



wwPDB EM Validation Summary Report ⓘ

Aug 4, 2026 – 03:05 PM EDT

PDB ID : 9NR1 / pdb_00009nr1
EMDB ID : EMD-49709
Title : CCT G beta 5 G257E complex state 1
Authors : Mack, D.C.; Shen, P.S.
Deposited on : 2025-03-13
Resolution : 3.20 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:

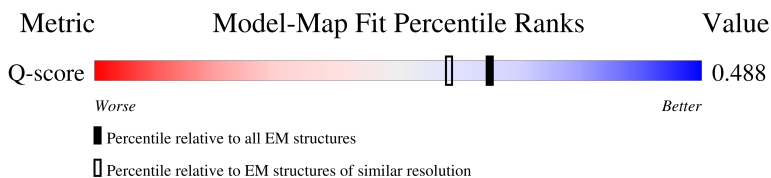
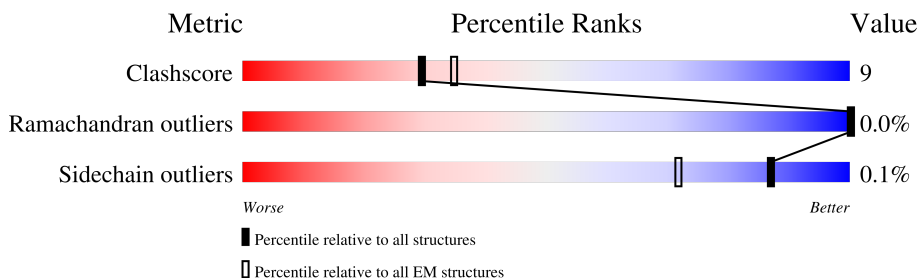
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 3.20 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	15020 (2.70 - 3.70)

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	556	 75% 21% .
1	a	556	 74% 22% .
2	B	535	 81% 17% .
2	b	535	 75% 23% .

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Mol	Chain	Length	Quality of chain
3	D	539	 75% 22% .
3	d	539	 76% 21% .
4	E	541	 76% 23% .
4	e	541	 78% 21% .
5	G	545	 73% 23% .
5	g	545	 75% 21% .
6	H	543	 80% 17% .
6	h	543	 73% 23% .
7	Q	548	 76% 22% .
7	q	548	 76% 21% .
8	Z	531	 76% 23% .
8	z	531	 77% 22% .
9	N	441	 98% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
12	AF3	A	603	-	-	X	-
12	AF3	D	603	-	-	X	-
12	AF3	g	603	-	-	X	-
12	AF3	h	603	-	-	X	-
12	AF3	z	603	-	-	X	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 65214 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
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
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
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
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
5	G	526	Total	C	N	O	S	0	0
			4089	2548	726	785	30		
5	g	526	Total	C	N	O	S	0	0
			4088	2548	725	785	30		

- Molecule 6 is a protein called T-complex protein 1 subunit eta.

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

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

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

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

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

- Molecule 9 is a protein called Guanine nucleotide-binding protein subunit beta-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	10	Total	C	N	O	S	0	0
			80	49	15	14	2		

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-31	MET	-	initiating methionine	UNP O14775
N	-30	TRP	-	expression tag	UNP O14775
N	-29	SER	-	expression tag	UNP O14775
N	-28	HIS	-	expression tag	UNP O14775

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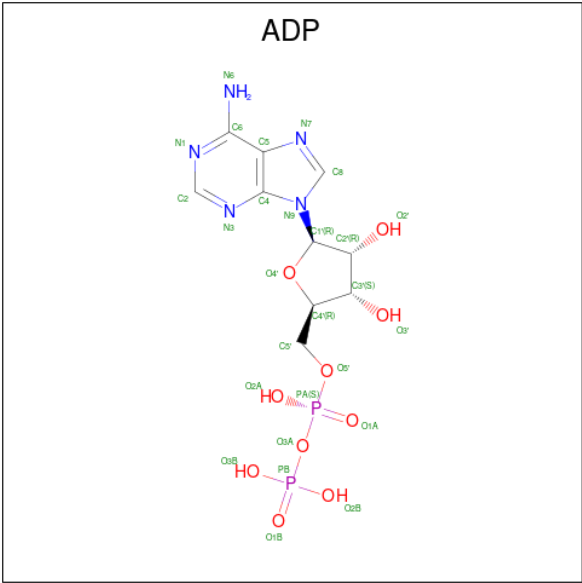
Chain	Residue	Modelled	Actual	Comment	Reference
N	-27	PRO	-	expression tag	UNP O14775
N	-26	GLN	-	expression tag	UNP O14775
N	-25	PHE	-	expression tag	UNP O14775
N	-24	GLU	-	expression tag	UNP O14775
N	-23	LYS	-	expression tag	UNP O14775
N	-22	GLY	-	expression tag	UNP O14775
N	-21	GLY	-	expression tag	UNP O14775
N	-20	GLY	-	expression tag	UNP O14775
N	-19	SER	-	expression tag	UNP O14775
N	-18	GLY	-	expression tag	UNP O14775
N	-17	GLY	-	expression tag	UNP O14775
N	-16	GLY	-	expression tag	UNP O14775
N	-15	SER	-	expression tag	UNP O14775
N	-14	GLY	-	expression tag	UNP O14775
N	-13	GLY	-	expression tag	UNP O14775
N	-12	SER	-	expression tag	UNP O14775
N	-11	SER	-	expression tag	UNP O14775
N	-10	ALA	-	expression tag	UNP O14775
N	-9	TRP	-	expression tag	UNP O14775
N	-8	SER	-	expression tag	UNP O14775
N	-7	HIS	-	expression tag	UNP O14775
N	-6	PRO	-	expression tag	UNP O14775
N	-5	GLN	-	expression tag	UNP O14775
N	-4	PHE	-	expression tag	UNP O14775
N	-3	GLU	-	expression tag	UNP O14775
N	-2	LYS	-	expression tag	UNP O14775
N	-1	ALA	-	expression tag	UNP O14775
N	0	ALA	-	expression tag	UNP O14775
N	257	GLU	GLY	engineered mutation	UNP O14775
N	396	GLY	-	expression tag	UNP O14775
N	397	GLY	-	expression tag	UNP O14775
N	398	GLU	-	expression tag	UNP O14775
N	399	ASP	-	expression tag	UNP O14775
N	400	GLN	-	expression tag	UNP O14775
N	401	VAL	-	expression tag	UNP O14775
N	402	ASP	-	expression tag	UNP O14775
N	403	PRO	-	expression tag	UNP O14775
N	404	ARG	-	expression tag	UNP O14775
N	405	LEU	-	expression tag	UNP O14775
N	406	ILE	-	expression tag	UNP O14775
N	407	ASP	-	expression tag	UNP O14775
N	408	GLY	-	expression tag	UNP O14775

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Chain	Residue	Modelled	Actual	Comment	Reference
N	409	LYS	-	expression tag	UNP O14775

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
10	A	1	Total 27	10	5	10	2	0
10	B	1	Total 27	10	5	10	2	0
10	D	1	Total 27	10	5	10	2	0
10	E	1	Total 27	10	5	10	2	0
10	G	1	Total 27	10	5	10	2	0
10	H	1	Total 27	10	5	10	2	0
10	Q	1	Total 27	10	5	10	2	0
10	Z	1	Total 27	10	5	10	2	0
10	a	1	Total 27	10	5	10	2	0
10	b	1	Total 27	10	5	10	2	0
10	d	1	Total 27	10	5	10	2	0

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

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

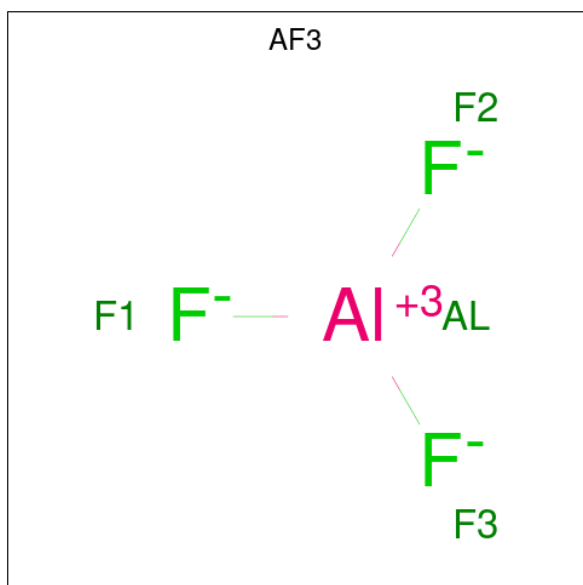
Mol	Chain	Residues	Atoms		AltConf
11	A	1	Total	Mg	0
			1	1	
11	B	1	Total	Mg	0
			1	1	
11	D	1	Total	Mg	0
			1	1	
11	E	1	Total	Mg	0
			1	1	
11	G	1	Total	Mg	0
			1	1	
11	H	1	Total	Mg	0
			1	1	
11	Q	1	Total	Mg	0
			1	1	
11	Z	1	Total	Mg	0
			1	1	
11	a	1	Total	Mg	0
			1	1	
11	b	1	Total	Mg	0
			1	1	
11	d	1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

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Mol	Chain	Residues	Atoms		AltConf
11	q	1	Total 1	Mg 1	0
11	z	1	Total 1	Mg 1	0

- Molecule 12 is ALUMINUM FLUORIDE (CCD ID: AF3) (formula: AlF_3).



Mol	Chain	Residues	Atoms			AltConf
12	A	1	Total 4	Al 1	F 3	0
12	B	1	Total 4	Al 1	F 3	0
12	D	1	Total 4	Al 1	F 3	0
12	E	1	Total 4	Al 1	F 3	0
12	G	1	Total 4	Al 1	F 3	0
12	H	1	Total 4	Al 1	F 3	0
12	Q	1	Total 4	Al 1	F 3	0
12	Z	1	Total 4	Al 1	F 3	0
12	a	1	Total 4	Al 1	F 3	0

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Mol	Chain	Residues	Atoms			AltConf
12	b	1	Total 4	Al 1	F 3	0
12	d	1	Total 4	Al 1	F 3	0
12	e	1	Total 4	Al 1	F 3	0
12	g	1	Total 4	Al 1	F 3	0
12	h	1	Total 4	Al 1	F 3	0
12	q	1	Total 4	Al 1	F 3	0
12	z	1	Total 4	Al 1	F 3	0

- Molecule 13 is water.

Mol	Chain	Residues	Atoms		AltConf
13	A	2	Total 2	O 2	0
13	B	2	Total 2	O 2	0
13	D	1	Total 1	O 1	0
13	E	1	Total 1	O 1	0
13	G	1	Total 1	O 1	0
13	H	1	Total 1	O 1	0
13	Q	1	Total 1	O 1	0
13	Z	1	Total 1	O 1	0
13	a	2	Total 2	O 2	0
13	b	1	Total 1	O 1	0
13	d	1	Total 1	O 1	0
13	e	1	Total 1	O 1	0

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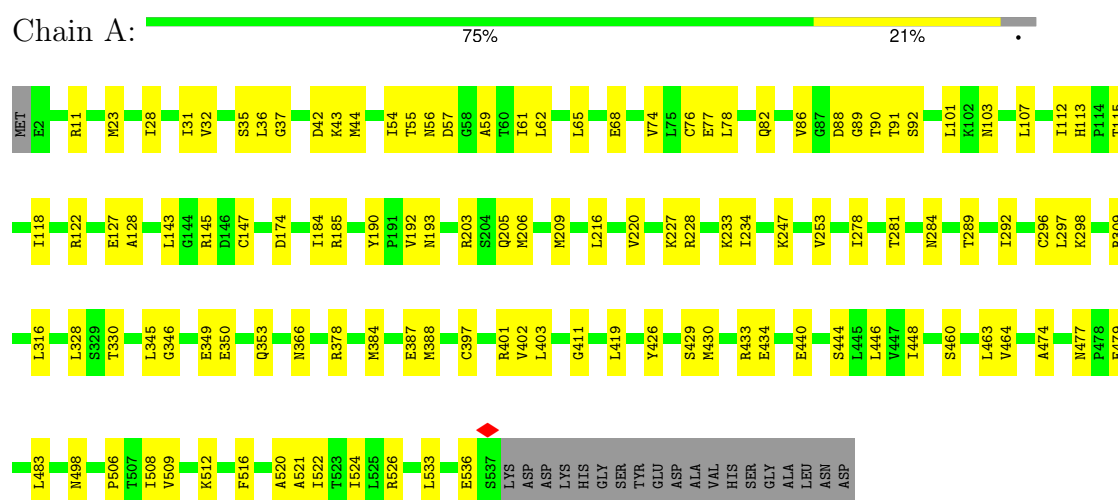
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Mol	Chain	Residues	Atoms		AltConf
13	g	1	Total 1	O 1	0
13	h	1	Total 1	O 1	0
13	q	1	Total 1	O 1	0
13	z	1	Total 1	O 1	0

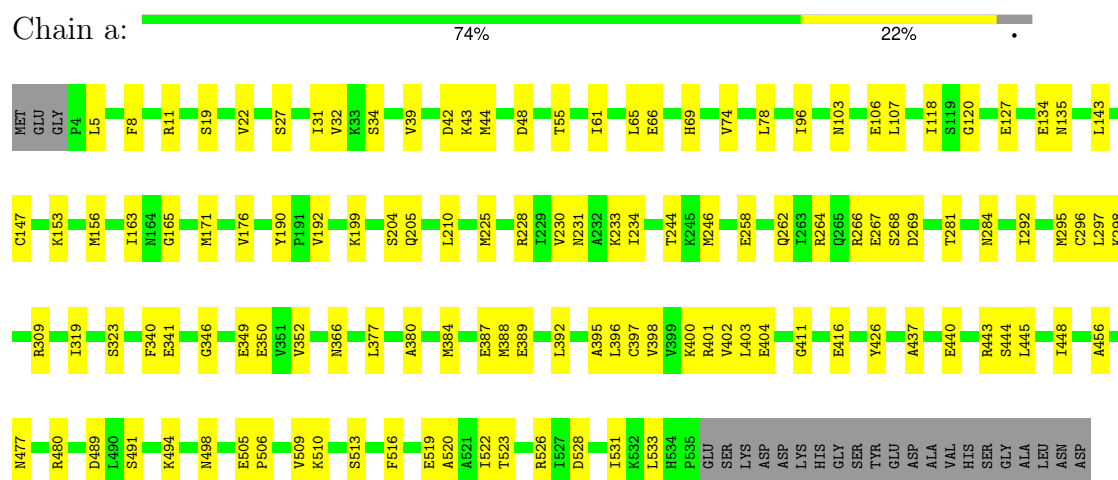
3 Residue-property plots

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.

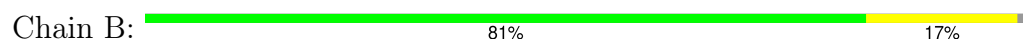
• Molecule 1: T-complex protein 1 subunit alpha



• Molecule 1: T-complex protein 1 subunit alpha

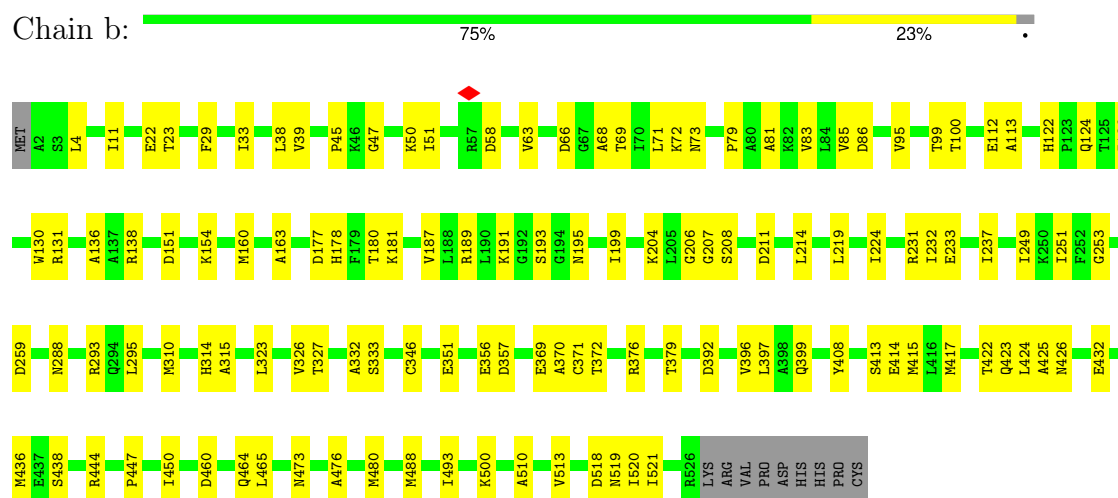


• Molecule 2: T-complex protein 1 subunit beta

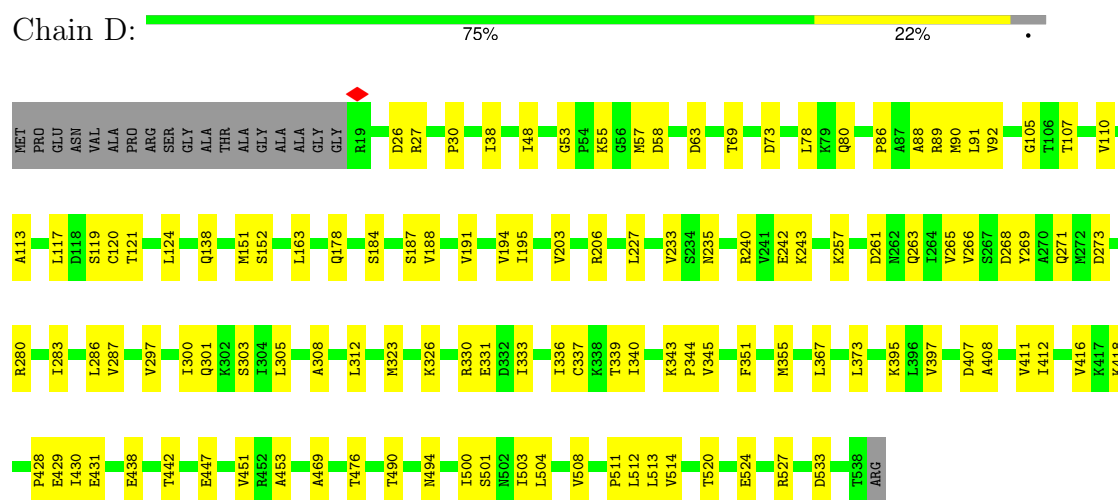




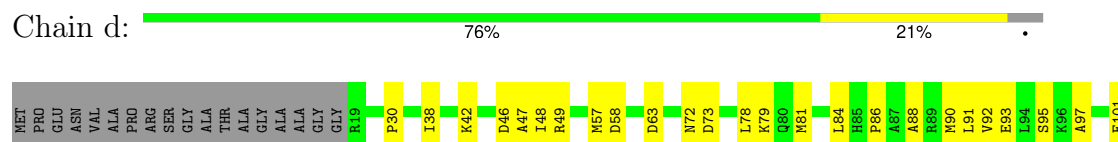
• Molecule 2: T-complex protein 1 subunit beta



• Molecule 3: T-complex protein 1 subunit delta

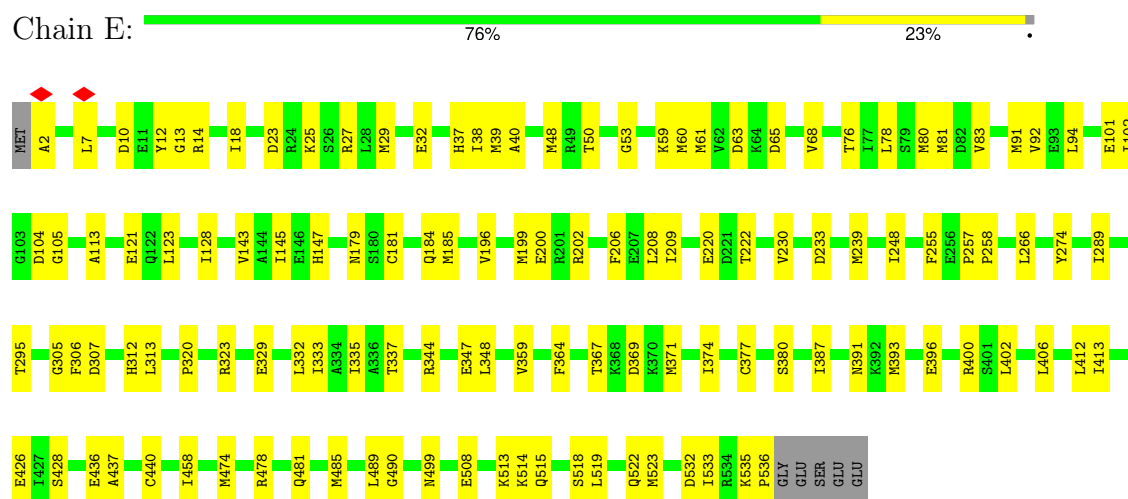


• Molecule 3: T-complex protein 1 subunit delta

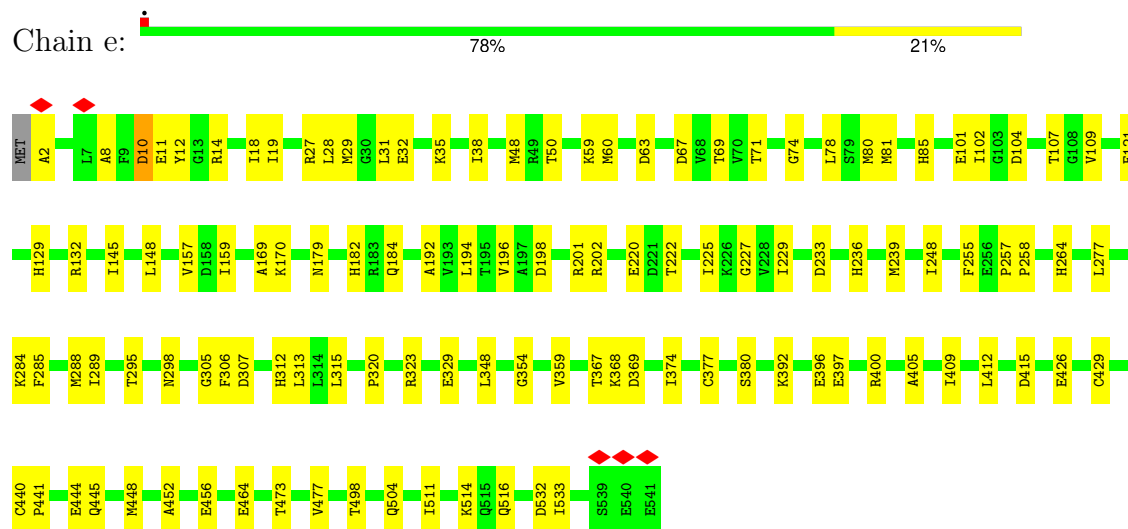




• Molecule 4: T-complex protein 1 subunit epsilon

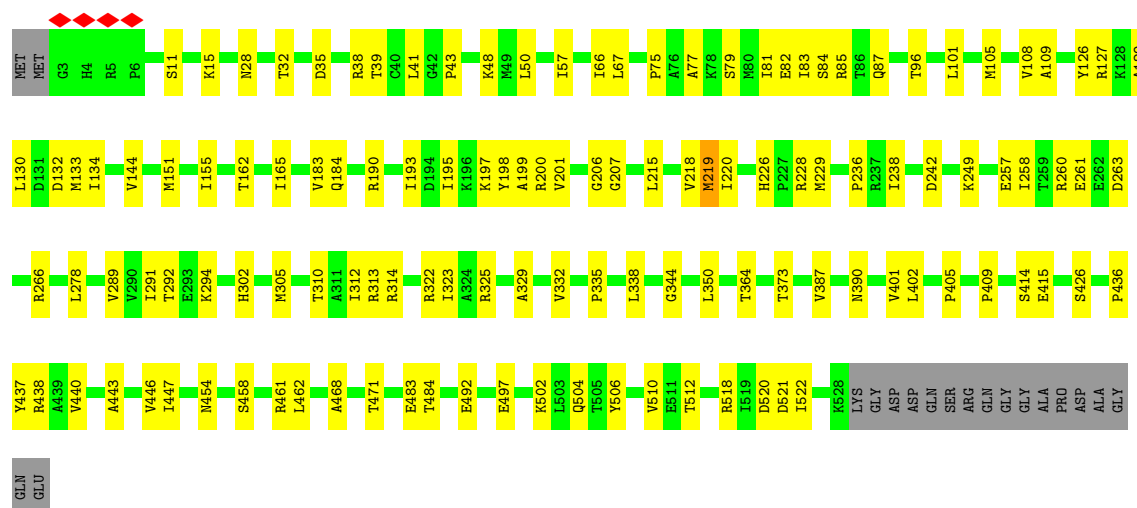


• Molecule 4: T-complex protein 1 subunit epsilon



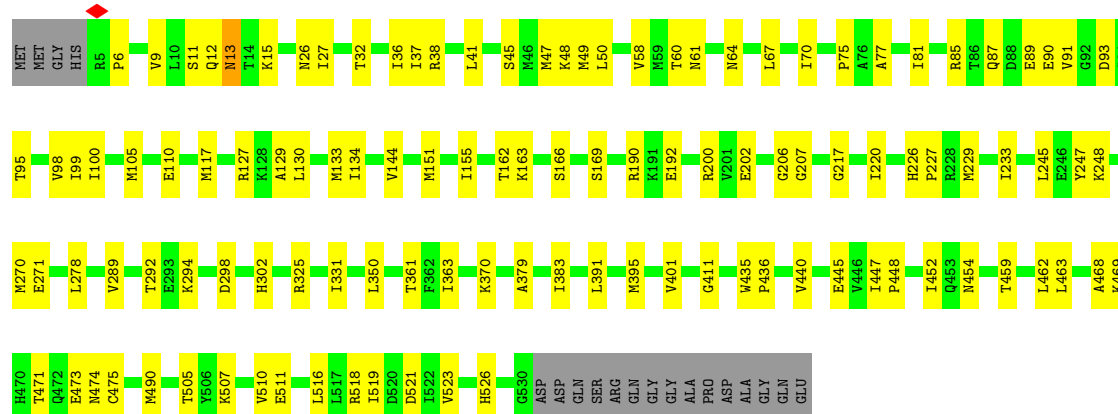
• Molecule 5: T-complex protein 1 subunit gamma





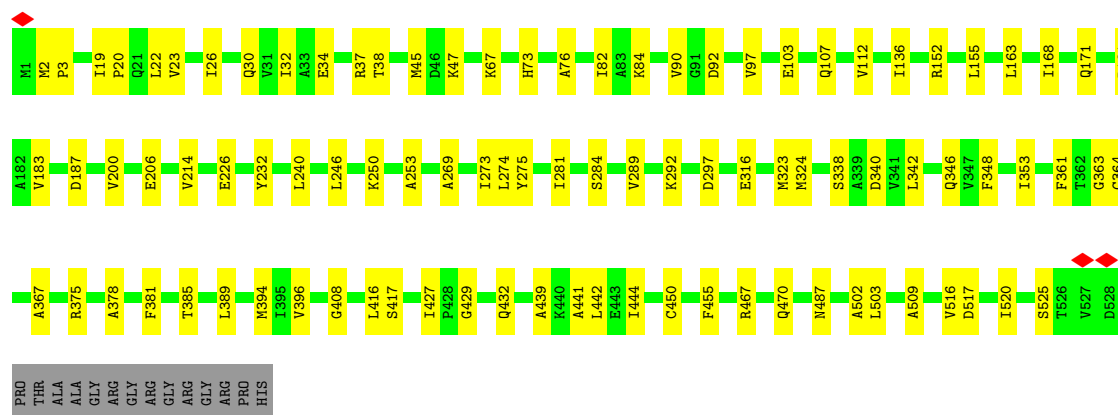
• Molecule 5: T-complex protein 1 subunit gamma

Chain g: 75% 21%



• Molecule 6: T-complex protein 1 subunit eta

Chain H: 80% 17%



• Molecule 6: T-complex protein 1 subunit eta

- Molecule 8: T-complex protein 1 subunit zeta

K449	R264	L103	Met
V450	R279	D107	A2
Q453	F289	L108	A3
K454		Y109	V4
S455	M293	E112	K5
L459	I297	I118	E12
Q460	D298	K127	V13
E461	P299	F133	A16
	F300	V137	T24
D480	E308	T147	L30
L481	G309	D150	Q31
M487	I310	V151	D32
V492	K321	A152	V33
	E322	R153	L34
M497	R323	T158	R35
V500	V331	T169	N37
K501	A332	K180	G39
K502	L333	F169	P40
Q503	N334	M190	L47
	C343	H198	A51
T509		K199	K58
I515	T373	S200	N61
	L374	E201	V62
D519	L375	L210	L63
M522	L376	L212	L64
R523	K377	D213	M67
	K399	H218	Q68
K526	I402	M221	I69
SER	D403	T232	T73
SER	L411	E235	A74
LEU	G412	S236	S75
LVS	G412	L237	L76
GLY	E415	E238	I77
	V416	Y239	V80
	A417	T242	I87
	M418	E243	T92
	K426	V244	T93
	K430	E257	S94
	G431	L435	L97
	R432	Q438	I98
	L435	L444	I99
		L445	G100
		L445	E101
		L446	L102

L459	K287	T149	M1
Q460	G288	D150	A2
E461		R153	A3
T462	V291	T158	V4
I466	I292	K159	R5
D480	N293	V160	T6
L481	T297	H161	L7
M487	D298	A162	
V488	E308	E163	M23
E491	V311	L164	G29
Q503	R314	A165	L30
L504	V331	D166	Q31
		T169	D32
I515	N334	E170	V33
L516	D338	A171	L34
L517	L339	S175	R35
V518	C343	I179	L38
M522	K359	M190	G39
R523	R370	I191	P40
A524	S371		M44
S527	V372	D203	I54
SER	L374	L206	T57
LEU	K377	I207	N61
LYS	I387	H218	V62
GLY	V398	M221	L63
	D404	D227	L64
	G406	A228	H65
	C406	Y229	E86
	V414	I230	M67
	E415	L231	Q68
	M418	V235	I69
	L444	S236	T73
	L445	L237	V80
	I446	E238	A81
	K449	Y239	T82
	Q453	F240	I87
	N454	R241	T92
	S455	R264	N95
		L277	V96
		K278	L103
		R279	R117
			S140
			R145

[illegible]

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

GLY GLY GLU ASP GLN VAL ASP PRO ARG LEU ILE ASP GLY LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54850	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.0	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	0.776	Depositor
Minimum map value	-0.257	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.0915	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	1.058, 1.058, 1.058	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: MG, ADP, AF3

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	0.11	0/4109	0.28	0/5548
1	a	0.11	0/4081	0.29	0/5510
2	B	0.10	0/3995	0.25	0/5386
2	b	0.11	0/3986	0.26	0/5375
3	D	0.10	0/3955	0.27	0/5338
3	d	0.11	0/3949	0.29	0/5331
4	E	0.12	0/4183	0.30	0/5635
4	e	0.11	0/4220	0.30	0/5684
5	G	0.12	0/4136	0.30	0/5579
5	g	0.12	0/4134	0.28	0/5575
6	H	0.12	0/4111	0.29	0/5550
6	h	0.11	0/4089	0.27	0/5519
7	Q	0.11	0/4147	0.28	0/5606
7	q	0.11	0/4112	0.29	0/5558
8	Z	0.10	0/4069	0.27	0/5486
8	z	0.11	0/4080	0.26	0/5501
9	N	0.09	0/81	0.23	0/108
All	All	0.11	0/65437	0.28	0/88289

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](#)

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	4069	0	4224	91	0
1	a	4041	0	4205	96	0
2	B	3952	0	4070	68	0
2	b	3943	0	4057	84	0
3	D	3923	0	4131	74	0
3	d	3917	0	4120	82	0
4	E	4132	0	4246	97	0
4	e	4169	0	4272	85	0
5	G	4089	0	4224	90	0
5	g	4088	0	4230	88	0
6	H	4054	0	4160	60	0
6	h	4032	0	4140	96	0
7	Q	4086	0	4160	82	0
7	q	4053	0	4125	83	0
8	Z	4022	0	4161	82	0
8	z	4033	0	4171	84	0
9	N	80	0	74	0	0
10	A	27	0	12	4	0
10	B	27	0	12	2	0
10	D	27	0	12	3	0
10	E	27	0	12	3	0
10	G	27	0	12	3	0
10	H	27	0	12	0	0
10	Q	27	0	12	1	0
10	Z	27	0	12	2	0
10	a	27	0	12	2	0
10	b	27	0	12	2	0
10	d	27	0	12	0	0
10	e	27	0	12	0	0
10	g	27	0	12	3	0
10	h	27	0	12	3	0
10	q	27	0	12	2	0
10	z	27	0	12	1	0
11	A	1	0	0	0	0
11	B	1	0	0	0	0
11	D	1	0	0	0	0
11	E	1	0	0	0	0
11	G	1	0	0	0	0
11	H	1	0	0	0	0
11	Q	1	0	0	0	0
11	Z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	a	1	0	0	0	0
11	b	1	0	0	0	0
11	d	1	0	0	0	0
11	e	1	0	0	0	0
11	g	1	0	0	0	0
11	h	1	0	0	0	0
11	q	1	0	0	0	0
11	z	1	0	0	0	0
12	A	4	0	0	2	0
12	B	4	0	0	1	0
12	D	4	0	0	2	0
12	E	4	0	0	0	0
12	G	4	0	0	1	0
12	H	4	0	0	0	0
12	Q	4	0	0	1	0
12	Z	4	0	0	1	0
12	a	4	0	0	1	0
12	b	4	0	0	1	0
12	d	4	0	0	1	0
12	e	4	0	0	0	0
12	g	4	0	0	2	0
12	h	4	0	0	4	0
12	q	4	0	0	1	0
12	z	4	0	0	3	0
13	A	2	0	0	1	0
13	B	2	0	0	0	0
13	D	1	0	0	0	0
13	E	1	0	0	0	0
13	G	1	0	0	0	0
13	H	1	0	0	0	0
13	Q	1	0	0	0	0
13	Z	1	0	0	0	0
13	a	2	0	0	0	0
13	b	1	0	0	0	0
13	d	1	0	0	0	0
13	e	1	0	0	0	0
13	g	1	0	0	0	0
13	h	1	0	0	0	0
13	q	1	0	0	0	0
13	z	1	0	0	0	0
All	All	65214	0	66962	1214	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 9.

The worst 5 of 1214 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)
6:h:201:GLN:HA	6:h:382:MET:HE1	1.55	0.89
6:h:22:LEU:HD22	6:h:112:VAL:HG11	1.58	0.85
3:d:119:SER:HB3	3:d:453:ALA:HB1	1.59	0.85
2:b:4:LEU:HD22	2:b:11:ILE:HD11	1.62	0.81
3:D:91:LEU:HD12	3:D:110:VAL:HG13	1.61	0.80

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	534/556 (96%)	515 (96%)	19 (4%)	0	100	100
1	a	530/556 (95%)	512 (97%)	18 (3%)	0	100	100
2	B	524/535 (98%)	508 (97%)	16 (3%)	0	100	100
2	b	523/535 (98%)	510 (98%)	13 (2%)	0	100	100
3	D	518/539 (96%)	513 (99%)	5 (1%)	0	100	100
3	d	518/539 (96%)	498 (96%)	20 (4%)	0	100	100
4	E	534/541 (99%)	516 (97%)	18 (3%)	0	100	100
4	e	539/541 (100%)	531 (98%)	7 (1%)	1 (0%)	43	73
5	G	524/545 (96%)	511 (98%)	13 (2%)	0	100	100
5	g	524/545 (96%)	508 (97%)	16 (3%)	0	100	100
6	H	526/543 (97%)	502 (95%)	24 (5%)	0	100	100
6	h	523/543 (96%)	506 (97%)	17 (3%)	0	100	100
7	Q	536/548 (98%)	518 (97%)	18 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	q	531/548 (97%)	518 (98%)	13 (2%)	0	100	100
8	Z	523/531 (98%)	510 (98%)	13 (2%)	0	100	100
8	z	525/531 (99%)	511 (97%)	14 (3%)	0	100	100
9	N	8/441 (2%)	8 (100%)	0	0	100	100
All	All	8440/9117 (93%)	8195 (97%)	244 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	e	10	ASP

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	447/463 (96%)	447 (100%)	0	100	100
1	a	444/463 (96%)	444 (100%)	0	100	100
2	B	418/427 (98%)	418 (100%)	0	100	100
2	b	417/427 (98%)	417 (100%)	0	100	100
3	D	442/452 (98%)	441 (100%)	1 (0%)	87	89
3	d	441/452 (98%)	441 (100%)	0	100	100
4	E	452/456 (99%)	452 (100%)	0	100	100
4	e	456/456 (100%)	456 (100%)	0	100	100
5	G	456/469 (97%)	454 (100%)	2 (0%)	84	86
5	g	456/469 (97%)	455 (100%)	1 (0%)	87	89
6	H	435/443 (98%)	434 (100%)	1 (0%)	87	89
6	h	432/443 (98%)	432 (100%)	0	100	100
7	Q	442/452 (98%)	442 (100%)	0	100	100
7	q	438/452 (97%)	438 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	Z	437/442 (99%)	437 (100%)	0	100	100
8	z	438/442 (99%)	438 (100%)	0	100	100
9	N	9/367 (2%)	9 (100%)	0	100	100
All	All	7060/7575 (93%)	7055 (100%)	5 (0%)	87	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	397	VAL
5	G	201	VAL
5	G	219	MET
6	H	323	MET
5	g	13	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
7	q	79	GLN
7	q	303	HIS
8	z	380	ASN
7	Q	50	ASN
6	H	390	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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
12	AF3	E	603	10	0,3,3	-	-	-		
10	ADP	E	601	11,12	28,29,29	1.41	4 (14%)	43,45,45	1.80	9 (20%)
10	ADP	e	601	11,12	28,29,29	1.43	5 (17%)	43,45,45	1.81	9 (20%)
12	AF3	g	603	10,5	0,3,3	-	-	-		
12	AF3	z	603	-	0,3,3	-	-	-		
12	AF3	Z	603	10	0,3,3	-	-	-		
10	ADP	Z	601	11,12	28,29,29	1.41	4 (14%)	43,45,45	1.84	8 (18%)
12	AF3	a	603	10	0,3,3	-	-	-		
10	ADP	d	601	11,12	28,29,29	1.42	4 (14%)	43,45,45	1.81	9 (20%)
10	ADP	b	601	11,12	28,29,29	1.42	5 (17%)	43,45,45	1.82	10 (23%)
10	ADP	A	601	11,12	28,29,29	1.41	4 (14%)	43,45,45	1.83	10 (23%)
12	AF3	G	603	10,5	0,3,3	-	-	-		
12	AF3	h	603	10	0,3,3	-	-	-		
10	ADP	g	601	11,12	28,29,29	1.42	4 (14%)	43,45,45	1.83	9 (20%)
10	ADP	z	601	11	28,29,29	1.42	4 (14%)	43,45,45	1.83	8 (18%)
12	AF3	d	603	10	0,3,3	-	-	-		
12	AF3	q	603	10	0,3,3	-	-	-		
10	ADP	q	601	11,12	28,29,29	1.40	4 (14%)	43,45,45	1.83	10 (23%)
12	AF3	Q	603	7,10	0,3,3	-	-	-		
12	AF3	D	603	10	0,3,3	-	-	-		
12	AF3	B	603	10	0,3,3	-	-	-		
10	ADP	D	601	11,12	28,29,29	1.41	4 (14%)	43,45,45	1.78	10 (23%)
10	ADP	a	601	11,12	28,29,29	1.42	4 (14%)	43,45,45	1.83	10 (23%)
12	AF3	e	603	10	0,3,3	-	-	-		
12	AF3	A	603	10	0,3,3	-	-	-		
10	ADP	Q	601	11,12	28,29,29	1.42	4 (14%)	43,45,45	1.83	9 (20%)
10	ADP	H	601	11,12	28,29,29	1.40	4 (14%)	43,45,45	1.83	9 (20%)
10	ADP	B	601	11,12	28,29,29	1.40	5 (17%)	43,45,45	1.80	10 (23%)
12	AF3	b	603	10	0,3,3	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	AF3	H	603	10	0,3,3	-	-	-		
10	ADP	G	601	11,12	28,29,29	1.41	4 (14%)	43,45,45	1.81	9 (20%)
10	ADP	h	601	11,12	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)

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
10	ADP	b	601	11,12	-	1/16/32/32	0/3/3/3
10	ADP	E	601	11,12	-	2/16/32/32	0/3/3/3
10	ADP	Q	601	11,12	-	6/16/32/32	0/3/3/3
10	ADP	A	601	11,12	-	4/16/32/32	0/3/3/3
10	ADP	g	601	11,12	-	5/16/32/32	0/3/3/3
10	ADP	e	601	11,12	-	1/16/32/32	0/3/3/3
10	ADP	h	601	11,12	-	1/16/32/32	0/3/3/3
10	ADP	z	601	11	-	3/16/32/32	0/3/3/3
10	ADP	q	601	11,12	-	6/16/32/32	0/3/3/3
10	ADP	H	601	11,12	-	3/16/32/32	0/3/3/3
10	ADP	B	601	11,12	-	3/16/32/32	0/3/3/3
10	ADP	Z	601	11,12	-	5/16/32/32	0/3/3/3
10	ADP	G	601	11,12	-	4/16/32/32	0/3/3/3
10	ADP	D	601	11,12	-	8/16/32/32	0/3/3/3
10	ADP	a	601	11,12	-	5/16/32/32	0/3/3/3
10	ADP	d	601	11,12	-	0/16/32/32	0/3/3/3

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	Q	601	ADP	C5-C4	4.74	1.47	1.39
10	Z	601	ADP	C5-C4	4.74	1.47	1.39
10	z	601	ADP	C5-C4	4.70	1.47	1.39
10	A	601	ADP	C5-C4	4.69	1.47	1.39
10	e	601	ADP	C5-C4	4.68	1.47	1.39

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	z	601	ADP	C5-C4-N3	-5.97	118.49	126.72
10	Z	601	ADP	C5-C4-N3	-5.90	118.59	126.72
10	Q	601	ADP	C5-C4-N3	-5.84	118.68	126.72
10	d	601	ADP	C5-C4-N3	-5.83	118.69	126.72
10	H	601	ADP	C5-C4-N3	-5.83	118.69	126.72

There are no chirality outliers.

5 of 57 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	601	ADP	C5'-O5'-PA-O2A
10	A	601	ADP	C5'-O5'-PA-O3A
10	B	601	ADP	C5'-O5'-PA-O1A
10	D	601	ADP	C5'-O5'-PA-O1A
10	D	601	ADP	C5'-O5'-PA-O3A

There are no ring outliers.

26 monomers are involved in 40 short contacts:

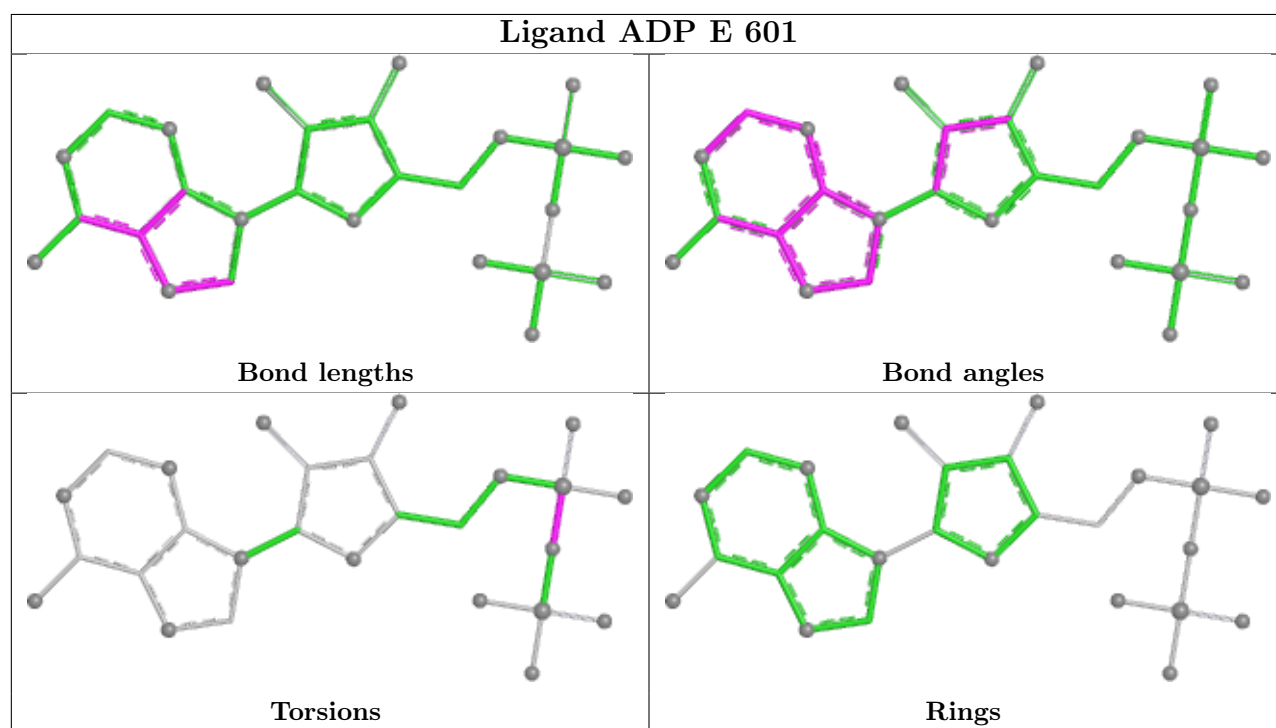
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	E	601	ADP	3	0
12	g	603	AF3	2	0
12	z	603	AF3	3	0
12	Z	603	AF3	1	0
10	Z	601	ADP	2	0
12	a	603	AF3	1	0
10	b	601	ADP	2	0
10	A	601	ADP	4	0
12	G	603	AF3	1	0
12	h	603	AF3	4	0
10	g	601	ADP	3	0
10	z	601	ADP	1	0
12	d	603	AF3	1	0
12	q	603	AF3	1	0
10	q	601	ADP	2	0
12	Q	603	AF3	1	0
12	D	603	AF3	2	0
12	B	603	AF3	1	0
10	D	601	ADP	3	0
10	a	601	ADP	2	0
12	A	603	AF3	2	0
10	Q	601	ADP	1	0

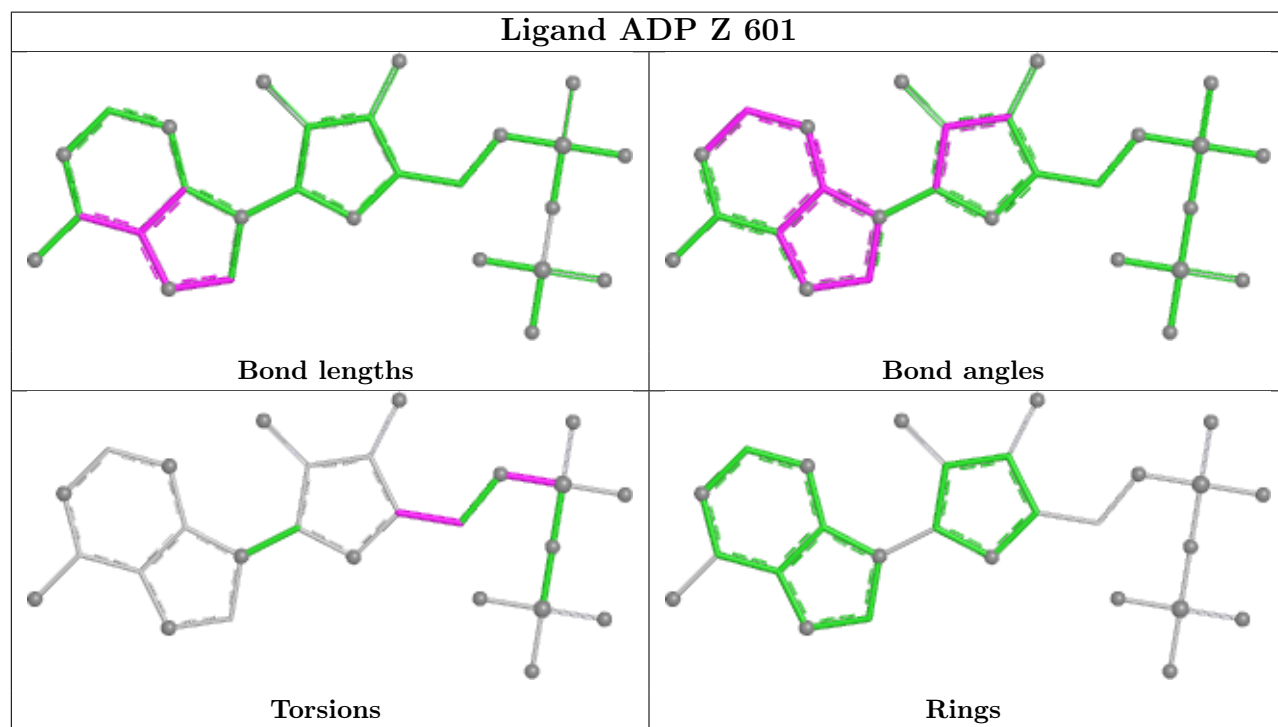
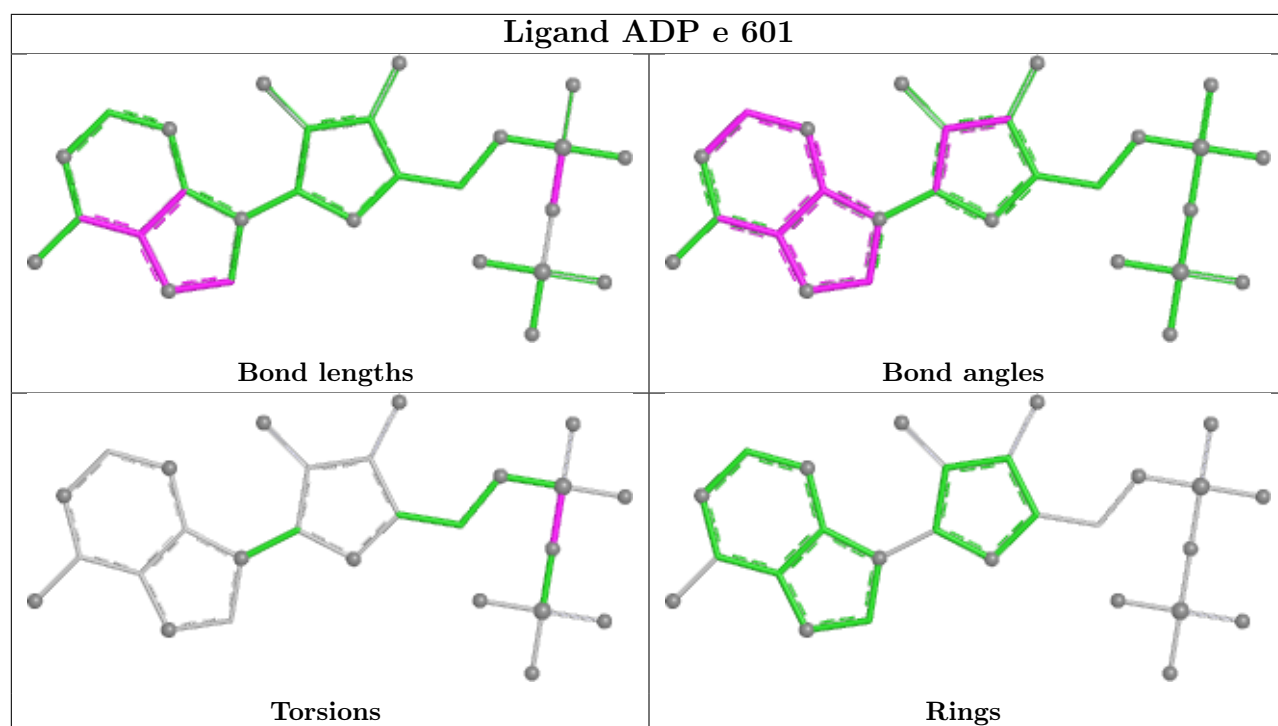
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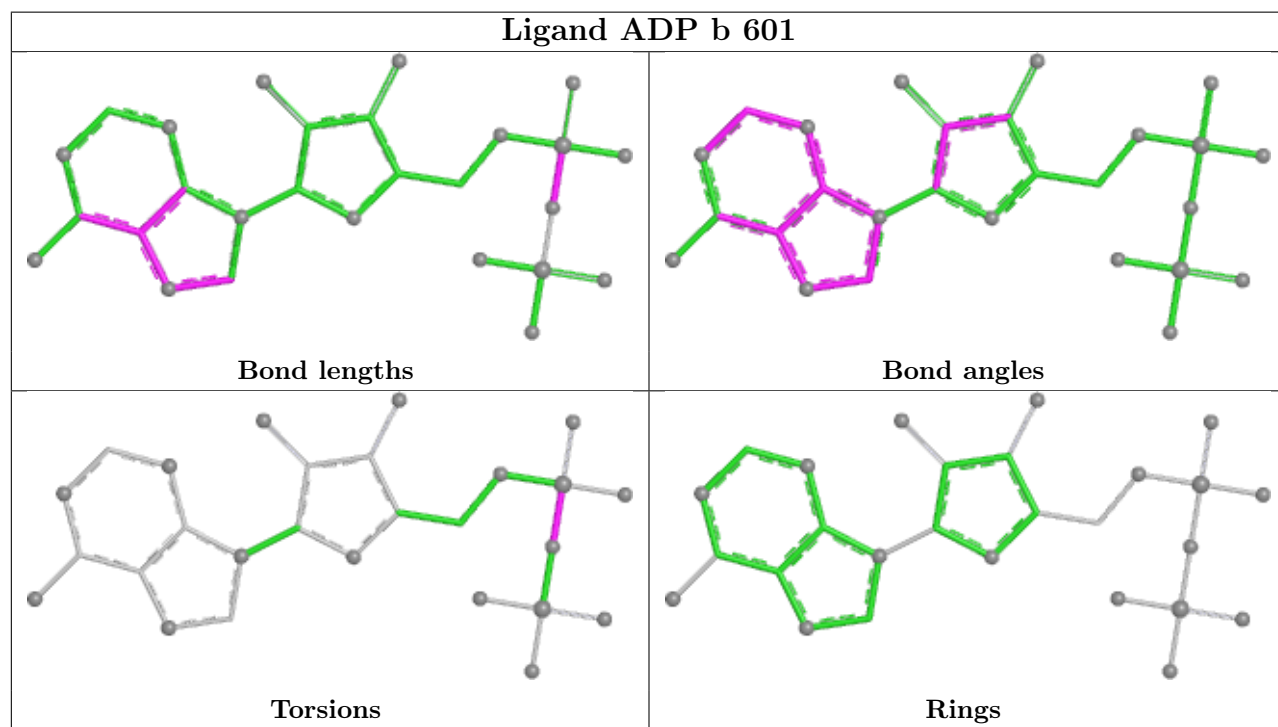
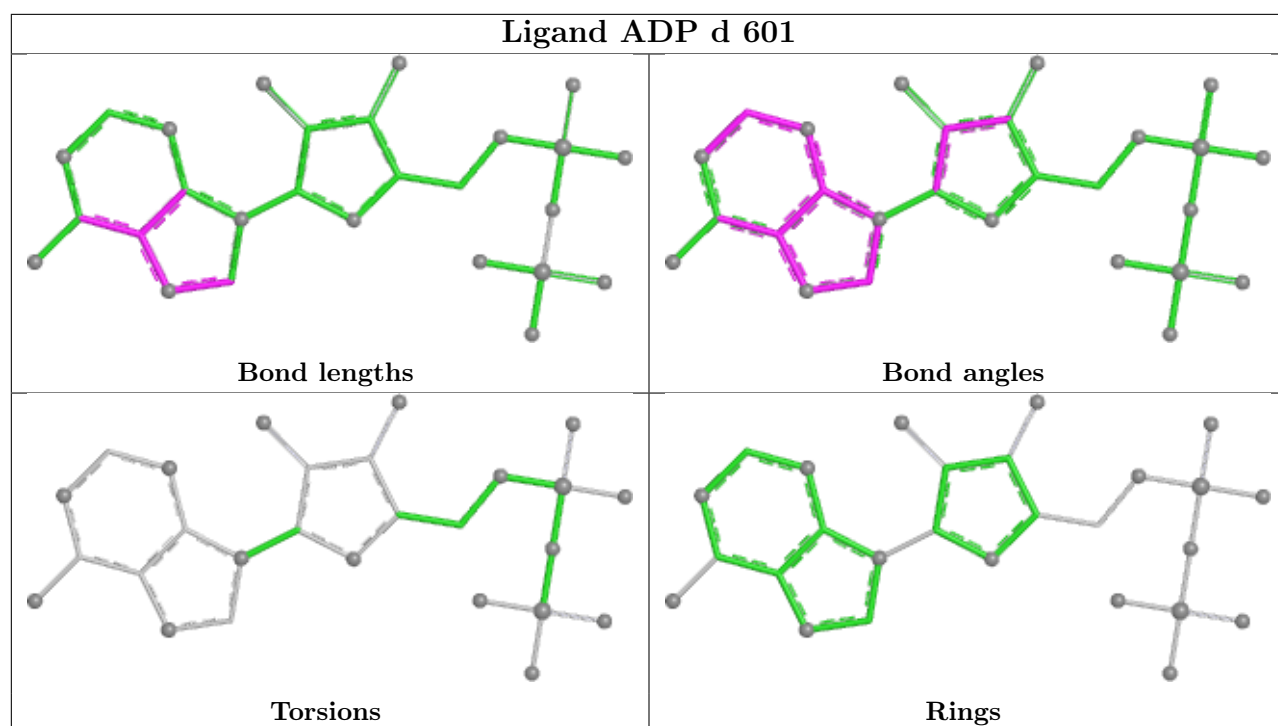
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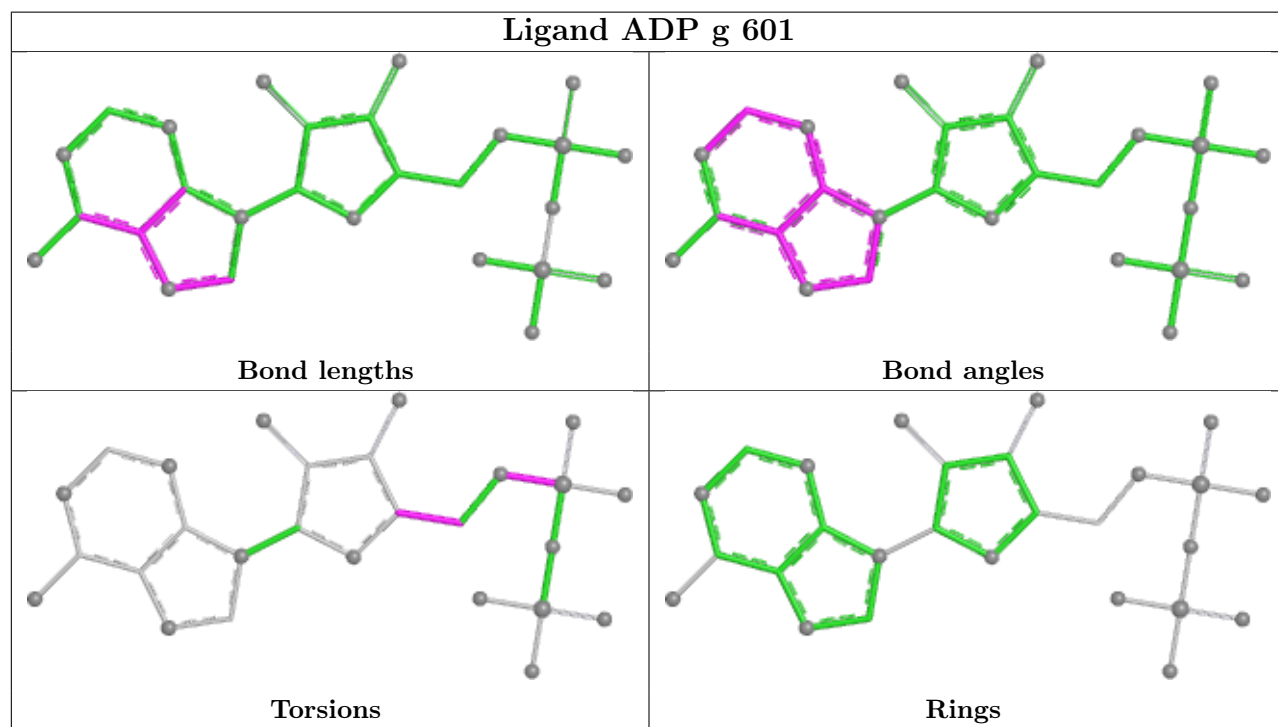
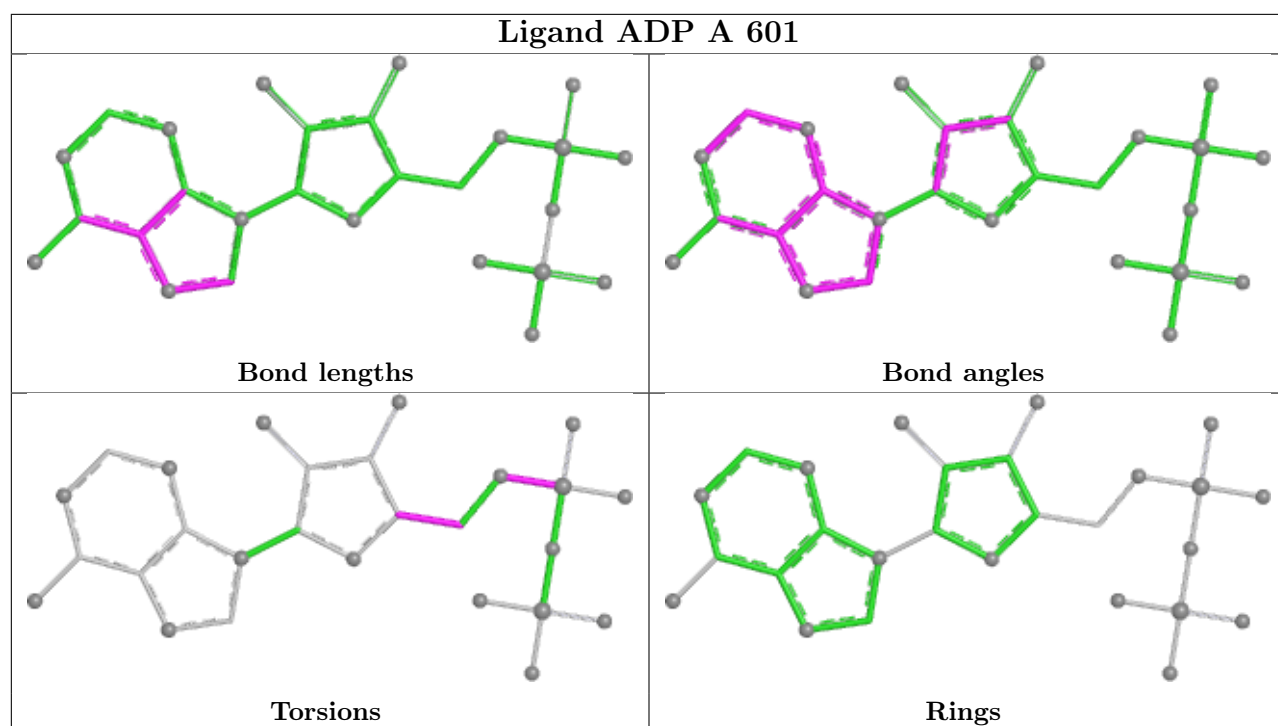
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	601	ADP	2	0
12	b	603	AF3	1	0
10	G	601	ADP	3	0
10	h	601	ADP	3	0

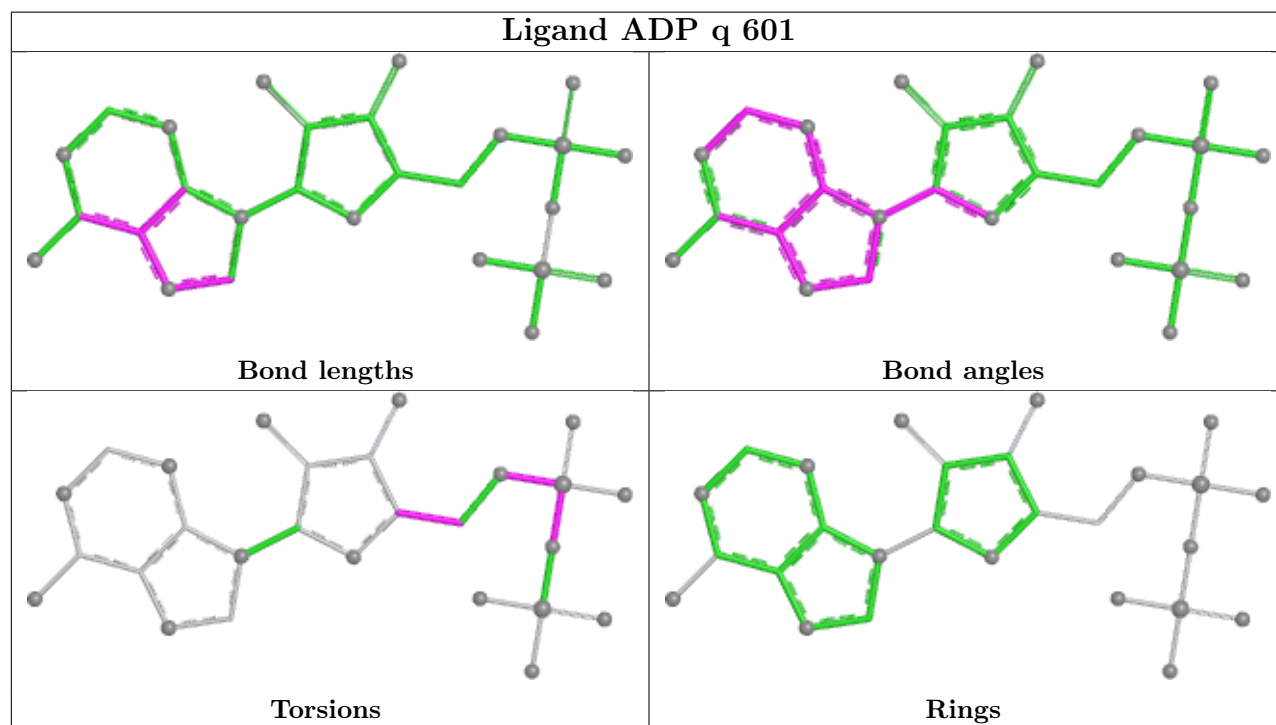
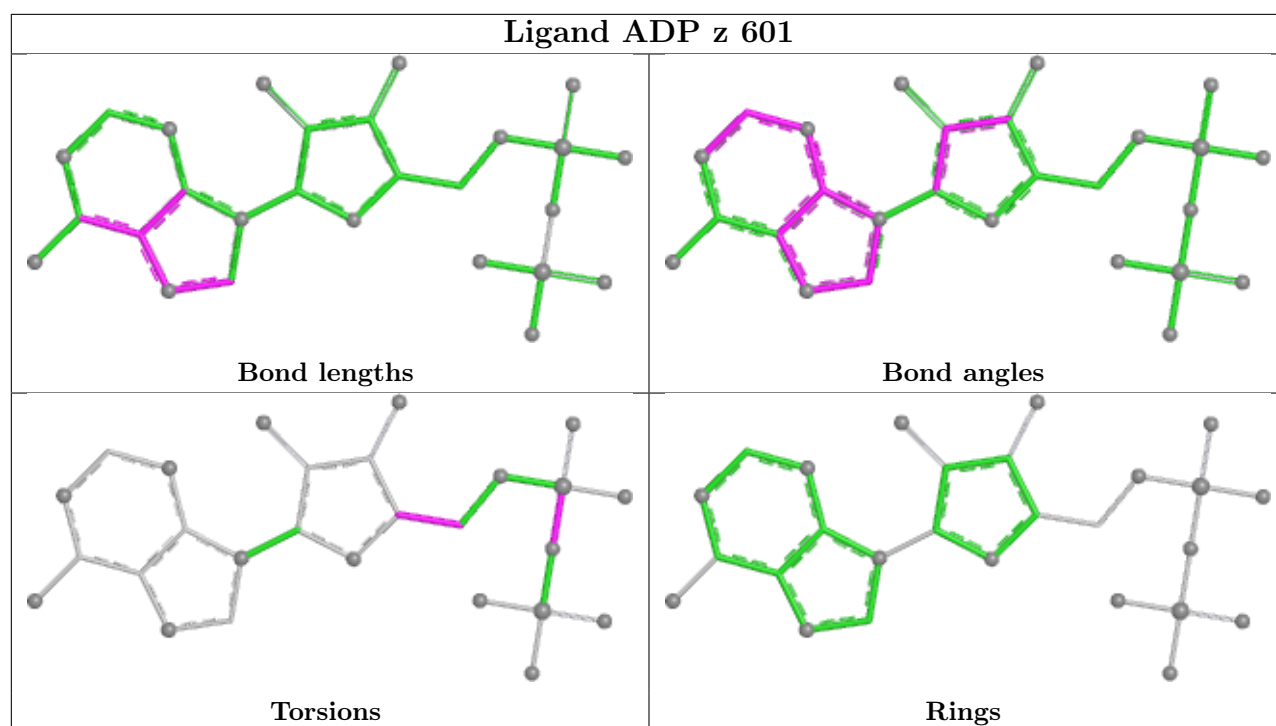
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

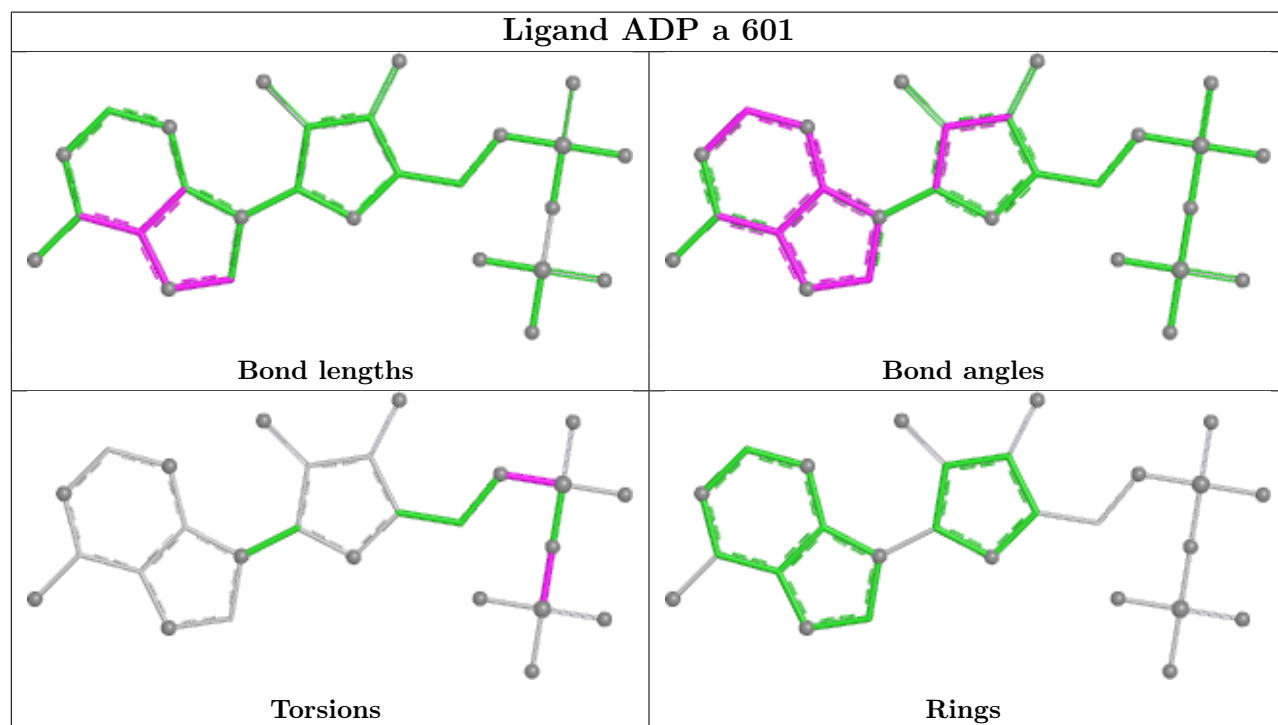
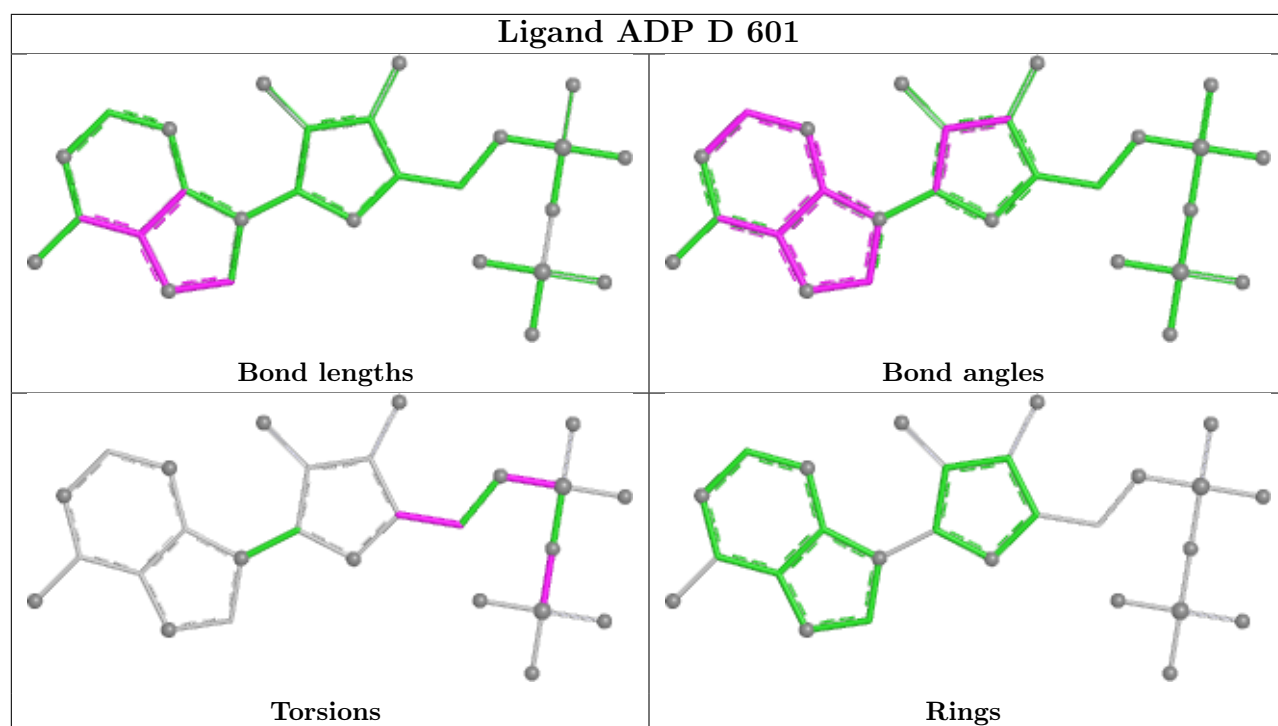


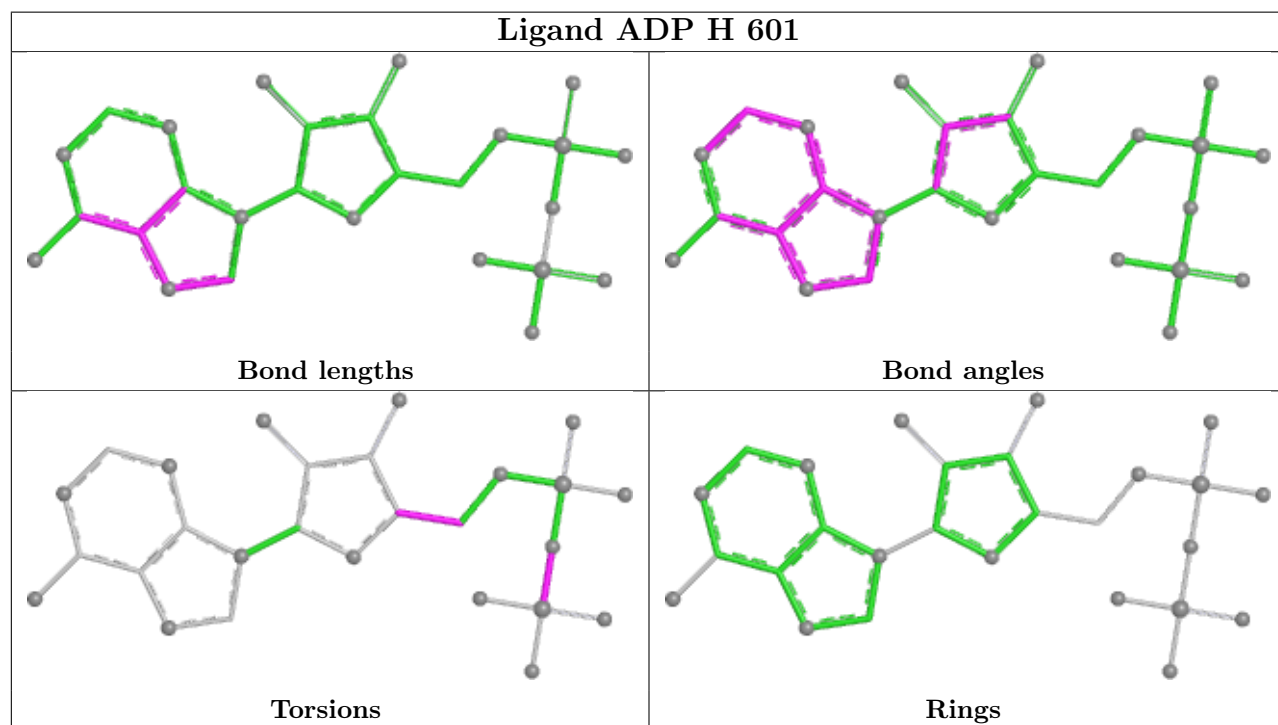
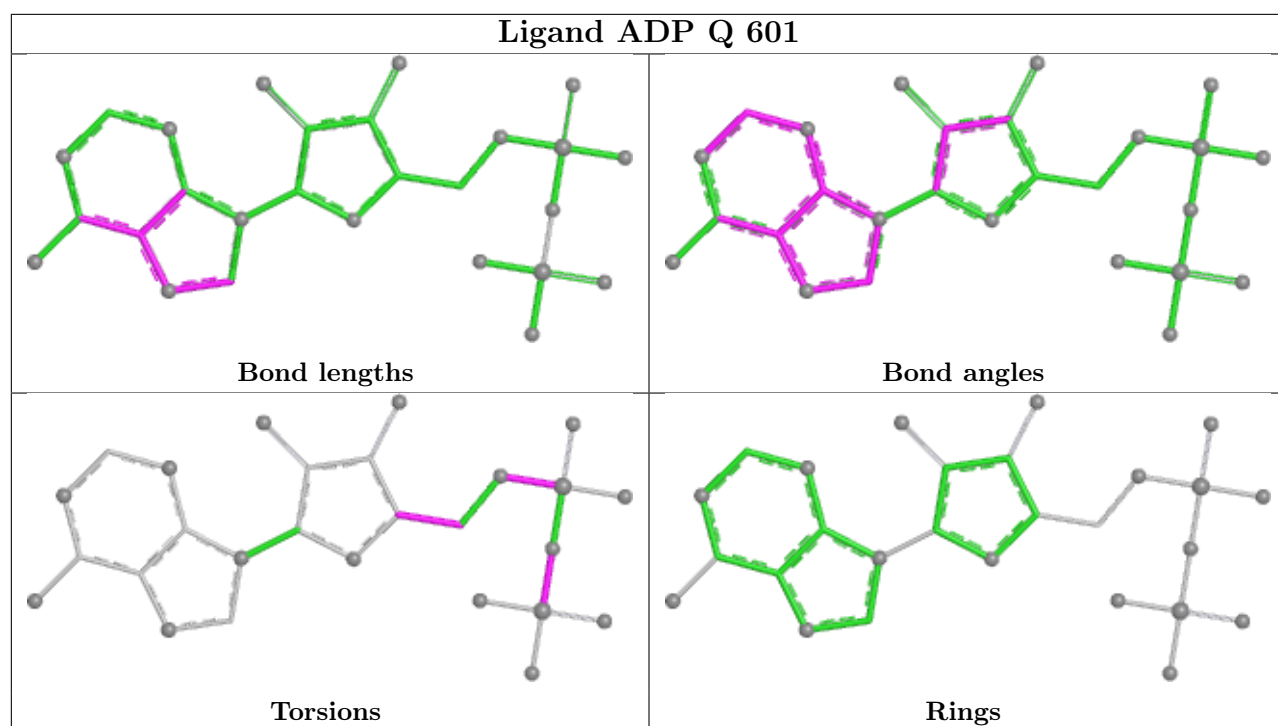


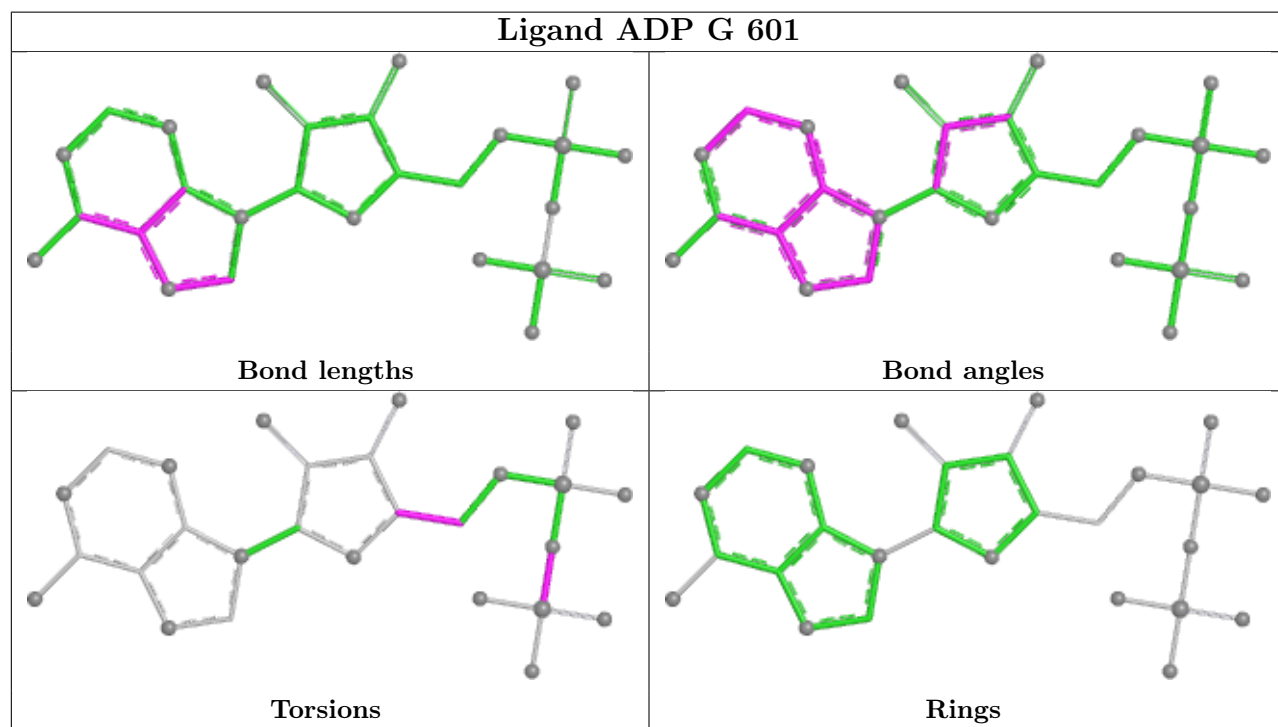
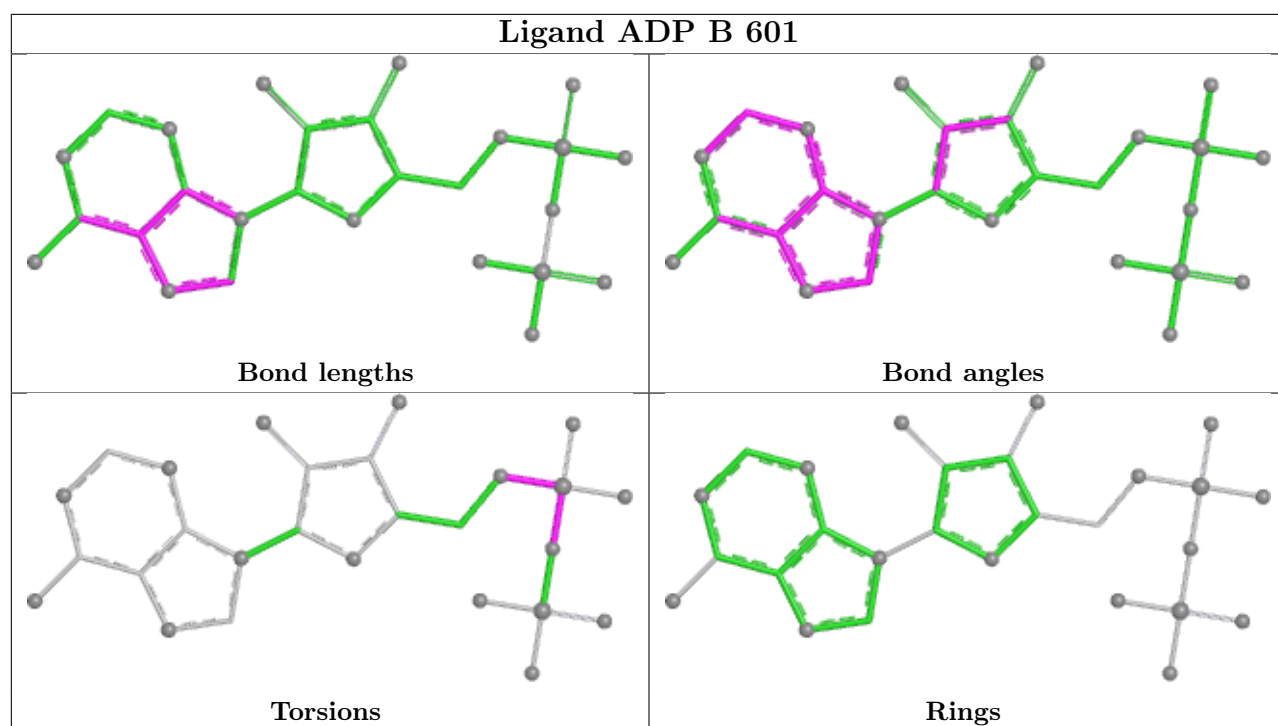


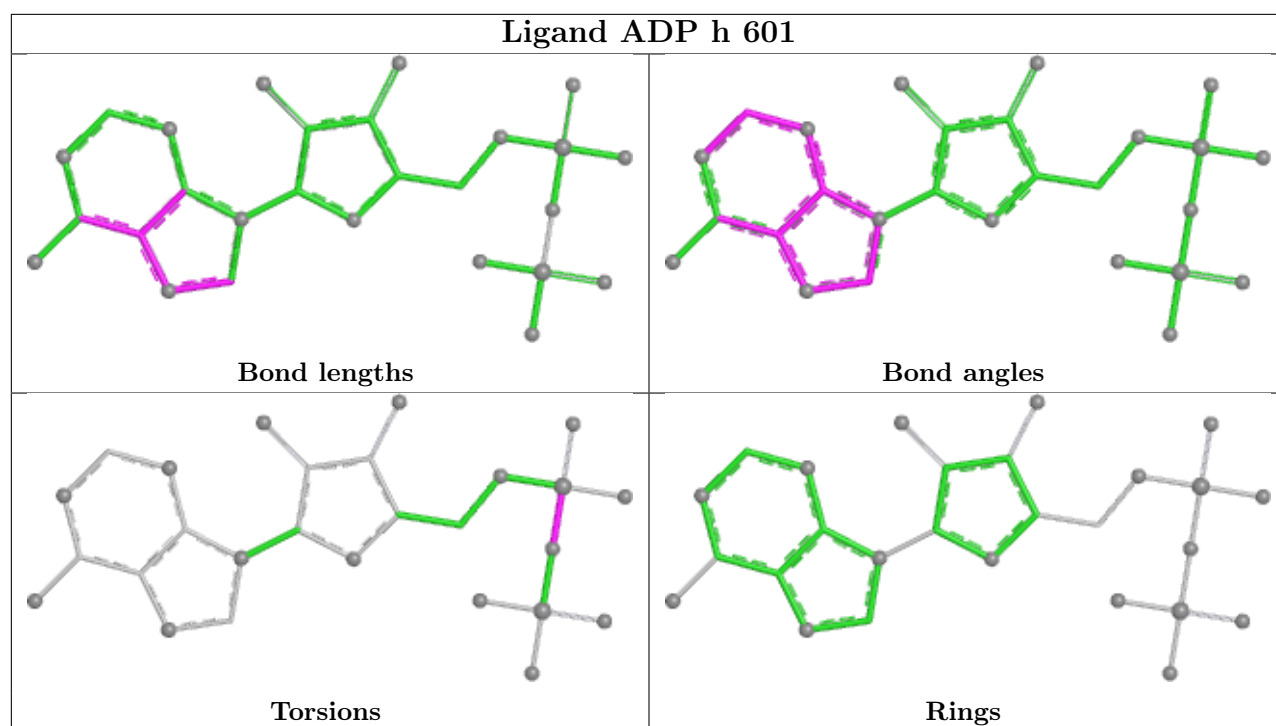












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

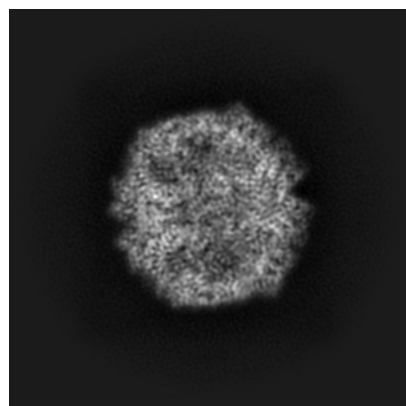
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49709. These allow visual inspection of the internal detail of the map and identification of artifacts.

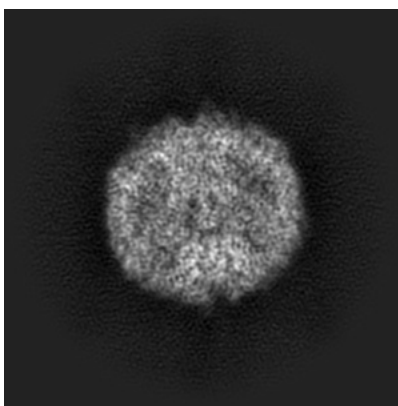
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

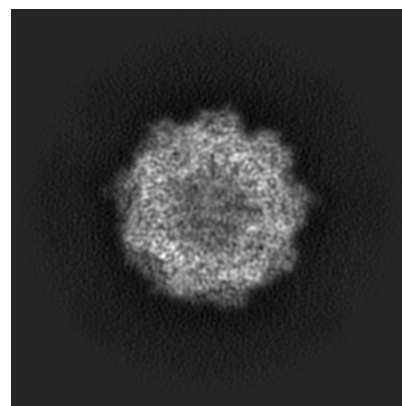
6.1.1 Primary map



X

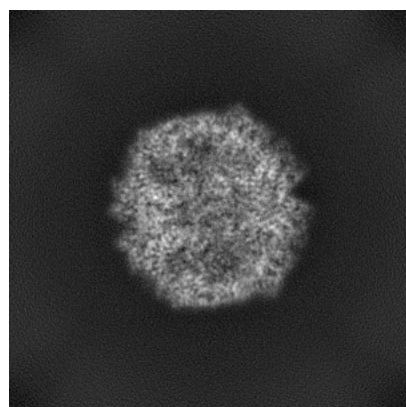


Y

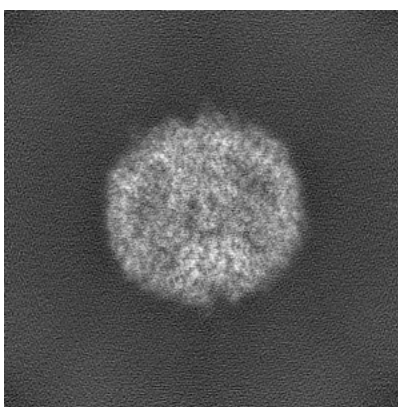


Z

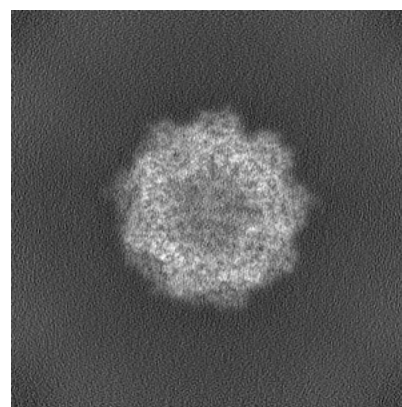
6.1.2 Raw map



X



Y

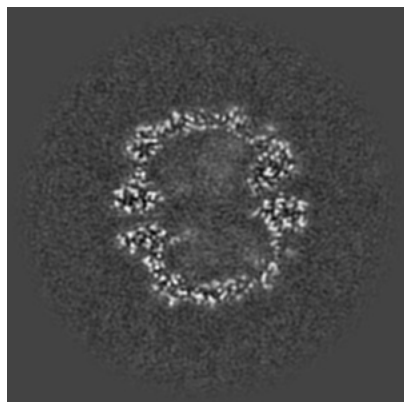


Z

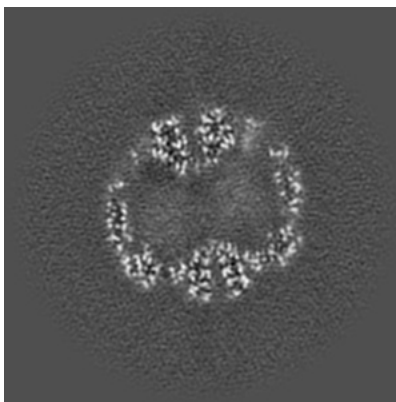
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

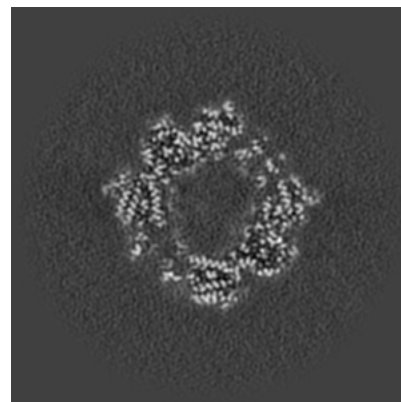
6.2.1 Primary map



X Index: 150

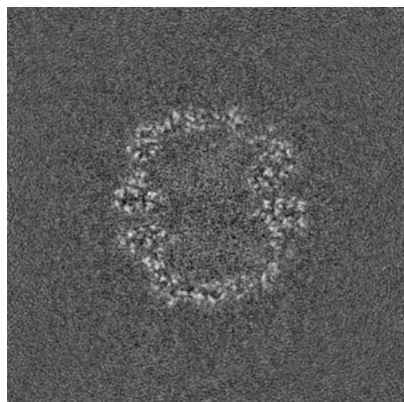


Y Index: 150

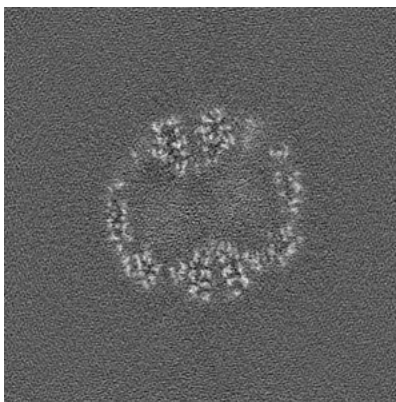


Z Index: 150

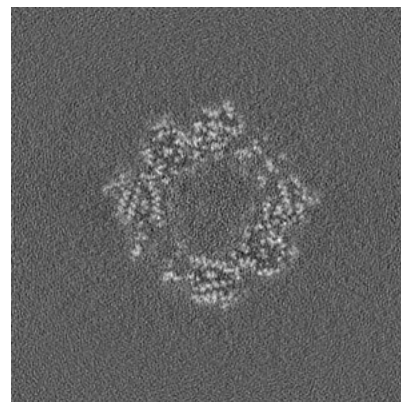
6.2.2 Raw map



X Index: 150



Y Index: 150

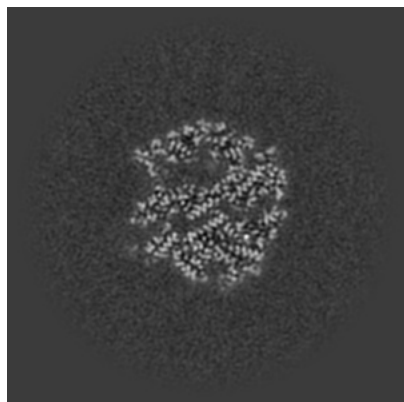


Z Index: 150

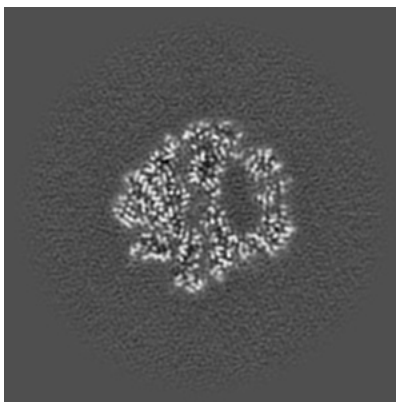
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

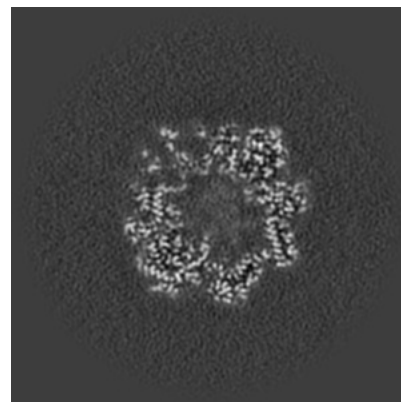
6.3.1 Primary map



X Index: 191

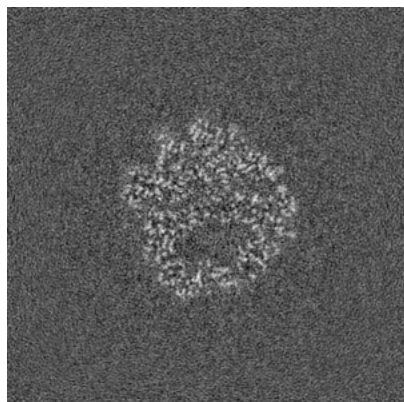


Y Index: 113

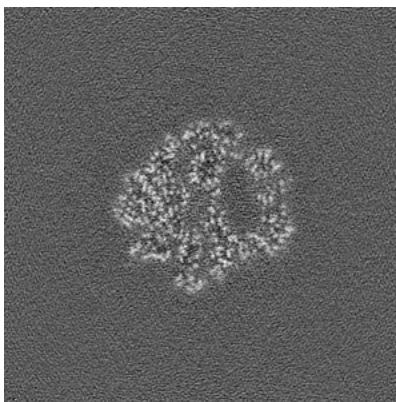


Z Index: 164

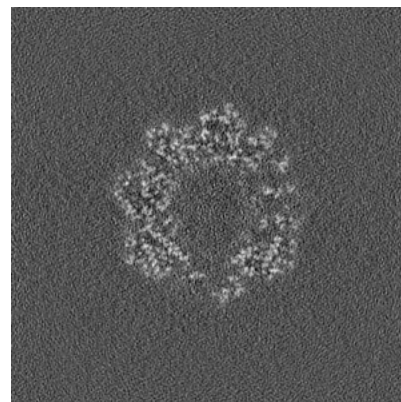
6.3.2 Raw map



X Index: 114



Y Index: 113

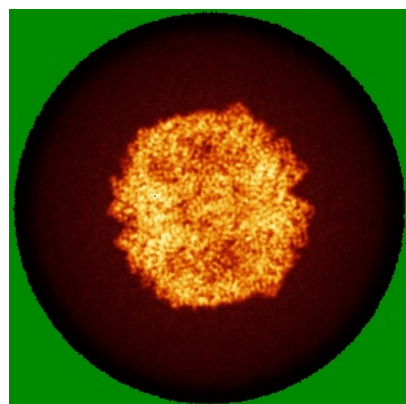


Z Index: 143

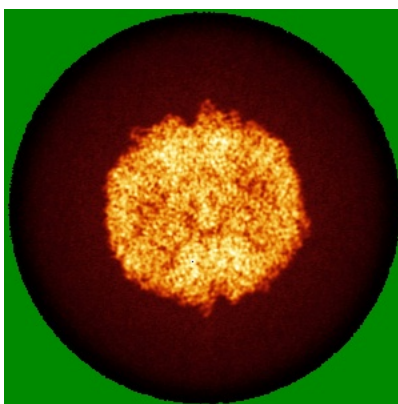
The images above show the largest variance slices of the map in three orthogonal directions.

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

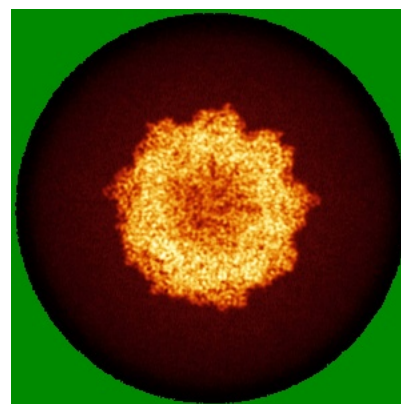
6.4.1 Primary map



X

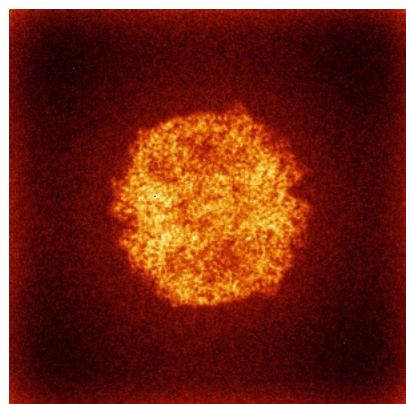


Y

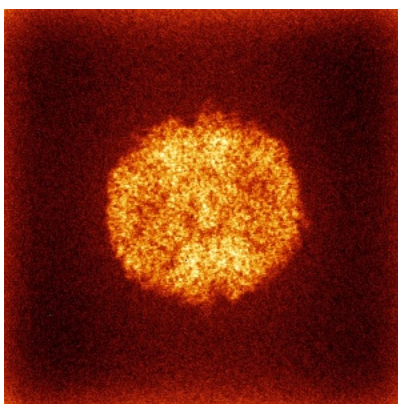


Z

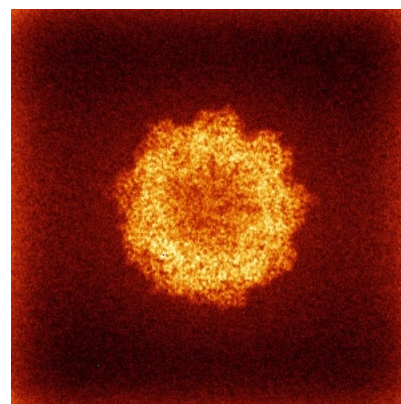
6.4.2 Raw map



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



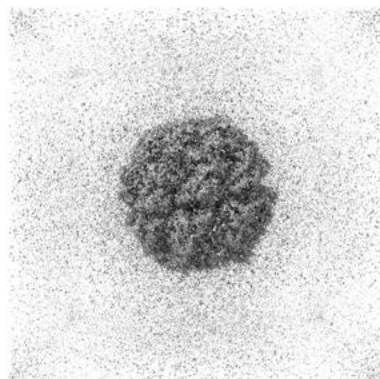
Y



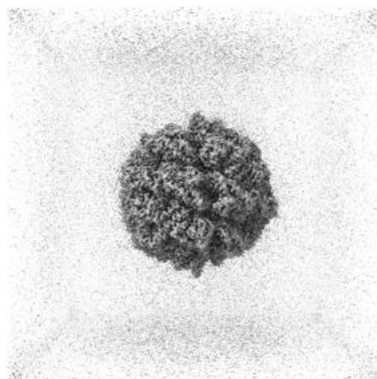
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0915. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

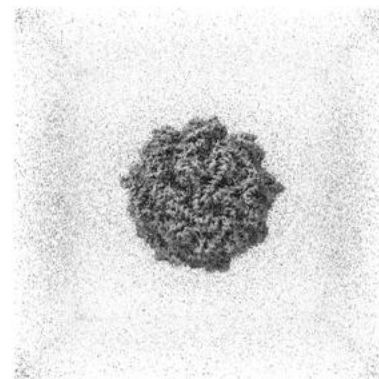
6.5.2 Raw map



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.

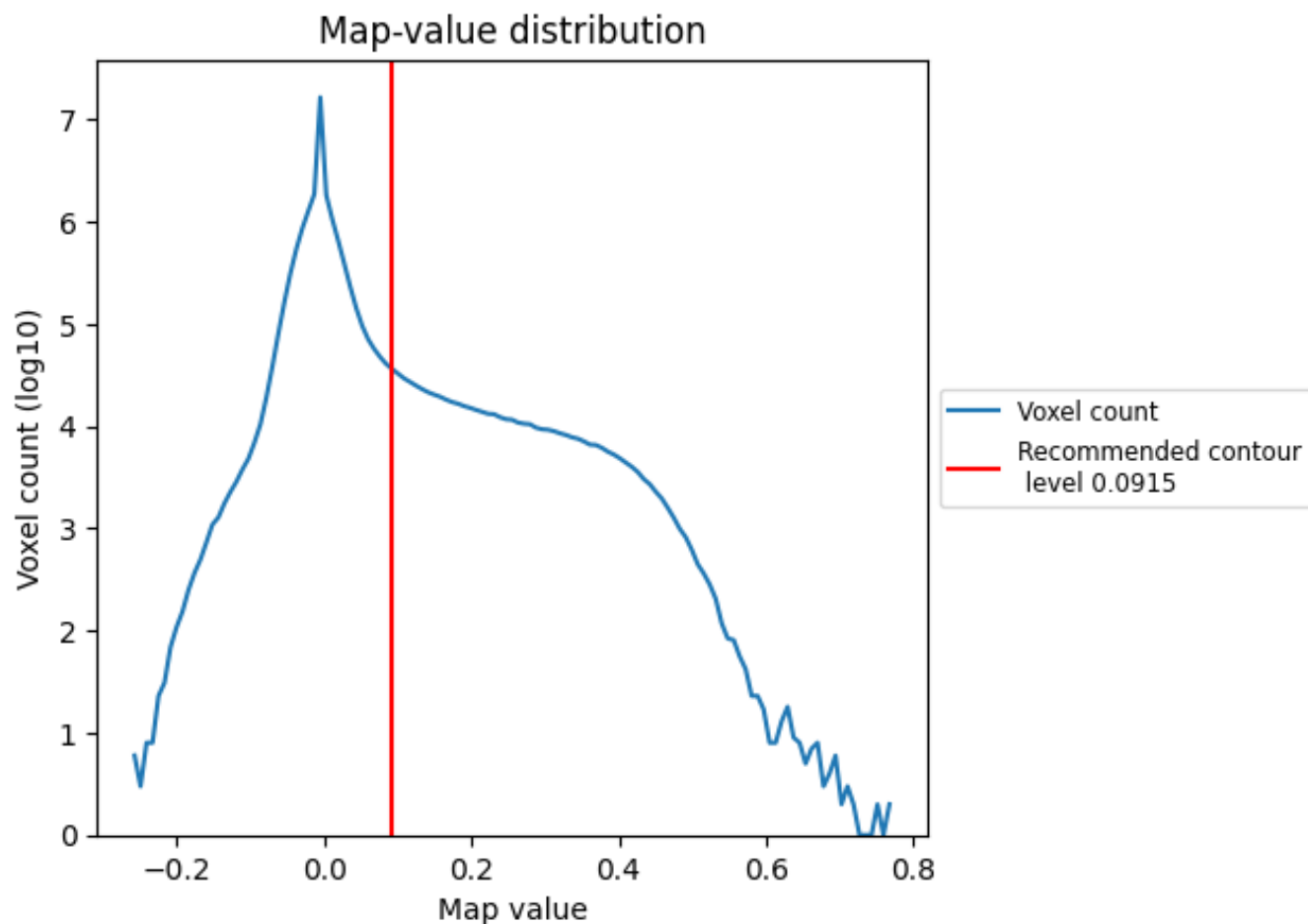
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

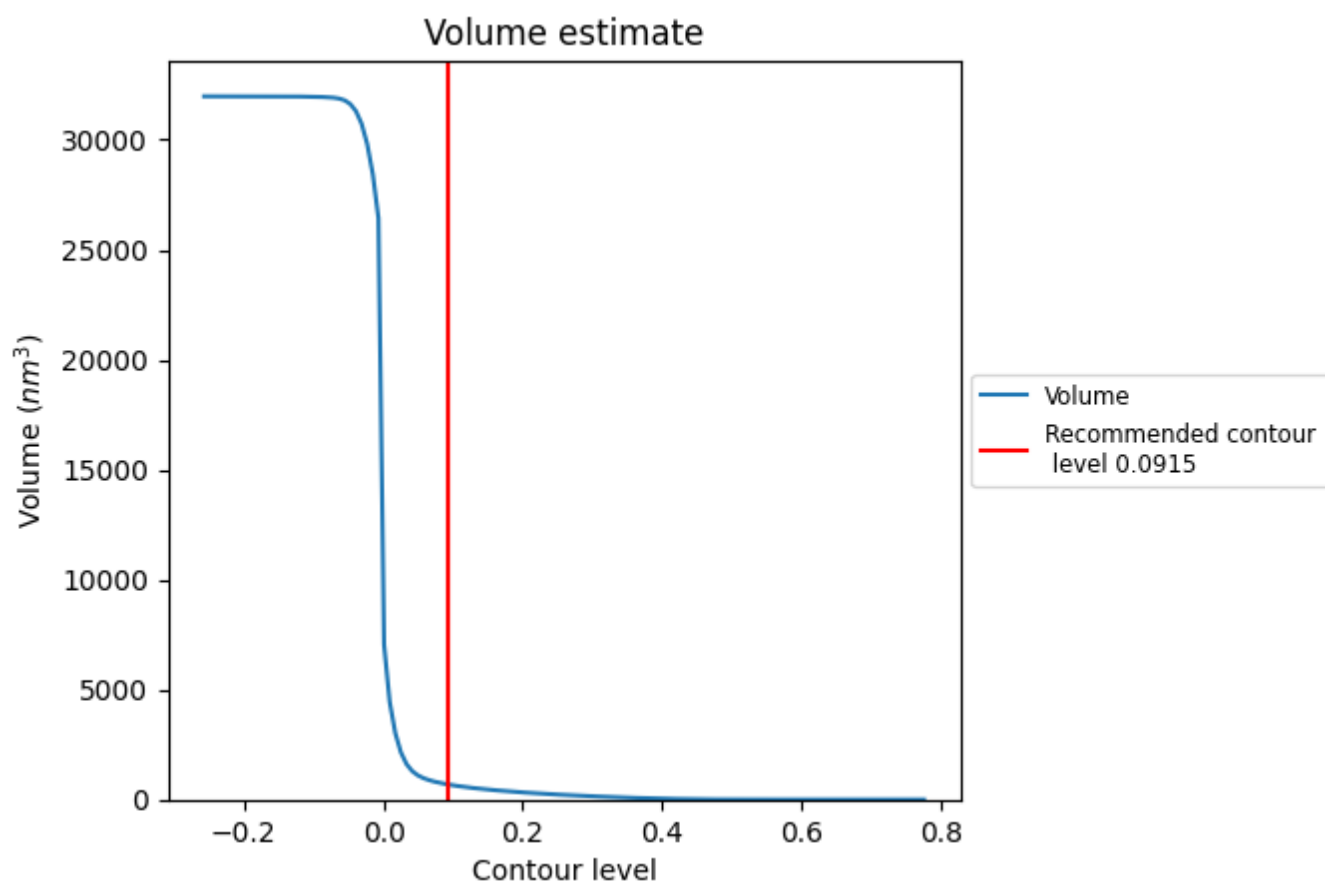
This section contains the results of statistical analysis of the map.

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.

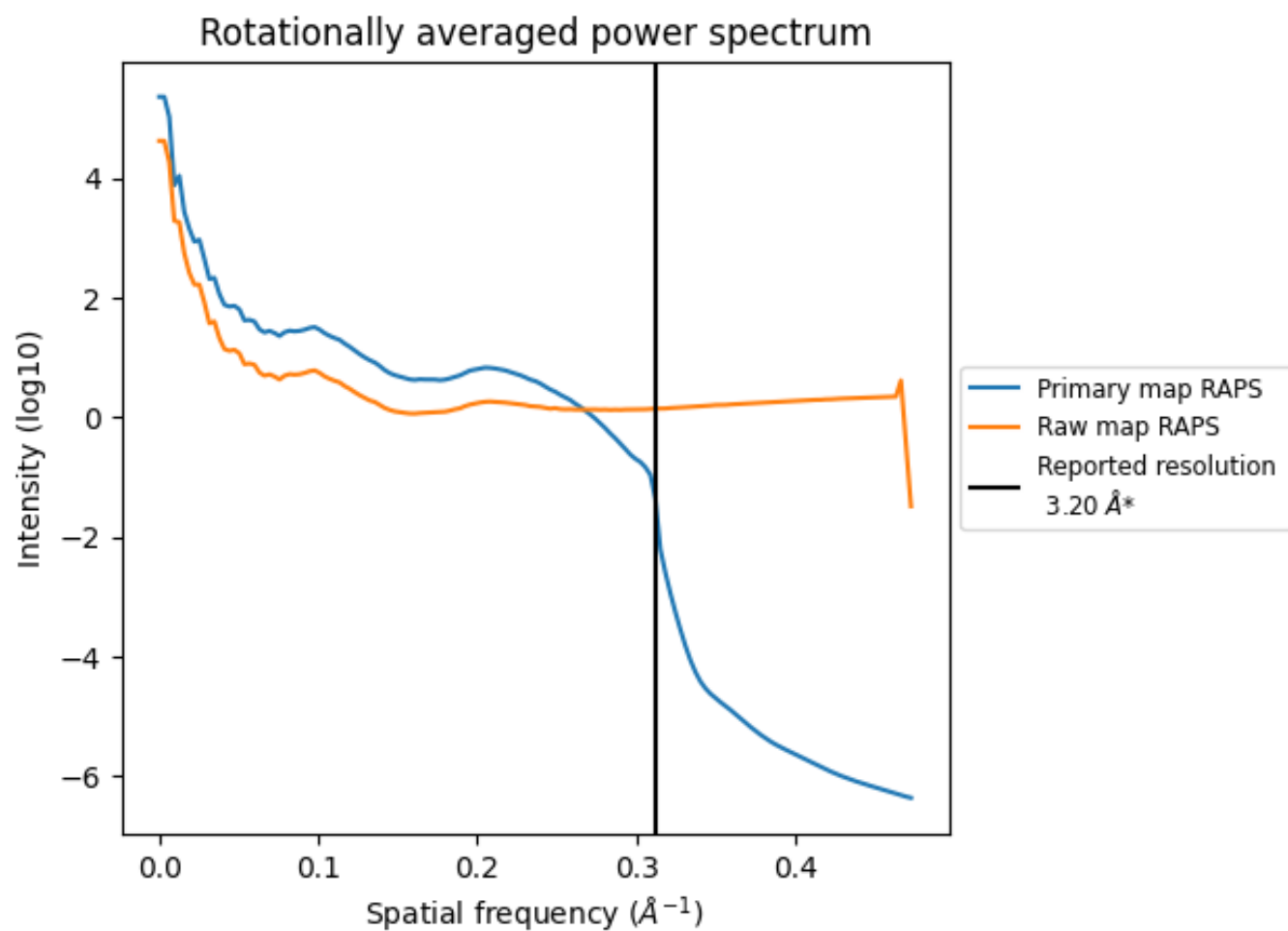
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 694 nm³; this corresponds to an approximate mass of 627 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 ⓘ

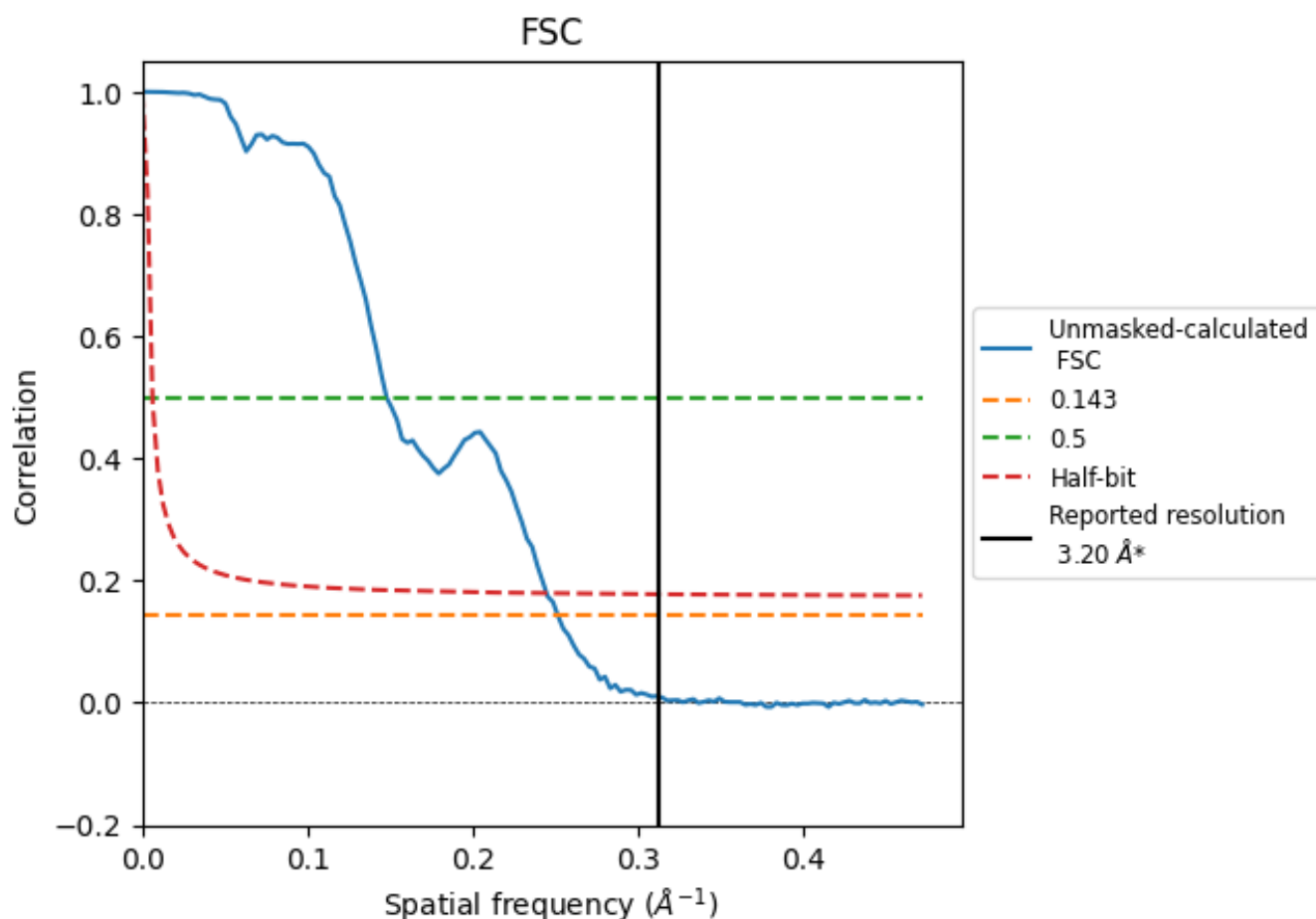


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

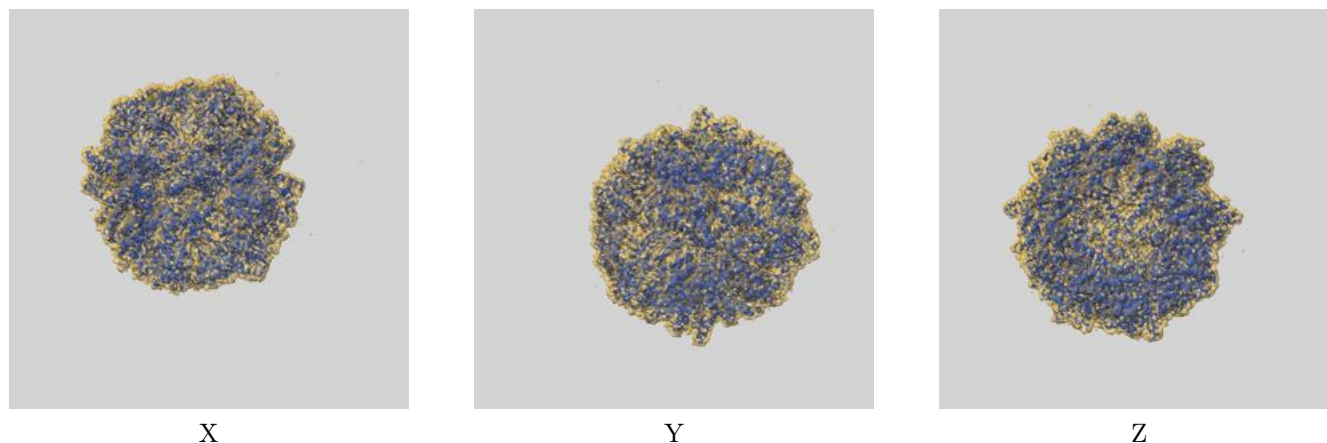
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.97	6.76	4.08

*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 3.97 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

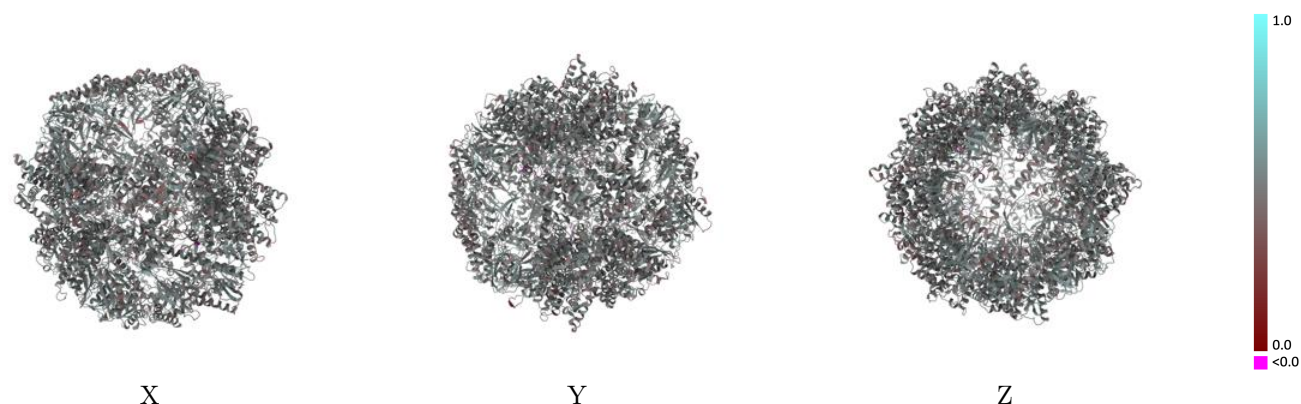
This section contains information regarding the fit between EMDB map EMD-49709 and PDB model 9NR1. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



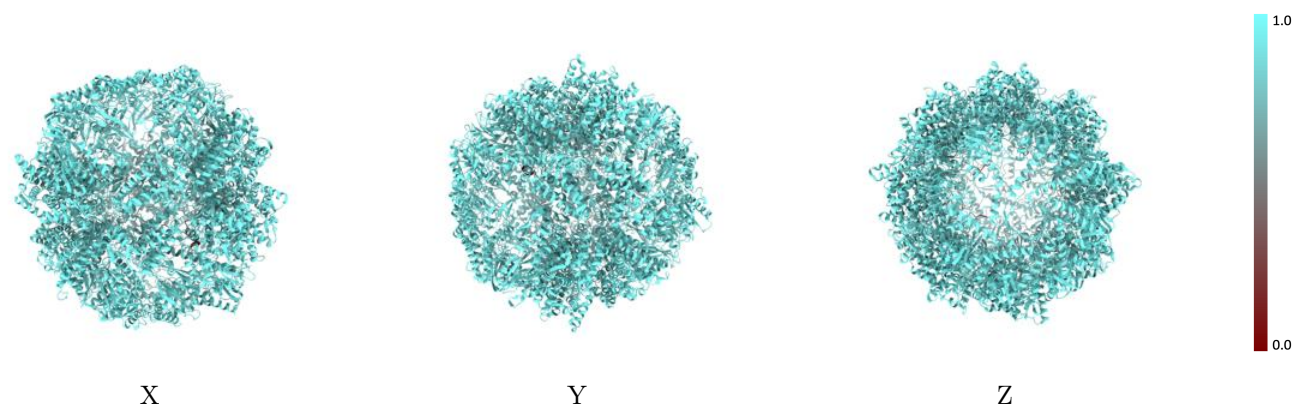
The images above show the 3D surface view of the map at the recommended contour level 0.0915 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



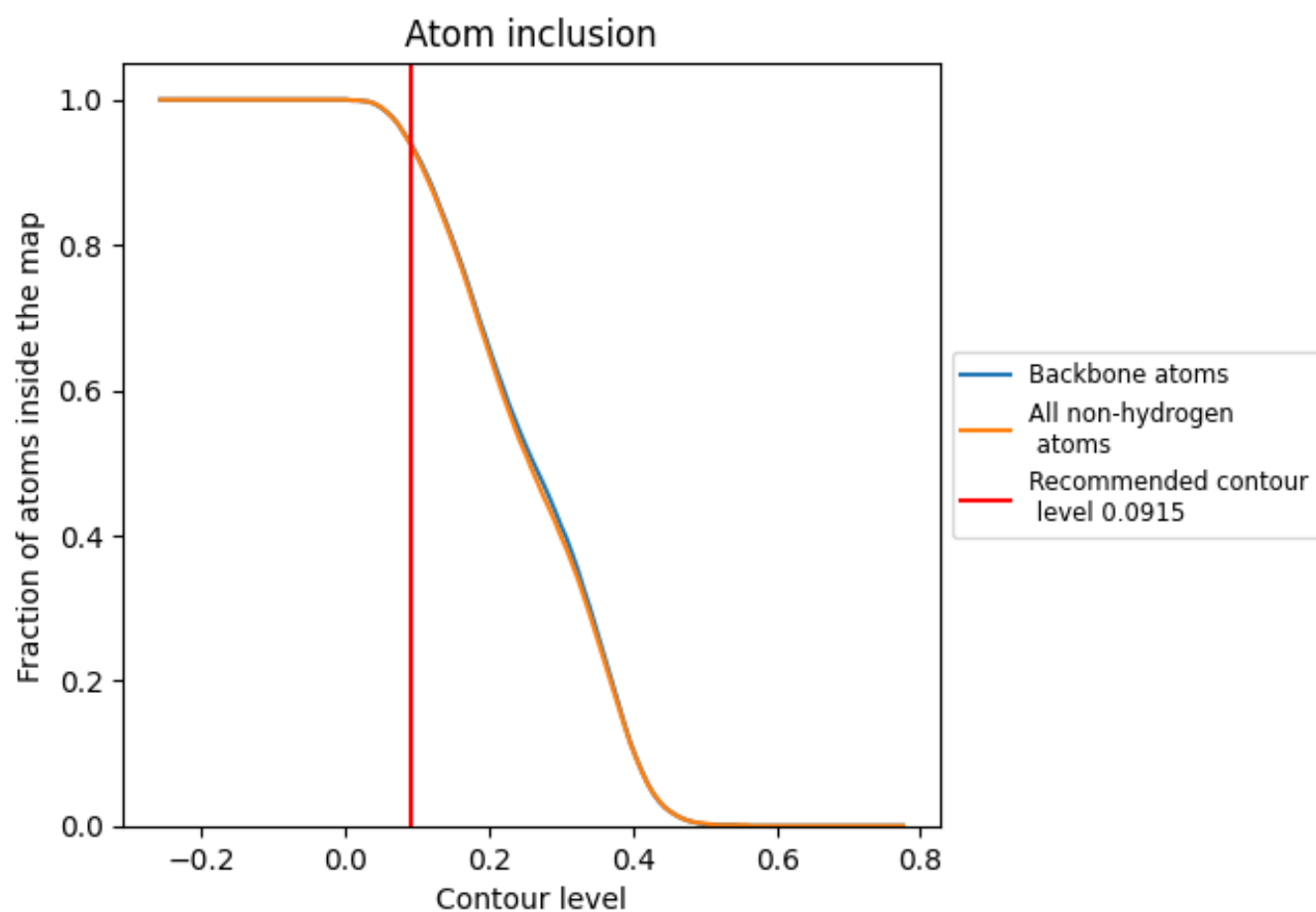
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0915).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.0915) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9370	 0.4880
A	 0.9280	 0.4800
B	 0.9460	 0.4940
D	 0.9410	 0.4900
E	 0.9470	 0.4920
G	 0.9330	 0.4870
H	 0.9420	 0.4920
N	 0.7010	 0.4910
Q	 0.9320	 0.4840
Z	 0.9370	 0.4880
a	 0.9350	 0.4840
b	 0.9430	 0.4930
d	 0.9490	 0.4880
e	 0.9410	 0.4890
g	 0.9340	 0.4870
h	 0.9430	 0.4870
q	 0.9390	 0.4830
z	 0.9320	 0.4840

