



wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 05:32 PM EDT

PDB ID : 9DMT / pdb_00009dmt
EMDB ID : EMD-47015
Title : Human muscle nAChR with fab7-bound
Authors : Li, H.; Hibbs, R.E.
Deposited on : 2024-09-14
Resolution : 2.18 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.dev117
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

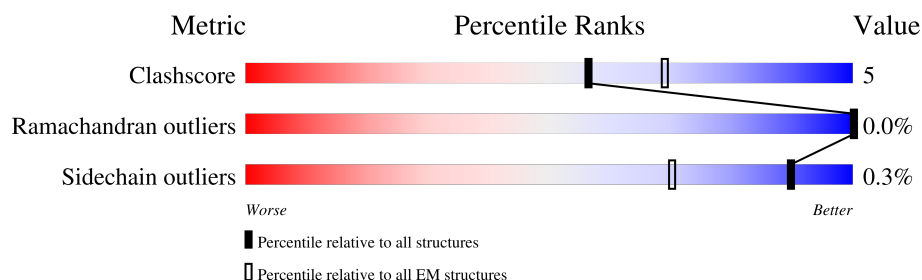
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.18 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.




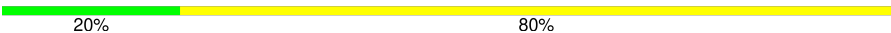


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	457	
1	C	457	
2	E	503	
3	D	517	
4	B	493	
5	F	295	
6	G	232	
7	H	5	

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Mol	Chain	Length	Quality of chain
7	I	5	 20%80%
7	J	5	 20%80%
7	L	5	 20%80%
8	K	6	 17%17%83%

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
9	POV	B	504	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 41045 atoms, of which 20581 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 Acetylcholine receptor subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	399	Total	C	H	N	O	S	0	0
			6433	2093	3231	513	577	19		
1	C	401	Total	C	H	N	O	S	0	0
			6486	2109	3263	516	579	19		

- Molecule 2 is a protein called Acetylcholine receptor subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	E	405	Total	C	H	N	O	S	0	0
			6575	2139	3294	541	591	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	479	SER	-	expression tag	UNP P11230
E	480	ARG	-	expression tag	UNP P11230

- Molecule 3 is a protein called Acetylcholine receptor subunit delta.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	433	Total	C	H	N	O	S	0	0
			7053	2295	3533	582	629	14		

- Molecule 4 is a protein called Acetylcholine receptor subunit epsilon.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	411	Total	C	H	N	O	S	0	0
			6480	2102	3228	533	603	14		

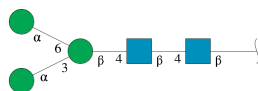
- Molecule 5 is a protein called Fab7 heavy chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	223	Total	C	H	N	O	S	0	0
			3315	1067	1634	283	325	6		

- Molecule 6 is a protein called Fab7 light chain.

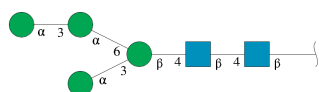
Mol	Chain	Residues	Atoms						AltConf	Trace
6	G	208	Total	C	H	N	O	S	0	0
			3171	1011	1561	269	325	5		

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	5	Total	C	H	N	O	0	0
			113	34	52	2	25		
7	I	5	Total	C	H	N	O	0	0
			113	34	52	2	25		
7	J	5	Total	C	H	N	O	0	0
			113	34	52	2	25		
7	L	5	Total	C	H	N	O	0	0
			113	34	52	2	25		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



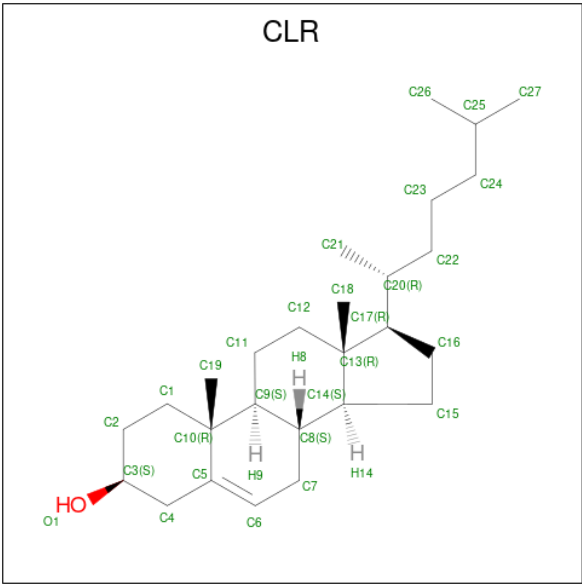
Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	6	Total	C	H	N	O	0	0
			133	40	61	2	30		

- Molecule 9 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P).



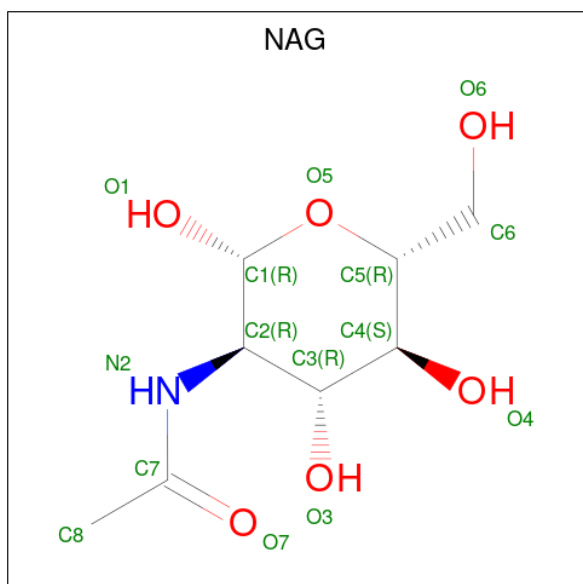
Mol	Chain	Residues	Atoms						AltConf
9	A	1	Total	C	H	N	O	P	0
			116	37	69	1	8	1	
9	E	1	Total	C	H	N	O	P	0
			134	42	82	1	8	1	
9	D	1	Total	C	H	N	O	P	0
			92	30	52	1	8	1	
9	B	1	Total	C	H	N	O	P	0
			107	34	63	1	8	1	

- Molecule 10 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms				AltConf
10	C	1	Total	C	H	O	0
			74	27	46	1	
10	E	1	Total	C	H	O	0
			74	27	46	1	
10	D	1	Total	C	H	O	0
			74	27	46	1	
10	D	1	Total	C	H	O	0
			74	27	46	1	
10	B	1	Total	C	H	O	0
			74	27	46	1	
10	B	1	Total	C	H	O	0
			74	27	46	1	

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					AltConf
11	D	1	Total	C	H	N	O	0
			27	8	13	1	5	
11	B	1	Total	C	H	N	O	0
			27	8	13	1	5	

- Molecule 1: Acetylcholine receptor subunit alpha



[illegible]

Protein	Residue	Score	Category																																																																																																															
Protein 1	SER	0.95	High																																																																																																															
	LEU	0.90	High																																																																																																															
	GLY	0.85	High																																																																																																															
	ALA	0.80	High																																																																																																															
	ALA	0.75	High																																																																																																															
	A397	0.70	High																																																																																																															
	P398	0.65	High																																																																																																															
	E399	0.60	High																																																																																																															
	V400	0.55	High																																																																																																															
	R401	0.50	High																																																																																																															
Protein 2	V410	0.45	High																																																																																																															
	N432	0.40	High																																																																																																															
	D435	0.35	High																																																																																																															
	C438	0.30	High																																																																																																															
	I453	0.25	High																																																																																																															
	F473	0.20	High																																																																																																															
	R332	0.15	High																																																																																																															
	I333	0.10	High																																																																																																															
	L334	0.05	High																																																																																																															
	GLY	0.00	High																																																																																																															
Protein 3	SER	0.95	High																																																																																																															
	PRO	0.90	High																																																																																																															
	PRO	0.85	High																																																																																																															
	PRO	0.80	High																																																																																																															
	PRO	0.75	High																																																																																																															
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	ALA	0.65	High																																																																																																															
	PRO	0.60	High																																																																																																															
	GLY	0.55	High																																																																																																															
	ALA	0.50	High																																																																																																															
Protein 4	ALA	0.45	High																																																																																																															
	ALA	0.40	High																																																																																																															
	SER	0.35	High																																																																																																															
	PRO	0.30	High																																																																																																															
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	ARG	0.20	High																																																																																																															
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	SER	0.05	High																																																																																																															
	SER	0.00	High																																																																																																															
Protein 5	VAL	0.95	High																																																																																																															
	GLY	0.90	High																																																																																																															
	LEU	0.85	High																																																																																																															
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	LEU	0.75	High																																																																																																															
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Protein 6	LEU	0.45	High																																																																																																															
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	VAL	0.05	High																																																																																																															
	PHE	0.00	High																																																																																																															
Protein 7	GLU	0.95	High																																																																																																															
	GLY	0.90	High																																																																																																															
	GLN	0.85	High																																																																																																															
	ARG	0.80	High																																																																																																															
	HIS	0.75	High																																																																																																															
	ARG	0.70	High																																																																																																															
	GLN	0.65	High																																																																																																															
	GLY	0.60	High																																																																																																															
	THR	0.55	High																																																																																																															
	TRP	0.50	High																																																																																																															
Protein 8	ALA	0.45	High																																																																																																															
	F267	0.40	High																																																																																																															
	L288	0.35	High																																																																																																															
	ALA	0.30	High																																																																																																															
	PHE	0.25	High																																																																																																															
	CYS	0.20	High																																																																																																															
	G200	0.15	High																																																																																																															
	G236	0.10	High																																																																																																															
	L237	0.05	High																																																																																																															
	V238	0.00	High																																																																																																															
Protein 9	Y242	0.95	High																																																																																																															
	F243	0.90	High																																																																																																															
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	L267	0.05	High																																																																																																															
	V281	0.00	High																																																																																																															
	R286	0.95	High</																																																																																																															

[illegible]

Protein	Residue	Score	Category
MET	GLY	0.00	Low
	TRP	0.00	Low
	SER	0.00	Low
	CYS	0.00	Low
	ILE	0.00	Low
	ILE	0.00	Low
	LEU	0.00	Low
	PHE	0.00	Low
	LEU	0.00	Low
	VAL	0.00	Low
ALA	THR	0.00	Low
	ALA	0.00	Low
	THR	0.00	Low
	GLY	0.00	Low
	VAL	0.00	Low
	SER	0.00	Low
	HIS	0.00	Low
	ASP	0.00	Low
	ILE	0.00	Low
	Q22	0.00	Low
M23	M23	0.00	Low
	A32	0.00	Low
	C42	0.00	Low
	Q46	0.00	Low
	S82	0.00	Low
	G85	0.00	Low
	S86	0.00	Low
	G87	0.00	Low
	F90	0.00	Low
	K125	0.00	Low
R126	T127	0.00	Low
	F134	0.00	Low
	I135	0.00	Low
	F136	0.00	Low
	P137	0.00	Low
	P138	0.00	Low
	S139	0.00	Low
	D140	0.00	Low
	L143	0.00	Low
	K144	0.00	Low
S145	G146	0.00	Low
	T147	0.00	Low
	A148	0.00	Low
	S149	0.00	Low
	C152	0.00	Low
	R160	0.00	Low
	E161	0.00	Low
	A162	0.00	Low
	K163	0.00	Low
	V164	0.00	Low
Q165	0.00	Low	
V168	D169	0.00	Low
	M170	0.00	Low
	A171	0.00	Low
	L172	0.00	Low
	Q173	0.00	Low
	S174	0.00	Low
	G175	0.00	Low
	M176	0.00	Low
	S177	0.00	Low
	Q178	0.00	Low
E179	E179	0.00	Low
	K187	0.00	Low
	D188	0.00	Low
	S189	0.00	Low
	T190	0.00	Low
	S194	0.00	Low
	S195	0.00	Low
	T196	0.00	Low
	L197	0.00	Low
	T198	0.00	Low
S200	L199	0.00	Low
	K201	0.00	Low
	A202	0.00	Low
	D203	0.00	Low
	Y204	0.00	Low
	E205	0.00	Low
	K206	0.00	Low
	H207	0.00	Low
	K208	0.00	Low
	V209	0.00	Low
Y210	A211	0.00	Low
	C212	0.00	Low
	E213	0.00	Low
	V214	0.00	Low
	T215	0.00	Low
	H216	0.00	Low
	Q217	0.00	Low
	G218	0.00	Low
	L219	0.00	Low
	S220	0.00	Low
T224	K225	0.00	Low
	S226	0.00	Low
	F227	0.00	Low
	N228	0.00	Low
	R229	0.00	Low
	R1V	0.00	Low

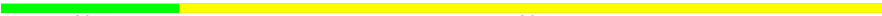
GLU
CYS

• Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  40% 60%

MAG1
MAG2
BNA3
MAN4
MAN5

• Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  20% 80%

MAG1
MAG2
BNA3
MAN4
MAN5

• Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  20% 80%

MAG1
MAG2
BNA3
MAN4
MAN5

• Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  20% 80%

MAG1
MAG2
BNA3
MAN4
MAN5

• Molecule 8: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  17% 17% 83%

MAG1
MAG2
BNA3
MAN4
MAN5
MAN6

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	307930	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)	1400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.268	Depositor
Minimum map value	-0.626	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.085	Depositor
Map size (Å)	374.0, 374.0, 374.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.935, 0.935, 0.935	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, POV, NAG, CLR, BMA

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	0.29	0/3285	0.56	0/4479
1	C	0.28	0/3306	0.55	0/4507
2	E	0.29	0/3367	0.58	0/4588
3	D	0.28	0/3616	0.57	0/4934
4	B	0.28	0/3330	0.57	0/4554
5	F	0.30	0/1725	0.64	0/2354
6	G	0.36	0/1647	0.62	0/2237
All	All	0.29	0/20276	0.58	0/27653

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	E	0	1
6	G	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	117	ARG	Sidechain
6	G	160	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3202	3231	3233	31	0
1	C	3223	3263	3265	10	0
2	E	3281	3294	3294	25	0
3	D	3520	3533	3536	39	0
4	B	3252	3228	3231	38	0
5	F	1681	1634	1632	8	0
6	G	1610	1561	1560	34	0
7	H	61	52	52	0	0
7	I	61	52	52	0	0
7	J	61	52	52	0	0
7	L	61	52	52	0	0
8	K	72	61	61	0	0
9	A	47	69	69	11	0
9	B	44	63	63	24	0
9	D	40	52	52	15	0
9	E	52	82	82	12	0
10	B	56	92	92	11	0
10	C	28	46	46	13	0
10	D	56	92	92	23	0
10	E	28	46	46	10	0
11	B	14	13	13	0	0
11	D	14	13	13	1	0
All	All	20464	20581	20588	192	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 5.

The worst 5 of 192 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:G:126:ARG:NH2	6:G:190:THR:CG2	2.01	1.22
3:D:290:LYS:NZ	9:D:504:POV:H12A	1.54	1.21
3:D:472:VAL:HG22	10:D:503:CLR:C7	1.72	1.20
3:D:472:VAL:HG22	10:D:503:CLR:H72	1.26	1.18
3:D:469:LEU:HD21	10:D:502:CLR:H152	1.28	1.11

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	395/457 (86%)	387 (98%)	8 (2%)	0	100	100
1	C	397/457 (87%)	387 (98%)	10 (2%)	0	100	100
2	E	397/503 (79%)	390 (98%)	6 (2%)	1 (0%)	37	40
3	D	429/517 (83%)	421 (98%)	8 (2%)	0	100	100
4	B	407/493 (83%)	398 (98%)	9 (2%)	0	100	100
5	F	219/295 (74%)	213 (97%)	6 (3%)	0	100	100
6	G	206/232 (89%)	199 (97%)	7 (3%)	0	100	100
All	All	2450/2954 (83%)	2395 (98%)	54 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	106	ILE

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	367/419 (88%)	366 (100%)	1 (0%)	91	95
1	C	370/419 (88%)	370 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	372/450 (83%)	371 (100%)	1 (0%)	91	95
3	D	399/466 (86%)	398 (100%)	1 (0%)	91	95
4	B	363/424 (86%)	361 (99%)	2 (1%)	84	91
5	F	186/251 (74%)	185 (100%)	1 (0%)	86	93
6	G	184/203 (91%)	183 (100%)	1 (0%)	86	93
All	All	2241/2632 (85%)	2234 (100%)	7 (0%)	90	95

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	147	ARG
4	B	435	ASP
6	G	82	SER
5	F	81	HIS
3	D	449	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	301	ASN
4	B	316	HIS
4	B	432	ASN
1	A	297	ASN
1	A	204	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 ⓘ

26 monosaccharides are modelled in this entry.

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	$\# Z > 2$
7	NAG	H	1	1,7	14,14,15	0.34	0	17,19,21	0.85	1 (5%)
7	NAG	H	2	7	14,14,15	0.34	0	17,19,21	0.90	2 (11%)
7	BMA	H	3	7	11,11,12	0.55	0	15,15,17	0.61	0
7	MAN	H	4	7	11,11,12	0.69	0	15,15,17	0.93	2 (13%)
7	MAN	H	5	7	11,11,12	0.57	0	15,15,17	0.82	0
7	NAG	I	1	1,7	14,14,15	0.80	1 (7%)	17,19,21	0.57	0
7	NAG	I	2	7	14,14,15	0.43	0	17,19,21	0.99	2 (11%)
7	BMA	I	3	7	11,11,12	0.56	0	15,15,17	0.61	0
7	MAN	I	4	7	11,11,12	0.66	0	15,15,17	0.93	2 (13%)
7	MAN	I	5	7	11,11,12	0.61	0	15,15,17	0.83	1 (6%)
7	NAG	J	1	7,2	14,14,15	0.26	0	17,19,21	0.88	1 (5%)
7	NAG	J	2	7	14,14,15	0.14	0	17,19,21	0.89	1 (5%)
7	BMA	J	3	7	11,11,12	0.44	0	15,15,17	0.70	0
7	MAN	J	4	7	11,11,12	0.60	0	15,15,17	0.94	2 (13%)
7	MAN	J	5	7	11,11,12	0.63	0	15,15,17	1.00	2 (13%)
8	NAG	K	1	3,8	14,14,15	0.32	0	17,19,21	0.81	1 (5%)
8	NAG	K	2	8	14,14,15	0.16	0	17,19,21	0.88	1 (5%)
8	BMA	K	3	8	11,11,12	0.45	0	15,15,17	0.62	0
8	MAN	K	4	8	11,11,12	0.78	0	15,15,17	1.14	2 (13%)
8	MAN	K	5	8	11,11,12	0.68	0	15,15,17	1.00	2 (13%)
8	MAN	K	6	8	11,11,12	0.57	0	15,15,17	1.00	2 (13%)
7	NAG	L	1	4,7	14,14,15	0.37	0	17,19,21	0.82	1 (5%)
7	NAG	L	2	7	14,14,15	0.22	0	17,19,21	0.79	1 (5%)
7	BMA	L	3	7	11,11,12	0.41	0	15,15,17	0.68	0
7	MAN	L	4	7	11,11,12	0.60	0	15,15,17	0.99	2 (13%)
7	MAN	L	5	7	11,11,12	0.69	0	15,15,17	0.89	2 (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
7	NAG	H	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	H	2	7	-	2/6/23/26	0/1/1/1
7	BMA	H	3	7	-	0/2/19/22	0/1/1/1
7	MAN	H	4	7	-	1/2/19/22	0/1/1/1
7	MAN	H	5	7	-	0/2/19/22	0/1/1/1
7	NAG	I	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	I	2	7	-	2/6/23/26	0/1/1/1
7	BMA	I	3	7	-	0/2/19/22	0/1/1/1
7	MAN	I	4	7	-	2/2/19/22	0/1/1/1
7	MAN	I	5	7	-	0/2/19/22	0/1/1/1
7	NAG	J	1	7,2	-	2/6/23/26	0/1/1/1
7	NAG	J	2	7	-	2/6/23/26	0/1/1/1
7	BMA	J	3	7	-	0/2/19/22	0/1/1/1
7	MAN	J	4	7	-	1/2/19/22	0/1/1/1
7	MAN	J	5	7	-	0/2/19/22	0/1/1/1
8	NAG	K	1	3,8	-	2/6/23/26	0/1/1/1
8	NAG	K	2	8	-	4/6/23/26	0/1/1/1
8	BMA	K	3	8	-	0/2/19/22	0/1/1/1
8	MAN	K	4	8	-	0/2/19/22	0/1/1/1
8	MAN	K	5	8	-	0/2/19/22	0/1/1/1
8	MAN	K	6	8	-	2/2/19/22	0/1/1/1
7	NAG	L	1	4,7	-	2/6/23/26	0/1/1/1
7	NAG	L	2	7	-	2/6/23/26	0/1/1/1
7	BMA	L	3	7	-	0/2/19/22	0/1/1/1
7	MAN	L	4	7	-	0/2/19/22	0/1/1/1
7	MAN	L	5	7	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	I	1	NAG	O5-C1	-2.91	1.38	1.43

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	K	4	MAN	C1-O5-C5	3.13	116.38	112.19
7	J	1	NAG	C2-N2-C7	3.07	127.02	122.90
7	L	1	NAG	C2-N2-C7	2.86	126.74	122.90
7	H	1	NAG	C2-N2-C7	2.84	126.71	122.90
8	K	2	NAG	C2-N2-C7	2.83	126.70	122.90

There are no chirality outliers.

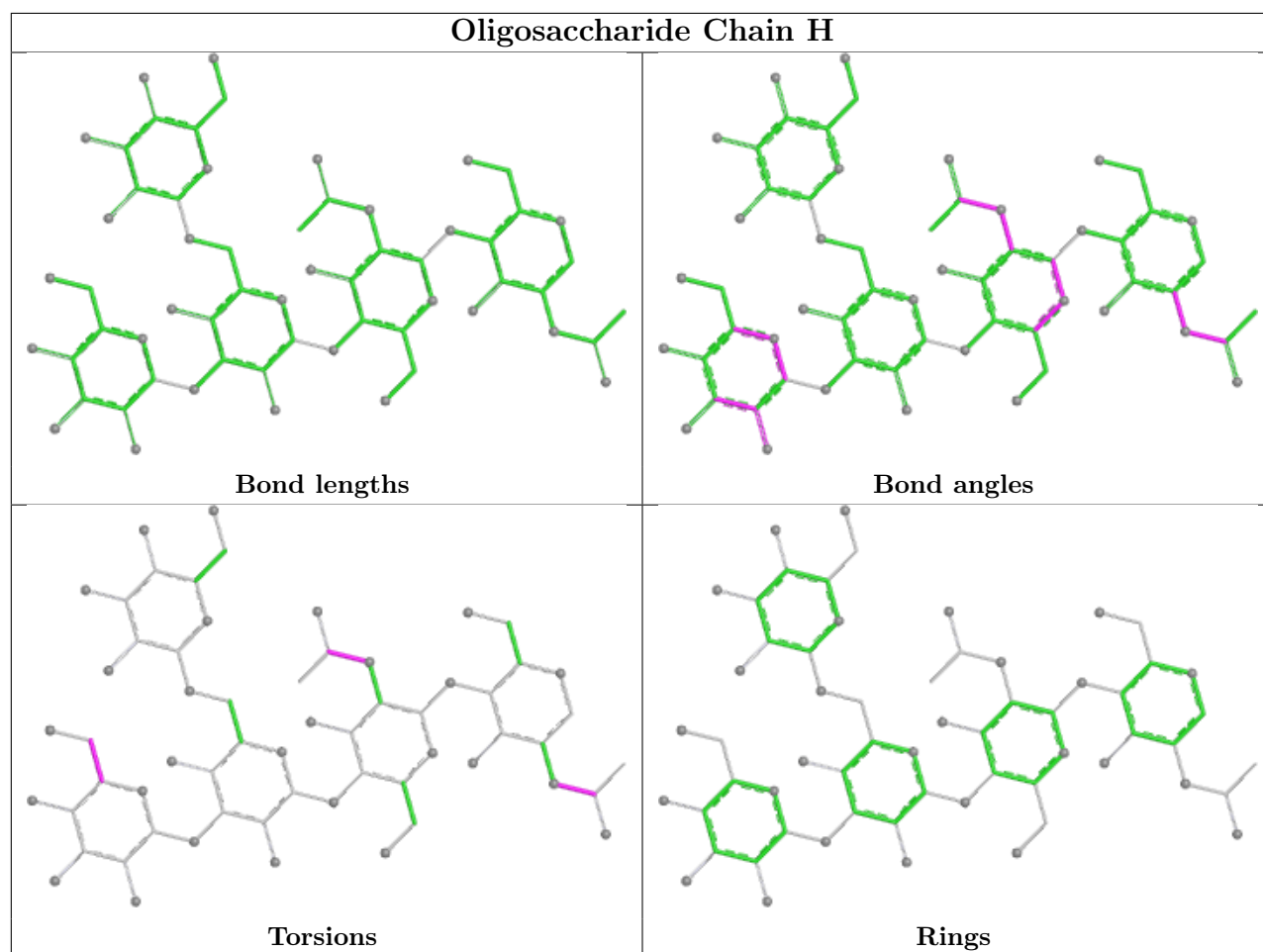
5 of 28 torsion outliers are listed below:

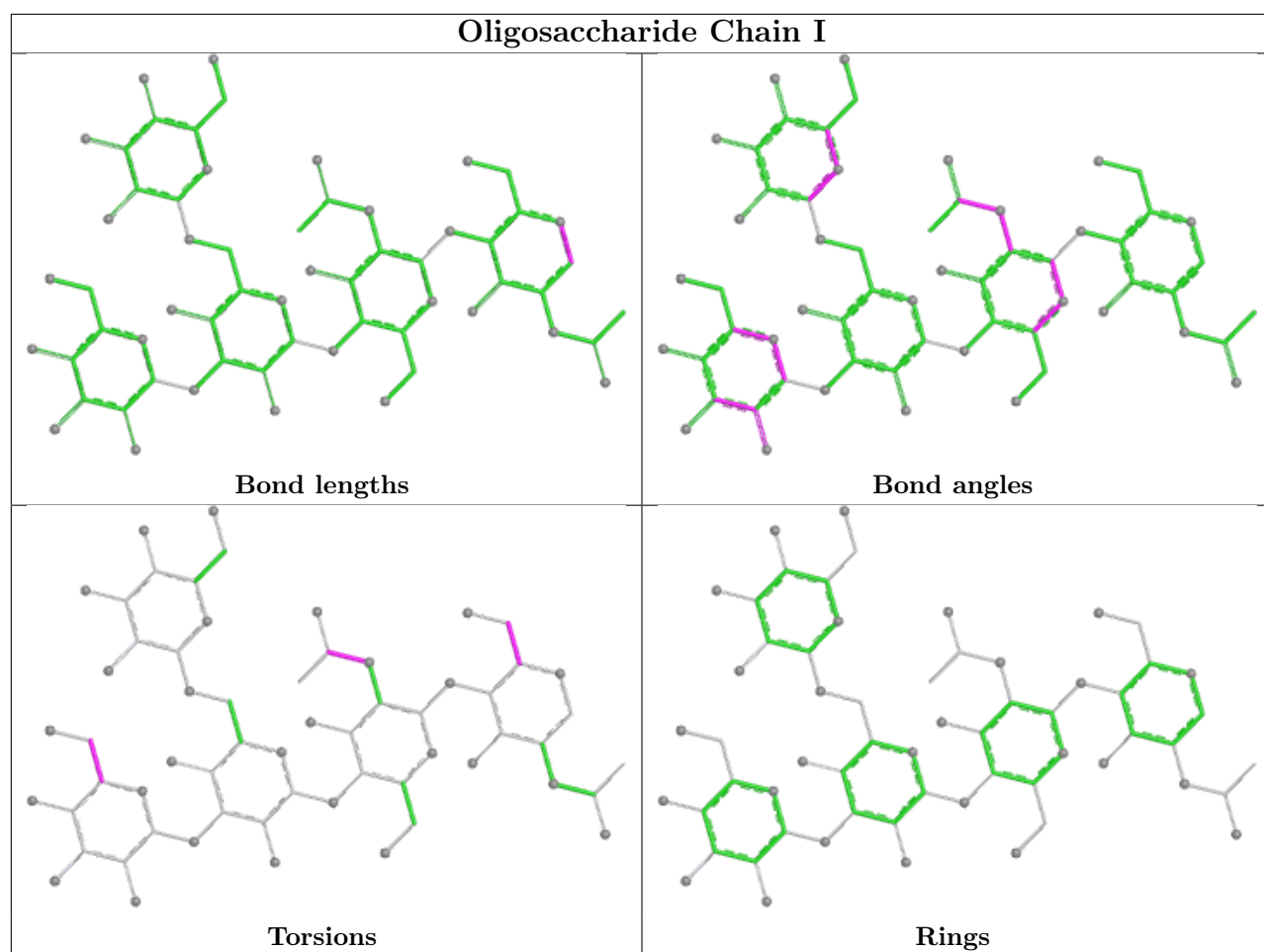
Mol	Chain	Res	Type	Atoms
7	H	1	NAG	C8-C7-N2-C2
7	H	1	NAG	O7-C7-N2-C2
7	H	2	NAG	C8-C7-N2-C2
7	H	2	NAG	O7-C7-N2-C2
7	I	2	NAG	C8-C7-N2-C2

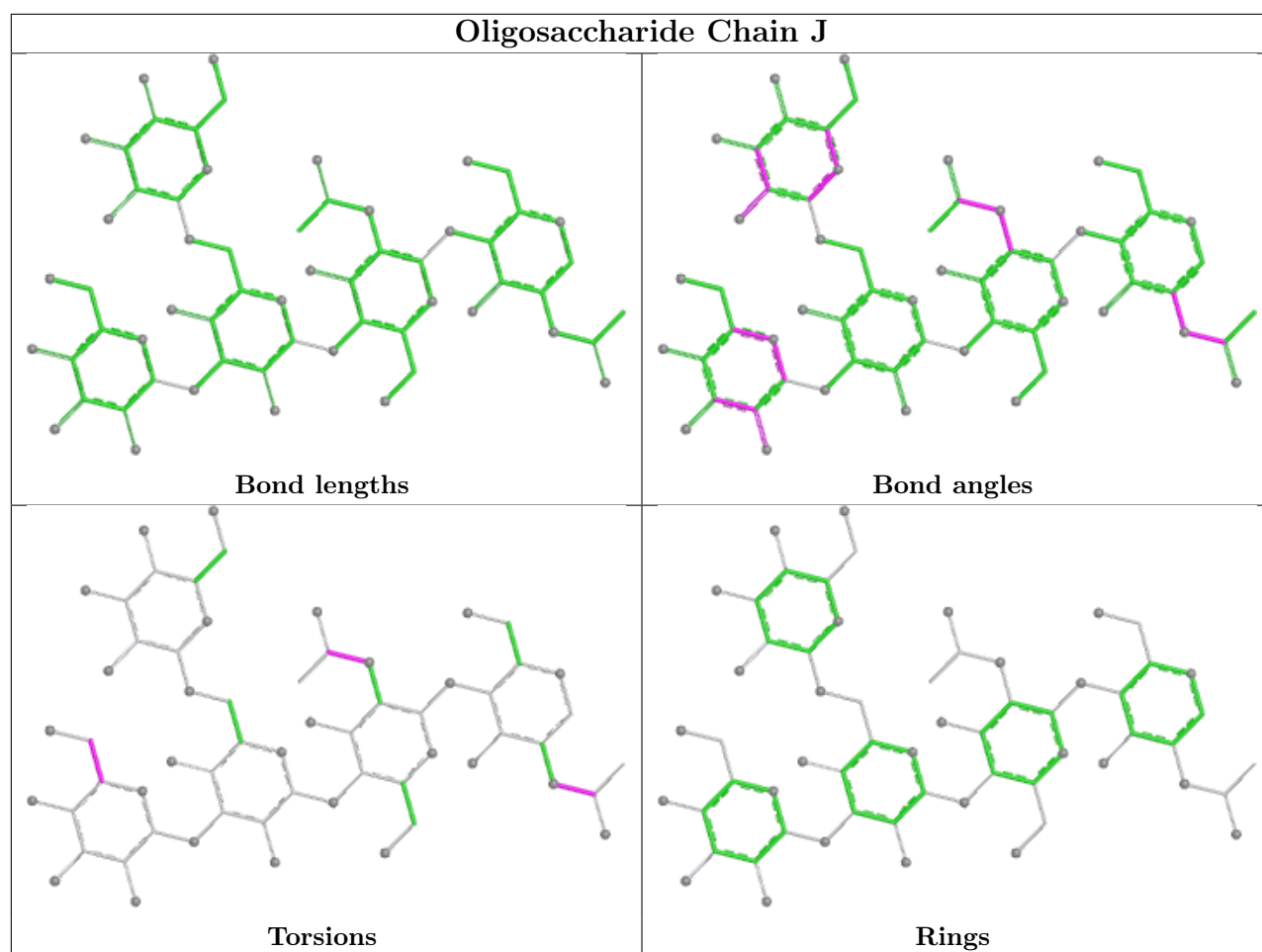
There are no ring outliers.

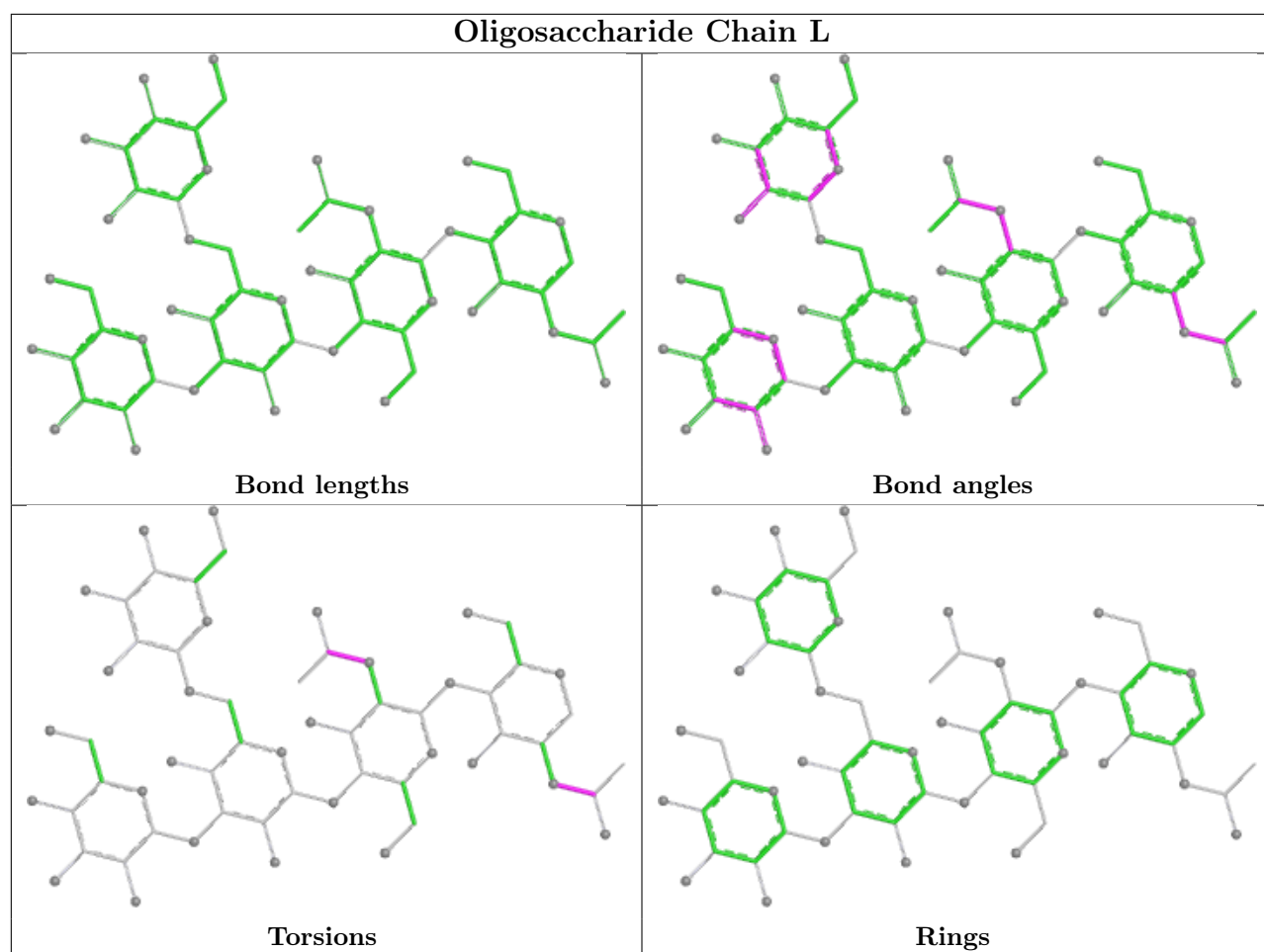
No monomer is involved in short contacts.

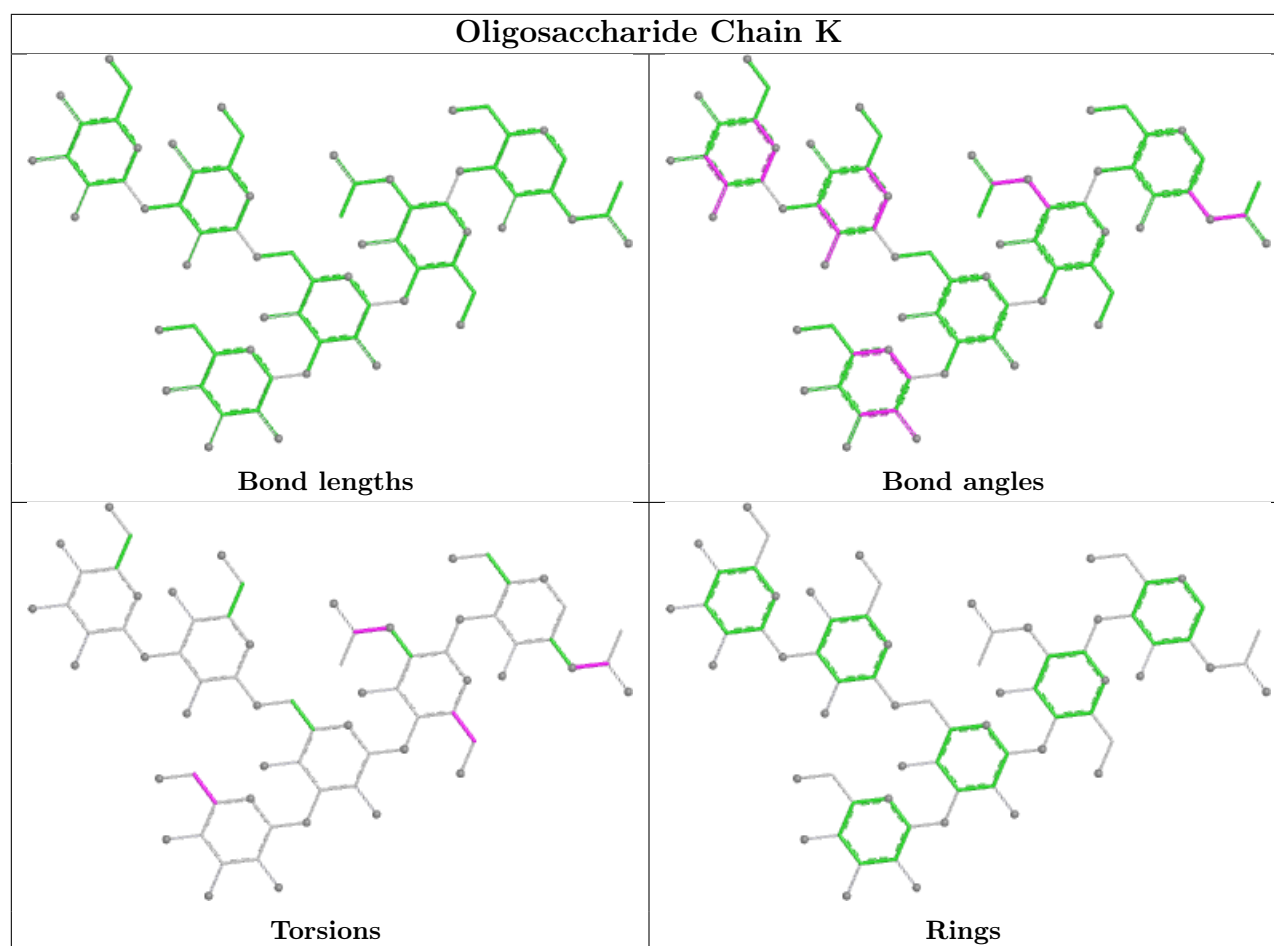
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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	POV	E	502	-	51,51,51	0.31	0	57,59,59	0.31	0
9	POV	D	504	-	39,39,51	0.32	0	45,47,59	0.34	0
10	CLR	B	503	-	31,31,31	0.30	0	48,48,48	0.40	0
11	NAG	B	501	4	14,14,15	0.72	1 (7%)	17,19,21	1.32	1 (5%)
9	POV	A	501	-	46,46,51	0.33	0	52,54,59	0.29	0
10	CLR	B	502	-	31,31,31	0.29	0	48,48,48	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	CLR	D	503	-	31,31,31	0.31	0	48,48,48	0.79	2 (4%)
11	NAG	D	501	3	14,14,15	0.44	0	17,19,21	1.62	3 (17%)
9	POV	B	504	-	43,43,51	0.33	0	49,51,59	0.33	0
10	CLR	C	501	-	31,31,31	0.30	0	48,48,48	0.46	0
10	CLR	D	502	-	31,31,31	0.27	0	48,48,48	0.69	1 (2%)
10	CLR	E	501	-	31,31,31	0.29	0	48,48,48	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	POV	E	502	-	-	13/55/55/55	-
9	POV	D	504	-	-	4/43/43/55	-
10	CLR	B	503	-	-	2/10/68/68	0/4/4/4
11	NAG	B	501	4	-	3/6/23/26	0/1/1/1
9	POV	A	501	-	-	11/50/50/55	-
10	CLR	B	502	-	-	2/10/68/68	0/4/4/4
10	CLR	D	503	-	-	4/10/68/68	0/4/4/4
11	NAG	D	501	3	-	4/6/23/26	0/1/1/1
9	POV	B	504	-	-	9/47/47/55	-
10	CLR	C	501	-	-	2/10/68/68	0/4/4/4
10	CLR	D	502	-	-	6/10/68/68	0/4/4/4
10	CLR	E	501	-	-	1/10/68/68	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B	501	NAG	C1-C2	2.25	1.55	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	501	NAG	C2-N2-C7	4.70	129.20	122.90
11	B	501	NAG	C2-N2-C7	4.15	128.46	122.90
11	D	501	NAG	C1-C2-N2	2.62	114.57	110.43
10	D	503	CLR	C9-C10-C5	-2.37	106.19	109.65
10	D	502	CLR	C16-C17-C20	2.24	115.57	112.18

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

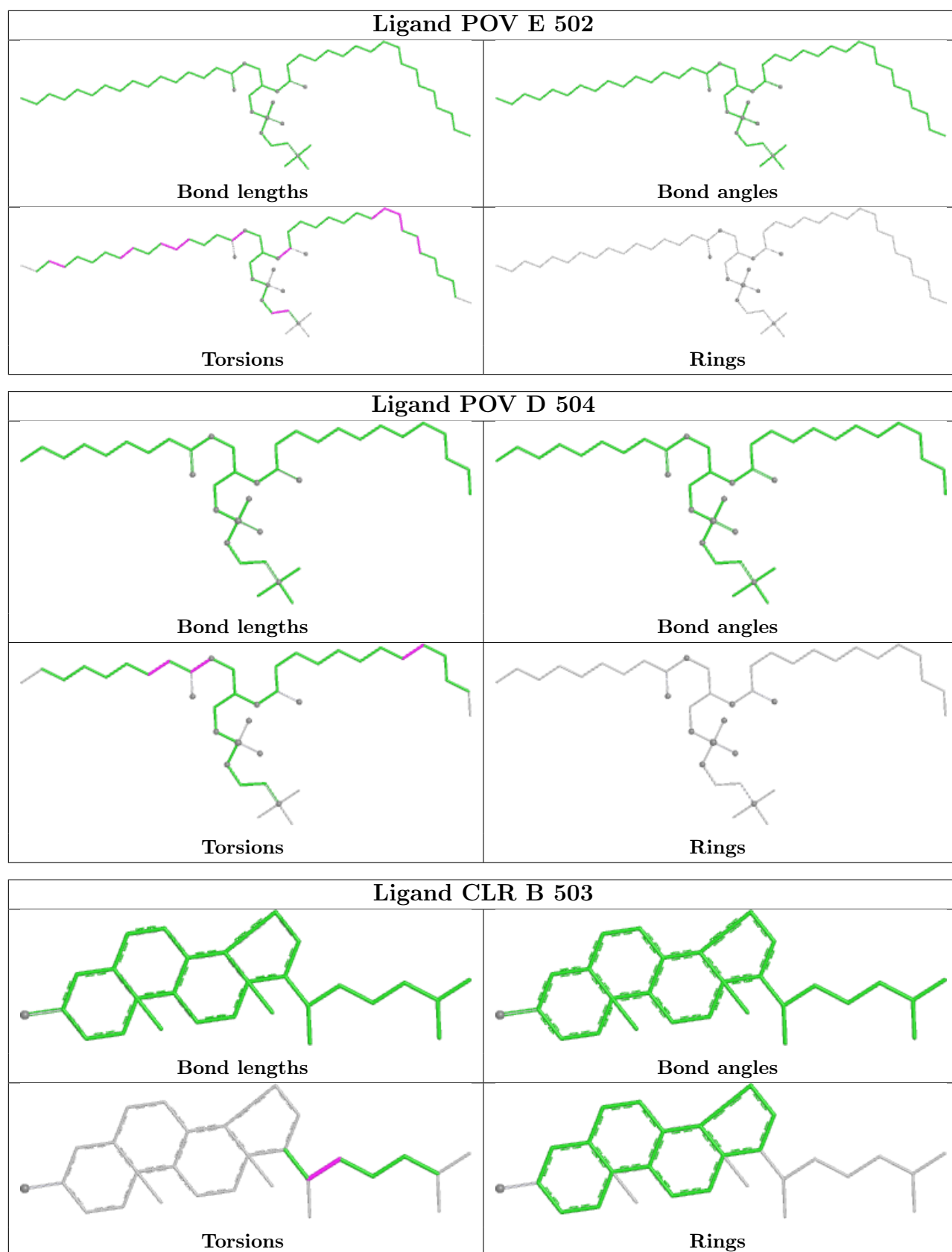
Mol	Chain	Res	Type	Atoms
9	A	501	POV	C11-O12-P-O14
9	E	502	POV	C22-C21-O21-C2
9	B	504	POV	O12-C11-C12-N
11	B	501	NAG	C3-C2-N2-C7
9	E	502	POV	O32-C31-O31-C3

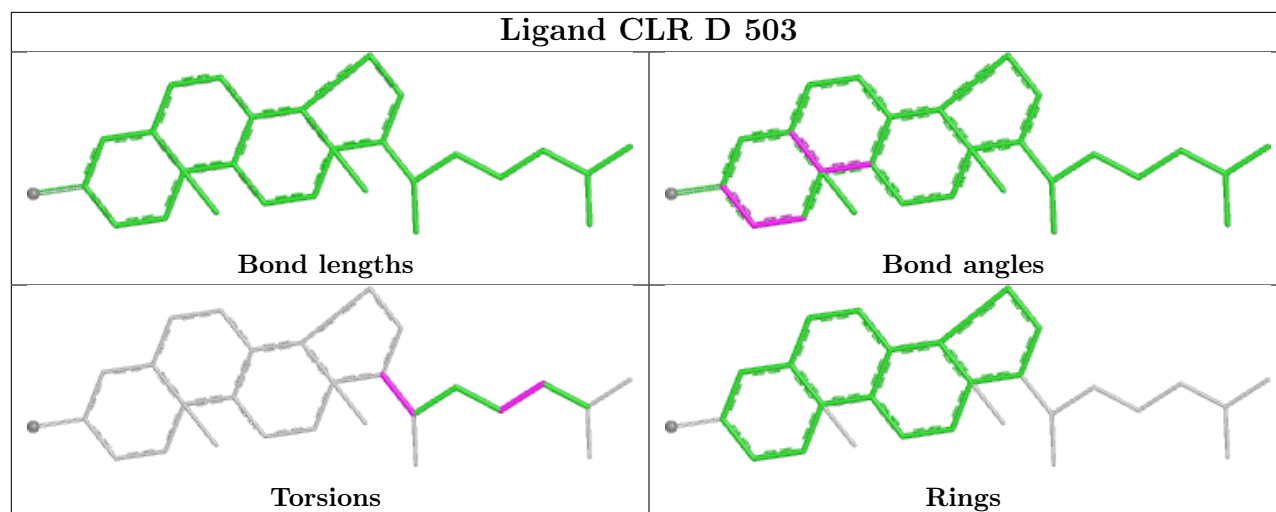
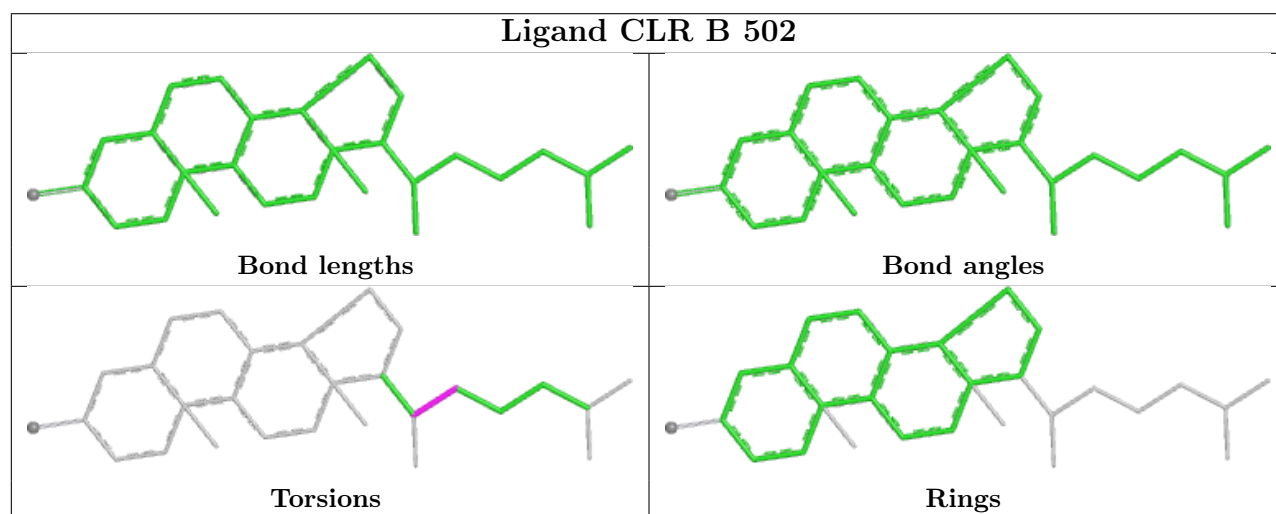
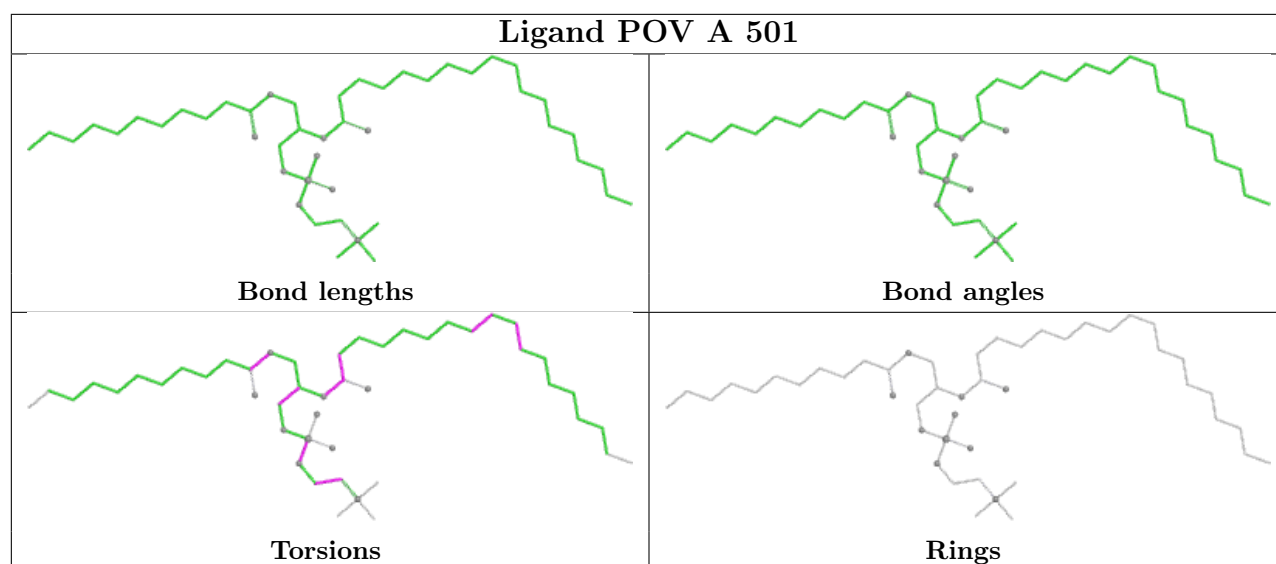
There are no ring outliers.

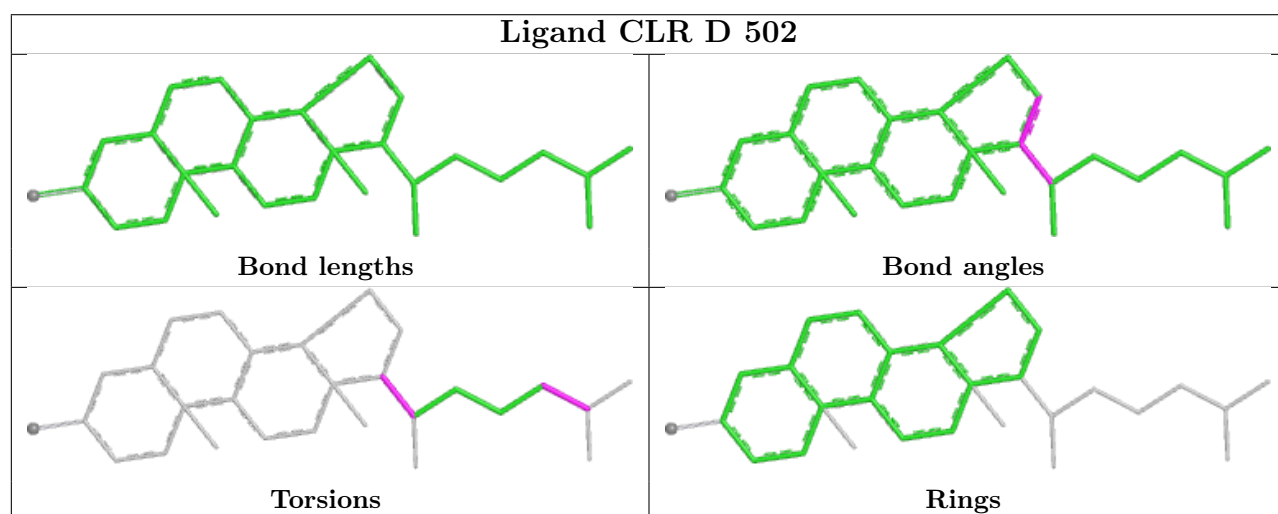
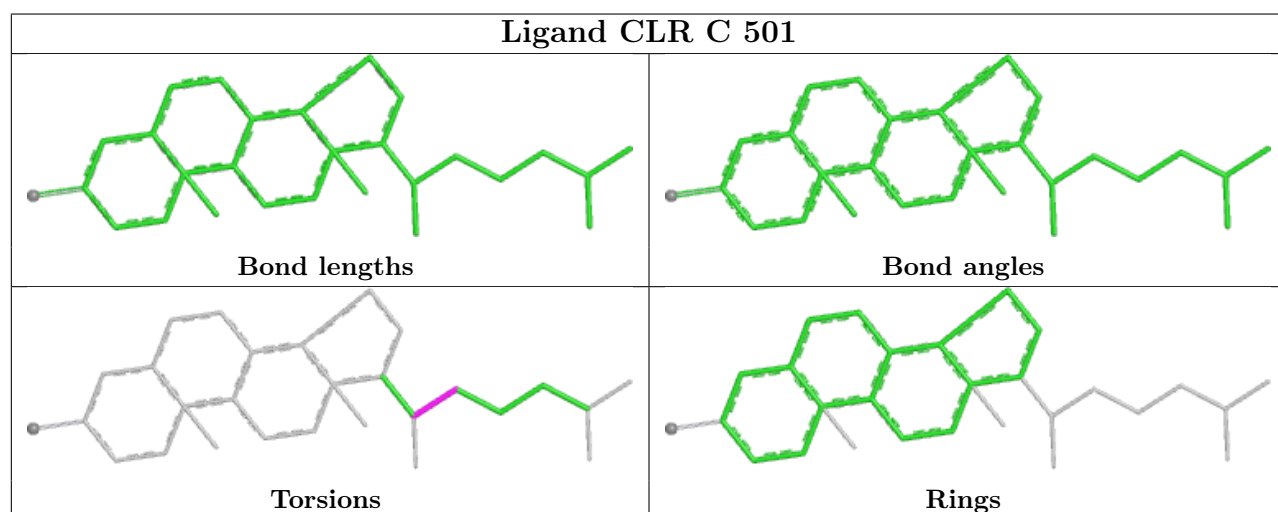
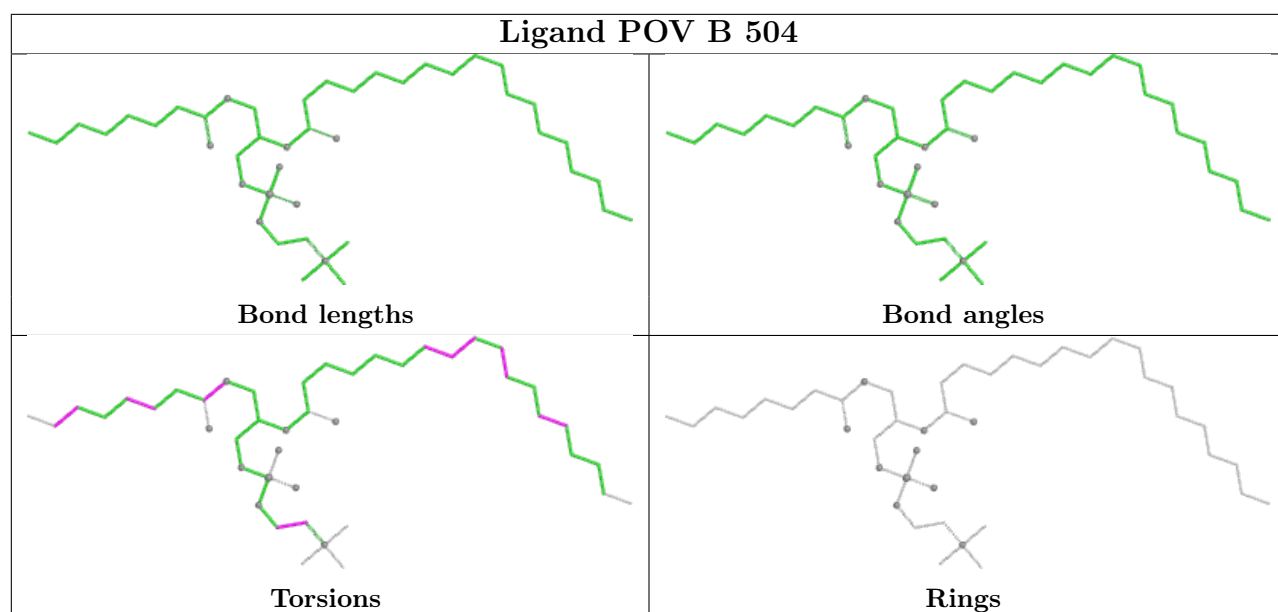
11 monomers are involved in 118 short contacts:

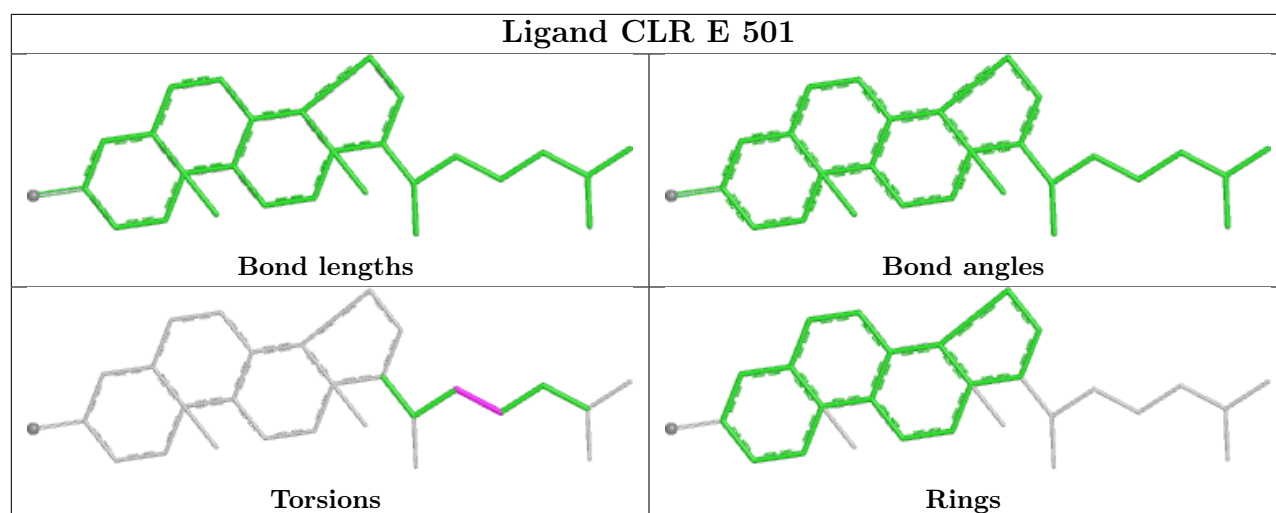
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	502	POV	12	0
9	D	504	POV	15	0
10	B	503	CLR	8	0
9	A	501	POV	11	0
10	B	502	CLR	3	0
10	D	503	CLR	18	0
11	D	501	NAG	1	0
9	B	504	POV	24	0
10	C	501	CLR	13	0
10	D	502	CLR	9	0
10	E	501	CLR	10	0

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.

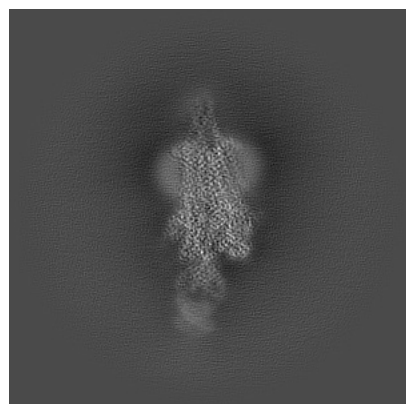
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47015. These allow visual inspection of the internal detail of the map and identification of artifacts.

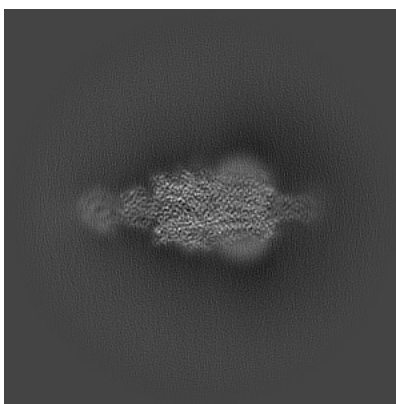
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

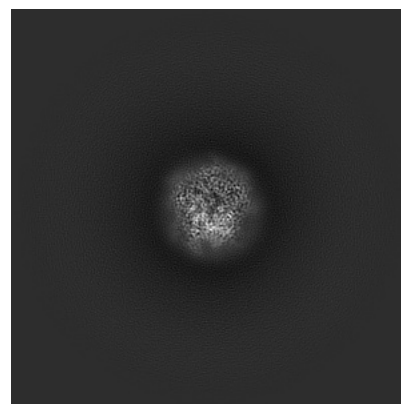
6.1.1 Primary map



X

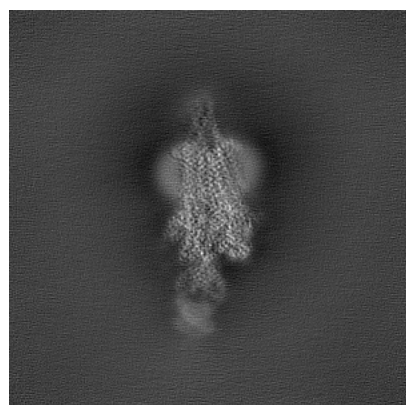


Y

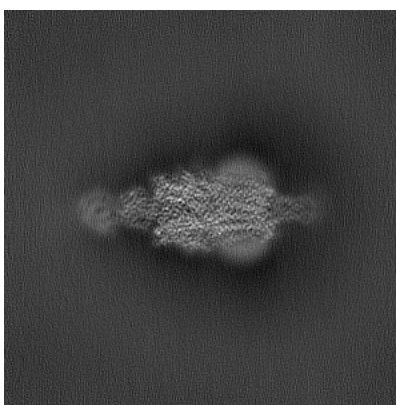


Z

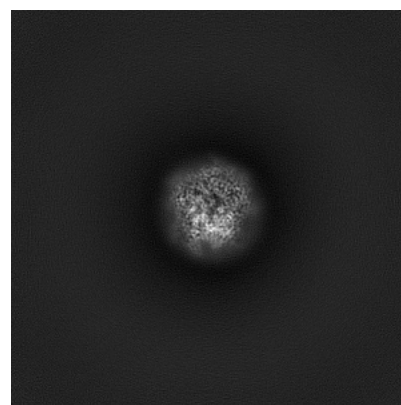
6.1.2 Raw map



X



Y

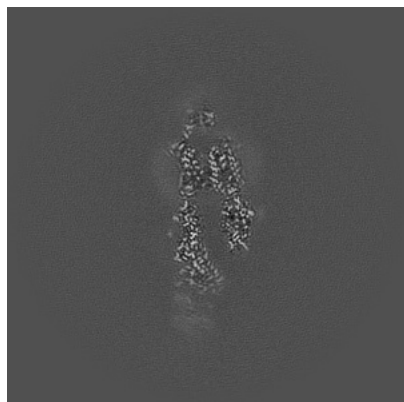


Z

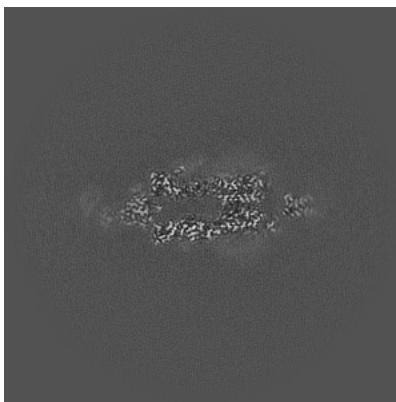
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

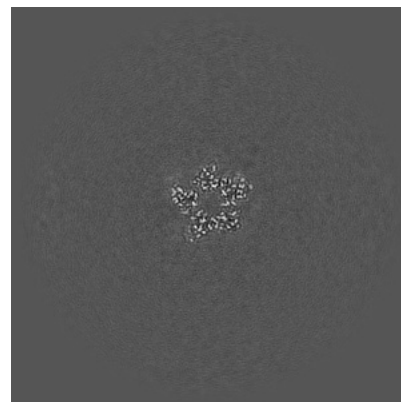
6.2.1 Primary map



X Index: 200

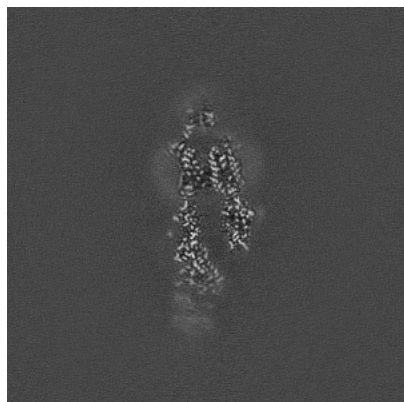


Y Index: 200

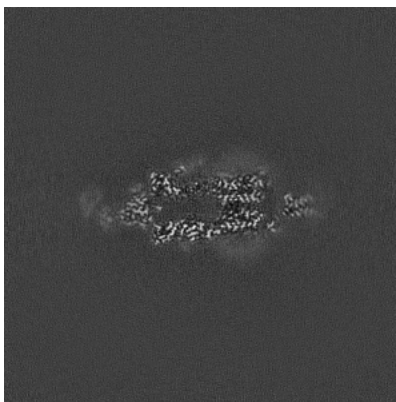


Z Index: 200

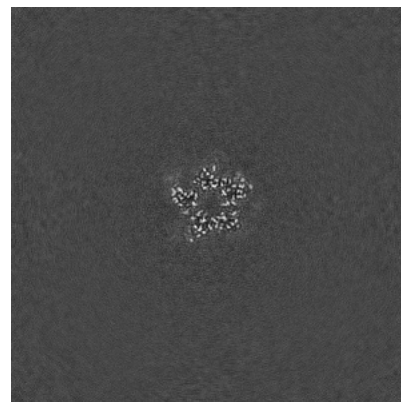
6.2.2 Raw map



X Index: 200



Y Index: 200

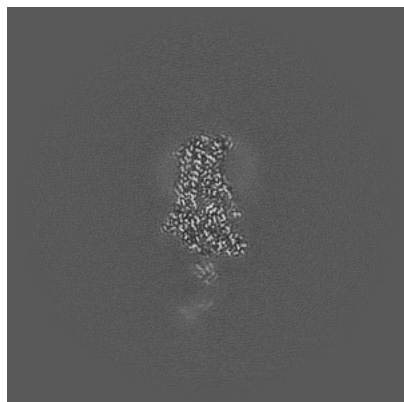


Z Index: 200

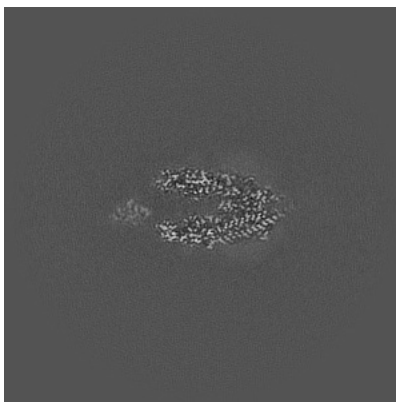
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

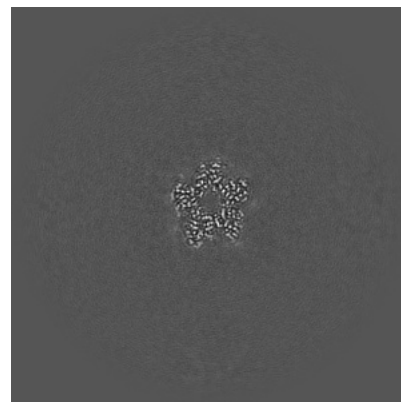
6.3.1 Primary map



X Index: 182

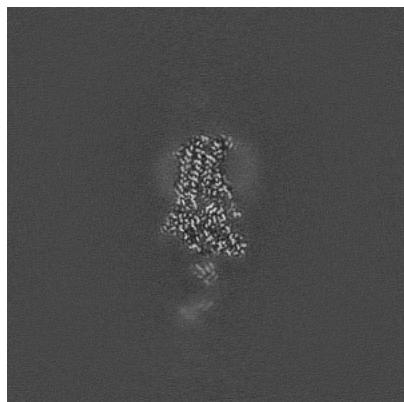


Y Index: 210

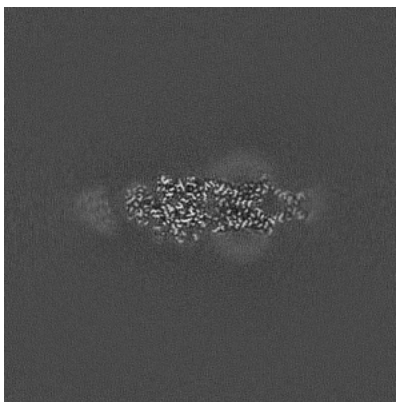


Z Index: 187

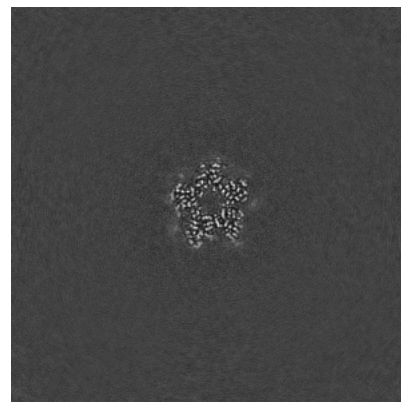
6.3.2 Raw map



X Index: 182



Y Index: 189

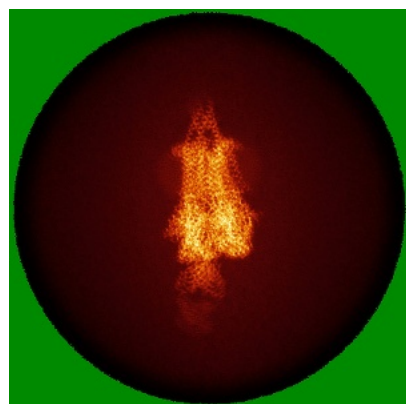


Z Index: 187

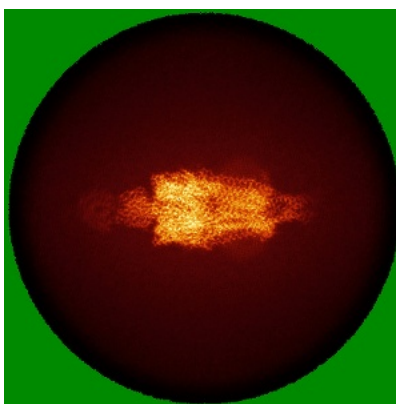
The images above show the largest variance slices of the map in three orthogonal directions.

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

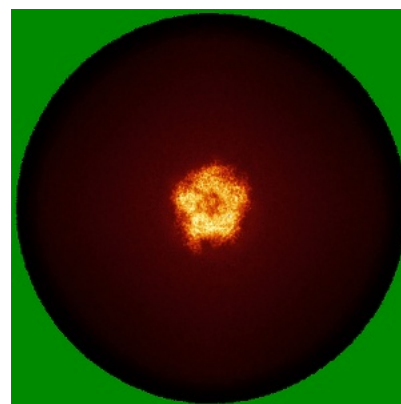
6.4.1 Primary map



X

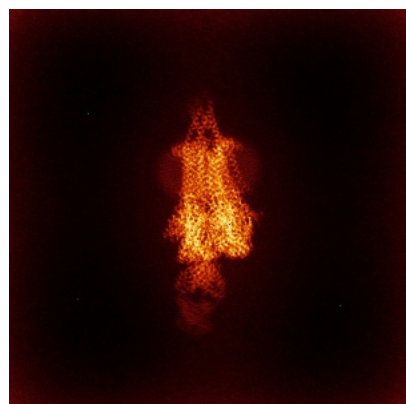


Y

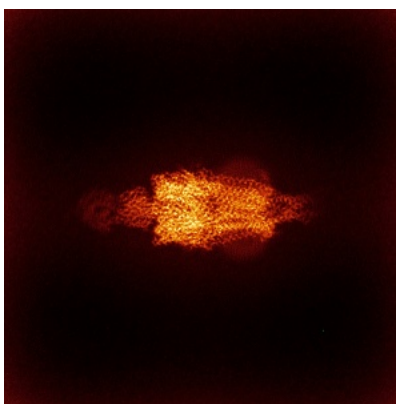


Z

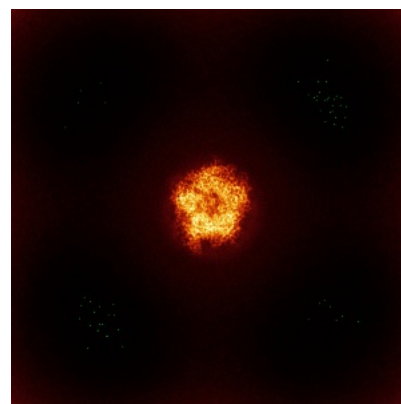
6.4.2 Raw map



X



Y

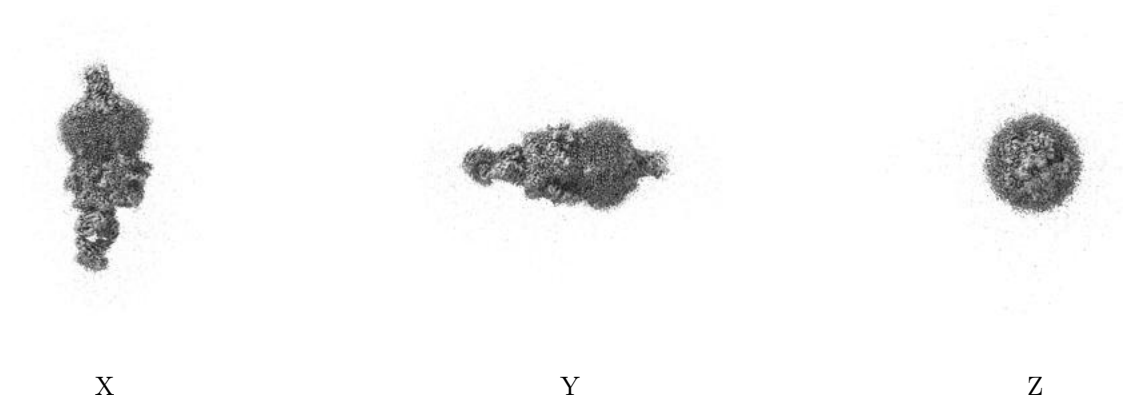


Z

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.

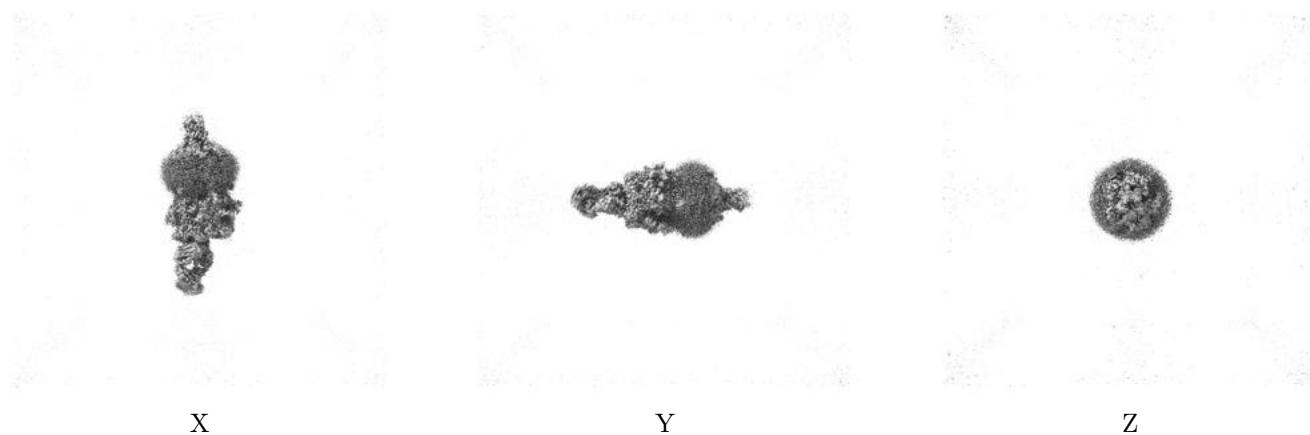
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.085. 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



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.

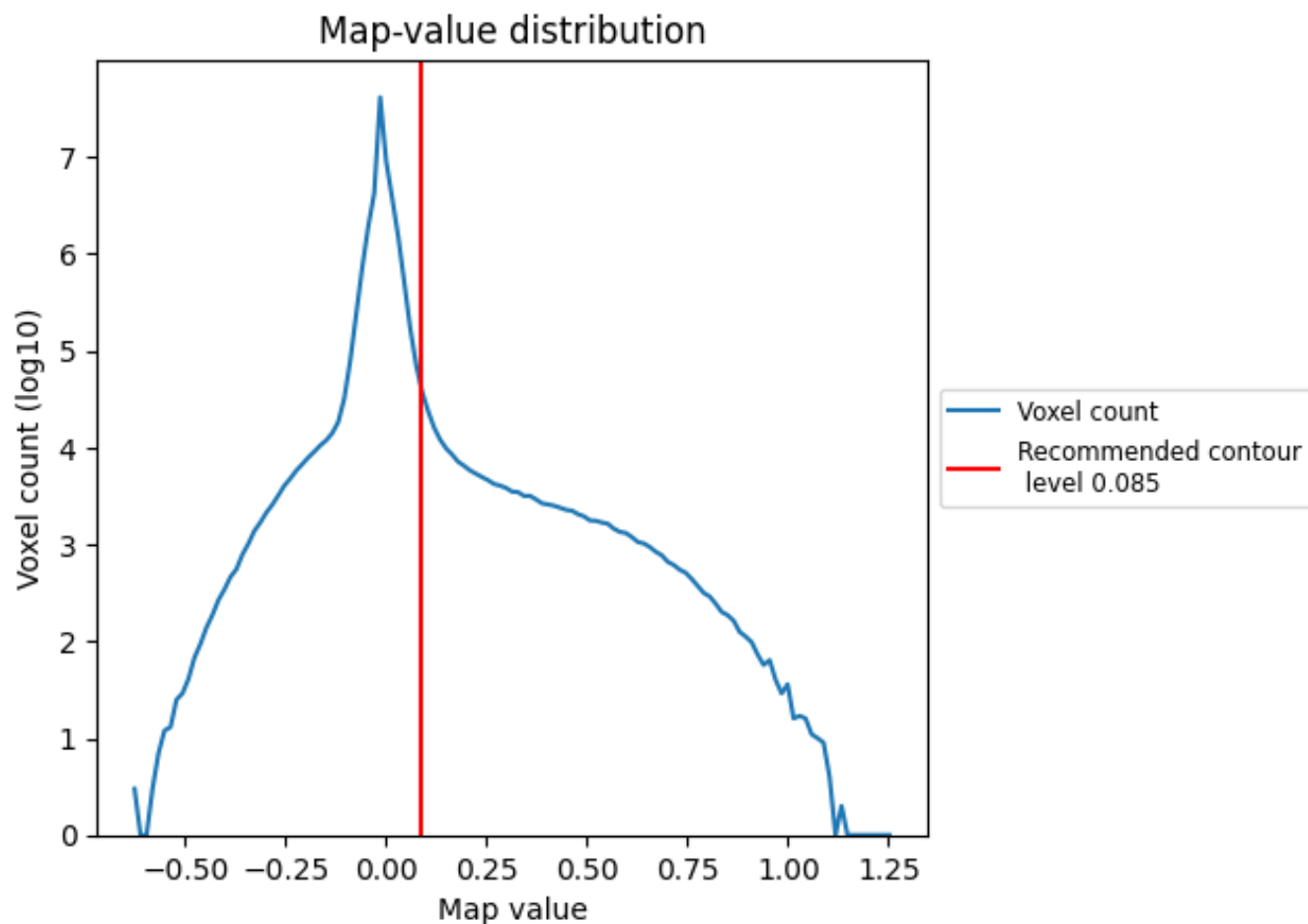
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

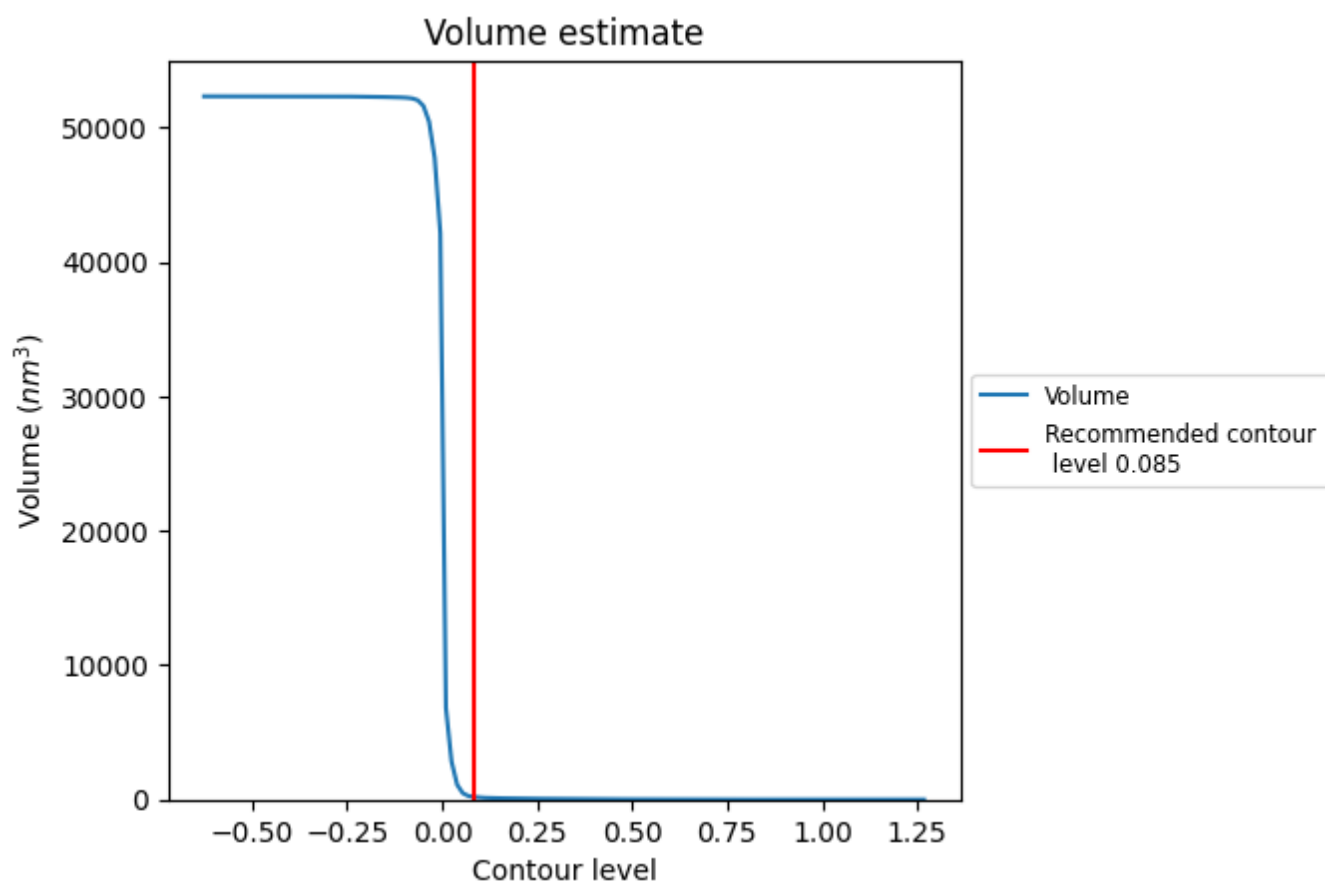
This section contains the results of statistical analysis of the map.

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.

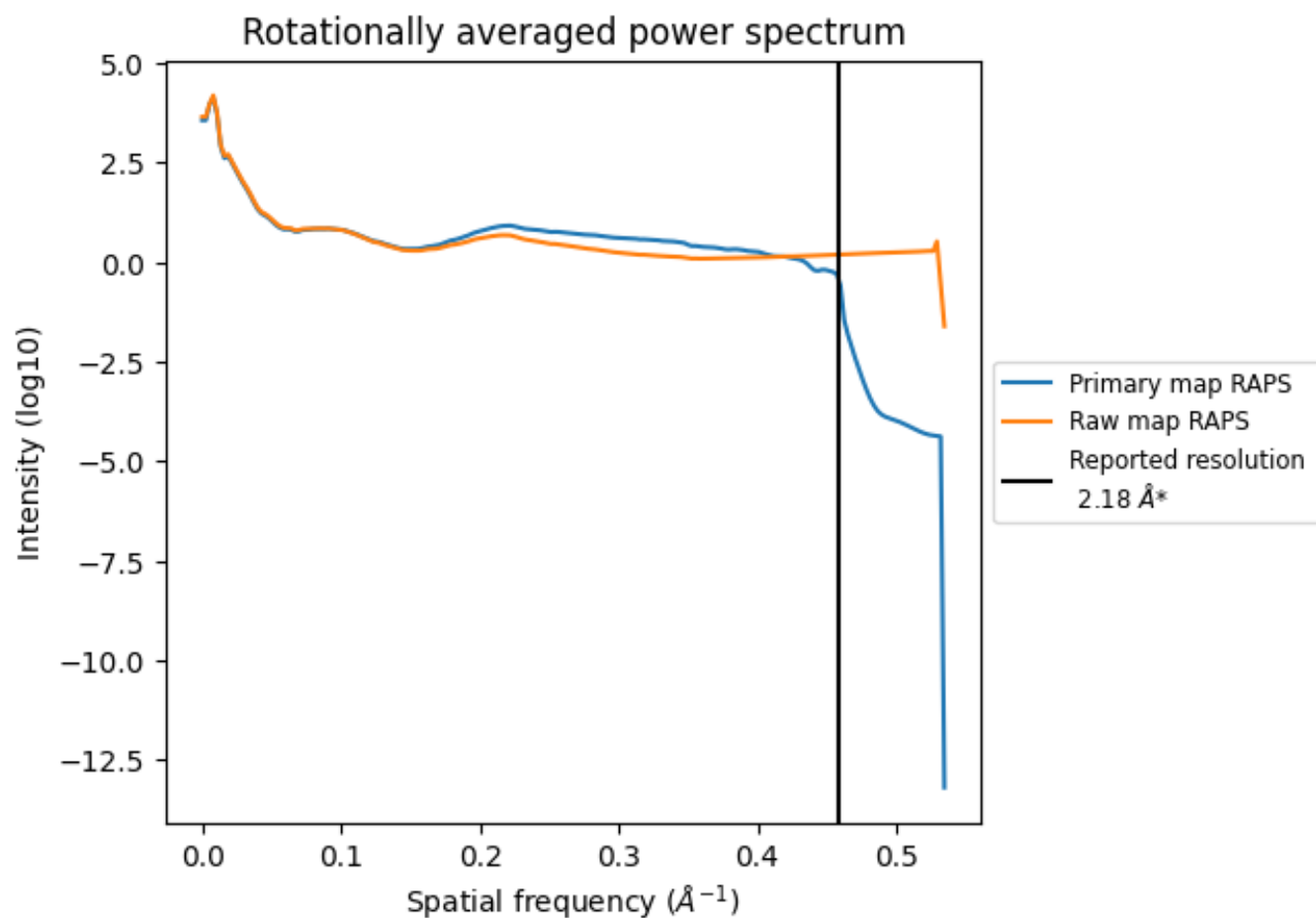
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 188 nm^3 ; this corresponds to an approximate mass of 170 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 ⓘ

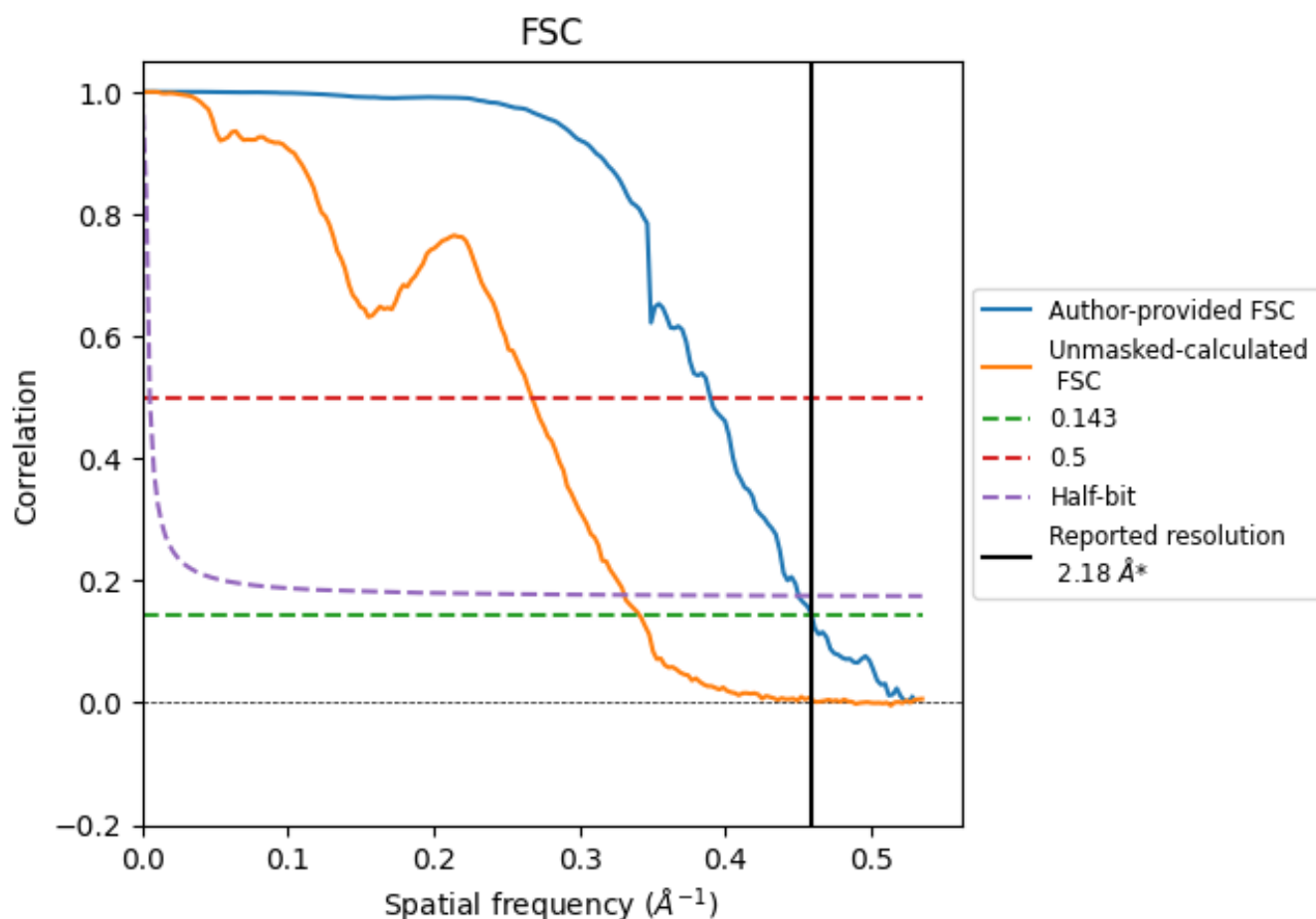


*Reported resolution corresponds to spatial frequency of 0.459 \AA^{-1}

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 0.459 \AA^{-1}

8.2 Resolution estimates [i](#)

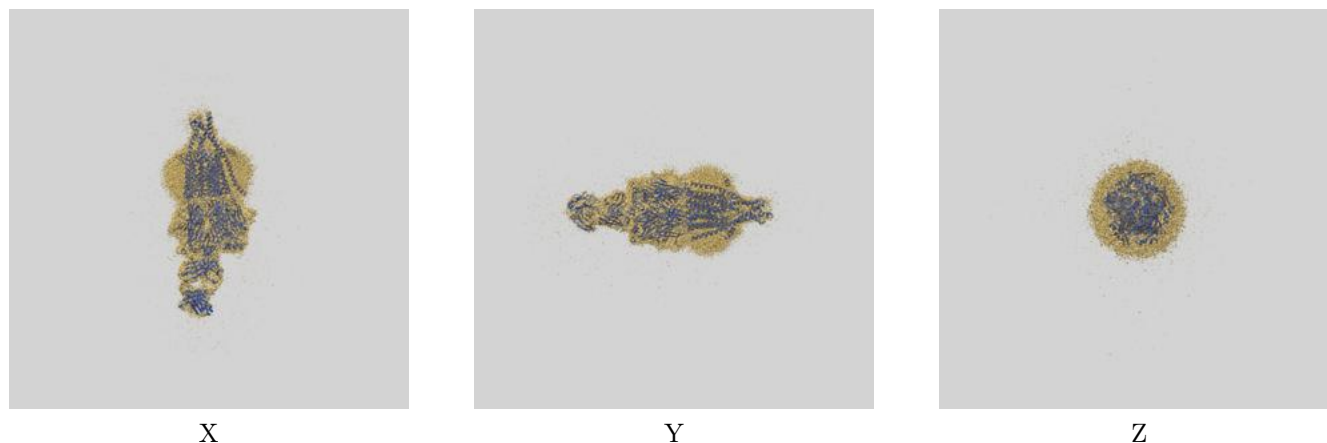
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.18	-	-
Author-provided FSC curve	2.18	2.57	2.22
Unmasked-calculated*	2.93	3.74	3.03

*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 2.93 differs from the reported value 2.18 by more than 10 %

9 Map-model fit [i](#)

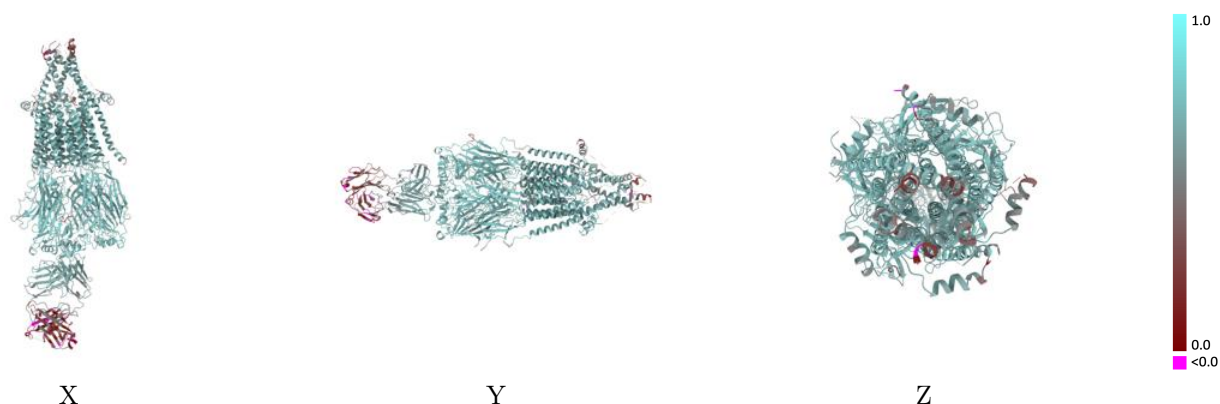
This section contains information regarding the fit between EMDB map EMD-47015 and PDB model 9DMT. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



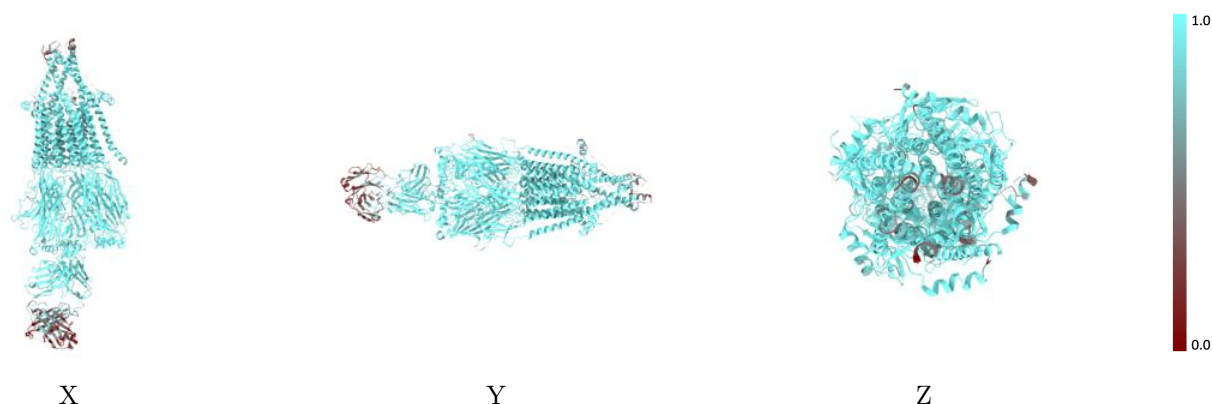
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



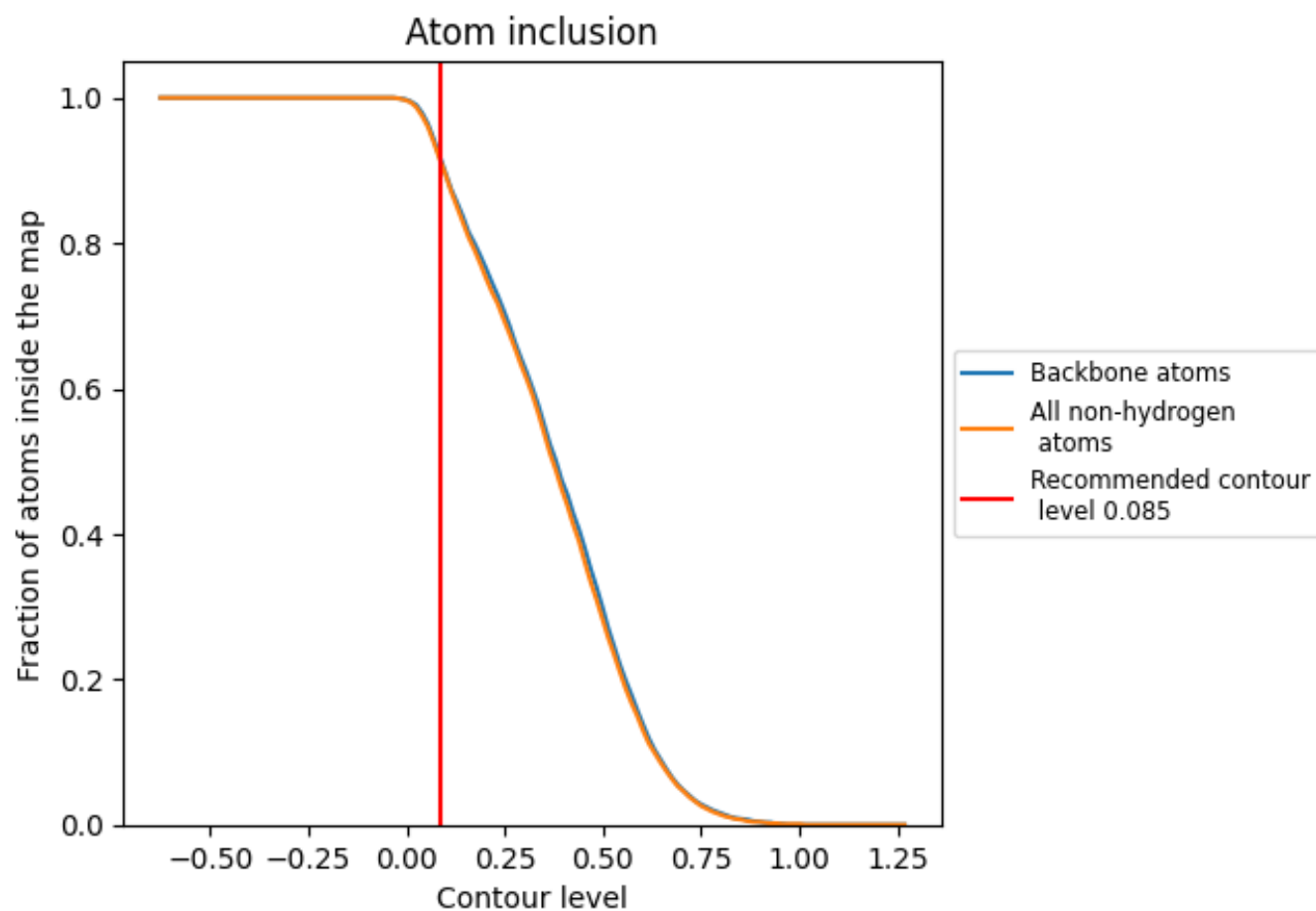
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9150	<div></div> 0.6270
A	<div></div> 0.9570	<div></div> 0.6650
B	<div></div> 0.9470	<div></div> 0.6540
C	<div></div> 0.9570	<div></div> 0.6640
D	<div></div> 0.9570	<div></div> 0.6660
E	<div></div> 0.9650	<div></div> 0.6670
F	<div></div> 0.7160	<div></div> 0.4550
G	<div></div> 0.6790	<div></div> 0.4370
H	<div></div> 0.9840	<div></div> 0.5790
I	<div></div> 0.9840	<div></div> 0.6060
J	<div></div> 0.9020	<div></div> 0.5440
K	<div></div> 0.8190	<div></div> 0.4950
L	<div></div> 0.8360	<div></div> 0.5410

1.0

0.0

<0.0