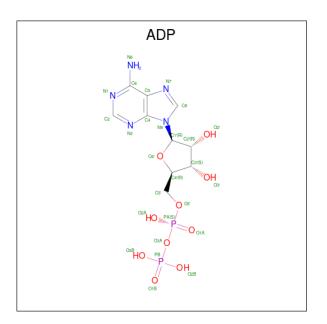
Mol	Chain	Residues	Atoms				AltConf	
0	Δ	1	Total	С	Ν	Ο	Р	0
9	A	1	31	10	5	13	3	0
0	р	1	Total	С	Ν	Ο	Р	0
9	D	1	31	10	5	13	3	0
0	С	1	Total	С	Ν	Ο	Р	0
9	U	1	31	10	5	13	3	U

• Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
10	А	1	Total Mg 1 1	0
10	В	1	Total Mg 1 1	0
10	С	1	Total Mg 1 1	0
10	Е	1	Total Mg 1 1	0

• Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).





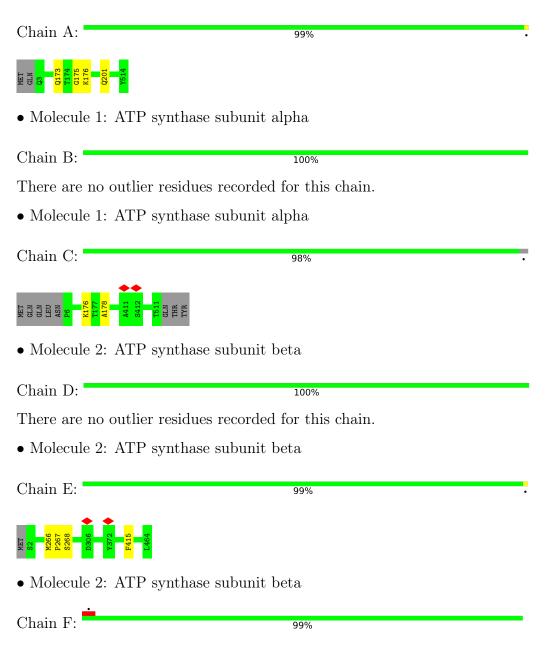
Mol	Chain	Residues	Atoms			AltConf		
11	F	1	Total	С	Ν	Ο	Р	0
11	Ľ	1	27	10	5	10	2	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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 3: ATP synthase subunit c



Chain P:	99% .
H1 619 A20 GLY GLY	
• Molecule 3: ATP synthase subunit c	
Chain Q:	99% •
HI CAR	
• Molecule 3: ATP synthase subunit c	
Chain R:	99% .
• Molecule 3: ATP synthase subunit c	
Chain S:	•
MET ES	
• Molecule 4: ATP synthase subunit a	
Chain a:	5%
MET ALA ALA ALA ALA CLU GLU HRS ALA CLU CLU CLU CLU CLU CLU CLU CLO CLO CLO CLO CLO CLO CLU CLO CLU CLO CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	N123 N125 M125 M126 L124 F21 F21 F21 F230 F243 I245 K290 H291 H291
• Molecule 5: ATP synthase subunit b	
Chain b:	· 7%
MET ASN ALL ASN ALLEU ALR ALA ALA ALA ALA ALA ALA ALA ALA AL3 AL3	
• Molecule 5: ATP synthase subunit b	
Chain p:	99% .
MET N2 L156	



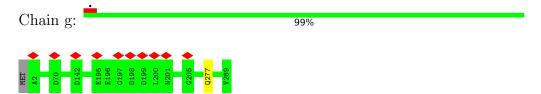
• Molecule 6: ATP synthase subunit delta

Chain d: 97% ··

• Molecule 7: ATP synthase epsilon chain

Chain e:	99%	
12 12 13 13 13 13 13 13 13 13 14 13 14 13 14 14 14 14 14 14 14 14 14 14 14 14 14		

• Molecule 8: ATP synthase gamma chain





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26147	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	60	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	85000	Depositor
Image detector	GATAN K3 $(6k \ge 4k)$	Depositor
Maximum map value	0.162	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0381	Depositor
Map size (Å)	382.5, 382.5, 382.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles ($^{\circ}$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

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

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
IVI01	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.34	0/3932	0.50	0/5321
1	В	0.33	0/3949	0.49	0/5343
1	С	0.33	0/3877	0.49	0/5246
2	D	0.33	0/3590	0.49	0/4864
2	Е	0.32	0/3582	0.49	0/4854
2	F	0.31	0/3582	0.49	0/4854
3	G	0.27	0/588	0.42	0/798
3	Н	0.31	0/596	0.48	0/808
3	J	0.30	0/596	0.52	0/808
3	К	0.30	0/588	0.54	0/798
3	L	0.31	0/588	0.51	0/798
3	0	0.30	0/596	0.50	0/808
3	Р	0.28	0/596	0.46	0/808
3	Q	0.30	0/596	0.50	0/808
3	R	0.29	0/596	0.51	0/808
3	S	0.29	0/588	0.46	0/798
4	a	0.29	0/2162	0.52	0/2953
5	b	0.36	0/1121	0.59	0/1508
5	р	0.29	0/1194	0.46	0/1608
6	d	0.32	0/1364	0.49	0/1854
7	е	0.28	0/1018	0.53	0/1383
8	g	0.31	0/2273	0.48	0/3062
All	All	0.32	0/37572	0.50	0/50890

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.



5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 PDB entries followed by that with respect to all EM entries.

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	Perce	ntiles
1	А	510/514~(99%)	465 (91%)	44 (9%)	1 (0%)	47	81
1	В	512/514~(100%)	474 (93%)	38 (7%)	0	100	100
1	С	504/514~(98%)	467 (93%)	36 (7%)	1 (0%)	47	81
2	D	462/464~(100%)	422 (91%)	40 (9%)	0	100	100
2	Ε	461/464~(99%)	423 (92%)	36 (8%)	2(0%)	34	72
2	F	461/464 (99%)	425 (92%)	35 (8%)	1 (0%)	47	81
3	G	77/81~(95%)	71 (92%)	6 (8%)	0	100	100
3	Н	78/81~(96%)	74 (95%)	4 (5%)	0	100	100
3	J	78/81~(96%)	71 (91%)	7 (9%)	0	100	100
3	К	77/81~(95%)	74 (96%)	3 (4%)	0	100	100
3	L	77/81~(95%)	71 (92%)	6 (8%)	0	100	100
3	О	78/81~(96%)	75~(96%)	3 (4%)	0	100	100
3	Р	78/81~(96%)	71 (91%)	7 (9%)	0	100	100
3	Q	78/81~(96%)	74 (95%)	4 (5%)	0	100	100
3	R	78/81~(96%)	72 (92%)	6 (8%)	0	100	100
3	S	77/81~(95%)	74 (96%)	3 (4%)	0	100	100
4	a	275/291~(94%)	242 (88%)	33 (12%)	0	100	100
5	b	143/156~(92%)	133 (93%)	9 (6%)	1 (1%)	22	62
5	р	153/156~(98%)	152 (99%)	1 (1%)	0	100	100
6	d	172/178~(97%)	159 (92%)	13 (8%)	0	100	100
7	е	136/139~(98%)	126 (93%)	10 (7%)	0	100	100



001000	iraca jien	i procio ao pago						
Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntile	\mathbf{s}
8	g	286/289~(99%)	269~(94%)	17 (6%)	0	100	100	
All	All	4851/4953~(98%)	4484 (92%)	361 (7%)	6 (0%)	54	85	

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Ε	268	SER
5	b	52	ALA
1	А	175	GLY
1	С	178	ALA
2	F	414	VAL
2	Е	267	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	А	404/406~(100%)	401 (99%)	3 (1%)	84 90
1	В	406/406~(100%)	406 (100%)	0	100 100
1	С	398/406~(98%)	397~(100%)	1 (0%)	92 95
2	D	379/379~(100%)	379~(100%)	0	100 100
2	Ε	378/379~(100%)	376 (100%)	2(0%)	88 93
2	F	378/379~(100%)	377 (100%)	1 (0%)	92 95
3	G	56/57~(98%)	56 (100%)	0	100 100
3	Н	57/57~(100%)	57 (100%)	0	100 100
3	J	57/57~(100%)	57~(100%)	0	100 100
3	K	56/57~(98%)	56 (100%)	0	100 100
3	L	56/57~(98%)	56 (100%)	0	100 100
3	О	57/57~(100%)	57 (100%)	0	100 100
3	Р	57/57~(100%)	57 (100%)	0	100 100
3	Q	57/57~(100%)	57~(100%)	0	100 100



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	R	57/57~(100%)	57~(100%)	0	100 100
3	S	56/57~(98%)	56 (100%)	0	100 100
4	a	216/246~(88%)	215 (100%)	1 (0%)	88 93
5	b	106/115~(92%)	106 (100%)	0	100 100
5	р	114/115~(99%)	114 (100%)	0	100 100
6	d	146/148~(99%)	144~(99%)	2(1%)	67 81
7	е	106/107~(99%)	106 (100%)	0	100 100
8	g	235/236~(100%)	234 (100%)	1 (0%)	91 94
All	All	3832/3892~(98%)	3821 (100%)	11 (0%)	92 95

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	173	GLN
1	А	176	LYS
1	А	201	GLN
1	С	176	LYS
2	Е	266	MET
2	Е	415	PHE
2	F	407	GLN
4	a	123	ASN
6	d	72	GLN
6	d	135	ASN
8	g	277	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	79	ASN
1	В	84	GLN
1	В	512	GLN
1	С	164	GLN
1	С	203	GLN
1	С	362	ASN
2	D	118	GLN
2	D	157	ASN
2	Е	169	HIS
2	Е	207	GLN



Mol	Chain	Res	Type
2	Е	358	HIS
2	F	196	ASN
3	J	41	GLN
4	a	213	ASN
5	b	45	ASN
5	b	60	GLN
5	b	63	GLN
5	b	137	ASN
6	d	135	ASN
7	е	46	GLN
8	g	41	GLN
5	р	139	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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	Turne	Chain	Dec	Res Link Bond lengths		В	ond ang	les		
	Type	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
9	ATP	В	601	10	26,33,33	0.67	0	31,52,52	0.87	0
9	ATP	А	601	10	26,33,33	0.67	0	31,52,52	0.87	2(6%)



Mol	Trune	Chain	Res Link		Bo	ond leng	\mathbf{ths}	В	ond ang	les
IVIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
11	ADP	Е	601	10	24,29,29	0.72	0	$29,\!45,\!45$	1.45	1 (3%)
9	ATP	С	601	10	26,33,33	0.66	0	$31,\!52,\!52$	0.86	1 (3%)

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
9	ATP	В	601	10	-	9/18/38/38	0/3/3/3
9	ATP	А	601	10	-	6/18/38/38	0/3/3/3
11	ADP	Е	601	10	-	3/12/32/32	0/3/3/3
9	ATP	С	601	10	-	8/18/38/38	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
11	Ε	601	ADP	C1'-N9-C4	6.73	138.47	126.64
9	А	601	ATP	C4-C5-N7	-2.02	107.29	109.40
9	С	601	ATP	C4-C5-N7	-2.01	107.31	109.40
9	А	601	ATP	C1'-N9-C4	-2.00	123.13	126.64

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	А	601	ATP	PB-O3B-PG-O2G
9	А	601	ATP	PB-O3B-PG-O3G
9	А	601	ATP	C5'-O5'-PA-O3A
9	В	601	ATP	PB-O3B-PG-O2G
9	В	601	ATP	C5'-O5'-PA-O1A
9	В	601	ATP	C5'-O5'-PA-O2A
9	В	601	ATP	C5'-O5'-PA-O3A
9	С	601	ATP	PB-O3B-PG-O2G
9	С	601	ATP	C5'-O5'-PA-O1A
9	С	601	ATP	C5'-O5'-PA-O2A
11	Е	601	ADP	C5'-O5'-PA-O1A
11	Е	601	ADP	C5'-O5'-PA-O3A
9	С	601	ATP	C4'-C5'-O5'-PA



Mol	Chain	Res	Type	Atoms
9	A	601	ATP	PB-O3A-PA-O5'
9	В	601	ATP	PB-O3A-PA-O5'
9	С	601	ATP	PB-O3A-PA-O5'
9	А	601	ATP	C4'-C5'-O5'-PA
9	В	601	ATP	C4'-C5'-O5'-PA
9	А	601	ATP	C5'-O5'-PA-O2A
9	В	601	ATP	O4'-C4'-C5'-O5'
9	С	601	ATP	PB-O3B-PG-O1G
9	В	601	ATP	PB-O3B-PG-O3G
9	С	601	ATP	PB-O3B-PG-O3G
11	Е	601	ADP	PA-O3A-PB-O2B
9	С	601	ATP	C5'-O5'-PA-O3A
9	В	601	ATP	PB-O3B-PG-O1G

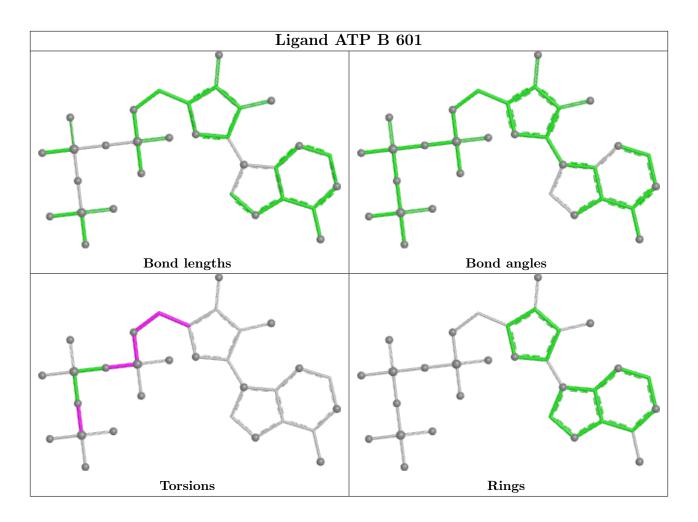
Continued from previous page...

There are no ring outliers.

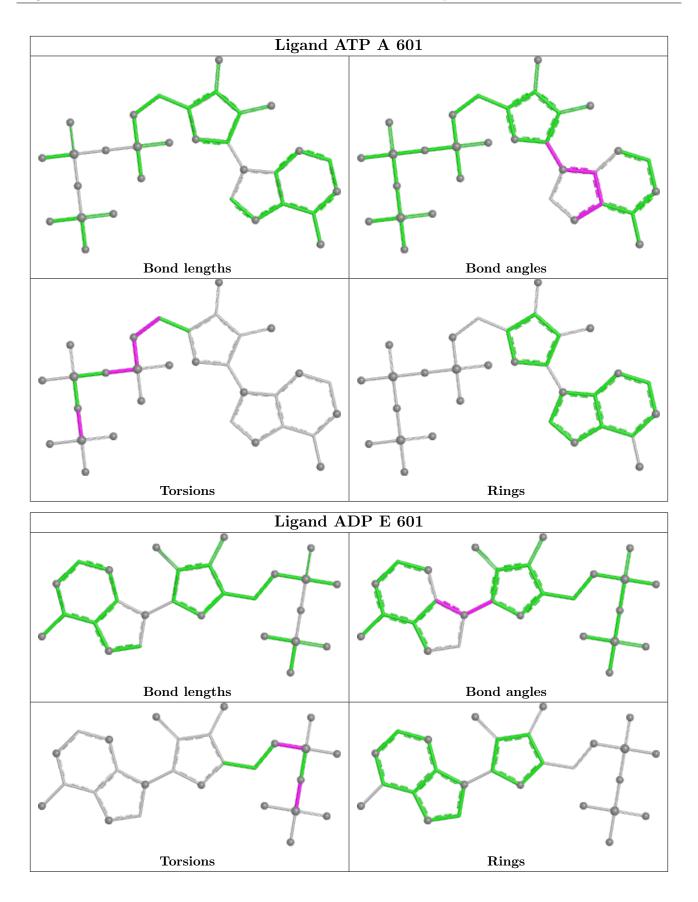
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

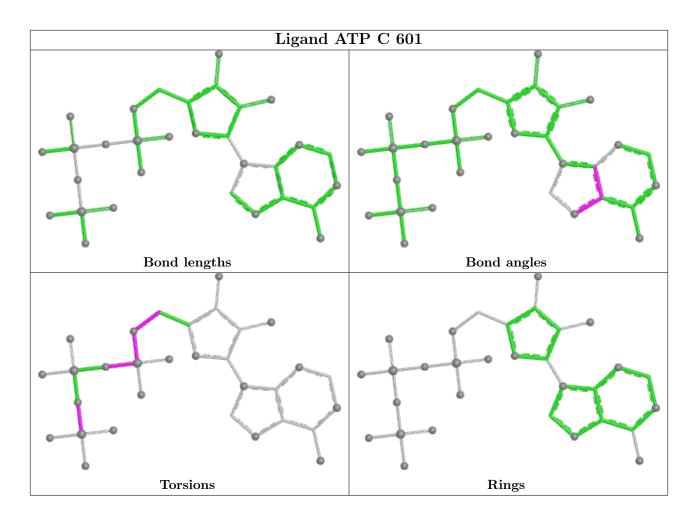












5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



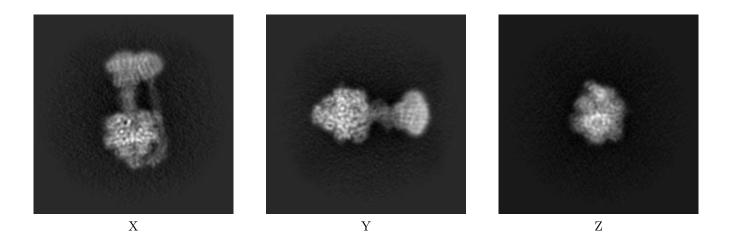
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-13181. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

Orthogonal projections (i) 6.1

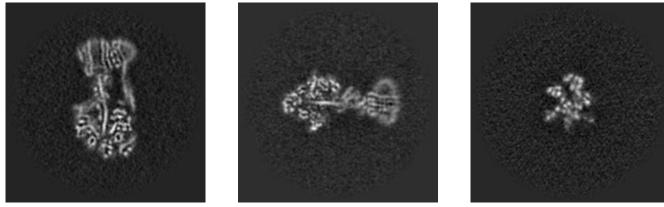
6.1.1Primary map



The images above show the map projected in three orthogonal directions.

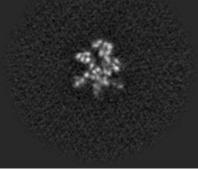
6.2Central slices (i)

6.2.1Primary map



X Index: 225

Y Index: 225

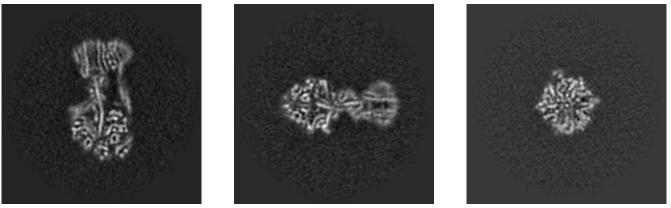


Z Index: 225

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 224

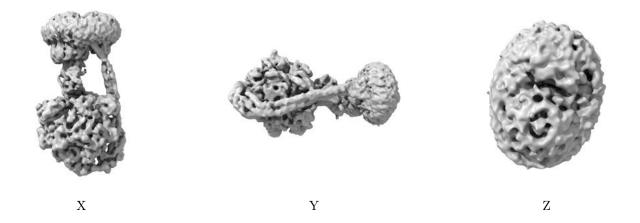
Y Index: 213

Z Index: 171

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0381. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



6.5 Mask visualisation (i)

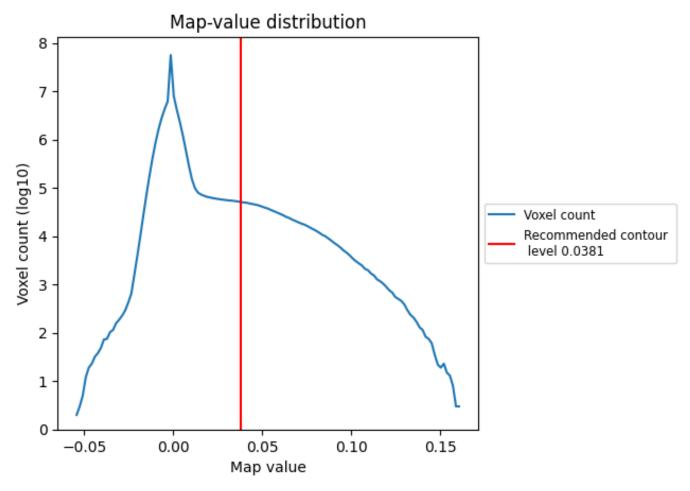
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

This section contains the results of statistical analysis of the map.

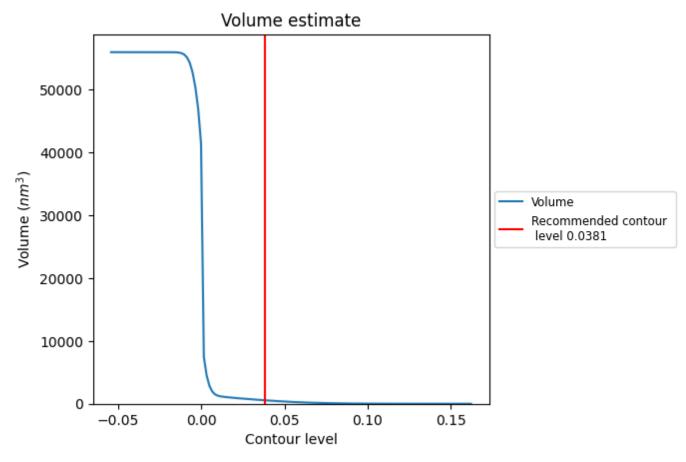
7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)

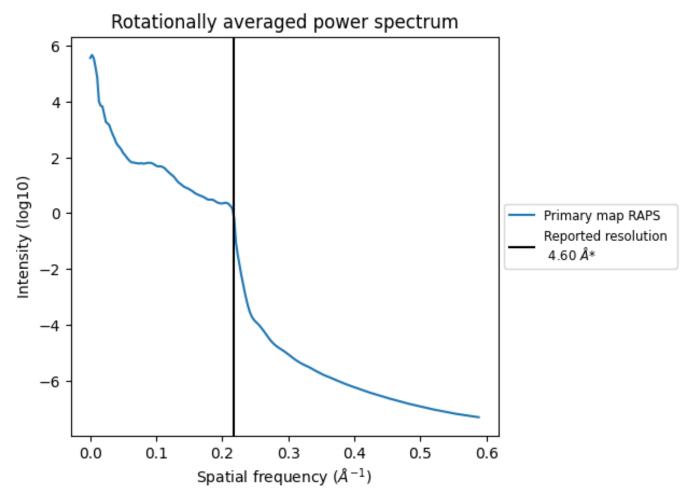


The volume at the recommended contour level is 559 $\rm nm^3;$ this corresponds to an approximate mass of 505 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.217 \AA^{-1}



8 Fourier-Shell correlation (i)

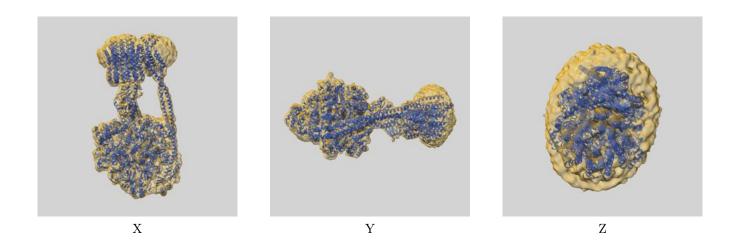
This section was not generated. No FSC curve or half-maps provided.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-13181 and PDB model 7P3N. Per-residue inclusion information can be found in section 3 on page 8.

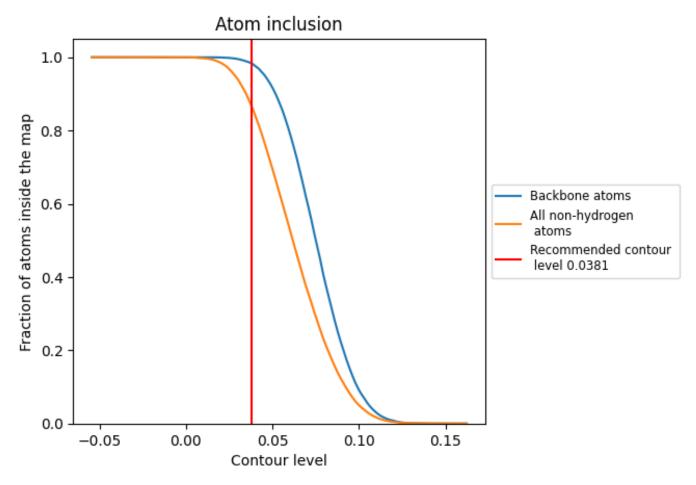
9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0381 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

