



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 05:16 PM UTC

PDB ID : 7NJS / pdb_00007njs
EMDB ID : EMD-12417
Title : Mycobacterium smegmatis ATP synthase state 3c
Authors : Montgomery, M.G.; Petri, J.; Spikes, T.E.; Walker, J.E.
Deposited on : 2021-02-17
Resolution : 2.46 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

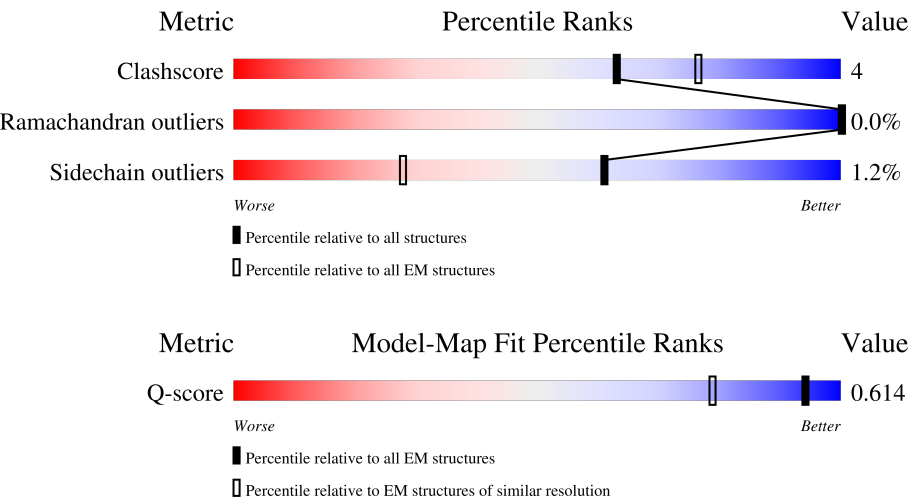
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.46 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.



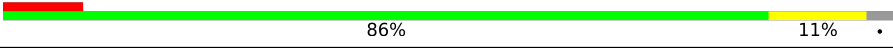
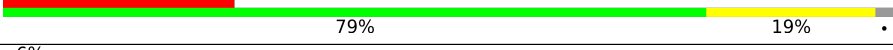
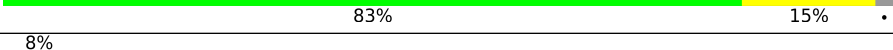
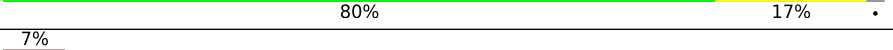
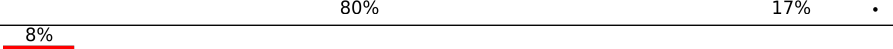
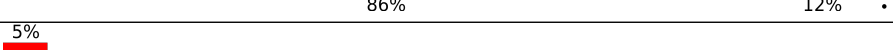
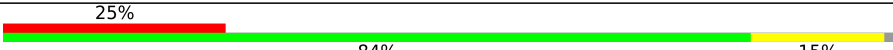
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6014 (1.96 - 2.96)

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 $\leq 5\%$. 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	A	548	
1	B	548	
1	C	548	
2	D	475	

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Mol	Chain	Length	Quality of chain
2	E	475	 88% 9% .
2	F	475	 88% 10% ..
3	G	307	 9% 86% 11% .
4	H	121	 26% 79% 19% .
5	L	86	 6% 81% 16% .
5	M	86	 5% 84% 14% .
5	N	86	 5% 83% 15% .
5	O	86	 8% 80% 17% .
5	P	86	 7% 80% 17% .
5	Q	86	 8% 86% 12% .
5	R	86	 5% 84% 14% .
5	S	86	 5% 86% 10% ..
5	T	86	 88% 10% .
6	a	252	 12% 80% 14% . 6%
7	b	180	 23% 67% 13% 20%
8	d	445	 25% 84% 15% .

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 74714 atoms, of which 37418 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.

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

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	517	Total	C	H	N	O	S	0	0
			7808	2451	3904	674	769	10		
1	B	503	Total	C	H	N	O	S	2	0
			7623	2393	3815	658	747	10		
1	C	521	Total	C	H	N	O	S	3	0
			7942	2496	3977	685	774	10		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	468	Total	C	H	N	O	S	2	0
			7162	2265	3573	616	695	13		
2	E	464	Total	C	H	N	O	S	0	0
			7087	2243	3533	609	689	13		
2	F	468	Total	C	H	N	O	S	0	0
			7144	2260	3564	614	693	13		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	G	297	Total	C	H	N	O	S	0	0
			4567	1418	2290	412	441	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	H	118	Total	C	H	N	O	S	0	0
			1802	565	891	161	184	1		

- Molecule 5 is a protein called ATP synthase subunit c.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	L	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	M	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	N	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	O	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	P	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	Q	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	R	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	S	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
5	T	85	Total	C	H	N	O	S	0	0
			1204	391	607	97	107	2		

- Molecule 6 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	a	238	Total	C	H	N	O	S	0	0
			3767	1252	1916	292	301	6		

- Molecule 7 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	b	144	Total	C	H	N	O	S	0	0
			2161	664	1090	193	212	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	171	HIS	-	expression tag	UNP A0R204
b	172	HIS	-	expression tag	UNP A0R204
b	173	HIS	-	expression tag	UNP A0R204
b	174	HIS	-	expression tag	UNP A0R204
b	175	HIS	-	expression tag	UNP A0R204
b	176	HIS	-	expression tag	UNP A0R204
b	177	HIS	-	expression tag	UNP A0R204
b	178	HIS	-	expression tag	UNP A0R204
b	179	HIS	-	expression tag	UNP A0R204

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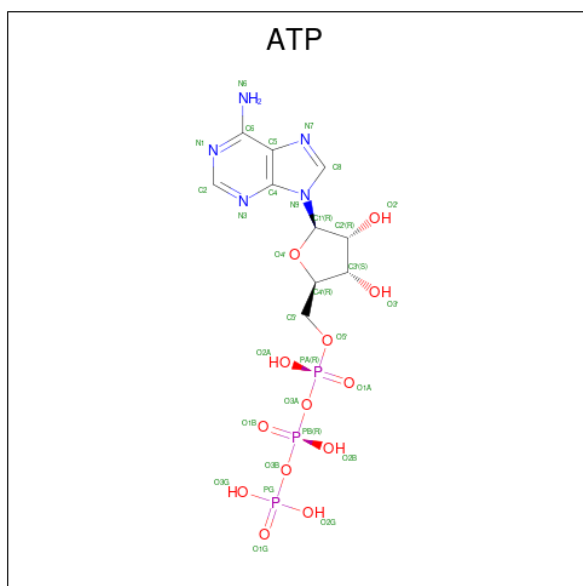
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Chain	Residue	Modelled	Actual	Comment	Reference
b	180	HIS	-	expression tag	UNP A0R204

- Molecule 8 is a protein called ATP synthase subunit b-delta.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	d	437	Total	C	H	N	O	S	0	0
			6640	2029	3362	596	648	5		

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



Mol	Chain	Residues	Atoms						AltConf
9	A	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
9	B	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
9	C	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
9	F	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

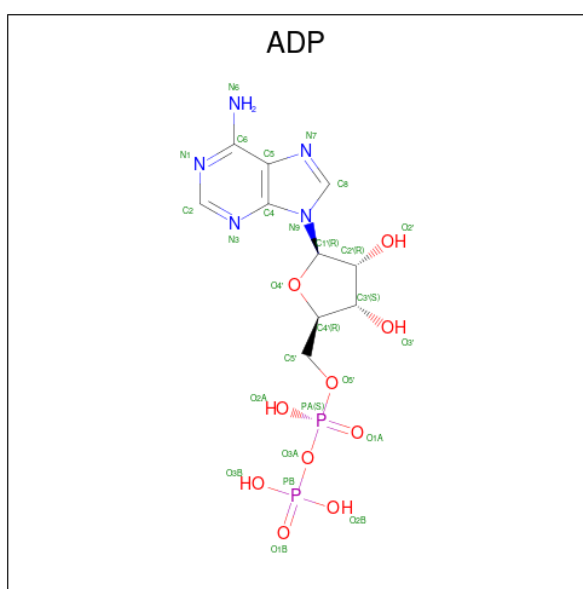
Mol	Chain	Residues	Atoms		AltConf
10	A	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
10	B	1	Total	Mg	0
			1	1	
10	C	1	Total	Mg	0
			1	1	
10	D	1	Total	Mg	0
			1	1	
10	F	1	Total	Mg	0
			1	1	

- Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms						AltConf
11	D	1	Total 39	C 10	H 12	N 5	O 10	P 2	0
11	E	1	Total 39	C 10	H 12	N 5	O 10	P 2	0

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		AltConf
12	A	3	Total	O	0
			3	3	
12	B	3	Total	O	0
			3	3	
12	C	3	Total	O	0
			3	3	

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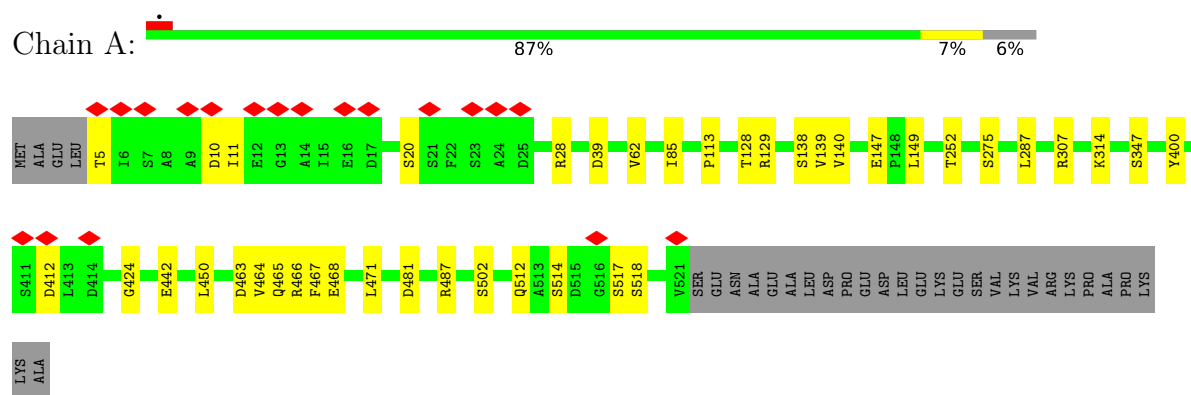
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Mol	Chain	Residues	Atoms		AltConf
12	D	4	Total	O	0
			4	4	
12	F	3	Total	O	0
			3	3	

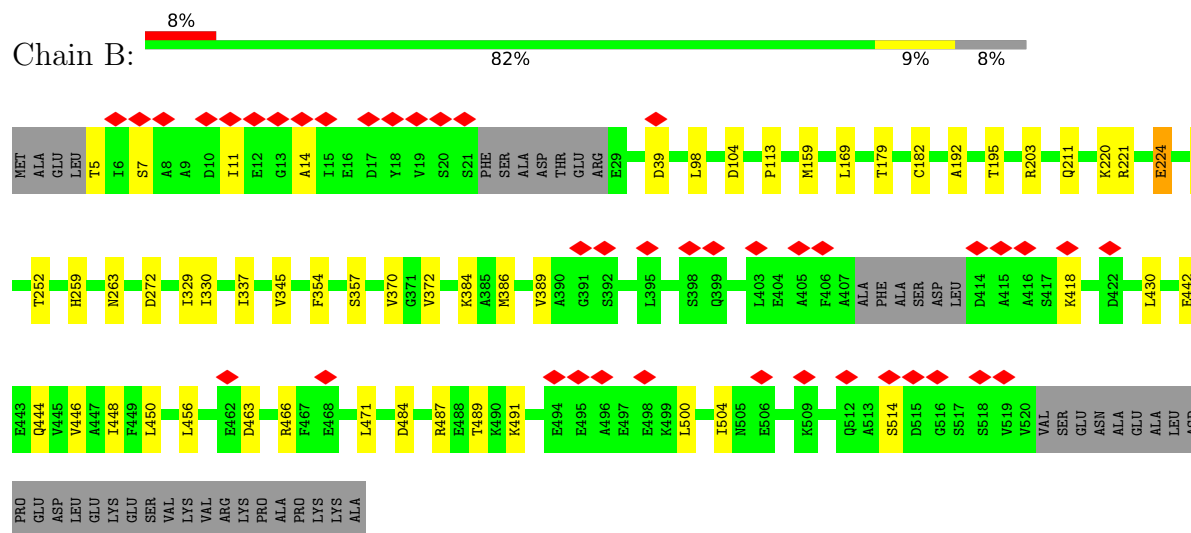
3 Residue-property plots

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.

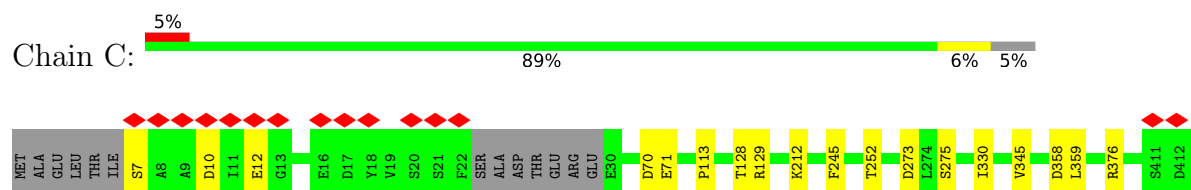
- Molecule 1: ATP synthase subunit alpha

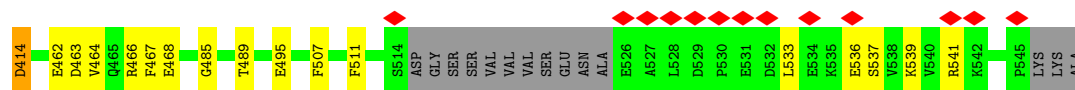


- Molecule 1: ATP synthase subunit alpha



- Molecule 1: ATP synthase subunit alpha

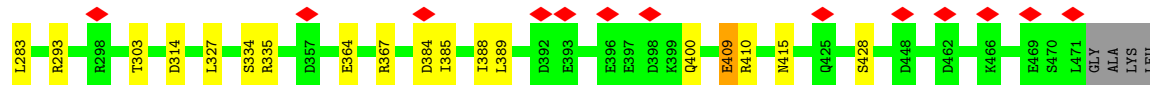
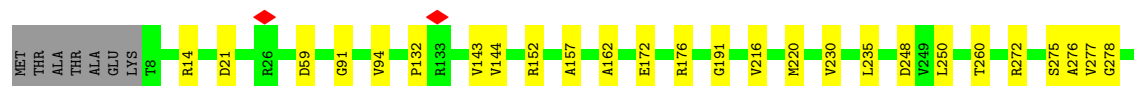
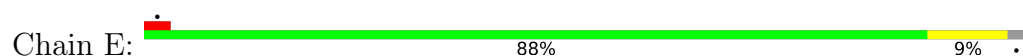




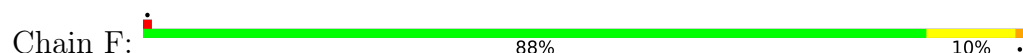
- Molecule 2: ATP synthase subunit beta



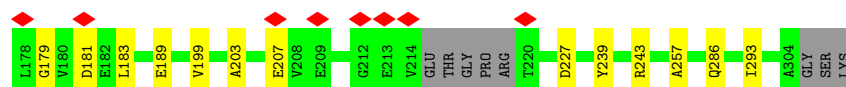
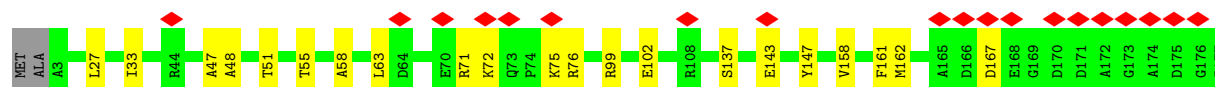
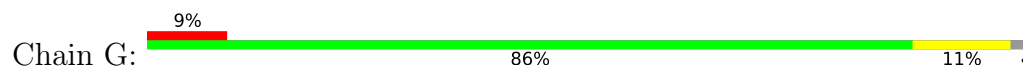
- Molecule 2: ATP synthase subunit beta



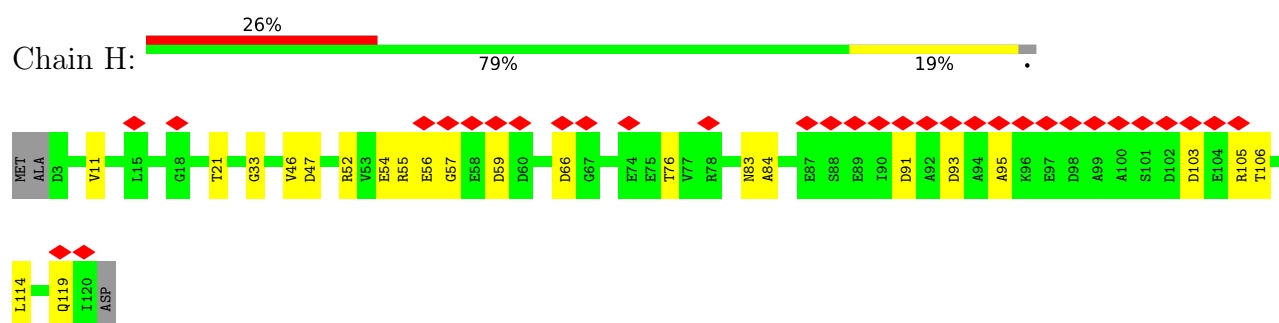
- Molecule 2: ATP synthase subunit beta



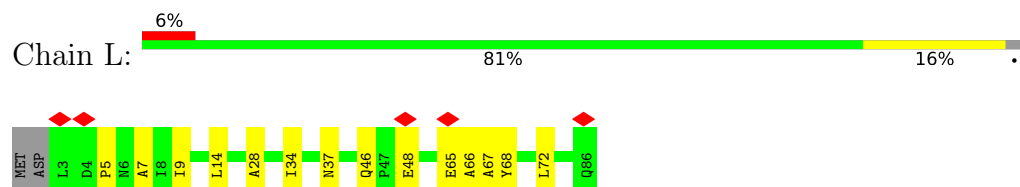
- Molecule 3: ATP synthase gamma chain



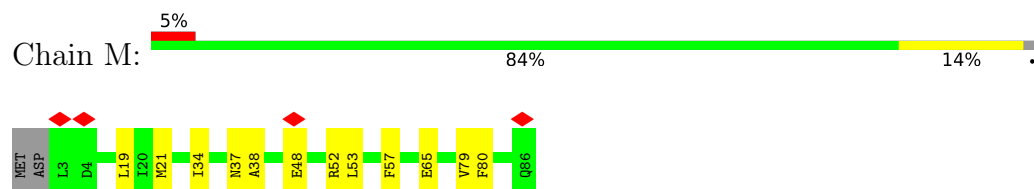
- Molecule 4: ATP synthase epsilon chain



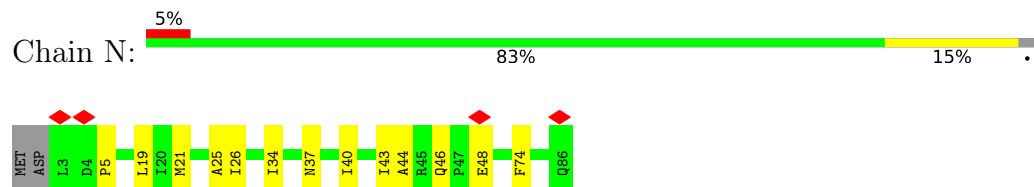
- Molecule 5: ATP synthase subunit c



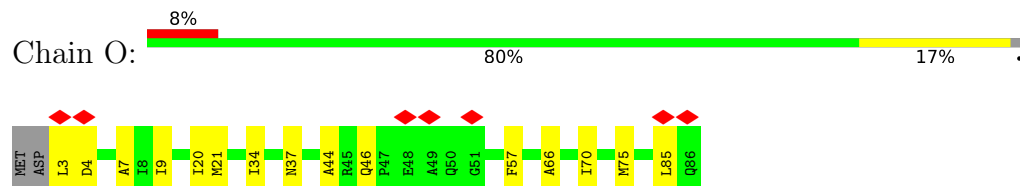
- Molecule 5: ATP synthase subunit c



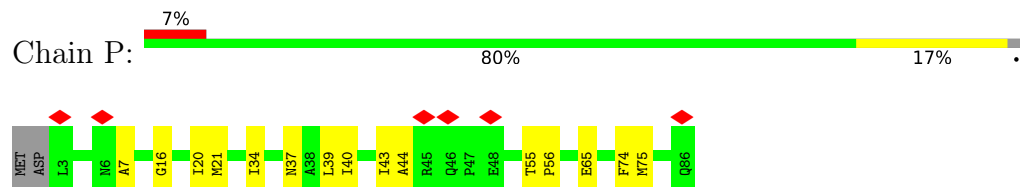
- Molecule 5: ATP synthase subunit c



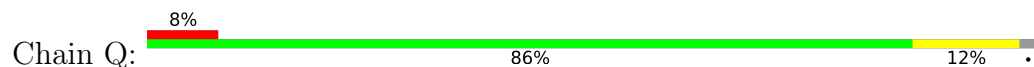
- Molecule 5: ATP synthase subunit c



- Molecule 5: ATP synthase subunit c

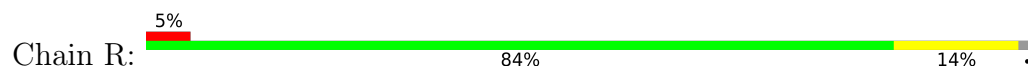


- Molecule 5: ATP synthase subunit c

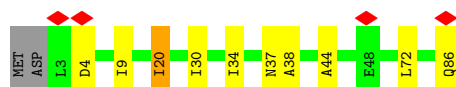
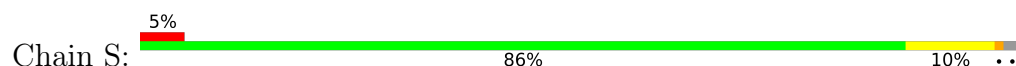




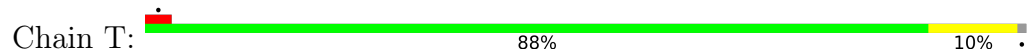
- Molecule 5: ATP synthase subunit c



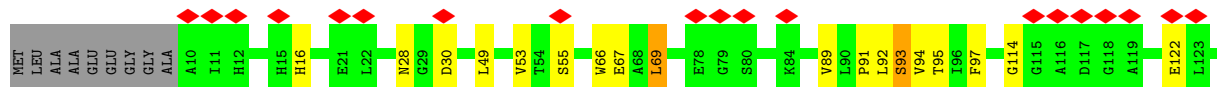
- Molecule 5: ATP synthase subunit c



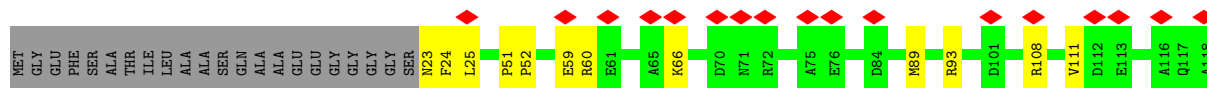
- Molecule 5: ATP synthase subunit c



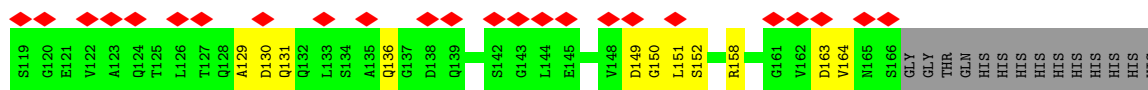
- Molecule 6: ATP synthase subunit a



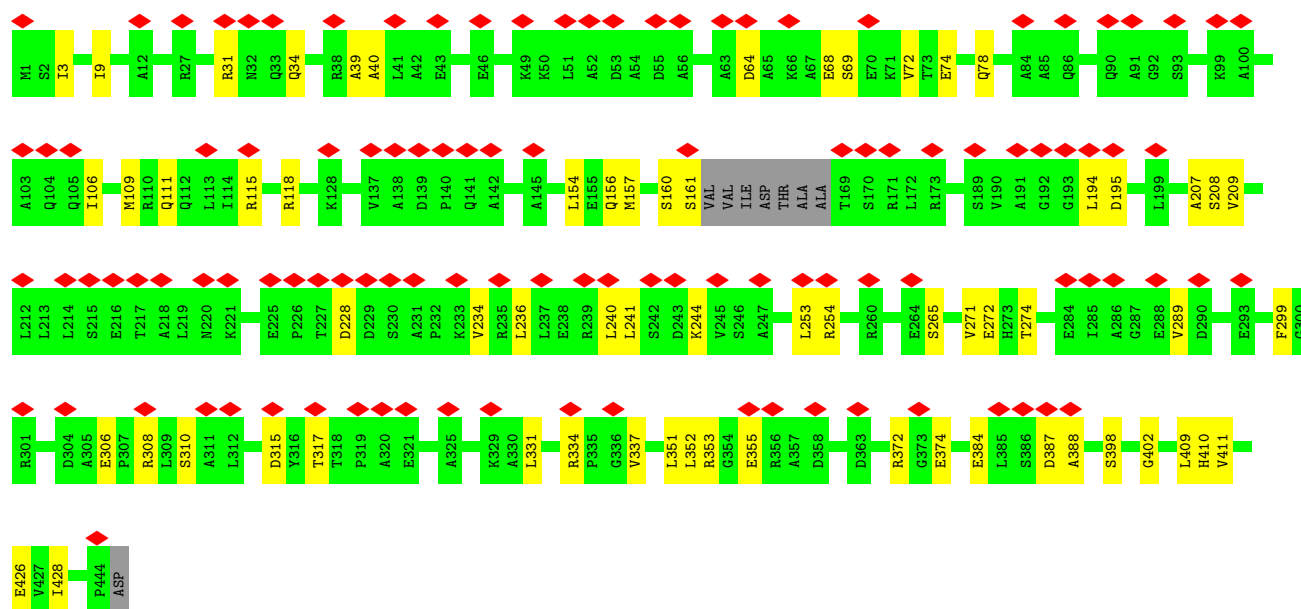
- Molecule 7: ATP synthase subunit b



- Molecule 8: ATP synthase subunit b-delta



Chain d:  25% 84% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37894	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 ($e^-/\text{\AA}^2$)	59.86	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.086	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0157	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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: ADP, MG, ATP

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	0.12	0/3964	0.25	0/5368
1	B	0.11	0/3873	0.26	0/5241
1	C	0.11	0/4038	0.25	0/5463
2	D	0.12	0/3659	0.26	0/4961
2	E	0.11	0/3619	0.24	0/4908
2	F	0.12	0/3645	0.26	0/4942
3	G	0.12	0/2306	0.25	0/3117
4	H	0.09	0/922	0.23	0/1252
5	L	0.14	0/600	0.29	0/814
5	M	0.14	0/600	0.31	0/814
5	N	0.13	0/600	0.25	0/814
5	O	0.13	0/600	0.28	0/814
5	P	0.14	0/600	0.28	0/814
5	Q	0.14	0/600	0.26	0/814
5	R	0.14	0/600	0.30	0/814
5	S	0.14	0/600	0.28	0/814
5	T	0.13	0/608	0.26	0/825
6	a	0.11	0/1905	0.26	0/2602
7	b	0.13	0/1080	0.27	0/1459
8	d	0.11	0/3307	0.25	0/4478
All	All	0.12	0/37726	0.26	0/51128

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 ⓘ

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	3904	3904	3904	23	0
1	B	3808	3815	3803	37	0
1	C	3965	3977	3965	23	0
2	D	3589	3573	3567	16	0
2	E	3554	3533	3533	26	0
2	F	3580	3564	3564	28	0
3	G	2277	2290	2290	26	0
4	H	911	891	891	13	0
5	L	589	603	603	11	0
5	M	589	603	603	11	0
5	N	589	603	603	14	0
5	O	589	603	603	13	0
5	P	589	603	603	14	0
5	Q	589	603	603	10	0
5	R	589	603	603	11	0
5	S	589	603	603	12	0
5	T	597	607	607	9	0
6	a	1851	1916	1916	24	0
7	b	1071	1090	1090	16	0
8	d	3278	3362	3362	45	0
9	A	31	12	12	0	0
9	B	31	12	12	0	0
9	C	31	12	12	0	0
9	F	31	12	12	0	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
10	C	1	0	0	0	0
10	D	1	0	0	0	0
10	F	1	0	0	0	0
11	D	27	12	12	2	0
11	E	27	12	12	0	0
12	A	3	0	0	0	0
12	B	3	0	0	1	0
12	C	3	0	0	0	0
12	D	4	0	0	1	0
12	F	3	0	0	1	0
All	All	37296	37418	37388	312	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 4.

The worst 5 of 312 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:273:ASP:OD2	1:C:275:SER:OG	1.98	0.82
8:d:109:MET:HE2	8:d:109:MET:HA	1.60	0.82
1:A:28:ARG:NH2	8:d:160:SER:OG	2.12	0.81
4:H:33:GLY:O	5:T:46:GLN:NE2	2.15	0.80
2:F:192:GLU:OE1	12:F:701:HOH:O	2.02	0.78

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 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	Percentiles	
1	A	515/548 (94%)	506 (98%)	9 (2%)	0	100	100
1	B	499/548 (91%)	495 (99%)	4 (1%)	0	100	100
1	C	518/548 (94%)	509 (98%)	9 (2%)	0	100	100
2	D	468/475 (98%)	461 (98%)	7 (2%)	0	100	100
2	E	462/475 (97%)	453 (98%)	8 (2%)	1 (0%)	43	54
2	F	466/475 (98%)	457 (98%)	9 (2%)	0	100	100
3	G	293/307 (95%)	289 (99%)	4 (1%)	0	100	100
4	H	116/121 (96%)	112 (97%)	4 (3%)	0	100	100
5	L	82/86 (95%)	77 (94%)	5 (6%)	0	100	100
5	M	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
5	N	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
5	O	82/86 (95%)	81 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	P	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
5	Q	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
5	R	82/86 (95%)	82 (100%)	0	0	100	100
5	S	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
5	T	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
6	a	236/252 (94%)	231 (98%)	5 (2%)	0	100	100
7	b	142/180 (79%)	139 (98%)	3 (2%)	0	100	100
8	d	433/445 (97%)	427 (99%)	6 (1%)	0	100	100
All	All	4887/5148 (95%)	4804 (98%)	82 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	277	VAL

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 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	A	415/441 (94%)	407 (98%)	8 (2%)	50	64
1	B	406/441 (92%)	403 (99%)	3 (1%)	76	84
1	C	422/441 (96%)	418 (99%)	4 (1%)	70	81
2	D	384/388 (99%)	382 (100%)	2 (0%)	81	87
2	E	381/388 (98%)	376 (99%)	5 (1%)	61	73
2	F	383/388 (99%)	377 (98%)	6 (2%)	55	69
3	G	231/238 (97%)	229 (99%)	2 (1%)	70	81
4	H	94/96 (98%)	92 (98%)	2 (2%)	47	62
5	L	54/56 (96%)	54 (100%)	0	100	100
5	M	54/56 (96%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	N	54/56 (96%)	54 (100%)	0	100	100
5	O	54/56 (96%)	53 (98%)	1 (2%)	50	64
5	P	54/56 (96%)	53 (98%)	1 (2%)	50	64
5	Q	54/56 (96%)	54 (100%)	0	100	100
5	R	54/56 (96%)	53 (98%)	1 (2%)	50	64
5	S	54/56 (96%)	53 (98%)	1 (2%)	50	64
5	T	55/56 (98%)	54 (98%)	1 (2%)	51	65
6	a	191/200 (96%)	187 (98%)	4 (2%)	47	62
7	b	110/134 (82%)	109 (99%)	1 (1%)	70	81
8	d	341/347 (98%)	336 (98%)	5 (2%)	57	70
All	All	3845/4006 (96%)	3798 (99%)	47 (1%)	61	74

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	137	SER
5	S	20	ILE
3	G	227	ASP
5	O	20	ILE
6	a	69	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
7	b	77	GLN
8	d	220	ASN
1	C	505	ASN
1	C	362	GLN
8	d	259	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
9	ATP	C	600	10	32,33,33	0.37	0	48,52,52	0.67	0
11	ADP	E	600	-	28,29,29	1.40	4 (14%)	43,45,45	1.92	11 (25%)
9	ATP	F	600	10	32,33,33	0.45	0	48,52,52	0.68	0
11	ADP	D	600	10	28,29,29	1.38	4 (14%)	43,45,45	1.87	10 (23%)
9	ATP	B	600	10	32,33,33	0.34	0	48,52,52	0.68	0
9	ATP	A	600	10	32,33,33	0.36	0	48,52,52	0.66	0

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	C	600	10	-	1/22/38/38	0/3/3/3
11	ADP	E	600	-	-	0/16/32/32	0/3/3/3
9	ATP	F	600	10	-	2/22/38/38	0/3/3/3
11	ADP	D	600	10	-	7/16/32/32	0/3/3/3
9	ATP	B	600	10	-	1/22/38/38	0/3/3/3
9	ATP	A	600	10	-	0/22/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	E	600	ADP	C5-C4	4.58	1.47	1.39
11	D	600	ADP	C5-C4	4.47	1.47	1.39
11	E	600	ADP	C5-C6	2.69	1.48	1.41
11	D	600	ADP	C5-C6	2.53	1.48	1.41
11	D	600	ADP	C5-N7	-2.50	1.34	1.39

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	E	600	ADP	C5-C4-N3	-5.92	118.57	126.72
11	D	600	ADP	C5-C4-N3	-5.82	118.70	126.72
11	D	600	ADP	N3-C4-N9	4.85	135.42	127.17
11	E	600	ADP	N3-C4-N9	4.77	135.29	127.17
11	E	600	ADP	C2-N3-C4	3.88	121.31	111.83

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

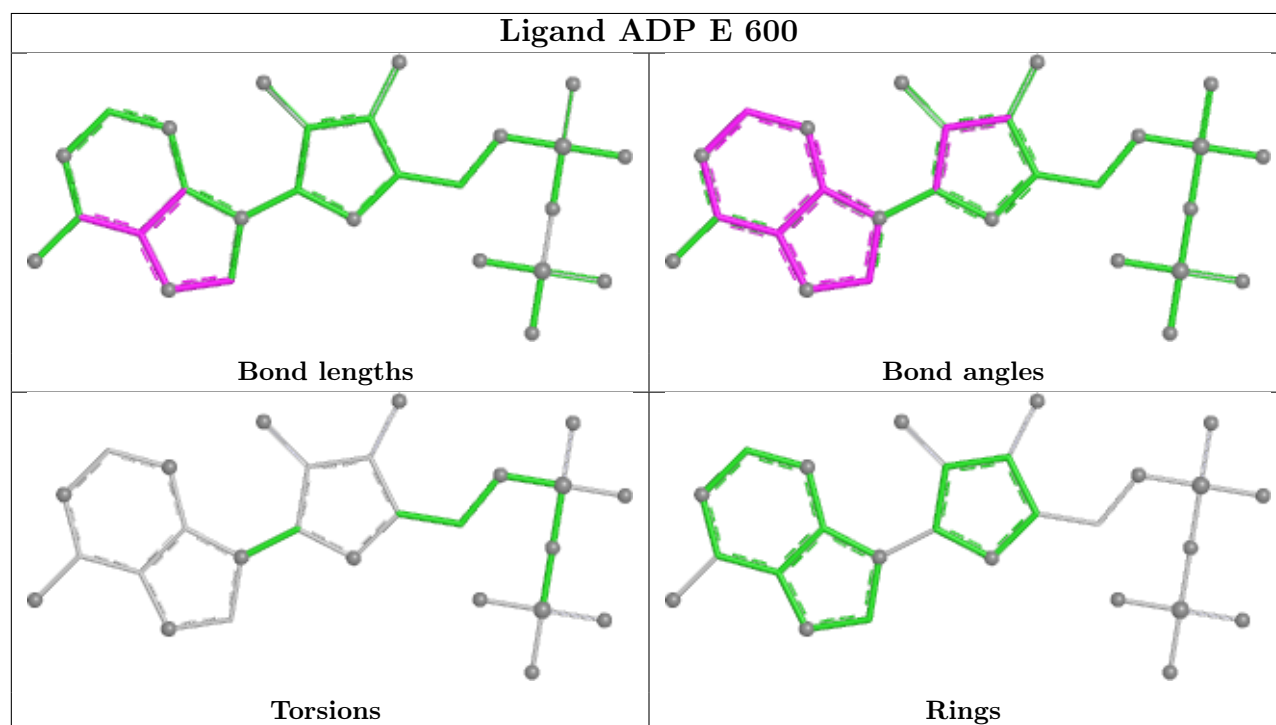
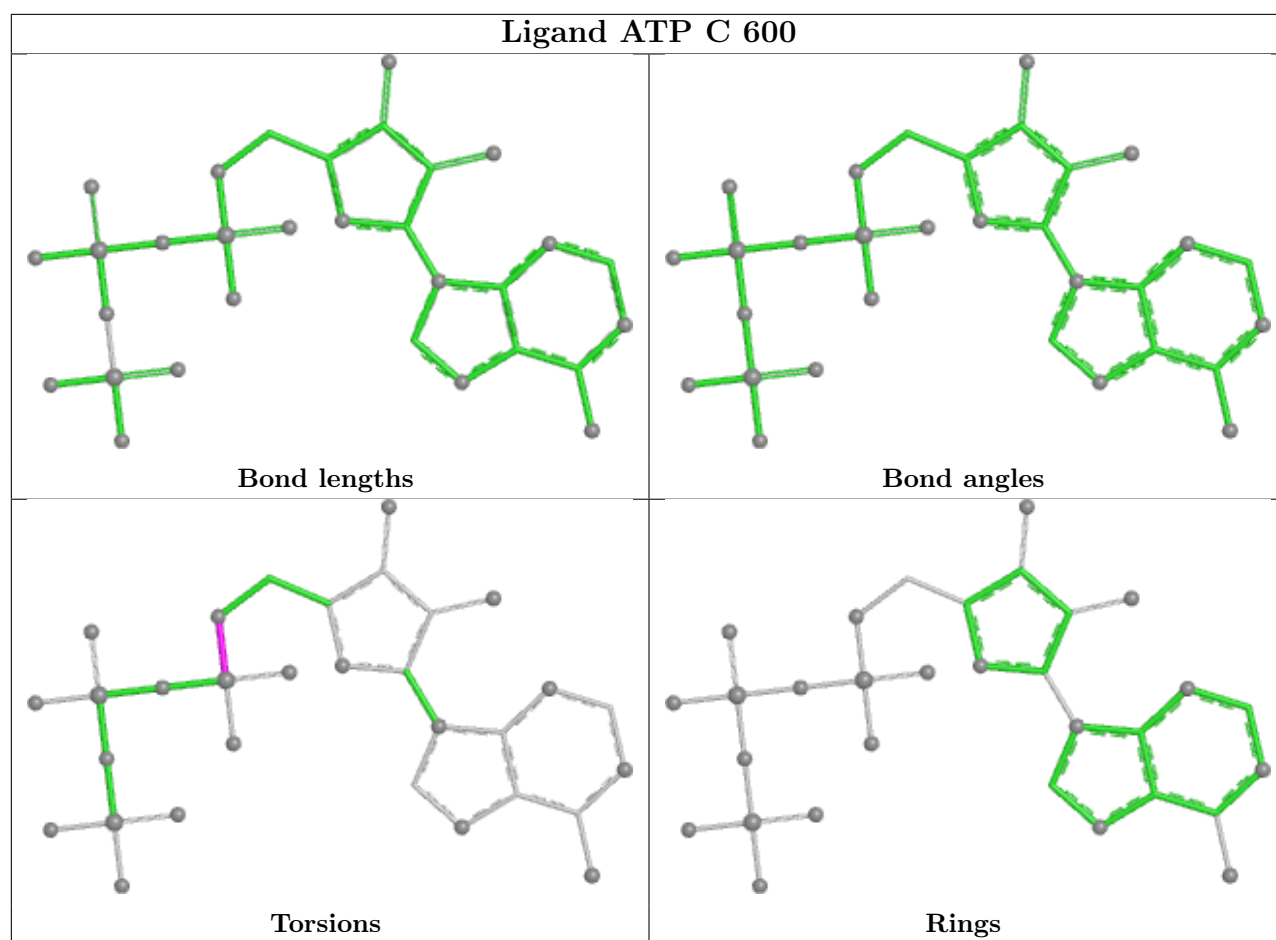
Mol	Chain	Res	Type	Atoms
9	F	600	ATP	PA-O3A-PB-O1B
11	D	600	ADP	PB-O3A-PA-O2A
9	B	600	ATP	C5'-O5'-PA-O1A
9	C	600	ATP	C5'-O5'-PA-O1A
11	D	600	ADP	C5'-O5'-PA-O1A

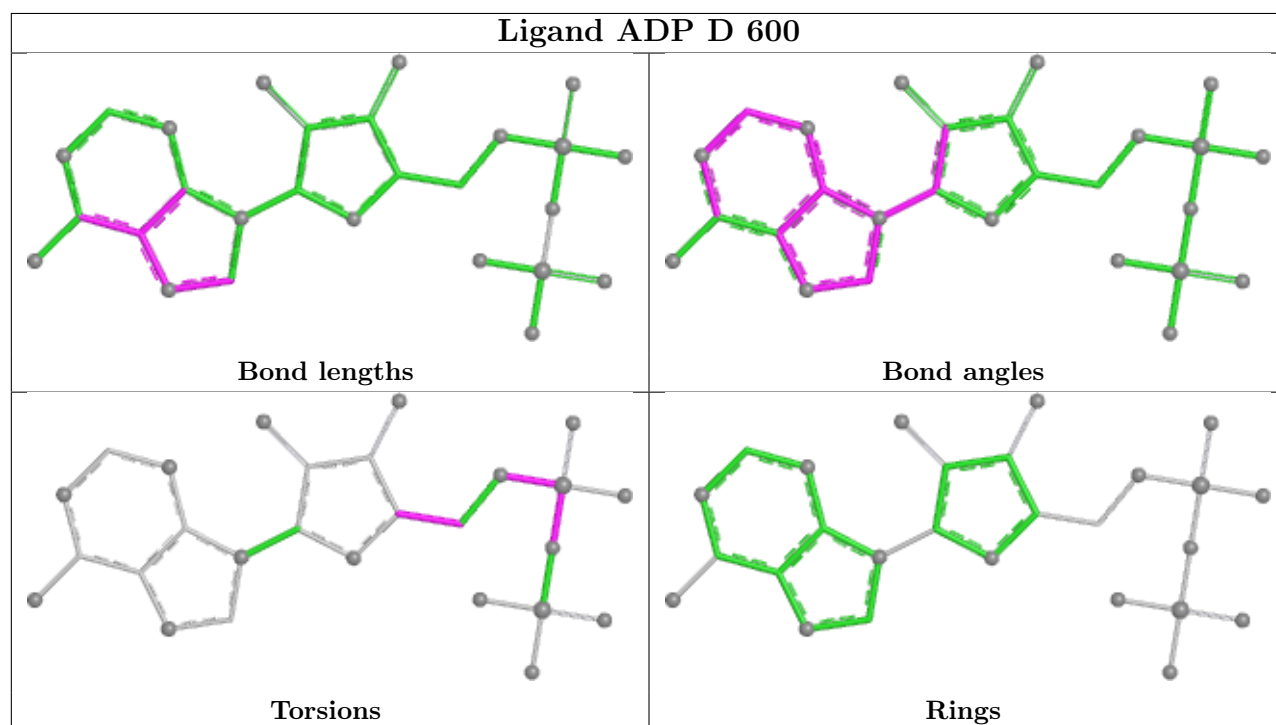
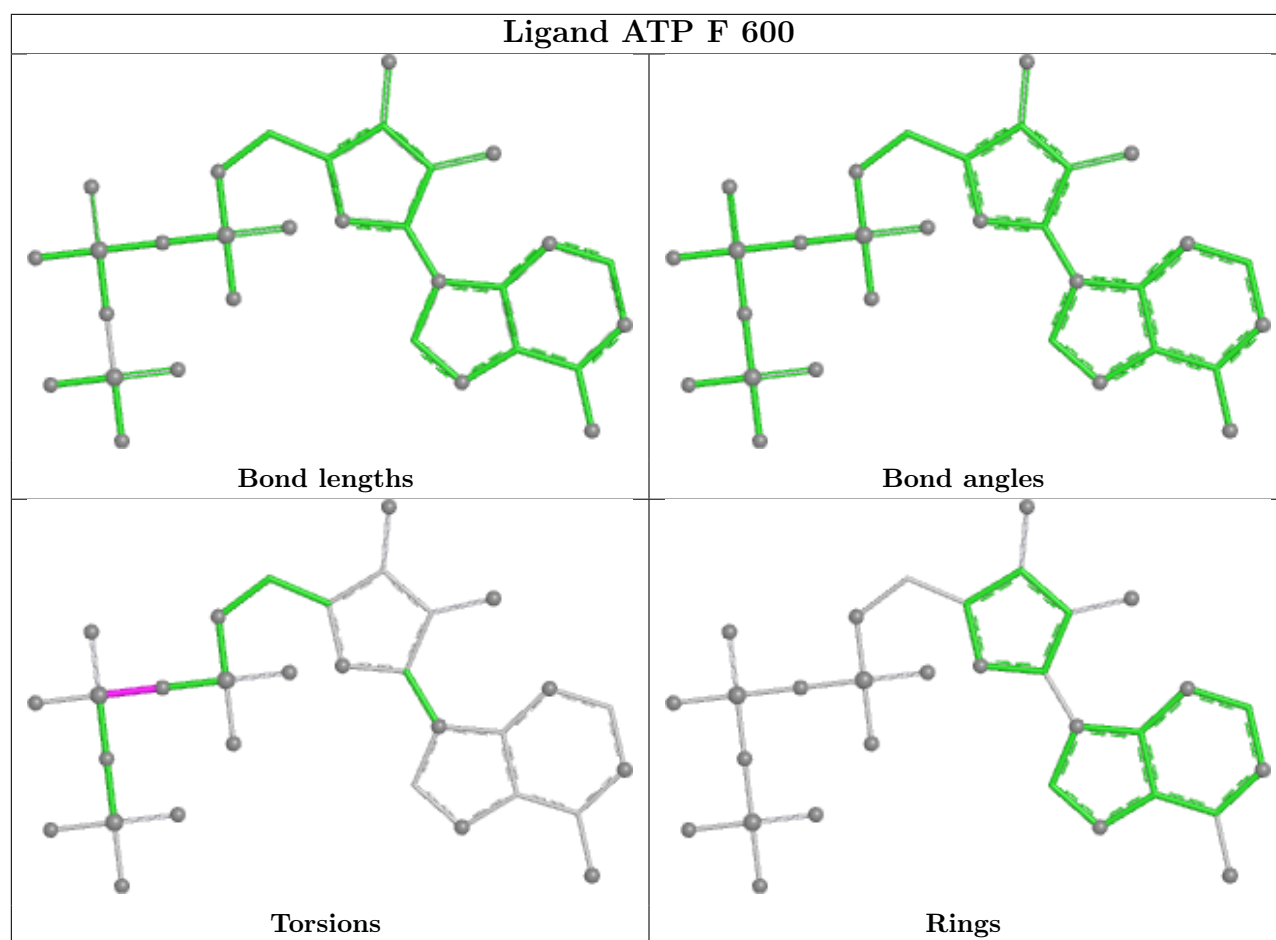
There are no ring outliers.

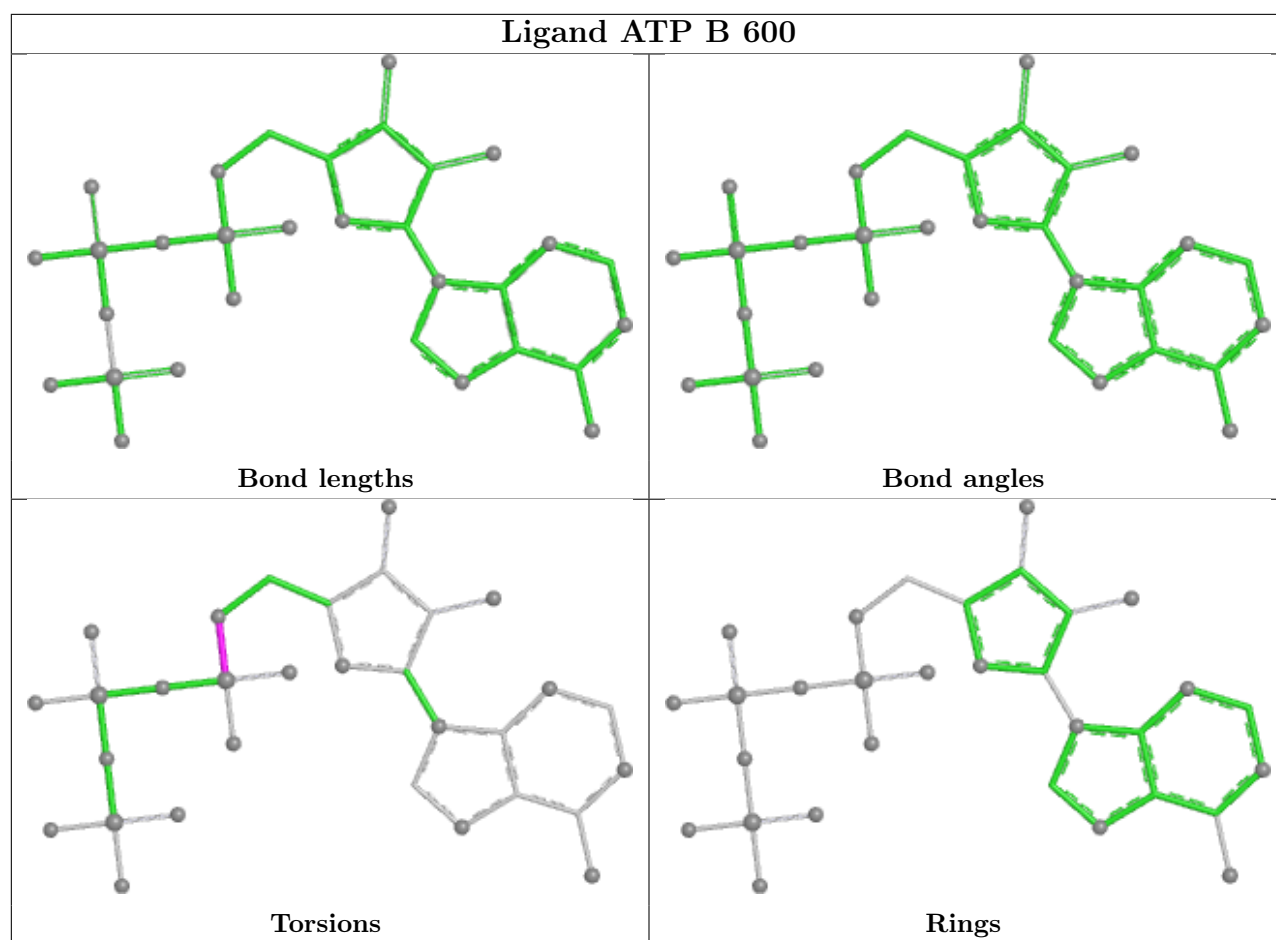
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	D	600	ADP	2	0

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 than 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.

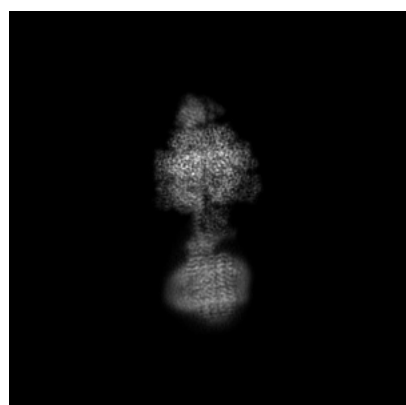
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12417. These allow visual inspection of the internal detail of the map and identification of artifacts.

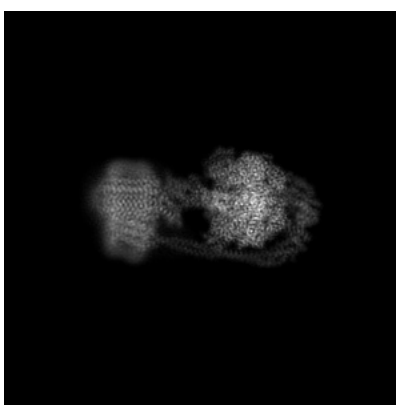
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

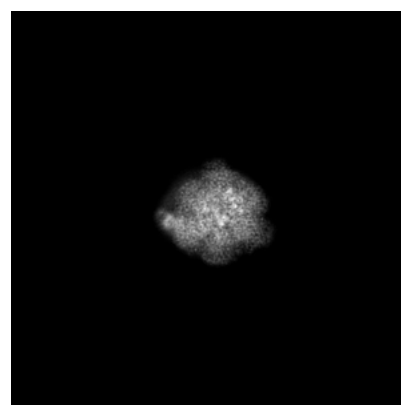
6.1.1 Primary map



X



Y

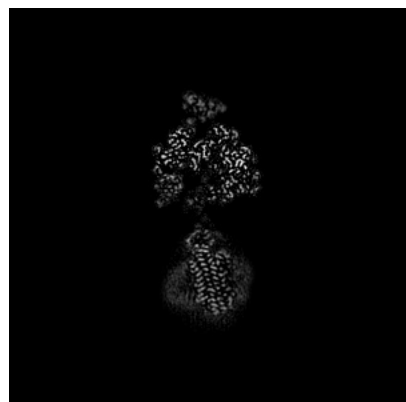


Z

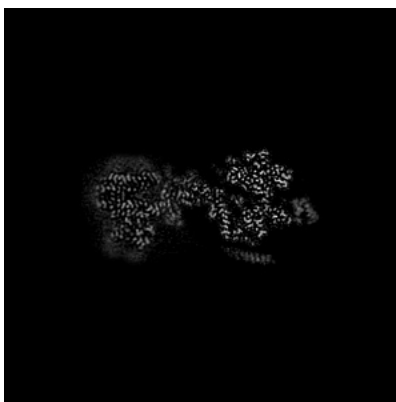
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

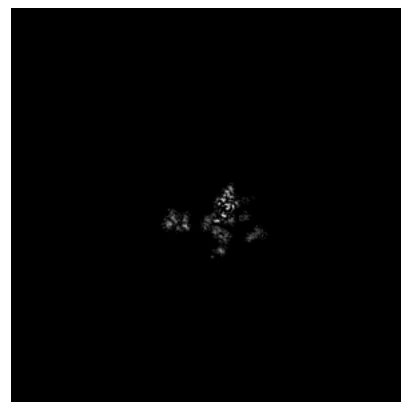
6.2.1 Primary map



X Index: 250



Y Index: 250

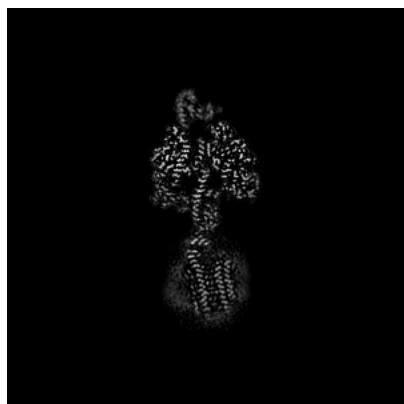


Z Index: 250

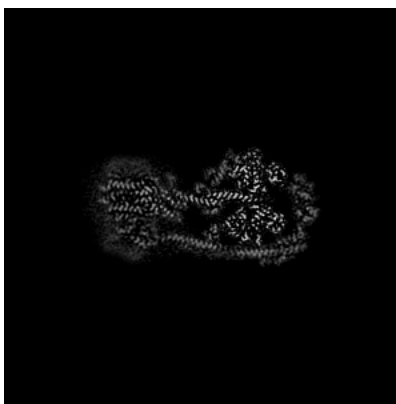
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

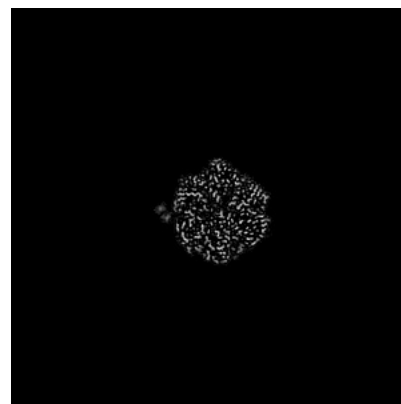
6.3.1 Primary map



X Index: 258



Y Index: 237

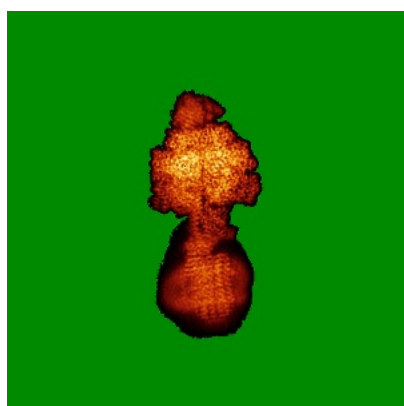


Z Index: 310

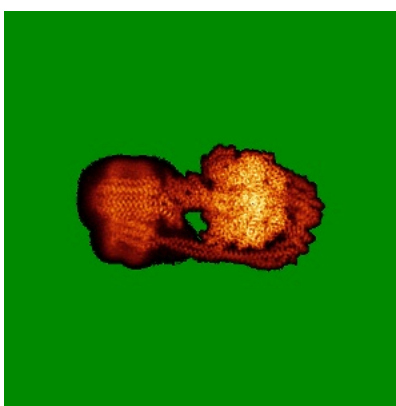
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

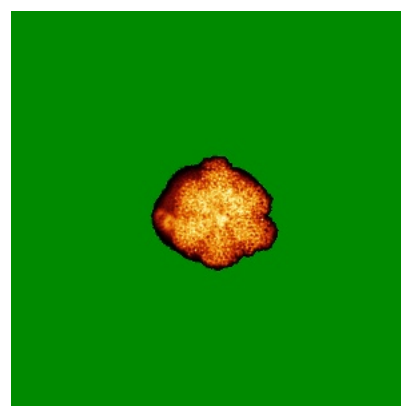
6.4.1 Primary map



X



Y



Z

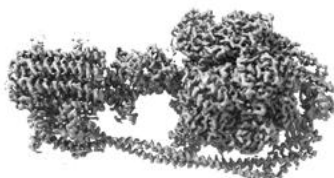
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

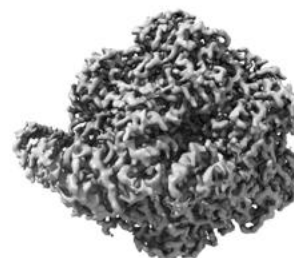
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0157. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

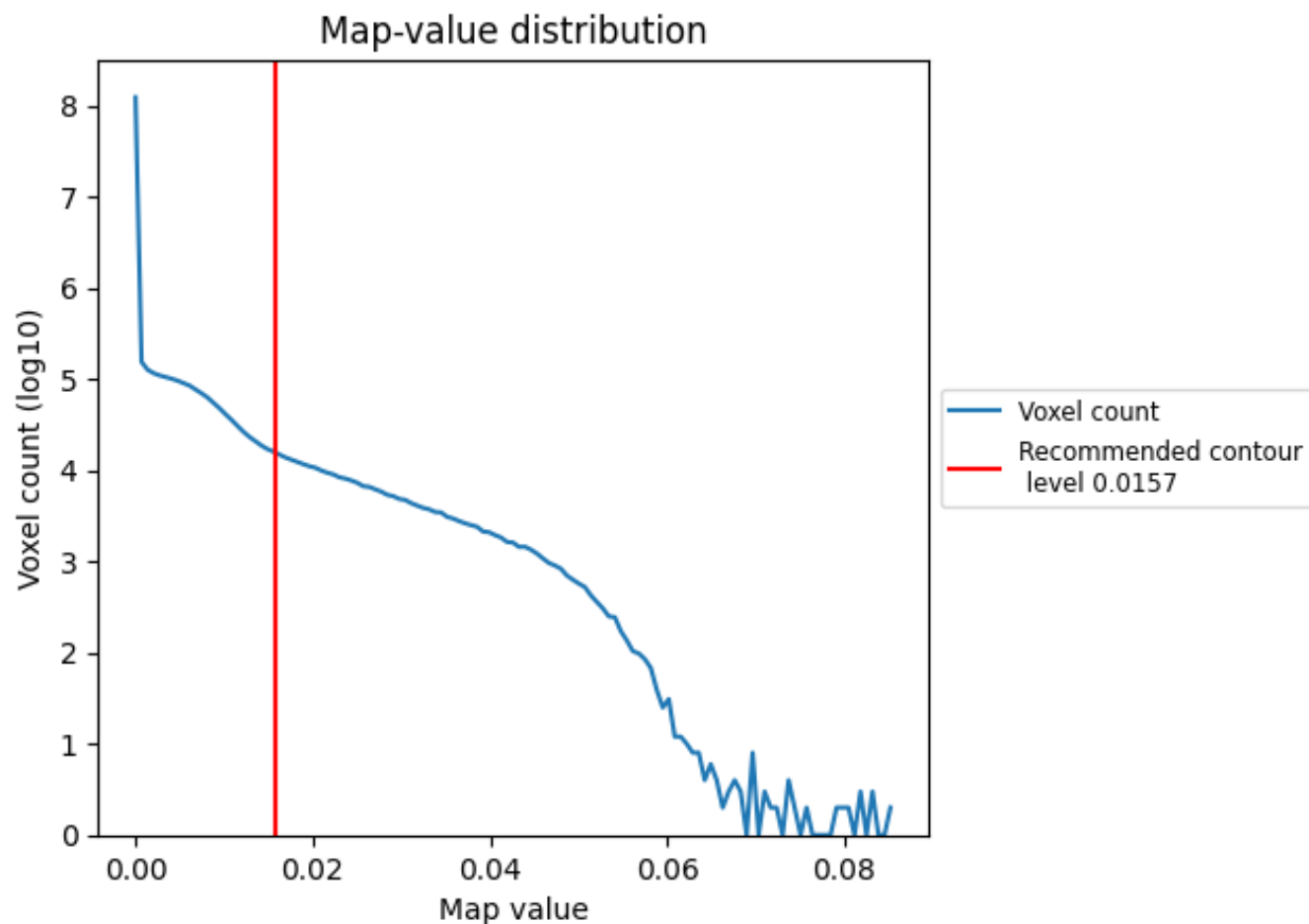
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

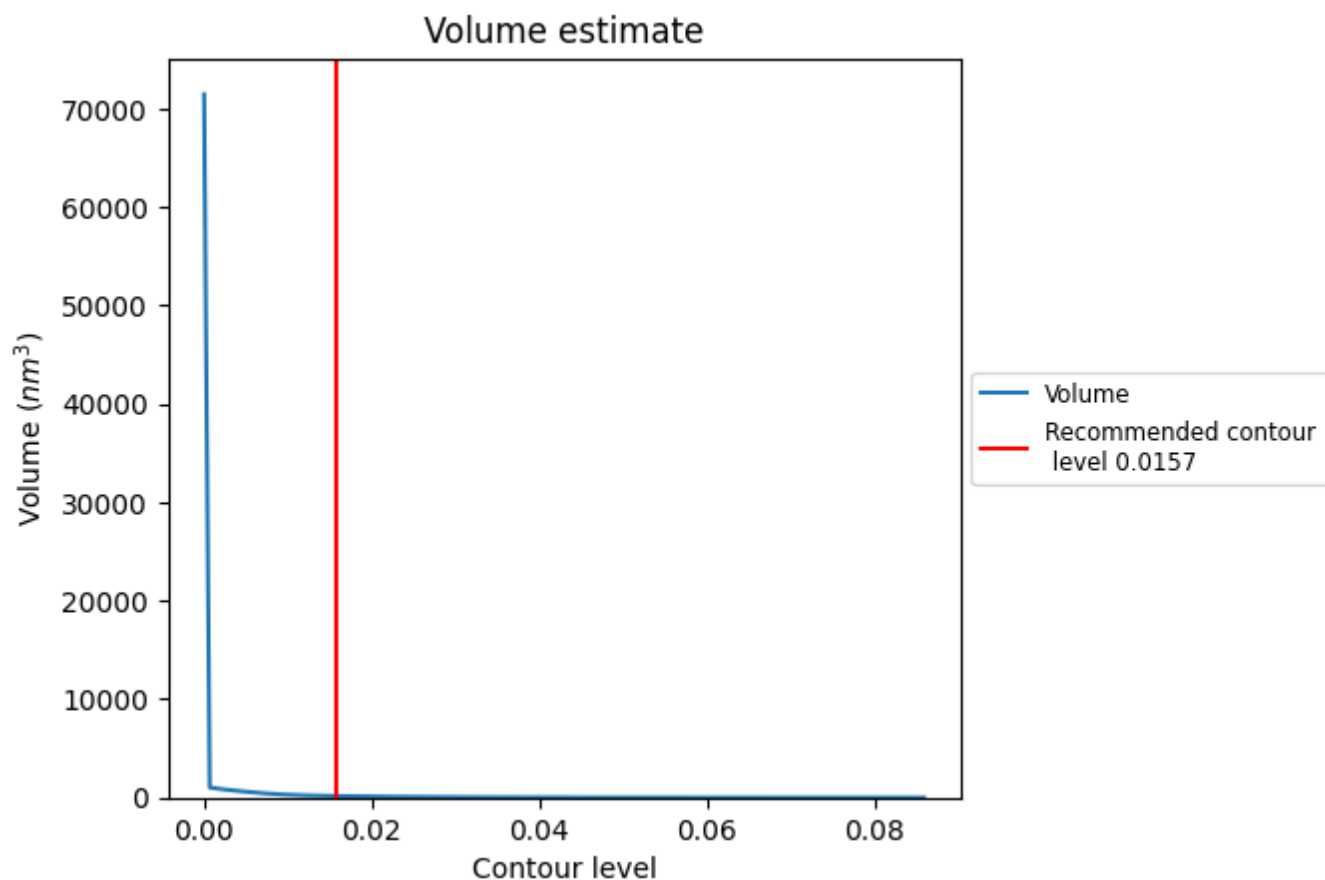
This section contains the results of statistical analysis of the map.

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.

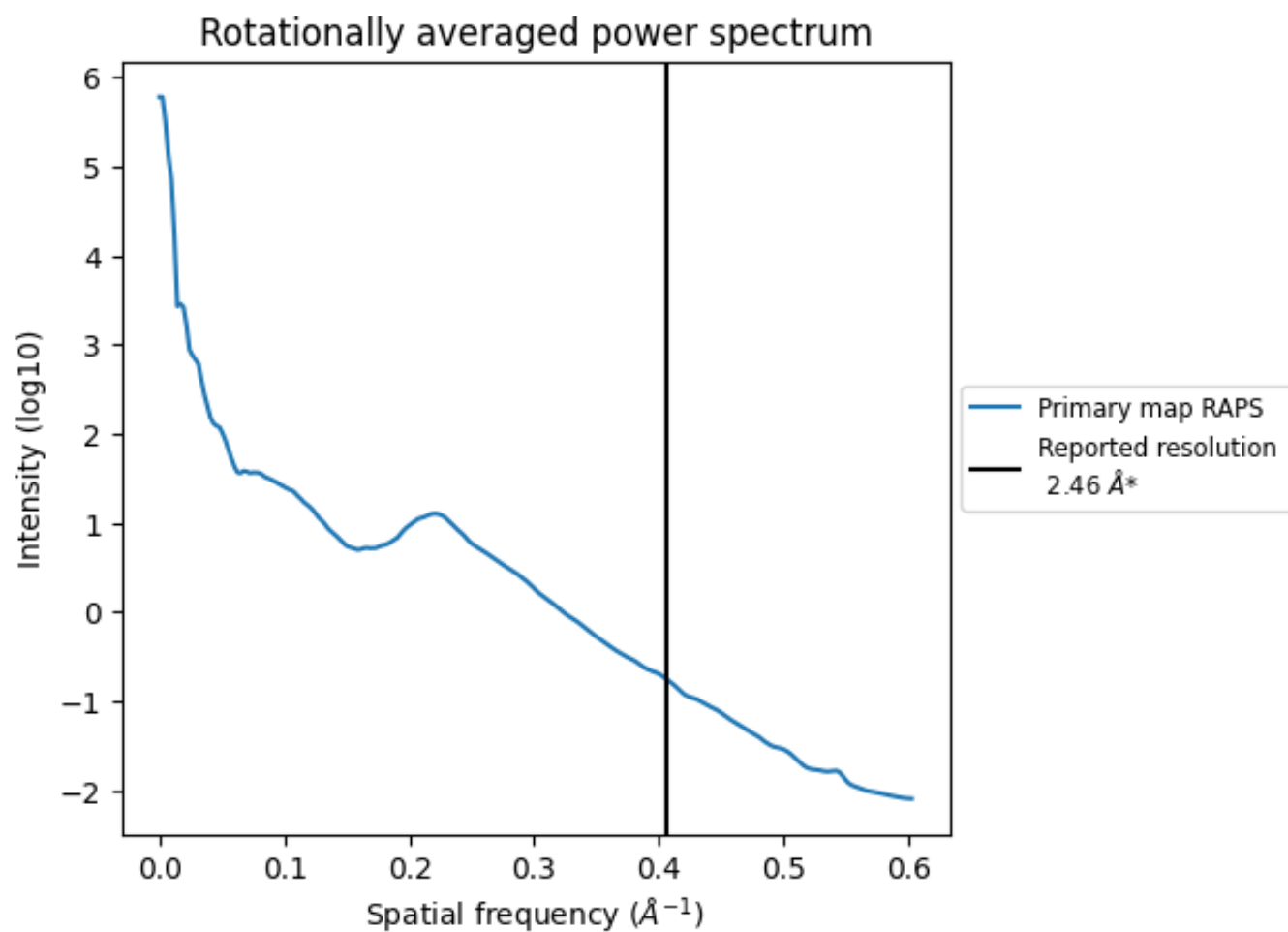
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 155 nm³; this corresponds to an approximate mass of 140 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.407 Å⁻¹

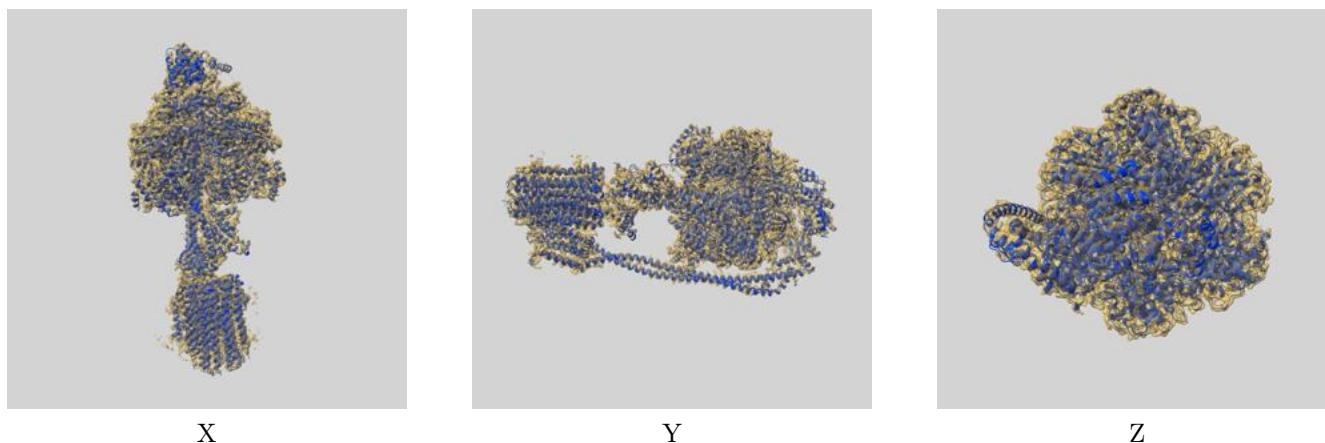
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

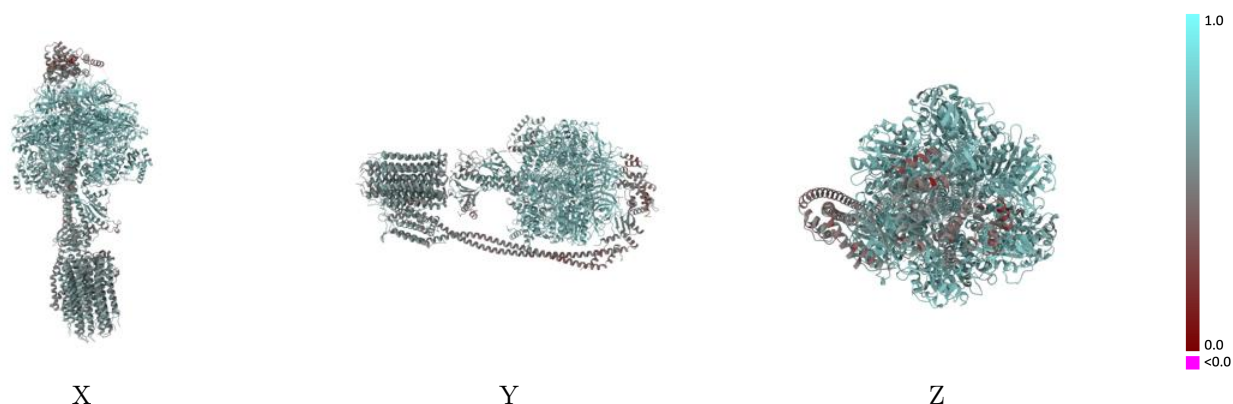
This section contains information regarding the fit between EMDB map EMD-12417 and PDB model 7NJS. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



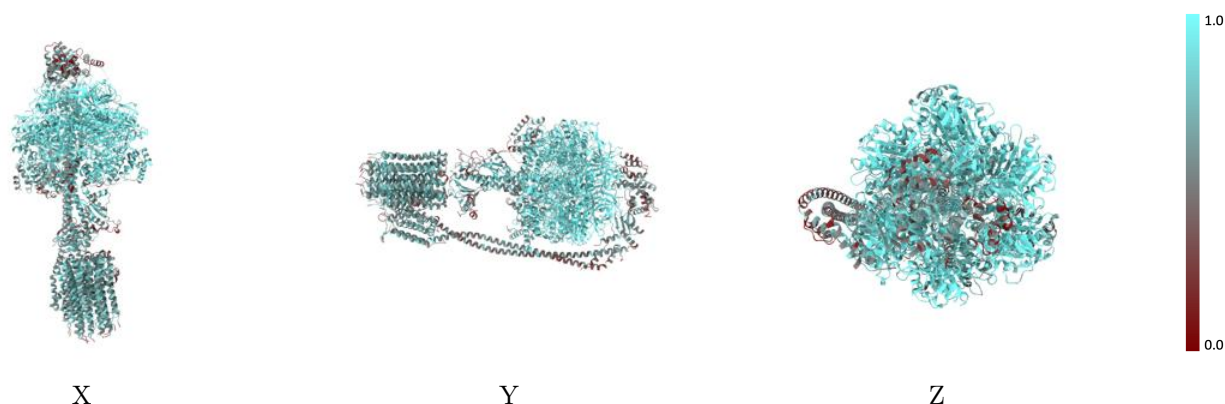
The images above show the 3D surface view of the map at the recommended contour level 0.0157 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



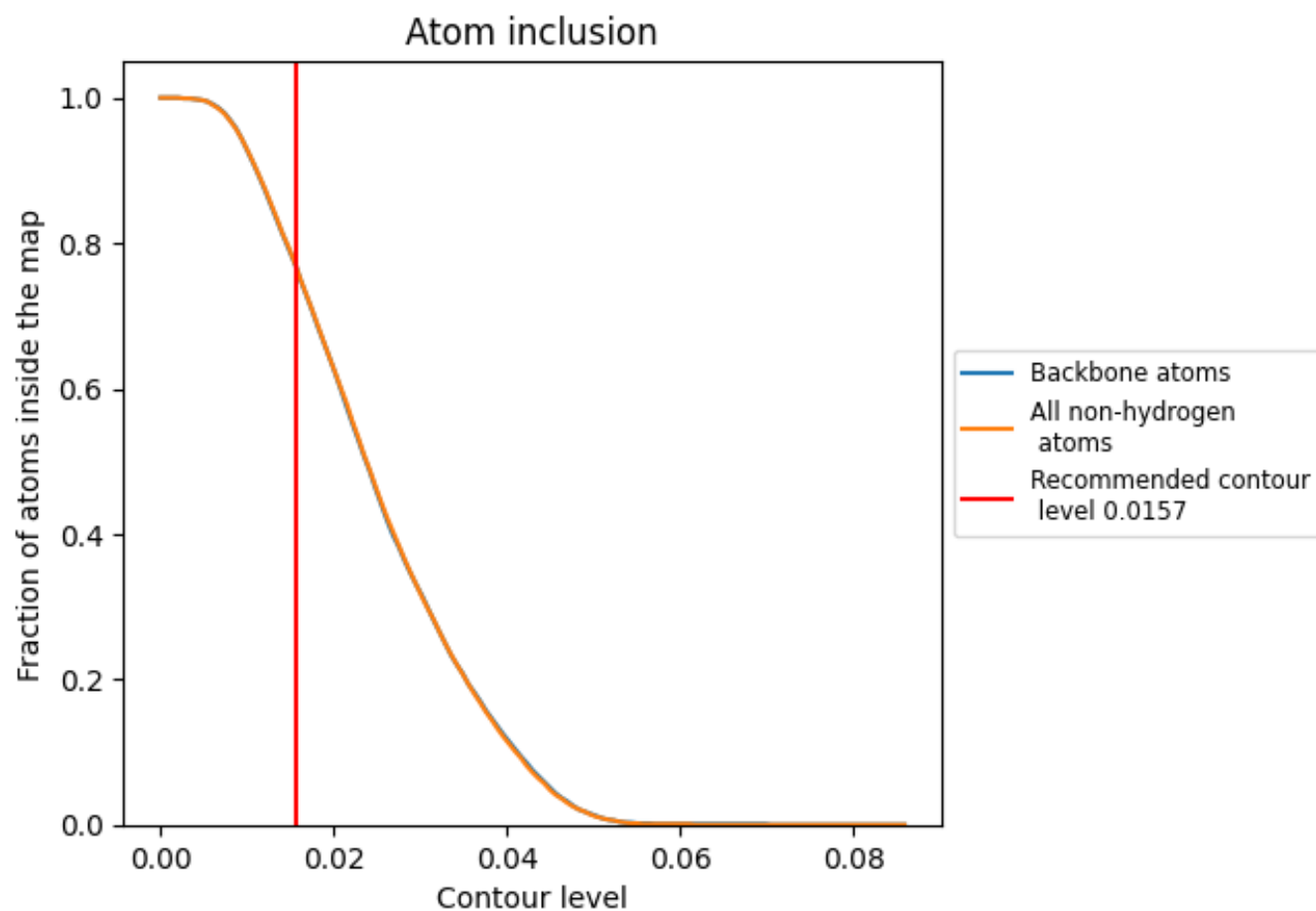
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0157).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0157) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7660	 0.6140
A	 0.8700	 0.6690
B	 0.8170	 0.6460
C	 0.8590	 0.6620
D	 0.9070	 0.6830
E	 0.8400	 0.6630
F	 0.9130	 0.6860
G	 0.7170	 0.5980
H	 0.5840	 0.5290
L	 0.6900	 0.5550
M	 0.6640	 0.5530
N	 0.6470	 0.5400
O	 0.6300	 0.5450
P	 0.6450	 0.5460
Q	 0.6420	 0.5410
R	 0.6510	 0.5610
S	 0.6750	 0.5570
T	 0.7060	 0.5630
a	 0.5930	 0.5350
b	 0.5280	 0.4670
d	 0.5390	 0.4750

