



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 11:39 AM UTC

PDB ID : 7C9I / pdb_00007c9i
EMDB ID : EMD-30312
Title : Human gamma-secretase in complex with small molecule L-685,458
Authors : Yang, G.; Zhou, R.; Guo, X.; Lei, J.; Yan, C.; Shi, Y.
Deposited on : 2020-06-05
Resolution : 3.10 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 EMD 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

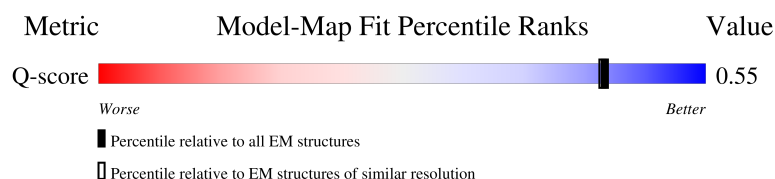
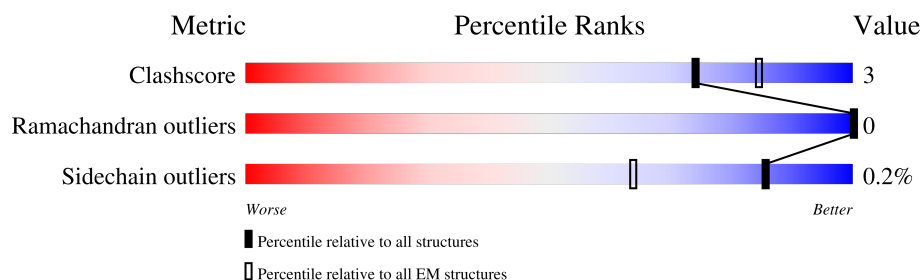
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



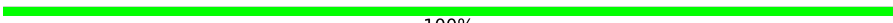
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	709	85% 9% 6%
2	B	467	61% 5% 34%
3	C	265	84% 8% 8%
4	D	143	62% 5% 33%

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Mol	Chain	Length	Quality of chain
5	E	2	 100%
5	G	2	 50%50%
5	H	2	 100%
5	I	2	 50%50%
5	J	2	 100%
6	F	5	 60%40%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 10853 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Nicastrin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	667	Total	C	N	O	S	0	0
			5235	3321	890	1003	21		

- Molecule 2 is a protein called Presenilin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	307	Total	C	N	O	S	0	0
			2436	1649	370	403	14		

- Molecule 3 is a protein called Gamma-secretase subunit APH-1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	243	Total	C	N	O	S	0	0
			1872	1254	299	315	4		

- Molecule 4 is a protein called Gamma-secretase subunit PEN-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	96	Total	C	N	O	S	0	0
			814	559	126	128	1		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-41	MET	-	initiating methionine	UNP Q9NZ42
D	-40	ALA	-	expression tag	UNP Q9NZ42
D	-39	SER	-	expression tag	UNP Q9NZ42
D	-38	TRP	-	expression tag	UNP Q9NZ42
D	-37	SER	-	expression tag	UNP Q9NZ42
D	-36	HIS	-	expression tag	UNP Q9NZ42
D	-35	PRO	-	expression tag	UNP Q9NZ42
D	-34	GLN	-	expression tag	UNP Q9NZ42
D	-33	PHE	-	expression tag	UNP Q9NZ42

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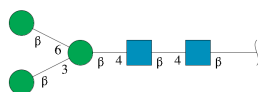
Chain	Residue	Modelled	Actual	Comment	Reference
D	-32	GLU	-	expression tag	UNP Q9NZ42
D	-31	LYS	-	expression tag	UNP Q9NZ42
D	-30	GLY	-	expression tag	UNP Q9NZ42
D	-29	GLY	-	expression tag	UNP Q9NZ42
D	-28	GLY	-	expression tag	UNP Q9NZ42
D	-27	ALA	-	expression tag	UNP Q9NZ42
D	-26	ARG	-	expression tag	UNP Q9NZ42
D	-25	GLY	-	expression tag	UNP Q9NZ42
D	-24	GLY	-	expression tag	UNP Q9NZ42
D	-23	SER	-	expression tag	UNP Q9NZ42
D	-22	GLY	-	expression tag	UNP Q9NZ42
D	-21	GLY	-	expression tag	UNP Q9NZ42
D	-20	GLY	-	expression tag	UNP Q9NZ42
D	-19	SER	-	expression tag	UNP Q9NZ42
D	-18	TRP	-	expression tag	UNP Q9NZ42
D	-17	SER	-	expression tag	UNP Q9NZ42
D	-16	HIS	-	expression tag	UNP Q9NZ42
D	-15	PRO	-	expression tag	UNP Q9NZ42
D	-14	GLN	-	expression tag	UNP Q9NZ42
D	-13	PHE	-	expression tag	UNP Q9NZ42
D	-12	GLU	-	expression tag	UNP Q9NZ42
D	-11	LYS	-	expression tag	UNP Q9NZ42
D	-10	GLY	-	expression tag	UNP Q9NZ42
D	-9	PHE	-	expression tag	UNP Q9NZ42
D	-8	ASP	-	expression tag	UNP Q9NZ42
D	-7	TYR	-	expression tag	UNP Q9NZ42
D	-6	LYS	-	expression tag	UNP Q9NZ42
D	-5	ASP	-	expression tag	UNP Q9NZ42
D	-4	ASP	-	expression tag	UNP Q9NZ42
D	-3	ASP	-	expression tag	UNP Q9NZ42
D	-2	ASP	-	expression tag	UNP Q9NZ42
D	-1	LYS	-	expression tag	UNP Q9NZ42
D	0	GLY	-	expression tag	UNP Q9NZ42
D	1	THR	-	expression tag	UNP Q9NZ42

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



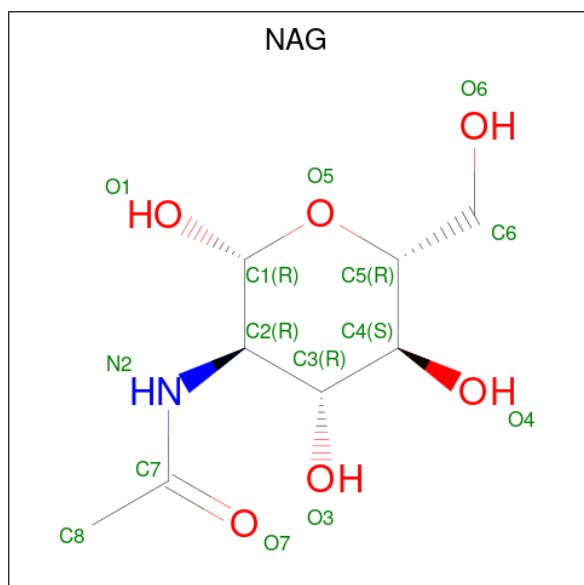
Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	2	Total	C	N	O	0	0
			28	16	2	10		
5	G	2	Total	C	N	O	0	0
			28	16	2	10		
5	H	2	Total	C	N	O	0	0
			28	16	2	10		
5	I	2	Total	C	N	O	0	0
			28	16	2	10		
5	J	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-3)-[beta-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.



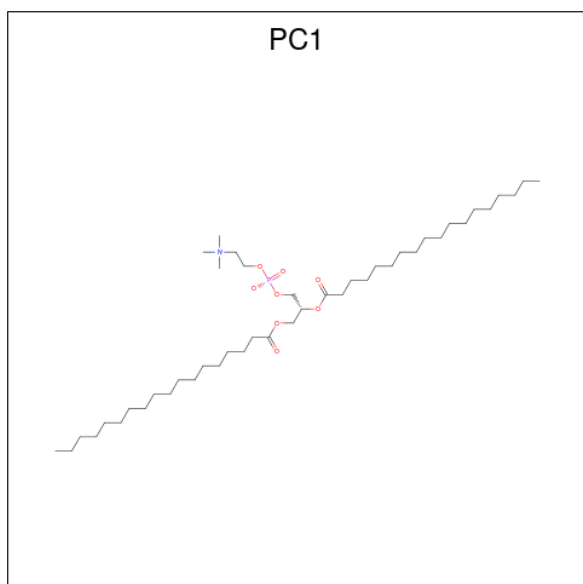
Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



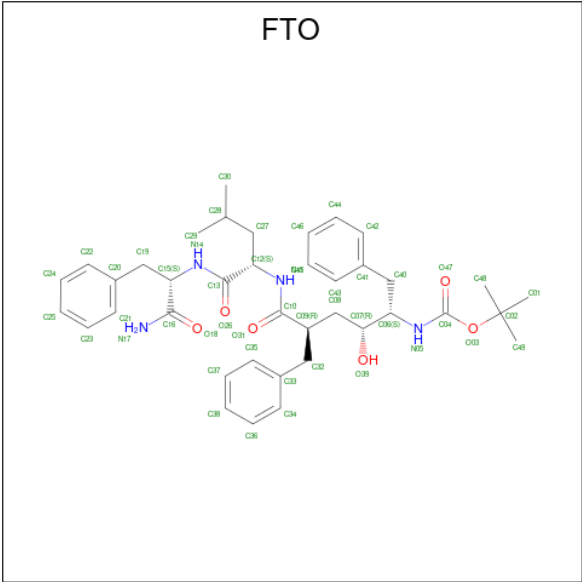
Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	A	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 8 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



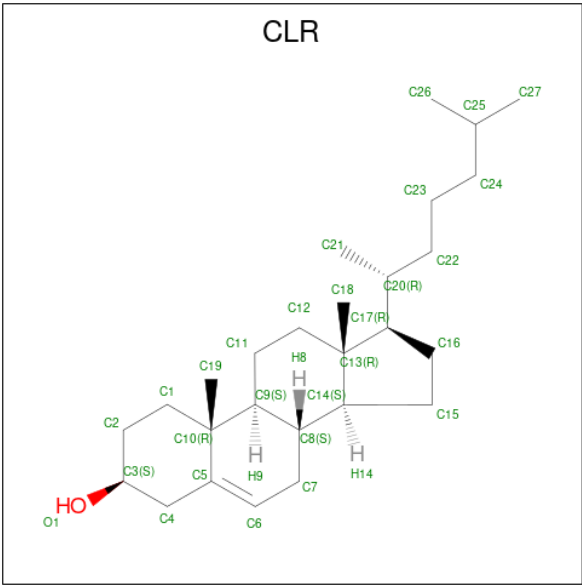
Mol	Chain	Residues	Atoms					AltConf
8	B	1	Total	C	N	O	P	0
			37	27	1	8	1	
8	C	1	Total	C	N	O	P	0
			41	31	1	8	1	

- Molecule 9 is {tert}-butyl {N}-[(2 {S},3 {R},5 {R})-6-[[[(2 {S})-1-[[[(2 {S})-1-azanyl-1-oxidanylidene-3-phenyl-propan-2-yl]amino]-4-methyl-1-oxidanylidene-pentan-2-yl]amino]-3-oxidanyl-6-oxidanylidene-1-phenyl-5-(phenylmethyl)hexan-2-yl]carbamate (CCD ID: FTO) (formula: $C_{39}H_{52}N_4O_6$).



Mol	Chain	Residues	Atoms				AltConf
9	B	1	Total	C	N	O	0
			49	39	4	6	

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



Mol	Chain	Residues	Atoms			AltConf
10	C	1	Total	C	O	0
			28	27	1	
10	C	1	Total	C	O	0
			28	27	1	
10	C	1	Total	C	O	0
			28	27	1	

GLU	ASP
SER	ARG
VAL	MET
TYR	VAL
SER	ALA
LEU	ARG
TLE	PRO
PRO	PRO
GLU	GLU
ASP	

- Molecule 4: Gamma-secretase subunit PEN-2



MET	ALA	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	GLY	GLY	ALA	ARG	GLY	GLY	SER	GLY	GLY	GLY	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	GLY	PHE	ASP	TYR	LYS	ASP	ASP	ASP	ASP	LYS	GLY	THR	ASN	LEU	GLU	ARG	V6	S7	R8	E9	R39	L43	W74	Q79
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	----	-----	-----	-----	-----

P97	P101
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- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



NAG1	NAG2
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- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



NAG1	NAG2
------	------

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



NAG1	NAG2
------	------

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



NAG1	NAG2
------	------

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



NAG1	NAG2
------	------

- Molecule 6: beta-D-mannopyranose-(1-3)-[beta-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 F: 

EM1	EM2	EM3	EM4	EM5
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	320661	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5625	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.242	Depositor
Minimum map value	-0.147	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.028	Depositor
Map size ($\text{\AA}$)	349.12, 349.12, 349.12	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.091, 1.091, 1.091	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PC1, CLR, BMA, FTO, NAG

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	0.31	0/5358	0.59	2/7302 (0.0%)
2	B	0.28	0/2499	0.56	2/3410 (0.1%)
3	C	0.29	0/1924	0.55	0/2624
4	D	0.23	0/847	0.49	0/1157
All	All	0.30	0/10628	0.57	4/14493 (0.0%)

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
1	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	224	VAL	CA-C-N	5.12	131.19	121.97
1	A	224	VAL	C-N-CA	5.12	131.19	121.97
2	B	86	PHE	CA-C-N	5.09	124.40	120.33
2	B	86	PHE	C-N-CA	5.09	124.40	120.33

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	VAL	Peptide

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	5235	0	5126	34	0
2	B	2436	0	2558	19	0
3	C	1872	0	1911	14	0
4	D	814	0	804	5	0
5	E	28	0	25	0	0
5	G	28	0	25	0	0
5	H	28	0	25	0	0
5	I	28	0	25	0	0
5	J	28	0	25	0	0
6	F	61	0	52	0	0
7	A	84	0	78	1	0
8	B	37	0	48	0	0
8	C	41	0	56	0	0
9	B	49	0	0	9	0
10	C	84	0	138	4	0
All	All	10853	0	10896	69	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 3.

All (69) 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)
2:B:381:LEU:HD23	2:B:386:PHE:CE2	2.21	0.76
2:B:286:LEU:HD12	9:B:502:FTO:C49	2.15	0.76
2:B:425:LEU:HD22	9:B:502:FTO:C30	2.17	0.74
2:B:405:ASN:HD22	2:B:454:GLN:HE22	1.36	0.72
2:B:106:TYR:HA	2:B:239:LYS:HD3	1.78	0.66
2:B:286:LEU:O	9:B:502:FTO:C48	2.48	0.61
1:A:282:LEU:HD11	1:A:567:VAL:HG21	1.83	0.60
1:A:530:ASN:OD1	1:A:535:GLN:NE2	2.36	0.59
1:A:112:LYS:NZ	1:A:175:ASP:O	2.36	0.58
1:A:296:GLU:HG2	1:A:369:ALA:HB3	1.86	0.58
1:A:265:THR:OG1	1:A:626:ARG:NH1	2.37	0.57
1:A:286:SER:OG	1:A:287:PHE:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ASP:OD1	1:A:561:THR:OG1	2.23	0.56
3:C:87:ARG:HH21	3:C:125:PHE:HD2	1.55	0.55
1:A:632:SER:OG	1:A:645:TYR:O	2.24	0.55
1:A:691:ASN:HD22	3:C:23:ILE:HG22	1.72	0.54
2:B:388:PHE:HE2	9:B:502:FTO:C45	2.19	0.54
3:C:227:TRP:HB2	10:C:302:CLR:H72	1.89	0.54
2:B:226:LEU:HD22	2:B:383:LEU:HD11	1.90	0.53
1:A:86:LEU:HD22	1:A:114:ARG:HD2	1.91	0.53
3:C:24:THR:O	3:C:31:ARG:NH1	2.43	0.52
2:B:192:ALA:O	4:D:79:GLN:NE2	2.38	0.52
4:D:39:ARG:HA	4:D:43:LEU:HD13	1.92	0.51
9:B:502:FTO:N05	9:B:502:FTO:C42	2.73	0.51
1:A:108:MET:HE1	1:A:121:LEU:HD21	1.93	0.50
1:A:36:VAL:HG21	3:C:137:ILE:HG22	1.93	0.50
1:A:52:ARG:NH1	1:A:223:ALA:O	2.39	0.50
3:C:17:ALA:HB2	3:C:168:ILE:HG21	1.95	0.49
3:C:7:PHE:HA	3:C:10:THR:HG22	1.95	0.49
2:B:119:THR:O	2:B:131:HIS:ND1	2.44	0.49
1:A:524:GLY:HA2	1:A:531:ASN:HD21	1.78	0.49
1:A:227:THR:HG21	1:A:647:THR:HB	1.95	0.49
2:B:434:ALA:HB2	9:B:502:FTO:C29	2.42	0.48
3:C:80:VAL:HG13	3:C:197:HIS:CD2	2.48	0.48
2:B:194:ASP:OD2	4:D:74:TRP:NE1	2.45	0.48
1:A:84:TRP:HA	1:A:88:ASP:HB2	1.96	0.48
1:A:285:ARG:HG2	1:A:454:GLN:HE21	1.77	0.47
9:B:502:FTO:C10	9:B:502:FTO:C34	2.92	0.47
2:B:416:ILE:HG13	3:C:40:PHE:HB2	1.96	0.47
2:B:464:GLN:NE2	3:C:160:SER:OG	2.45	0.47
1:A:200:ASN:HD21	1:A:213:CYS:HB3	1.80	0.46
9:B:502:FTO:N14	9:B:502:FTO:C21	2.78	0.46
2:B:96:VAL:HG21	2:B:390:SER:HB3	1.96	0.46
1:A:39:LYS:HB3	3:C:147:VAL:HG13	1.96	0.46
1:A:253:ASP:HB3	1:A:331:GLN:HG2	1.98	0.46
1:A:52:ARG:NH2	1:A:63:GLN:OE1	2.49	0.45
1:A:261:LYS:NZ	1:A:321:LEU:O	2.50	0.45
3:C:174:TRP:HE1	3:C:224:MET:HE3	1.81	0.45
3:C:159:THR:HG21	3:C:210:TYR:CD1	2.52	0.44
1:A:543:ARG:HD3	1:A:606:GLN:HE22	1.82	0.44
1:A:64:SER:HB2	1:A:179:PRO:HG3	1.99	0.43
2:B:211:ILE:HG23	2:B:215:TRP:HE3	1.84	0.43
2:B:192:ALA:HB2	4:D:97:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:7:SER:OG	4:D:9:GLU:OE1	2.29	0.43
1:A:274:ARG:HB2	1:A:323:ARG:HG2	2.01	0.43
1:A:560:PRO:HB2	1:A:565:TYR:CE2	2.54	0.43
1:A:56:ALA:HA	1:A:227:THR:HG22	2.01	0.43
2:B:194:ASP:OD1	2:B:194:ASP:N	2.49	0.42
10:C:302:CLR:H222	10:C:302:CLR:H162	1.64	0.42
1:A:49:PRO:HG3	1:A:656:ILE:HD13	2.01	0.42
1:A:350:GLY:HA2	1:A:355:GLN:HE22	1.83	0.42
3:C:227:TRP:CD1	10:C:302:CLR:H152	2.55	0.42
2:B:425:LEU:CD2	9:B:502:FTO:C30	2.94	0.41
1:A:120:GLY:H	1:A:178:PHE:HB2	1.85	0.41
10:C:301:CLR:H162	10:C:301:CLR:H222	1.65	0.41
1:A:266:THR:HB	7:A:804:NAG:HN2	1.84	0.41
1:A:422:LEU:HD12	1:A:423:PRO:HD2	2.03	0.41
1:A:310:GLU:HG3	1:A:574:LEU:HG	2.03	0.41
1:A:125:LEU:HD13	1:A:456:ILE:HD12	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	665/709 (94%)	615 (92%)	50 (8%)	0	100	100
2	B	303/467 (65%)	290 (96%)	13 (4%)	0	100	100
3	C	241/265 (91%)	227 (94%)	14 (6%)	0	100	100
4	D	94/143 (66%)	89 (95%)	5 (5%)	0	100	100
All	All	1303/1584 (82%)	1221 (94%)	82 (6%)	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	584/612 (95%)	583 (100%)	1 (0%)	87	89
2	B	265/408 (65%)	264 (100%)	1 (0%)	84	86
3	C	193/214 (90%)	193 (100%)	0	100	100
4	D	84/119 (71%)	84 (100%)	0	100	100
All	All	1126/1353 (83%)	1124 (100%)	2 (0%)	85	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	VAL
2	B	380	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
1	A	102	HIS
1	A	158	HIS
1	A	194	GLN
1	A	220	HIS
1	A	222	HIS
1	A	355	GLN
1	A	358	ASN
1	A	454	GLN
1	A	516	GLN
1	A	531	ASN
1	A	535	GLN
1	A	553	HIS
1	A	606	GLN
1	A	691	ASN
2	B	405	ASN
2	B	454	GLN

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Mol	Chain	Res	Type
2	B	464	GLN
4	D	33	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 ⓘ

15 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	$\# Z > 2$
5	NAG	E	1	1,5	14,14,15	0.30	0	17,19,21	0.43	0
5	NAG	E	2	5	14,14,15	0.30	0	17,19,21	0.63	0
6	NAG	F	1	6,1	14,14,15	0.31	0	17,19,21	0.70	0
6	NAG	F	2	6	14,14,15	0.26	0	17,19,21	0.52	0
6	BMA	F	3	6	11,11,12	0.67	0	15,15,17	0.87	0
6	BMA	F	4	6	11,11,12	0.69	0	15,15,17	0.89	1 (6%)
6	BMA	F	5	6	11,11,12	1.56	4 (36%)	15,15,17	1.59	2 (13%)
5	NAG	G	1	1,5	14,14,15	0.29	0	17,19,21	1.16	1 (5%)
5	NAG	G	2	5	14,14,15	0.44	0	17,19,21	0.65	0
5	NAG	H	1	1,5	14,14,15	0.23	0	17,19,21	0.63	0
5	NAG	H	2	5	14,14,15	0.26	0	17,19,21	0.58	0
5	NAG	I	1	1,5	14,14,15	0.27	0	17,19,21	0.49	0
5	NAG	I	2	5	14,14,15	0.86	1 (7%)	17,19,21	2.38	3 (17%)
5	NAG	J	1	1,5	14,14,15	0.40	0	17,19,21	0.49	0
5	NAG	J	2	5	14,14,15	0.32	0	17,19,21	0.59	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
5	NAG	E	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
6	NAG	F	1	6,1	-	4/6/23/26	0/1/1/1
6	NAG	F	2	6	-	1/6/23/26	0/1/1/1
6	BMA	F	3	6	-	2/2/19/22	0/1/1/1
6	BMA	F	4	6	-	1/2/19/22	0/1/1/1
6	BMA	F	5	6	-	0/2/19/22	0/1/1/1
5	NAG	G	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	G	2	5	-	4/6/23/26	0/1/1/1
5	NAG	H	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	H	2	5	-	3/6/23/26	0/1/1/1
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	4/6/23/26	0/1/1/1
5	NAG	J	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	1/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	5	BMA	C2-C3	2.71	1.56	1.52
5	I	2	NAG	C1-C2	2.61	1.55	1.52
6	F	5	BMA	C1-C2	2.43	1.58	1.52
6	F	5	BMA	O5-C5	2.34	1.48	1.43
6	F	5	BMA	O5-C1	2.14	1.47	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	2	NAG	C2-N2-C7	8.30	134.02	122.90
6	F	5	BMA	C1-O5-C5	4.79	118.60	112.19
5	I	2	NAG	C1-C2-N2	3.89	116.56	110.43
5	G	1	NAG	C2-N2-C7	3.40	127.46	122.90
6	F	5	BMA	C2-C3-C4	2.22	114.76	110.86
5	I	2	NAG	C8-C7-N2	2.15	119.68	116.12
6	F	4	BMA	C1-O5-C5	2.09	114.99	112.19

There are no chirality outliers.

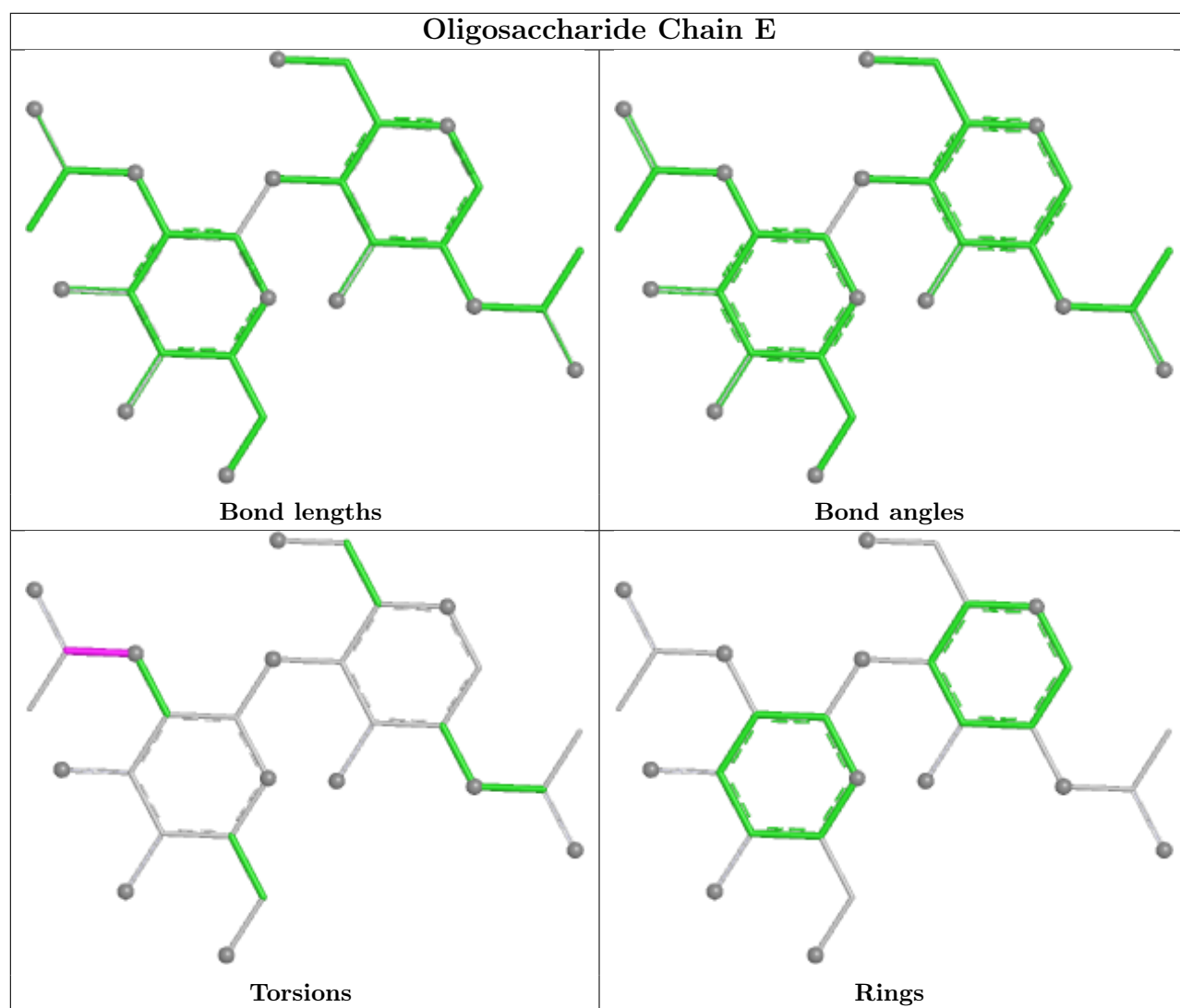
All (30) torsion outliers are listed below:

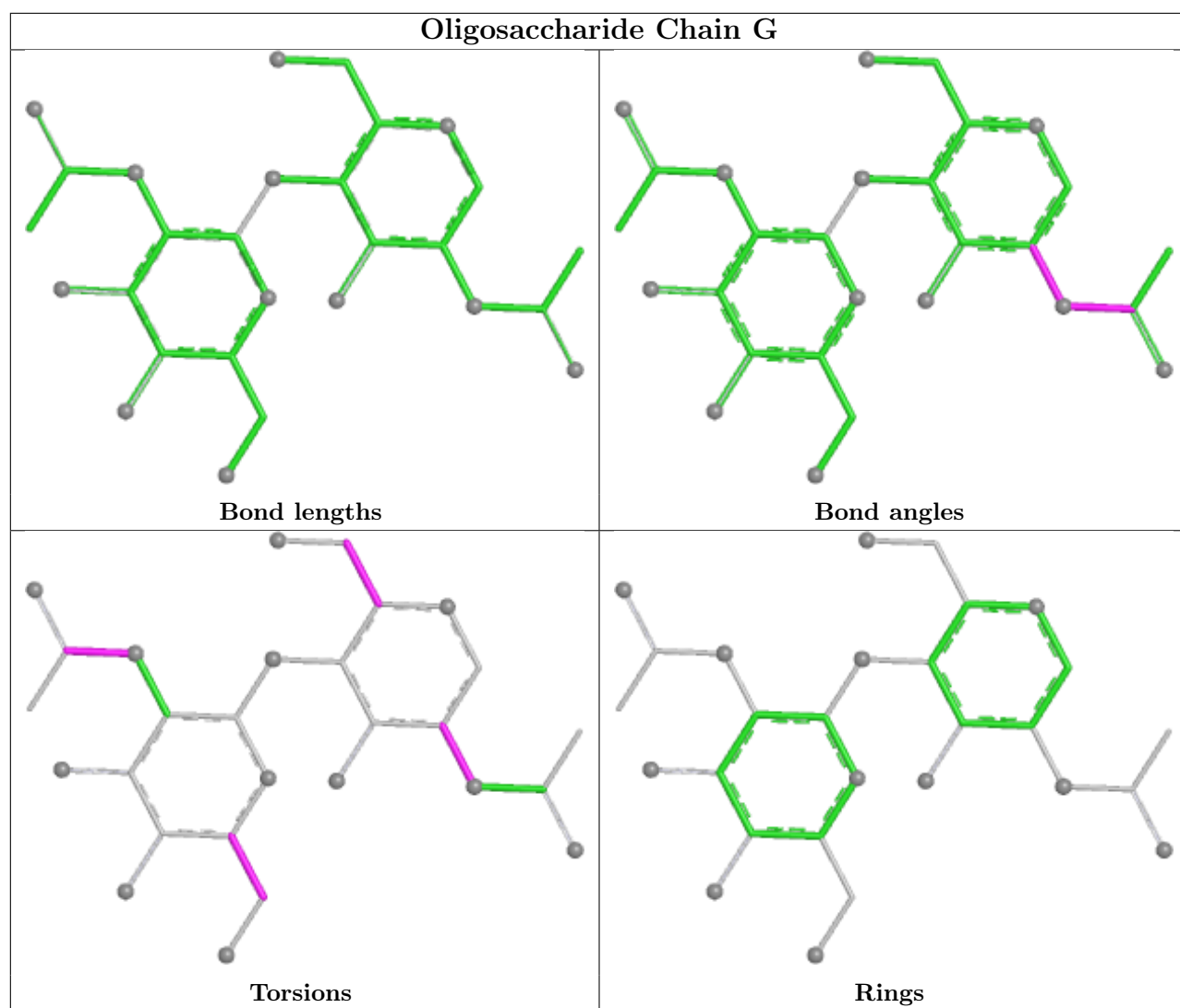
Mol	Chain	Res	Type	Atoms
6	F	3	BMA	C4-C5-C6-O6
6	F	3	BMA	O5-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
5	G	2	NAG	C4-C5-C6-O6
5	I	1	NAG	C4-C5-C6-O6
6	F	1	NAG	C4-C5-C6-O6
5	I	1	NAG	O5-C5-C6-O6
5	E	2	NAG	C8-C7-N2-C2
5	E	2	NAG	O7-C7-N2-C2
5	G	2	NAG	C8-C7-N2-C2
5	G	2	NAG	O7-C7-N2-C2
5	H	2	NAG	C8-C7-N2-C2
5	H	2	NAG	O7-C7-N2-C2
5	I	2	NAG	C8-C7-N2-C2
5	I	2	NAG	O7-C7-N2-C2
6	F	1	NAG	C8-C7-N2-C2
6	F	1	NAG	O7-C7-N2-C2
5	J	1	NAG	O5-C5-C6-O6
5	J	1	NAG	C4-C5-C6-O6
6	F	1	NAG	O5-C5-C6-O6
6	F	2	NAG	O5-C5-C6-O6
6	F	4	BMA	O5-C5-C6-O6
5	G	1	NAG	C4-C5-C6-O6
5	G	1	NAG	C1-C2-N2-C7
5	G	1	NAG	O5-C5-C6-O6
5	G	1	NAG	C3-C2-N2-C7
5	I	2	NAG	C1-C2-N2-C7
5	I	2	NAG	C3-C2-N2-C7
5	H	2	NAG	C4-C5-C6-O6
5	J	2	NAG	C4-C5-C6-O6

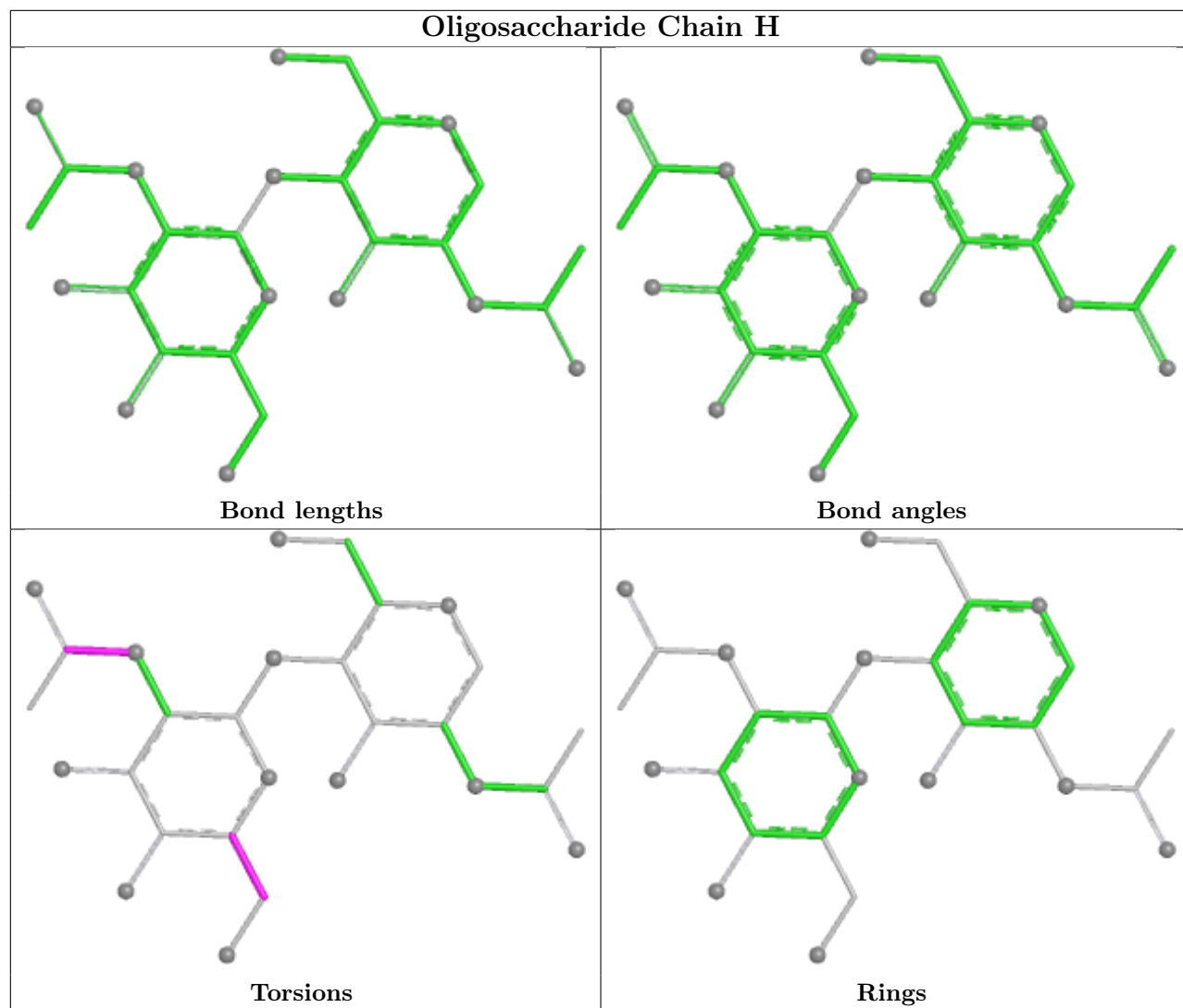
There are no ring outliers.

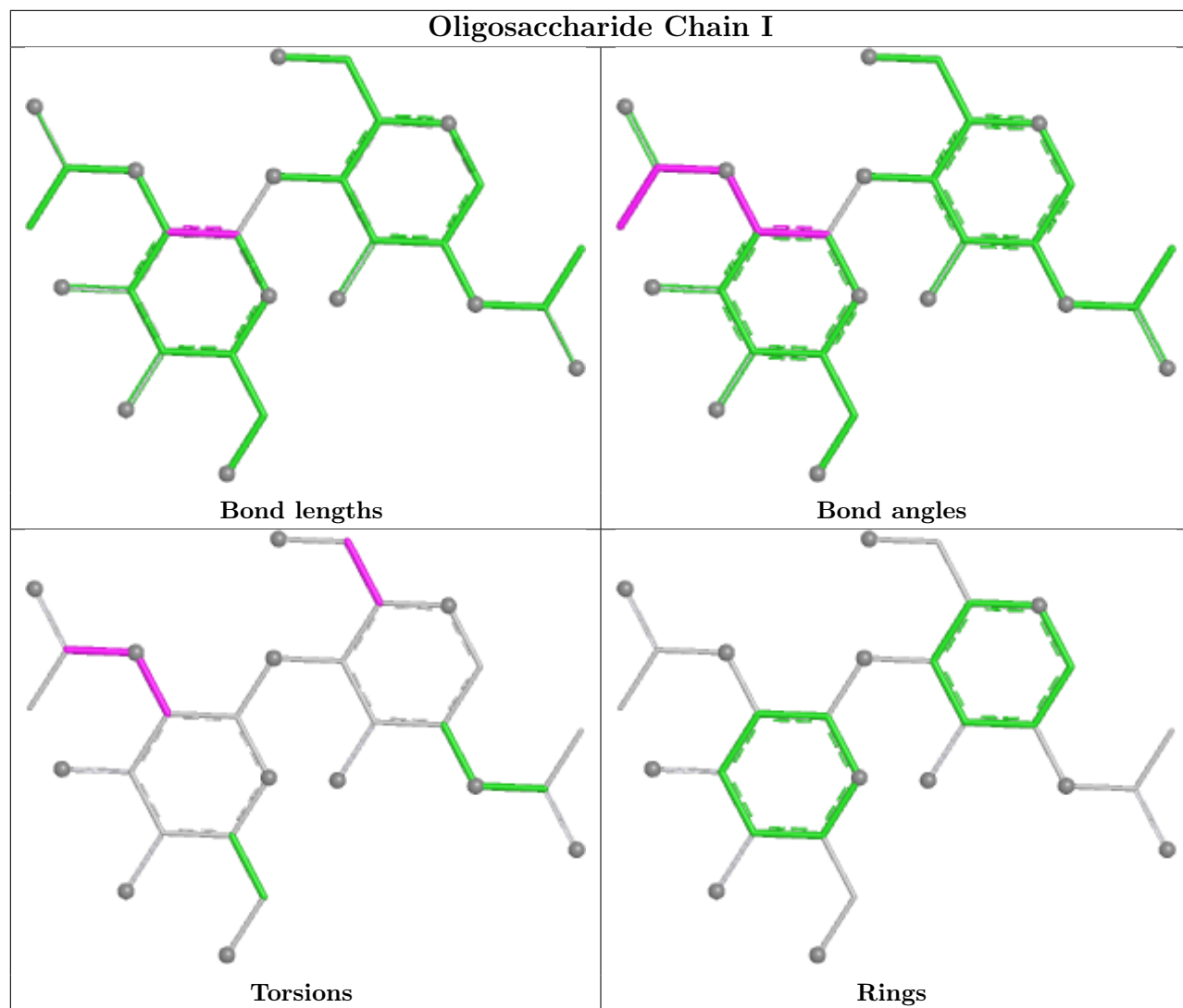
No monomer is involved in short contacts.

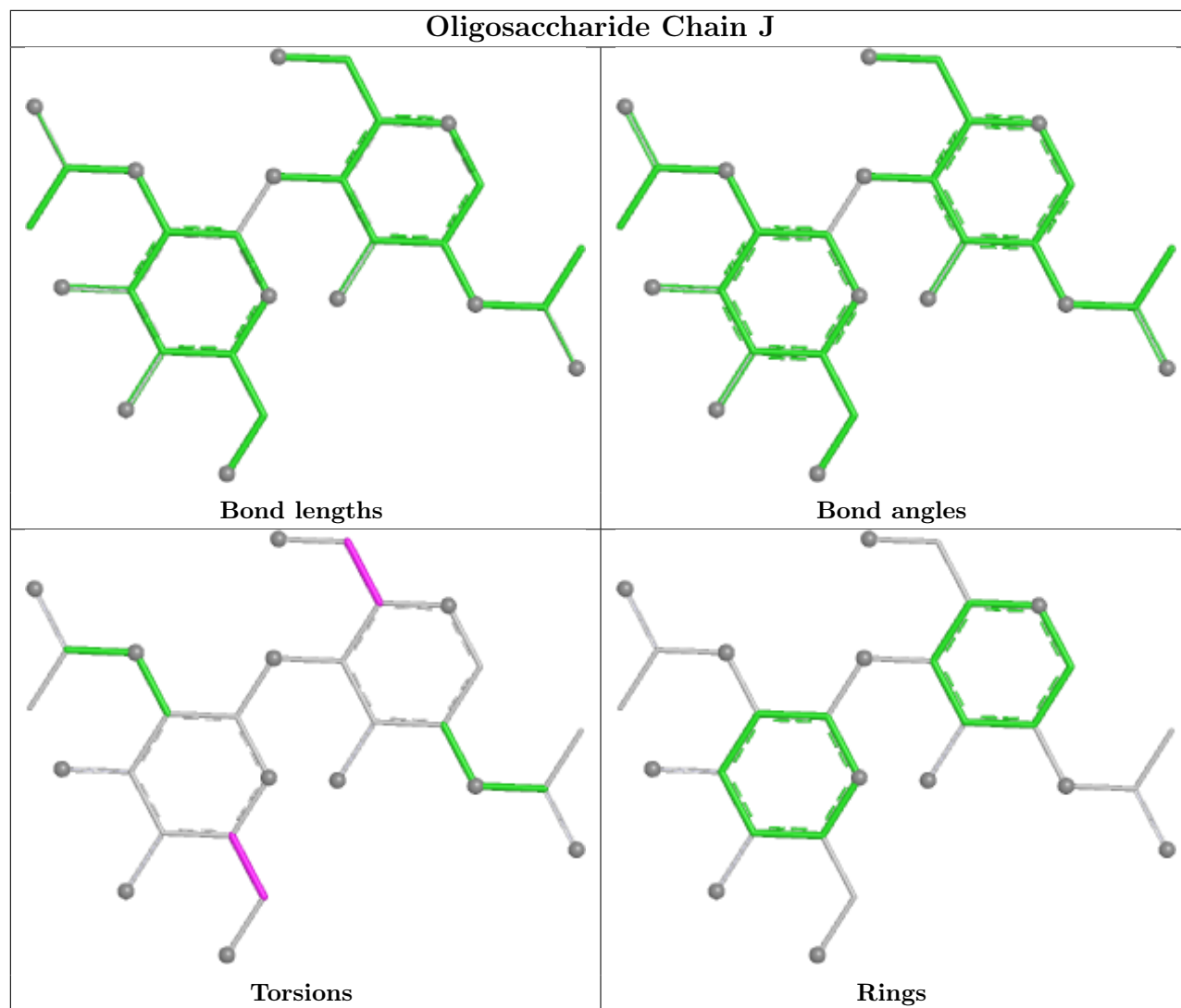
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

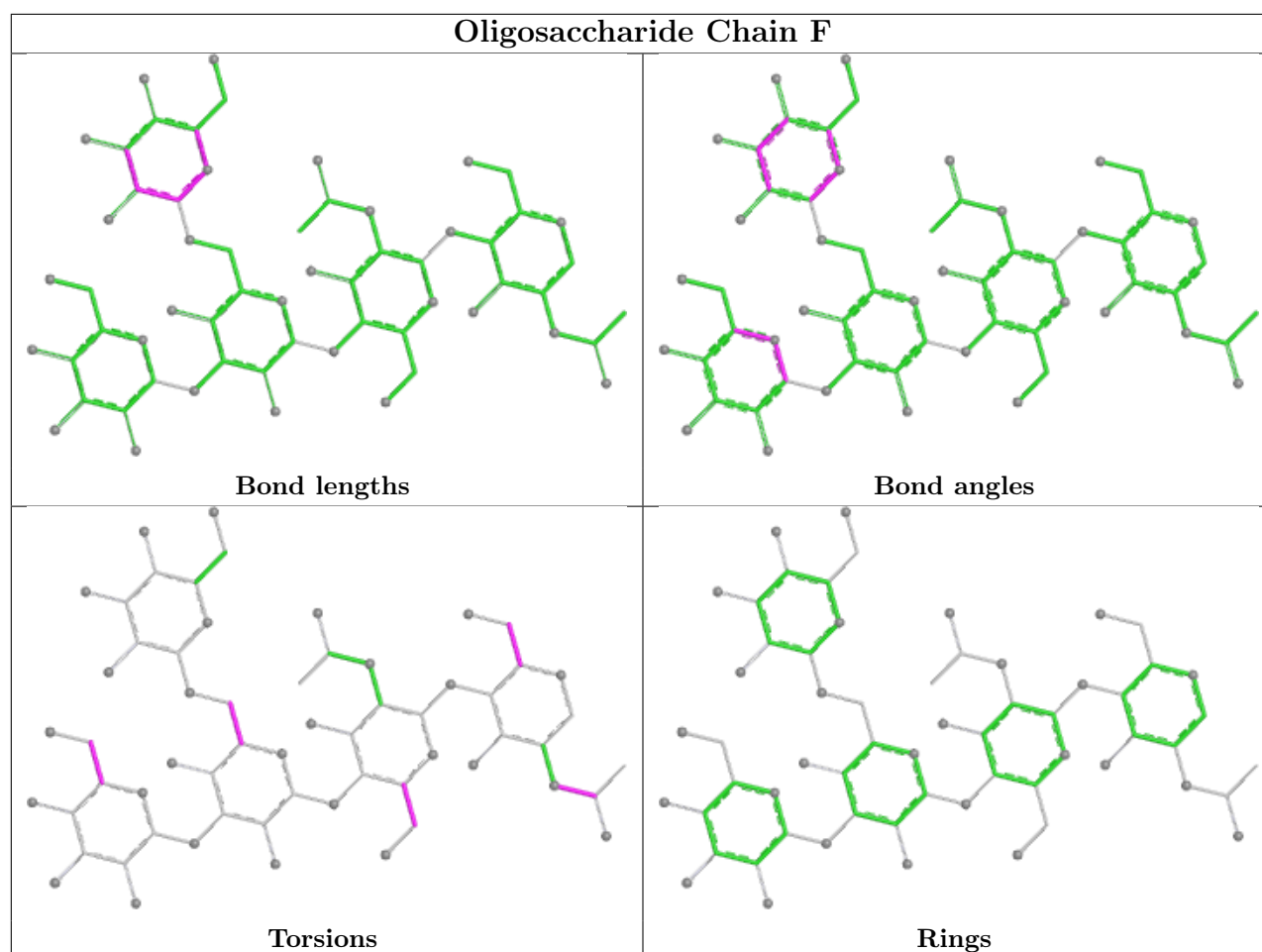












5.6 Ligand geometry [i](#)

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	$\# Z > 2$
7	NAG	A	804	1	14,14,15	1.03	1 (7%)	17,19,21	2.43	4 (23%)
10	CLR	C	302	-	31,31,31	0.34	0	48,48,48	0.63	0
10	CLR	C	301	-	31,31,31	0.36	0	48,48,48	0.57	0
8	PC1	C	304	-	40,40,53	0.31	0	46,48,61	0.41	0
10	CLR	C	303	-	31,31,31	0.33	0	48,48,48	0.65	0
7	NAG	A	803	1	14,14,15	0.41	0	17,19,21	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	A	802	1	14,14,15	0.63	1 (7%)	17,19,21	1.10	2 (11%)
7	NAG	A	806	1	14,14,15	0.28	0	17,19,21	0.69	1 (5%)
9	FTO	B	502	-	51,51,51	1.92	13 (25%)	65,69,69	1.51	9 (13%)
7	NAG	A	801	1	14,14,15	0.48	0	17,19,21	0.65	1 (5%)
7	NAG	A	805	1	14,14,15	0.27	0	17,19,21	0.49	0
8	PC1	B	501	-	36,36,53	0.33	0	42,44,61	0.47	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
7	NAG	A	804	1	-	6/6/23/26	0/1/1/1
10	CLR	C	302	-	-	5/10/68/68	0/4/4/4
10	CLR	C	301	-	-	4/10/68/68	0/4/4/4
8	PC1	C	304	-	-	7/44/44/57	-
10	CLR	C	303	-	-	6/10/68/68	0/4/4/4
7	NAG	A	803	1	-	2/6/23/26	0/1/1/1
7	NAG	A	802	1	-	4/6/23/26	0/1/1/1
7	NAG	A	806	1	-	0/6/23/26	0/1/1/1
9	FTO	B	502	-	-	10/53/53/53	0/3/3/3
7	NAG	A	801	1	-	0/6/23/26	0/1/1/1
7	NAG	A	805	1	-	0/6/23/26	0/1/1/1
8	PC1	B	501	-	-	5/40/40/57	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	502	FTO	C10-N11	5.41	1.45	1.34
9	B	502	FTO	C16-N17	5.37	1.45	1.32
9	B	502	FTO	C13-N14	5.36	1.45	1.34
9	B	502	FTO	O03-C02	-4.64	1.40	1.48
9	B	502	FTO	C04-N05	4.41	1.45	1.34
7	A	804	NAG	C1-C2	3.17	1.56	1.52
9	B	502	FTO	O03-C04	2.91	1.40	1.34
9	B	502	FTO	O18-C16	-2.76	1.18	1.23
9	B	502	FTO	C45-C43	-2.65	1.34	1.38
9	B	502	FTO	C44-C42	2.62	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	502	FTO	O31-C10	-2.33	1.18	1.23
9	B	502	FTO	O26-C13	-2.32	1.18	1.23
9	B	502	FTO	C46-C44	2.15	1.43	1.38
7	A	802	NAG	C1-C2	2.12	1.55	1.52
9	B	502	FTO	C43-C41	-2.11	1.34	1.38

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	804	NAG	C2-N2-C7	8.38	134.13	122.90
9	B	502	FTO	O03-C04-N05	6.08	119.99	110.03
9	B	502	FTO	C02-O03-C04	-4.59	114.01	120.97
7	A	804	NAG	C1-C2-N2	4.11	116.91	110.43
9	B	502	FTO	C45-C43-C41	3.27	125.21	120.61
7	A	802	NAG	C2-N2-C7	3.23	127.23	122.90
9	B	502	FTO	O03-C04-O47	-3.17	120.01	125.64
9	B	502	FTO	O47-C04-N05	-2.97	120.00	124.86
7	A	806	NAG	C1-O5-C5	2.35	115.33	112.19
9	B	502	FTO	C33-C32-C09	-2.26	109.44	113.74
7	A	801	NAG	C1-O5-C5	2.23	115.18	112.19
7	A	804	NAG	C1-O5-C5	2.23	115.18	112.19
9	B	502	FTO	C41-C40-C06	-2.23	109.62	113.40
7	A	802	NAG	C1-C2-N2	2.16	113.83	110.43
9	B	502	FTO	C28-C27-C12	-2.15	109.62	115.40
9	B	502	FTO	C09-C10-N11	2.08	119.77	116.19
7	A	804	NAG	C8-C7-N2	2.08	119.56	116.12

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	501	PC1	O32-C31-O31-C3
8	B	501	PC1	C32-C31-O31-C3
8	C	304	PC1	O22-C21-O21-C2
9	B	502	FTO	C19-C15-C16-O18
9	B	502	FTO	C19-C15-C16-N17
10	C	302	CLR	C16-C17-C20-C22
10	C	303	CLR	C13-C17-C20-C21
10	C	303	CLR	C13-C17-C20-C22
10	C	302	CLR	C16-C17-C20-C21
10	C	303	CLR	C16-C17-C20-C21
10	C	302	CLR	C13-C17-C20-C21

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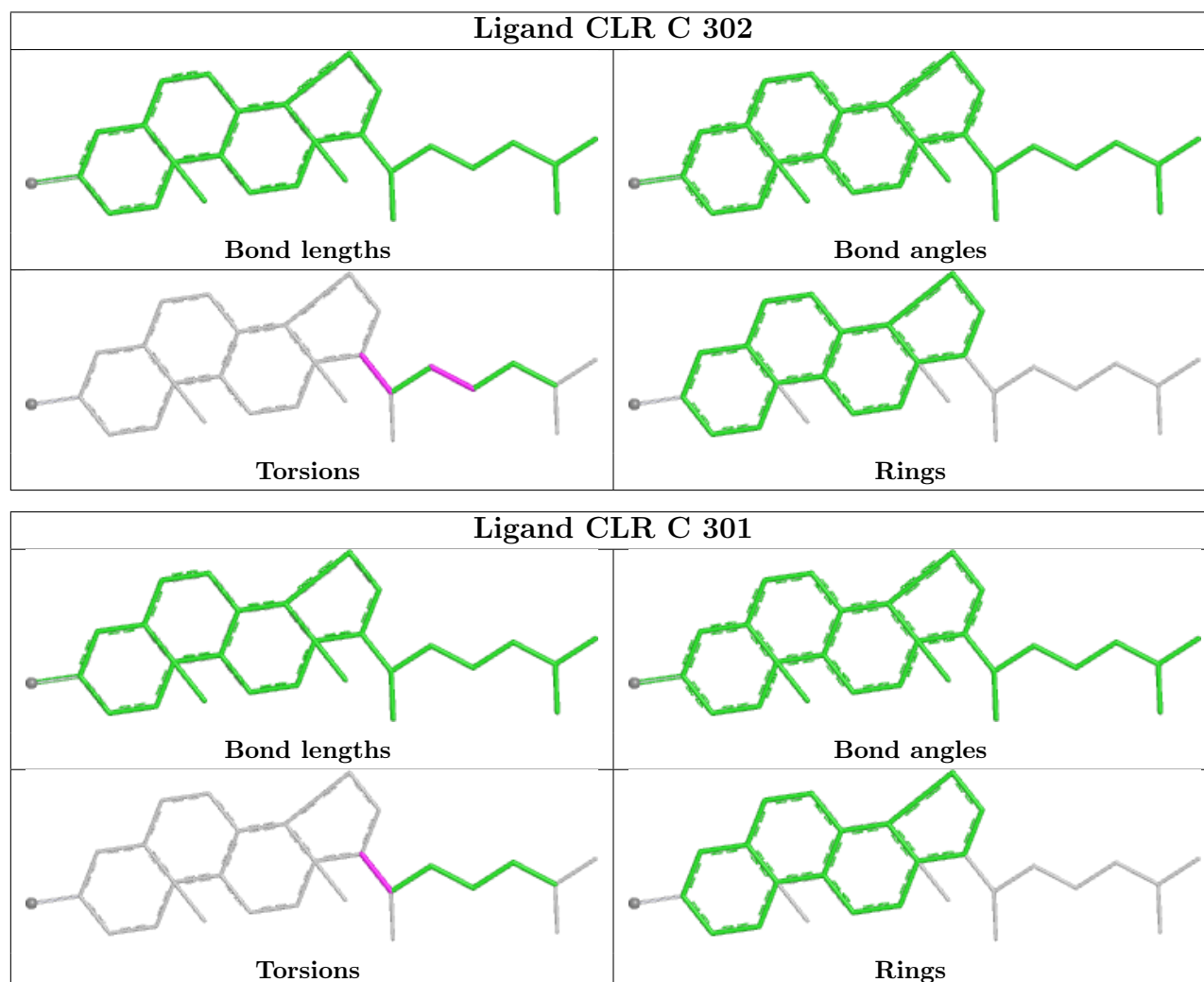
Mol	Chain	Res	Type	Atoms
10	C	303	CLR	C16-C17-C20-C22
8	C	304	PC1	C22-C21-O21-C2
10	C	302	CLR	C13-C17-C20-C22
7	A	804	NAG	O5-C5-C6-O6
7	A	802	NAG	O5-C5-C6-O6
7	A	804	NAG	C4-C5-C6-O6
7	A	803	NAG	O5-C5-C6-O6
10	C	303	CLR	C21-C20-C22-C23
7	A	803	NAG	C4-C5-C6-O6
7	A	802	NAG	C4-C5-C6-O6
9	B	502	FTO	C12-C27-C28-C30
7	A	804	NAG	C8-C7-N2-C2
7	A	804	NAG	O7-C7-N2-C2
10	C	303	CLR	C17-C20-C22-C23
9	B	502	FTO	C12-C27-C28-C29
9	B	502	FTO	N05-C06-C40-C41
8	C	304	PC1	C21-C22-C23-C24
10	C	301	CLR	C16-C17-C20-C22
10	C	301	CLR	C13-C17-C20-C22
9	B	502	FTO	N05-C04-O03-C02
8	C	304	PC1	O13-C11-C12-N
10	C	301	CLR	C16-C17-C20-C21
8	C	304	PC1	C11-O13-P-O14
9	B	502	FTO	O47-C04-O03-C02
9	B	502	FTO	C08-C09-C10-O31
10	C	301	CLR	C13-C17-C20-C21
10	C	302	CLR	C20-C22-C23-C24
7	A	802	NAG	C1-C2-N2-C7
7	A	804	NAG	C1-C2-N2-C7
7	A	802	NAG	C3-C2-N2-C7
7	A	804	NAG	C3-C2-N2-C7
8	C	304	PC1	C1-C2-O21-C21
8	B	501	PC1	C12-C11-O13-P
8	C	304	PC1	C12-C11-O13-P
8	B	501	PC1	O21-C21-C22-C23
9	B	502	FTO	O03-C04-N05-C06
8	B	501	PC1	O22-C21-C22-C23
9	B	502	FTO	C32-C09-C10-O31

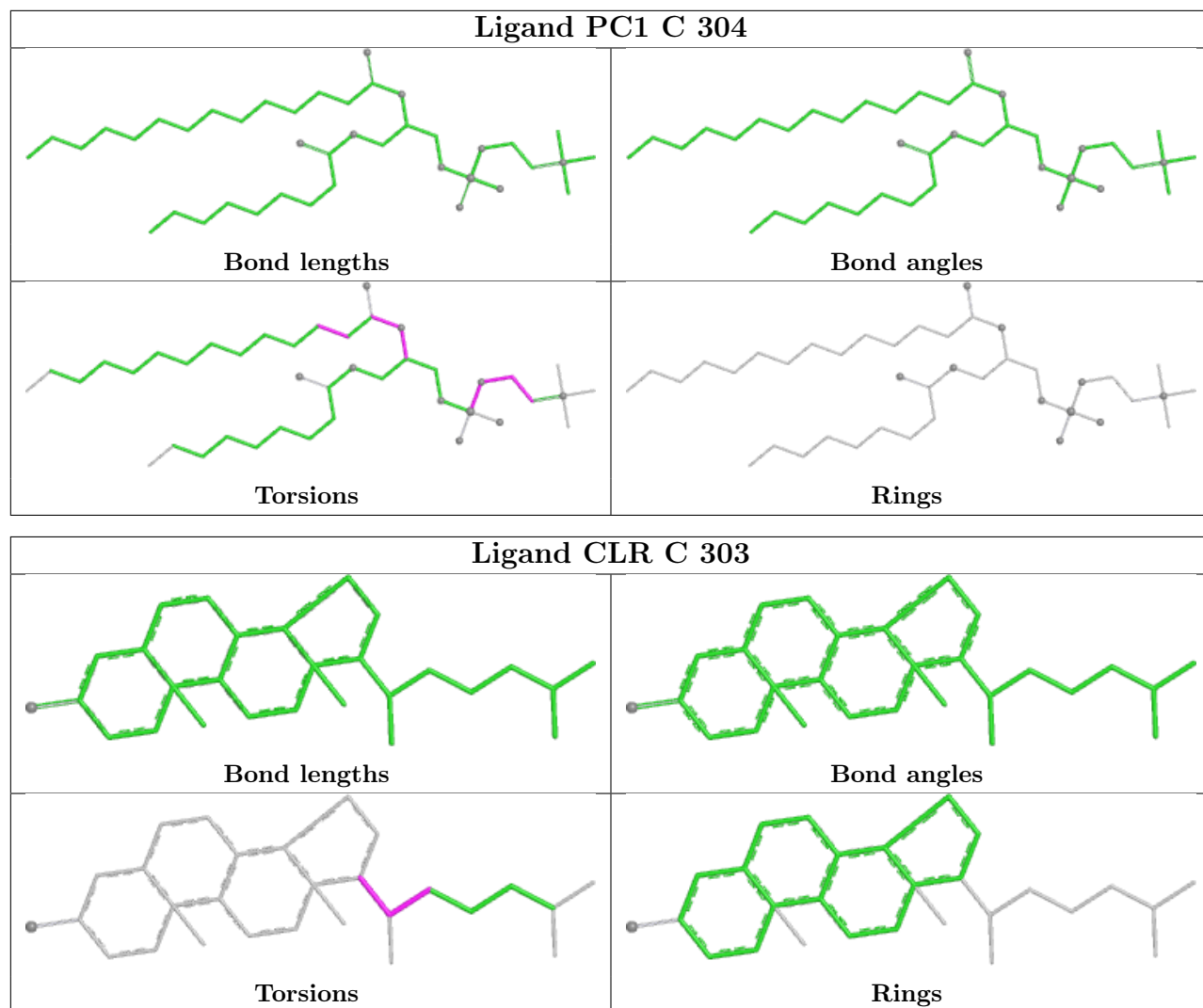
There are no ring outliers.

4 monomers are involved in 14 short contacts:

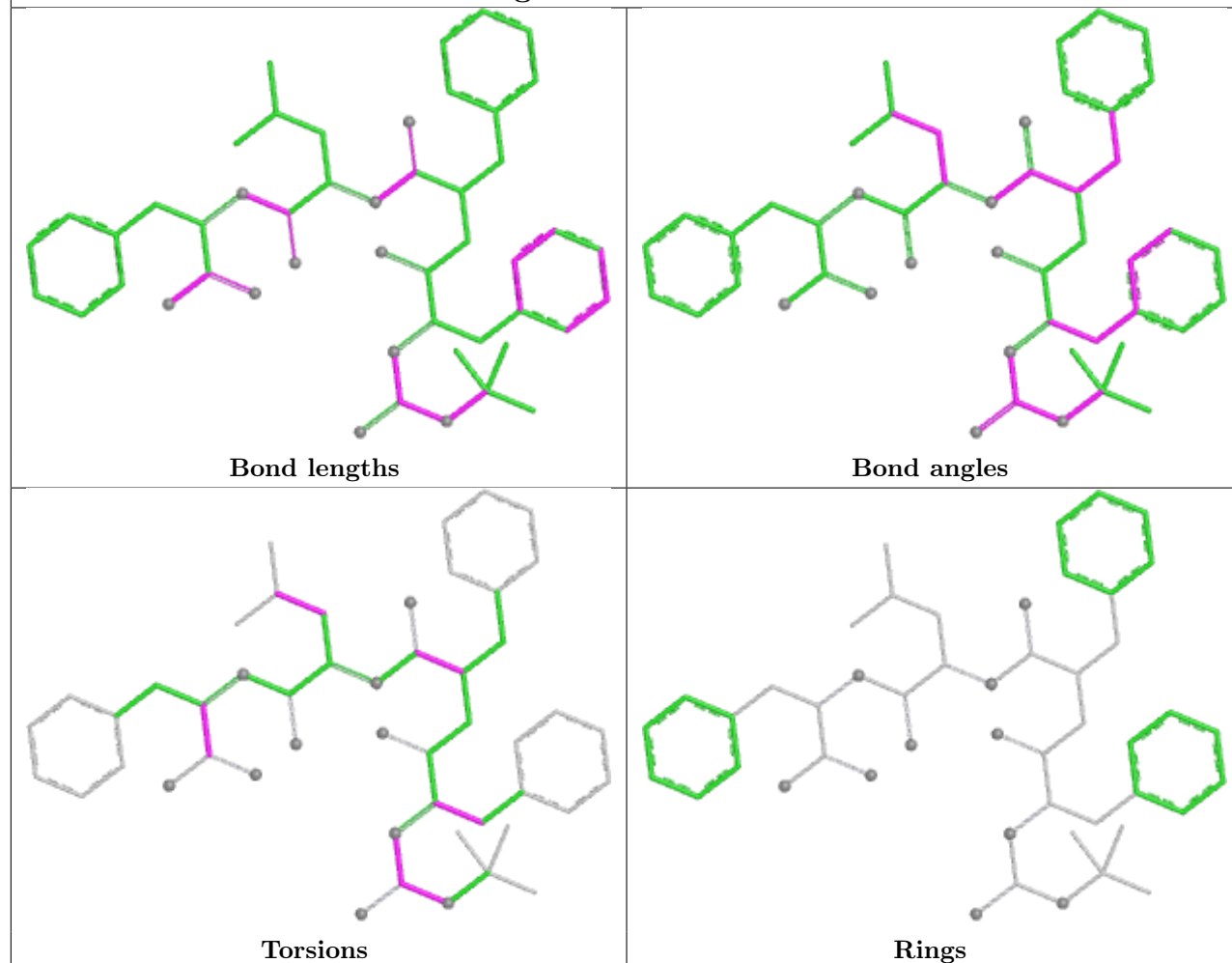
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	804	NAG	1	0
10	C	302	CLR	3	0
10	C	301	CLR	1	0
9	B	502	FTO	9	0

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.

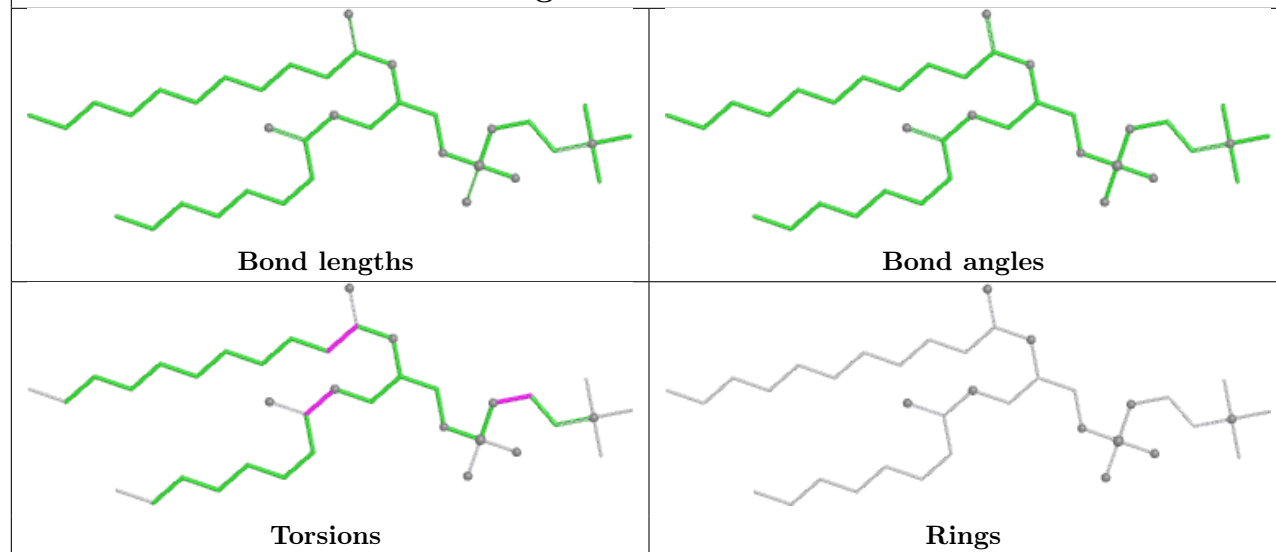




Ligand FTO B 502



Ligand PC1 B 501



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.

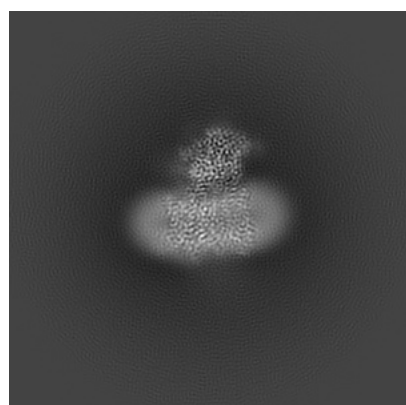
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30312. These allow visual inspection of the internal detail of the map and identification of artifacts.

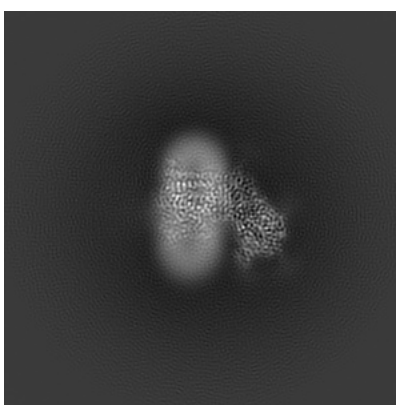
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

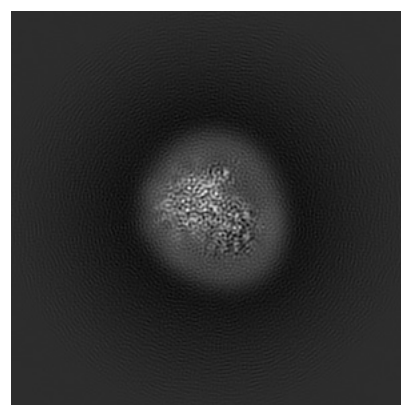
6.1.1 Primary map



X



Y

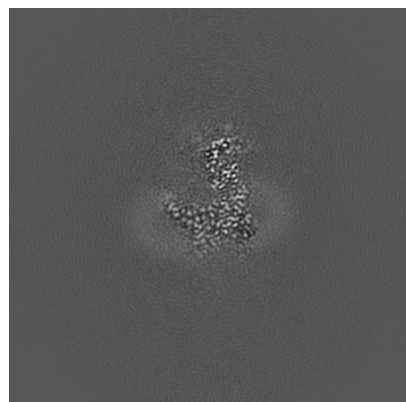


Z

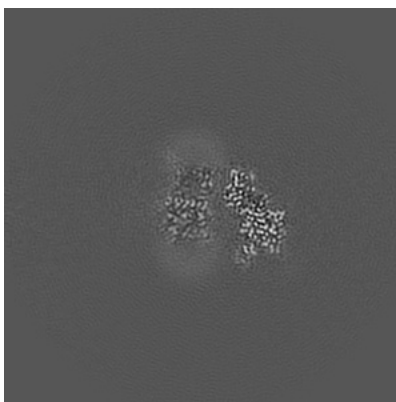
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

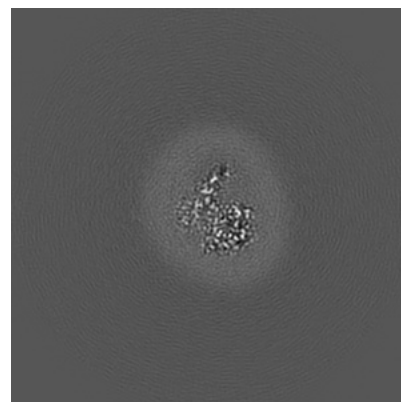
6.2.1 Primary map



X Index: 160



Y Index: 160

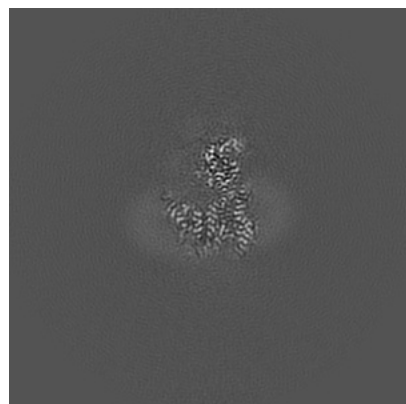


Z Index: 160

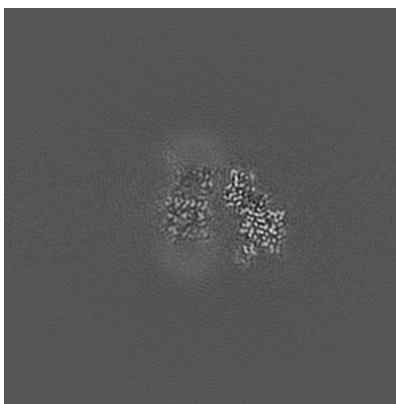
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

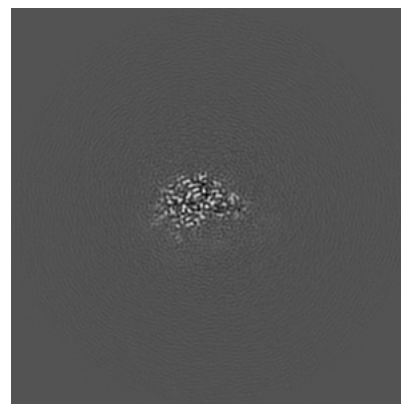
6.3.1 Primary map



X Index: 162



Y Index: 160

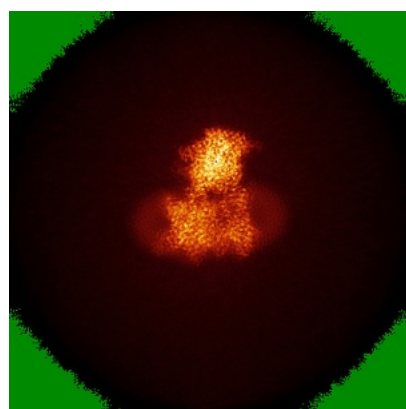


Z Index: 196

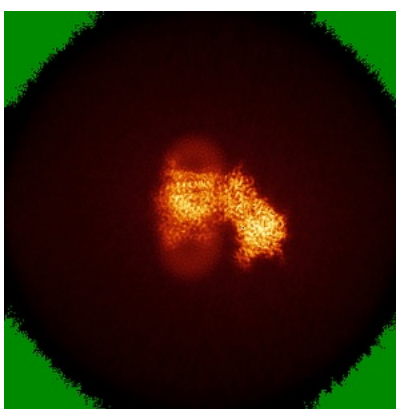
The images above show the largest variance slices of the map in three orthogonal directions.

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

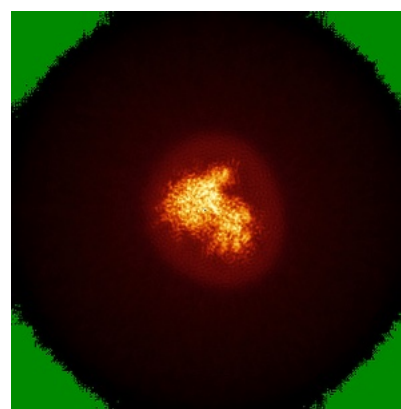
6.4.1 Primary map



X



Y

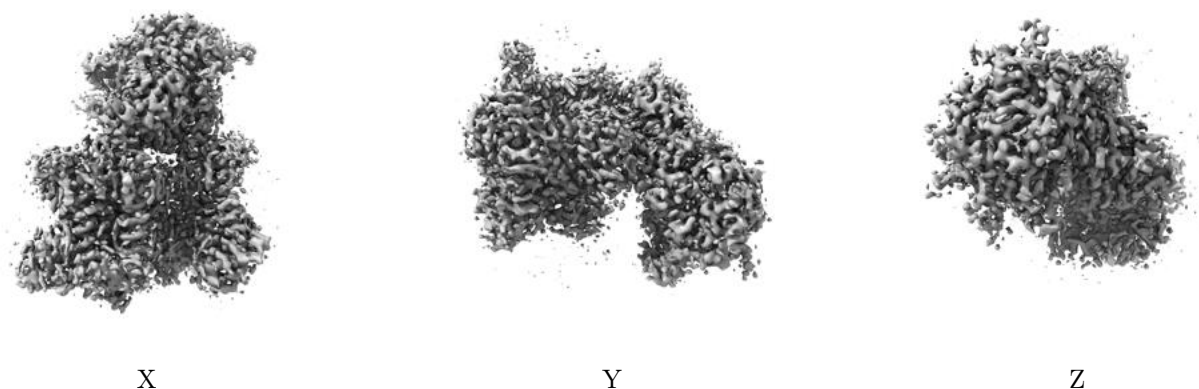


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.028. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

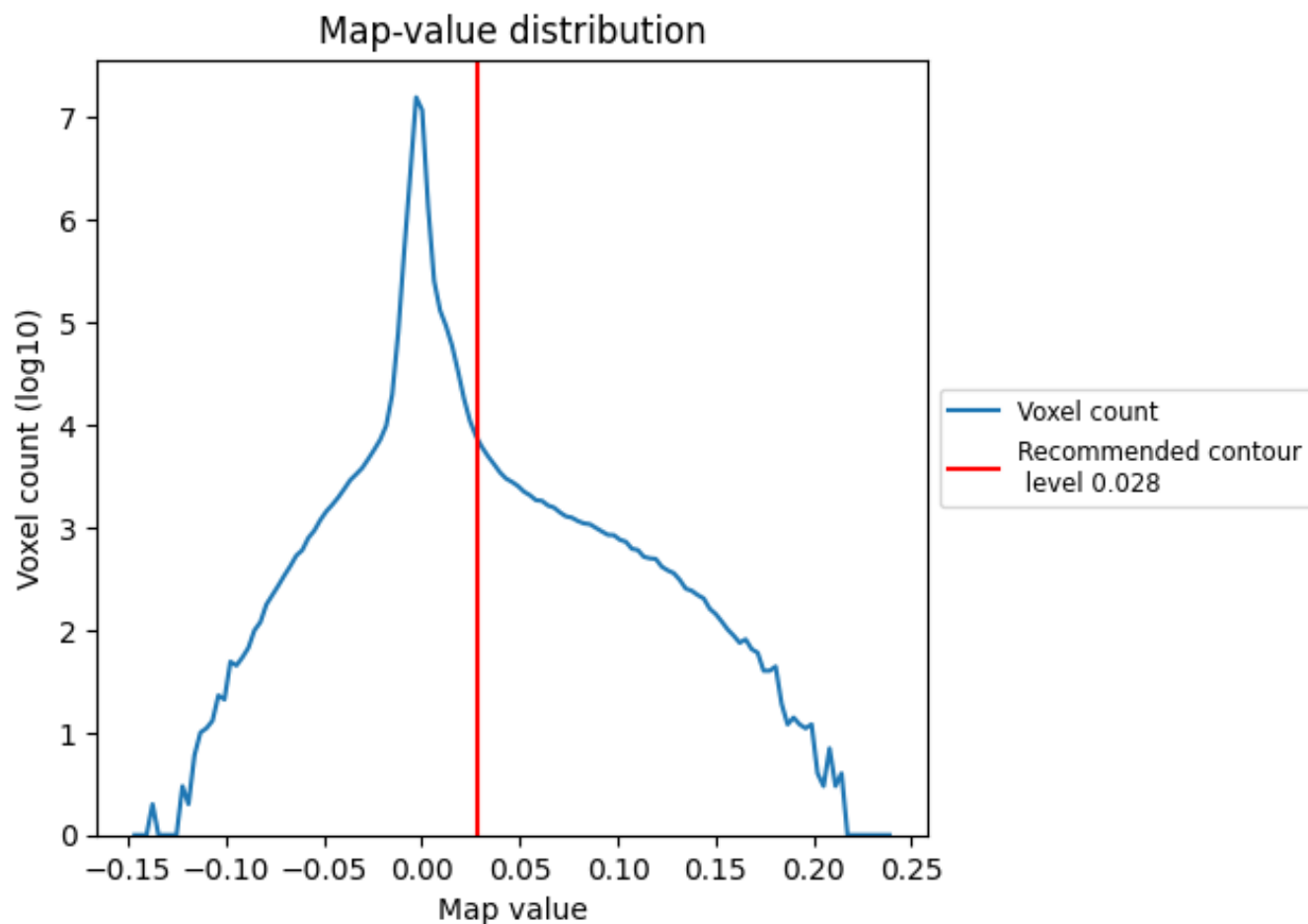
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

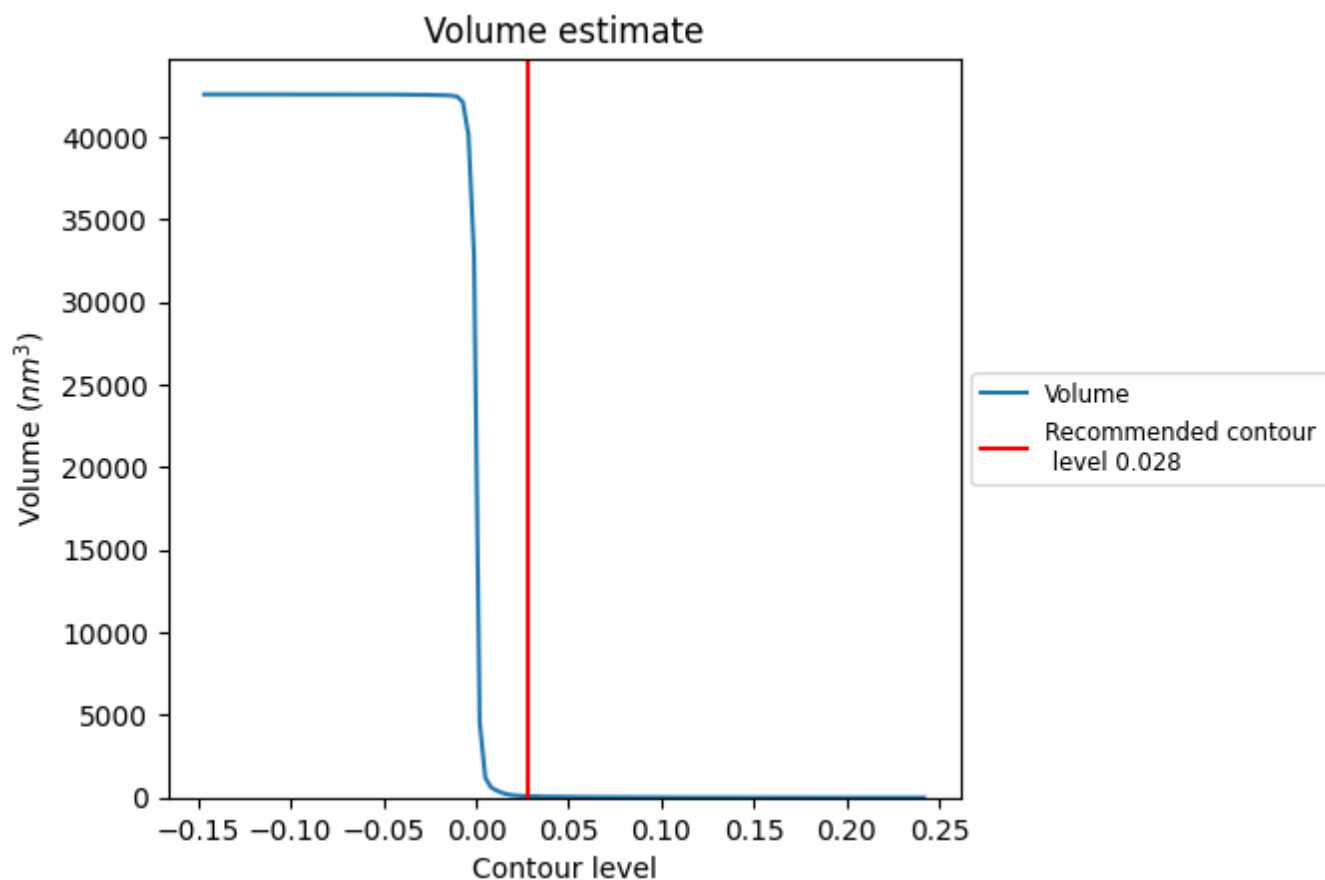
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

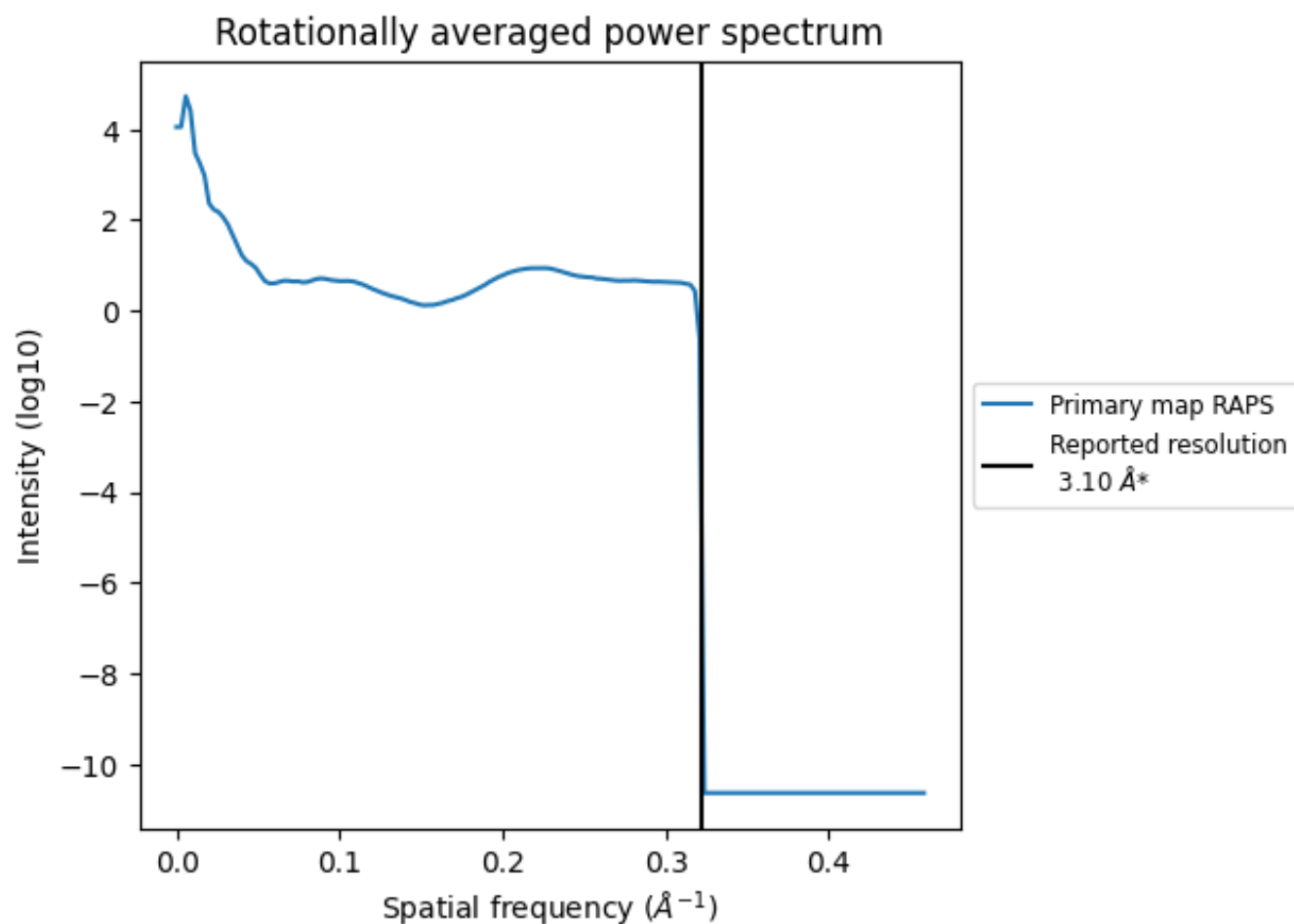
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 83 nm³; this corresponds to an approximate mass of 75 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 0.323 Å⁻¹

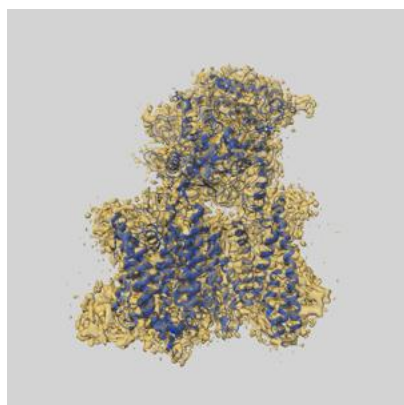
8 Fourier-Shell correlation

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

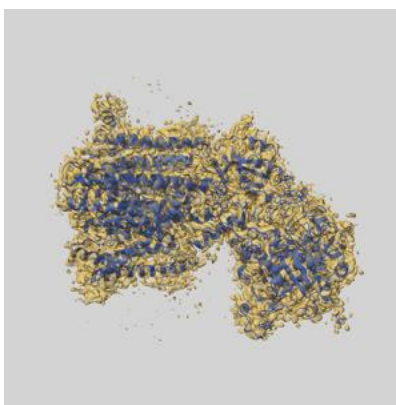
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30312 and PDB model 7C9I. Per-residue inclusion information can be found in section 3 on page 9.

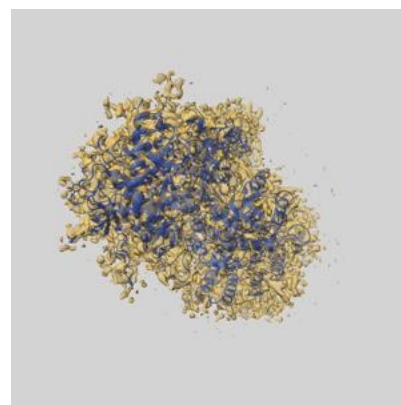
9.1 Map-model overlay [i](#)



X



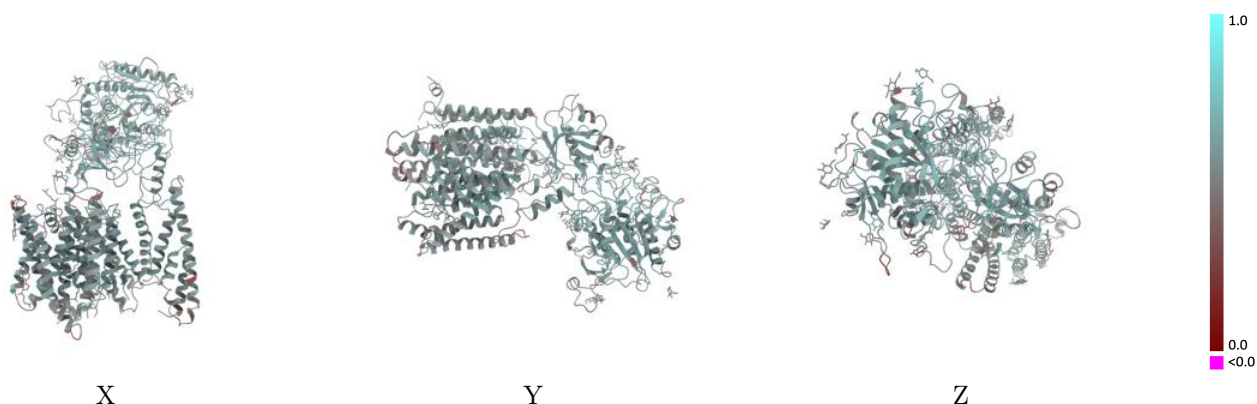
Y



Z

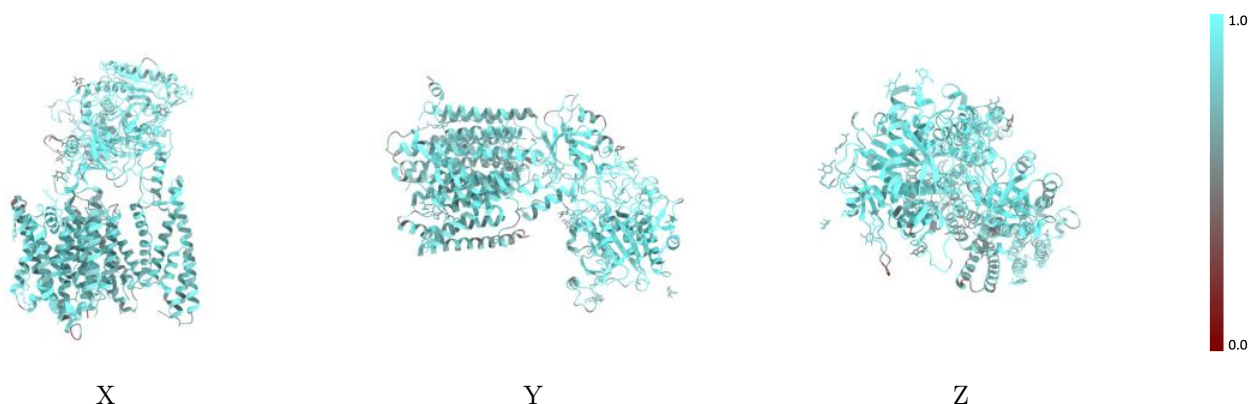
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



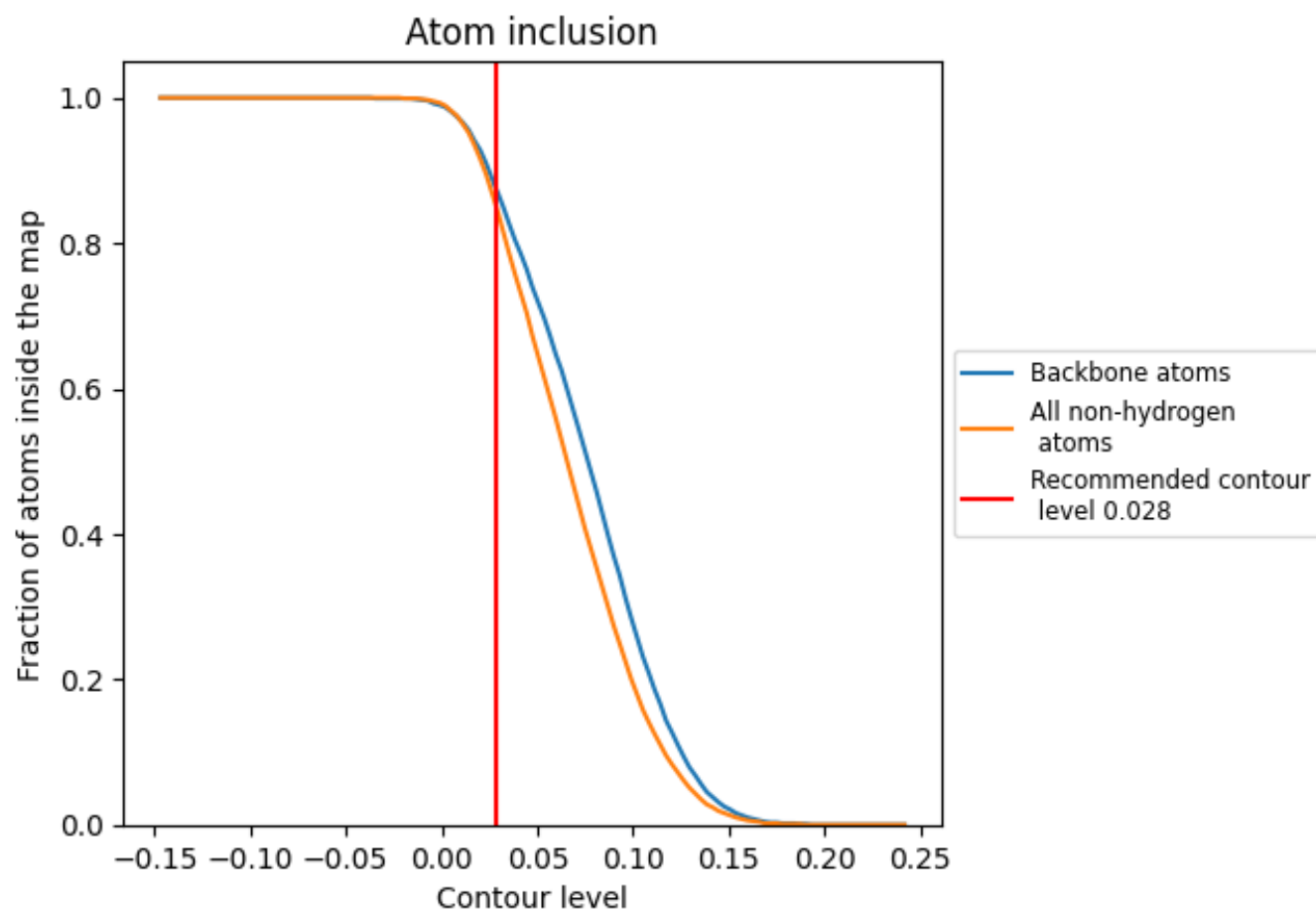
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.028).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8560	0.5500
A	0.8880	0.5670
B	0.8080	0.5350
C	0.8400	0.5380
D	0.8460	0.5190
E	0.7140	0.4940
F	0.8200	0.5150
G	0.9640	0.5580
H	0.8570	0.5450
I	0.6430	0.4050
J	0.7500	0.5140

1.0

0.0

<0.0