



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 03:51 PM UTC

PDB ID : 9H9E / pdb_00009h9e
EMDB ID : EMD-51963
Title : Cryo-EM structure of the human GABAA receptor alpha1 subunit in complex with the assembly factor NACHO/TMEM35A
Authors : Hooda, Y.; Sente, A.; Judy, R.M.; Smalinskaite, L.; Peak-Chew, S.; Naydenova, K.; Malinauskas, T.; Hardwick, S.W.; Chirgadze, D.Y.; Aricescu, A.R.; Hegde, R.S.
Deposited on : 2024-10-30
Resolution : 3.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

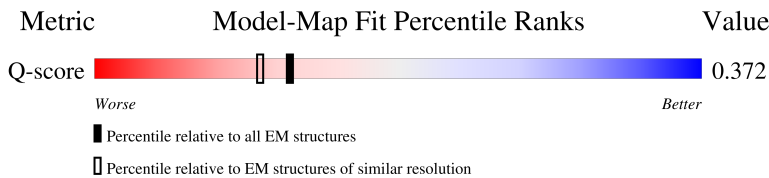
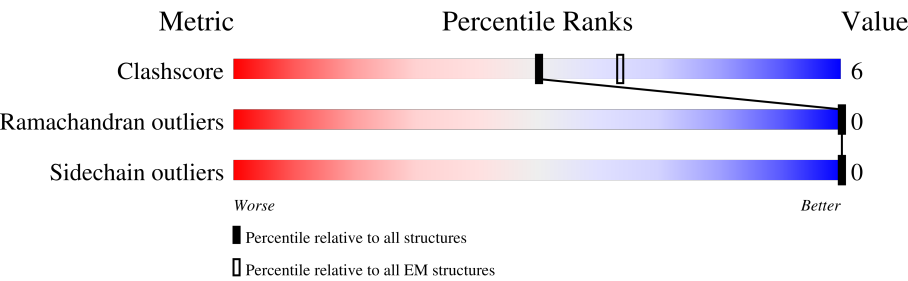
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	484	7% 60% 9% 31%
1	D	484	7% 60% 9% 31%
2	B	187	63% 8% 29%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	C	187	
3	a	5	
3	d	5	

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
6	PGT	A	503	X	-	-	-
6	PGT	D	503	X	-	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16266 atoms, of which 8324 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 Gamma-aminobutyric acid receptor subunit alpha-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	334	Total	C	H	N	O	S	0	0
			5397	1746	2696	453	486	16		
1	D	334	Total	C	H	N	O	S	0	0
			5397	1746	2696	453	486	16		

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-54	MET	-	initiating methionine	UNP P14867
A	-53	GLY	-	expression tag	UNP P14867
A	-52	ILE	-	expression tag	UNP P14867
A	-51	LEU	-	expression tag	UNP P14867
A	-50	PRO	-	expression tag	UNP P14867
A	-49	SER	-	expression tag	UNP P14867
A	-48	PRO	-	expression tag	UNP P14867
A	-47	GLY	-	expression tag	UNP P14867
A	-46	MET	-	expression tag	UNP P14867
A	-45	PRO	-	expression tag	UNP P14867
A	-44	ALA	-	expression tag	UNP P14867
A	-43	LEU	-	expression tag	UNP P14867
A	-42	LEU	-	expression tag	UNP P14867
A	-41	SER	-	expression tag	UNP P14867
A	-40	LEU	-	expression tag	UNP P14867
A	-39	VAL	-	expression tag	UNP P14867
A	-38	SER	-	expression tag	UNP P14867
A	-37	LEU	-	expression tag	UNP P14867
A	-36	LEU	-	expression tag	UNP P14867
A	-35	SER	-	expression tag	UNP P14867
A	-34	VAL	-	expression tag	UNP P14867
A	-33	LEU	-	expression tag	UNP P14867
A	-32	LEU	-	expression tag	UNP P14867
A	-31	MET	-	expression tag	UNP P14867
A	-30	GLY	-	expression tag	UNP P14867
A	-29	CYS	-	expression tag	UNP P14867

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	VAL	-	expression tag	UNP P14867
A	-27	ALA	-	expression tag	UNP P14867
A	-26	GLU	-	expression tag	UNP P14867
A	-25	THR	-	expression tag	UNP P14867
A	-24	GLY	-	expression tag	UNP P14867
A	-23	TRP	-	expression tag	UNP P14867
A	-22	SER	-	expression tag	UNP P14867
A	-21	HIS	-	expression tag	UNP P14867
A	-20	PRO	-	expression tag	UNP P14867
A	-19	GLN	-	expression tag	UNP P14867
A	-18	PHE	-	expression tag	UNP P14867
A	-17	GLU	-	expression tag	UNP P14867
A	-16	LYS	-	expression tag	UNP P14867
A	-15	GLY	-	expression tag	UNP P14867
A	-14	GLY	-	expression tag	UNP P14867
A	-13	GLY	-	expression tag	UNP P14867
A	-12	SER	-	expression tag	UNP P14867
A	-11	GLY	-	expression tag	UNP P14867
A	-10	GLY	-	expression tag	UNP P14867
A	-9	GLY	-	expression tag	UNP P14867
A	-8	SER	-	expression tag	UNP P14867
A	-7	GLY	-	expression tag	UNP P14867
A	-6	GLY	-	expression tag	UNP P14867
A	-5	SER	-	expression tag	UNP P14867
A	-4	ALA	-	expression tag	UNP P14867
A	-3	TRP	-	expression tag	UNP P14867
A	-2	SER	-	expression tag	UNP P14867
A	-1	HIS	-	expression tag	UNP P14867
A	0	PRO	-	expression tag	UNP P14867
A	1	GLN	-	expression tag	UNP P14867
A	2	PHE	-	expression tag	UNP P14867
A	3	GLU	-	expression tag	UNP P14867
A	4	LYS	-	expression tag	UNP P14867
A	5	GLY	-	expression tag	UNP P14867
A	6	GLY	-	expression tag	UNP P14867
A	7	SER	-	expression tag	UNP P14867
A	8	THR	-	expression tag	UNP P14867
A	9	GLY	-	expression tag	UNP P14867
D	-54	MET	-	initiating methionine	UNP P14867
D	-53	GLY	-	expression tag	UNP P14867
D	-52	ILE	-	expression tag	UNP P14867
D	-51	LEU	-	expression tag	UNP P14867

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-50	PRO	-	expression tag	UNP P14867
D	-49	SER	-	expression tag	UNP P14867
D	-48	PRO	-	expression tag	UNP P14867
D	-47	GLY	-	expression tag	UNP P14867
D	-46	MET	-	expression tag	UNP P14867
D	-45	PRO	-	expression tag	UNP P14867
D	-44	ALA	-	expression tag	UNP P14867
D	-43	LEU	-	expression tag	UNP P14867
D	-42	LEU	-	expression tag	UNP P14867
D	-41	SER	-	expression tag	UNP P14867
D	-40	LEU	-	expression tag	UNP P14867
D	-39	VAL	-	expression tag	UNP P14867
D	-38	SER	-	expression tag	UNP P14867
D	-37	LEU	-	expression tag	UNP P14867
D	-36	LEU	-	expression tag	UNP P14867
D	-35	SER	-	expression tag	UNP P14867
D	-34	VAL	-	expression tag	UNP P14867
D	-33	LEU	-	expression tag	UNP P14867
D	-32	LEU	-	expression tag	UNP P14867
D	-31	MET	-	expression tag	UNP P14867
D	-30	GLY	-	expression tag	UNP P14867
D	-29	CYS	-	expression tag	UNP P14867
D	-28	VAL	-	expression tag	UNP P14867
D	-27	ALA	-	expression tag	UNP P14867
D	-26	GLU	-	expression tag	UNP P14867
D	-25	THR	-	expression tag	UNP P14867
D	-24	GLY	-	expression tag	UNP P14867
D	-23	TRP	-	expression tag	UNP P14867
D	-22	SER	-	expression tag	UNP P14867
D	-21	HIS	-	expression tag	UNP P14867
D	-20	PRO	-	expression tag	UNP P14867
D	-19	GLN	-	expression tag	UNP P14867
D	-18	PHE	-	expression tag	UNP P14867
D	-17	GLU	-	expression tag	UNP P14867
D	-16	LYS	-	expression tag	UNP P14867
D	-15	GLY	-	expression tag	UNP P14867
D	-14	GLY	-	expression tag	UNP P14867
D	-13	GLY	-	expression tag	UNP P14867
D	-12	SER	-	expression tag	UNP P14867
D	-11	GLY	-	expression tag	UNP P14867
D	-10	GLY	-	expression tag	UNP P14867
D	-9	GLY	-	expression tag	UNP P14867

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	SER	-	expression tag	UNP P14867
D	-7	GLY	-	expression tag	UNP P14867
D	-6	GLY	-	expression tag	UNP P14867
D	-5	SER	-	expression tag	UNP P14867
D	-4	ALA	-	expression tag	UNP P14867
D	-3	TRP	-	expression tag	UNP P14867
D	-2	SER	-	expression tag	UNP P14867
D	-1	HIS	-	expression tag	UNP P14867
D	0	PRO	-	expression tag	UNP P14867
D	1	GLN	-	expression tag	UNP P14867
D	2	PHE	-	expression tag	UNP P14867
D	3	GLU	-	expression tag	UNP P14867
D	4	LYS	-	expression tag	UNP P14867
D	5	GLY	-	expression tag	UNP P14867
D	6	GLY	-	expression tag	UNP P14867
D	7	SER	-	expression tag	UNP P14867
D	8	THR	-	expression tag	UNP P14867
D	9	GLY	-	expression tag	UNP P14867

- Molecule 2 is a protein called Novel acetylcholine receptor chaperone.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	133	Total	C	H	N	O	S	0	0
			2181	688	1147	177	163	6		
2	C	133	Total	C	H	N	O	S	0	0
			2181	688	1147	177	163	6		

There are 40 discrepancies between the modelled and reference sequences:

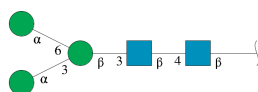
Chain	Residue	Modelled	Actual	Comment	Reference
B	168	GLY	-	expression tag	UNP Q53FP2
B	169	GLY	-	expression tag	UNP Q53FP2
B	170	SER	-	expression tag	UNP Q53FP2
B	171	GLY	-	expression tag	UNP Q53FP2
B	172	GLY	-	expression tag	UNP Q53FP2
B	173	SER	-	expression tag	UNP Q53FP2
B	174	GLY	-	expression tag	UNP Q53FP2
B	175	GLY	-	expression tag	UNP Q53FP2
B	176	SER	-	expression tag	UNP Q53FP2
B	177	GLY	-	expression tag	UNP Q53FP2
B	178	LYS	-	expression tag	UNP Q53FP2
B	179	THR	-	expression tag	UNP Q53FP2

Continued on next page...

Continued from previous page...

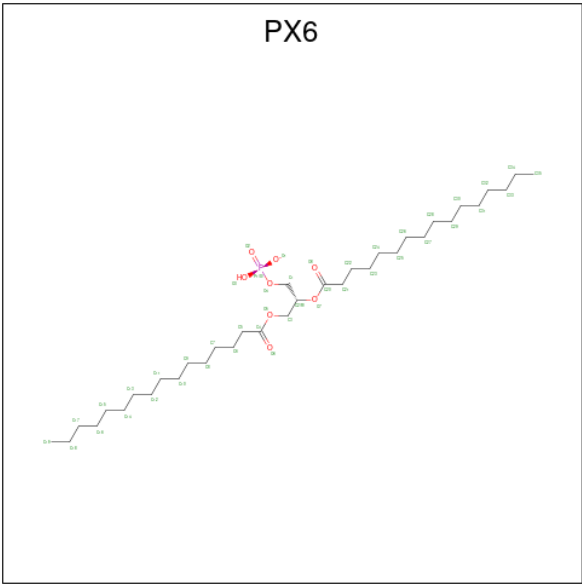
Chain	Residue	Modelled	Actual	Comment	Reference
B	180	GLU	-	expression tag	UNP Q53FP2
B	181	THR	-	expression tag	UNP Q53FP2
B	182	SER	-	expression tag	UNP Q53FP2
B	183	GLN	-	expression tag	UNP Q53FP2
B	184	VAL	-	expression tag	UNP Q53FP2
B	185	ALA	-	expression tag	UNP Q53FP2
B	186	PRO	-	expression tag	UNP Q53FP2
B	187	ALA	-	expression tag	UNP Q53FP2
C	168	GLY	-	expression tag	UNP Q53FP2
C	169	GLY	-	expression tag	UNP Q53FP2
C	170	SER	-	expression tag	UNP Q53FP2
C	171	GLY	-	expression tag	UNP Q53FP2
C	172	GLY	-	expression tag	UNP Q53FP2
C	173	SER	-	expression tag	UNP Q53FP2
C	174	GLY	-	expression tag	UNP Q53FP2
C	175	GLY	-	expression tag	UNP Q53FP2
C	176	SER	-	expression tag	UNP Q53FP2
C	177	GLY	-	expression tag	UNP Q53FP2
C	178	LYS	-	expression tag	UNP Q53FP2
C	179	THR	-	expression tag	UNP Q53FP2
C	180	GLU	-	expression tag	UNP Q53FP2
C	181	THR	-	expression tag	UNP Q53FP2
C	182	SER	-	expression tag	UNP Q53FP2
C	183	GLN	-	expression tag	UNP Q53FP2
C	184	VAL	-	expression tag	UNP Q53FP2
C	185	ALA	-	expression tag	UNP Q53FP2
C	186	PRO	-	expression tag	UNP Q53FP2
C	187	ALA	-	expression tag	UNP Q53FP2

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



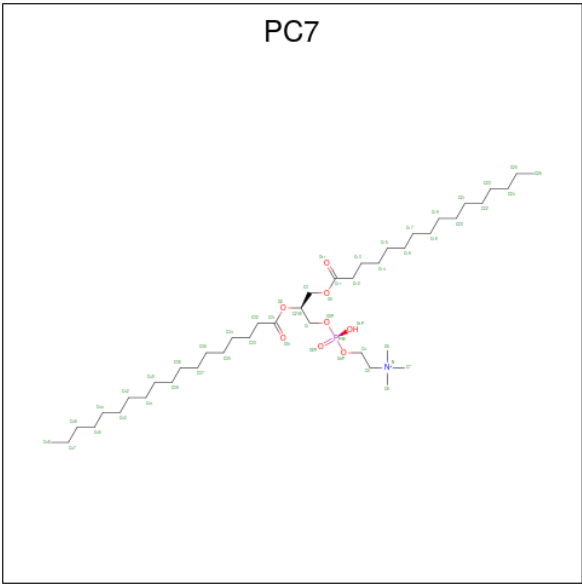
Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	5	Total	C	H	N	O	0	0
			113	34	52	2	25		
3	d	5	Total	C	H	N	O	0	0
			113	34	52	2	25		

- Molecule 4 is 1,2-DIPALMITOYL-SN-GLYCERO-3-PHOSPHATE (CCD ID: PX6) (formula: C₃₅H₆₈O₈P).



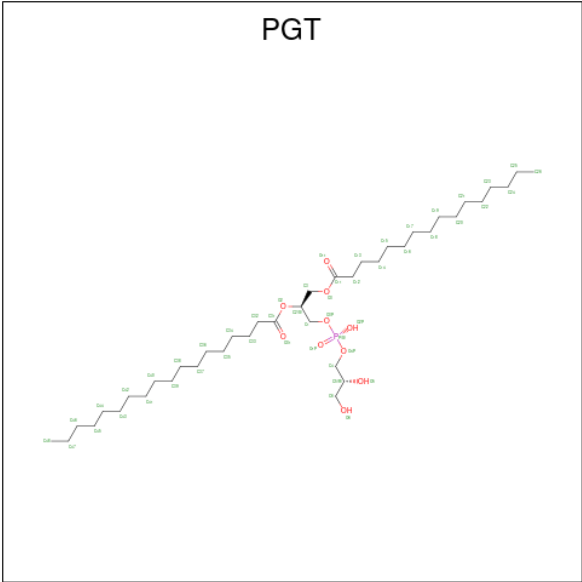
Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	O	P	
4	A	1	111	35	67	8	1	0
4	D	1	111	35	67	8	1	0

- Molecule 5 is (7S)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSAN-1-AMINIUM 4-OXIDE (CCD ID: PC7) (formula: C₄₂H₈₅NO₈P).



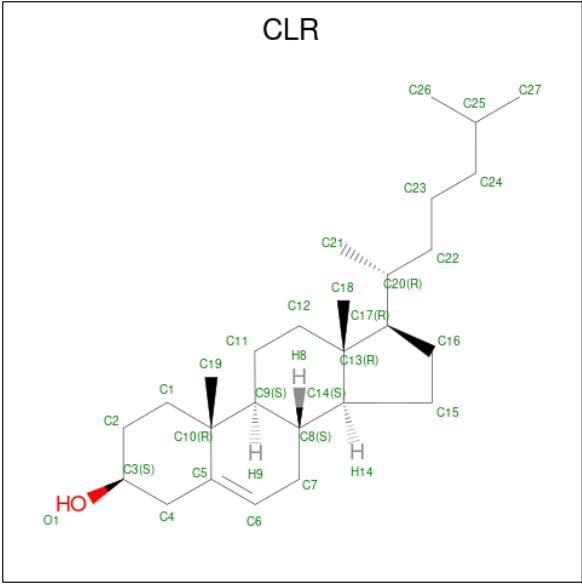
Mol	Chain	Residues	Atoms						AltConf
5	A	1	Total 132	C 42	H 80	N 1	O 8	P 1	0
5	D	1	Total 132	C 42	H 80	N 1	O 8	P 1	0

- Molecule 6 is (1S)-2-{{[(2R)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL STEARATE (CCD ID: PGT) (formula: C₄₀H₇₉O₁₀P).

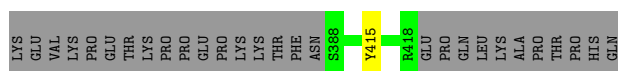


Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	H	O	P	0
			125	40	74	10	1	
6	D	1	Total	C	H	O	P	0
			125	40	74	10	1	

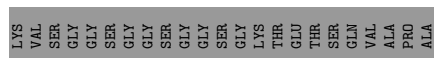
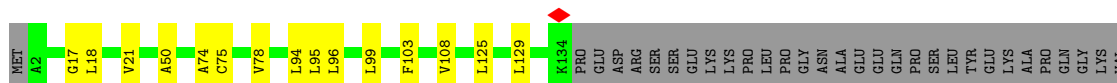
- Molecule 7 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



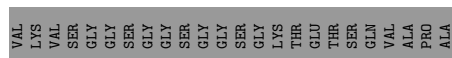
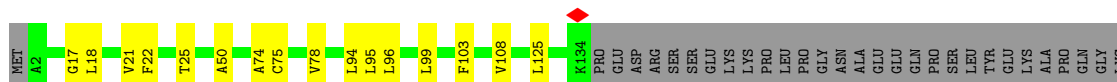
Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	H	O	0
			74	27	46	1	
7	D	1	Total	C	H	O	0
			74	27	46	1	



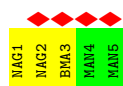
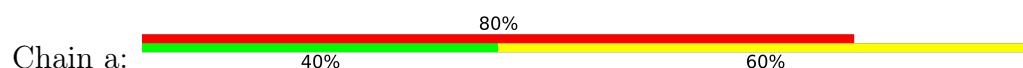
- Molecule 2: Novel acetylcholine receptor chaperone



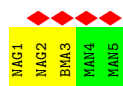
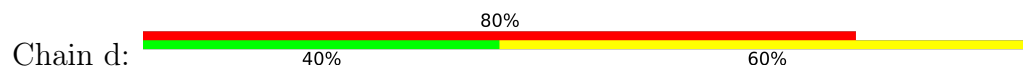
- Molecule 2: Novel acetylcholine receptor chaperone



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	304241	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	11.087	Depositor
Minimum map value	-8.331	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.112	Depositor
Recommended contour level	0.811	Depositor
Map size (Å)	375.232, 375.232, 375.232	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.46575, 1.46575, 1.46575	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: PC7, PGT, NAG, MAN, CLR, BMA, PX6

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	0/2768	0.25	0/3761
1	D	0.11	0/2768	0.25	0/3761
2	B	0.12	0/1053	0.19	0/1422
2	C	0.12	0/1053	0.19	0/1422
All	All	0.11	0/7642	0.23	0/10366

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	2701	2696	2694	33	0
1	D	2701	2696	2694	36	0
2	B	1034	1147	1146	14	0
2	C	1034	1147	1146	13	0
3	a	61	52	52	2	0
3	d	61	52	52	2	0
4	A	44	67	68	0	0
4	D	44	67	68	0	0
5	A	52	80	84	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	52	80	84	3	0
6	A	51	74	78	0	0
6	D	51	74	78	0	0
7	A	28	46	46	1	0
7	D	28	46	46	1	0
All	All	7942	8324	8336	91	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 6.

All (91) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:LEU:HD21	1:D:240:LEU:HD21	1.72	0.70
1:A:272:SER:HB3	1:D:228:ILE:HG22	1.75	0.68
1:D:118:LEU:HD21	1:D:120:ARG:NE	2.10	0.67
1:A:118:LEU:HD21	1:A:120:ARG:NE	2.10	0.67
2:B:95:LEU:HB3	1:D:302:ILE:HD12	1.76	0.67
1:A:236:MET:CE	5:A:502:PC7:H402	2.26	0.65
1:D:236:MET:CE	5:D:502:PC7:H402	2.25	0.65
1:A:240:LEU:O	1:A:243:VAL:HG22	1.97	0.65
1:A:236:MET:HE3	5:A:502:PC7:H402	1.80	0.64
1:D:175:PRO:O	1:D:198:VAL:HG11	1.98	0.64
1:A:175:PRO:O	1:A:198:VAL:HG11	1.98	0.64
1:D:240:LEU:O	1:D:243:VAL:HG22	1.97	0.64
1:D:236:MET:HE3	5:D:502:PC7:H402	1.82	0.62
1:D:30:LEU:HB2	1:D:34:LEU:HD13	1.83	0.60
2:B:50:ALA:O	7:D:504:CLR:H193	2.01	0.60
1:A:30:LEU:HB2	1:A:34:LEU:HD13	1.83	0.60
1:A:228:ILE:HG22	1:D:272:SER:HB3	1.84	0.59
1:A:302:ILE:HD12	2:C:95:LEU:HB3	1.85	0.58
1:A:82:THR:O	1:A:123:GLU:N	2.37	0.57
1:D:82:THR:O	1:D:123:GLU:N	2.37	0.57
1:A:114:MET:SD	1:A:114:MET:N	2.78	0.57
2:C:99:LEU:O	2:C:103:PHE:N	2.37	0.57
1:D:114:MET:N	1:D:114:MET:SD	2.78	0.57
2:B:99:LEU:O	2:B:103:PHE:N	2.37	0.56
1:D:90:MET:HE3	1:D:94:ILE:HD11	1.89	0.55
1:A:94:ILE:HG22	1:A:95:TRP:H	1.71	0.55
1:A:90:MET:HE3	1:A:94:ILE:HD11	1.89	0.54
2:C:95:LEU:HD23	2:C:125:LEU:HD23	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:504:CLR:H193	2:C:50:ALA:O	2.08	0.53
1:D:94:ILE:HG22	1:D:95:TRP:H	1.71	0.53
2:B:95:LEU:HD23	2:B:125:LEU:HD23	1.89	0.53
1:D:15:PHE:CE2	1:D:19:LEU:HD11	2.44	0.52
1:A:15:PHE:CE2	1:A:19:LEU:HD11	2.44	0.52
2:C:108:VAL:HG12	2:C:108:VAL:O	2.09	0.52
1:A:94:ILE:HG22	1:A:95:TRP:N	2.25	0.52
1:A:118:LEU:HD21	1:A:120:ARG:HE	1.75	0.52
1:A:175:PRO:C	1:A:198:VAL:HG11	2.35	0.52
1:A:110:HIS:HA	3:a:1:NAG:H82	1.92	0.51
1:D:94:ILE:HG22	1:D:95:TRP:N	2.25	0.51
2:B:108:VAL:O	2:B:108:VAL:HG12	2.09	0.51
1:D:110:HIS:HA	3:d:1:NAG:H82	1.92	0.51
1:D:42:LYS:HB3	1:D:172:THR:HG22	1.93	0.51
1:D:175:PRO:C	1:D:198:VAL:HG11	2.35	0.51
1:D:118:LEU:HD21	1:D:120:ARG:HE	1.74	0.51
1:A:42:LYS:HB3	1:A:172:THR:HG22	1.93	0.50
2:B:129:LEU:HD23	1:D:305:ALA:HB1	1.94	0.50
1:D:86:LEU:HD23	1:D:90:MET:HG2	1.93	0.50
1:A:87:ASN:OD1	1:A:88:ASN:N	2.45	0.49
1:A:86:LEU:HD23	1:A:90:MET:HG2	1.93	0.49
3:a:2:NAG:O4	3:a:3:BMA:C1	2.60	0.49
2:C:96:LEU:O	2:C:96:LEU:HD23	2.13	0.49
3:d:2:NAG:O4	3:d:3:BMA:C1	2.60	0.49
1:A:99:THR:OG1	1:A:169:TYR:OH	2.23	0.49
1:A:280:VAL:HG21	1:A:282:TYR:CZ	2.48	0.49
2:B:96:LEU:O	2:B:96:LEU:HD23	2.13	0.49
1:A:121:ILE:HD12	1:A:121:ILE:N	2.28	0.48
1:D:87:ASN:OD1	1:D:88:ASN:N	2.45	0.48
2:C:74:ALA:O	2:C:78:VAL:HG23	2.13	0.48
1:D:121:ILE:N	1:D:121:ILE:HD12	2.28	0.48
1:D:12:THR:O	1:D:16:THR:HG23	2.15	0.47
1:D:280:VAL:HG21	1:D:282:TYR:CZ	2.48	0.47
2:B:74:ALA:O	2:B:78:VAL:HG23	2.13	0.47
1:A:12:THR:O	1:A:16:THR:HG23	2.15	0.46
2:B:75:CYS:HB2	2:B:94:LEU:HD21	1.97	0.46
2:B:103:PHE:CD1	1:D:291:ALA:HB1	2.50	0.46
1:D:32:PRO:O	1:D:39:THR:OG1	2.34	0.45
2:C:94:LEU:HB2	2:C:125:LEU:HD21	1.98	0.45
1:A:32:PRO:O	1:A:39:THR:OG1	2.35	0.45
2:C:75:CYS:HB2	2:C:94:LEU:HD21	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:VAL:O	1:A:179:VAL:HG13	2.17	0.45
1:A:30:LEU:HD13	1:A:34:LEU:HD22	1.99	0.44
2:C:18:LEU:C	2:C:18:LEU:HD23	2.42	0.44
2:B:94:LEU:HB2	2:B:125:LEU:HD21	1.98	0.44
1:D:236:MET:HE1	5:D:502:PC7:H402	1.96	0.44
1:D:270:SER:OG	1:D:274:ARG:NH2	2.51	0.44
2:B:18:LEU:C	2:B:18:LEU:HD23	2.42	0.44
1:D:285:ALA:HB2	1:D:415:TYR:CE2	2.53	0.44
1:D:30:LEU:HD13	1:D:34:LEU:HD22	1.99	0.43
1:D:179:VAL:HG13	1:D:179:VAL:O	2.17	0.43
1:A:285:ALA:HB2	1:A:415:TYR:CE2	2.53	0.43
2:C:22:PHE:O	2:C:25:THR:OG1	2.35	0.42
1:A:270:SER:OG	1:A:274:ARG:NH2	2.51	0.41
1:D:237:THR:HG21	1:D:266:MET:SD	2.61	0.41
2:C:94:LEU:CB	2:C:125:LEU:HD21	2.51	0.41
2:B:94:LEU:CB	2:B:125:LEU:HD21	2.51	0.40
1:D:156:LYS:HG2	1:D:214:THR:HG22	2.02	0.40
1:A:237:THR:HG21	1:A:266:MET:SD	2.61	0.40
2:B:17:GLY:O	2:B:21:VAL:HG12	2.21	0.40
1:D:15:PHE:CZ	1:D:19:LEU:HD11	2.56	0.40
1:A:15:PHE:CZ	1:A:19:LEU:HD11	2.56	0.40
2:C:17:GLY:O	2:C:21:VAL:HG12	2.21	0.40

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	330/484 (68%)	323 (98%)	7 (2%)	0	100	100
1	D	330/484 (68%)	323 (98%)	7 (2%)	0	100	100
2	B	131/187 (70%)	130 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	131/187 (70%)	130 (99%)	1 (1%)	0	100	100
All	All	922/1342 (69%)	906 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	299/419 (71%)	299 (100%)	0	100	100
1	D	299/419 (71%)	299 (100%)	0	100	100
2	B	112/153 (73%)	112 (100%)	0	100	100
2	C	112/153 (73%)	112 (100%)	0	100	100
All	All	822/1144 (72%)	822 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	91	ASN
2	C	91	ASN
1	D	229	GLN
1	D	308	ASN

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 ⓘ

10 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	$\# Z > 2$
3	NAG	a	1	1,3	14,14,15	0.23	0	17,19,21	0.51	0
3	NAG	a	2	3	14,14,15	0.24	0	17,19,21	0.50	0
3	BMA	a	3	3	11,11,12	0.18	0	15,15,17	0.35	0
3	MAN	a	4	3	11,11,12	0.18	0	15,15,17	0.36	0
3	MAN	a	5	3	11,11,12	0.18	0	15,15,17	0.36	0
3	NAG	d	1	1,3	14,14,15	0.23	0	17,19,21	0.51	0
3	NAG	d	2	3	14,14,15	0.24	0	17,19,21	0.50	0
3	BMA	d	3	3	11,11,12	0.18	0	15,15,17	0.34	0
3	MAN	d	4	3	11,11,12	0.18	0	15,15,17	0.36	0
3	MAN	d	5	3	11,11,12	0.18	0	15,15,17	0.36	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
3	NAG	a	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	a	2	3	-	0/6/23/26	0/1/1/1
3	BMA	a	3	3	-	0/2/19/22	0/1/1/1
3	MAN	a	4	3	-	1/2/19/22	0/1/1/1
3	MAN	a	5	3	-	0/2/19/22	0/1/1/1
3	NAG	d	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	d	2	3	-	0/6/23/26	0/1/1/1
3	BMA	d	3	3	-	0/2/19/22	0/1/1/1
3	MAN	d	4	3	-	1/2/19/22	0/1/1/1
3	MAN	d	5	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

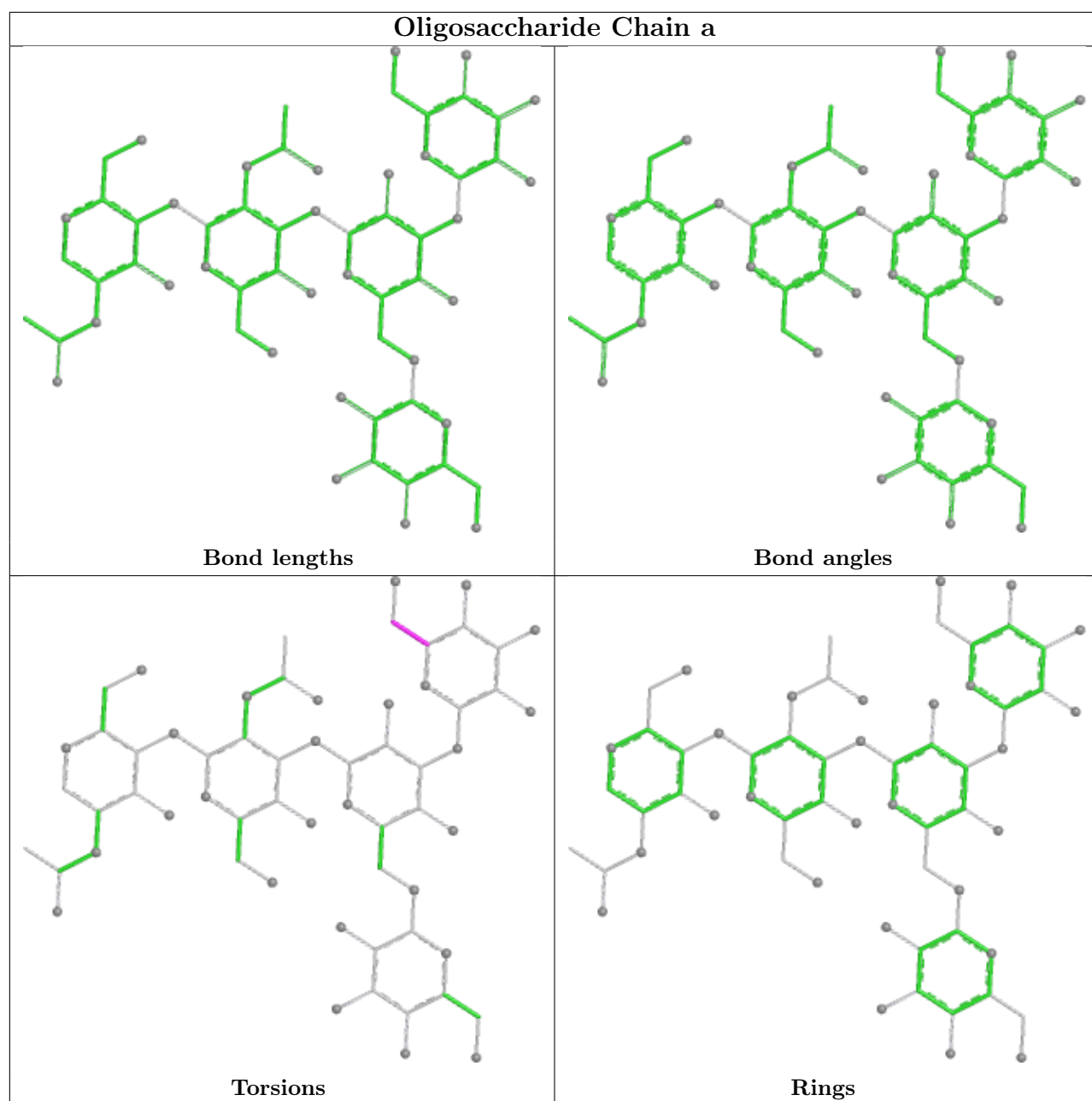
Mol	Chain	Res	Type	Atoms
3	a	4	MAN	O5-C5-C6-O6
3	d	4	MAN	O5-C5-C6-O6

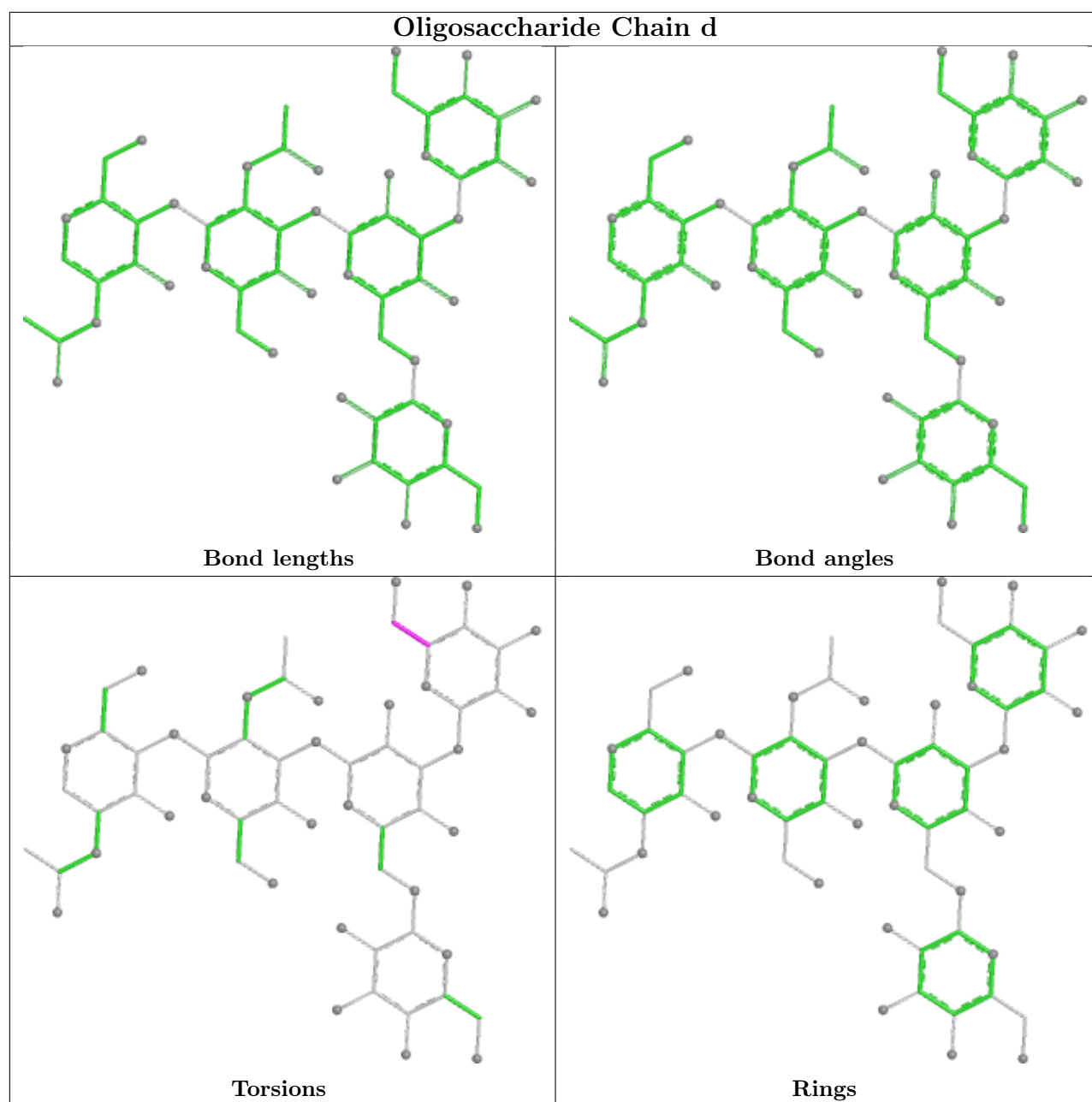
There are no ring outliers.

6 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	d	1	NAG	1	0
3	a	1	NAG	1	0
3	a	3	BMA	1	0
3	d	2	NAG	1	0
3	a	2	NAG	1	0
3	d	3	BMA	1	0

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](#)

8 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
6	PGT	D	503	-	50,50,50	0.40	0	53,56,56	0.34	0
7	CLR	A	504	-	31,31,31	0.14	0	48,48,48	0.28	0
6	PGT	A	503	-	50,50,50	0.40	0	53,56,56	0.34	0
5	PC7	D	502	-	51,51,51	0.41	0	57,59,59	0.45	0
7	CLR	D	504	-	31,31,31	0.14	0	48,48,48	0.28	0
5	PC7	A	502	-	51,51,51	0.41	0	57,59,59	0.45	0
4	PX6	D	501	-	43,43,43	0.28	0	46,48,48	0.29	0
4	PX6	A	501	-	43,43,43	0.28	0	46,48,48	0.29	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
6	PGT	D	503	-	1/1/5/5	13/55/55/55	-
7	CLR	A	504	-	-	4/10/68/68	0/4/4/4
6	PGT	A	503	-	1/1/5/5	13/55/55/55	-
5	PC7	D	502	-	-	11/55/55/55	-
7	CLR	D	504	-	-	4/10/68/68	0/4/4/4
5	PC7	A	502	-	-	11/55/55/55	-
4	PX6	D	501	-	-	2/45/45/45	-
4	PX6	A	501	-	-	2/45/45/45	-

There are no bond length outliers.

There are no bond angle outliers.

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	503	PGT	C2
6	D	503	PGT	C2

All (60) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	PX6	O7-C2-C3-O5
4	D	501	PX6	O7-C2-C3-O5
5	A	502	PC7	O2-C2-C3-O3
5	A	502	PC7	C1-O3P-P-O1P

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	A	502	PC7	C1-O3P-P-O4P
5	A	502	PC7	C4-O4P-P-O3P
5	A	502	PC7	C4-O4P-P-O1P
5	D	502	PC7	O2-C2-C3-O3
5	D	502	PC7	C1-O3P-P-O1P
5	D	502	PC7	C1-O3P-P-O4P
5	D	502	PC7	C4-O4P-P-O3P
5	D	502	PC7	C4-O4P-P-O1P
6	A	503	PGT	C1-O3P-P-O2P
6	A	503	PGT	C1-O3P-P-O4P
6	D	503	PGT	C1-O3P-P-O2P
6	D	503	PGT	C1-O3P-P-O4P
7	A	504	CLR	C13-C17-C20-C22
7	D	504	CLR	C13-C17-C20-C22
7	A	504	CLR	C16-C17-C20-C21
7	D	504	CLR	C16-C17-C20-C21
7	A	504	CLR	C16-C17-C20-C22
7	D	504	CLR	C16-C17-C20-C22
6	A	503	PGT	C37-C38-C39-C40
6	D	503	PGT	C37-C38-C39-C40
6	A	503	PGT	C16-C17-C18-C19
6	D	503	PGT	C16-C17-C18-C19
5	A	502	PC7	C38-C39-C40-C41
5	D	502	PC7	C38-C39-C40-C41
5	A	502	PC7	C37-C38-C39-C40
5	D	502	PC7	C37-C38-C39-C40
4	A	501	PX6	C1-C2-C3-O5
4	D	501	PX6	C1-C2-C3-O5
6	A	503	PGT	C39-C40-C41-C42
6	D	503	PGT	C39-C40-C41-C42
5	A	502	PC7	C1-C2-C3-O3
5	D	502	PC7	C1-C2-C3-O3
5	A	502	PC7	C39-C40-C41-C42
5	D	502	PC7	C39-C40-C41-C42
6	A	503	PGT	O3P-C1-C2-O2
6	D	503	PGT	O3P-C1-C2-O2
6	A	503	PGT	O3P-C1-C2-C3
6	D	503	PGT	O3P-C1-C2-C3
7	A	504	CLR	C13-C17-C20-C21
7	D	504	CLR	C13-C17-C20-C21
5	A	502	PC7	O4P-C4-C5-N
5	D	502	PC7	O4P-C4-C5-N

Continued on next page...

Continued from previous page...

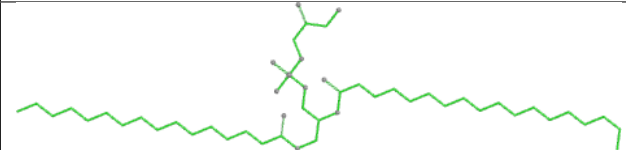
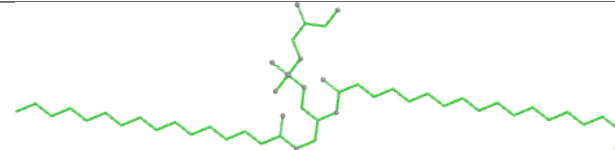
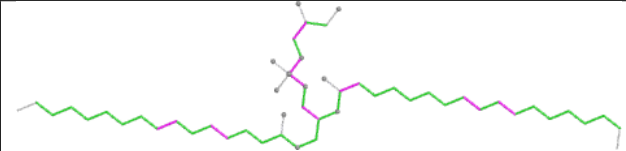
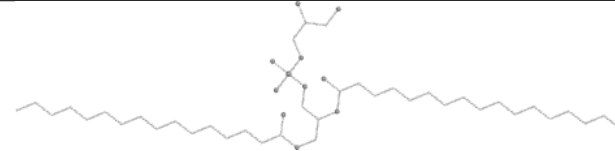
Mol	Chain	Res	Type	Atoms
6	A	503	PGT	C4-O4P-P-O3P
6	A	503	PGT	C4-O4P-P-O1P
6	A	503	PGT	C4-O4P-P-O2P
6	D	503	PGT	C4-O4P-P-O3P
6	D	503	PGT	C4-O4P-P-O1P
6	D	503	PGT	C4-O4P-P-O2P
6	A	503	PGT	C13-C14-C15-C16
6	D	503	PGT	C13-C14-C15-C16
6	A	503	PGT	O2-C31-C32-C33
6	D	503	PGT	O2-C31-C32-C33
6	A	503	PGT	O4P-C4-C5-O5
6	D	503	PGT	O4P-C4-C5-O5
5	A	502	PC7	C1-C2-O2-C31
5	D	502	PC7	C1-C2-O2-C31

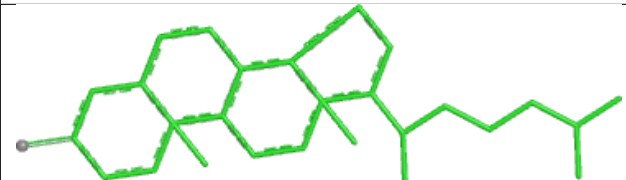
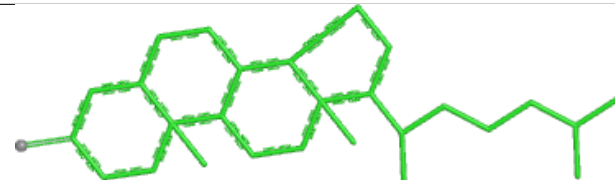
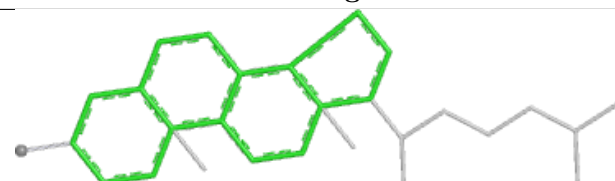
There are no ring outliers.

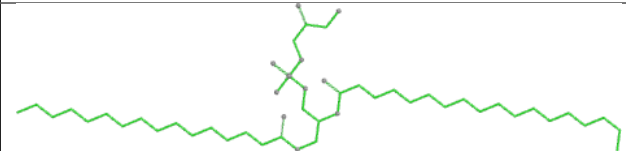
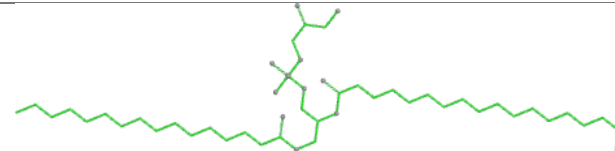
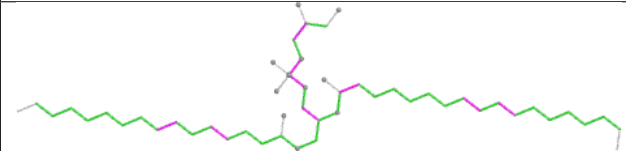
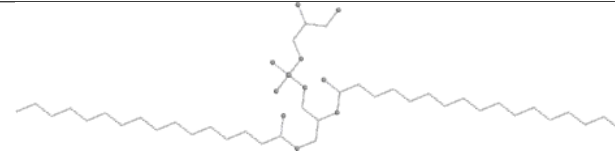
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	504	CLR	1	0
5	D	502	PC7	3	0
7	D	504	CLR	1	0
5	A	502	PC7	2	0

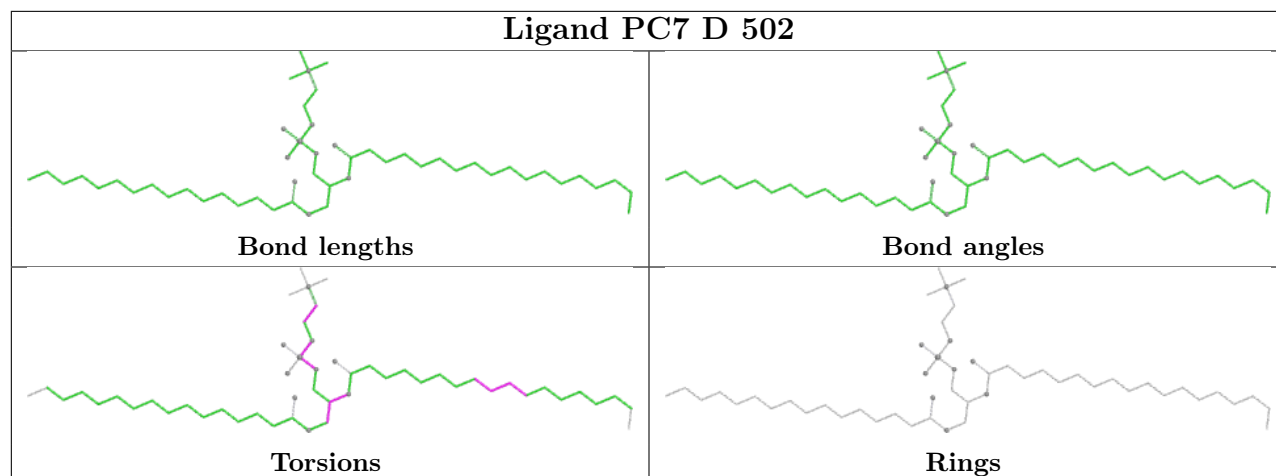
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand PGT D 503	
	
Bond lengths	Bond angles
	
Torsions	Rings

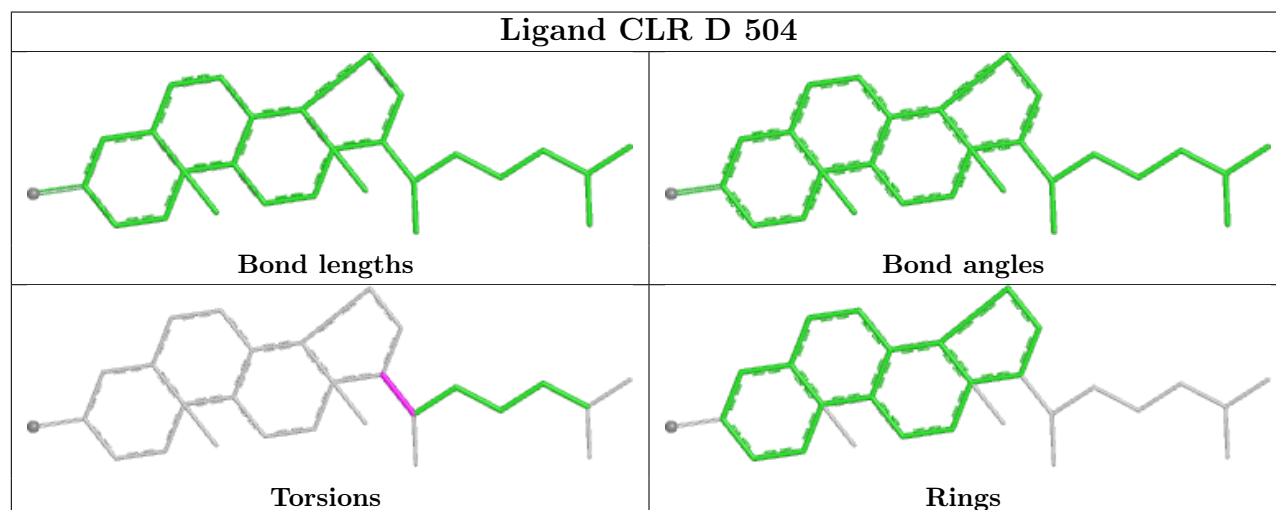
Ligand CLR A 504	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PGT A 503	
	
Bond lengths	Bond angles
	
Torsions	Rings

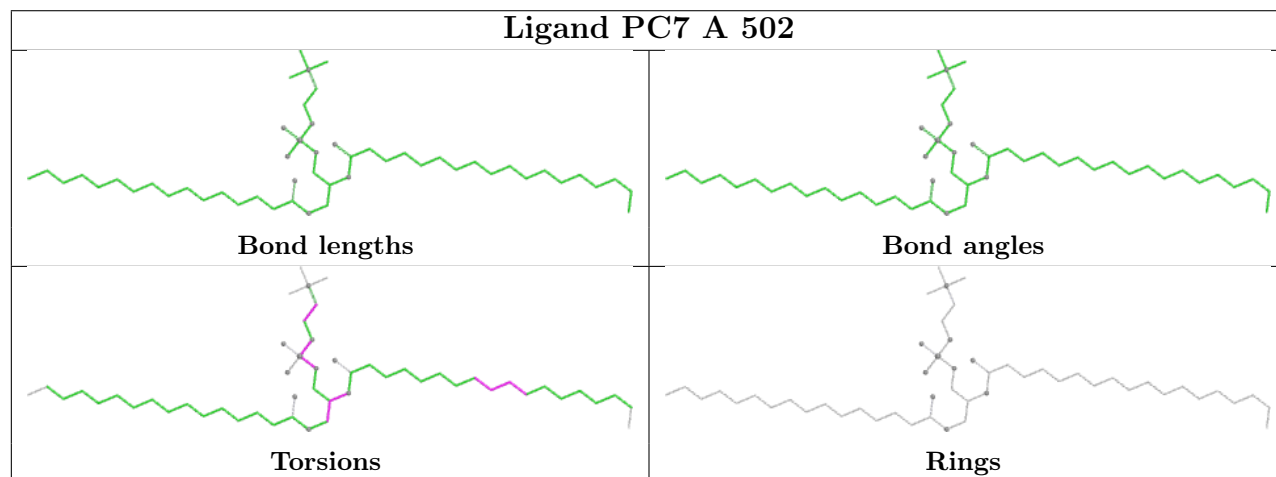
Ligand PC7 D 502

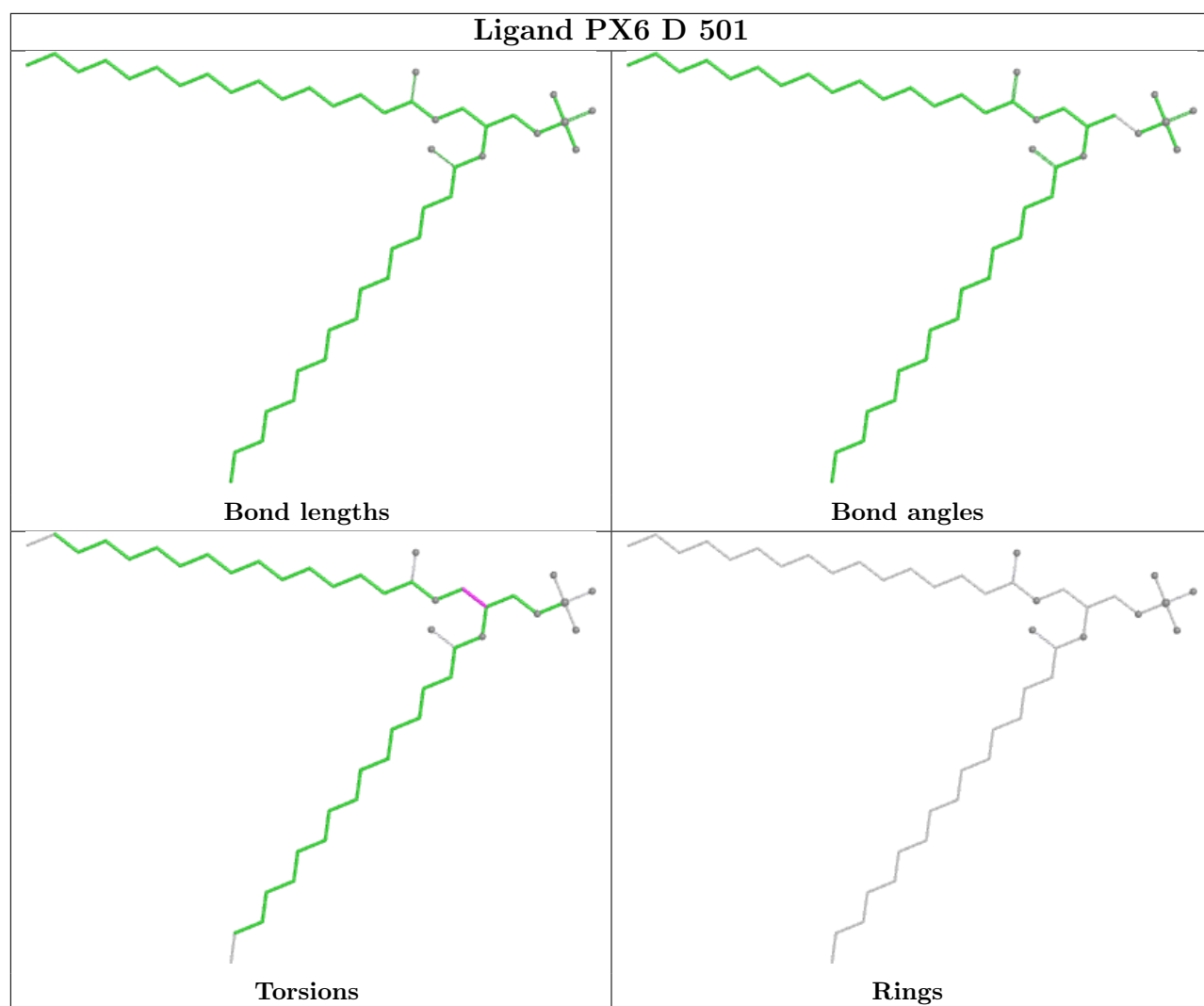


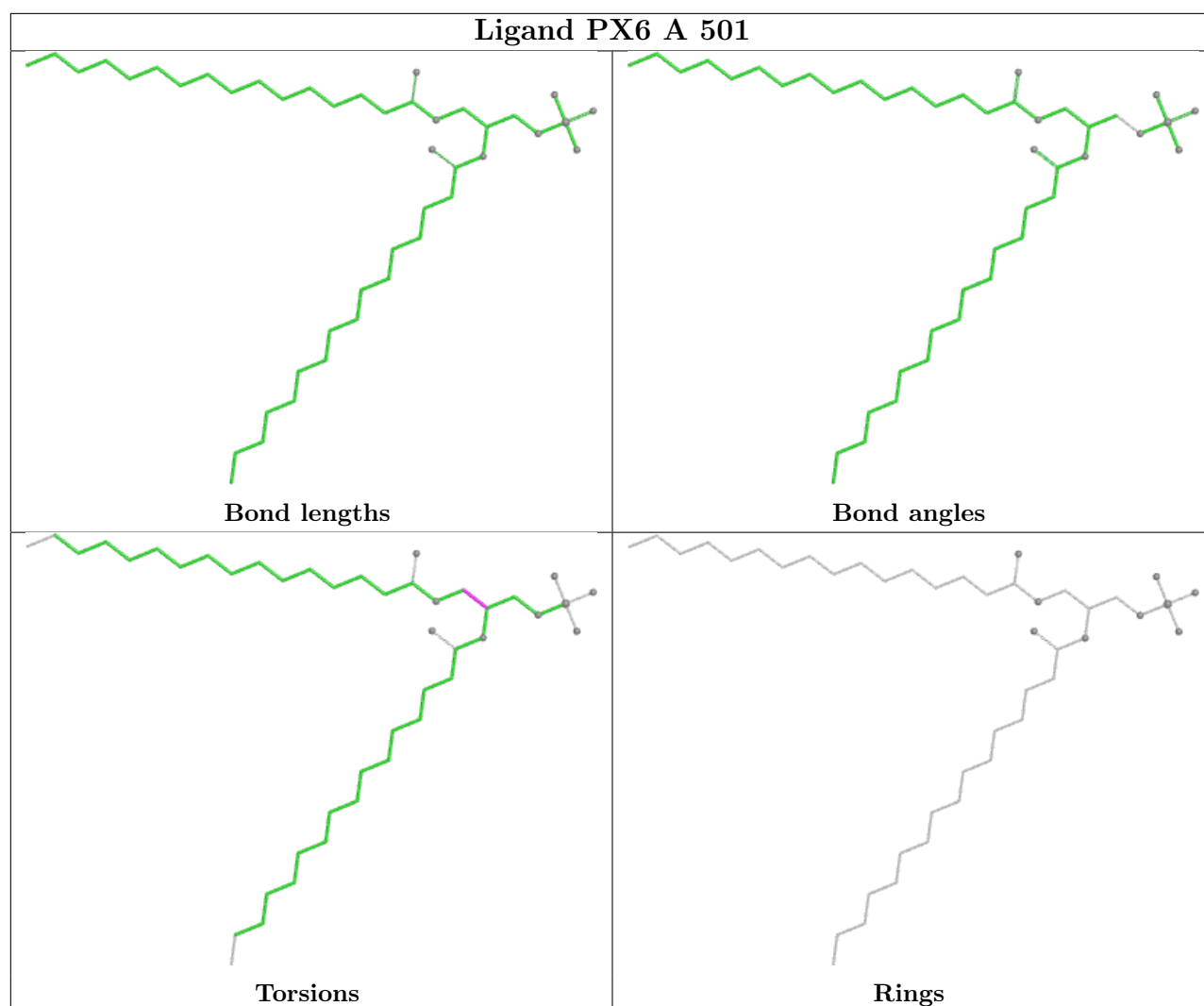
Ligand CLR D 504



Ligand PC7 A 502







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.

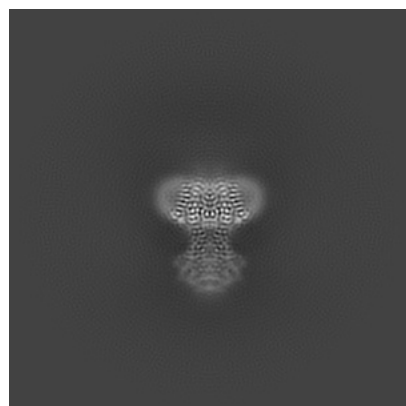
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51963. These allow visual inspection of the internal detail of the map and identification of artifacts.

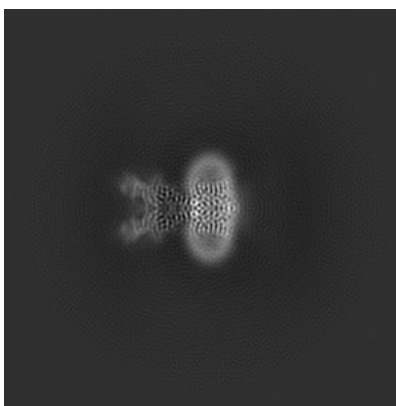
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

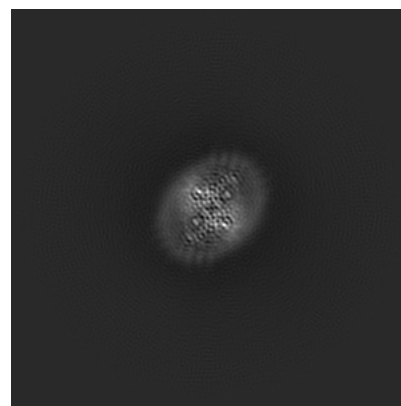
6.1.1 Primary map



X

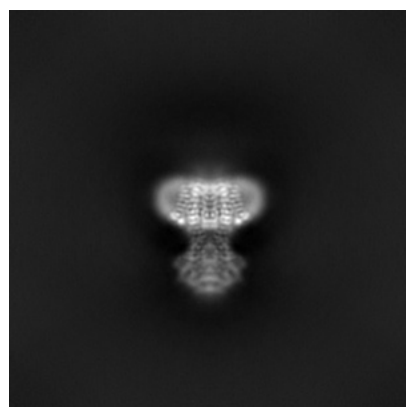


Y

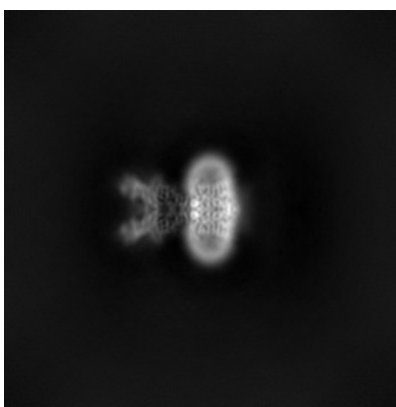


Z

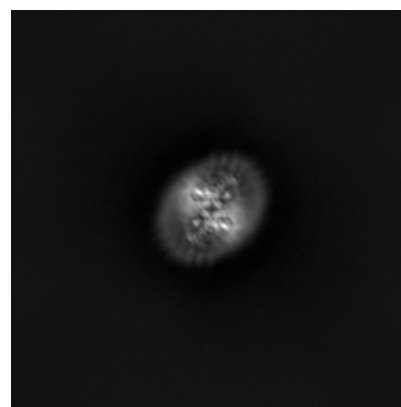
6.1.2 Raw map



X



Y

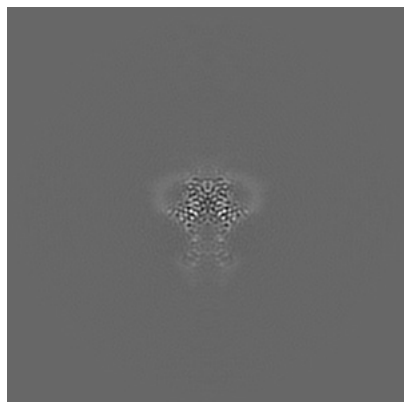


Z

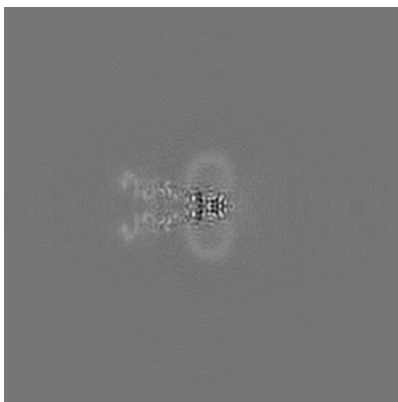
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

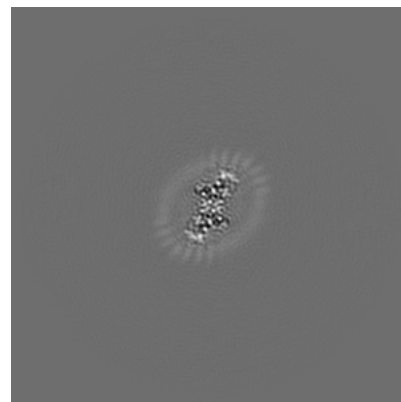
6.2.1 Primary map



X Index: 128

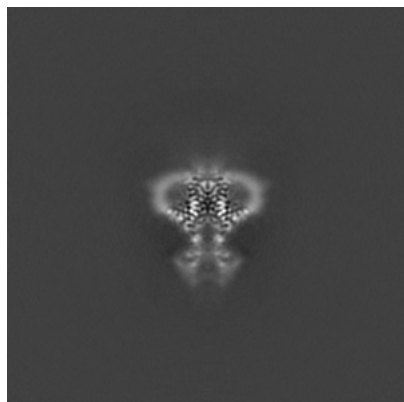


Y Index: 128

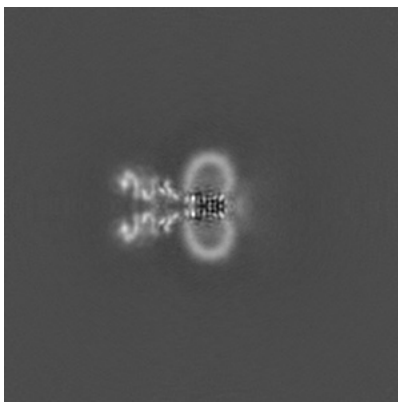


Z Index: 128

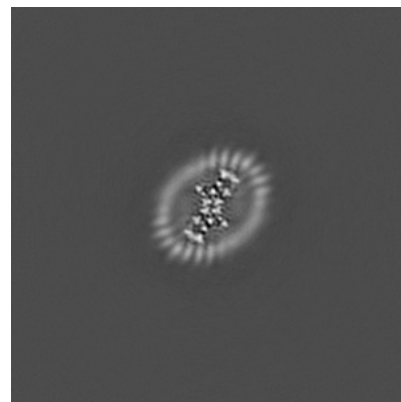
6.2.2 Raw map



X Index: 128



Y Index: 128

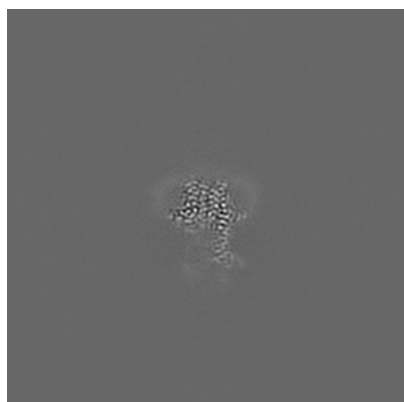


Z Index: 128

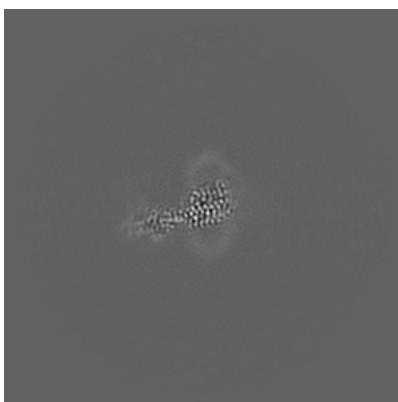
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

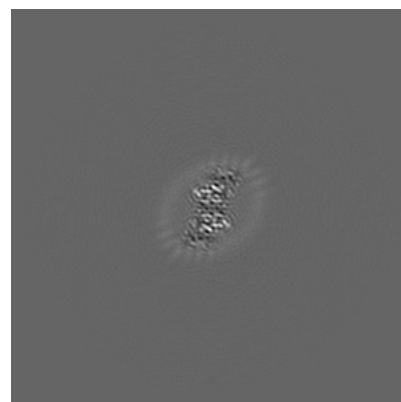
6.3.1 Primary map



X Index: 125

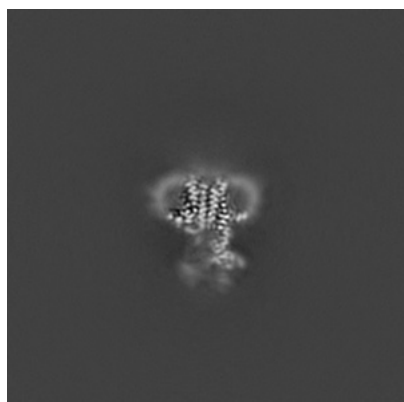


Y Index: 138

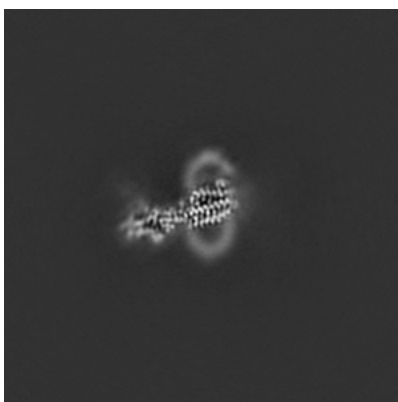


Z Index: 126

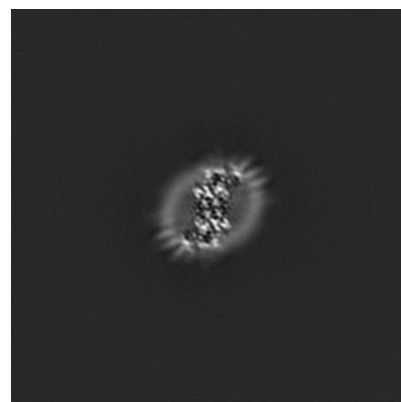
6.3.2 Raw map



X Index: 125



Y Index: 138

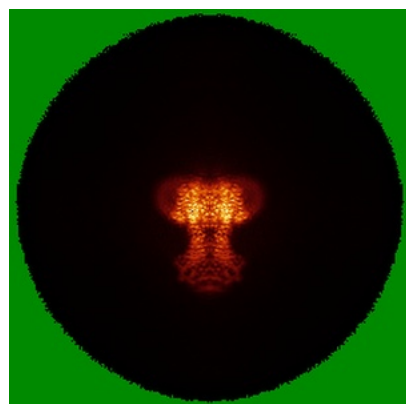


Z Index: 123

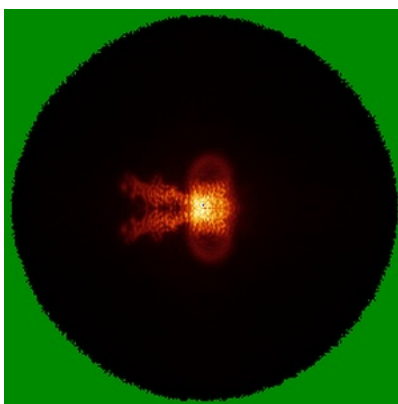
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

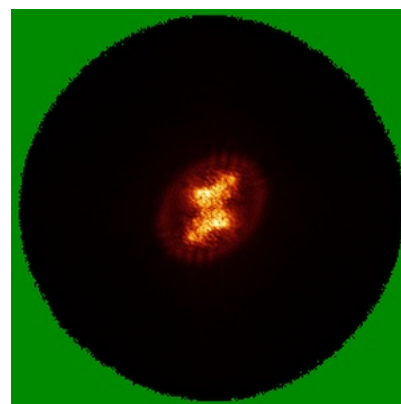
6.4.1 Primary map



X

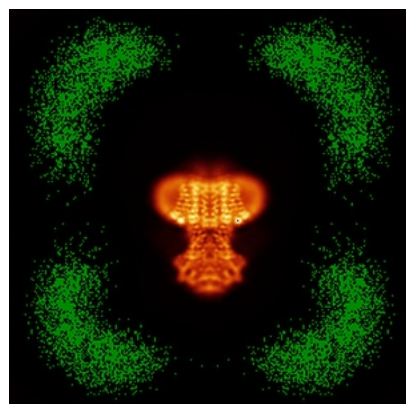


Y

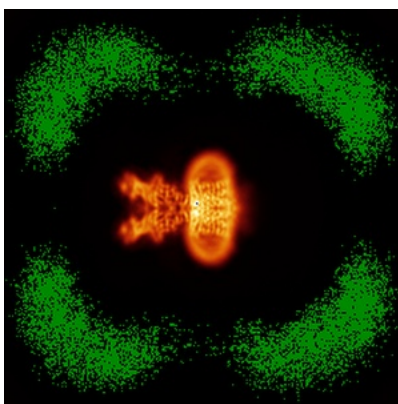


Z

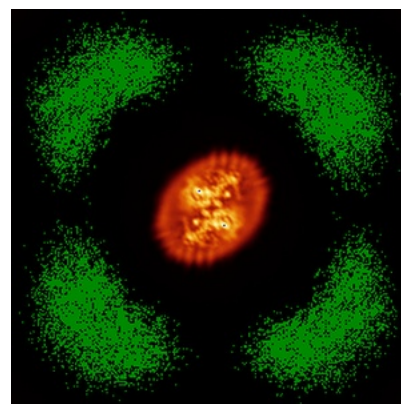
6.4.2 Raw map



X



Y

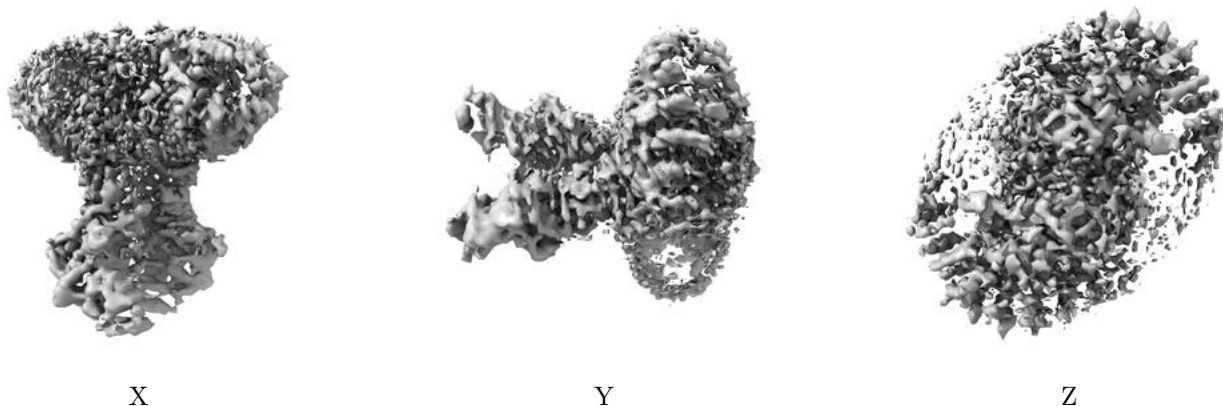


Z

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.

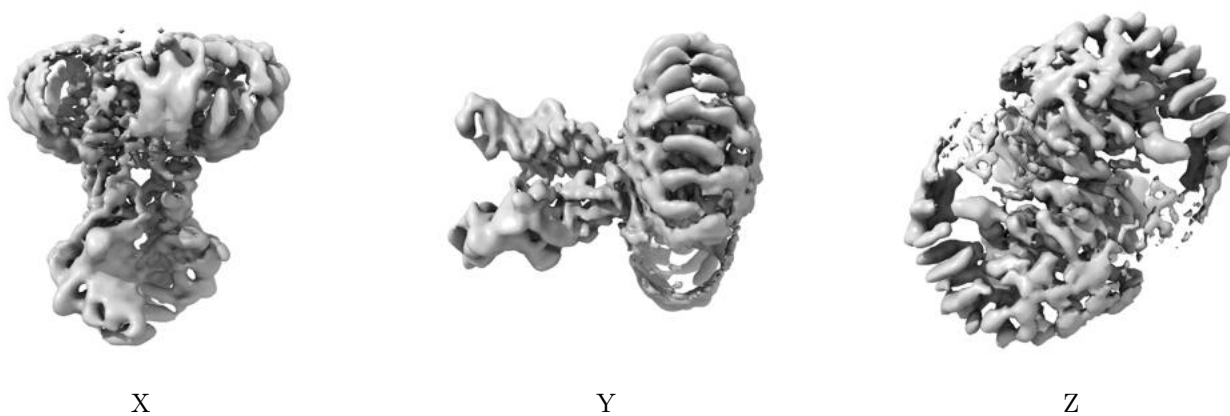
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.811. 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.

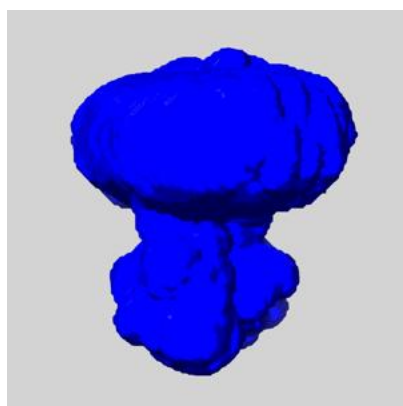
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

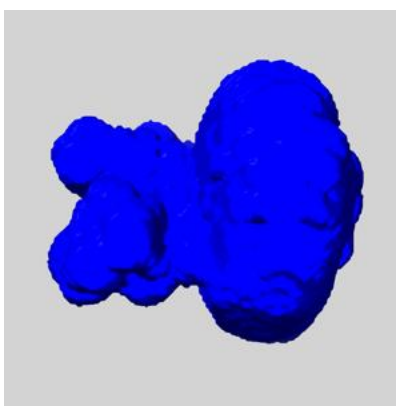
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

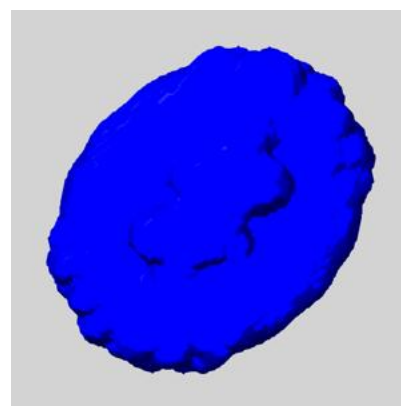
6.6.1 emd_51963_msk_1.map [i](#)



X



Y

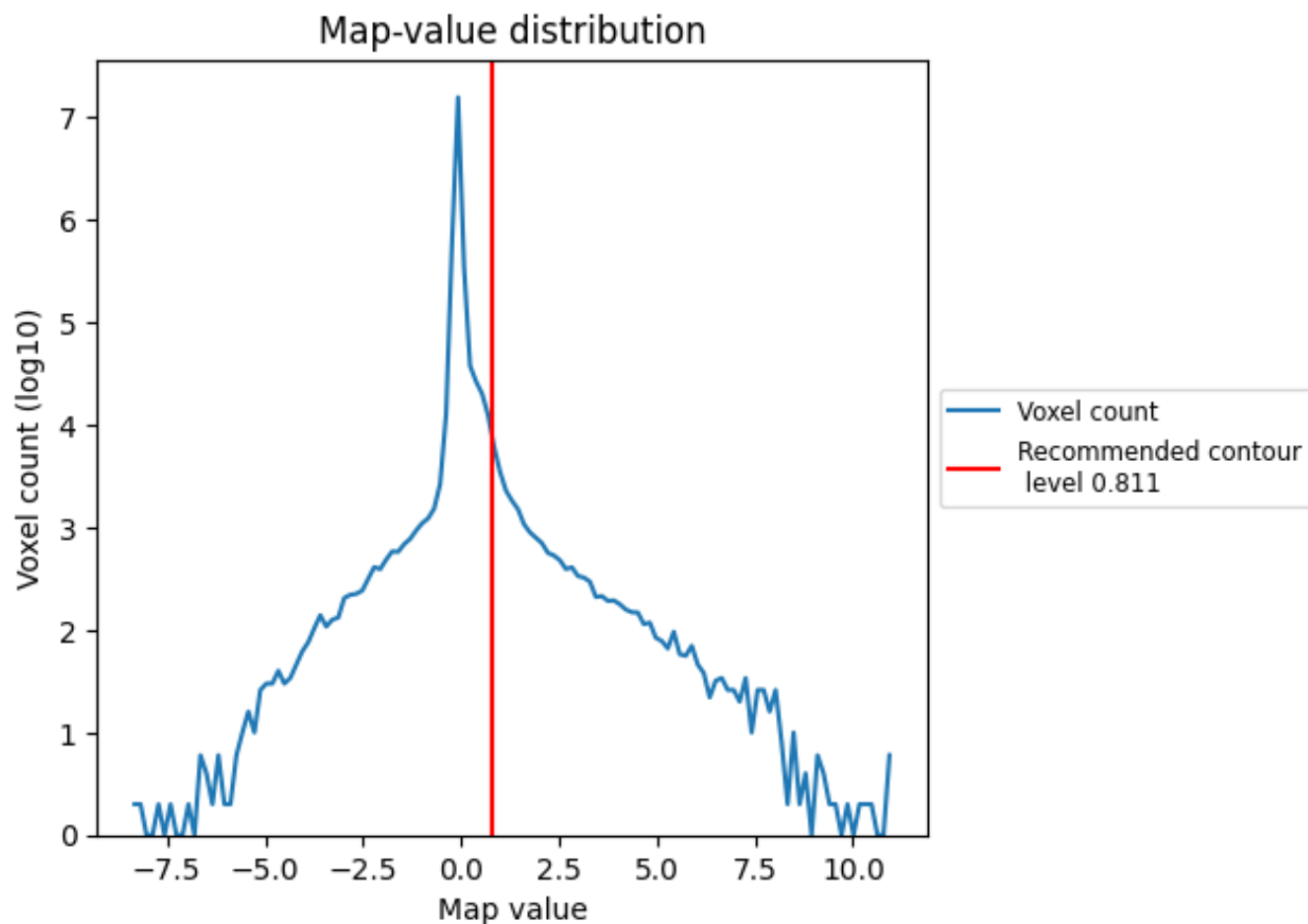


Z

7 Map analysis [i](#)

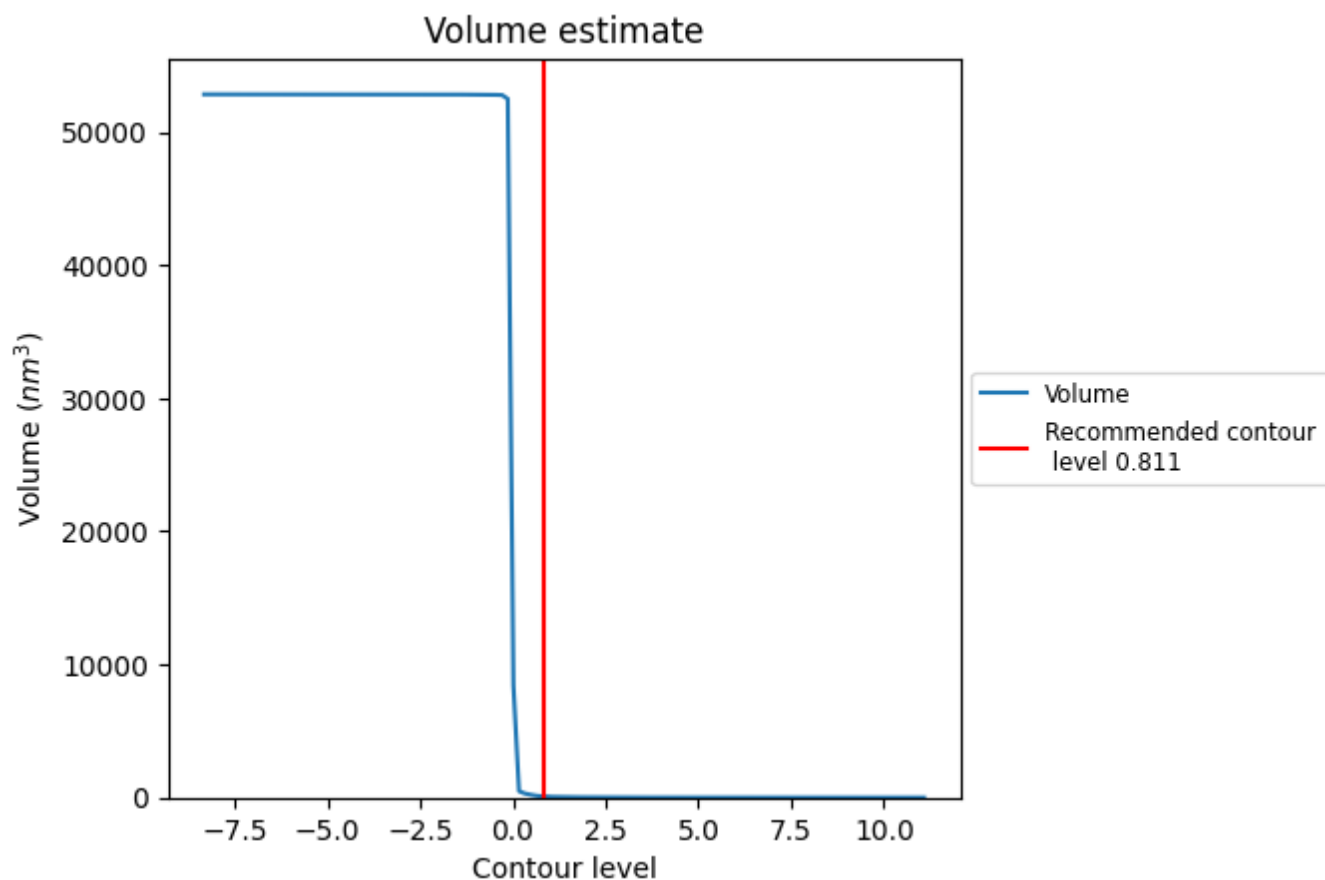
This section contains the results of statistical analysis of the map.

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.

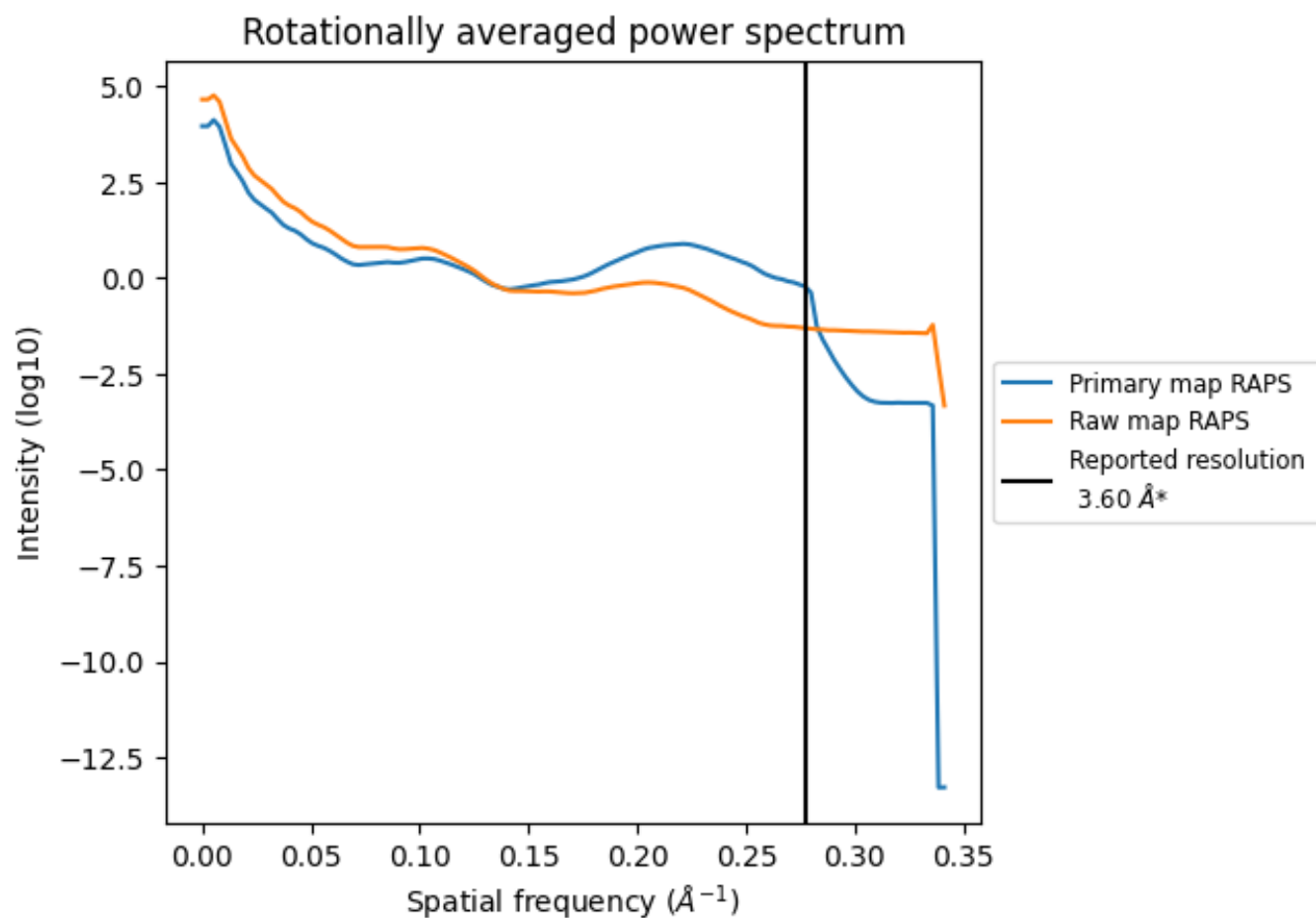
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 86 nm^3 ; this corresponds to an approximate mass of 78 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 ⓘ

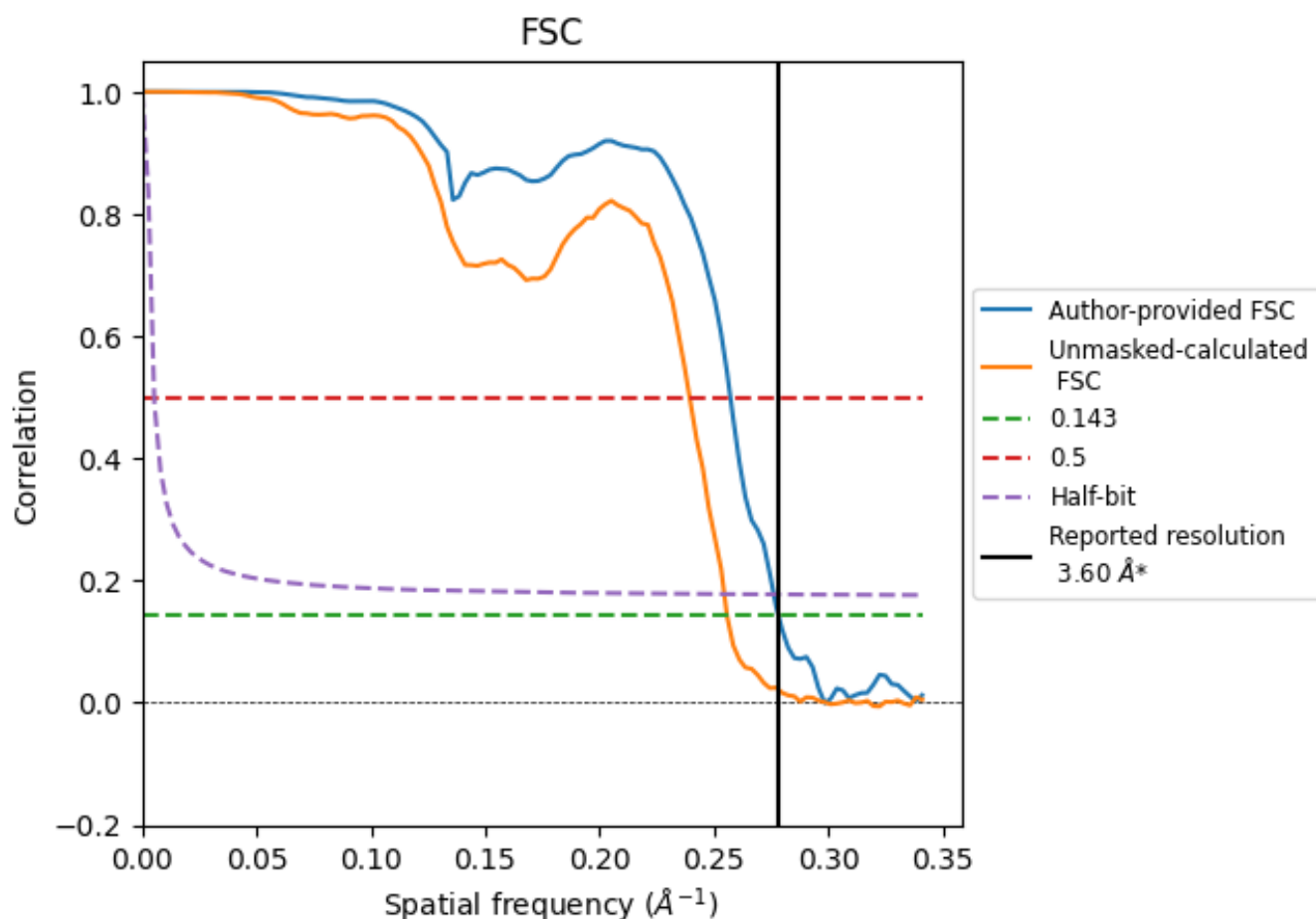


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

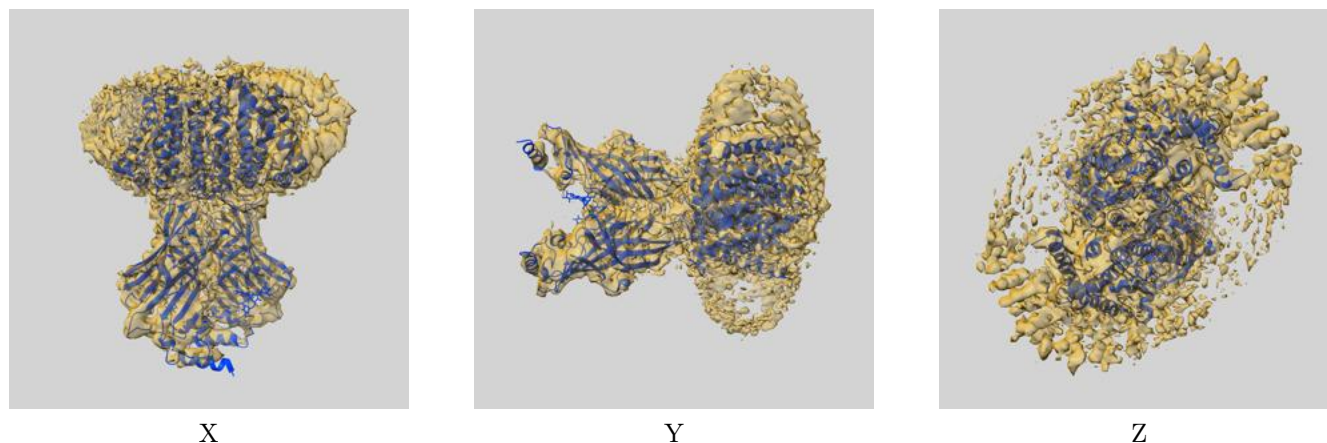
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	3.89	3.62
Unmasked-calculated*	3.91	4.18	3.93

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

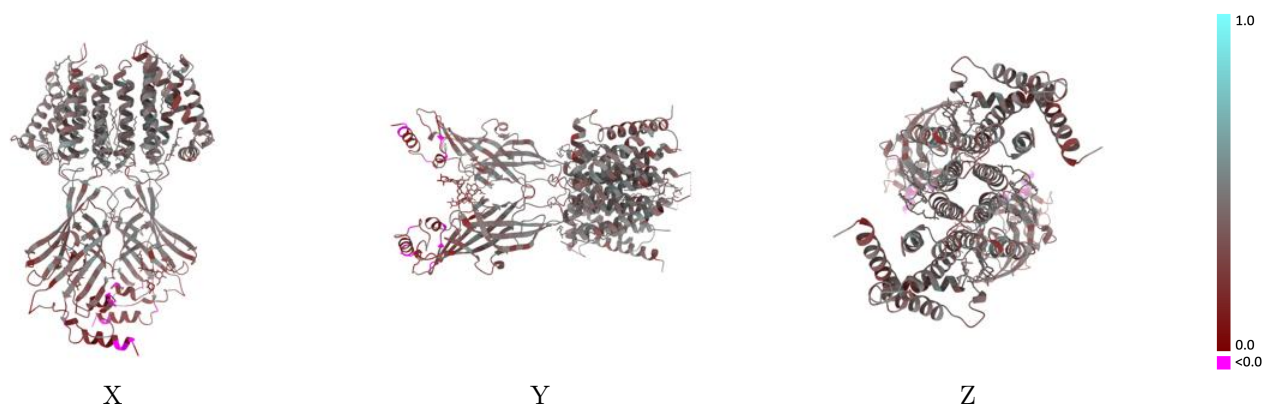
This section contains information regarding the fit between EMDB map EMD-51963 and PDB model 9H9E. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



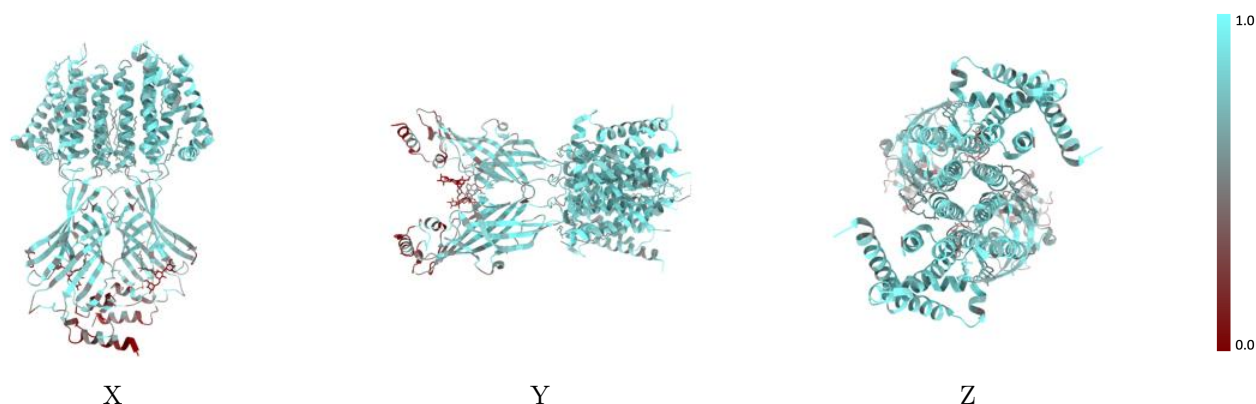
The images above show the 3D surface view of the map at the recommended contour level 0.811 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



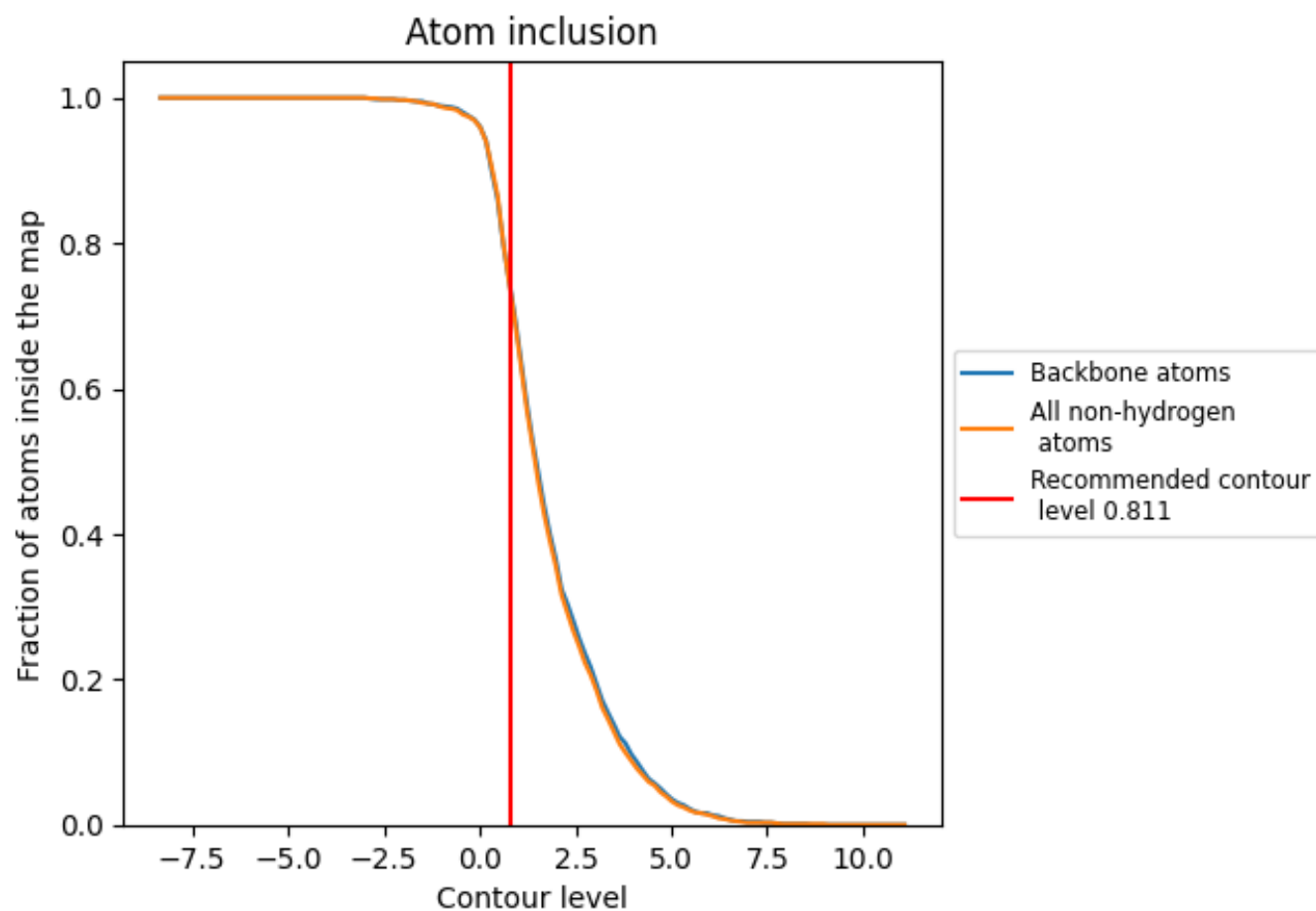
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.811).

9.4 Atom inclusion ⓘ



At the recommended contour level, 73% of all backbone atoms, 73% 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 (0.811) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7300	0.3720
A	0.7060	0.3640
B	0.8120	0.4030
C	0.8170	0.4070
D	0.7070	0.3620
a	0.1970	0.2230
d	0.1800	0.2260

1.0

0.0

<0.0