



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 02:49 AM UTC

PDB ID : 7TXZ / pdb_00007txz
EMDB ID : EMD-26162
Title : Nipah Virus attachment (G) glycoprotein ectodomain in complex with nAH1.3 neutralizing antibody Fab fragment (local refinement of the distal region)
Authors : Wang, Z.Q.; Seattle Structural Genomics Center for Infectious Disease (SSG-CID); Veesler, D.
Deposited on : 2022-02-10
Resolution : 3.20 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:

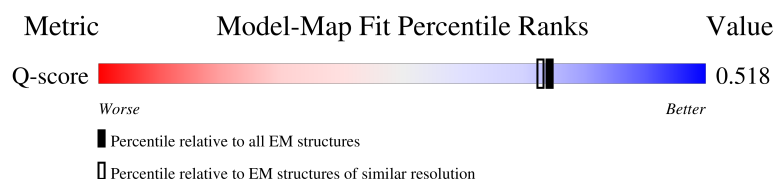
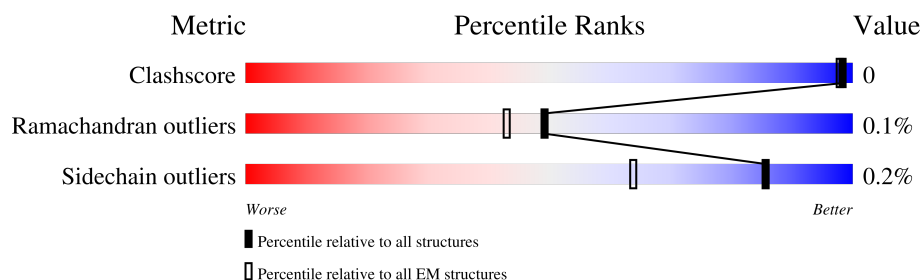
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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

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

The reported resolution of this entry is 3.20 Å.

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



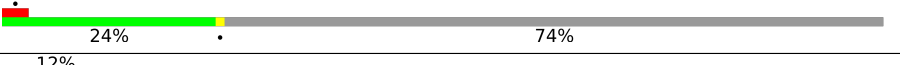
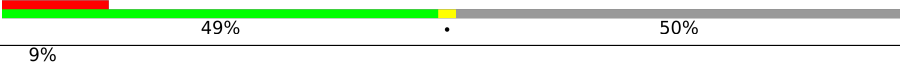
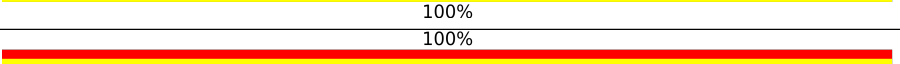
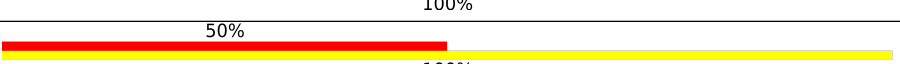
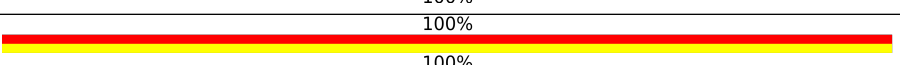
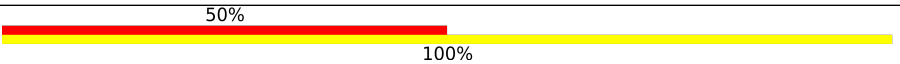
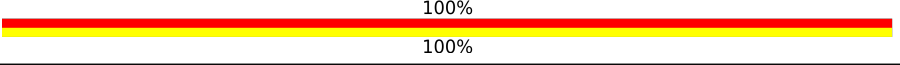
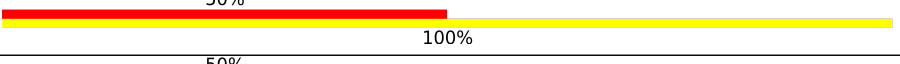
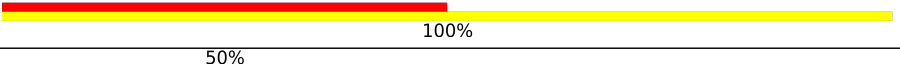
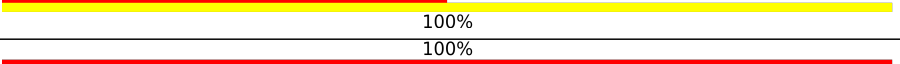
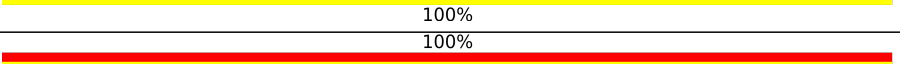
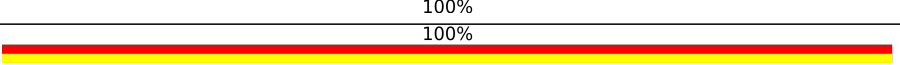
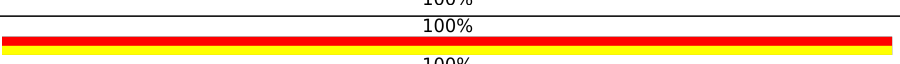
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	539	12% 83% 13%
1	B	539	8% 82% 5% 13%
1	C	539	6% 94%
1	D	539	6% 94%

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Mol	Chain	Length	Quality of chain
2	E	458	
2	H	458	
3	F	218	
3	L	218	
4	G	2	
4	I	2	
4	K	2	
4	M	2	
4	N	2	
4	O	2	
4	P	2	
4	Q	2	
4	S	2	
4	T	2	
4	U	2	
5	J	3	
5	R	3	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11303 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 Glycoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	470	Total	C	N	O	S	0	0
			3513	2270	606	613	24		
1	B	471	Total	C	N	O	S	0	0
			3579	2304	618	633	24		
1	D	34	Total	C	N	O	S	0	0
			212	130	40	39	3		
1	C	34	Total	C	N	O	S	0	0
			205	129	38	35	3		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	64	HIS	-	expression tag	UNP Q9IH62
A	65	HIS	-	expression tag	UNP Q9IH62
A	66	HIS	-	expression tag	UNP Q9IH62
A	67	HIS	-	expression tag	UNP Q9IH62
A	68	HIS	-	expression tag	UNP Q9IH62
A	69	HIS	-	expression tag	UNP Q9IH62
A	602	TYR	-	expression tag	UNP Q9IH62
B	64	HIS	-	expression tag	UNP Q9IH62
B	65	HIS	-	expression tag	UNP Q9IH62
B	66	HIS	-	expression tag	UNP Q9IH62
B	67	HIS	-	expression tag	UNP Q9IH62
B	68	HIS	-	expression tag	UNP Q9IH62
B	69	HIS	-	expression tag	UNP Q9IH62
B	602	TYR	-	expression tag	UNP Q9IH62
D	64	HIS	-	expression tag	UNP Q9IH62
D	65	HIS	-	expression tag	UNP Q9IH62
D	66	HIS	-	expression tag	UNP Q9IH62
D	67	HIS	-	expression tag	UNP Q9IH62
D	68	HIS	-	expression tag	UNP Q9IH62
D	69	HIS	-	expression tag	UNP Q9IH62
D	602	TYR	-	expression tag	UNP Q9IH62
C	64	HIS	-	expression tag	UNP Q9IH62

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Chain	Residue	Modelled	Actual	Comment	Reference
C	65	HIS	-	expression tag	UNP Q9IH62
C	66	HIS	-	expression tag	UNP Q9IH62
C	67	HIS	-	expression tag	UNP Q9IH62
C	68	HIS	-	expression tag	UNP Q9IH62
C	69	HIS	-	expression tag	UNP Q9IH62
C	602	TYR	-	expression tag	UNP Q9IH62

- Molecule 2 is a protein called nAH1.3 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	117	Total	C	N	O	S	0	0
			882	572	153	152	5		
2	H	117	Total	C	N	O	S	0	0
			874	563	152	154	5		

- Molecule 3 is a protein called nAH1.3 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	110	Total	C	N	O	S	0	0
			835	527	140	163	5		
3	L	111	Total	C	N	O	S	0	0
			805	515	140	145	5		

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



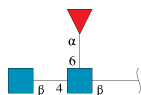
Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		

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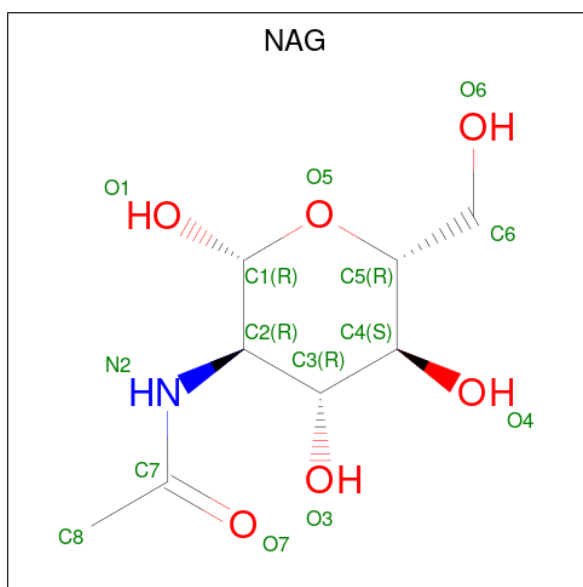
Mol	Chain	Residues	Atoms				AltConf	Trace
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	2	10		
4	Q	2	Total	C	N	O	0	0
			28	16	2	10		
4	S	2	Total	C	N	O	0	0
			28	16	2	10		
4	T	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	J	3	Total	C	N	O	0	0
			38	22	2	14		
5	R	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

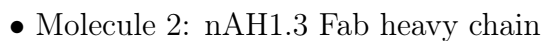
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• Molecule 1: Glycoprotein G

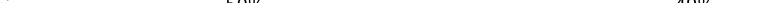


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• Molecule 2: nAH1.3 Fab heavy chain

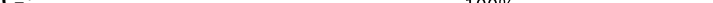


THR LEU THR THR LYS ASP GLU TYR GLU ARG HIS ASN SER TYR THR CYS GLU ALA THR HIS LYS THR SER THR THR PRO PRO ILE VAL LYS SER SER PHE ASN ARG ASN GLU CYS

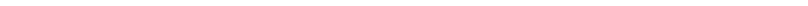
Chain L: 

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

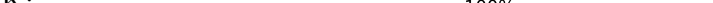
GLU
ALA
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ASN
ARG
ASN
GLU
CYS

Chain G: 

NAG1
NAG2

Chain I: 

NAG1
NAG2

Chain K:  50% 100%

NAG1
NAG2

Chain M:	100%
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- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



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



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



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



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	168035	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 ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.519	Depositor
Minimum map value	-3.761	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	1	Depositor
Map size (Å)	482.99997, 482.99997, 482.99997	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, FUC

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	0.83	0/3603	1.15	42/4925 (0.9%)
1	B	0.87	0/3669	1.14	49/5009 (1.0%)
1	C	0.69	0/209	1.38	6/290 (2.1%)
1	D	0.76	0/216	1.09	2/299 (0.7%)
2	E	0.80	0/905	0.98	4/1232 (0.3%)
2	H	0.86	0/897	1.00	6/1222 (0.5%)
3	F	0.83	0/855	1.07	6/1156 (0.5%)
3	L	0.82	0/825	1.06	6/1119 (0.5%)
All	All	0.84	0/11179	1.12	121/15252 (0.8%)

There are no bond length outliers.

All (121) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	493	CYS	CA-C-N	8.04	127.93	120.21
1	A	493	CYS	C-N-CA	8.04	127.93	120.21
1	B	302	ASP	CA-C-N	7.99	127.71	119.56
1	B	302	ASP	C-N-CA	7.99	127.71	119.56
1	A	391	LYS	CA-C-N	7.66	127.37	119.56
1	A	391	LYS	C-N-CA	7.66	127.37	119.56
1	B	272	THR	CA-C-N	7.60	125.13	119.66
1	B	272	THR	C-N-CA	7.60	125.13	119.66
1	A	322	LYS	CA-C-N	7.29	127.29	119.78
1	A	322	LYS	C-N-CA	7.29	127.29	119.78
1	C	150	LEU	CA-C-N	6.92	127.51	120.38
1	C	150	LEU	C-N-CA	6.92	127.51	120.38
1	A	273	PRO	CA-C-N	6.88	126.51	119.56
1	A	273	PRO	C-N-CA	6.88	126.51	119.56
1	B	423	ASN	CA-C-N	6.77	127.16	119.92
1	B	423	ASN	C-N-CA	6.77	127.16	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	ASN	CA-C-N	6.76	126.73	120.03
1	A	164	ASN	C-N-CA	6.76	126.73	120.03
1	A	597	ILE	CA-C-N	6.73	126.49	119.76
1	A	597	ILE	C-N-CA	6.73	126.49	119.76
1	A	199	LYS	CA-C-N	6.70	126.66	119.76
1	A	199	LYS	C-N-CA	6.70	126.66	119.76
1	B	273	PRO	N-CA-C	-6.61	103.51	110.58
1	C	162	CYS	CA-C-N	6.54	126.52	119.78
1	C	162	CYS	C-N-CA	6.54	126.52	119.78
1	A	150	LEU	CA-C-N	6.45	127.02	120.38
1	A	150	LEU	C-N-CA	6.45	127.02	120.38
1	A	302	ASP	CA-C-N	6.41	126.54	119.87
1	A	302	ASP	C-N-CA	6.41	126.54	119.87
1	B	322	LYS	CA-C-N	6.38	126.36	119.78
1	B	322	LYS	C-N-CA	6.38	126.36	119.78
1	B	164	ASN	CA-C-N	6.37	125.99	119.56
1	B	164	ASN	C-N-CA	6.37	125.99	119.56
1	B	597	ILE	CA-C-N	6.33	126.24	119.85
1	B	597	ILE	C-N-CA	6.33	126.24	119.85
1	B	487	ARG	CA-C-N	6.33	126.29	120.03
1	B	487	ARG	C-N-CA	6.33	126.29	120.03
3	F	46	GLN	CA-C-N	6.28	126.84	120.38
3	F	46	GLN	C-N-CA	6.28	126.84	120.38
1	B	219	ASP	CA-C-N	6.16	126.07	119.85
1	B	219	ASP	C-N-CA	6.16	126.07	119.85
1	A	151	PRO	CA-C-N	6.07	126.01	119.76
1	A	151	PRO	C-N-CA	6.07	126.01	119.76
1	B	493	CYS	CA-C-N	6.05	126.02	120.03
1	B	493	CYS	C-N-CA	6.05	126.02	120.03
3	L	62	VAL	CA-C-N	6.05	126.02	120.03
3	L	62	VAL	C-N-CA	6.05	126.02	120.03
1	A	172	ARG	CA-C-N	6.03	126.00	120.03
1	A	172	ARG	C-N-CA	6.03	126.00	120.03
3	F	62	VAL	CA-C-N	5.99	125.96	120.03
3	F	62	VAL	C-N-CA	5.99	125.96	120.03
1	B	273	PRO	CA-C-N	5.84	125.95	119.87
1	B	273	PRO	C-N-CA	5.84	125.95	119.87
1	B	391	LYS	CA-C-N	5.82	125.50	119.56
1	B	391	LYS	C-N-CA	5.82	125.50	119.56
1	A	423	ASN	CA-C-N	5.82	125.73	119.85
1	A	423	ASN	C-N-CA	5.82	125.73	119.85
1	B	199	LYS	CA-C-N	5.82	125.75	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	199	LYS	C-N-CA	5.82	125.75	119.76
1	B	162	CYS	CA-C-N	5.80	125.76	119.78
1	B	162	CYS	C-N-CA	5.80	125.76	119.78
1	B	275	ASN	CA-C-N	5.77	125.87	119.87
1	B	275	ASN	C-N-CA	5.77	125.87	119.87
1	B	349	MET	CA-C-N	5.75	125.69	119.76
1	B	349	MET	C-N-CA	5.75	125.69	119.76
1	A	540	PHE	N-CA-C	5.75	117.81	109.07
1	A	450	GLN	CA-C-N	5.73	125.66	119.76
1	A	450	GLN	C-N-CA	5.73	125.66	119.76
1	A	352	GLY	CA-C-N	5.61	125.72	119.32
1	A	352	GLY	C-N-CA	5.61	125.72	119.32
1	D	162	CYS	CA-C-N	5.61	125.51	119.85
1	D	162	CYS	C-N-CA	5.61	125.51	119.85
3	F	47	PRO	CA-C-N	5.58	125.50	119.76
3	F	47	PRO	C-N-CA	5.58	125.50	119.76
1	A	402	ARG	CA-C-N	5.55	126.77	119.84
1	A	402	ARG	C-N-CA	5.55	126.77	119.84
1	B	450	GLN	CA-C-N	5.54	125.46	119.76
1	B	450	GLN	C-N-CA	5.54	125.46	119.76
1	B	586	ASN	CB-CA-C	-5.53	110.22	116.63
2	H	13	GLN	CA-C-N	5.52	125.53	119.90
2	H	13	GLN	C-N-CA	5.52	125.53	119.90
1	B	585	ASP	N-CA-C	5.49	116.31	108.74
1	A	275	ASN	CA-C-N	5.47	125.56	119.87
1	A	275	ASN	C-N-CA	5.47	125.56	119.87
1	A	499	CYS	CA-C-N	5.47	125.78	119.93
1	A	499	CYS	C-N-CA	5.47	125.78	119.93
2	E	40	SER	CA-C-N	5.42	125.50	119.32
2	E	40	SER	C-N-CA	5.42	125.50	119.32
1	B	352	GLY	CA-C-N	5.41	125.49	119.32
1	B	352	GLY	C-N-CA	5.41	125.49	119.32
1	B	150	LEU	CA-C-N	5.35	125.89	120.38
1	B	150	LEU	C-N-CA	5.35	125.89	120.38
2	H	40	SER	CA-C-N	5.34	125.67	119.47
2	H	40	SER	C-N-CA	5.34	125.67	119.47
1	B	540	PHE	N-CA-C	5.34	117.19	109.07
2	H	89	ARG	CA-C-N	5.30	125.62	119.47
2	H	89	ARG	C-N-CA	5.30	125.62	119.47
1	B	402	ARG	CA-C-N	5.30	125.62	119.47
1	B	402	ARG	C-N-CA	5.30	125.62	119.47
1	B	420	ASP	CA-CB-CG	5.25	117.85	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	46	GLN	CA-C-N	5.25	125.78	120.38
3	L	46	GLN	C-N-CA	5.25	125.78	120.38
1	A	589	ARG	CA-C-N	5.24	125.16	119.76
1	A	589	ARG	C-N-CA	5.24	125.16	119.76
1	B	499	CYS	CA-C-N	5.24	125.53	119.93
1	B	499	CYS	C-N-CA	5.24	125.53	119.93
2	E	13	GLN	CA-C-N	5.20	125.20	119.90
2	E	13	GLN	C-N-CA	5.20	125.20	119.90
1	A	162	CYS	CA-C-N	5.13	125.04	119.76
1	A	162	CYS	C-N-CA	5.13	125.04	119.76
3	L	47	PRO	CA-C-N	5.12	125.03	119.76
3	L	47	PRO	C-N-CA	5.12	125.03	119.76
1	C	151	PRO	CA-C-N	5.10	125.03	119.78
1	C	151	PRO	C-N-CA	5.10	125.03	119.78
1	B	151	PRO	CA-C-N	5.05	124.96	119.76
1	B	151	PRO	C-N-CA	5.05	124.96	119.76
1	B	364	PHE	CA-C-N	5.05	124.81	119.76
1	B	364	PHE	C-N-CA	5.05	124.81	119.76
1	A	272	THR	CA-C-N	5.03	125.56	120.38
1	A	272	THR	C-N-CA	5.03	125.56	120.38
1	A	148	PHE	N-CA-C	5.01	116.45	110.44

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	3513	0	3287	2	0
1	B	3579	0	3398	2	0
1	C	205	0	151	0	0
1	D	212	0	154	0	0
2	E	882	0	814	2	0
2	H	874	0	785	1	0
3	F	835	0	806	0	0
3	L	805	0	737	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	28	0	25	0	0
4	I	28	0	25	0	0
4	K	28	0	25	0	0
4	M	28	0	25	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	Q	28	0	25	0	0
4	S	28	0	25	0	0
4	T	28	0	25	0	0
4	U	28	0	25	0	0
5	J	38	0	34	0	0
5	R	38	0	34	0	0
6	A	14	0	13	0	0
All	All	11303	0	10488	7	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 0.

All (7) 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:420:ASP:OD2	1:A:425:LYS:NZ	2.42	0.52
2:E:102:ILE:O	2:E:103:THR:C	2.55	0.50
2:H:102:ILE:O	2:H:103:THR:C	2.56	0.46
2:E:27:PHE:CE2	2:E:100:ARG:HD3	2.52	0.45
1:B:601:CYS:O	1:B:602:TYR:C	2.60	0.44
1:B:155:ILE:O	1:B:155:ILE:HG22	2.19	0.42
1:A:454:TYR:CD1	1:A:454:TYR:C	2.98	0.41

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	466/539 (86%)	457 (98%)	9 (2%)	0	100	100
1	B	469/539 (87%)	458 (98%)	11 (2%)	0	100	100
1	C	32/539 (6%)	31 (97%)	1 (3%)	0	100	100
1	D	32/539 (6%)	30 (94%)	1 (3%)	1 (3%)	3	22
2	E	115/458 (25%)	113 (98%)	2 (2%)	0	100	100
2	H	115/458 (25%)	113 (98%)	2 (2%)	0	100	100
3	F	108/218 (50%)	107 (99%)	1 (1%)	0	100	100
3	L	109/218 (50%)	108 (99%)	1 (1%)	0	100	100
All	All	1446/3508 (41%)	1417 (98%)	28 (2%)	1 (0%)	49	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	156	HIS

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	347/483 (72%)	346 (100%)	1 (0%)	86	88
1	B	364/483 (75%)	364 (100%)	0	100	100
1	C	14/483 (3%)	14 (100%)	0	100	100
1	D	16/483 (3%)	16 (100%)	0	100	100
2	E	80/408 (20%)	80 (100%)	0	100	100
2	H	78/408 (19%)	78 (100%)	0	100	100
3	F	92/191 (48%)	91 (99%)	1 (1%)	65	79
3	L	74/191 (39%)	74 (100%)	0	100	100
All	All	1065/3130 (34%)	1063 (100%)	2 (0%)	85	89

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

Mol	Chain	Res	Type
1	A	150	LEU
3	F	52	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	332	GLN
1	A	358	GLN
1	A	455	GLN
1	B	186	ASN
1	B	450	GLN
2	E	84	GLN
2	E	86	ASN
1	C	156	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

28 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	$\# Z > 2$
4	NAG	G	1	4,1	14,14,15	1.58	2 (14%)	17,19,21	0.99	1 (5%)
4	NAG	G	2	4	14,14,15	1.42	2 (14%)	17,19,21	0.86	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	I	1	4,1	14,14,15	1.46	1 (7%)	17,19,21	1.20	2 (11%)
4	NAG	I	2	4	14,14,15	1.42	2 (14%)	17,19,21	0.91	1 (5%)
5	NAG	J	1	5,1	14,14,15	1.32	1 (7%)	17,19,21	1.19	1 (5%)
5	NAG	J	2	5	14,14,15	1.52	2 (14%)	17,19,21	0.86	1 (5%)
5	FUC	J	3	5	10,10,11	1.44	3 (30%)	14,14,16	0.55	0
4	NAG	K	1	4,1	14,14,15	1.50	2 (14%)	17,19,21	1.17	3 (17%)
4	NAG	K	2	4	14,14,15	1.46	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	M	1	4,1	14,14,15	1.67	2 (14%)	17,19,21	0.92	1 (5%)
4	NAG	M	2	4	14,14,15	1.51	2 (14%)	17,19,21	0.95	1 (5%)
4	NAG	N	1	4,1	14,14,15	1.66	2 (14%)	17,19,21	0.85	1 (5%)
4	NAG	N	2	4	14,14,15	1.48	2 (14%)	17,19,21	0.95	1 (5%)
4	NAG	O	1	4,1	14,14,15	1.60	2 (14%)	17,19,21	0.94	1 (5%)
4	NAG	O	2	4	14,14,15	1.46	2 (14%)	17,19,21	0.84	1 (5%)
4	NAG	P	1	4,1	14,14,15	1.52	2 (14%)	17,19,21	0.89	1 (5%)
4	NAG	P	2	4	14,14,15	1.45	2 (14%)	17,19,21	0.89	1 (5%)
4	NAG	Q	1	4,1	14,14,15	1.52	2 (14%)	17,19,21	0.95	1 (5%)
4	NAG	Q	2	4	14,14,15	1.53	2 (14%)	17,19,21	0.91	1 (5%)
5	NAG	R	1	5,1	14,14,15	1.12	1 (7%)	17,19,21	1.05	2 (11%)
5	NAG	R	2	5	14,14,15	1.56	2 (14%)	17,19,21	0.80	1 (5%)
5	FUC	R	3	5	10,10,11	1.42	2 (20%)	14,14,16	0.51	0
4	NAG	S	1	4,1	14,14,15	1.59	2 (14%)	17,19,21	1.09	1 (5%)
4	NAG	S	2	4	14,14,15	1.47	2 (14%)	17,19,21	0.89	1 (5%)
4	NAG	T	1	4,1	14,14,15	1.65	2 (14%)	17,19,21	0.90	1 (5%)
4	NAG	T	2	4	14,14,15	1.45	2 (14%)	17,19,21	0.87	1 (5%)
4	NAG	U	1	4,1	14,14,15	1.62	2 (14%)	17,19,21	0.95	1 (5%)
4	NAG	U	2	4	14,14,15	1.41	2 (14%)	17,19,21	0.87	1 (5%)

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
4	NAG	G	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	1/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	J	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	J	2	5	-	0/6/23/26	0/1/1/1
5	FUC	J	3	5	-	-	0/1/1/1
4	NAG	K	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	0/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	0/6/23/26	0/1/1/1
5	NAG	R	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	R	2	5	-	0/6/23/26	0/1/1/1
5	FUC	R	3	5	-	-	0/1/1/1
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	1/6/23/26	0/1/1/1
4	NAG	T	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	T	2	4	-	1/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	1	NAG	C1-C2	4.65	1.58	1.52
4	G	1	NAG	C1-C2	4.39	1.58	1.52
4	O	1	NAG	C1-C2	4.38	1.58	1.52
4	M	1	NAG	C1-C2	4.36	1.58	1.52
4	S	1	NAG	C1-C2	4.33	1.58	1.52
4	T	1	NAG	C1-C2	4.27	1.58	1.52
4	U	1	NAG	C1-C2	4.22	1.58	1.52
5	R	2	NAG	C1-C2	4.18	1.58	1.52
5	J	1	NAG	C1-C2	3.99	1.57	1.52
4	P	1	NAG	C1-C2	3.94	1.57	1.52
4	Q	2	NAG	C1-C2	3.87	1.57	1.52
4	O	2	NAG	C1-C2	3.79	1.57	1.52
4	N	2	NAG	C1-C2	3.74	1.57	1.52
4	P	2	NAG	C1-C2	3.72	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	2	NAG	C1-C2	3.72	1.57	1.52
4	K	1	NAG	C1-C2	3.70	1.57	1.52
4	K	2	NAG	C1-C2	3.68	1.57	1.52
4	M	2	NAG	C1-C2	3.68	1.57	1.52
4	I	1	NAG	C1-C2	3.60	1.57	1.52
5	J	2	NAG	C1-C2	3.60	1.57	1.52
4	T	2	NAG	C1-C2	3.60	1.57	1.52
4	G	2	NAG	C1-C2	3.57	1.57	1.52
4	Q	1	NAG	C1-C2	3.52	1.57	1.52
4	U	2	NAG	C1-C2	3.51	1.57	1.52
4	I	2	NAG	C1-C2	3.43	1.57	1.52
5	R	1	NAG	C1-C2	3.20	1.56	1.52
5	J	2	NAG	O5-C5	2.70	1.48	1.43
4	M	2	NAG	O5-C5	2.61	1.48	1.43
4	U	1	NAG	O5-C5	2.60	1.48	1.43
4	Q	2	NAG	O5-C5	2.59	1.48	1.43
4	M	1	NAG	O5-C5	2.58	1.48	1.43
4	T	1	NAG	O5-C5	2.51	1.48	1.43
4	T	2	NAG	O5-C5	2.50	1.48	1.43
4	I	2	NAG	O5-C5	2.49	1.48	1.43
4	Q	1	NAG	O5-C5	2.48	1.48	1.43
4	U	2	NAG	O5-C5	2.45	1.48	1.43
5	R	2	NAG	O5-C5	2.42	1.48	1.43
5	R	3	FUC	O5-C5	2.41	1.48	1.43
4	S	2	NAG	O5-C5	2.41	1.48	1.43
4	O	2	NAG	O5-C5	2.40	1.48	1.43
4	N	2	NAG	O5-C5	2.40	1.48	1.43
4	G	2	NAG	O5-C5	2.39	1.48	1.43
4	N	1	NAG	O5-C5	2.35	1.48	1.43
5	J	3	FUC	O5-C5	2.35	1.48	1.43
4	P	1	NAG	O5-C5	2.35	1.48	1.43
4	P	2	NAG	O5-C5	2.33	1.48	1.43
4	K	2	NAG	O5-C5	2.31	1.47	1.43
4	O	1	NAG	O5-C5	2.29	1.47	1.43
4	S	1	NAG	O5-C5	2.27	1.47	1.43
5	J	3	FUC	C2-C3	2.26	1.55	1.52
4	K	1	NAG	O5-C5	2.25	1.47	1.43
4	G	1	NAG	O5-C5	2.17	1.47	1.43
5	J	3	FUC	C1-C2	2.08	1.57	1.52
5	R	3	FUC	C1-C2	2.06	1.57	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	1	NAG	C8-C7-N2	2.78	120.73	116.12
4	S	1	NAG	C8-C7-N2	2.63	120.48	116.12
4	K	1	NAG	C8-C7-N2	2.61	120.45	116.12
4	N	2	NAG	C8-C7-N2	2.53	120.32	116.12
5	J	2	NAG	C8-C7-N2	2.46	120.20	116.12
4	I	1	NAG	C8-C7-N2	2.46	120.20	116.12
4	I	1	NAG	C1-C2-N2	-2.45	106.57	110.43
4	M	2	NAG	C8-C7-N2	2.44	120.16	116.12
4	Q	2	NAG	C8-C7-N2	2.38	120.07	116.12
4	P	2	NAG	C8-C7-N2	2.38	120.06	116.12
4	K	2	NAG	C8-C7-N2	2.37	120.05	116.12
5	R	1	NAG	C8-C7-N2	2.36	120.04	116.12
4	I	2	NAG	C8-C7-N2	2.34	119.99	116.12
4	K	1	NAG	O4-C4-C5	-2.32	103.61	109.32
5	R	1	NAG	C2-N2-C7	-2.30	119.82	122.90
5	R	2	NAG	C8-C7-N2	2.28	119.89	116.12
4	Q	1	NAG	C8-C7-N2	2.27	119.88	116.12
4	S	2	NAG	C8-C7-N2	2.26	119.86	116.12
4	G	2	NAG	C8-C7-N2	2.26	119.86	116.12
4	U	2	NAG	C8-C7-N2	2.25	119.85	116.12
4	U	1	NAG	C8-C7-N2	2.24	119.84	116.12
4	M	1	NAG	C8-C7-N2	2.19	119.75	116.12
4	O	2	NAG	C8-C7-N2	2.18	119.74	116.12
4	O	1	NAG	C8-C7-N2	2.18	119.74	116.12
4	G	1	NAG	C8-C7-N2	2.15	119.68	116.12
4	T	1	NAG	C8-C7-N2	2.12	119.64	116.12
4	T	2	NAG	C8-C7-N2	2.12	119.64	116.12
4	P	1	NAG	C8-C7-N2	2.08	119.56	116.12
4	N	1	NAG	C8-C7-N2	2.04	119.50	116.12
4	K	1	NAG	O7-C7-C8	-2.01	118.48	122.05

There are no chirality outliers.

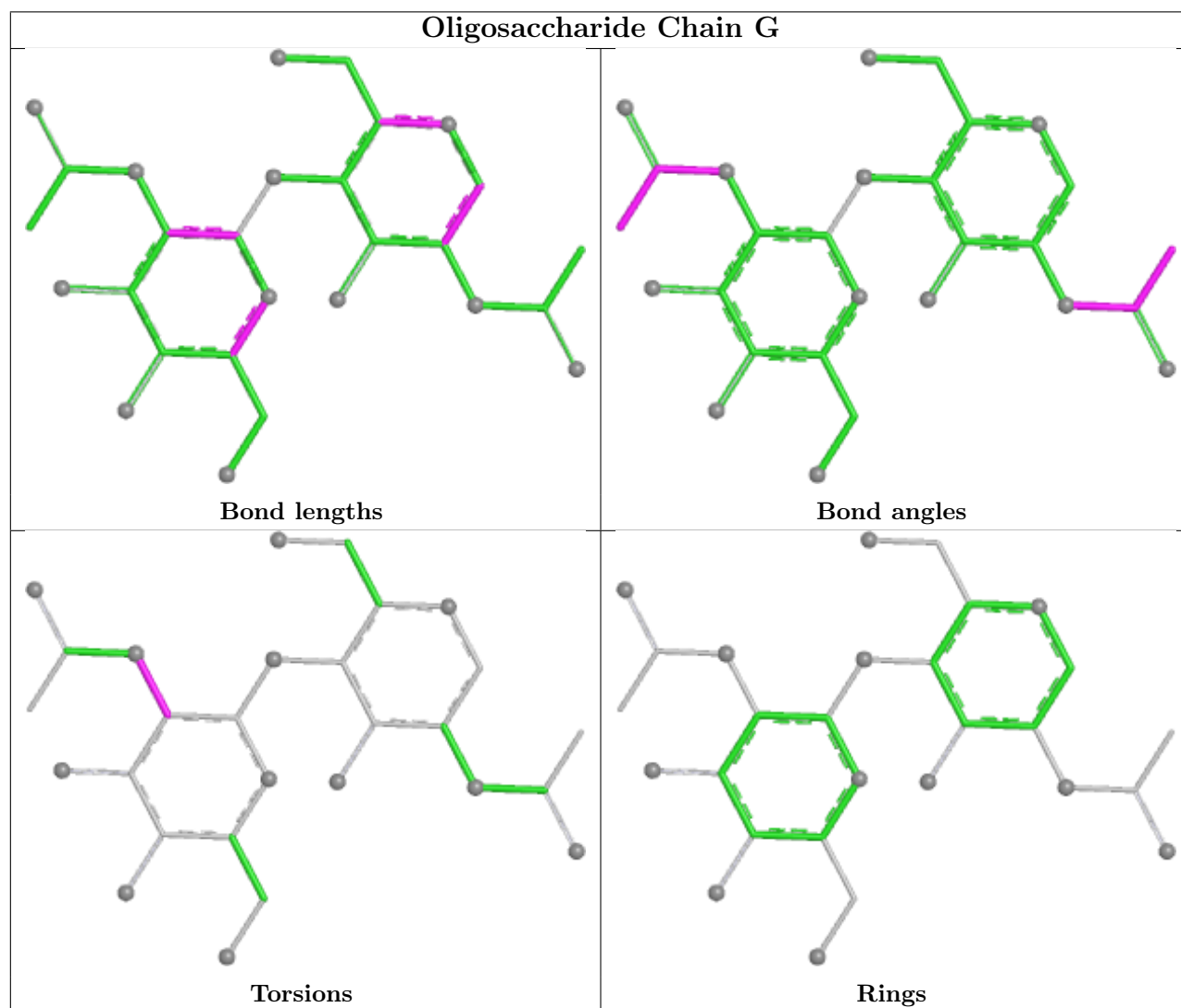
All (5) torsion outliers are listed below:

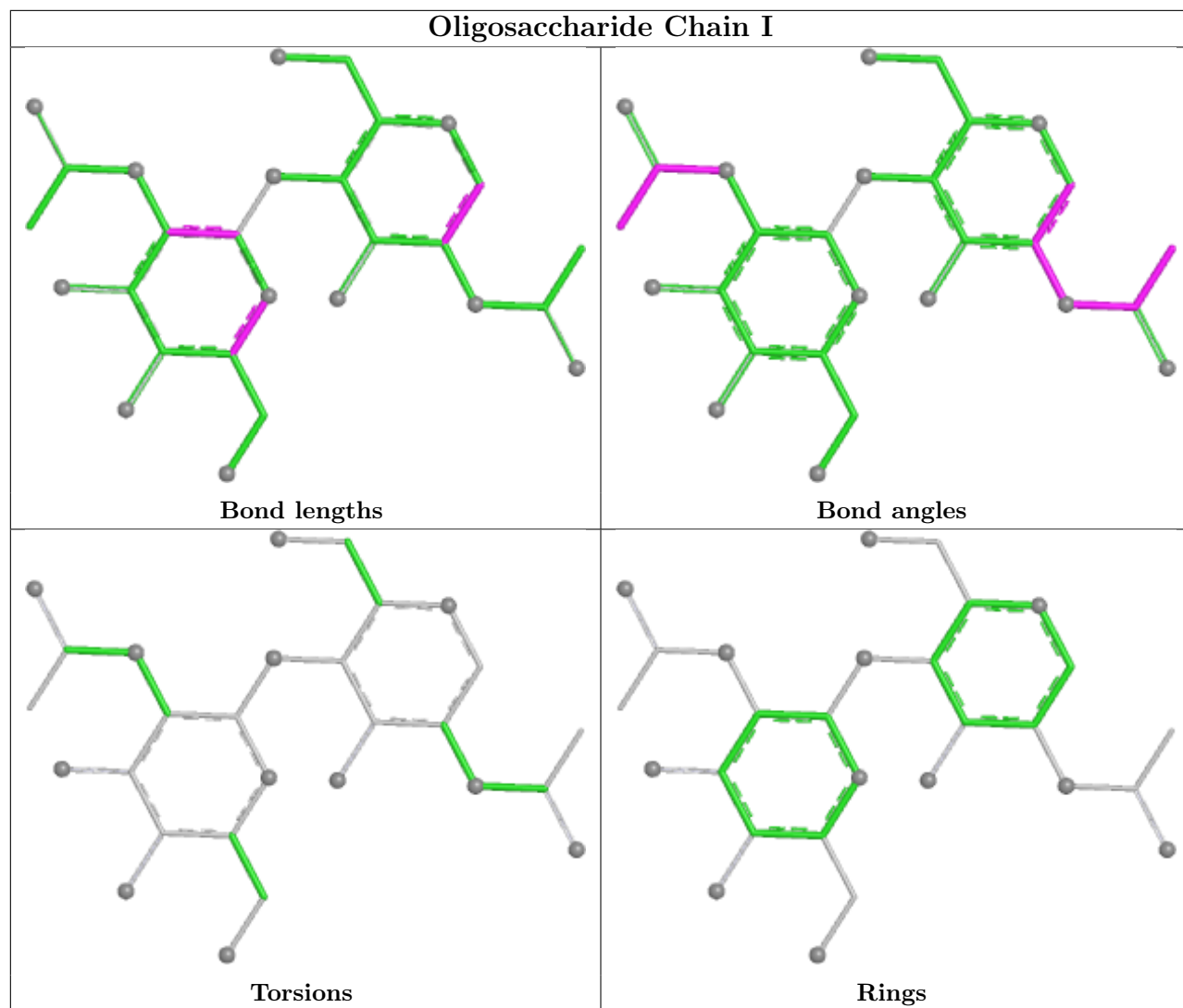
Mol	Chain	Res	Type	Atoms
4	S	2	NAG	O5-C5-C6-O6
4	T	2	NAG	O5-C5-C6-O6
4	G	2	NAG	C1-C2-N2-C7
4	T	1	NAG	C1-C2-N2-C7
5	R	1	NAG	C1-C2-N2-C7

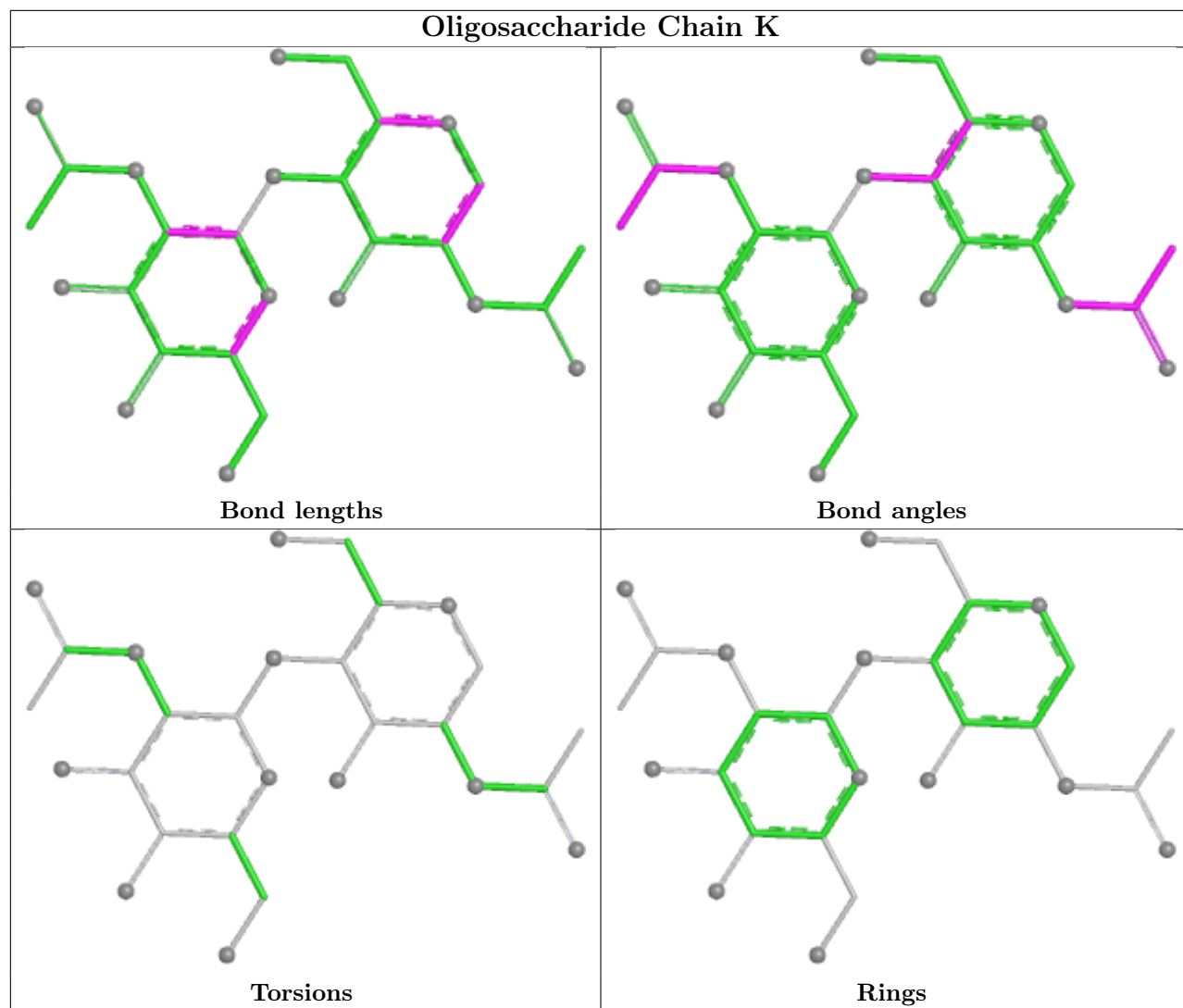
There are no ring outliers.

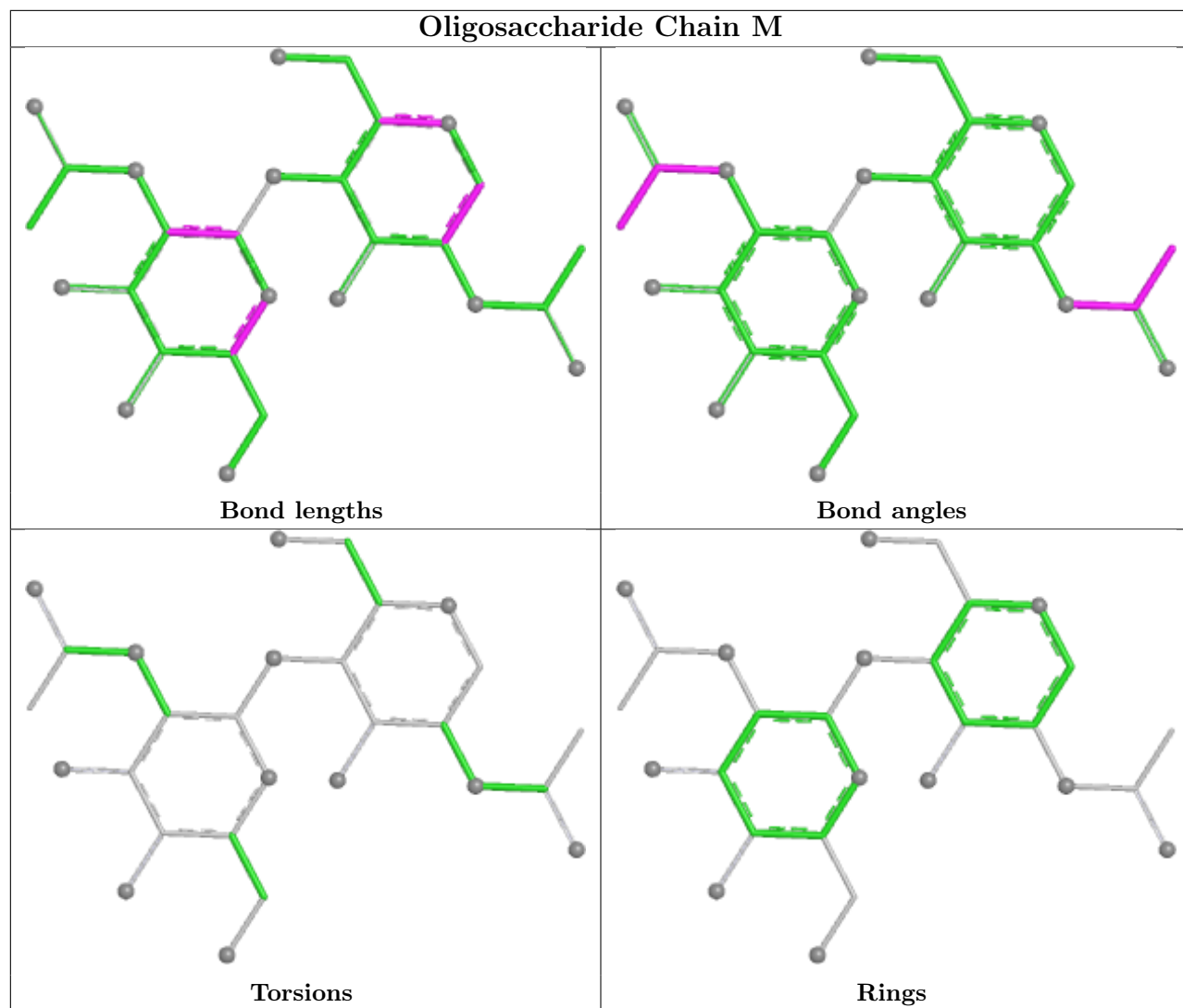
No monomer is involved in short contacts.

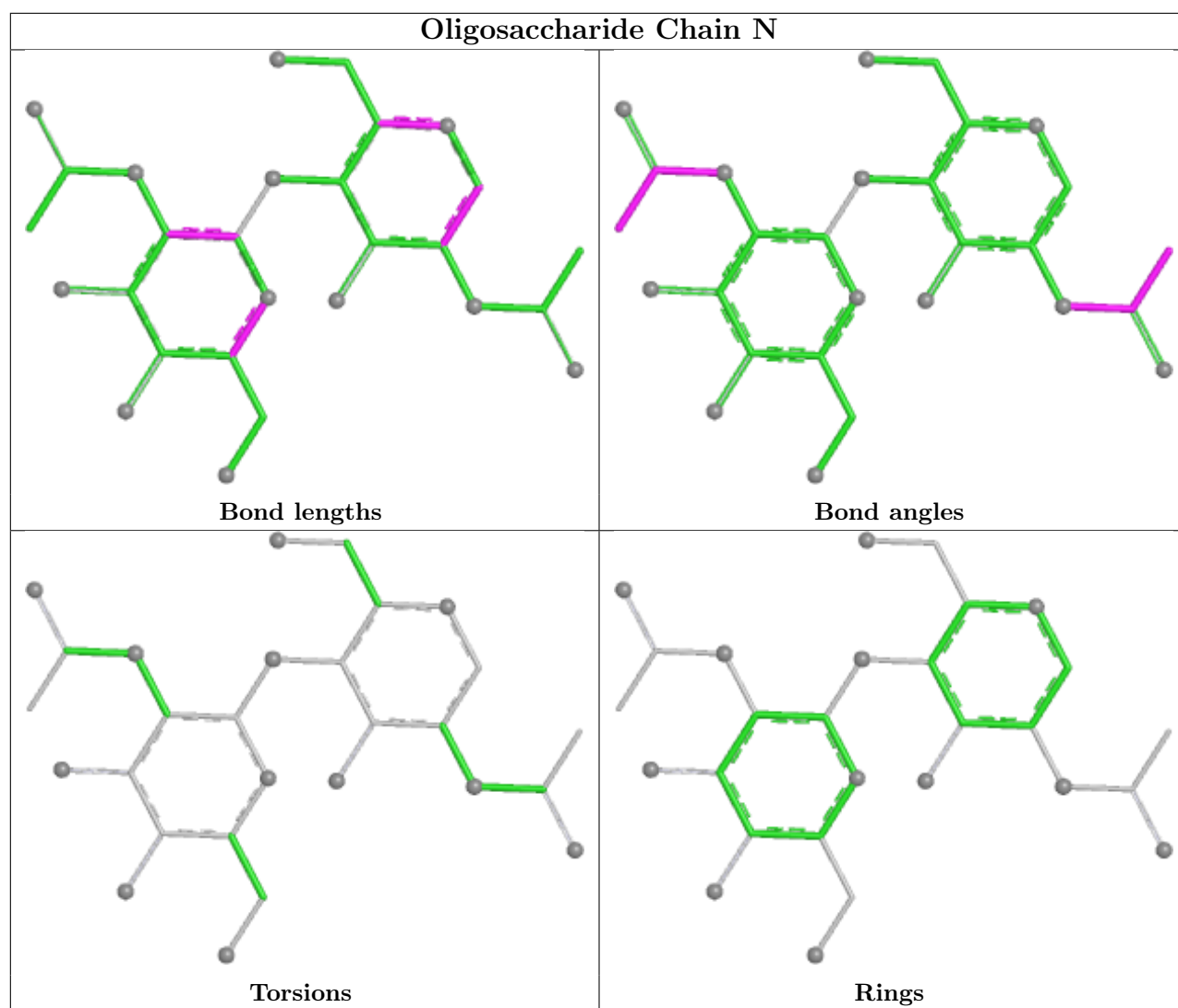
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

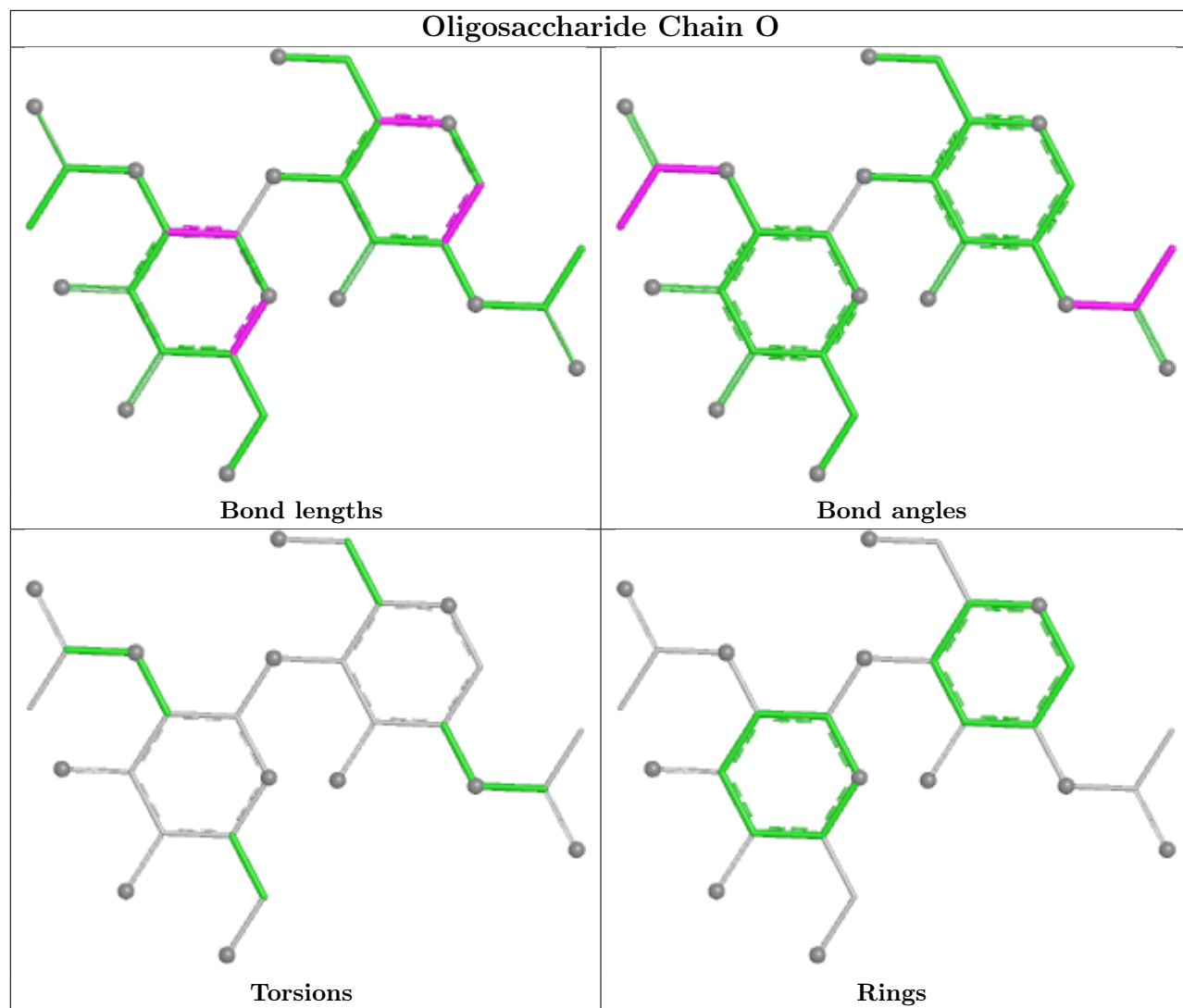


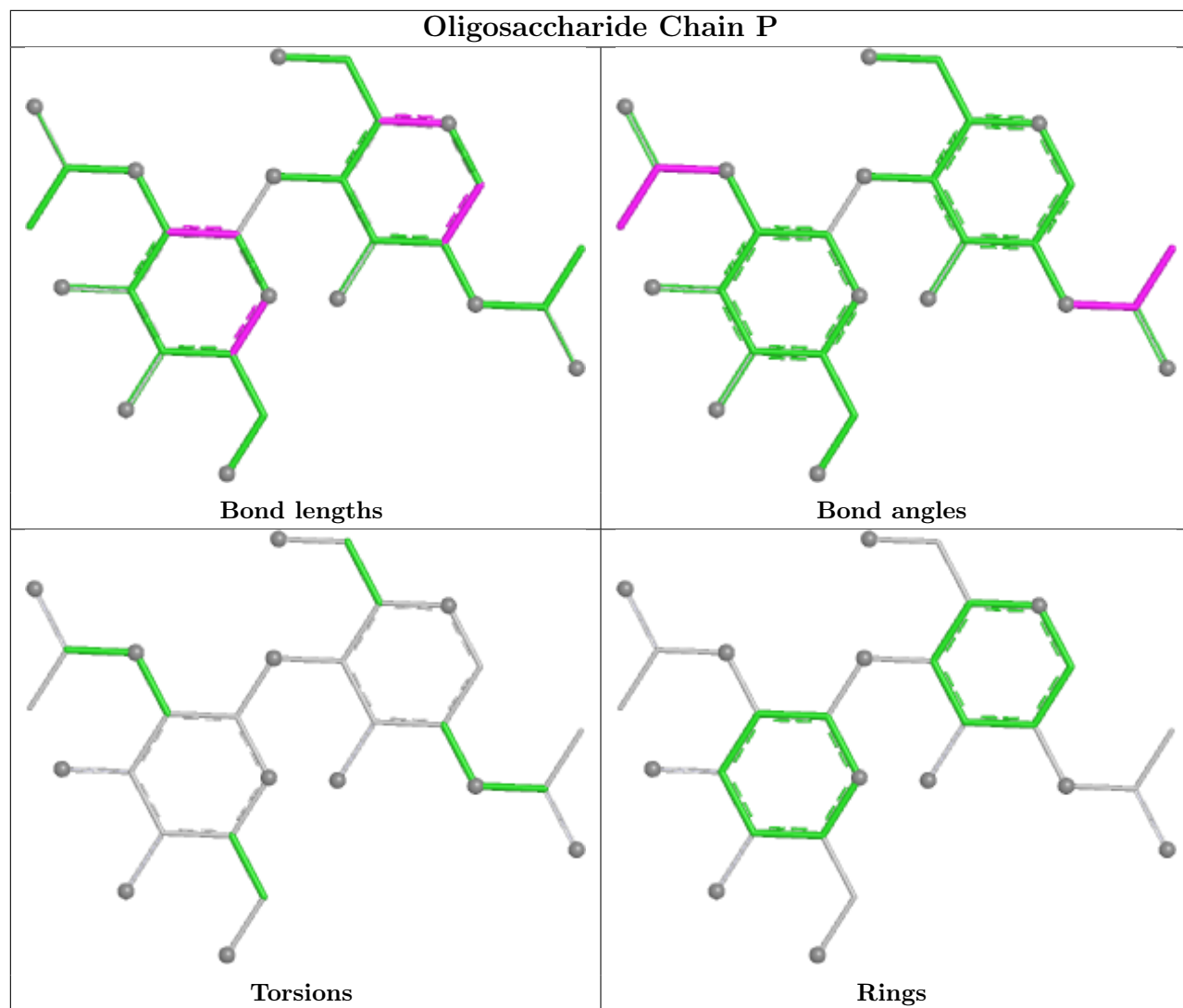


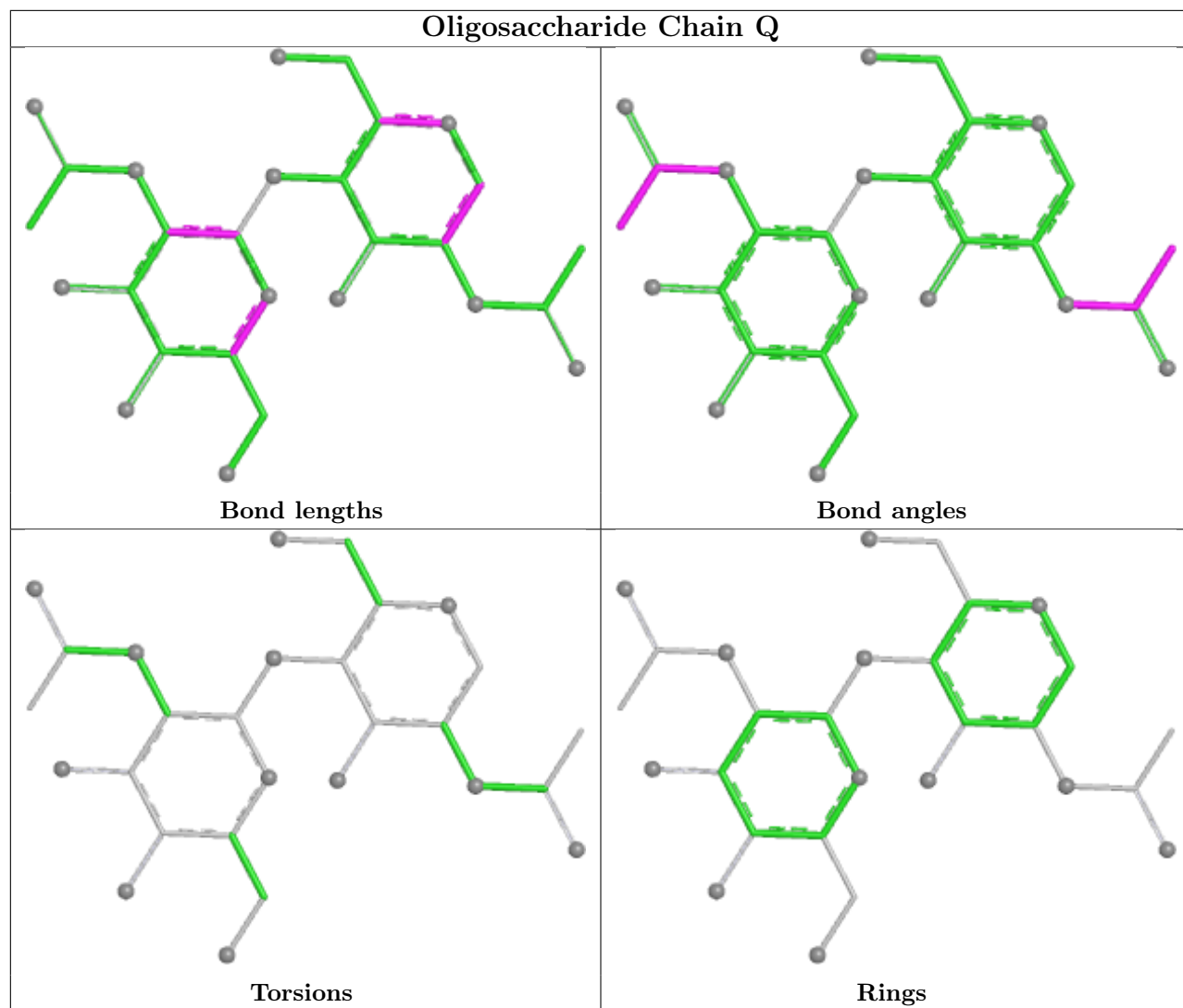


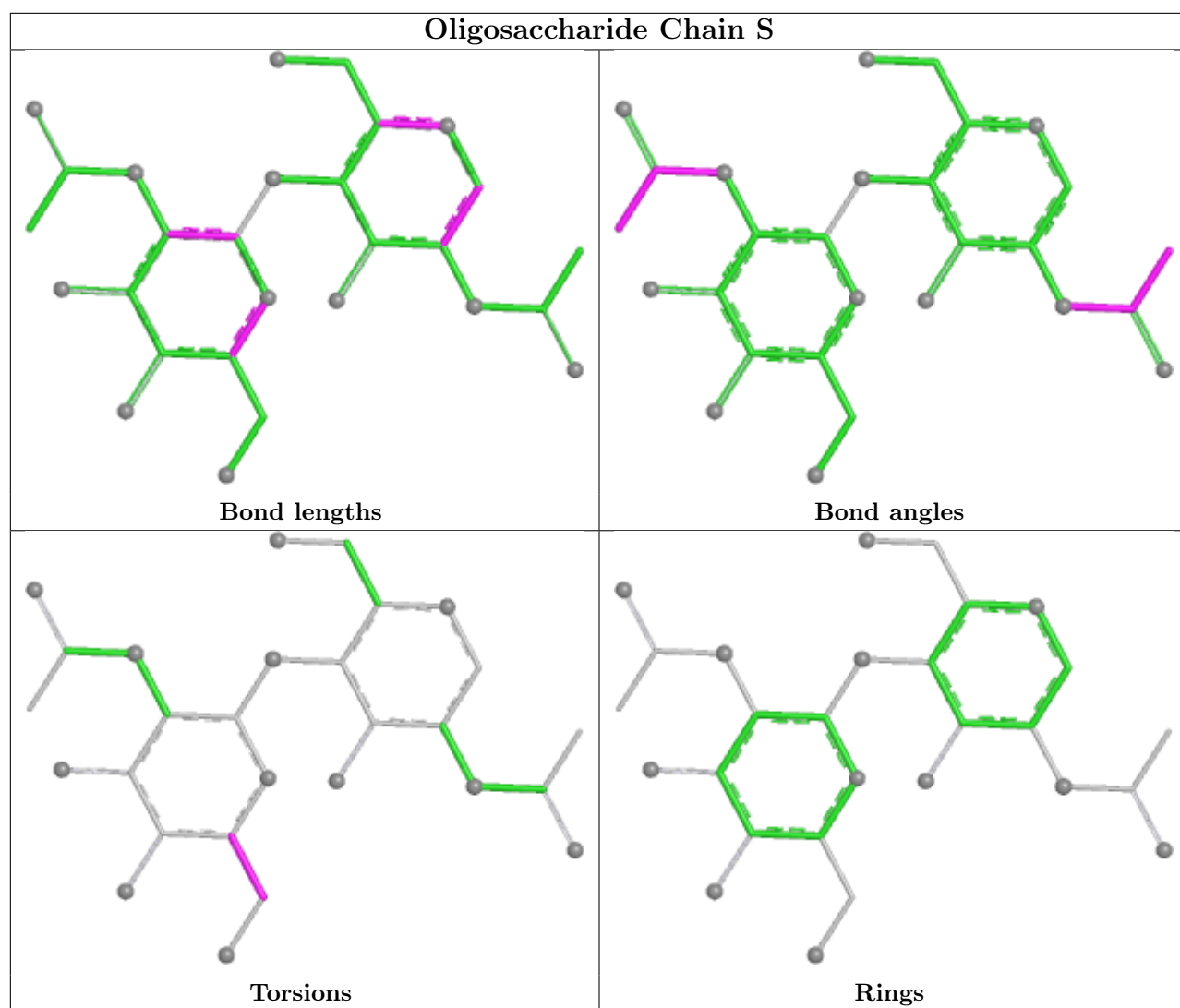


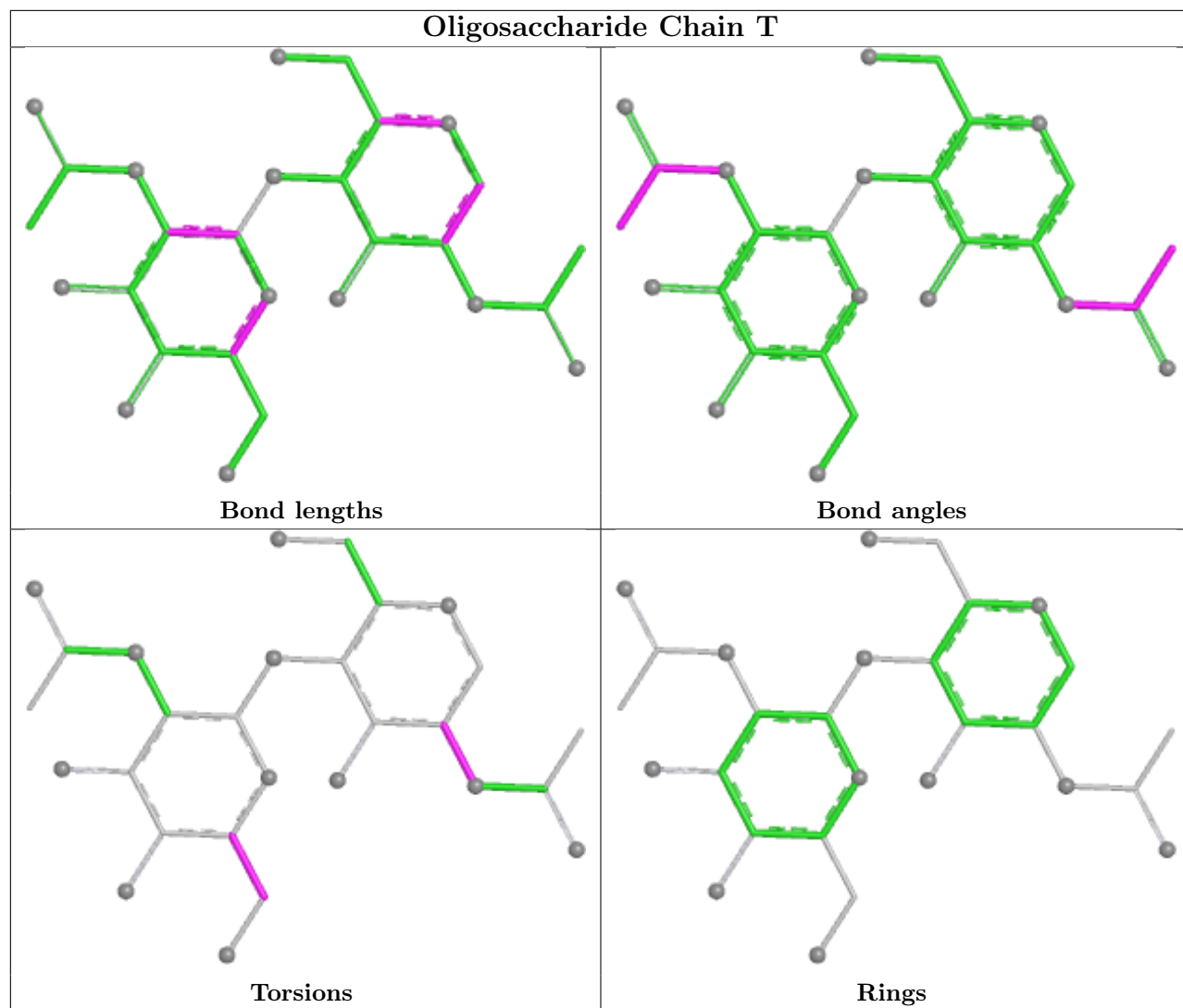


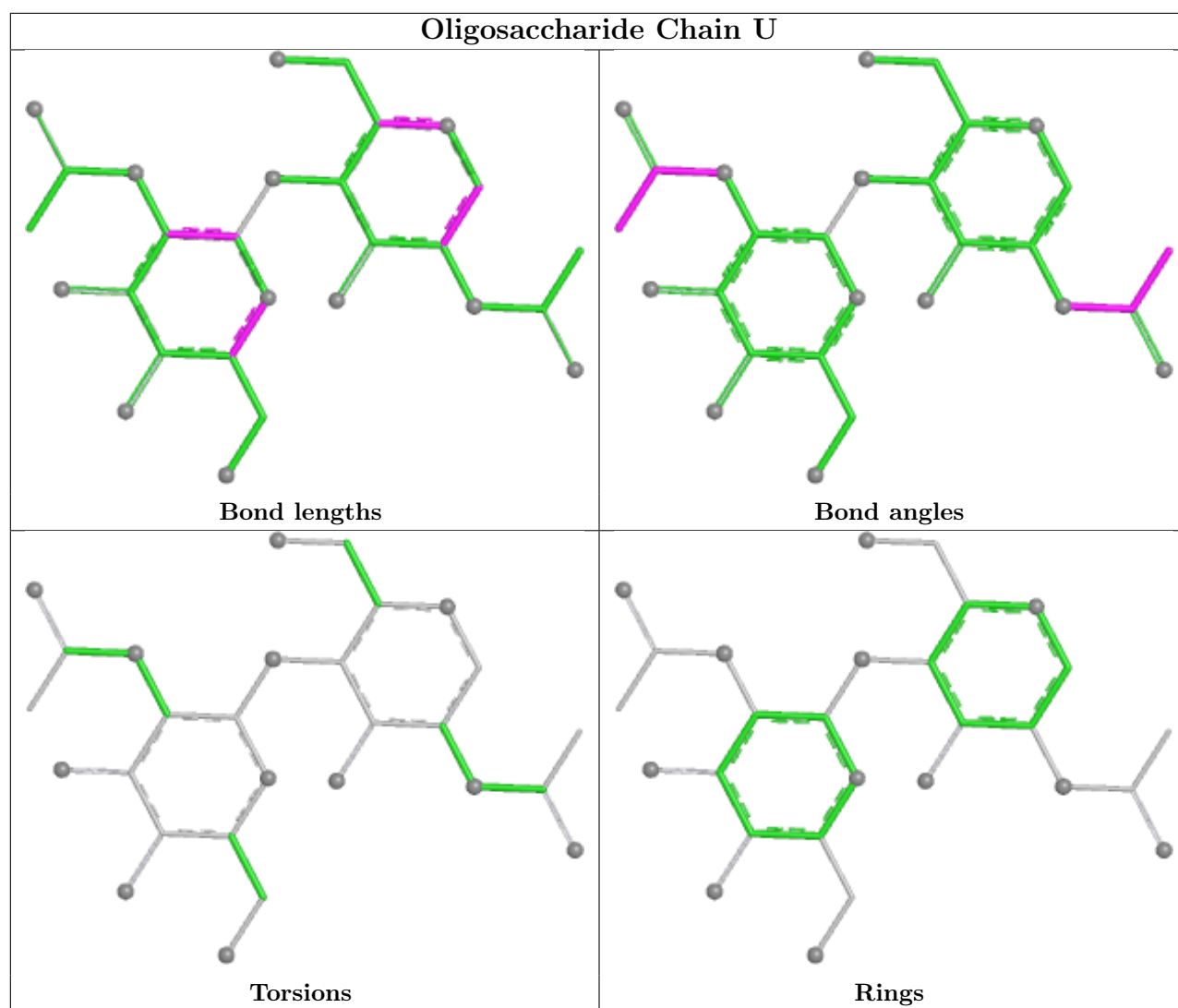


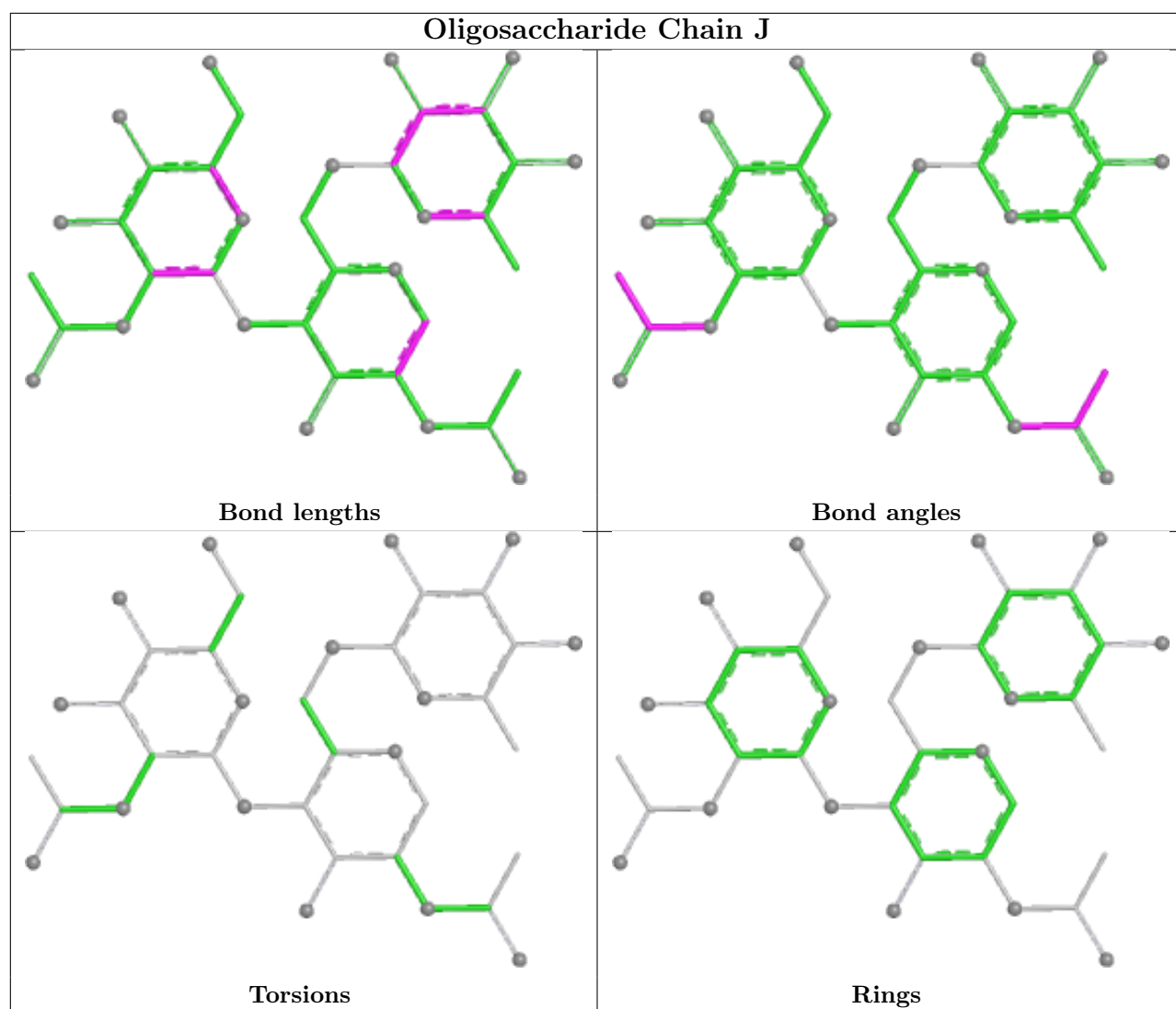


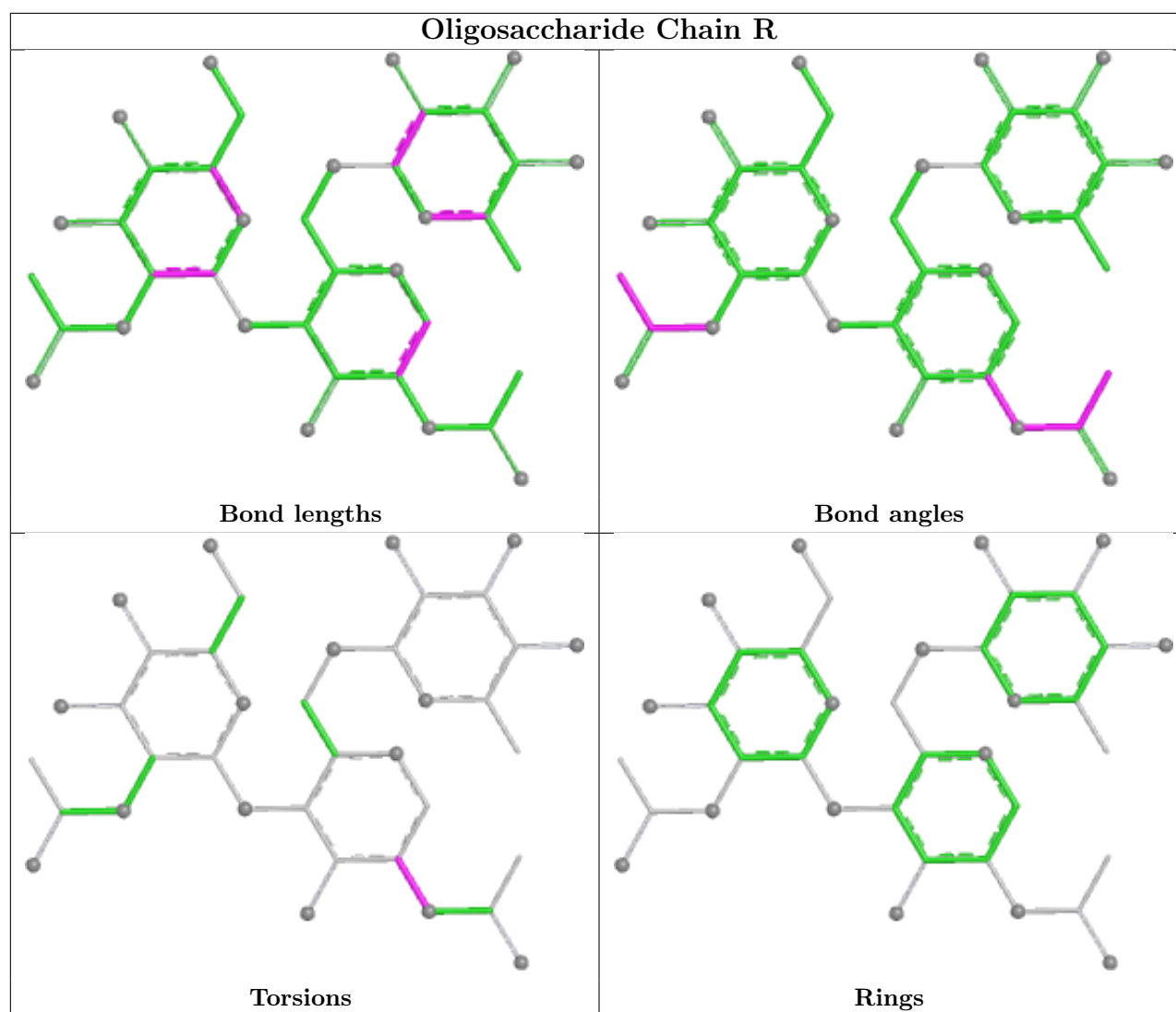












5.6 Ligand geometry [i](#)

1 ligand is 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	NAG	A	701	1	14,14,15	1.57	2 (14%)	17,19,21	0.92	1 (5%)

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	NAG	A	701	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	701	NAG	C1-C2	4.25	1.58	1.52
6	A	701	NAG	O5-C5	2.38	1.48	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	701	NAG	C8-C7-N2	2.24	119.83	116.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

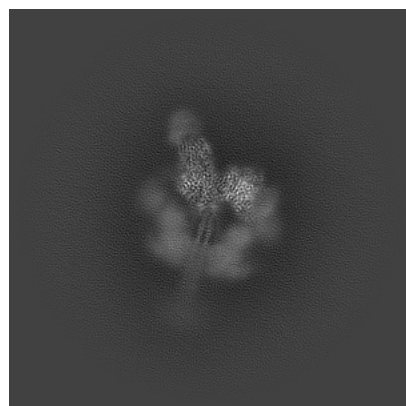
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26162. These allow visual inspection of the internal detail of the map and identification of artifacts.

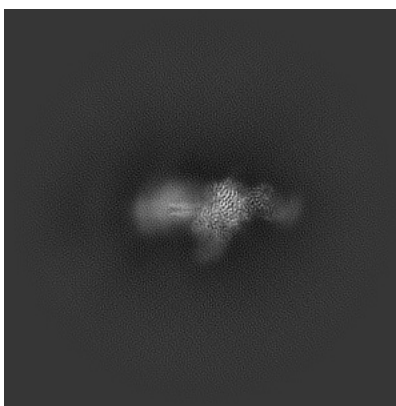
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

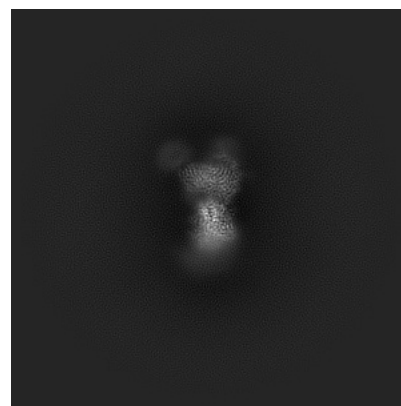
6.1.1 Primary map



X

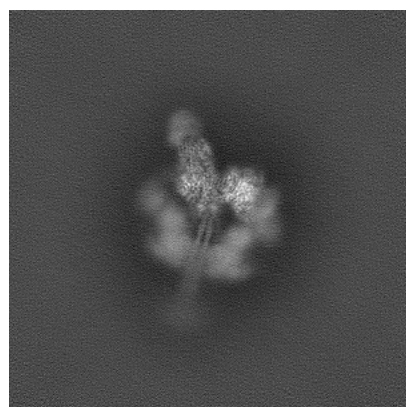


Y

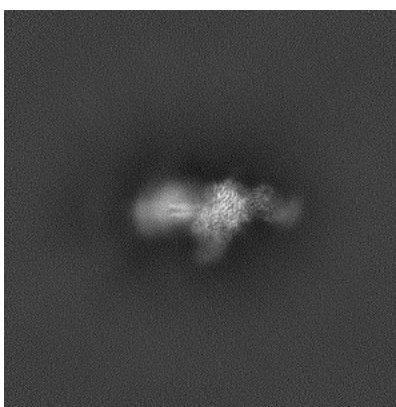


Z

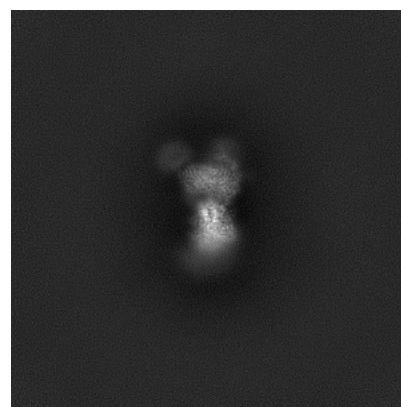
6.1.2 Raw map



X



Y

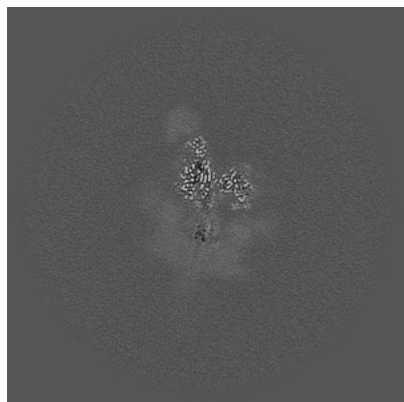


Z

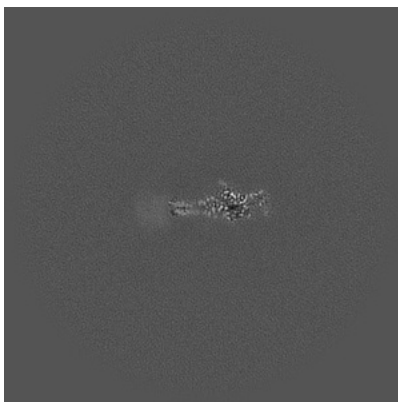
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

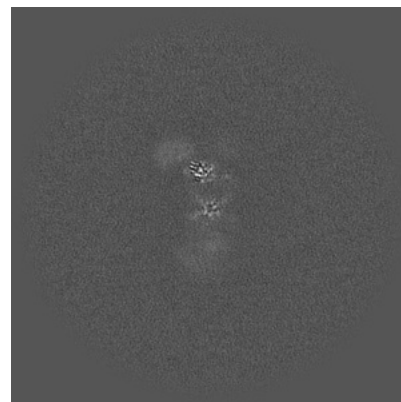
6.2.1 Primary map



X Index: 230

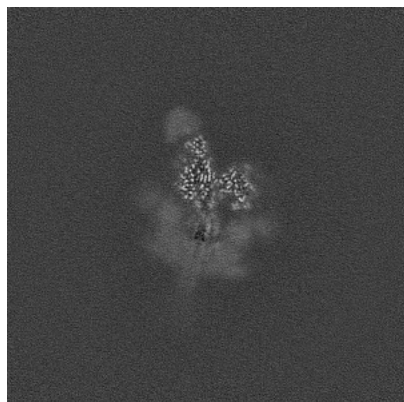


Y Index: 230



Z Index: 230

6.2.2 Raw map



X Index: 230



Y Index: 230



Z Index: 230

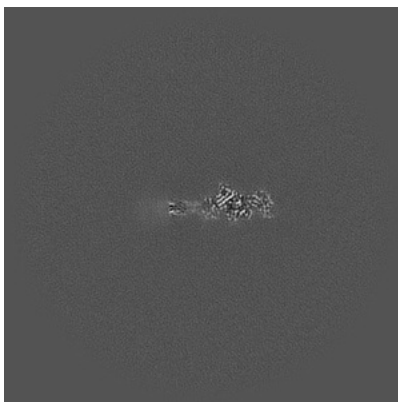
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

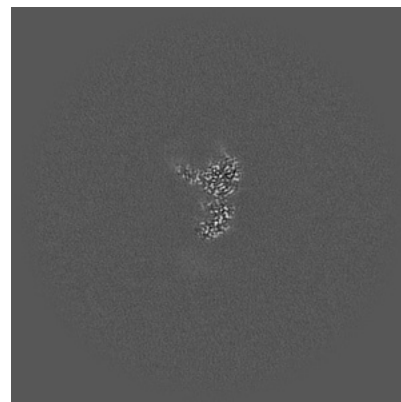
6.3.1 Primary map



X Index: 234



Y Index: 225

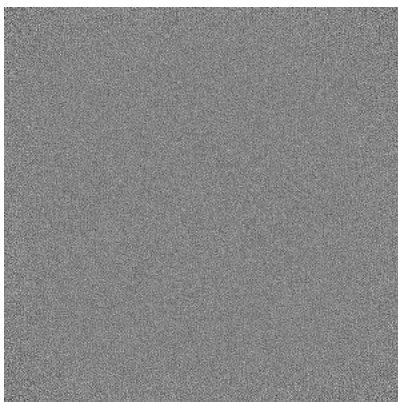


Z Index: 253

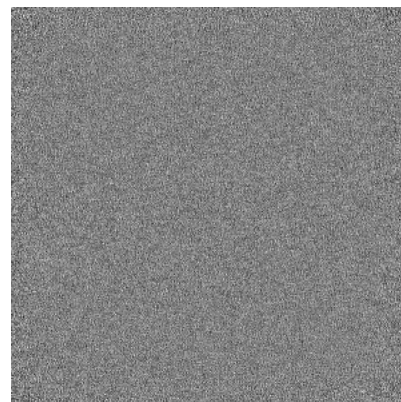
6.3.2 Raw map



X Index: 234



Y Index: 0

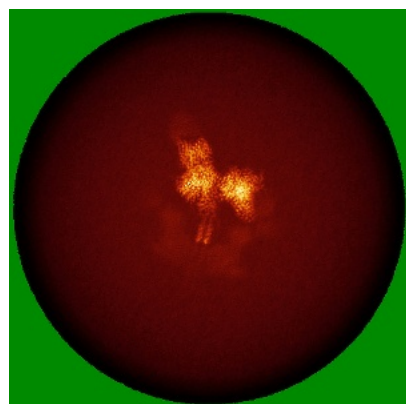


Z Index: 0

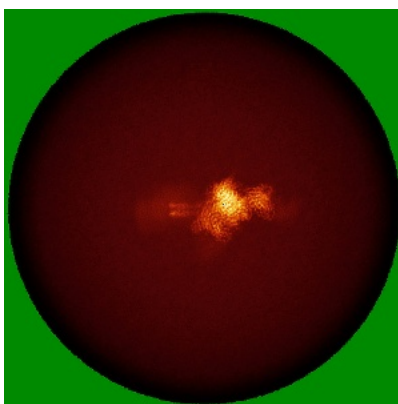
The images above show the largest variance slices of the map in three orthogonal directions.

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

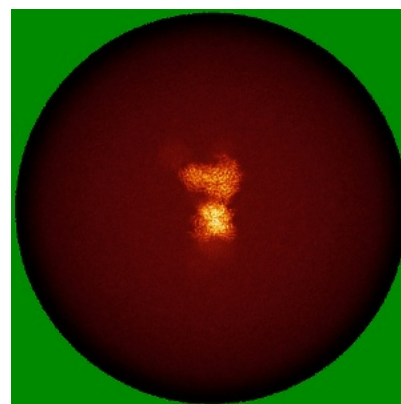
6.4.1 Primary map



X

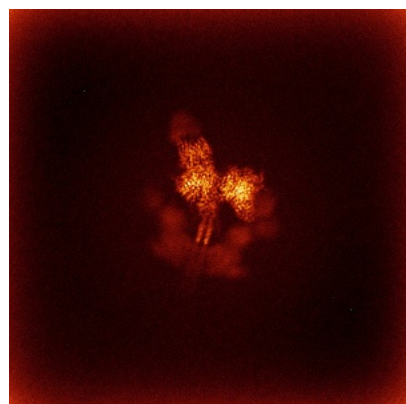


Y

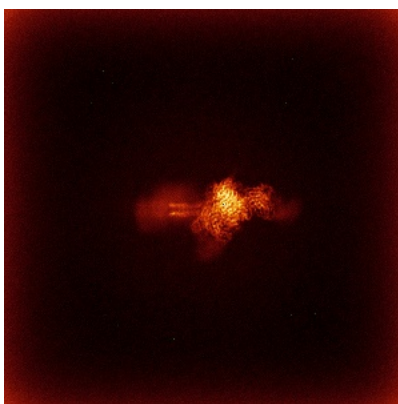


Z

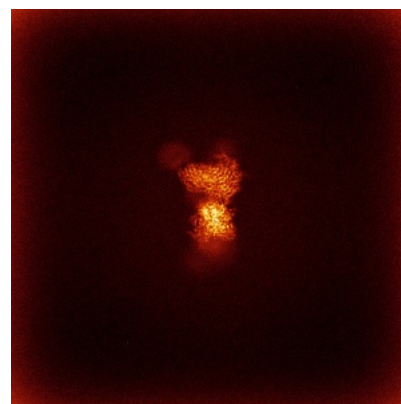
6.4.2 Raw map



X



Y

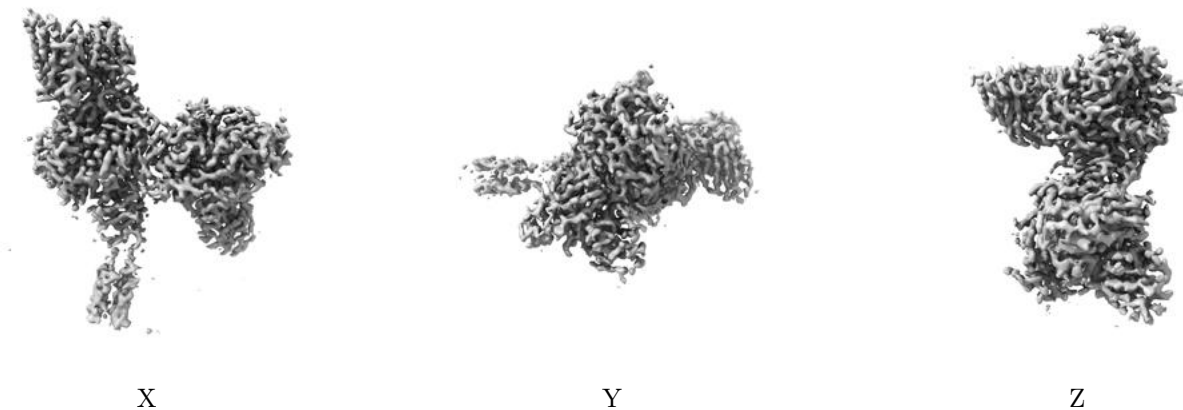


Z

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.

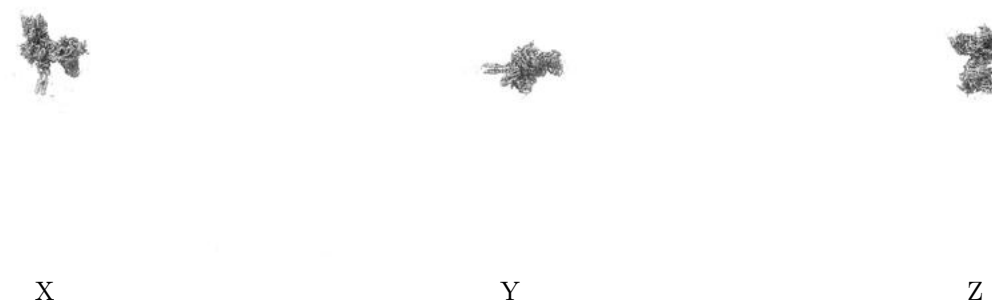
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

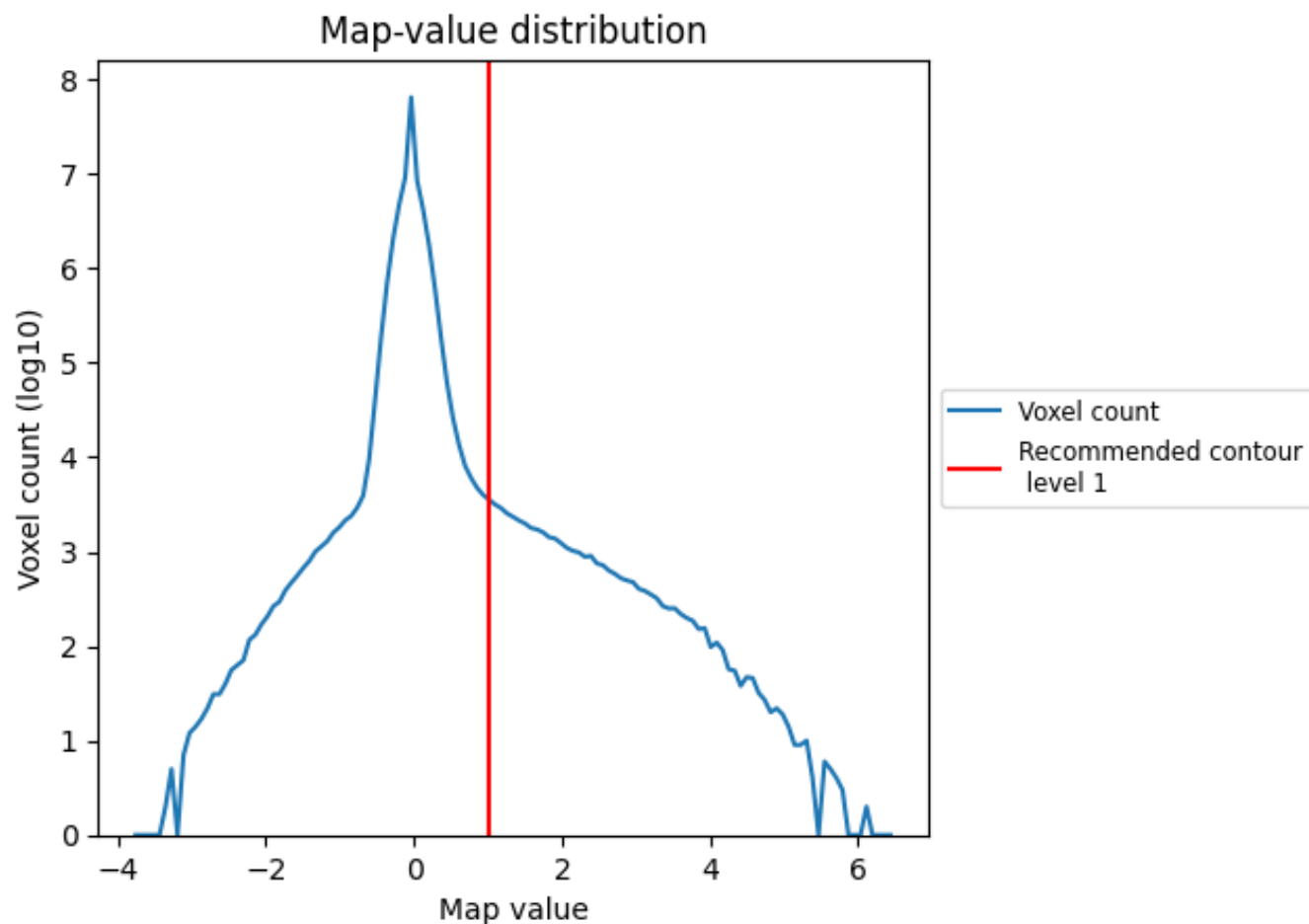
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

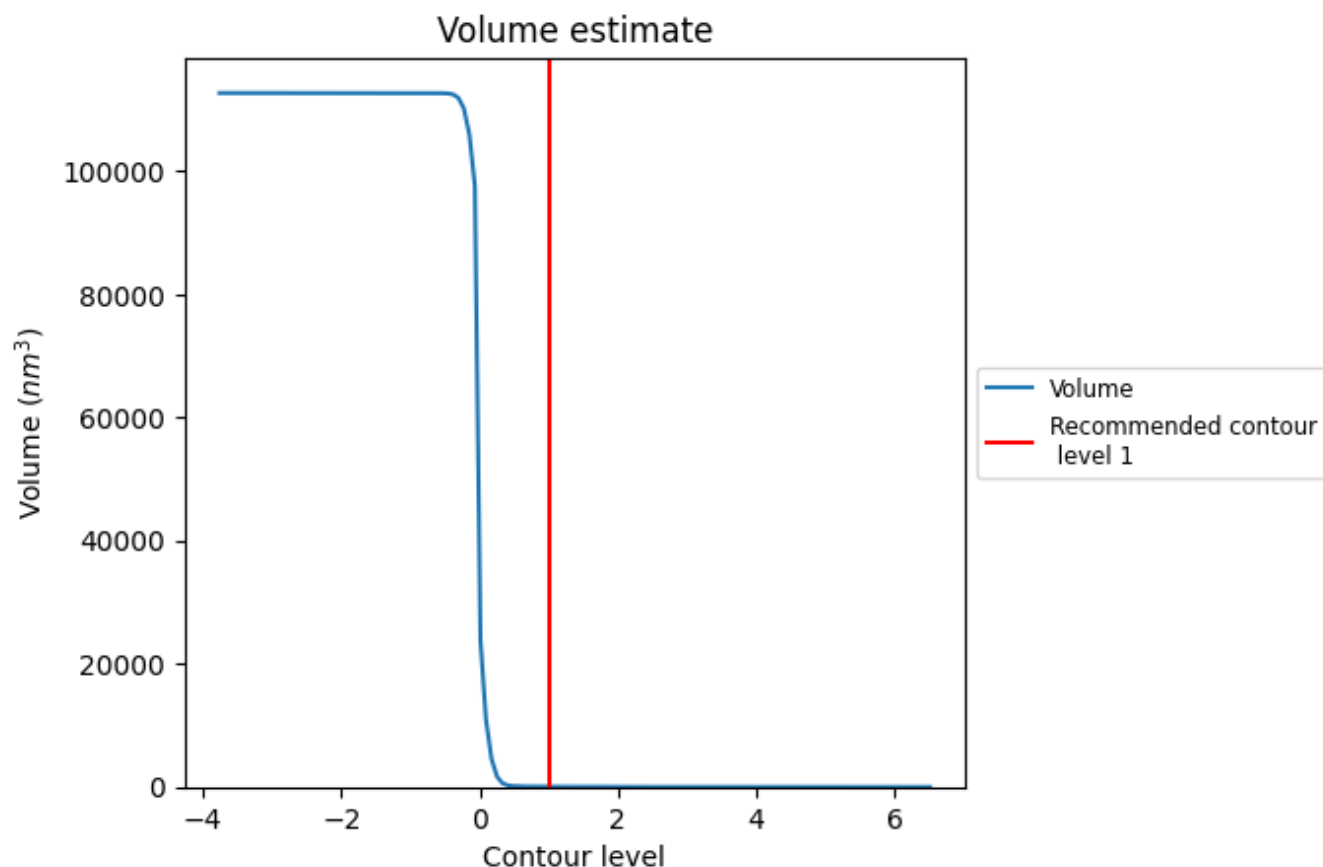
This section contains the results of statistical analysis of the map.

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.

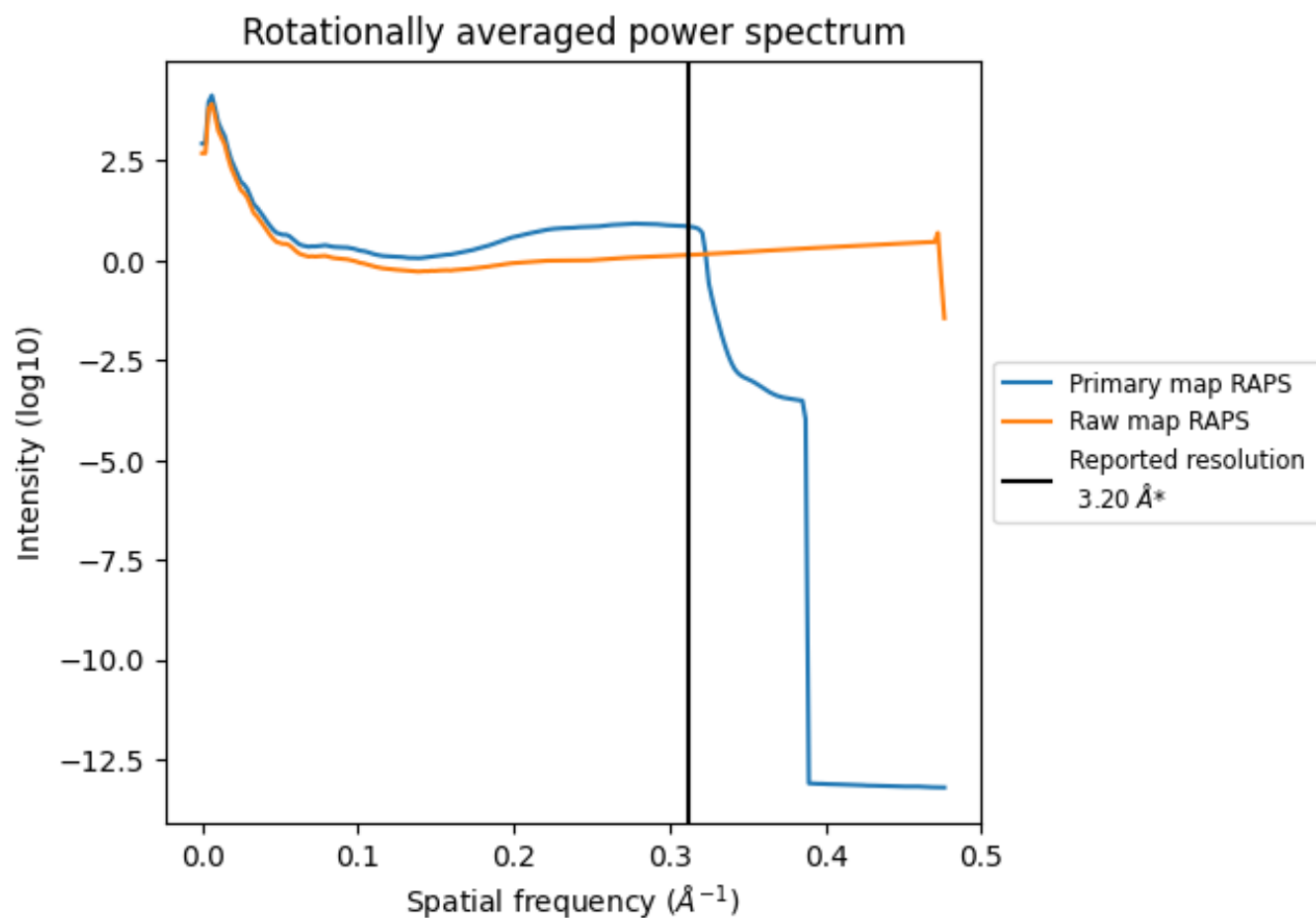
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 48 nm^3 ; this corresponds to an approximate mass of 43 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

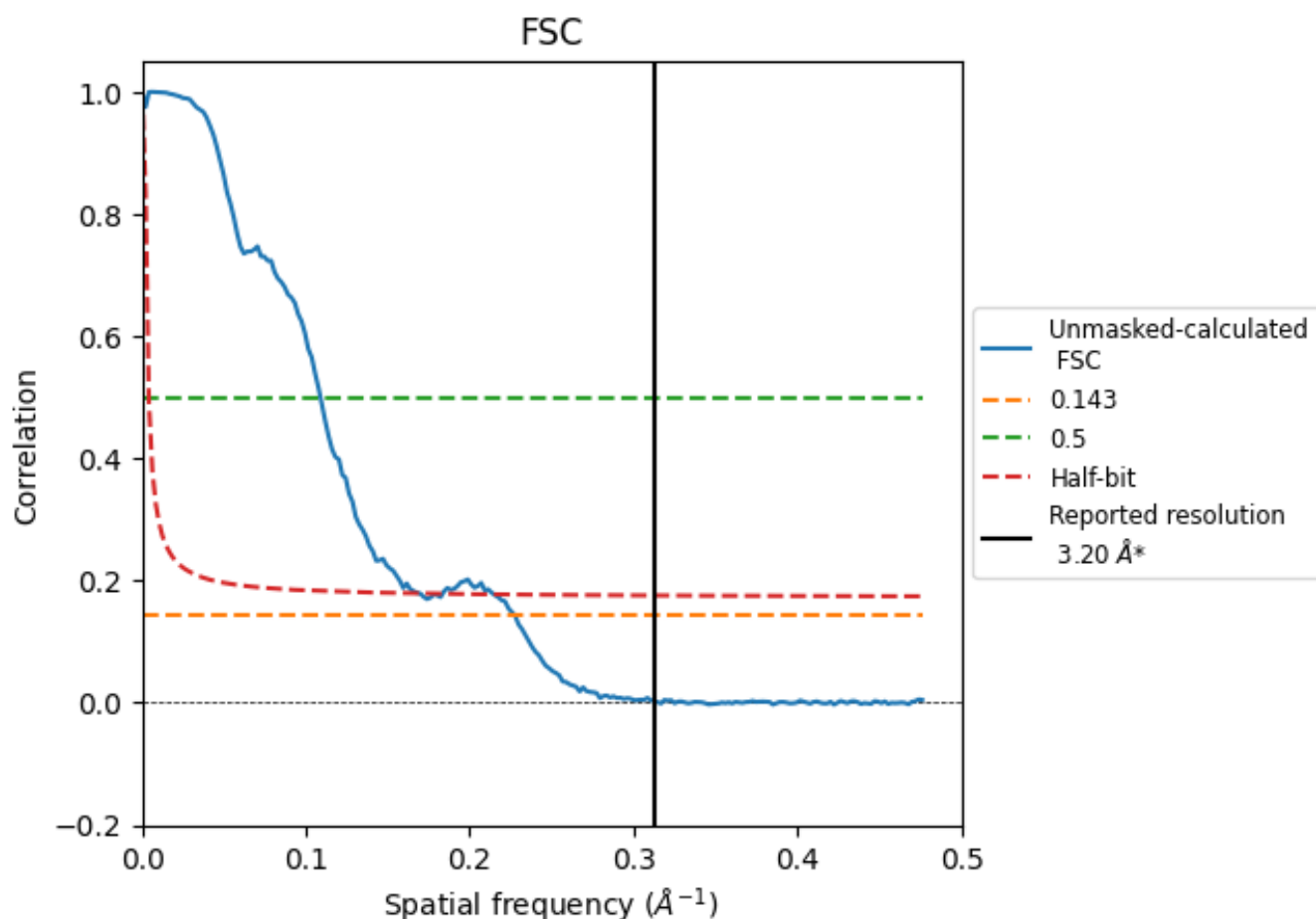


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

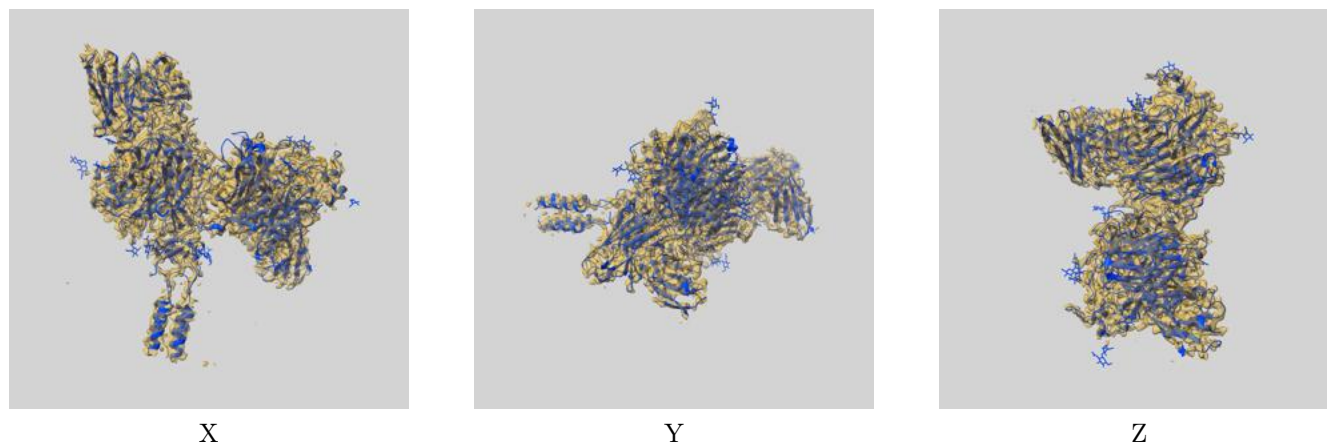
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.40	9.19	5.90

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

9 Map-model fit [i](#)

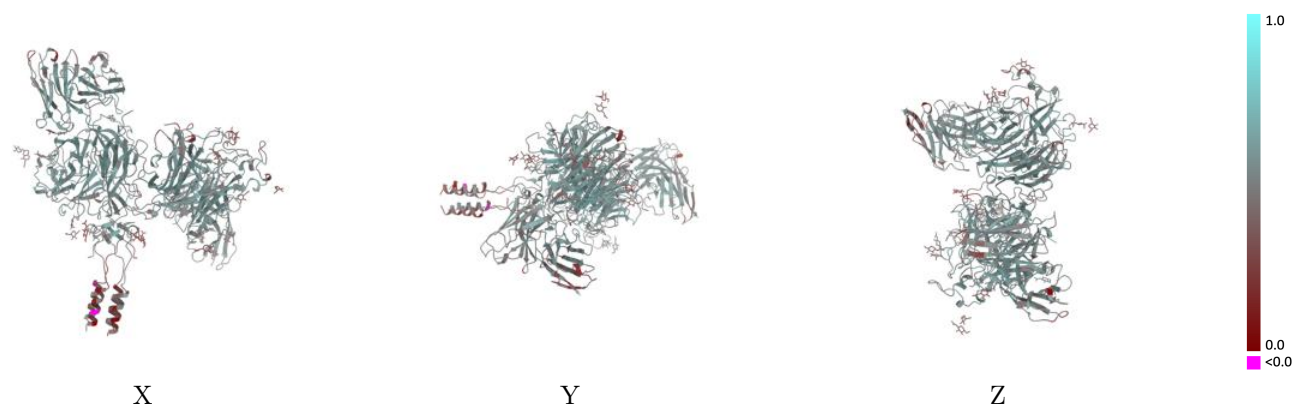
This section contains information regarding the fit between EMDB map EMD-26162 and PDB model 7TXZ. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



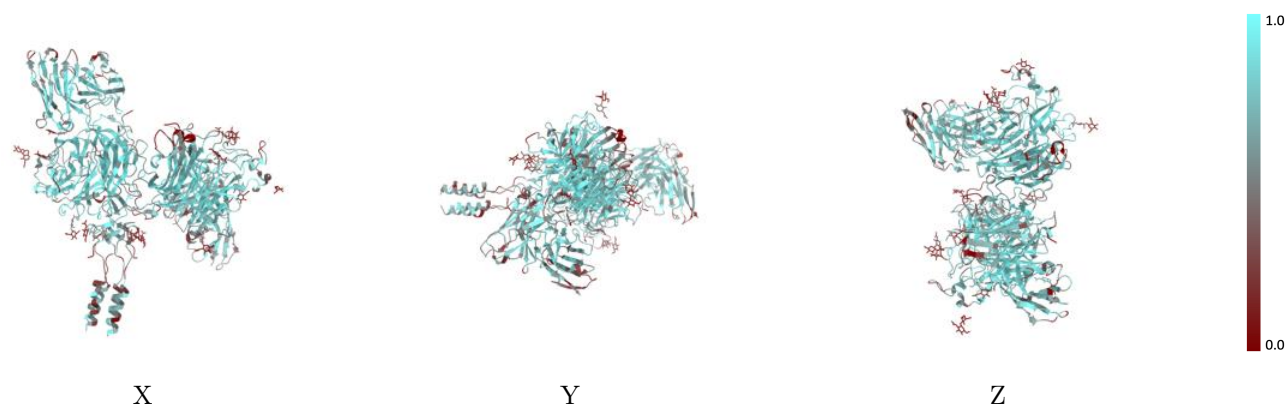
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



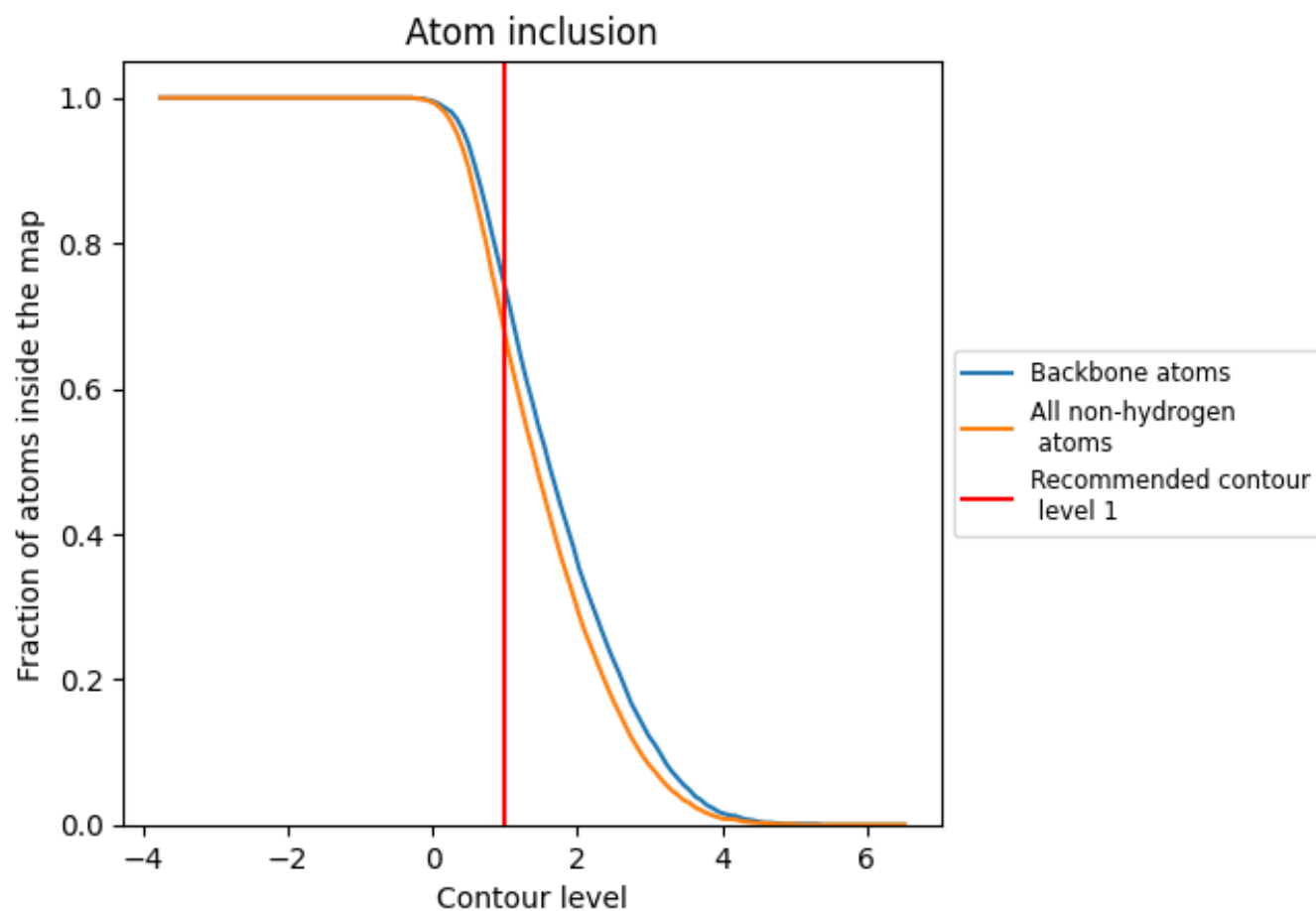
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 67% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.5180
A	 0.6920	 0.5320
B	 0.7430	 0.5440
C	 0.4830	 0.3830
D	 0.5000	 0.4010
E	 0.6630	 0.5150
F	 0.6170	 0.4840
G	 0.2140	 0.3370
H	 0.7050	 0.5290
I	 0.1430	 0.3250
J	 0.0790	 0.3700
K	 0.2500	 0.3920
L	 0.6510	 0.5120
M	 0.0000	 0.1890
N	 0.2500	 0.4040
O	 0.0000	 0.3660
P	 0.3930	 0.4700
Q	 0.3570	 0.3830
R	 0.1580	 0.4370
S	 0.2860	 0.3410
T	 0.0360	 0.3600
U	 0.1070	 0.3690

