



wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 12:26 PM JST

PDB ID : 8J0T
EMDB ID : EMD-35911
Title : Cryo-EM structure of Mycobacterium tuberculosis ATP synthase in the apo-form
Authors : Zhang, Y.; Lai, Y.; Liu, F.; Rao, Z.; Gong, H.
Deposited on : 2023-04-11
Resolution : 2.80 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:

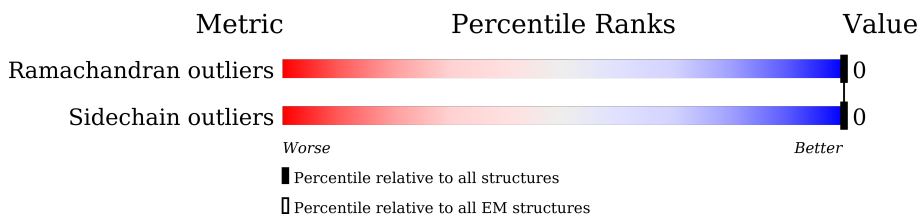
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance

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

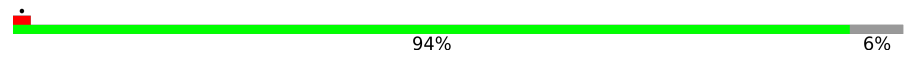
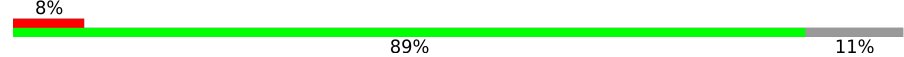
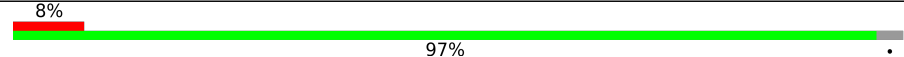
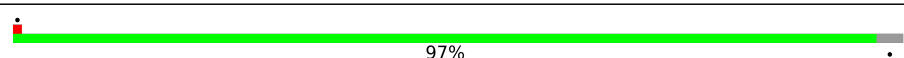
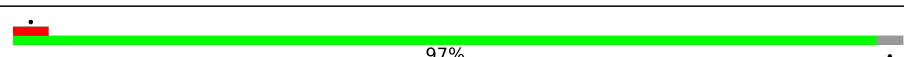
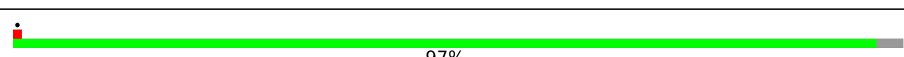
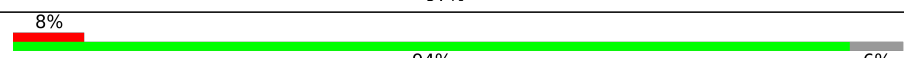
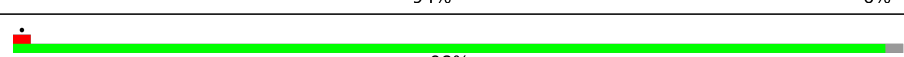
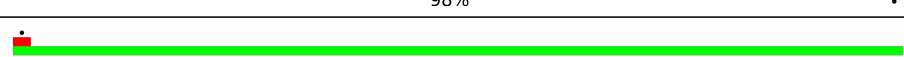
The reported resolution of this entry is 2.80 Å.

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)
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 $\leq 5\%$. 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	549	 94% 6%
1	B	549	 8% 89% 11%
1	C	549	 8% 97% .
2	D	486	 97% .
2	E	486	 97% .
2	F	486	 97% .
3	G	305	 8% 94% 6%
4	H	121	 98% .
5	1	81	 100%

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Mol	Chain	Length	Quality of chain
5	2	81	 100%
5	3	81	 100%
5	4	81	 100%
5	5	81	 100%
5	6	81	 100%
5	7	81	 100%
5	8	81	 100%
5	9	81	 100%
6	a	250	 15% 88% 12%
7	b	171	 9% 84% 16%
8	d	446	 17% 100%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 37208 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.

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	517	Total 3916	C 2449	N 684	O 772	S 11	0	0
1	B	491	Total 3740	C 2341	N 654	O 734	S 11	0	0
1	C	534	Total 4061	C 2544	N 708	O 798	S 11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	469	Total 3614	C 2279	N 622	O 701	S 12	0	0
2	E	469	Total 3614	C 2279	N 622	O 701	S 12	0	0
2	F	469	Total 3614	C 2279	N 622	O 701	S 12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	287	Total 2251	C 1415	N 398	O 430	S 8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	H	119	Total 906	C 562	N 162	O 181	S 1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	2	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	3	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	4	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	5	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	6	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	7	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	8	81	Total	C	N	O	S	0	0
			567	373	92	99	3		
5	9	81	Total	C	N	O	S	0	0
			567	373	92	99	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	220	Total	C	N	O	S	0	0
			1706	1145	269	286	6		

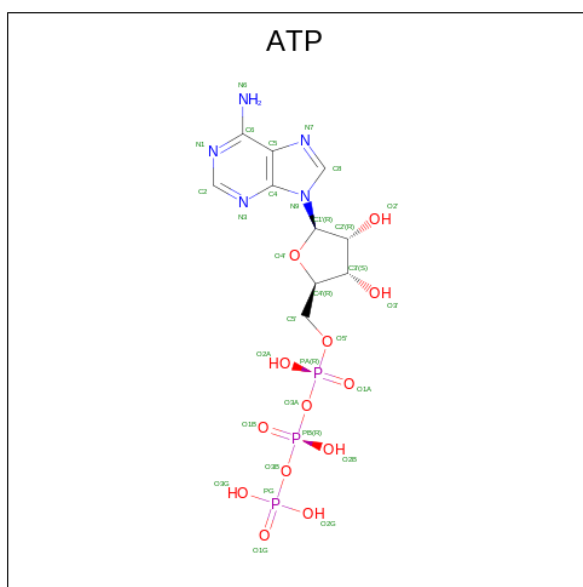
- Molecule 7 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	b	144	Total	C	N	O	S	0	0
			1107	691	201	212	3		

- Molecule 8 is a protein called Multifunctional fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	d	445	Total	C	N	O	S	0	0
			3424	2131	637	649	7		

- Molecule 9 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
9	A	1	31	10	5	13	3	0
9	B	1	31	10	5	13	3	0
9	C	1	31	10	5	13	3	0

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

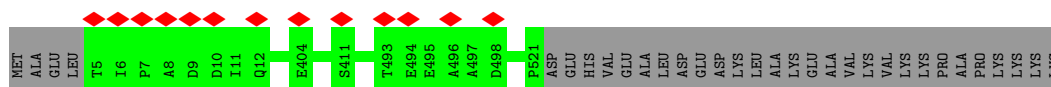
- Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

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.

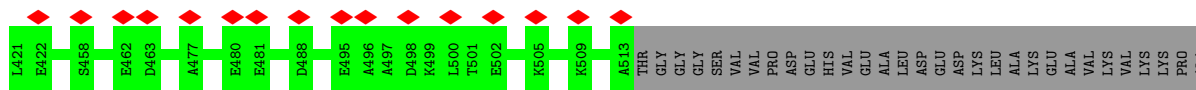
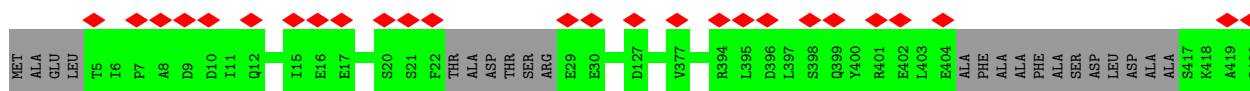
- Molecule 1: ATP synthase subunit alpha

Chain A:  94% 6%



- Molecule 1: ATP synthase subunit alpha

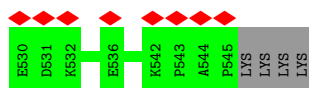
Chain B:  8% 89% 11%



PRO
LYS
LYS
LYS

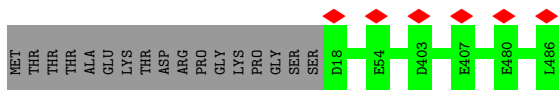
- Molecule 1: ATP synthase subunit alpha

Chain C:  8% 97% .

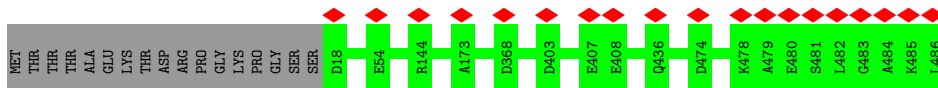


- Molecule 2: ATP synthase subunit beta

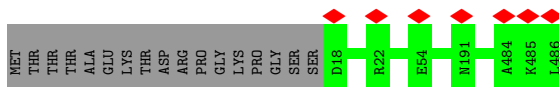
Chain D:  97% .



- Molecule 2: ATP synthase subunit beta



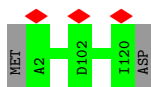
- Molecule 2: ATP synthase subunit beta



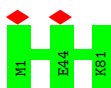
- Molecule 3: ATP synthase gamma chain



- Molecule 4: ATP synthase epsilon chain



- Molecule 5: ATP synthase subunit c



- Molecule 5: ATP synthase subunit c



- Molecule 5: ATP synthase subunit c

Chain 3:  100%



- Molecule 5: ATP synthase subunit c

Chain 4:  100%



- Molecule 5: ATP synthase subunit c

Chain 5:  100%



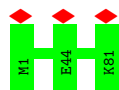
- Molecule 5: ATP synthase subunit c

Chain 6:  100%



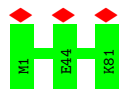
- Molecule 5: ATP synthase subunit c

Chain 7:  100%



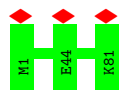
- Molecule 5: ATP synthase subunit c

Chain 8:  100%

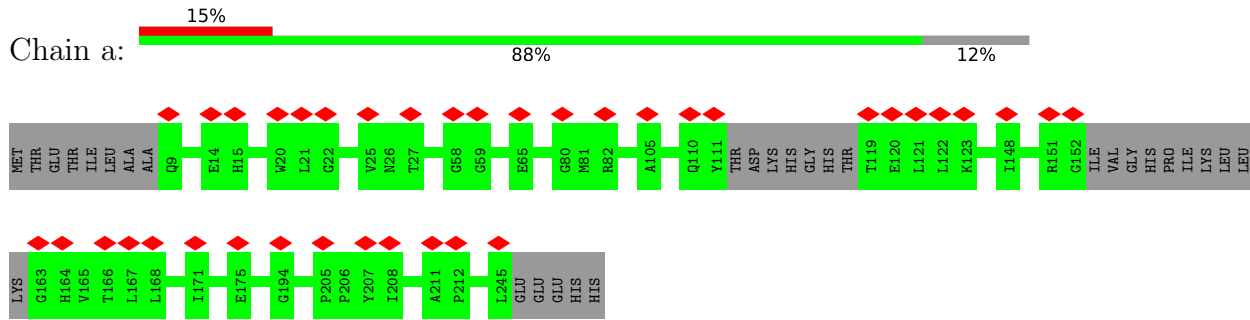


- Molecule 5: ATP synthase subunit c

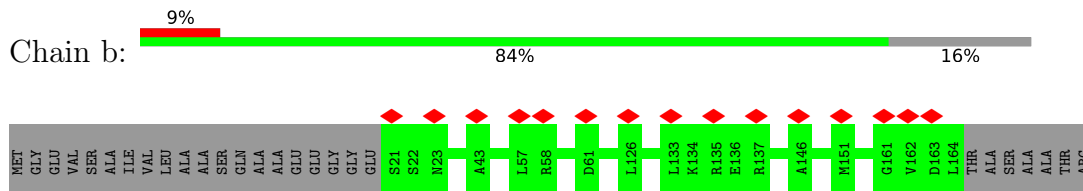
Chain 9:  100%



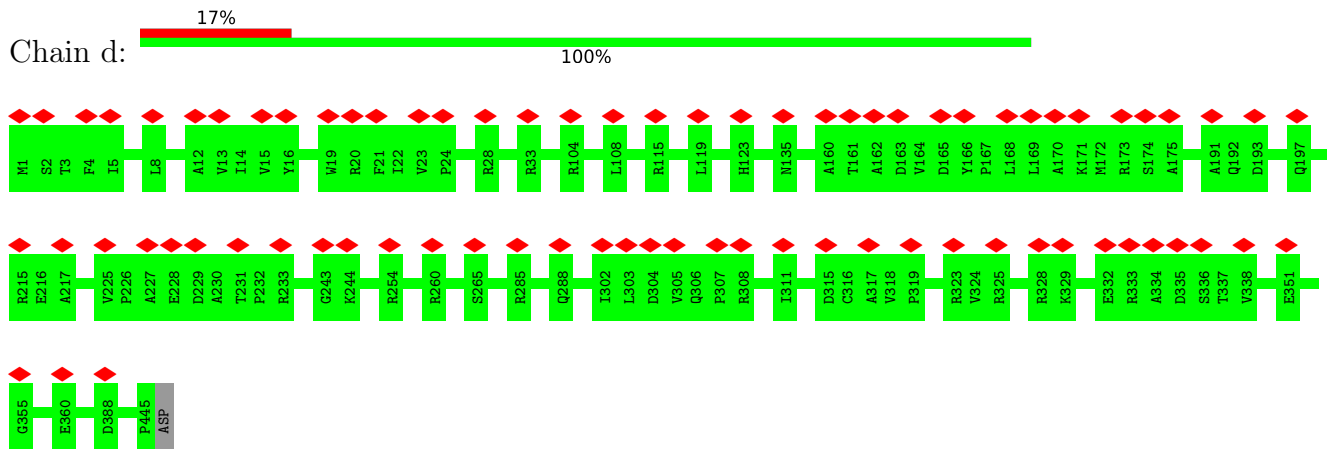
• Molecule 6: ATP synthase subunit a



• Molecule 7: ATP synthase subunit b



• Molecule 8: Multifunctional fusion protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66593	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	44.692	Depositor
Minimum map value	-25.990	Depositor
Average map value	0.009	Depositor
Map value standard deviation	1.095	Depositor
Recommended contour level	5.6	Depositor
Map size (\AA)	373.76, 373.76, 373.76	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.73, 0.73, 0.73	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, ATP, 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	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/3976	0.46	0/5387
1	B	0.32	0/3795	0.46	0/5137
1	C	0.33	0/4122	0.45	0/5580
2	D	0.32	0/3680	0.45	0/4990
2	E	0.31	0/3680	0.45	0/4990
2	F	0.31	0/3680	0.45	0/4990
3	G	0.32	0/2286	0.46	0/3092
4	H	0.35	0/915	0.51	0/1237
5	1	0.40	0/578	0.49	0/784
5	2	0.41	0/578	0.49	0/784
5	3	0.41	0/578	0.49	0/784
5	4	0.40	0/578	0.49	0/784
5	5	0.37	0/578	0.47	0/784
5	6	0.37	0/578	0.47	0/784
5	7	0.37	0/578	0.47	0/784
5	8	0.37	0/578	0.47	0/784
5	9	0.37	0/578	0.47	0/784
6	a	0.33	0/1748	0.52	0/2390
7	b	0.36	0/1118	0.62	0/1512
8	d	0.34	0/3462	0.58	0/4697
All	All	0.33	0/37664	0.48	0/51058

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	Percentiles	
1	A	515/549 (94%)	490 (95%)	25 (5%)	0	100	100
1	B	485/549 (88%)	463 (96%)	22 (4%)	0	100	100
1	C	528/549 (96%)	503 (95%)	25 (5%)	0	100	100
2	D	467/486 (96%)	446 (96%)	21 (4%)	0	100	100
2	E	467/486 (96%)	453 (97%)	14 (3%)	0	100	100
2	F	467/486 (96%)	446 (96%)	21 (4%)	0	100	100
3	G	283/305 (93%)	272 (96%)	11 (4%)	0	100	100
4	H	117/121 (97%)	113 (97%)	4 (3%)	0	100	100
5	1	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
5	2	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
5	3	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
5	4	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
5	5	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
5	6	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
5	7	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
5	8	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
5	9	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
6	a	214/250 (86%)	201 (94%)	13 (6%)	0	100	100
7	b	142/171 (83%)	127 (89%)	15 (11%)	0	100	100
8	d	443/446 (99%)	415 (94%)	28 (6%)	0	100	100
All	All	4839/5127 (94%)	4607 (95%)	232 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	417/444 (94%)	417 (100%)	0	100	100
1	B	400/444 (90%)	400 (100%)	0	100	100
1	C	433/444 (98%)	433 (100%)	0	100	100
2	D	389/403 (96%)	389 (100%)	0	100	100
2	E	389/403 (96%)	389 (100%)	0	100	100
2	F	389/403 (96%)	389 (100%)	0	100	100
3	G	235/248 (95%)	235 (100%)	0	100	100
4	H	94/96 (98%)	94 (100%)	0	100	100
5	1	52/52 (100%)	52 (100%)	0	100	100
5	2	52/52 (100%)	52 (100%)	0	100	100
5	3	52/52 (100%)	52 (100%)	0	100	100
5	4	52/52 (100%)	52 (100%)	0	100	100
5	5	52/52 (100%)	52 (100%)	0	100	100
5	6	52/52 (100%)	52 (100%)	0	100	100
5	7	52/52 (100%)	52 (100%)	0	100	100
5	8	52/52 (100%)	52 (100%)	0	100	100
5	9	52/52 (100%)	52 (100%)	0	100	100
6	a	178/204 (87%)	178 (100%)	0	100	100
7	b	117/133 (88%)	117 (100%)	0	100	100
8	d	356/357 (100%)	356 (100%)	0	100	100
All	All	3865/4047 (96%)	3865 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
5	5	67	ASN
6	a	227	GLN
5	6	67	ASN
5	9	67	ASN
8	d	123	HIS

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 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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	A	600	10	26,33,33	0.91	1 (3%)	31,52,52	1.52	5 (16%)
9	ATP	B	600	10	26,33,33	0.90	1 (3%)	31,52,52	1.53	5 (16%)
9	ATP	C	600	10	26,33,33	0.90	1 (3%)	31,52,52	1.52	5 (16%)
11	ADP	F	600	10	24,29,29	0.92	1 (4%)	29,45,45	1.41	4 (13%)
11	ADP	D	600	10	24,29,29	0.93	1 (4%)	29,45,45	1.40	4 (13%)

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	A	600	10	-	2/18/38/38	0/3/3/3
9	ATP	B	600	10	-	2/18/38/38	0/3/3/3
9	ATP	C	600	10	-	2/18/38/38	0/3/3/3
11	ADP	F	600	10	-	0/12/32/32	0/3/3/3
11	ADP	D	600	10	-	0/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	600	ATP	C5-C4	2.23	1.46	1.40
9	A	600	ATP	C5-C4	2.21	1.46	1.40
11	D	600	ADP	C5-C4	2.20	1.46	1.40
9	C	600	ATP	C5-C4	2.19	1.46	1.40
11	F	600	ADP	C5-C4	2.19	1.46	1.40

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	600	ADP	C3'-C2'-C1'	3.42	106.13	100.98
11	F	600	ADP	C3'-C2'-C1'	3.41	106.12	100.98
9	A	600	ATP	PB-O3B-PG	-3.38	121.21	132.83
9	C	600	ATP	PB-O3B-PG	-3.38	121.23	132.83
9	B	600	ATP	PB-O3B-PG	-3.37	121.25	132.83

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

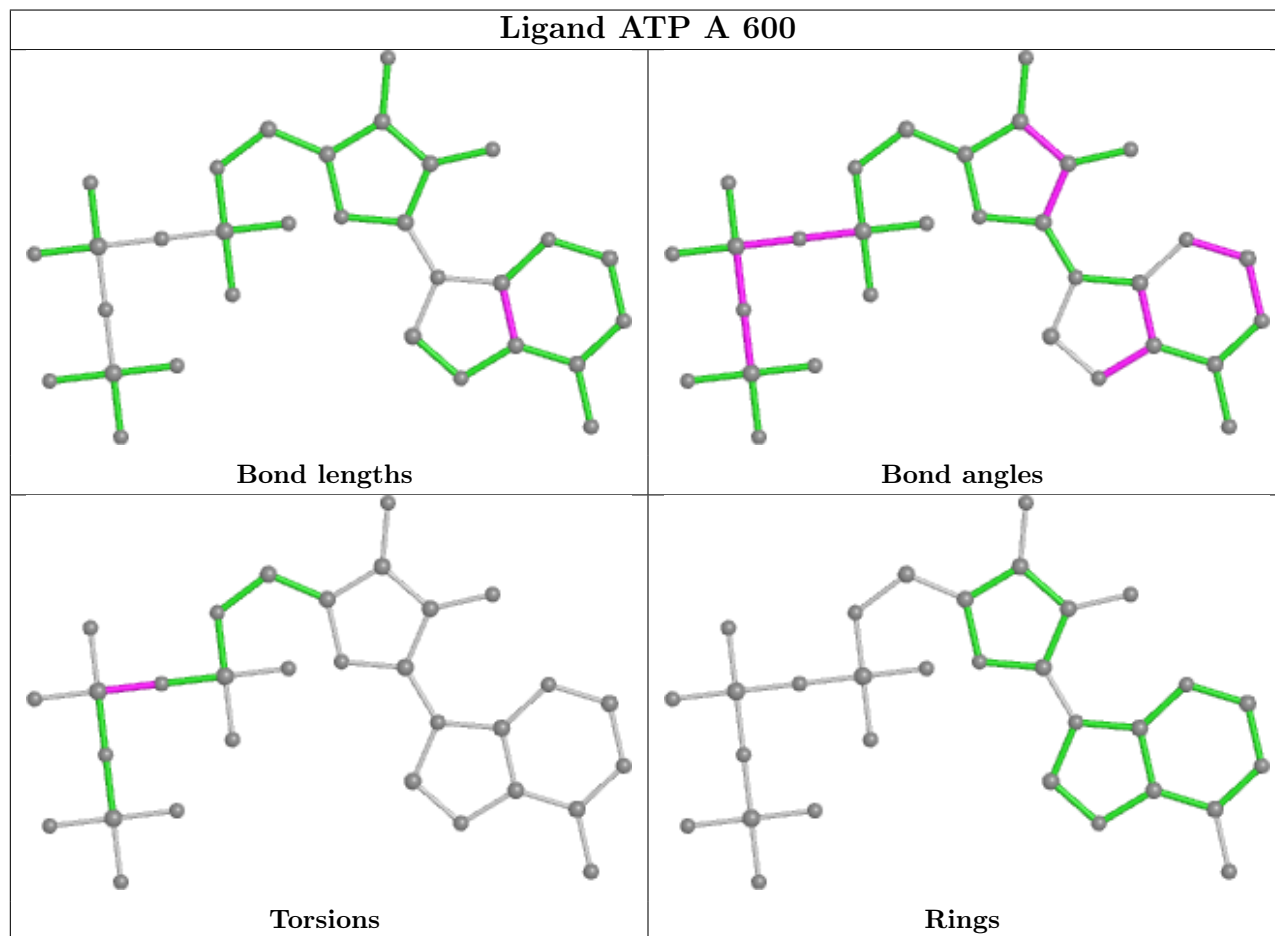
Mol	Chain	Res	Type	Atoms
9	A	600	ATP	PA-O3A-PB-O1B
9	B	600	ATP	PA-O3A-PB-O1B
9	C	600	ATP	PA-O3A-PB-O1B
9	A	600	ATP	PA-O3A-PB-O2B
9	B	600	ATP	PA-O3A-PB-O2B

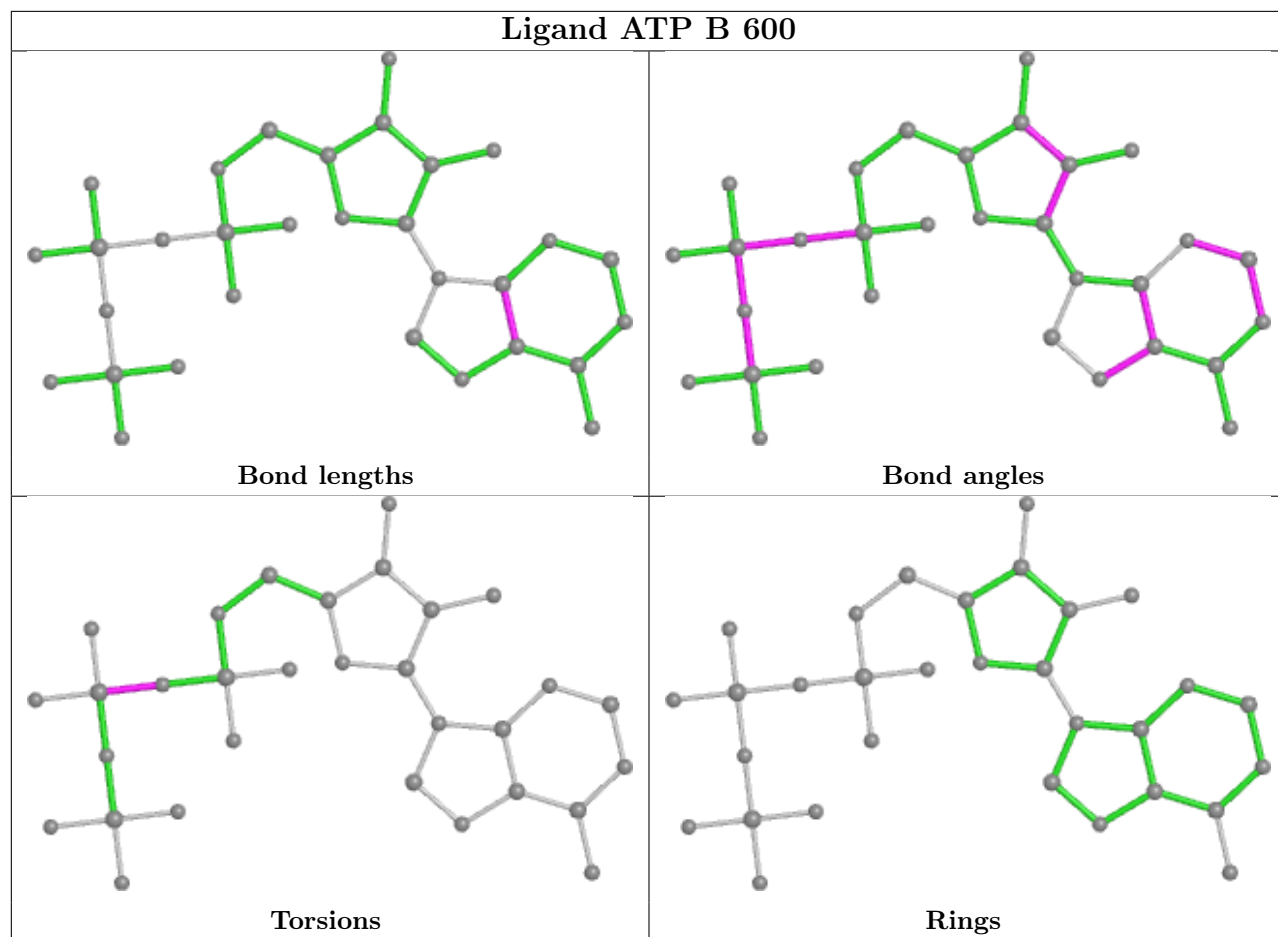
There are no ring outliers.

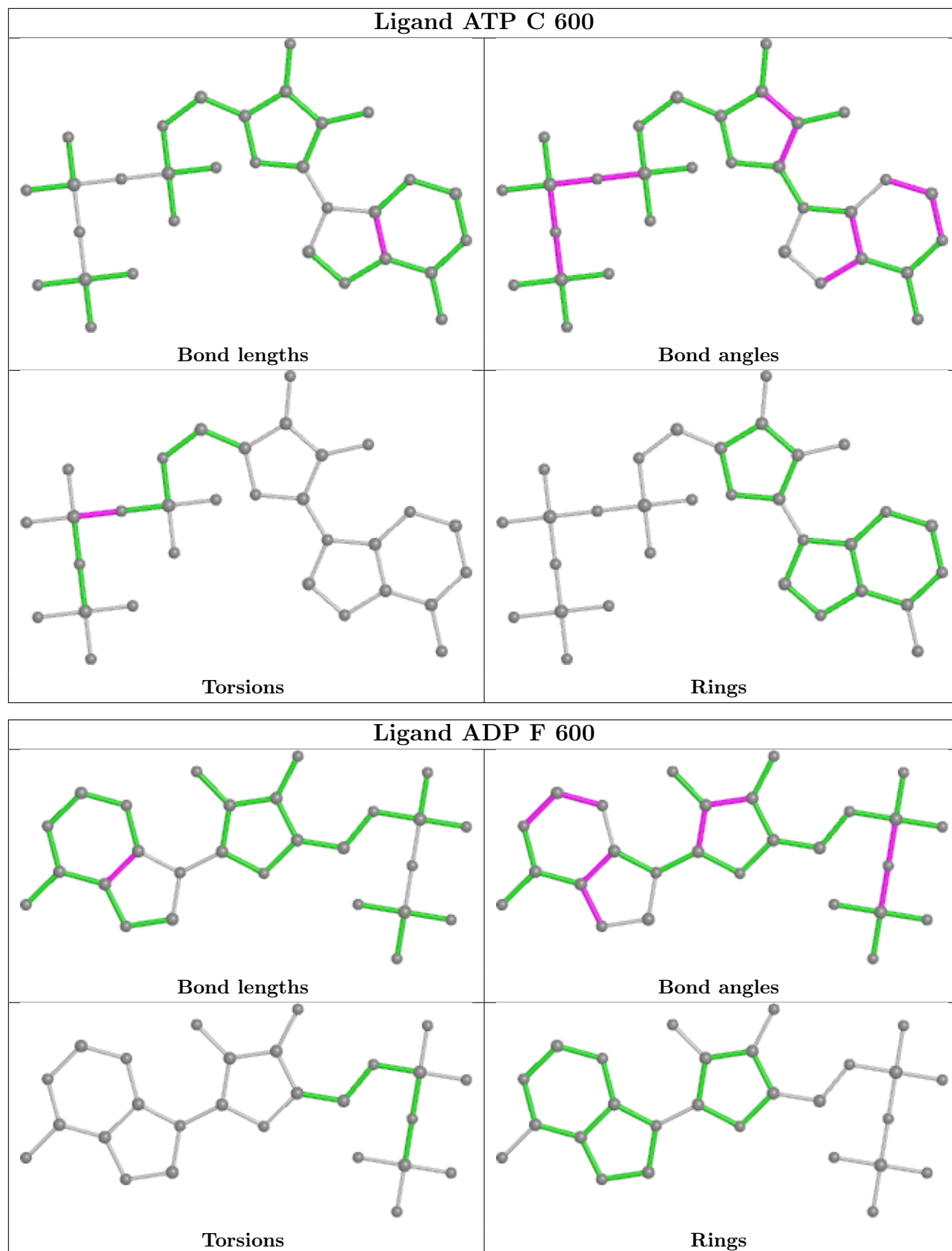
No monomer is involved in short contacts.

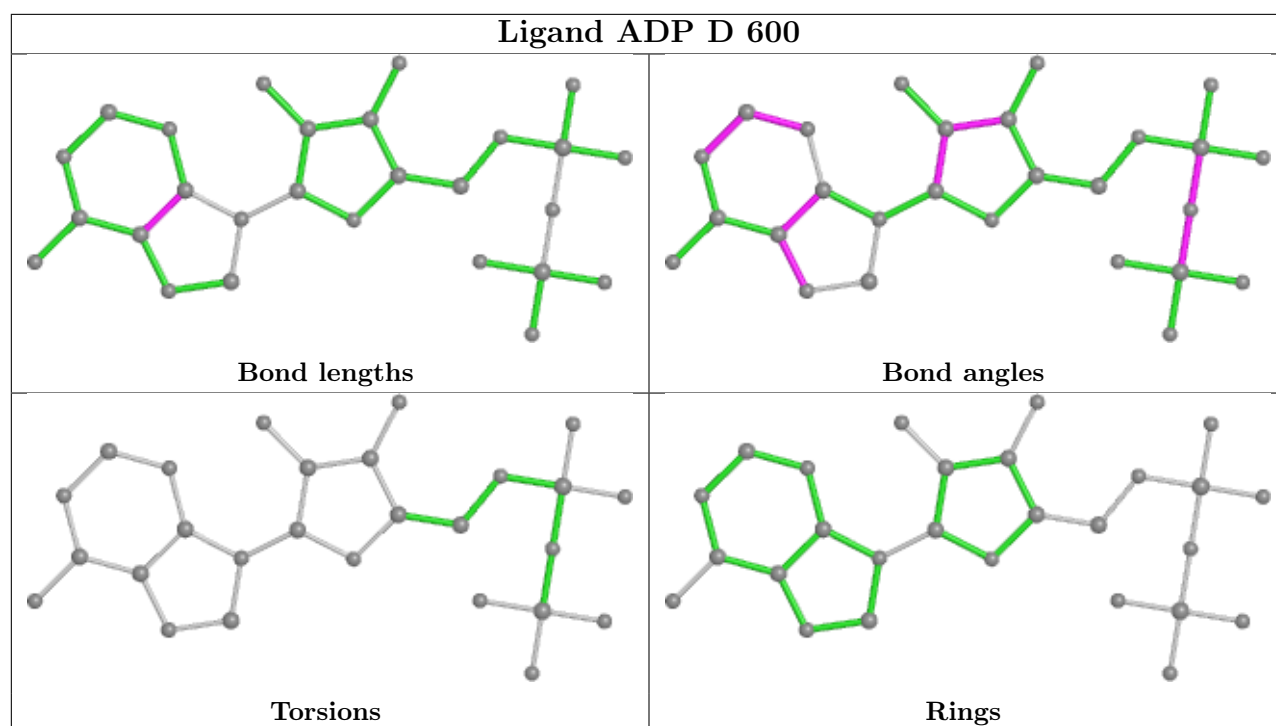
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

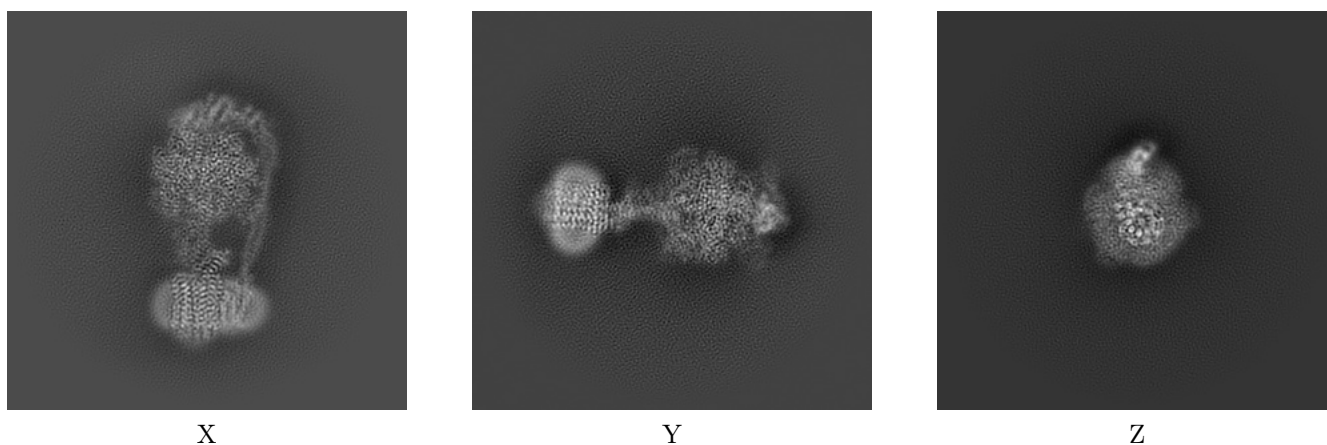
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35911. 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](#)

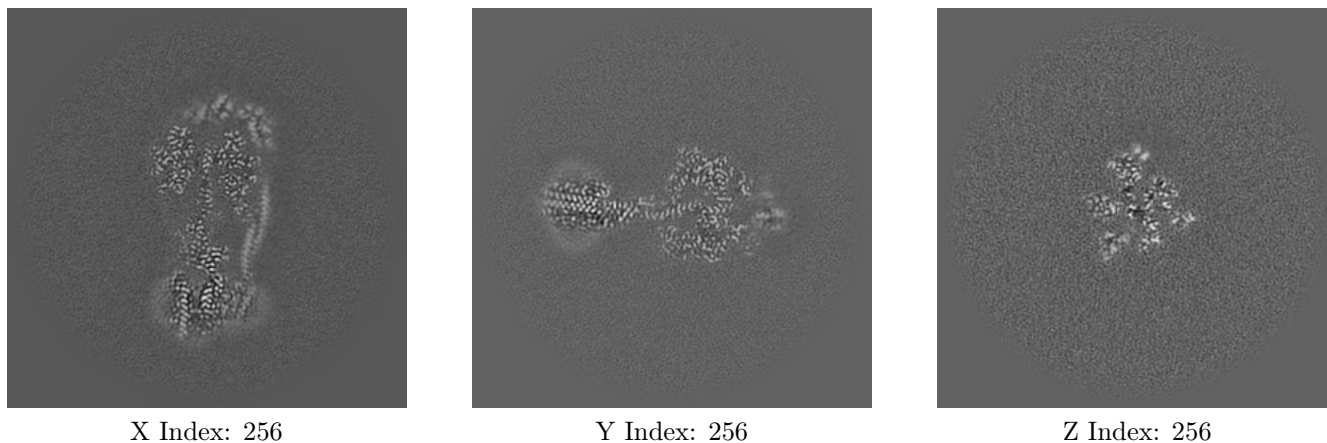
6.1.1 Primary map



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

6.2 Central slices [i](#)

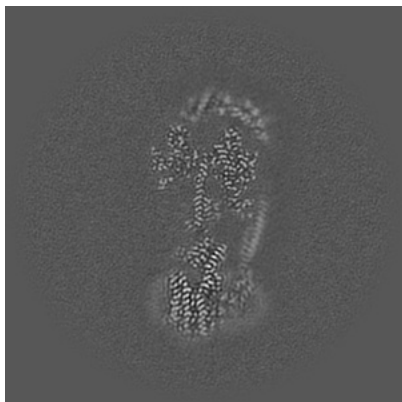
6.2.1 Primary map



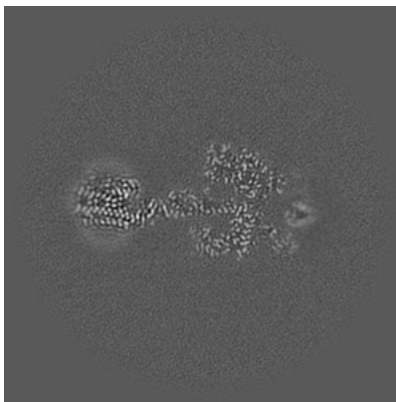
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

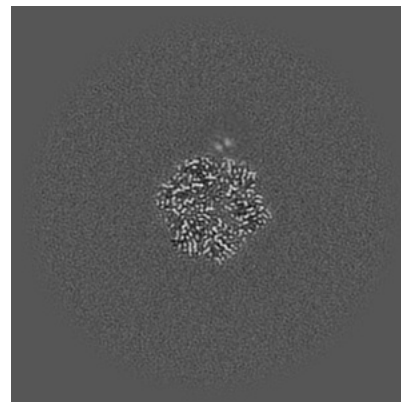
6.3.1 Primary map



X Index: 251



Y Index: 251

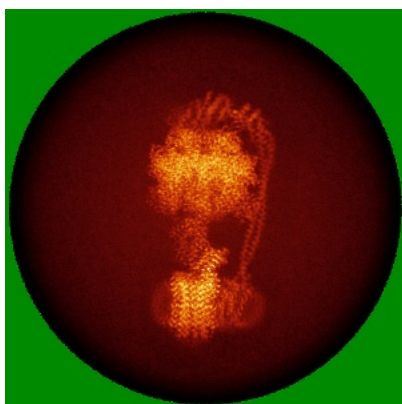


Z Index: 309

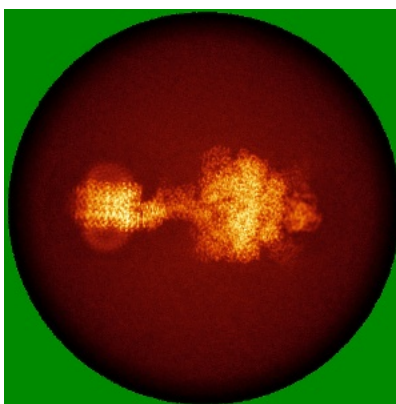
The images above show the largest variance slices of the map in three orthogonal directions.

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

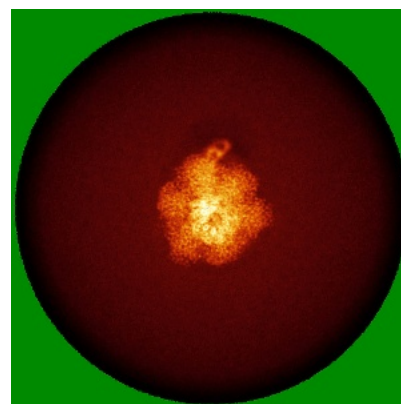
6.4.1 Primary map



X



Y



Z

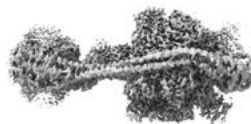
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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 5.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

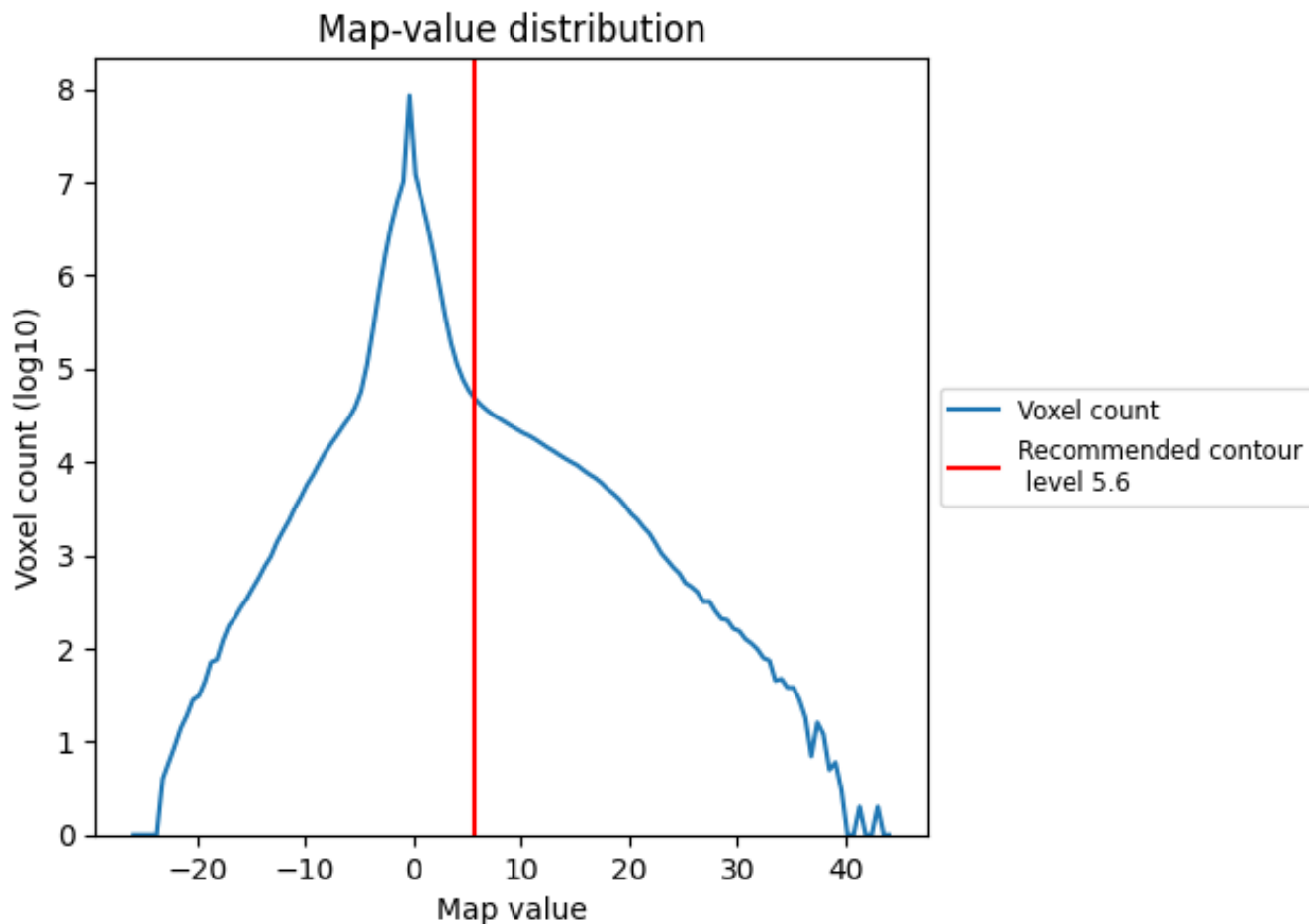
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

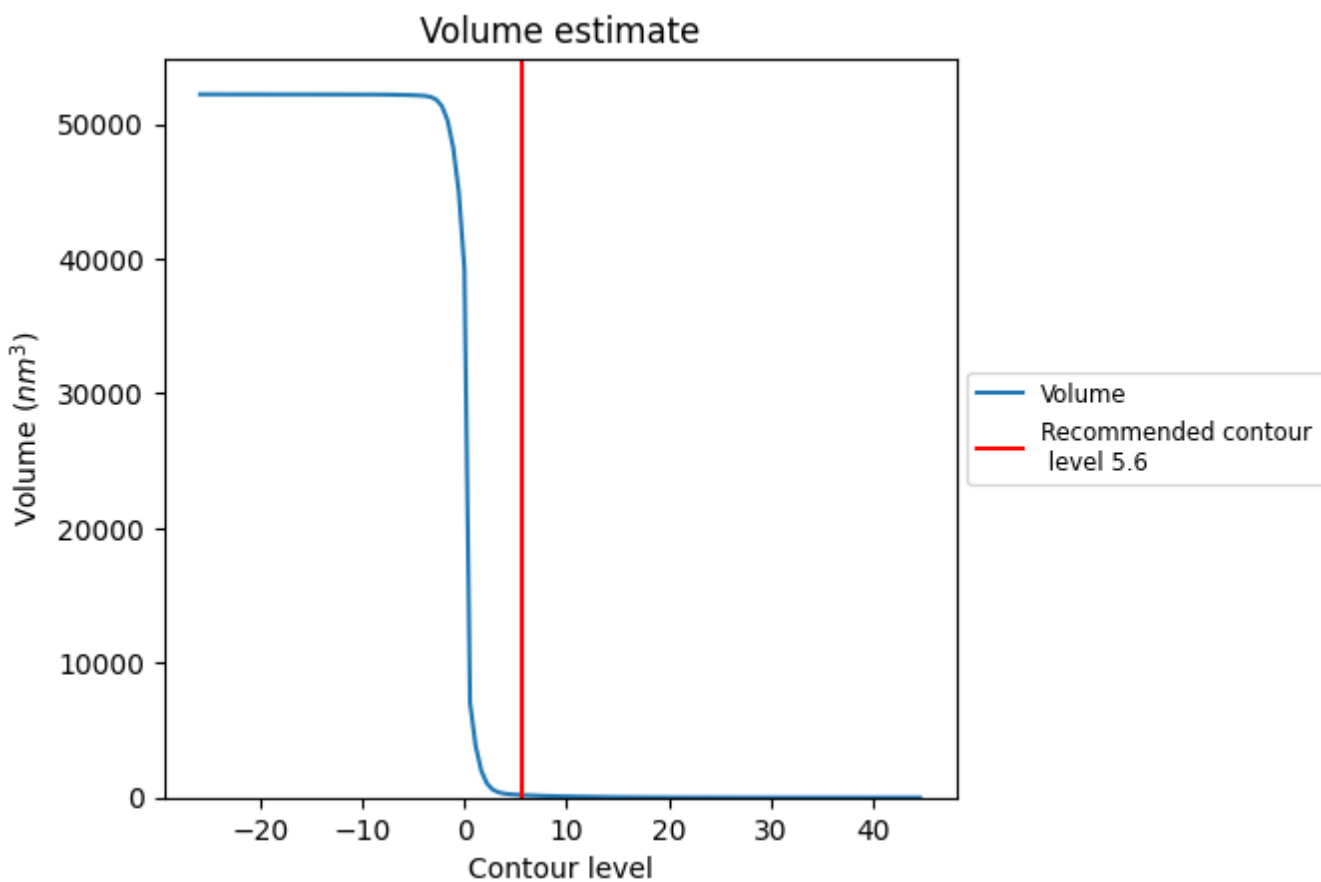
This section contains the results of statistical analysis of the map.

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.

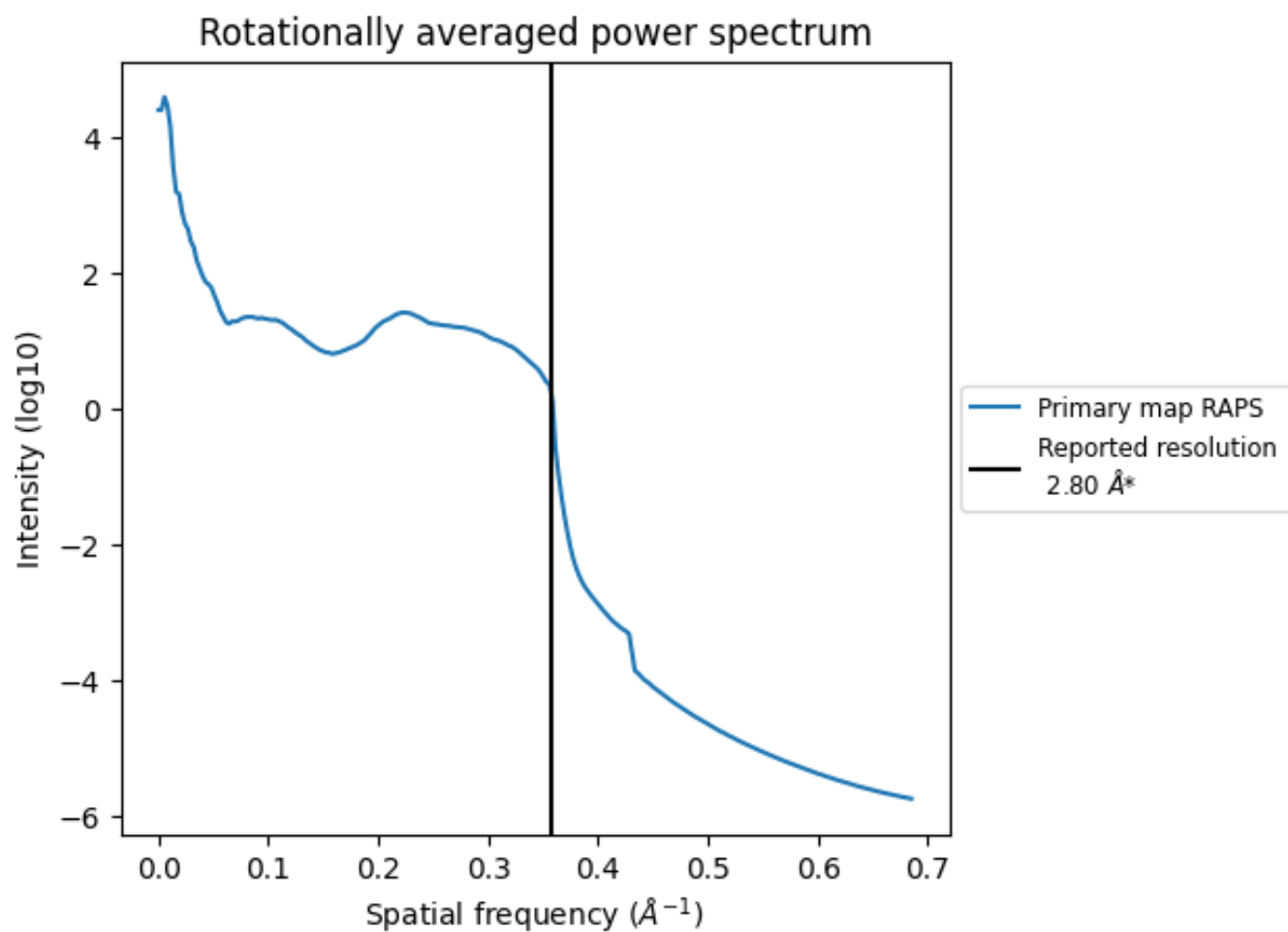
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 185 nm³; this corresponds to an approximate mass of 167 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 0.357\AA^{-1}

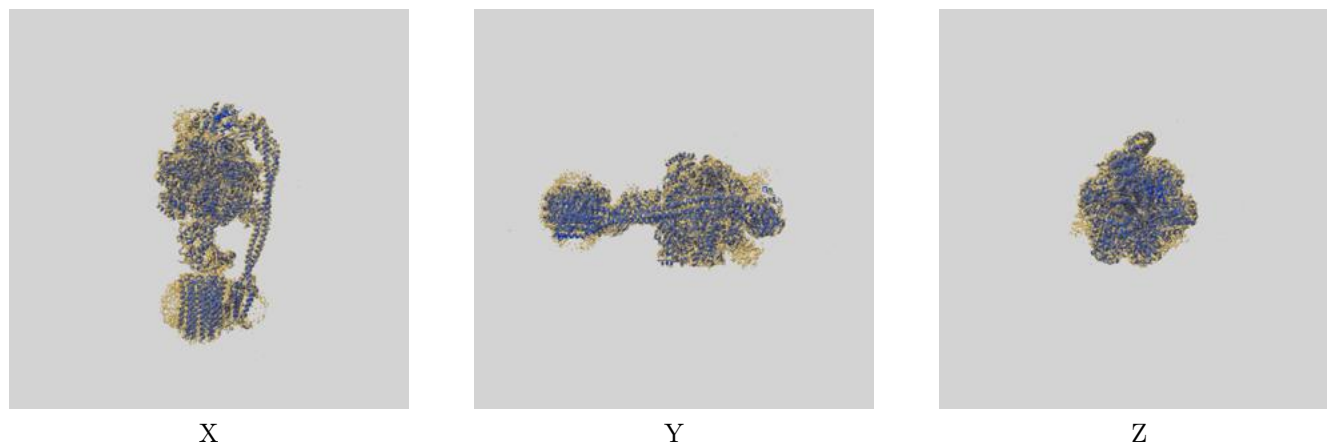
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

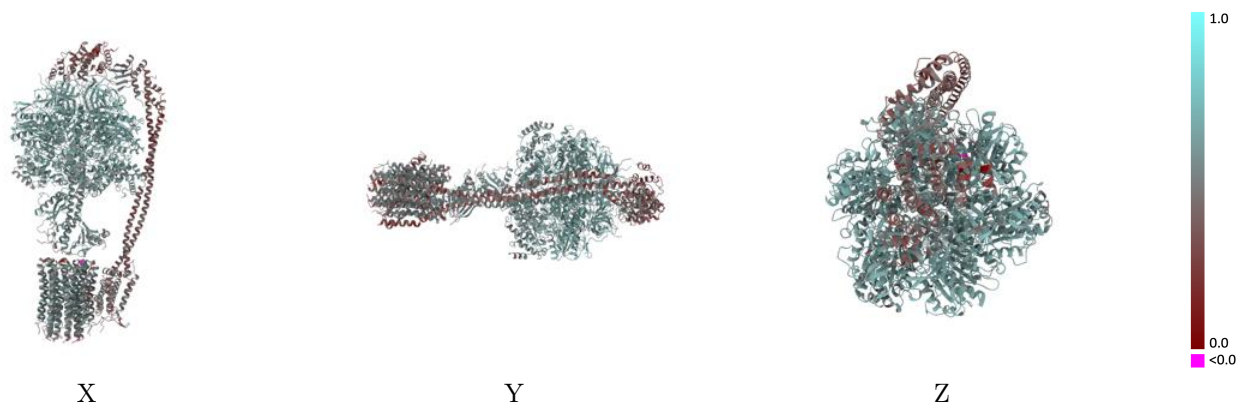
This section contains information regarding the fit between EMDB map EMD-35911 and PDB model 8J0T. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



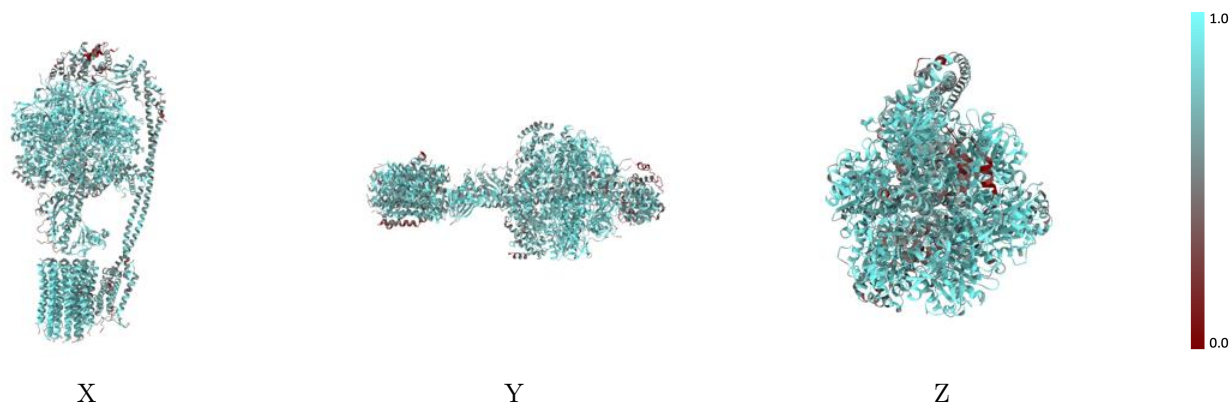
The images above show the 3D surface view of the map at the recommended contour level 5.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



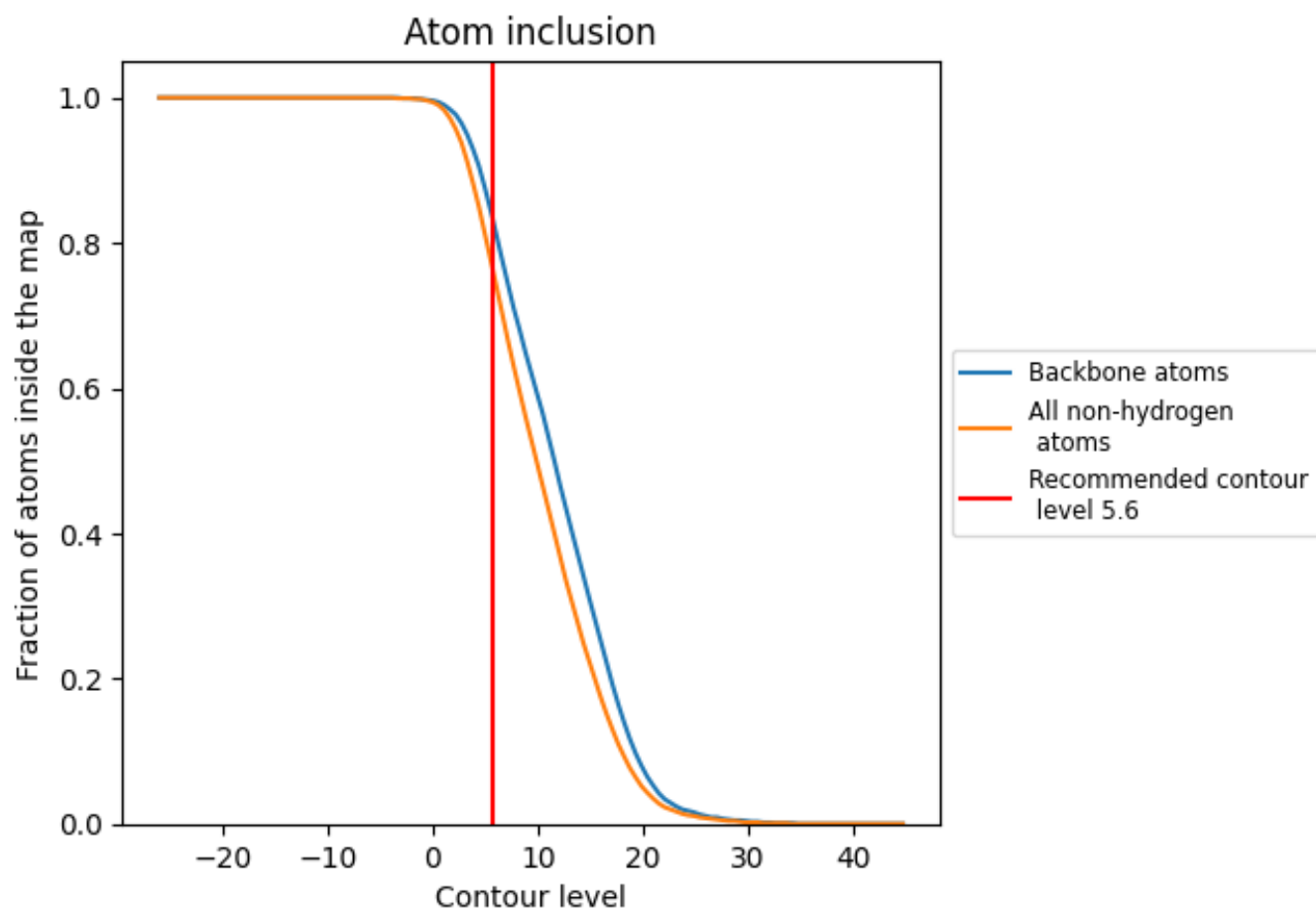
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.6).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% 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 (5.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7700	 0.5430
1	 0.8130	 0.4980
2	 0.8200	 0.4910
3	 0.8100	 0.4950
4	 0.8040	 0.5040
5	 0.8150	 0.4910
6	 0.8100	 0.5080
7	 0.8130	 0.5000
8	 0.8310	 0.4990
9	 0.8290	 0.4980
A	 0.8300	 0.5970
B	 0.7760	 0.5820
C	 0.7710	 0.5830
D	 0.8390	 0.6110
E	 0.8040	 0.6010
F	 0.8400	 0.6130
G	 0.6970	 0.5500
H	 0.8100	 0.5340
a	 0.6250	 0.4170
b	 0.6380	 0.3620
d	 0.5960	 0.3620

