



wwPDB EM Validation Summary Report ⓘ

Nov 8, 2023 – 05:39 PM EST

PDB ID : 8SHT
EMDB ID : EMD-40494
Title : CCT G beta 5 complex closed state 14
Authors : Wang, S.; Sass, M.; Willardson, B.M.; Shen, P.S.
Deposited on : 2023-04-14
Resolution : 3.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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<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:

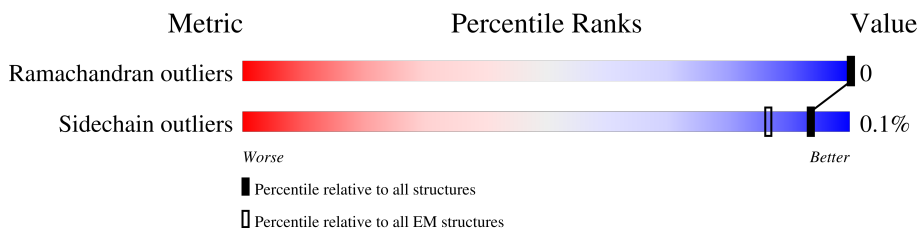
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



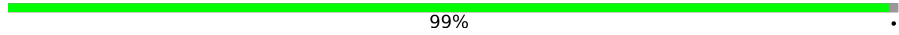
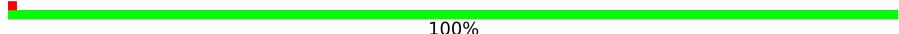
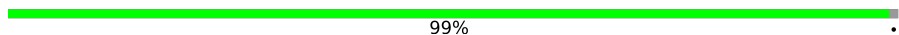
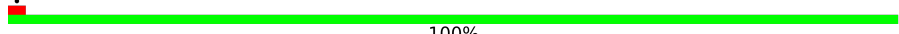



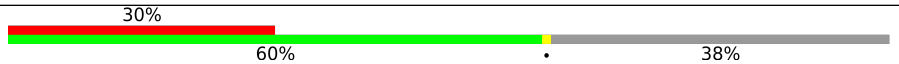

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	536	100%
1	a	536	99%
2	B	526	100%
2	b	526	100%
3	D	520	100%
3	d	520	100%
4	E	540	99%
4	e	540	100%
5	G	528	100%

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Mol	Chain	Length	Quality of chain
5	g	528	 99%
6	H	528	 100%
6	h	528	 99%
7	Q	538	 100%
7	q	538	 99%
8	Z	527	 100%
8	z	527	 100%
9	P	301	 30% 60% 38%
10	N	395	 54% 46%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 68272 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 T-complex protein 1 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	536	Total	C	N	O	S	0	0
			4069	2548	711	787	23		
1	a	532	Total	C	N	O	S	0	0
			4041	2533	707	778	23		

- Molecule 2 is a protein called T-complex protein 1 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	526	Total	C	N	O	S	0	0
			3952	2473	696	764	19		
2	b	525	Total	C	N	O	S	0	0
			3943	2467	694	763	19		

- Molecule 3 is a protein called T-complex protein 1 subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	520	Total	C	N	O	S	0	0
			3923	2453	683	764	23		
3	d	520	Total	C	N	O	S	0	0
			3917	2450	680	764	23		

- Molecule 4 is a protein called T-complex protein 1 subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	535	Total	C	N	O	S	1	0
			4132	2590	719	792	31		
4	e	540	Total	C	N	O	S	1	0
			4169	2610	724	804	31		

- Molecule 5 is a protein called T-complex protein 1 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	526	4089	2548	726	785	30	0	0
5	g	523	4063	2532	719	782	30	0	0

- Molecule 6 is a protein called T-complex protein 1 subunit eta, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	528	4054	2561	699	769	25	0	0
6	h	525	4032	2548	696	763	25	0	0

- Molecule 7 is a protein called T-complex protein 1 subunit theta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	Q	538	4086	2579	696	784	27	0	0
7	q	533	4053	2558	690	778	27	0	0

- Molecule 8 is a protein called T-complex protein 1 subunit zeta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	Z	525	4022	2528	704	769	21	0	0
8	z	527	4033	2534	706	772	21	0	0

- Molecule 9 is a protein called Phosducin-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	P	186	1507	955	256	284	12	0	0

- Molecule 10 is a protein called Guanine nucleotide-binding protein subunit beta-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	N	214	1656	1031	287	326	12	0	0

- Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

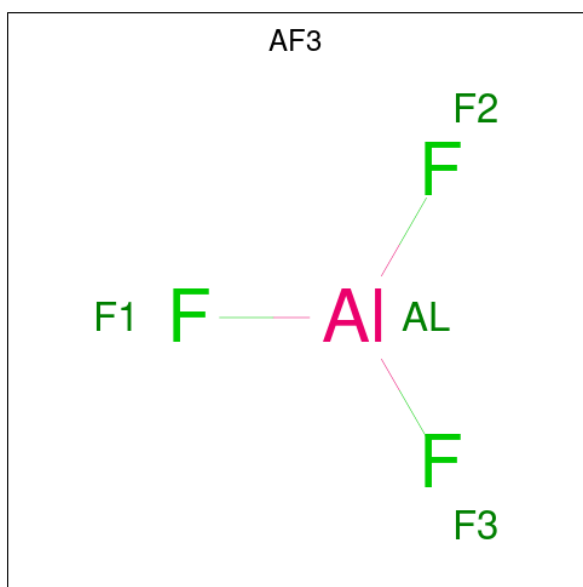
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
11	q	1	27	10	5	10	2	0
11	z	1	27	10	5	10	2	0

- Molecule 12 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
12	A	1	1	1	0
12	B	1	1	1	0
12	D	1	1	1	0
12	E	1	1	1	0
12	G	1	1	1	0
12	H	1	1	1	0
12	Q	1	1	1	0
12	Z	1	1	1	0
12	a	1	1	1	0
12	b	1	1	1	0
12	d	1	1	1	0
12	e	1	1	1	0
12	g	1	1	1	0
12	h	1	1	1	0
12	q	1	1	1	0
12	z	1	1	1	0

- Molecule 13 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula: AlF₃).



Mol	Chain	Residues	Atoms			AltConf
			Total	Al	F	
13	A	1	4	1	3	0
13	B	1	4	1	3	0
13	D	1	4	1	3	0
13	E	1	4	1	3	0
13	G	1	4	1	3	0
13	H	1	4	1	3	0
13	Q	1	4	1	3	0
13	Z	1	4	1	3	0
13	a	1	4	1	3	0
13	b	1	4	1	3	0
13	d	1	4	1	3	0
13	e	1	4	1	3	0
13	g	1	4	1	3	0
13	h	1	4	1	3	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	Al	F	
13	q	1	4	1	3	0
13	z	1	4	1	3	0

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
14	A	2	2	2	0
14	B	2	2	2	0
14	D	1	1	1	0
14	E	1	1	1	0
14	G	1	1	1	0
14	H	1	1	1	0
14	Q	1	1	1	0
14	Z	1	1	1	0
14	a	2	2	2	0
14	b	1	1	1	0
14	d	1	1	1	0
14	e	1	1	1	0
14	g	1	1	1	0
14	h	1	1	1	0
14	q	1	1	1	0
14	z	1	1	1	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.

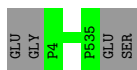
- Molecule 1: T-complex protein 1 subunit alpha

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: T-complex protein 1 subunit alpha

Chain a:  99%



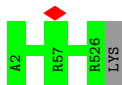
- Molecule 2: T-complex protein 1 subunit beta

Chain B:  100%



- Molecule 2: T-complex protein 1 subunit beta

Chain b:  100%



- Molecule 3: T-complex protein 1 subunit delta

Chain D:  100%



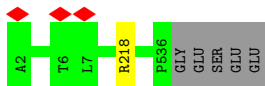
- Molecule 3: T-complex protein 1 subunit delta

Chain d:  100%



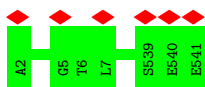
- Molecule 4: T-complex protein 1 subunit epsilon

Chain E:  99%



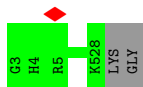
- Molecule 4: T-complex protein 1 subunit epsilon

Chain e:  100%



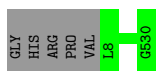
- Molecule 5: T-complex protein 1 subunit gamma

Chain G:  100%



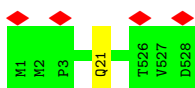
- Molecule 5: T-complex protein 1 subunit gamma

Chain g:  99%



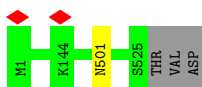
- Molecule 6: T-complex protein 1 subunit eta, N-terminally processed

Chain H:  100%

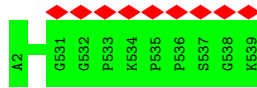


- Molecule 6: T-complex protein 1 subunit eta, N-terminally processed

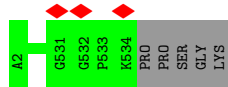
Chain h:  99%



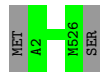
- Molecule 7: T-complex protein 1 subunit theta



- Molecule 7: T-complex protein 1 subunit theta



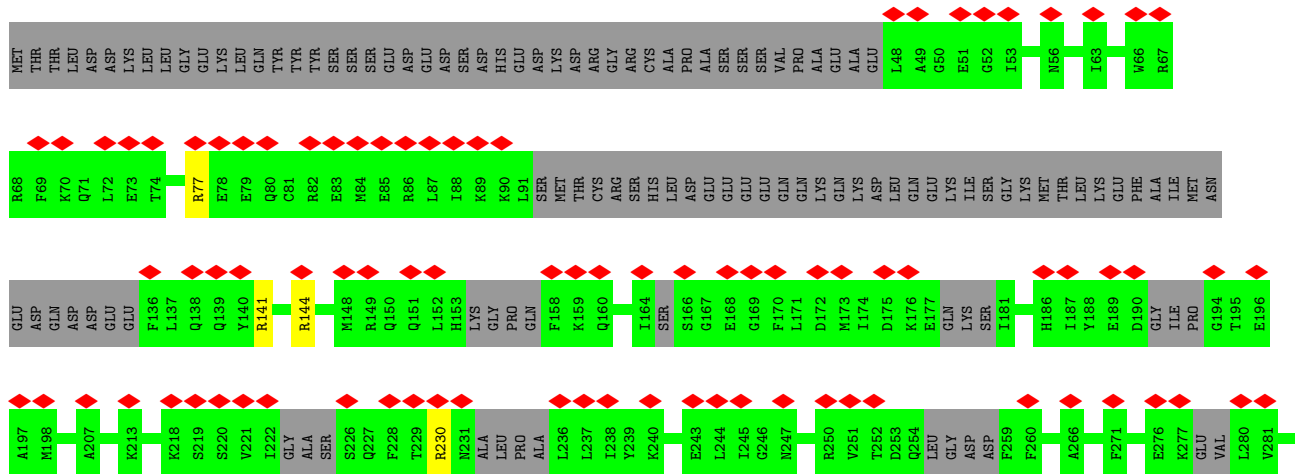
- Molecule 8: T-complex protein 1 subunit zeta

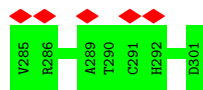


- Molecule 8: T-complex protein 1 subunit zeta



- Molecule 9: Phosducin-like protein





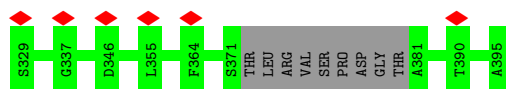
- Molecule 10: Guanine nucleotide-binding protein subunit beta-5

Chain N: 54% 46%

MET CYS ASP GLN THR PHE LEU VAL ASN VAL PHE GLY SER CYS ASP LYS HIS VAL PHE LYS GLN ARG ALA VAL ARG PRO VAL PHE LYS SER LYS GLN GLN LEU SER MET TYR CYS SER THR CYS ALA GLU ILE MET ALA THR GLU MET ASP TRP HIS CYS LYS ASN GLU THR LYS ARG ALA ARG LYS ILE VAL SER LEU SER SER

ALA GLU SER LEU GLY LYS LEU GLU ARG LYS LEU HIS GLN VAL ALA ARG VAL VAL MET K96 K102 GLY HIS GLY ASN ILE LYS VAL LEU CYS MET ASP TRP HIS CYS LYS ASP LYS ARG ARG ILE VAL SER SER

GLN ASP GLY LYS ILE VAL TRP ASP PHE THR THR ASN LYS GLU HIS ALA VAL THR MET PRO CYS THR TRP VAL MET ALA CYS ALA TYR ALA PRO SER GLY CYS ALA ILE ALA CYS GLY GLY LEU ASP ASN CYS S172 E281 S320 LYS GLU SER ILE PHE GLY ALA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33752	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.086	Depositor
Minimum map value	-0.393	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.129	Depositor
Map size (\AA)	317.4, 317.4, 317.4	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.058, 1.058, 1.058	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AF3, MG, ADP

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	0.25	0/4109	0.48	0/5548
1	a	0.25	0/4081	0.47	0/5510
2	B	0.25	0/3995	0.47	0/5386
2	b	0.25	0/3986	0.47	0/5375
3	D	0.25	0/3955	0.48	0/5338
3	d	0.25	0/3949	0.48	0/5331
4	E	0.25	0/4183	0.48	0/5635
4	e	0.25	0/4220	0.47	0/5684
5	G	0.25	0/4136	0.48	0/5579
5	g	0.25	0/4108	0.48	0/5539
6	H	0.26	0/4111	0.47	0/5550
6	h	0.26	0/4089	0.46	0/5519
7	Q	0.25	0/4147	0.45	0/5606
7	q	0.25	0/4112	0.46	0/5558
8	Z	0.25	0/4069	0.47	0/5486
8	z	0.25	0/4080	0.47	0/5501
9	P	0.24	0/1521	0.50	0/2024
10	N	0.25	0/1689	0.52	0/2280
All	All	0.25	0/68540	0.47	0/92449

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

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

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 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	534/536 (100%)	515 (96%)	19 (4%)	0	100	100
1	a	530/536 (99%)	509 (96%)	21 (4%)	0	100	100
2	B	524/526 (100%)	510 (97%)	14 (3%)	0	100	100
2	b	523/526 (99%)	507 (97%)	16 (3%)	0	100	100
3	D	518/520 (100%)	510 (98%)	8 (2%)	0	100	100
3	d	518/520 (100%)	498 (96%)	20 (4%)	0	100	100
4	E	534/540 (99%)	512 (96%)	22 (4%)	0	100	100
4	e	539/540 (100%)	527 (98%)	12 (2%)	0	100	100
5	G	524/528 (99%)	508 (97%)	16 (3%)	0	100	100
5	g	521/528 (99%)	508 (98%)	13 (2%)	0	100	100
6	H	526/528 (100%)	510 (97%)	16 (3%)	0	100	100
6	h	523/528 (99%)	506 (97%)	17 (3%)	0	100	100
7	Q	536/538 (100%)	522 (97%)	14 (3%)	0	100	100
7	q	531/538 (99%)	517 (97%)	14 (3%)	0	100	100
8	Z	523/527 (99%)	509 (97%)	14 (3%)	0	100	100
8	z	525/527 (100%)	511 (97%)	14 (3%)	0	100	100
9	P	166/301 (55%)	150 (90%)	16 (10%)	0	100	100
10	N	206/395 (52%)	182 (88%)	24 (12%)	0	100	100
All	All	8801/9182 (96%)	8511 (97%)	290 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	447/447 (100%)	447 (100%)	0	100	100
1	a	444/447 (99%)	444 (100%)	0	100	100
2	B	418/418 (100%)	418 (100%)	0	100	100
2	b	417/418 (100%)	417 (100%)	0	100	100
3	D	442/442 (100%)	442 (100%)	0	100	100
3	d	441/442 (100%)	441 (100%)	0	100	100
4	E	452/455 (99%)	451 (100%)	1 (0%)	93	98
4	e	456/455 (100%)	456 (100%)	0	100	100
5	G	456/457 (100%)	456 (100%)	0	100	100
5	g	453/457 (99%)	453 (100%)	0	100	100
6	H	435/435 (100%)	434 (100%)	1 (0%)	93	98
6	h	432/435 (99%)	431 (100%)	1 (0%)	93	98
7	Q	442/442 (100%)	442 (100%)	0	100	100
7	q	438/442 (99%)	438 (100%)	0	100	100
8	Z	437/439 (100%)	437 (100%)	0	100	100
8	z	438/439 (100%)	437 (100%)	1 (0%)	93	98
9	P	166/266 (62%)	162 (98%)	4 (2%)	49	79
10	N	180/334 (54%)	180 (100%)	0	100	100
All	All	7394/7670 (96%)	7386 (100%)	8 (0%)	93	98

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	P	230	ARG
9	P	144	ARG
9	P	77	ARG
8	z	526	MET
9	P	141	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
8	Z	334	ASN

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Mol	Chain	Res	Type
8	Z	514	ASN
8	z	70	GLN
4	e	139	GLN
6	h	30	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 48 ligands modelled in this entry, 16 are monoatomic - leaving 32 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
13	AF3	h	603	-	0,3,3	-	-	-		
13	AF3	G	603	-	0,3,3	-	-	-		
11	ADP	A	601	12	24,29,29	0.92	1 (4%)	29,45,45	1.47	4 (13%)
13	AF3	d	603	-	0,3,3	-	-	-		
11	ADP	B	601	12	24,29,29	0.95	1 (4%)	29,45,45	1.39	4 (13%)
11	ADP	q	601	12	24,29,29	0.94	1 (4%)	29,45,45	1.51	4 (13%)
13	AF3	E	603	-	0,3,3	-	-	-		
11	ADP	z	601	12	24,29,29	0.92	1 (4%)	29,45,45	1.52	4 (13%)
11	ADP	e	601	12	24,29,29	0.94	1 (4%)	29,45,45	1.35	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	AF3	a	603	-	0,3,3	-	-	-		
13	AF3	H	603	-	0,3,3	-	-	-		
13	AF3	Z	603	-	0,3,3	-	-	-		
11	ADP	g	601	12	24,29,29	0.93	1 (4%)	29,45,45	1.48	4 (13%)
13	AF3	g	603	-	0,3,3	-	-	-		
11	ADP	a	601	12	24,29,29	0.93	1 (4%)	29,45,45	1.46	4 (13%)
11	ADP	h	601	12	24,29,29	0.92	1 (4%)	29,45,45	1.37	4 (13%)
13	AF3	b	603	-	0,3,3	-	-	-		
11	ADP	G	601	12	24,29,29	0.92	1 (4%)	29,45,45	1.46	4 (13%)
13	AF3	q	603	-	0,3,3	-	-	-		
11	ADP	b	601	12	24,29,29	0.94	1 (4%)	29,45,45	1.38	4 (13%)
11	ADP	d	601	12	24,29,29	0.93	1 (4%)	29,45,45	1.40	4 (13%)
13	AF3	e	603	-	0,3,3	-	-	-		
11	ADP	Q	601	12	24,29,29	0.93	1 (4%)	29,45,45	1.52	4 (13%)
13	AF3	A	603	-	0,3,3	-	-	-		
11	ADP	E	601	12	24,29,29	0.94	1 (4%)	29,45,45	1.35	4 (13%)
13	AF3	B	603	-	0,3,3	-	-	-		
13	AF3	z	603	-	0,3,3	-	-	-		
13	AF3	Q	603	-	0,3,3	-	-	-		
11	ADP	H	601	12	24,29,29	0.94	1 (4%)	29,45,45	1.39	4 (13%)
11	ADP	Z	601	12	24,29,29	0.93	1 (4%)	29,45,45	1.50	4 (13%)
11	ADP	D	601	12	24,29,29	0.93	1 (4%)	29,45,45	1.36	4 (13%)
13	AF3	D	603	-	0,3,3	-	-	-		

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
11	ADP	G	601	12	-	1/12/32/32	0/3/3/3
11	ADP	e	601	12	-	3/12/32/32	0/3/3/3
11	ADP	A	601	12	-	3/12/32/32	0/3/3/3
11	ADP	b	601	12	-	3/12/32/32	0/3/3/3
11	ADP	H	601	12	-	6/12/32/32	0/3/3/3
11	ADP	d	601	12	-	1/12/32/32	0/3/3/3
11	ADP	Q	601	12	-	7/12/32/32	0/3/3/3
11	ADP	q	601	12	-	5/12/32/32	0/3/3/3
11	ADP	E	601	12	-	1/12/32/32	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	ADP	B	601	12	-	3/12/32/32	0/3/3/3
11	ADP	Z	601	12	-	4/12/32/32	0/3/3/3
11	ADP	z	601	12	-	3/12/32/32	0/3/3/3
11	ADP	g	601	12	-	2/12/32/32	0/3/3/3
11	ADP	a	601	12	-	5/12/32/32	0/3/3/3
11	ADP	D	601	12	-	1/12/32/32	0/3/3/3
11	ADP	h	601	12	-	4/12/32/32	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	Z	601	ADP	C5-C4	2.41	1.47	1.40
11	G	601	ADP	C5-C4	2.39	1.47	1.40
11	B	601	ADP	C5-C4	2.39	1.47	1.40
11	d	601	ADP	C5-C4	2.38	1.47	1.40
11	e	601	ADP	C5-C4	2.37	1.47	1.40

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Q	601	ADP	PA-O3A-PB	-3.99	119.14	132.83
11	q	601	ADP	PA-O3A-PB	-3.89	119.47	132.83
11	a	601	ADP	PA-O3A-PB	-3.89	119.47	132.83
11	z	601	ADP	PA-O3A-PB	-3.87	119.53	132.83
11	A	601	ADP	PA-O3A-PB	-3.86	119.58	132.83

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

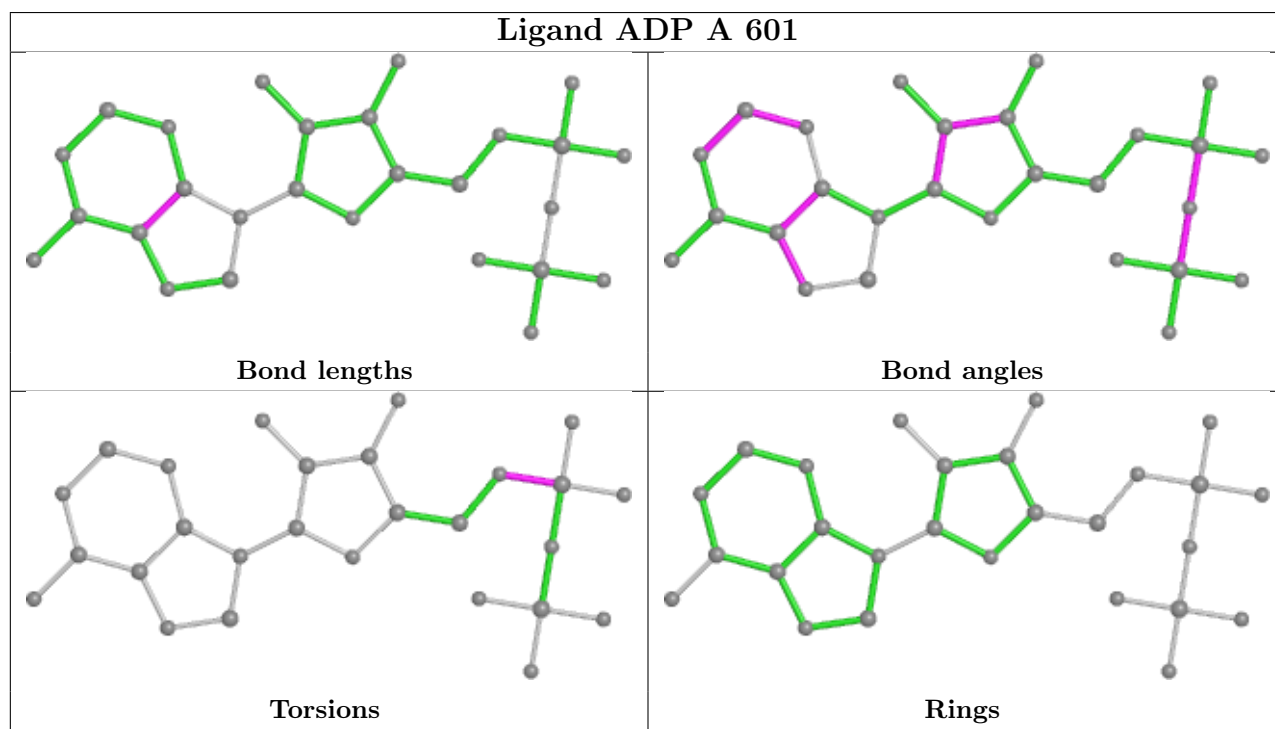
Mol	Chain	Res	Type	Atoms
11	A	601	ADP	C5'-O5'-PA-O1A
11	A	601	ADP	C5'-O5'-PA-O2A
11	B	601	ADP	C5'-O5'-PA-O1A
11	H	601	ADP	C5'-O5'-PA-O3A
11	Q	601	ADP	C5'-O5'-PA-O1A

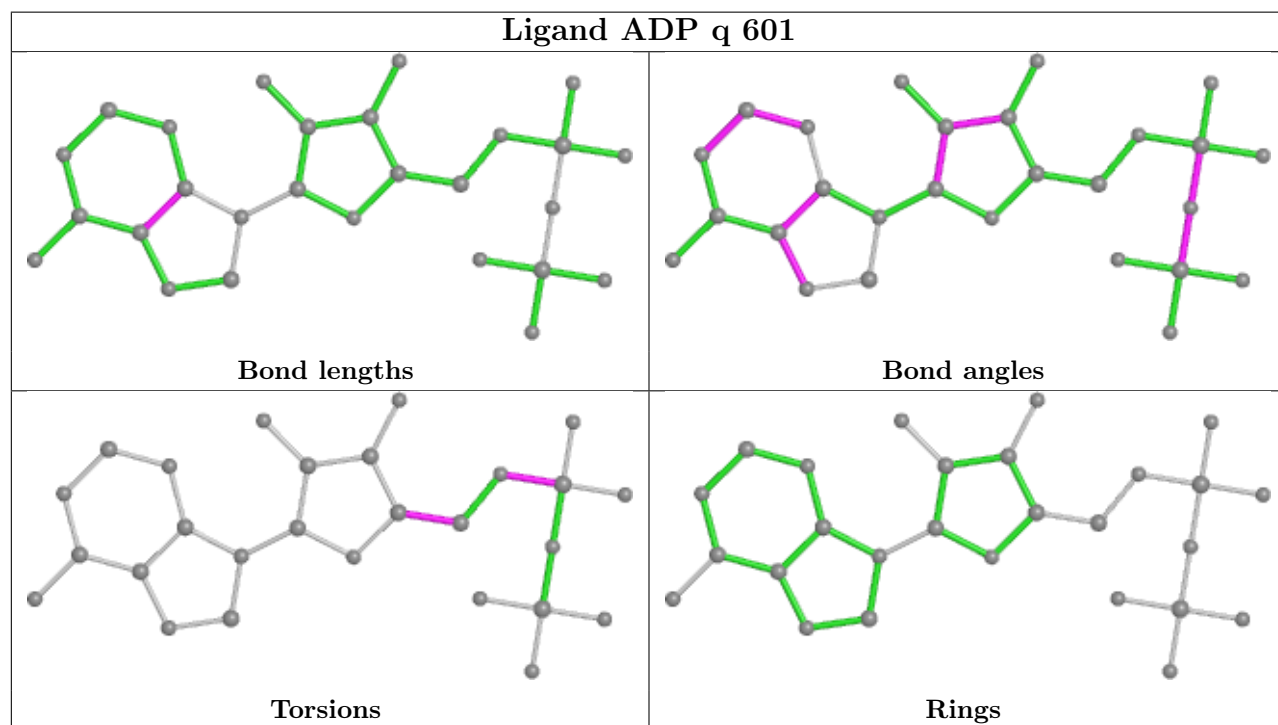
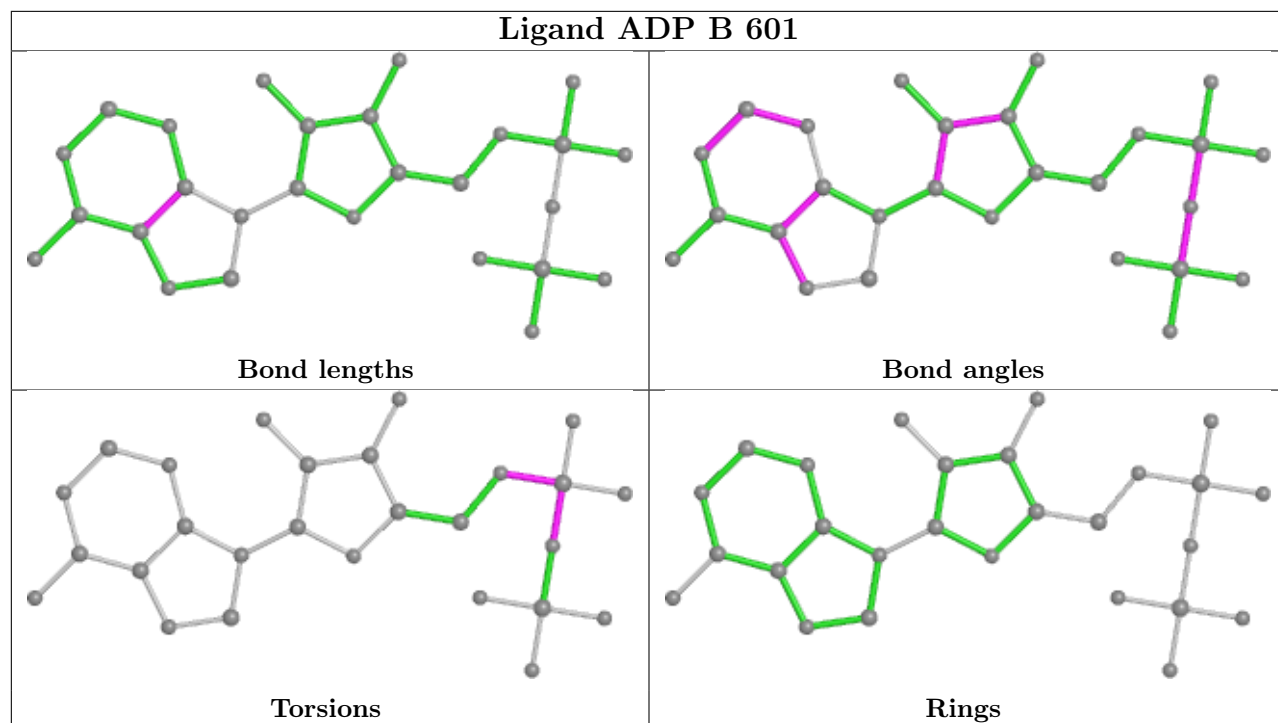
There are no ring outliers.

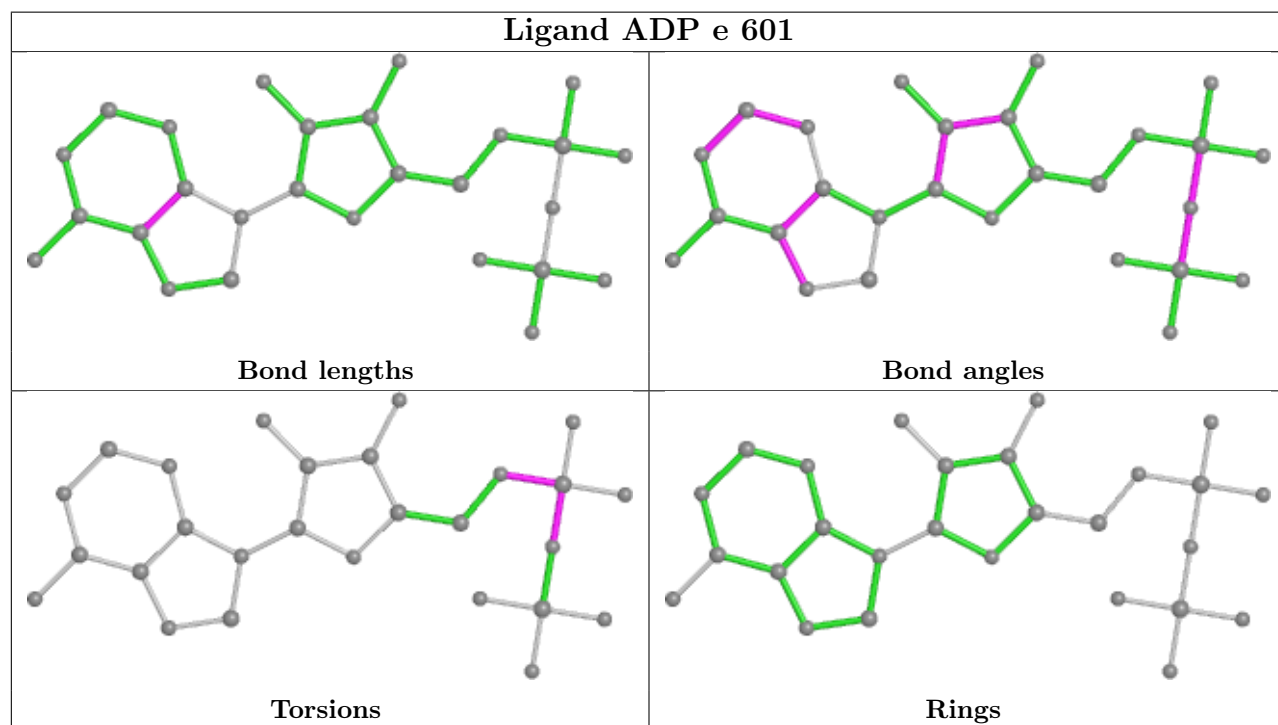
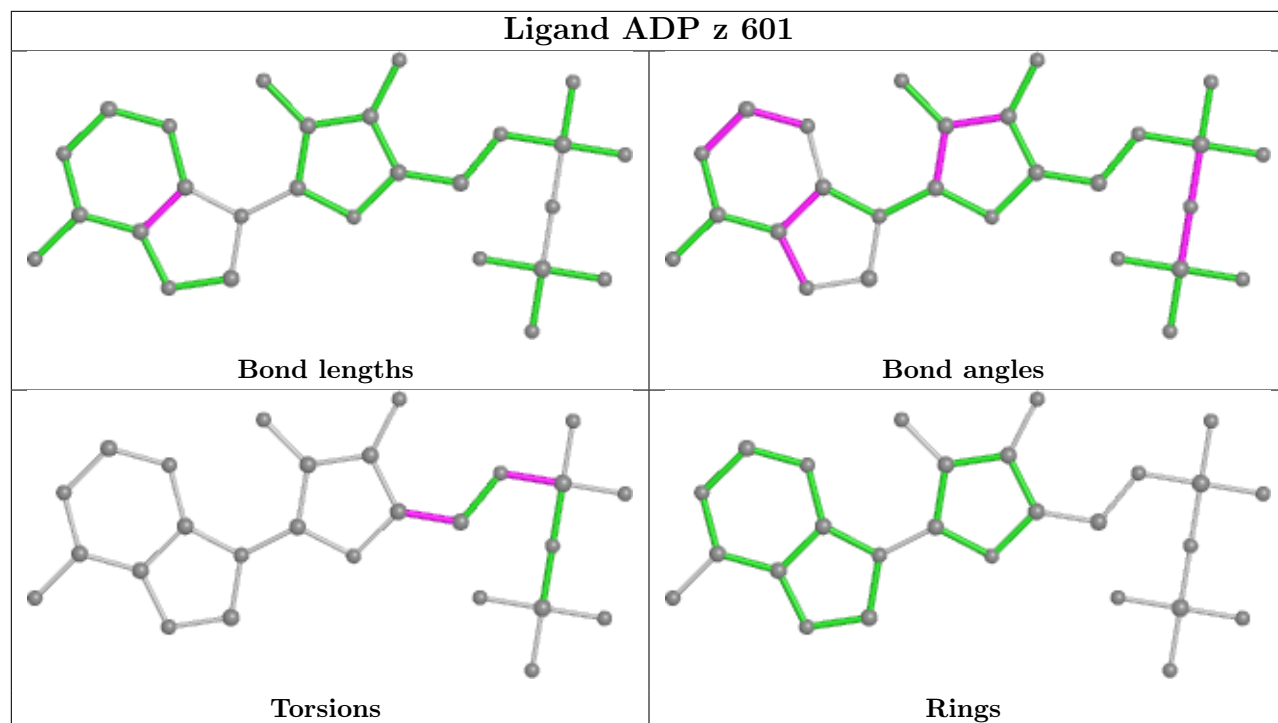
No monomer is involved in short contacts.

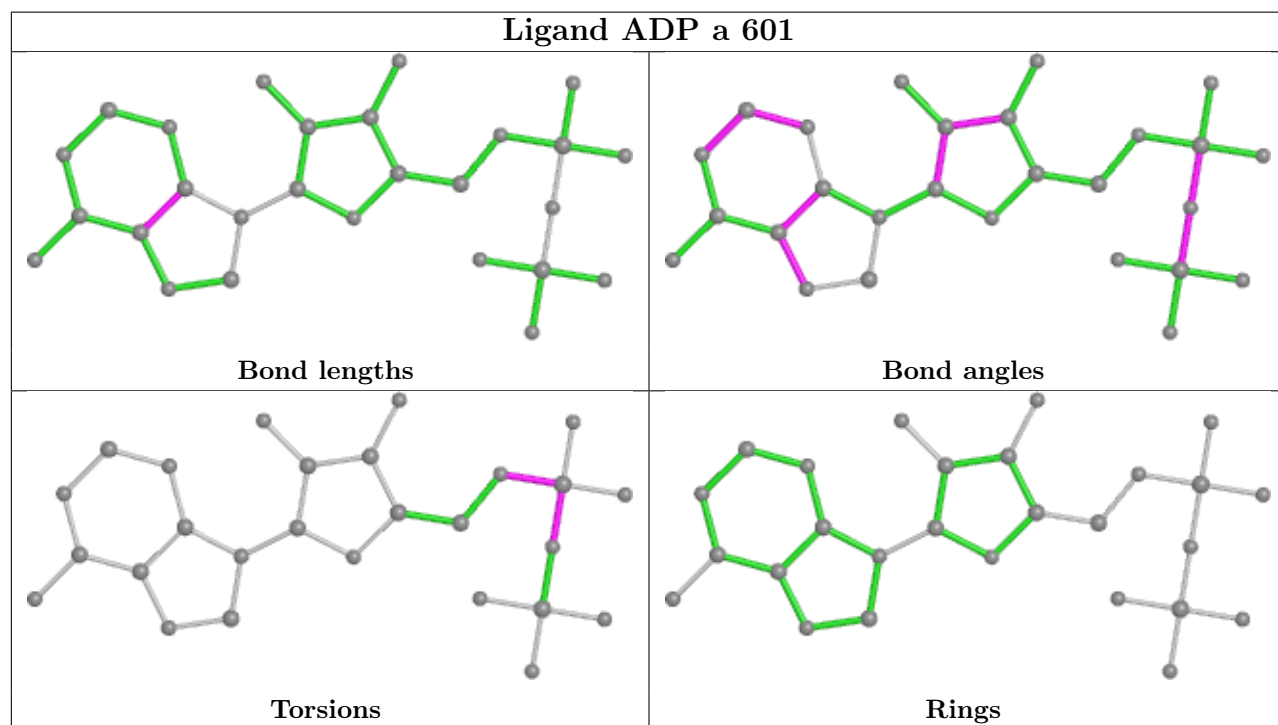
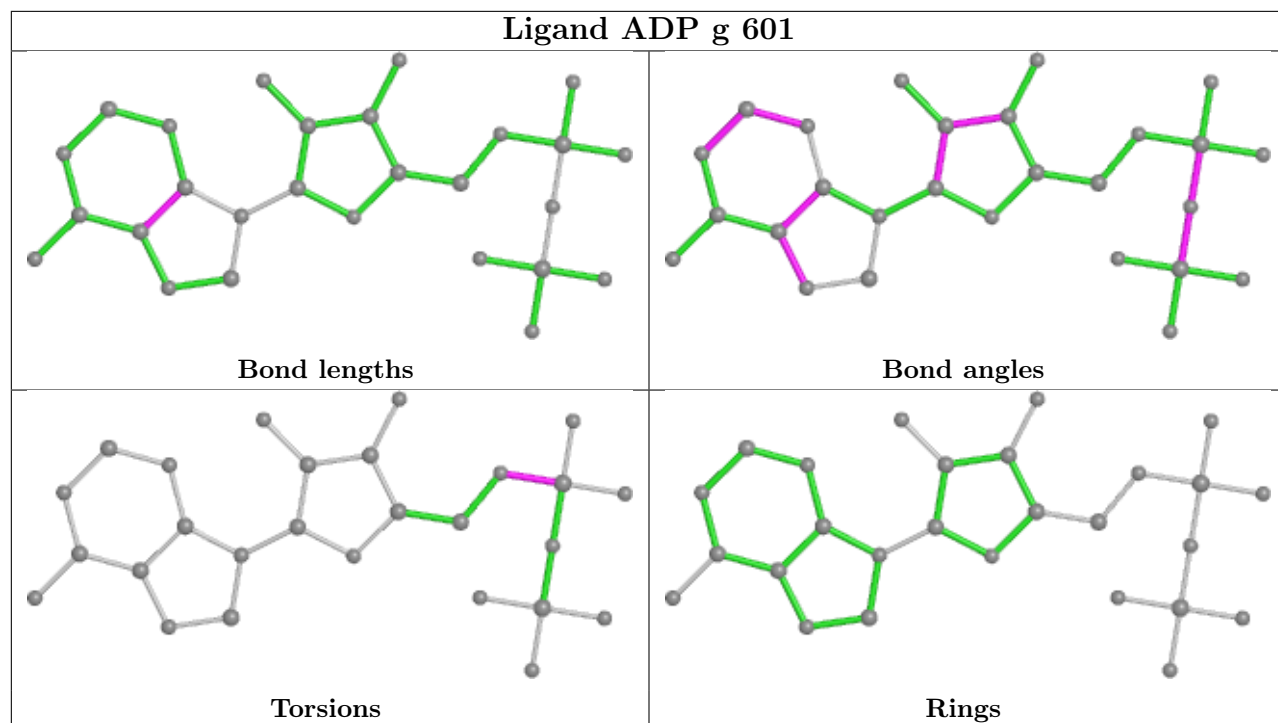
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

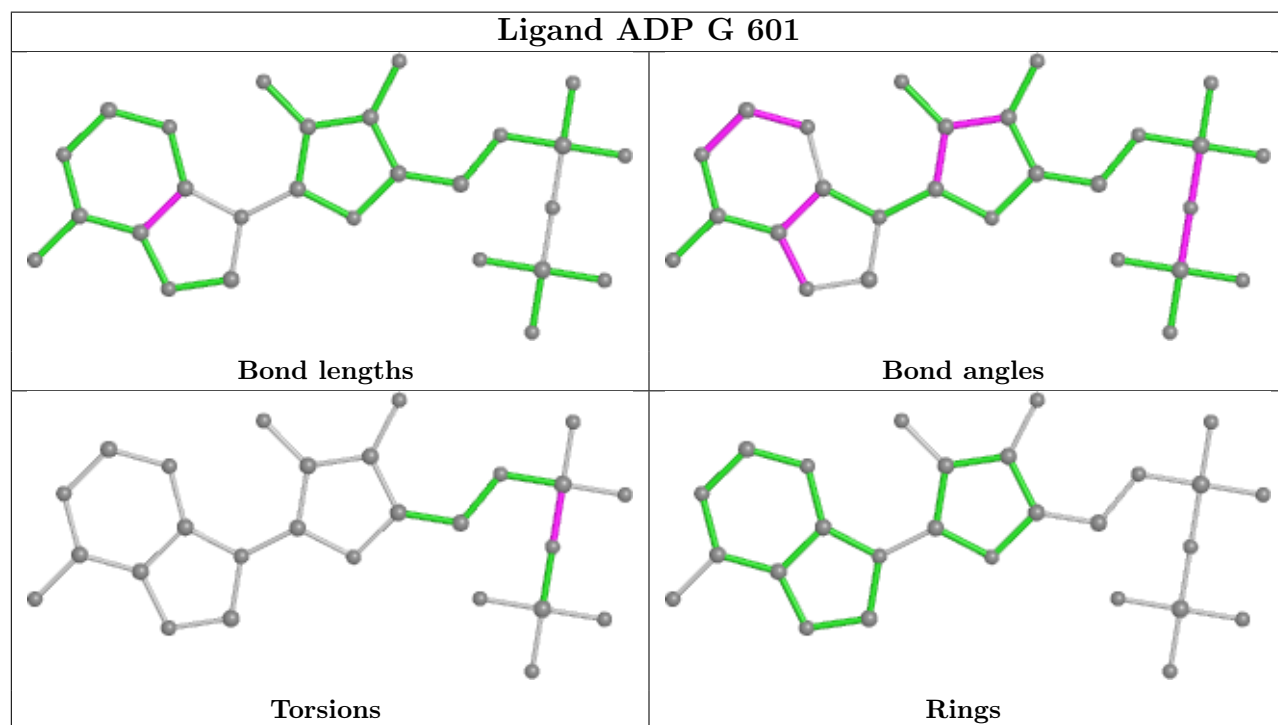
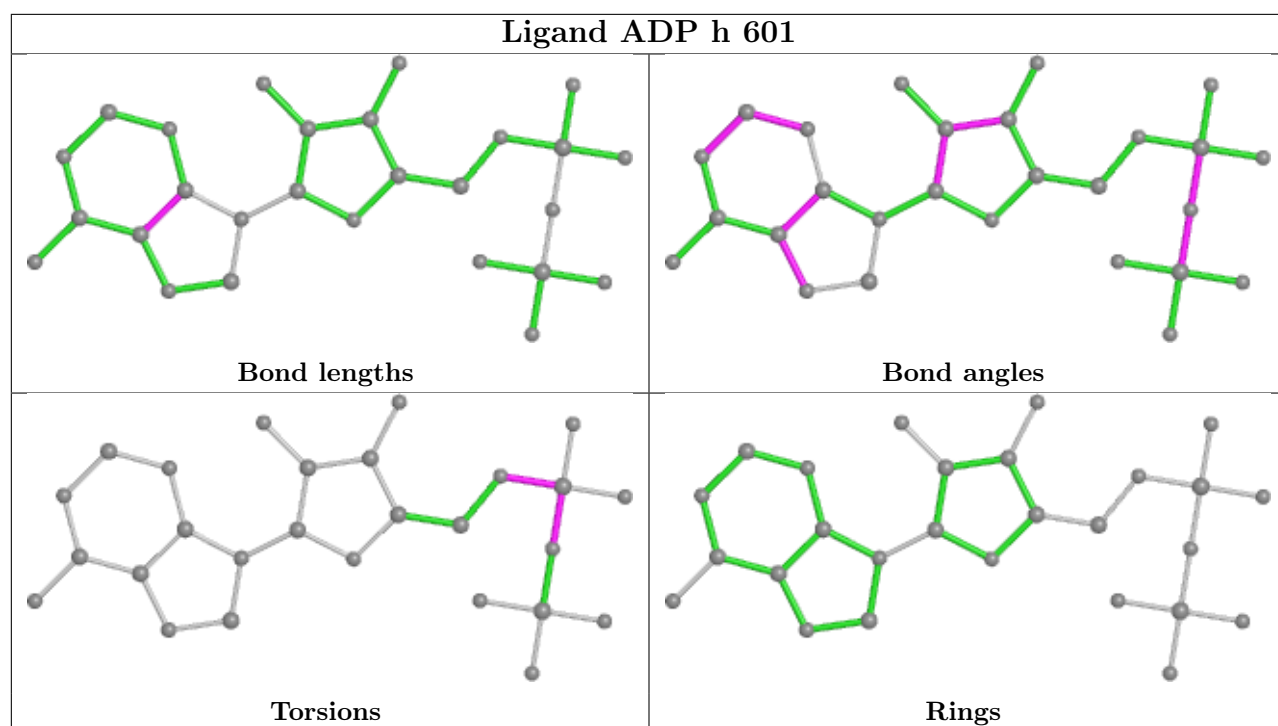
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.

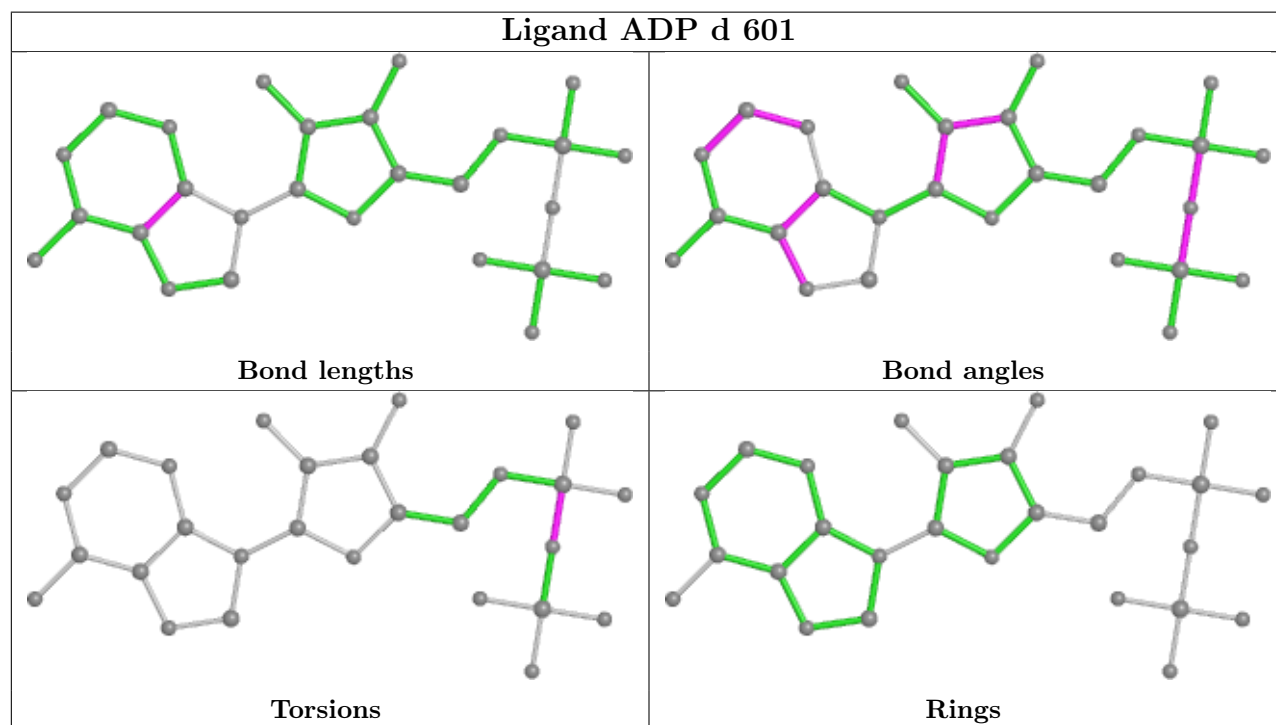
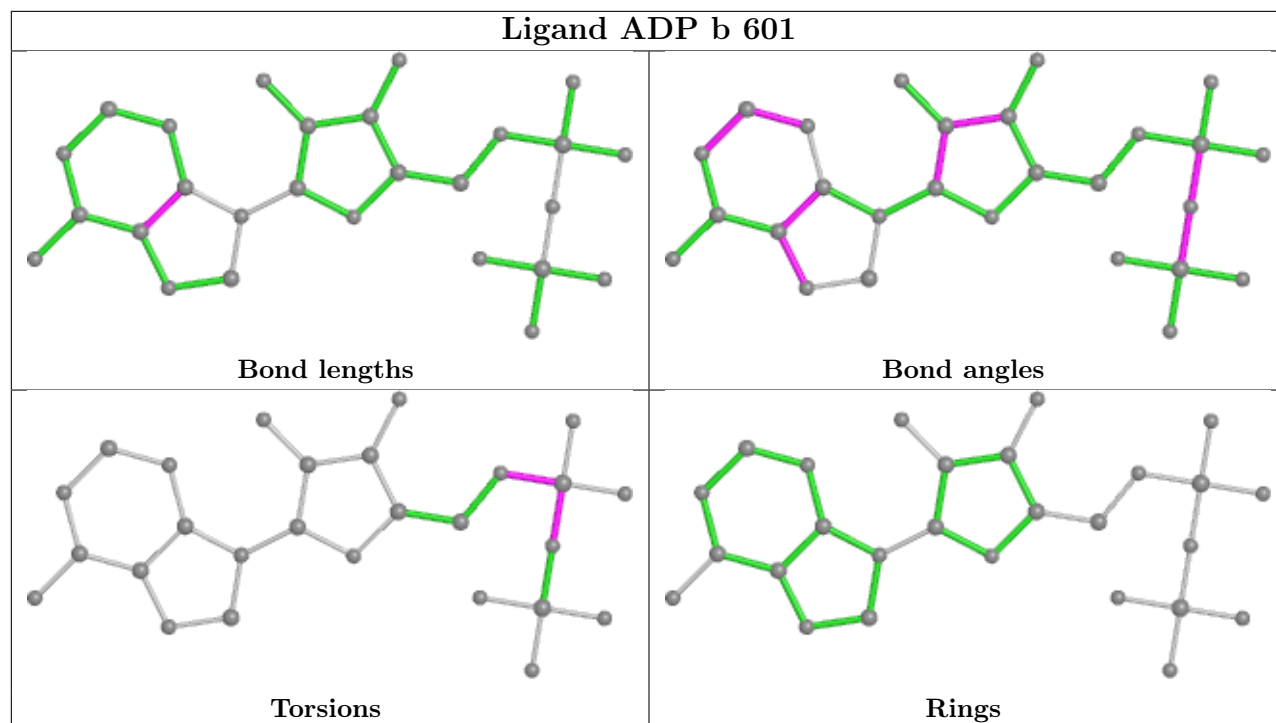


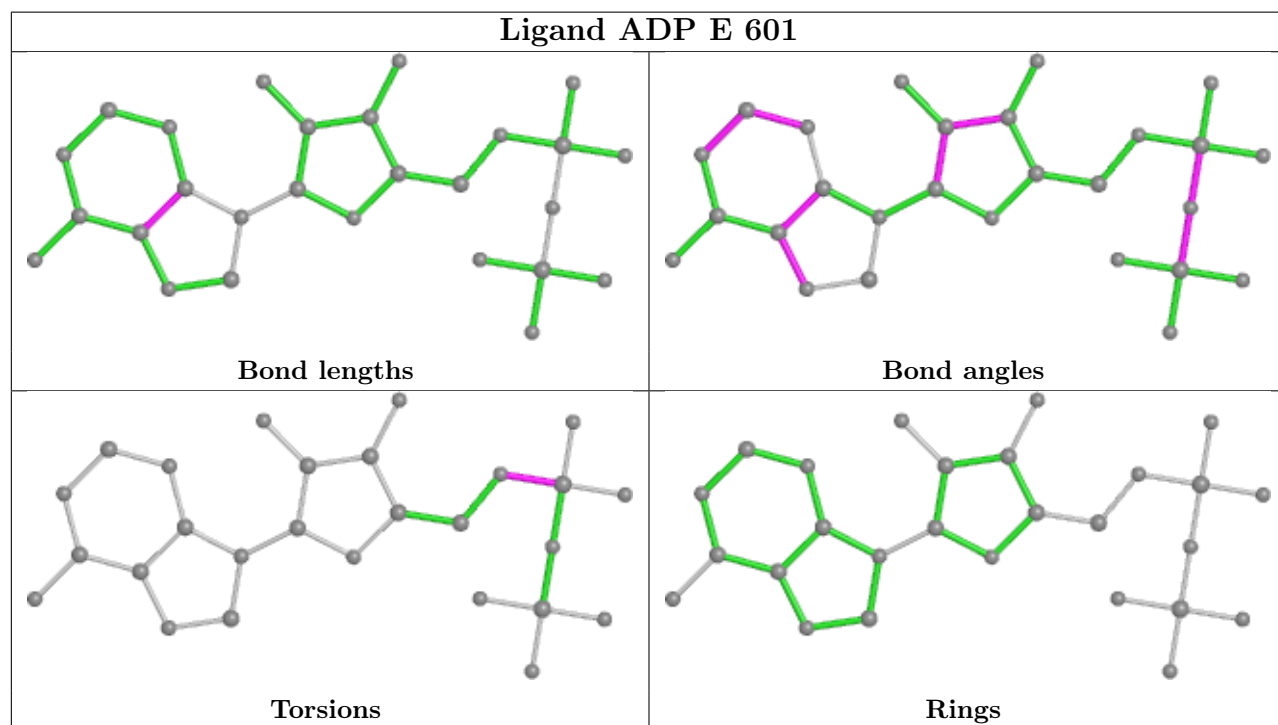
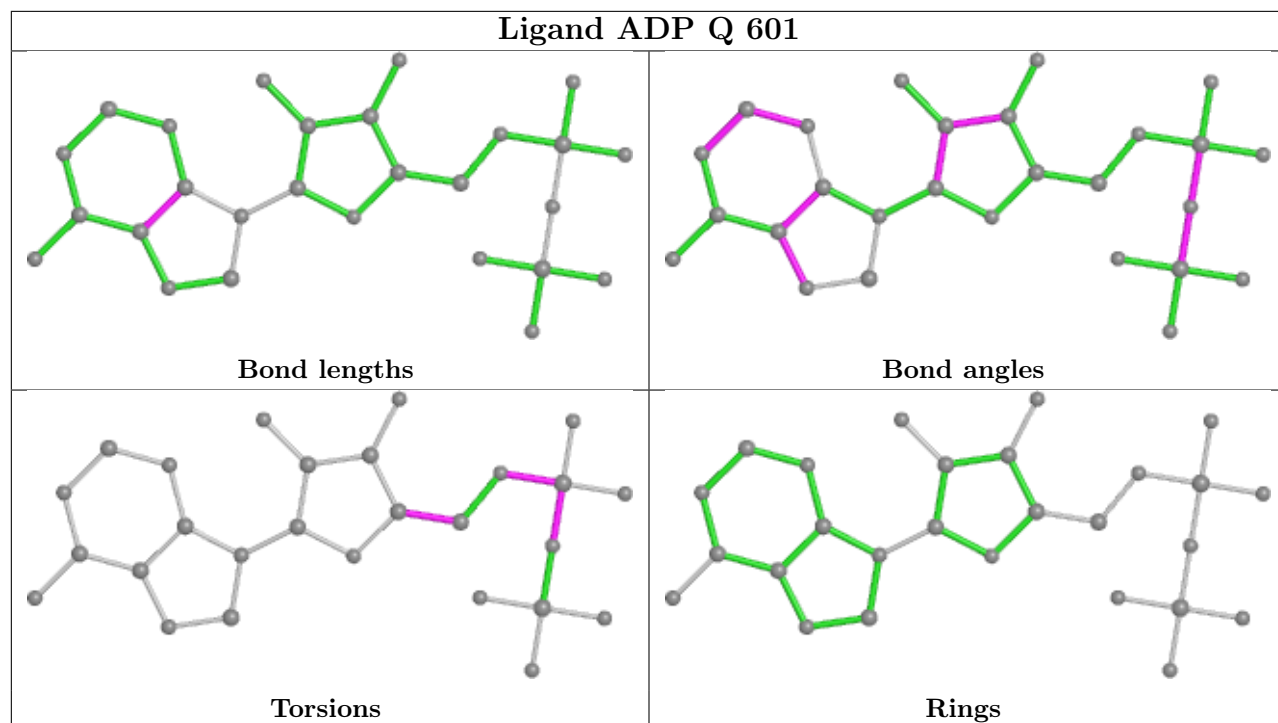


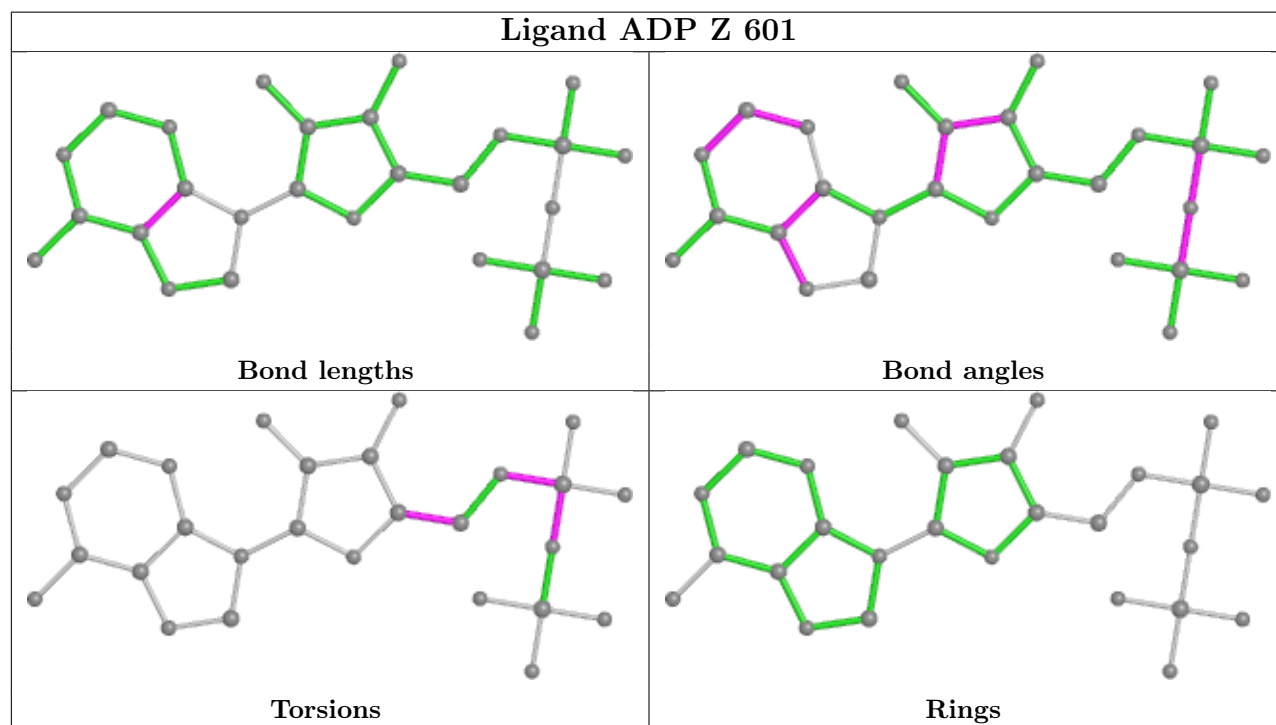
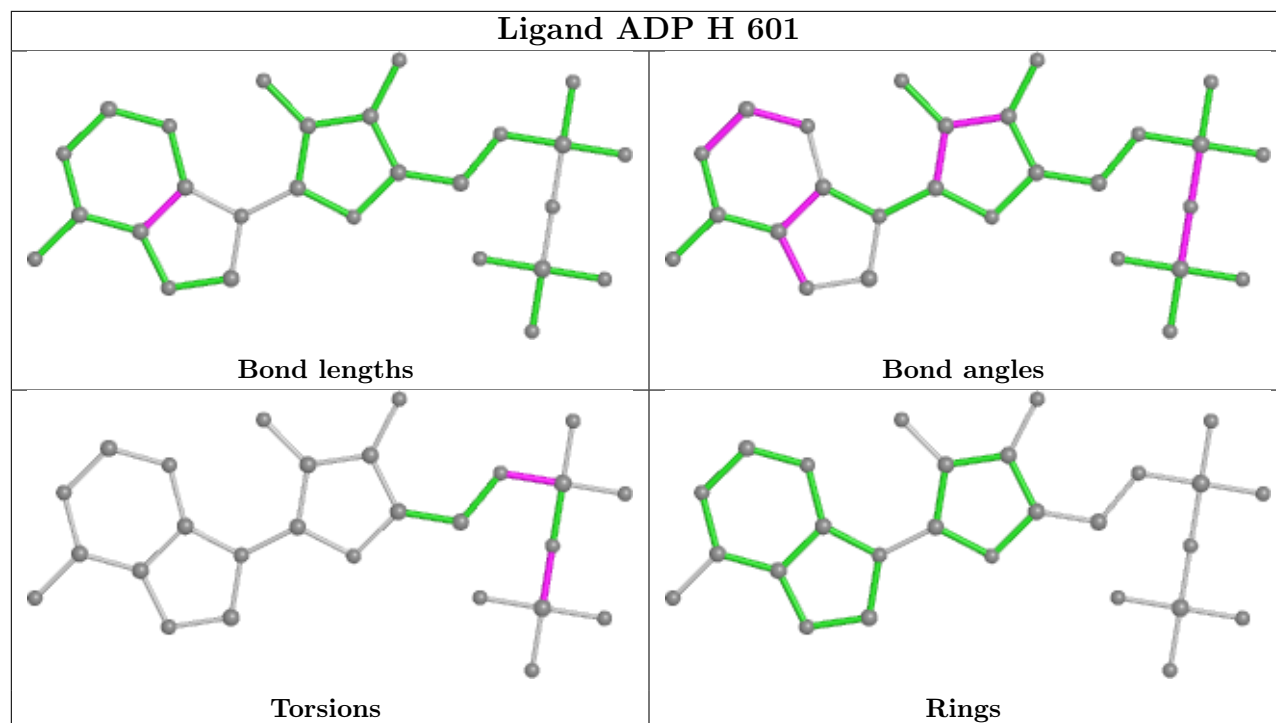


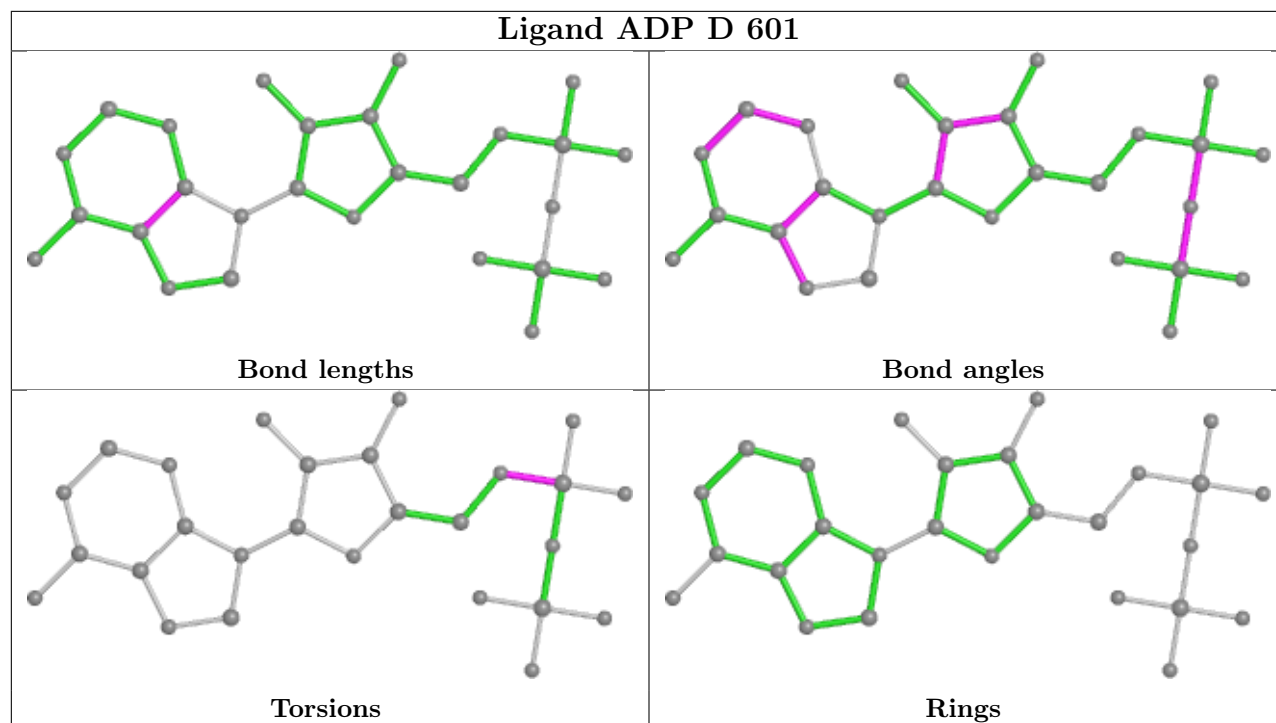












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

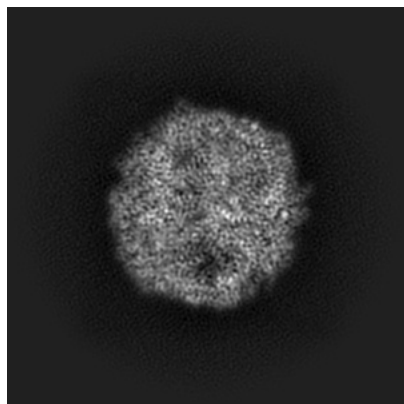
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40494. These allow visual inspection of the internal detail of the map and identification of artifacts.

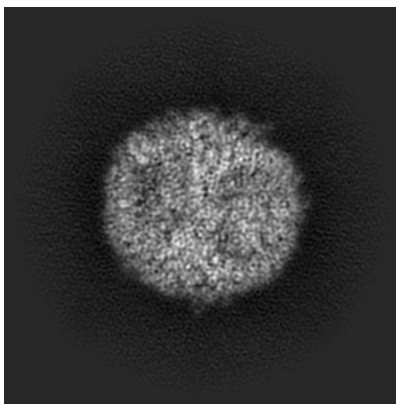
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

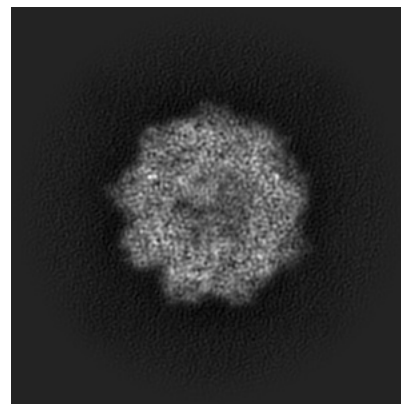
6.1.1 Primary map



X

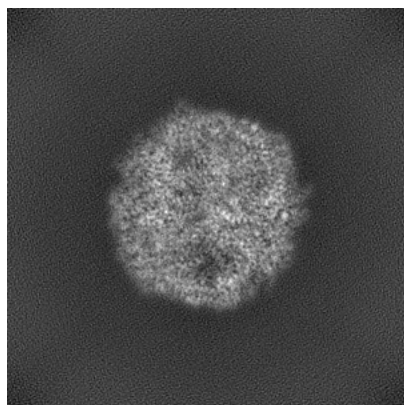


Y

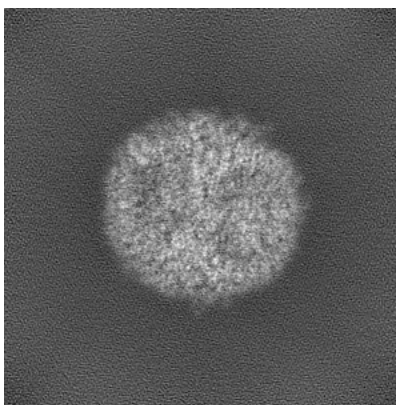


Z

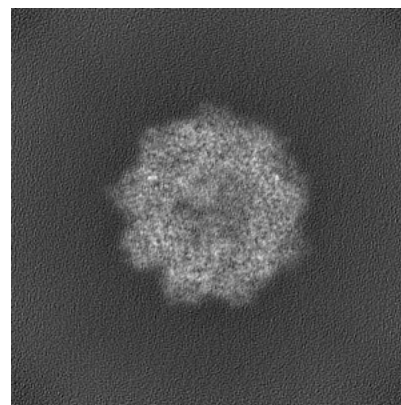
6.1.2 Raw map



X



Y

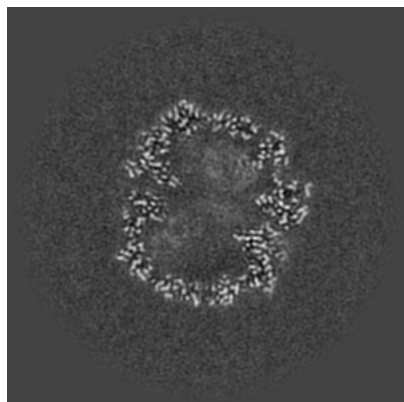


Z

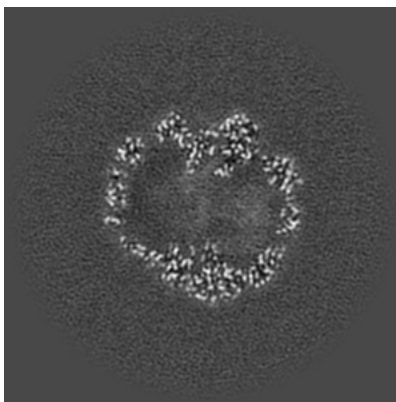
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

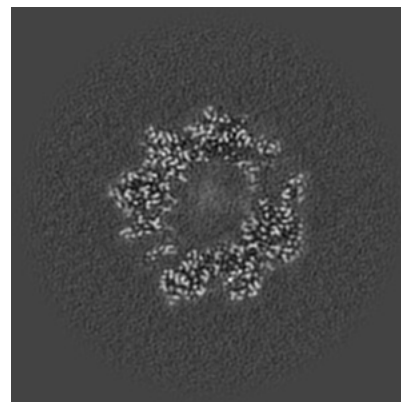
6.2.1 Primary map



X Index: 150

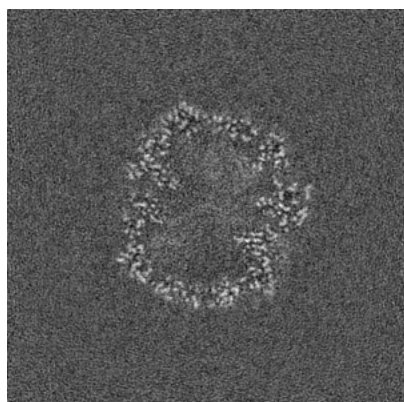


Y Index: 150

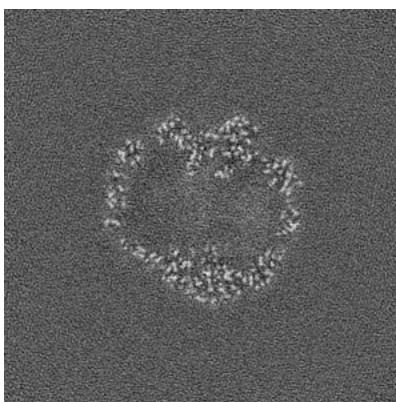


Z Index: 150

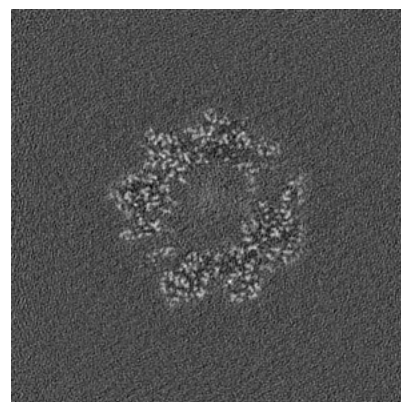
6.2.2 Raw map



X Index: 150



Y Index: 150

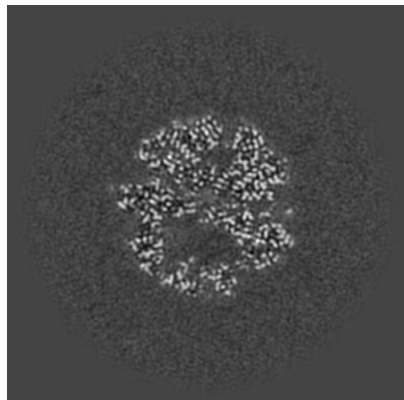


Z Index: 150

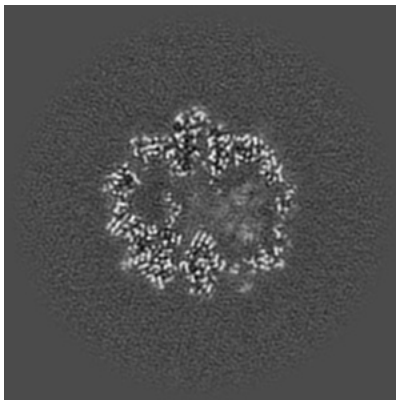
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

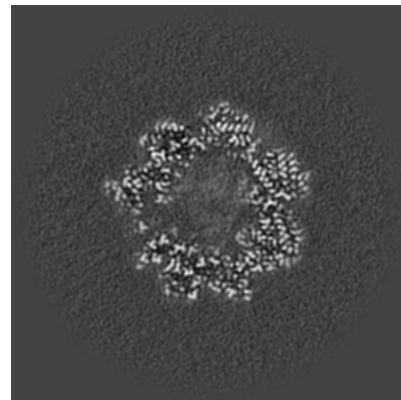
6.3.1 Primary map



X Index: 182

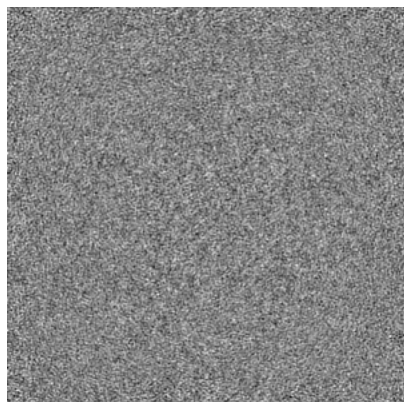


Y Index: 172

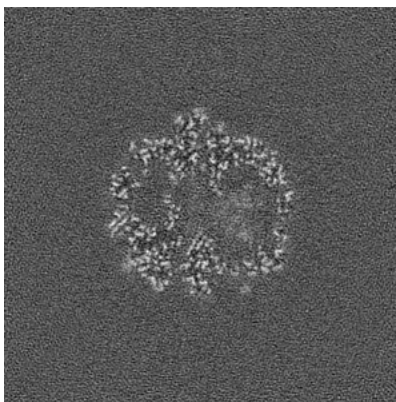


Z Index: 143

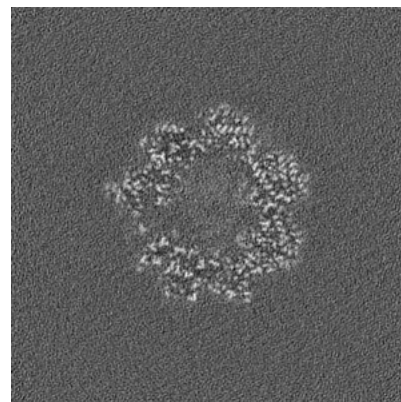
6.3.2 Raw map



X Index: 0



Y Index: 173

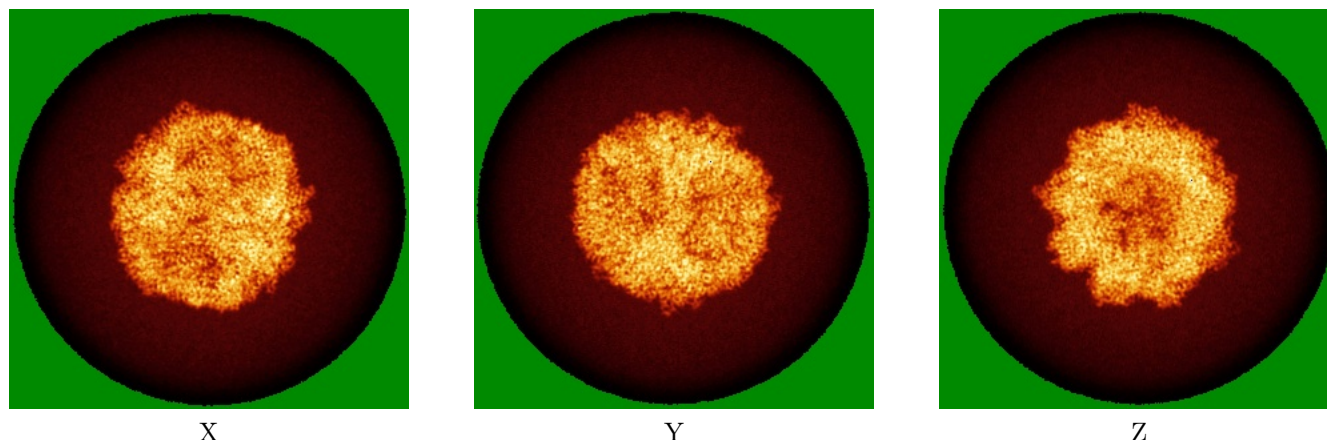


Z Index: 143

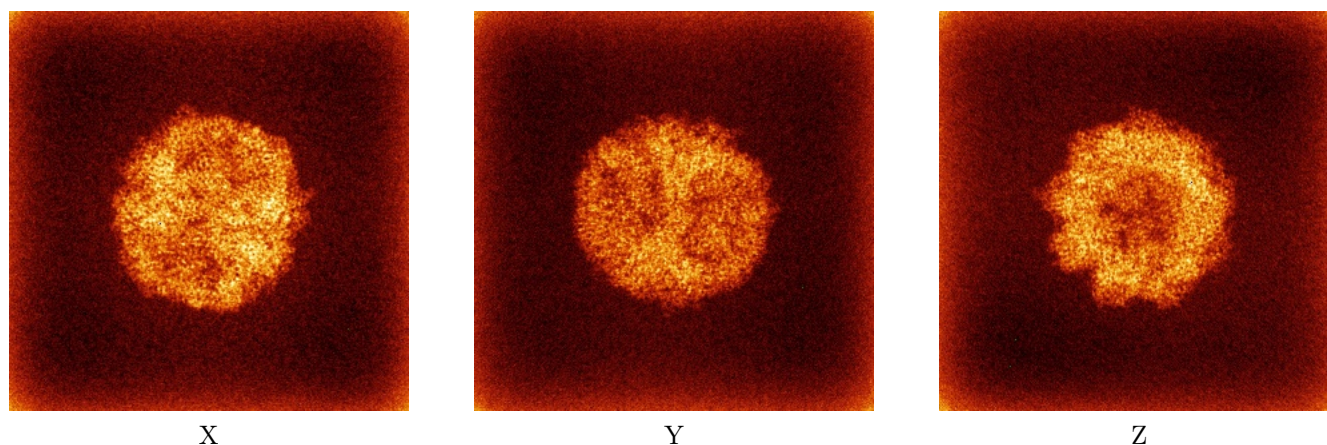
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



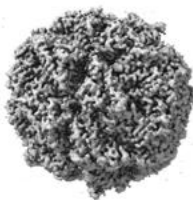
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



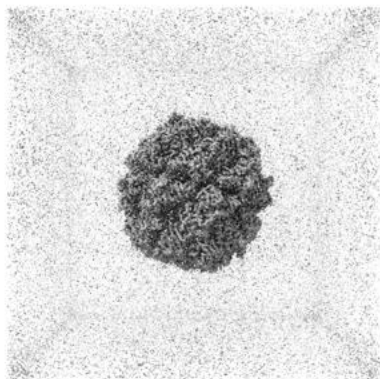
Y



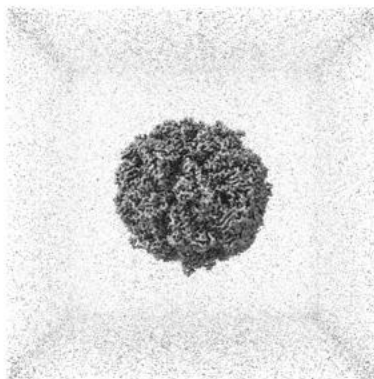
Z

The images above show the 3D surface view of the map at the recommended contour level 0.129. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

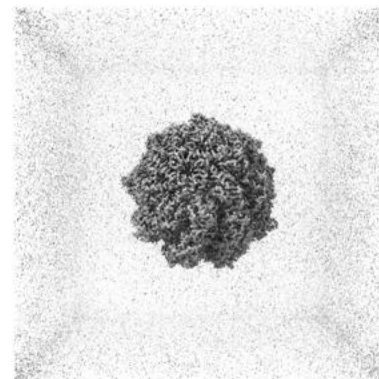
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

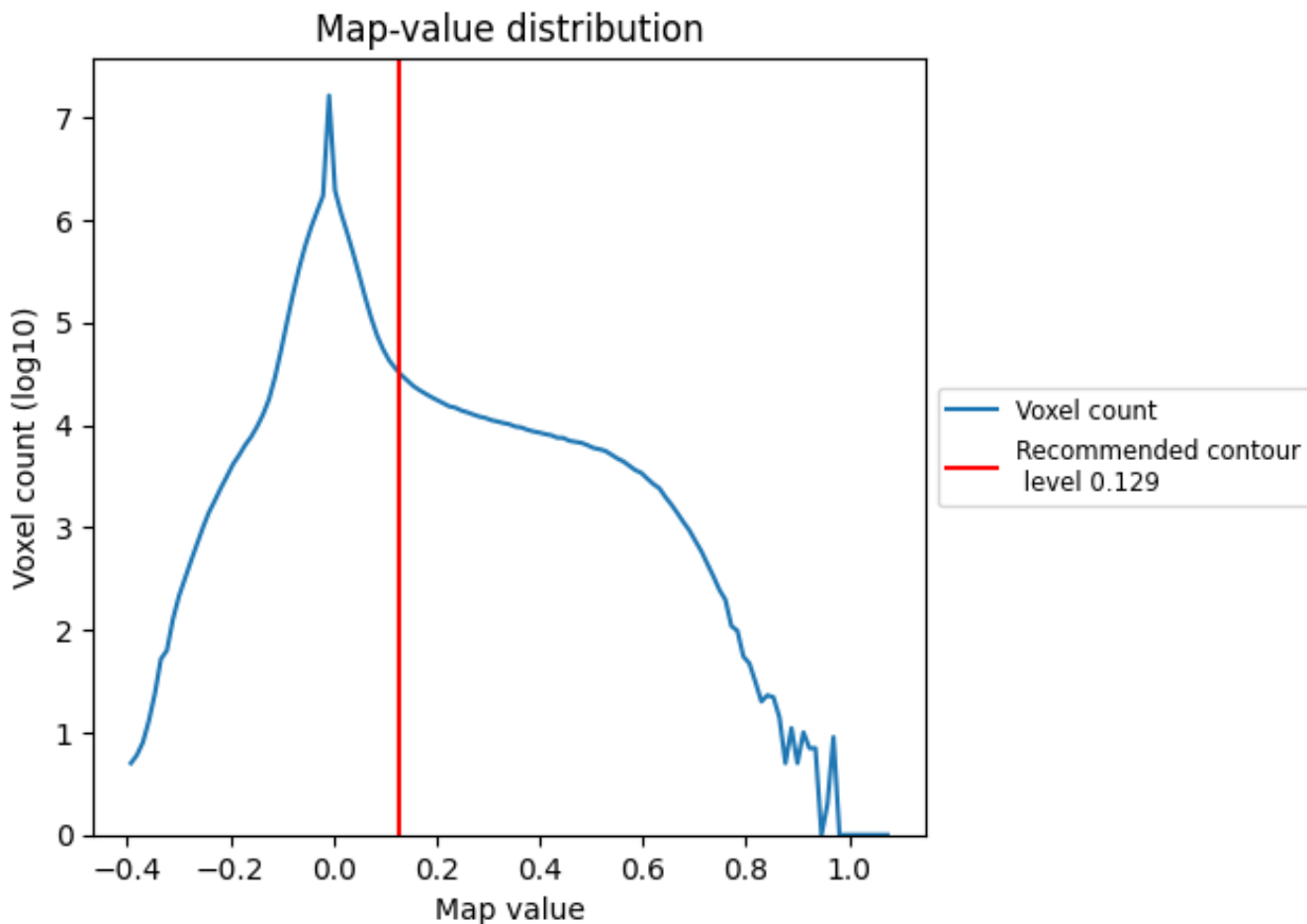
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

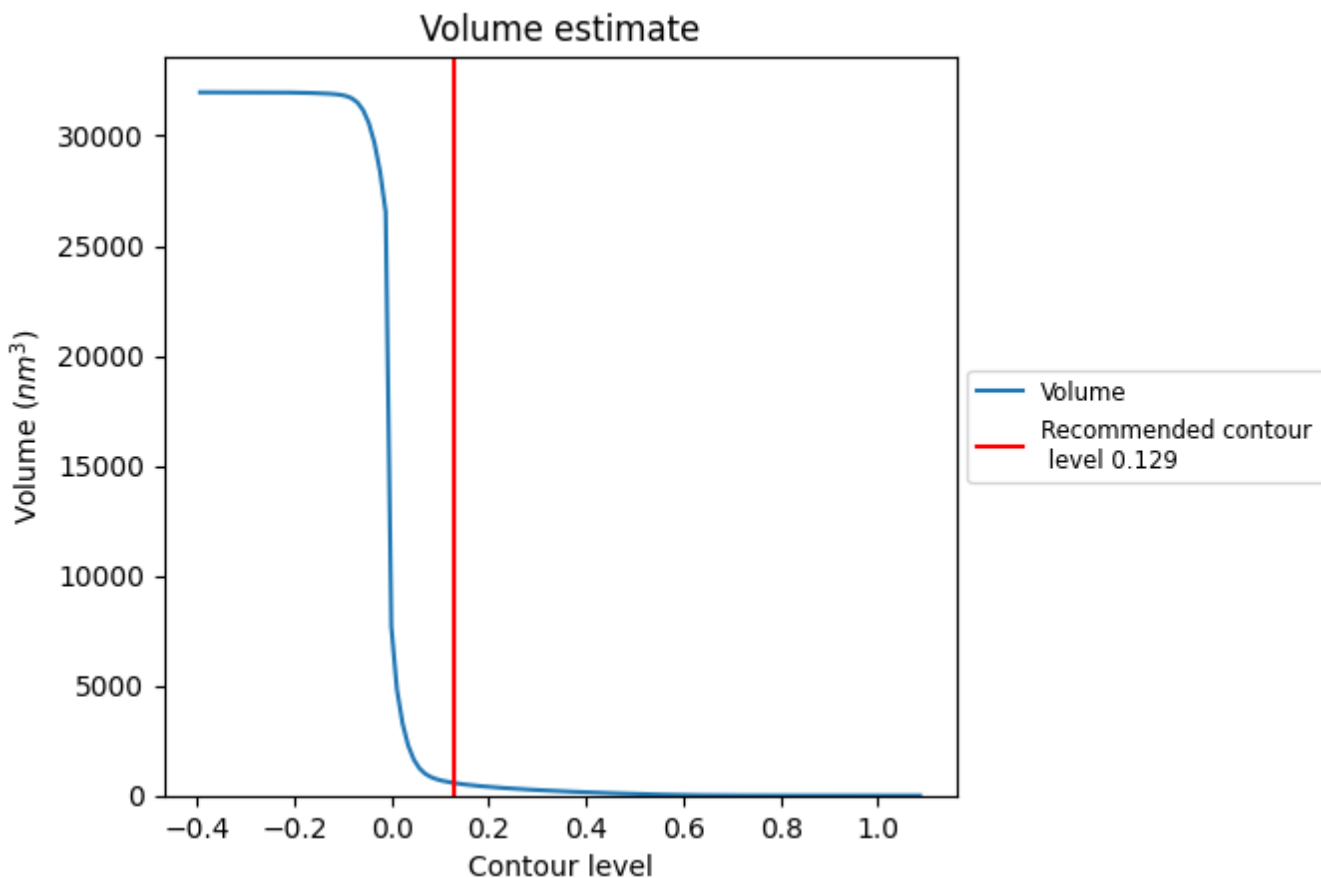
This section contains the results of statistical analysis of the map.

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.

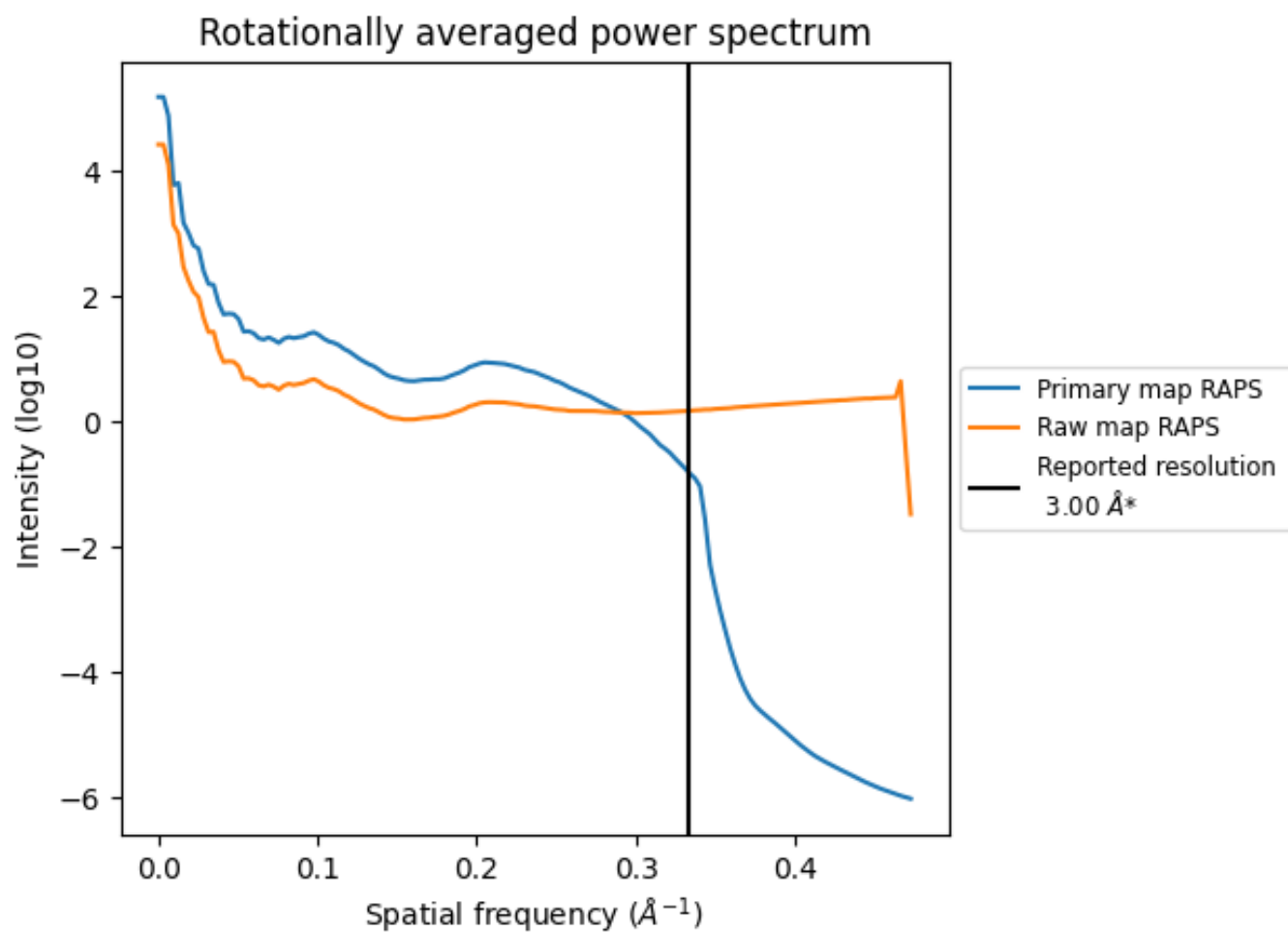
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 572 nm³; this corresponds to an approximate mass of 516 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

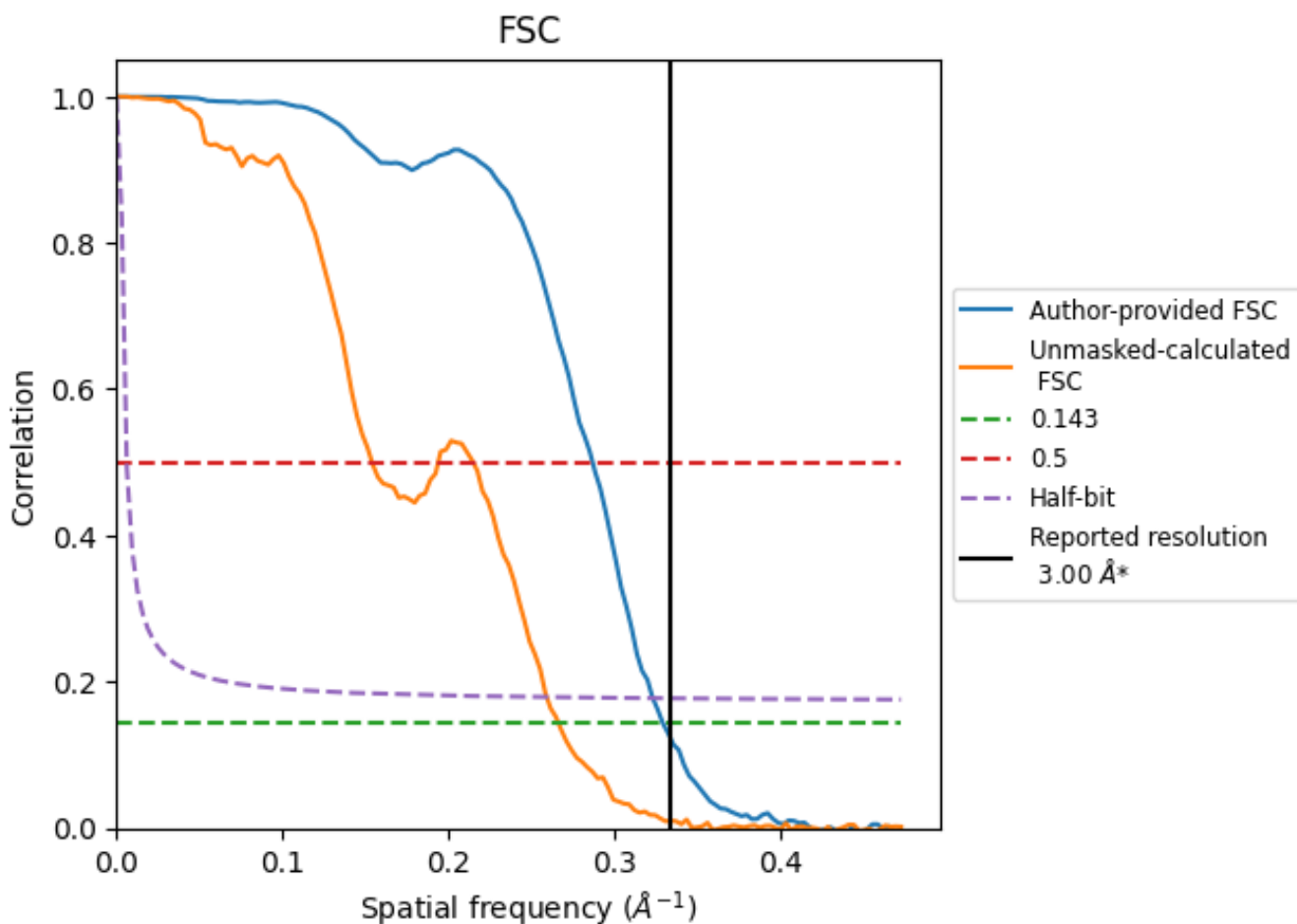


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

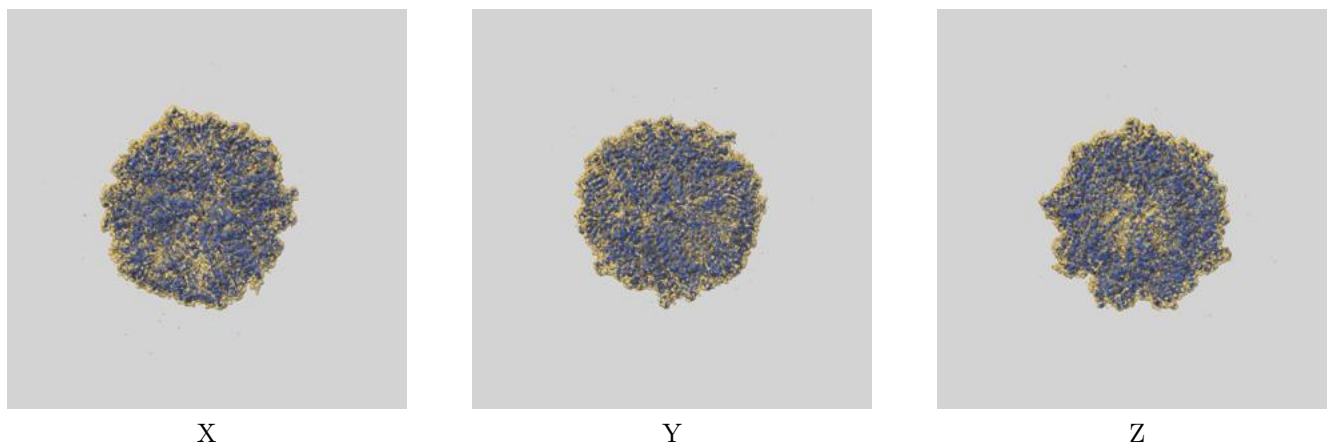
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.49	3.10
Unmasked-calculated*	3.76	6.50	3.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.76 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

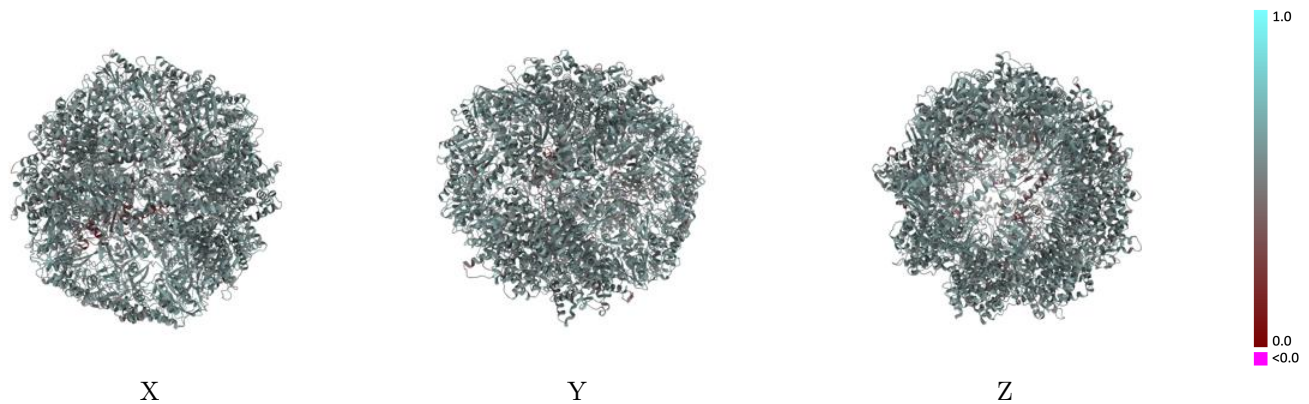
This section contains information regarding the fit between EMDB map EMD-40494 and PDB model 8SHT. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



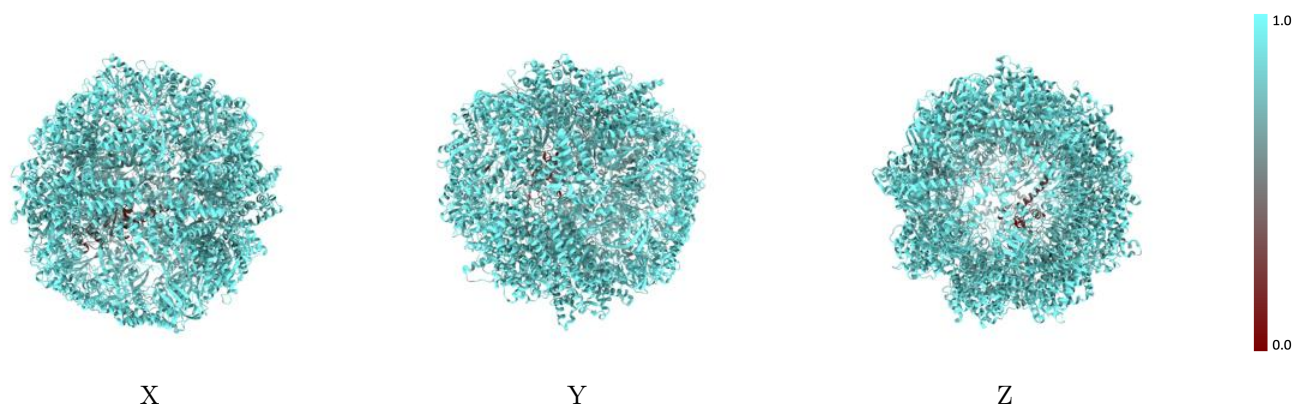
The images above show the 3D surface view of the map at the recommended contour level 0.129 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



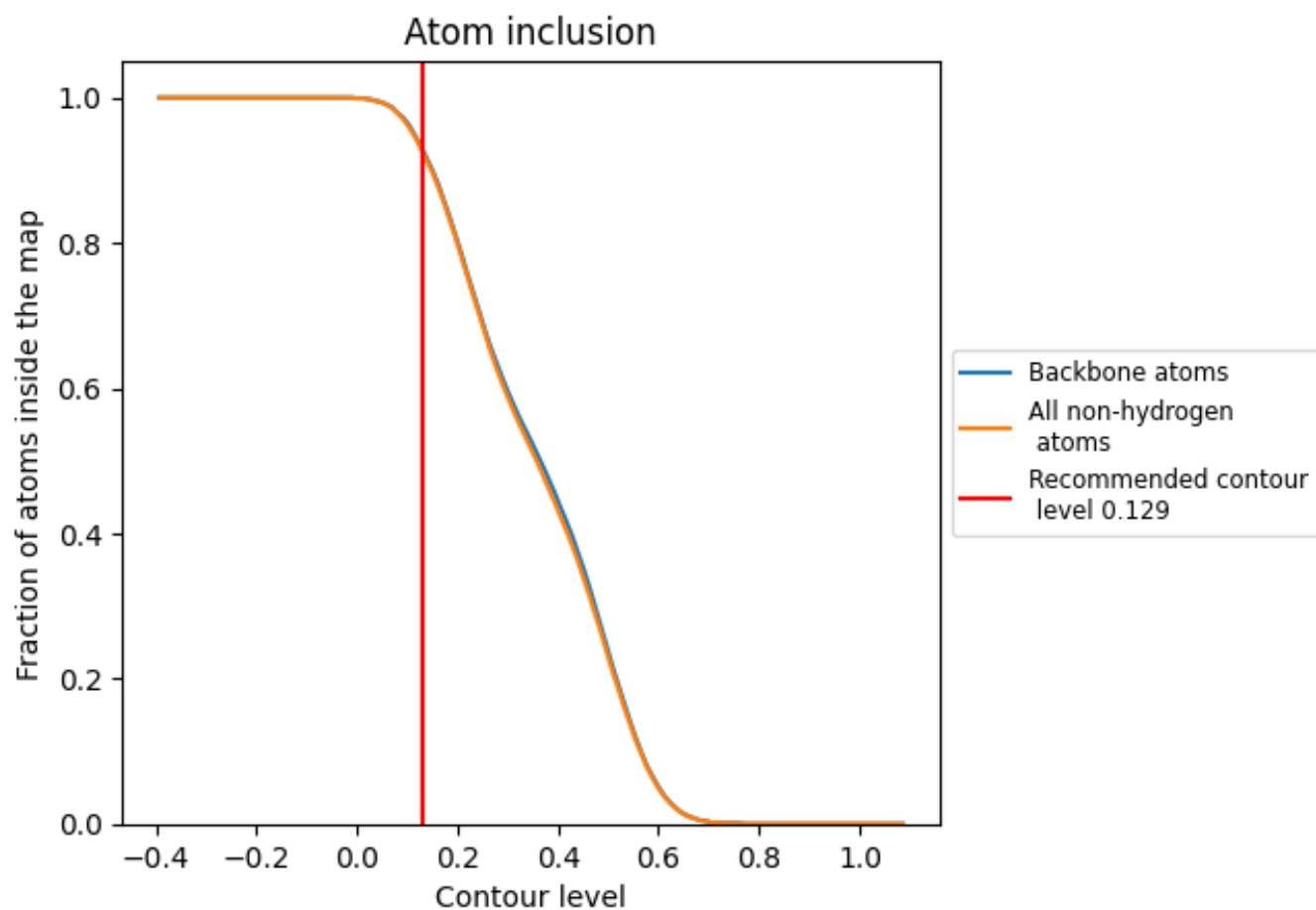
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.129).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.129) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.5420
A	 0.9420	 0.5480
B	 0.9500	 0.5560
D	 0.9500	 0.5500
E	 0.9410	 0.5500
G	 0.9430	 0.5520
H	 0.9470	 0.5520
N	 0.7870	 0.4130
P	 0.4160	 0.3330
Q	 0.9350	 0.5460
Z	 0.9460	 0.5480
a	 0.9450	 0.5470
b	 0.9540	 0.5560
d	 0.9470	 0.5490
e	 0.9380	 0.5490
g	 0.9490	 0.5530
h	 0.9470	 0.5550
q	 0.9450	 0.5480
z	 0.9420	 0.5490

