



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:23 PM UTC

PDB ID : 7TN9 / pdb_00007tn9
EMDB ID : EMD-26005
Title : Structure of the Inmazed cocktail and resistance to escape against Ebola virus
Authors : Rayaprolu, V.; Fulton, B.; Rafique, A.; Arturo, E.; Williams, D.; Hariharan, C.; Callaway, H.; Parvate, A.; Schendel, S.L.; Parekh, D.; Hui, S.; Shaffer, K.; Pascal, K.E.; Wloga, E.; Giordano, S.; Copin, R.; Franklin, M.; Boytz, R.M.; Donahue, C.; Davey, R.; Baum, A.; Kyratsous, C.A.; Sapphire, E.O.
Deposited on : 2022-01-20
Resolution : 3.10 Å(reported)
Based on initial model : 5JQ3

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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)

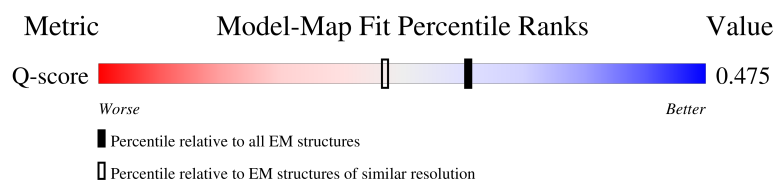
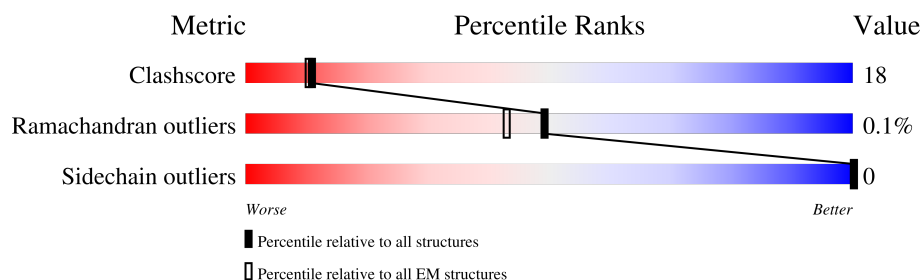
1 Overall quality at a glance

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)

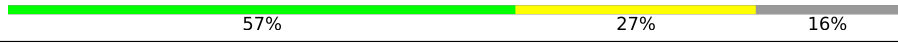
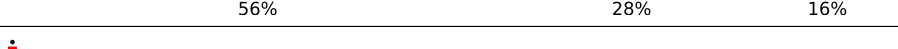
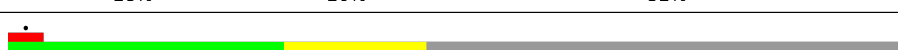
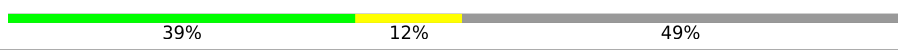
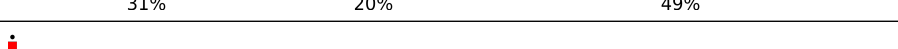
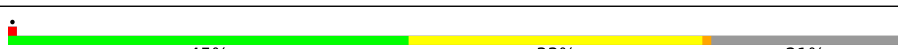
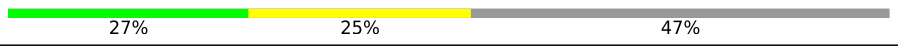
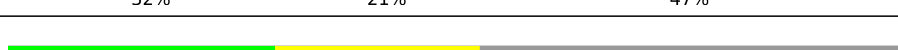
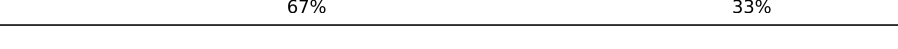
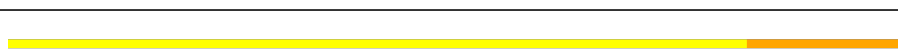
The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment 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	217	
1	C	217	
1	E	217	

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Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
2	S	321	
2	T	321	
2	U	321	
3	N	213	
3	P	213	
3	R	213	
4	B	220	
4	D	220	
4	F	220	
5	V	140	
5	W	140	
5	X	140	
6	M	217	
6	O	217	
6	Q	217	
7	G	215	
7	I	215	
8	H	215	
8	J	215	
9	K	6	
9	L	6	
9	Y	6	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 22621 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 REGN3471 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	116	Total	C	N	O	S	0	0
			895	570	151	170	4		
1	C	116	Total	C	N	O	S	0	0
			895	570	151	170	4		
1	E	116	Total	C	N	O	S	0	0
			895	570	151	170	4		

- Molecule 2 is a protein called Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	T	269	Total	C	N	O	S	0	0
			2127	1359	361	402	5		
2	S	237	Total	C	N	O	S	0	0
			1872	1205	313	349	5		
2	U	269	Total	C	N	O	S	0	0
			2127	1359	361	402	5		

There are 123 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	31	ARG	-	expression tag	UNP Q05320
T	312	ASN	-	expression tag	UNP Q05320
T	313	THR	-	expression tag	UNP Q05320
T	314	HIS	-	expression tag	UNP Q05320
T	315	HIS	-	expression tag	UNP Q05320
T	316	GLN	-	expression tag	UNP Q05320
T	317	ASP	-	expression tag	UNP Q05320
T	318	THR	-	expression tag	UNP Q05320
T	319	GLY	-	expression tag	UNP Q05320
T	320	GLU	-	expression tag	UNP Q05320
T	321	GLU	-	expression tag	UNP Q05320
T	322	SER	-	expression tag	UNP Q05320
T	323	ALA	-	expression tag	UNP Q05320

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Chain	Residue	Modelled	Actual	Comment	Reference
T	324	SER	-	expression tag	UNP Q05320
T	325	SER	-	expression tag	UNP Q05320
T	326	GLY	-	expression tag	UNP Q05320
T	327	LYS	-	expression tag	UNP Q05320
T	328	LEU	-	expression tag	UNP Q05320
T	329	GLY	-	expression tag	UNP Q05320
T	330	LEU	-	expression tag	UNP Q05320
T	331	ILE	-	expression tag	UNP Q05320
T	332	THR	-	expression tag	UNP Q05320
T	333	ASN	-	expression tag	UNP Q05320
T	334	THR	-	expression tag	UNP Q05320
T	335	ILE	-	expression tag	UNP Q05320
T	336	ALA	-	expression tag	UNP Q05320
T	337	GLY	-	expression tag	UNP Q05320
T	338	VAL	-	expression tag	UNP Q05320
T	339	ALA	-	expression tag	UNP Q05320
T	340	GLY	-	expression tag	UNP Q05320
T	341	LEU	-	expression tag	UNP Q05320
T	342	ILE	-	expression tag	UNP Q05320
T	343	THR	-	expression tag	UNP Q05320
T	344	GLY	-	expression tag	UNP Q05320
T	345	GLY	-	expression tag	UNP Q05320
T	346	ARG	-	expression tag	UNP Q05320
T	347	ARG	-	expression tag	UNP Q05320
T	348	THR	-	expression tag	UNP Q05320
T	349	ARG	-	expression tag	UNP Q05320
T	350	ARG	-	expression tag	UNP Q05320
T	351	GLU	-	expression tag	UNP Q05320
S	31	ARG	-	expression tag	UNP Q05320
S	312	ASN	-	expression tag	UNP Q05320
S	313	THR	-	expression tag	UNP Q05320
S	314	HIS	-	expression tag	UNP Q05320
S	315	HIS	-	expression tag	UNP Q05320
S	316	GLN	-	expression tag	UNP Q05320
S	317	ASP	-	expression tag	UNP Q05320
S	318	THR	-	expression tag	UNP Q05320
S	319	GLY	-	expression tag	UNP Q05320
S	320	GLU	-	expression tag	UNP Q05320
S	321	GLU	-	expression tag	UNP Q05320
S	322	SER	-	expression tag	UNP Q05320
S	323	ALA	-	expression tag	UNP Q05320
S	324	SER	-	expression tag	UNP Q05320

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Chain	Residue	Modelled	Actual	Comment	Reference
S	325	SER	-	expression tag	UNP Q05320
S	326	GLY	-	expression tag	UNP Q05320
S	327	LYS	-	expression tag	UNP Q05320
S	328	LEU	-	expression tag	UNP Q05320
S	329	GLY	-	expression tag	UNP Q05320
S	330	LEU	-	expression tag	UNP Q05320
S	331	ILE	-	expression tag	UNP Q05320
S	332	THR	-	expression tag	UNP Q05320
S	333	ASN	-	expression tag	UNP Q05320
S	334	THR	-	expression tag	UNP Q05320
S	335	ILE	-	expression tag	UNP Q05320
S	336	ALA	-	expression tag	UNP Q05320
S	337	GLY	-	expression tag	UNP Q05320
S	338	VAL	-	expression tag	UNP Q05320
S	339	ALA	-	expression tag	UNP Q05320
S	340	GLY	-	expression tag	UNP Q05320
S	341	LEU	-	expression tag	UNP Q05320
S	342	ILE	-	expression tag	UNP Q05320
S	343	THR	-	expression tag	UNP Q05320
S	344	GLY	-	expression tag	UNP Q05320
S	345	GLY	-	expression tag	UNP Q05320
S	346	ARG	-	expression tag	UNP Q05320
S	347	ARG	-	expression tag	UNP Q05320
S	348	THR	-	expression tag	UNP Q05320
S	349	ARG	-	expression tag	UNP Q05320
S	350	ARG	-	expression tag	UNP Q05320
S	351	GLU	-	expression tag	UNP Q05320
U	31	ARG	-	expression tag	UNP Q05320
U	312	ASN	-	expression tag	UNP Q05320
U	313	THR	-	expression tag	UNP Q05320
U	314	HIS	-	expression tag	UNP Q05320
U	315	HIS	-	expression tag	UNP Q05320
U	316	GLN	-	expression tag	UNP Q05320
U	317	ASP	-	expression tag	UNP Q05320
U	318	THR	-	expression tag	UNP Q05320
U	319	GLY	-	expression tag	UNP Q05320
U	320	GLU	-	expression tag	UNP Q05320
U	321	GLU	-	expression tag	UNP Q05320
U	322	SER	-	expression tag	UNP Q05320
U	323	ALA	-	expression tag	UNP Q05320
U	324	SER	-	expression tag	UNP Q05320
U	325	SER	-	expression tag	UNP Q05320

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Chain	Residue	Modelled	Actual	Comment	Reference
U	326	GLY	-	expression tag	UNP Q05320
U	327	LYS	-	expression tag	UNP Q05320
U	328	LEU	-	expression tag	UNP Q05320
U	329	GLY	-	expression tag	UNP Q05320
U	330	LEU	-	expression tag	UNP Q05320
U	331	ILE	-	expression tag	UNP Q05320
U	332	THR	-	expression tag	UNP Q05320
U	333	ASN	-	expression tag	UNP Q05320
U	334	THR	-	expression tag	UNP Q05320
U	335	ILE	-	expression tag	UNP Q05320
U	336	ALA	-	expression tag	UNP Q05320
U	337	GLY	-	expression tag	UNP Q05320
U	338	VAL	-	expression tag	UNP Q05320
U	339	ALA	-	expression tag	UNP Q05320
U	340	GLY	-	expression tag	UNP Q05320
U	341	LEU	-	expression tag	UNP Q05320
U	342	ILE	-	expression tag	UNP Q05320
U	343	THR	-	expression tag	UNP Q05320
U	344	GLY	-	expression tag	UNP Q05320
U	345	GLY	-	expression tag	UNP Q05320
U	346	ARG	-	expression tag	UNP Q05320
U	347	ARG	-	expression tag	UNP Q05320
U	348	THR	-	expression tag	UNP Q05320
U	349	ARG	-	expression tag	UNP Q05320
U	350	ARG	-	expression tag	UNP Q05320
U	351	GLU	-	expression tag	UNP Q05320

- Molecule 3 is a protein called REGN3479 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	105	Total	C	N	O	S	0	0
			796	498	132	163	3		
3	N	103	Total	C	N	O	S	0	0
			779	487	130	159	3		
3	P	101	Total	C	N	O	S	0	0
			760	475	125	157	3		

- Molecule 4 is a protein called REGN3471 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	113	Total	C	N	O	S	0	0
			873	552	142	176	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	113	Total	C	N	O	S	0	0
			873	552	142	176	3		
4	D	113	Total	C	N	O	S	0	0
			873	552	142	176	3		

- Molecule 5 is a protein called GP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	110	Total	C	N	O	S	0	0
			862	549	151	156	6		
5	V	110	Total	C	N	O	S	0	0
			862	549	151	156	6		
5	X	107	Total	C	N	O	S	0	0
			839	534	147	152	6		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	544	THR	ILE	conflict	UNP Q05320
W	638	ASP	-	expression tag	UNP Q05320
W	639	ASP	-	expression tag	UNP Q05320
W	640	ASP	-	expression tag	UNP Q05320
W	641	ASP	-	expression tag	UNP Q05320
W	642	LYS	-	expression tag	UNP Q05320
V	544	THR	ILE	conflict	UNP Q05320
V	638	ASP	-	expression tag	UNP Q05320
V	639	ASP	-	expression tag	UNP Q05320
V	640	ASP	-	expression tag	UNP Q05320
V	641	ASP	-	expression tag	UNP Q05320
V	642	LYS	-	expression tag	UNP Q05320
X	544	THR	ILE	conflict	UNP Q05320
X	638	ASP	-	expression tag	UNP Q05320
X	639	ASP	-	expression tag	UNP Q05320
X	640	ASP	-	expression tag	UNP Q05320
X	641	ASP	-	expression tag	UNP Q05320
X	642	LYS	-	expression tag	UNP Q05320

- Molecule 6 is a protein called REGN3479 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	116	Total	C	N	O	S	0	0
			878	549	152	171	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	115	Total 869	C 544	N 151	O 168	S 6	0	0
6	O	115	Total 869	C 544	N 151	O 168	S 6	0	0

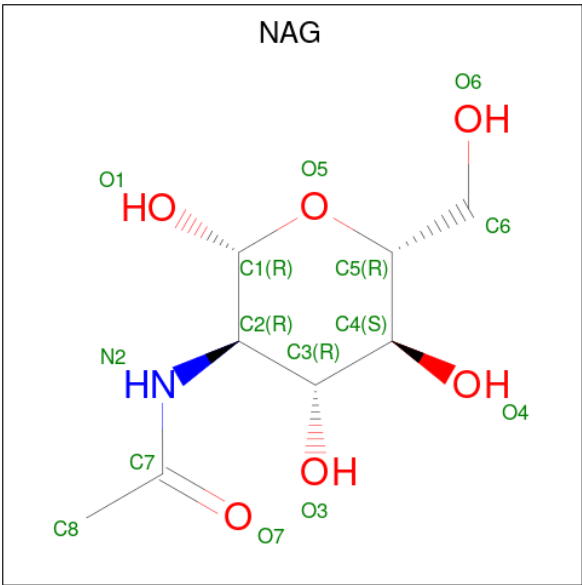
- | Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|-------|
| 7 | G | 115 | Total
912 | C
577 | N
161 | O
169 | S
5 | 0 | 0 |
| 7 | I | 113 | Total
899 | C
569 | N
159 | O
166 | S
5 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|-------|
| 8 | H | 107 | Total
810 | C
511 | N
134 | O
162 | S
3 | 0 | 0 |
| 8 | J | 95 | Total
728 | C
461 | N
119 | O
145 | S
3 | 0 | 0 |

-
- Diagram illustrating a tree structure with 10 nodes. The root node is green and has three children: a green node (left), a green node (middle), and a blue node (right). The left green node has two children: a green node (left) and a green node (right). The middle green node has two children: a green node (left) and a blue node (right). The right blue node has two children: a blue node (left) and a blue node (right). The leftmost green node has two children: a green node (left) and a green node (right). The rightmost blue node has two children: a blue node (left) and a blue node (right). The diagram is labeled with Greek letters and numbers.

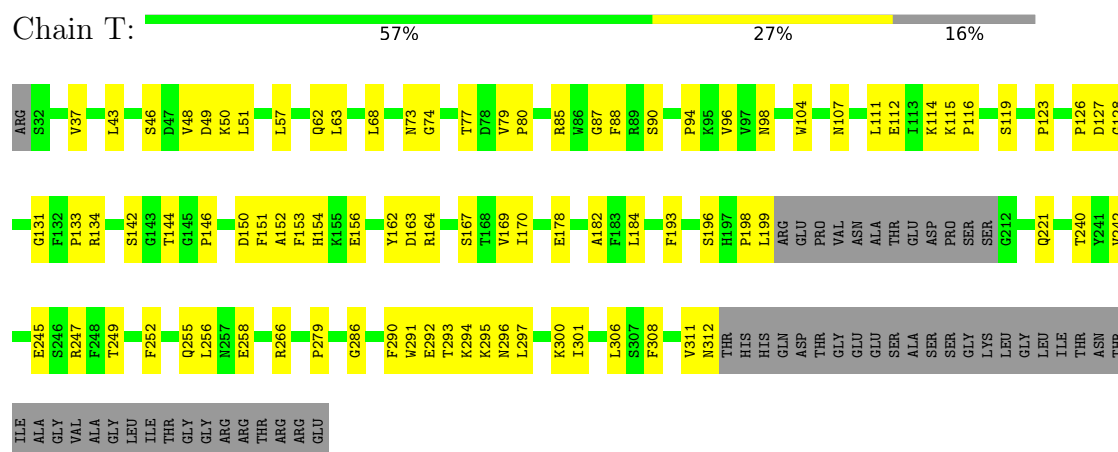
Mol	Chain	Residues	Atoms				AltConf	Trace
9	K	6	Total 72	C 40	N 2	O 30	0	0
9	L	6	Total 72	C 40	N 2	O 30	0	0
9	Y	6	Total 72	C 40	N 2	O 30	0	0

- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

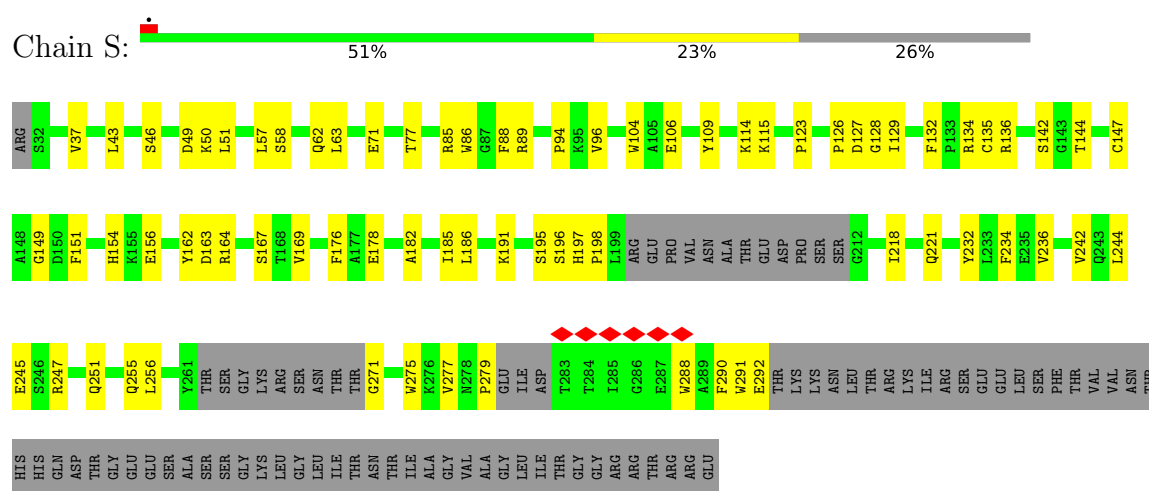


Mol	Chain	Residues	Atoms				AltConf
10	T	1	Total	C	N	O	0
			14	8	1	5	
10	T	1	Total	C	N	O	0
			14	8	1	5	
10	T	1	Total	C	N	O	0
			14	8	1	5	
10	S	1	Total	C	N	O	0
			14	8	1	5	
10	S	1	Total	C	N	O	0
			14	8	1	5	
10	U	1	Total	C	N	O	0
			14	8	1	5	
10	U	1	Total	C	N	O	0
			14	8	1	5	
10	U	1	Total	C	N	O	0
			14	8	1	5	

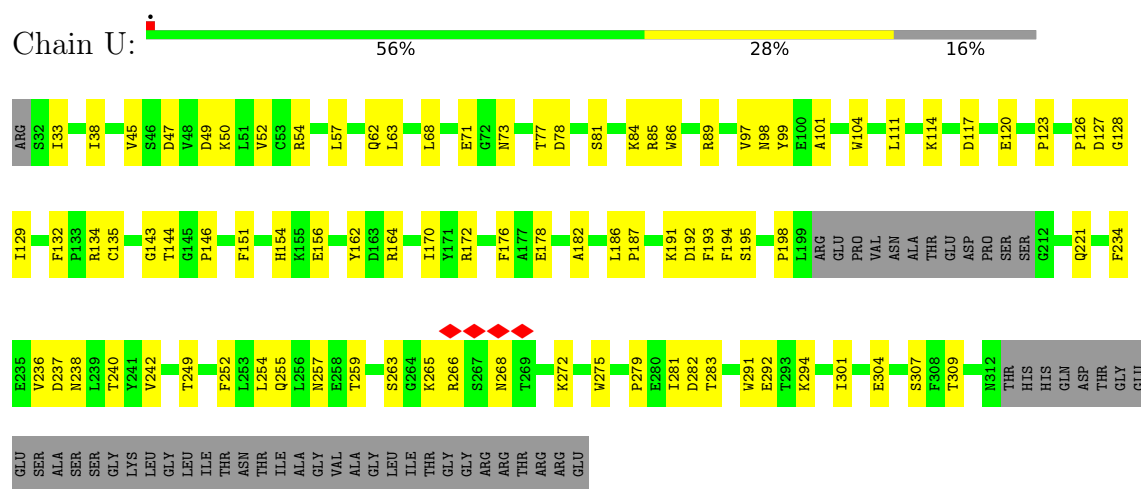
- Molecule 2: Envelope glycoprotein



- Molecule 2: Envelope glycoprotein

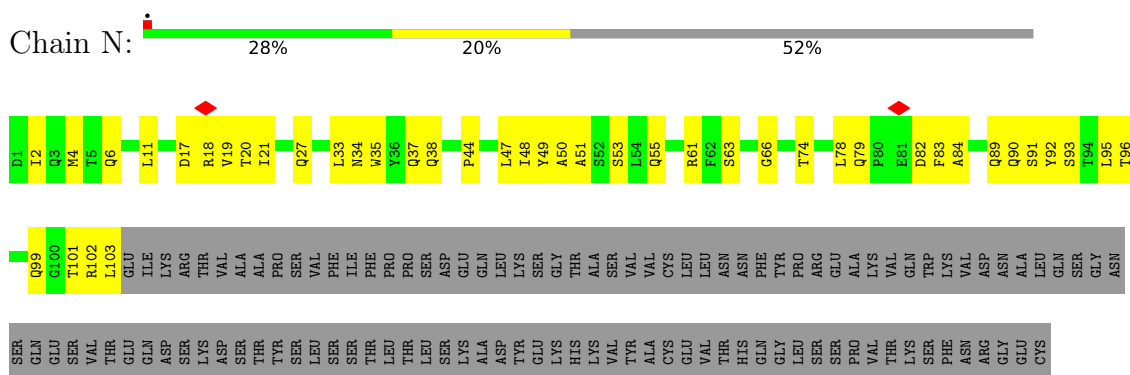


- Molecule 2: Envelope glycoprotein

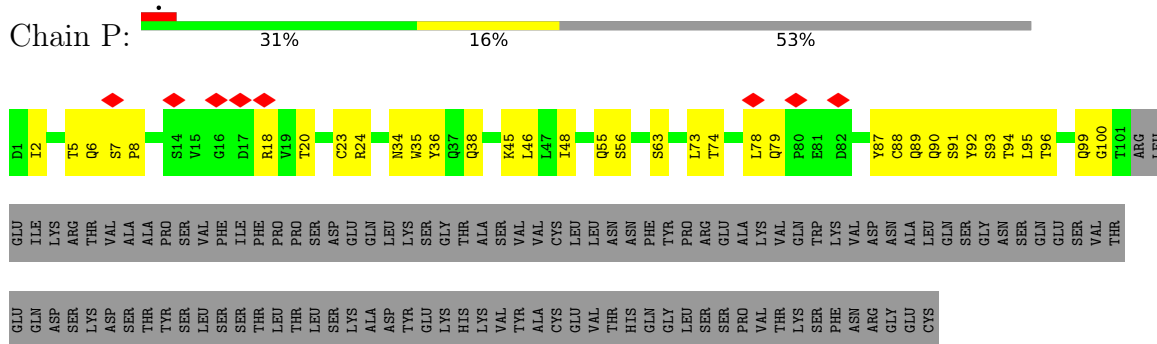


- Molecule 3: REGN3479 light chain

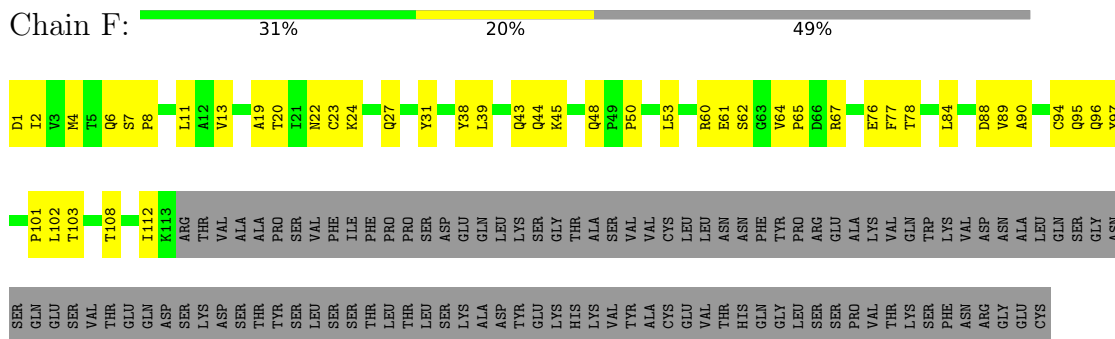
- Molecule 3: REGN3479 light chain



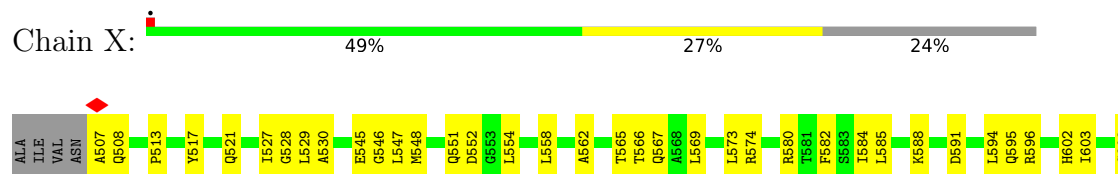
- Molecule 3: REGN3479 light chain

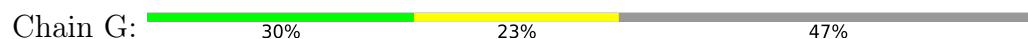


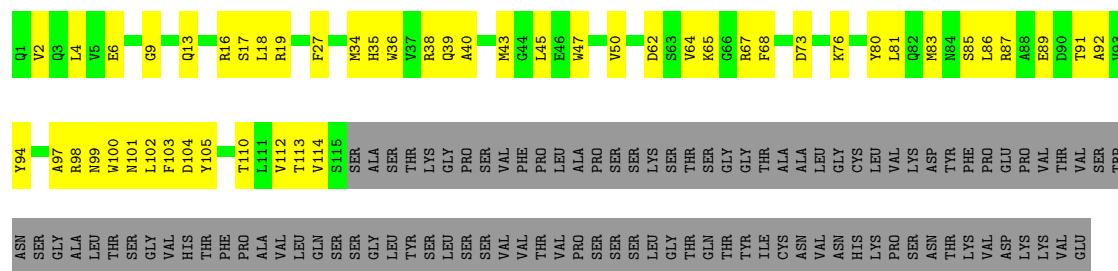
- Molecule 4: REGN3471 light chain



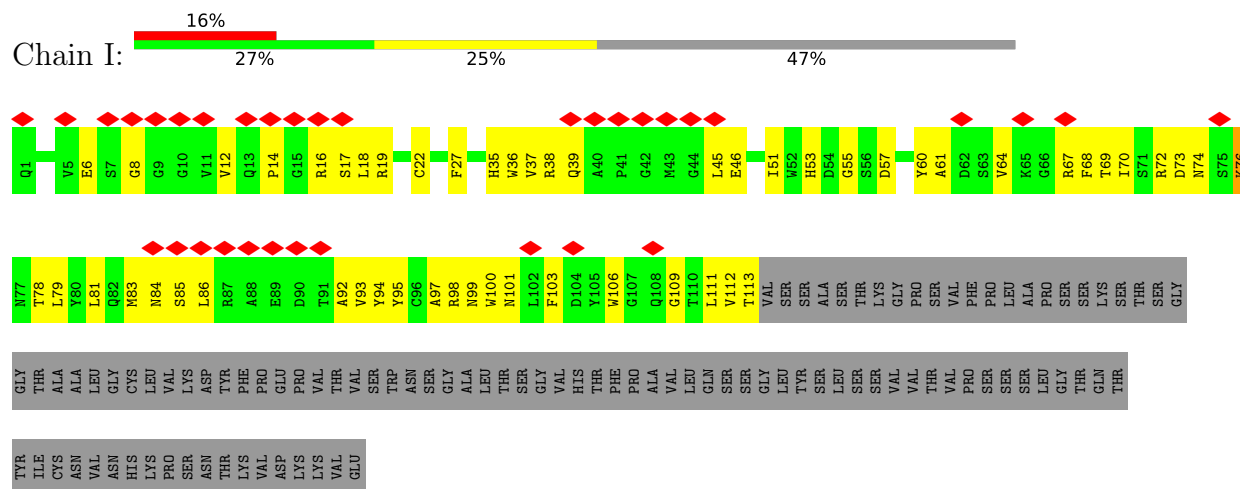
- Molecule 4: REGN3471 light chain



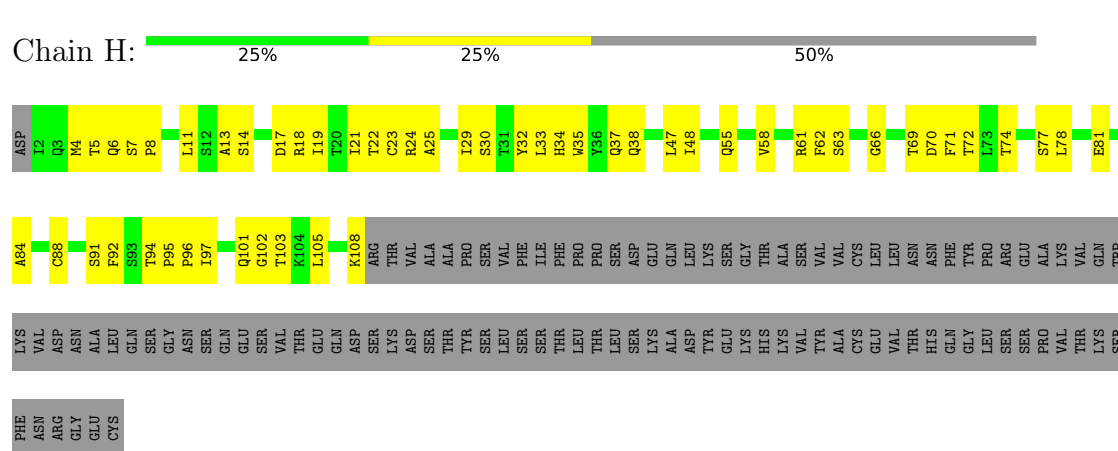




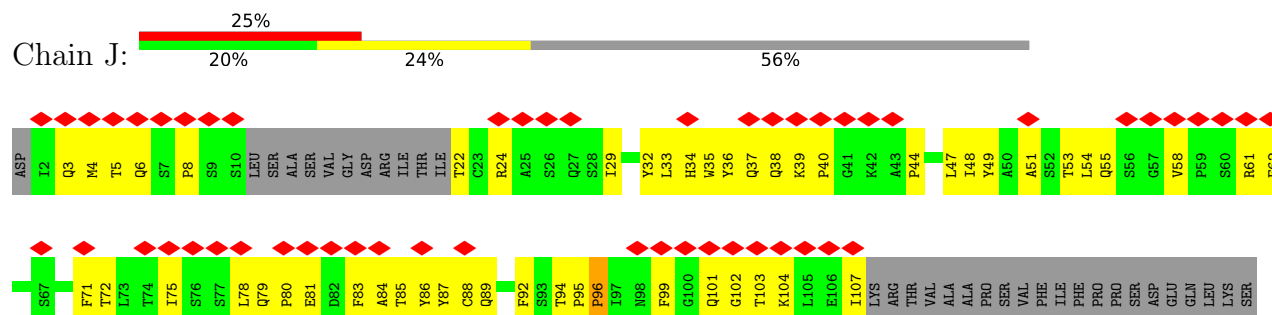
• Molecule 7: REGN3470 heavy chain



• Molecule 8: REGN3470 light chain



• Molecule 8: REGN3470 light chain



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

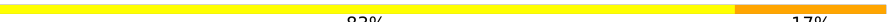
LYS HIS
LYS VAL
TYR VAL
ALA CYS
GLU VAL
THR THR
HIS HIS
GLN GLY
LEU LEU
SER SER
SER PRO
VAL THR
THR LYS
SER SER
PHE PHE
ASN ASN
ARG ARG
GLY GLY
GLU CYS

- Molecule 9: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  67% 33%

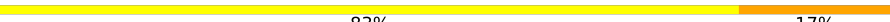
MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

- Molecule 9: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  83% 17%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

- Molecule 9: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:  83% 17%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	276715	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 ($e^-/\text{\AA}^2$)	52.4	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.718	Depositor
Minimum map value	-0.619	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	537.8048, 537.8048, 537.8048	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0504, 1.0504, 1.0504	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, BMA, 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	0/918	0.43	0/1245
1	C	0.29	0/918	0.41	0/1245
1	E	0.30	0/918	0.42	0/1245
2	S	0.27	0/1921	0.40	0/2609
2	T	0.30	0/2179	0.48	0/2958
2	U	0.28	0/2178	0.46	0/2955
3	N	0.19	0/795	0.43	0/1078
3	P	0.18	0/776	0.40	0/1053
3	R	0.23	0/812	0.45	0/1101
4	B	0.29	0/893	0.44	0/1214
4	D	0.29	0/893	0.44	0/1214
4	F	0.30	0/893	0.49	0/1214
5	V	0.31	0/884	0.57	0/1205
5	W	0.34	0/884	0.64	2/1205 (0.2%)
5	X	0.32	0/861	0.61	0/1173
6	M	0.20	0/888	0.44	0/1201
6	O	0.20	0/888	0.40	0/1201
6	Q	0.22	0/897	0.41	0/1213
7	G	0.22	0/936	0.44	0/1271
7	I	0.21	0/923	0.56	1/1253 (0.1%)
8	H	0.20	0/829	0.50	0/1126
8	J	0.18	0/746	0.48	0/1012
All	All	0.27	0/22830	0.47	3/30991 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	I	76	LYS	CB-CG-CD	6.21	125.59	111.30
5	W	507	ALA	CA-C-N	5.01	127.61	120.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	W	507	ALA	C-N-CA	5.01	127.61	120.49

There are no chirality outliers.

There are no planarity outliers.

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	895	0	851	35	0
1	C	895	0	851	36	0
1	E	895	0	851	31	0
2	S	1872	0	1810	57	0
2	T	2127	0	2079	77	0
2	U	2127	0	2077	80	0
3	N	779	0	758	35	0
3	P	760	0	734	28	0
3	R	796	0	775	21	0
4	B	873	0	848	19	0
4	D	873	0	848	21	0
4	F	873	0	848	35	0
5	V	862	0	835	43	0
5	W	862	0	836	58	0
5	X	839	0	809	46	0
6	M	869	0	837	58	0
6	O	869	0	837	43	0
6	Q	878	0	846	42	0
7	G	912	0	864	38	0
7	I	899	0	850	55	0
8	H	810	0	789	47	0
8	J	728	0	703	47	0
9	K	72	0	61	7	0
9	L	72	0	61	4	0
9	Y	72	0	61	4	0
10	S	28	0	26	0	0
10	T	42	0	39	2	0
10	U	42	0	39	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	22621	0	21823	819	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 18.

The worst 5 of 819 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:O:57:SER:HB3	6:O:59:TYR:HE1	1.31	0.94
2:T:73:ASN:HB3	5:W:508:GLN:HE21	1.34	0.92
7:I:17:SER:HB3	7:I:83:MET:HG3	1.53	0.91
2:S:104:TRP:NE1	5:V:545:GLU:OE1	2.06	0.88
2:S:128:GLY:HA3	5:V:580:ARG:HH22	1.37	0.86

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	114/217 (52%)	113 (99%)	1 (1%)	0	100	100
1	C	114/217 (52%)	111 (97%)	3 (3%)	0	100	100
1	E	114/217 (52%)	111 (97%)	3 (3%)	0	100	100
2	S	229/321 (71%)	225 (98%)	4 (2%)	0	100	100
2	T	265/321 (83%)	260 (98%)	5 (2%)	0	100	100
2	U	264/321 (82%)	257 (97%)	7 (3%)	0	100	100
3	N	101/213 (47%)	97 (96%)	4 (4%)	0	100	100
3	P	99/213 (46%)	98 (99%)	1 (1%)	0	100	100
3	R	103/213 (48%)	99 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	111/220 (50%)	106 (96%)	5 (4%)	0	100	100
4	D	111/220 (50%)	105 (95%)	6 (5%)	0	100	100
4	F	111/220 (50%)	105 (95%)	6 (5%)	0	100	100
5	V	108/140 (77%)	106 (98%)	2 (2%)	0	100	100
5	W	108/140 (77%)	106 (98%)	2 (2%)	0	100	100
5	X	105/140 (75%)	102 (97%)	3 (3%)	0	100	100
6	M	113/217 (52%)	110 (97%)	2 (2%)	1 (1%)	14	44
6	O	113/217 (52%)	109 (96%)	4 (4%)	0	100	100
6	Q	114/217 (52%)	113 (99%)	1 (1%)	0	100	100
7	G	113/215 (53%)	110 (97%)	3 (3%)	0	100	100
7	I	111/215 (52%)	109 (98%)	2 (2%)	0	100	100
8	H	105/215 (49%)	99 (94%)	6 (6%)	0	100	100
8	J	91/215 (42%)	89 (98%)	1 (1%)	1 (1%)	11	39
All	All	2817/4844 (58%)	2740 (97%)	75 (3%)	2 (0%)	49	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	102	PRO
8	J	96	PRO

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	91/178 (51%)	91 (100%)	0	100	100
1	C	91/178 (51%)	91 (100%)	0	100	100
1	E	91/178 (51%)	91 (100%)	0	100	100
2	S	201/273 (74%)	201 (100%)	0	100	100
2	T	232/273 (85%)	232 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U	232/273 (85%)	232 (100%)	0	100	100
3	N	89/188 (47%)	89 (100%)	0	100	100
3	P	87/188 (46%)	87 (100%)	0	100	100
3	R	91/188 (48%)	91 (100%)	0	100	100
4	B	98/194 (50%)	98 (100%)	0	100	100
4	D	98/194 (50%)	98 (100%)	0	100	100
4	F	98/194 (50%)	98 (100%)	0	100	100
5	V	90/119 (76%)	90 (100%)	0	100	100
5	W	90/119 (76%)	90 (100%)	0	100	100
5	X	87/119 (73%)	87 (100%)	0	100	100
6	M	92/180 (51%)	92 (100%)	0	100	100
6	O	92/180 (51%)	92 (100%)	0	100	100
6	Q	93/180 (52%)	93 (100%)	0	100	100
7	G	95/181 (52%)	95 (100%)	0	100	100
7	I	93/181 (51%)	93 (100%)	0	100	100
8	H	92/190 (48%)	92 (100%)	0	100	100
8	J	83/190 (44%)	83 (100%)	0	100	100
All	All	2406/4138 (58%)	2406 (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. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
6	M	3	GLN
1	E	81	GLN
3	P	6	GLN
1	C	35	HIS
8	H	34	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

18 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
9	NAG	K	1	9,5	14,14,15	0.45	0	17,19,21	0.69	0
9	NAG	K	2	9	14,14,15	0.28	0	17,19,21	0.56	0
9	BMA	K	3	9	11,11,12	0.86	0	15,15,17	1.12	2 (13%)
9	MAN	K	4	9	11,11,12	1.09	1 (9%)	15,15,17	2.42	5 (33%)
9	MAN	K	5	9	11,11,12	0.64	0	15,15,17	0.91	1 (6%)
9	MAN	K	6	9	11,11,12	0.86	1 (9%)	15,15,17	0.90	1 (6%)
9	NAG	L	1	9,5	14,14,15	0.38	0	17,19,21	0.53	0
9	NAG	L	2	9	14,14,15	0.18	0	17,19,21	0.48	0
9	BMA	L	3	9	11,11,12	0.67	0	15,15,17	1.01	1 (6%)
9	MAN	L	4	9	11,11,12	0.60	0	15,15,17	1.03	2 (13%)
9	MAN	L	5	9	11,11,12	0.74	0	15,15,17	0.88	1 (6%)
9	MAN	L	6	9	11,11,12	0.78	1 (9%)	15,15,17	0.82	1 (6%)
9	NAG	Y	1	9,5	14,14,15	0.42	0	17,19,21	0.46	0
9	NAG	Y	2	9	14,14,15	0.44	0	17,19,21	0.43	0
9	BMA	Y	3	9	11,11,12	0.66	0	15,15,17	1.14	2 (13%)
9	MAN	Y	4	9	11,11,12	0.76	1 (9%)	15,15,17	1.10	2 (13%)
9	MAN	Y	5	9	11,11,12	1.00	1 (9%)	15,15,17	0.83	1 (6%)
9	MAN	Y	6	9	11,11,12	0.77	0	15,15,17	0.91	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	K	1	9,5	-	0/6/23/26	0/1/1/1
9	NAG	K	2	9	-	2/6/23/26	0/1/1/1
9	BMA	K	3	9	-	2/2/19/22	0/1/1/1
9	MAN	K	4	9	-	2/2/19/22	0/1/1/1
9	MAN	K	5	9	-	1/2/19/22	0/1/1/1
9	MAN	K	6	9	-	0/2/19/22	0/1/1/1
9	NAG	L	1	9,5	-	0/6/23/26	0/1/1/1
9	NAG	L	2	9	-	3/6/23/26	0/1/1/1
9	BMA	L	3	9	-	2/2/19/22	0/1/1/1
9	MAN	L	4	9	-	1/2/19/22	1/1/1/1
9	MAN	L	5	9	-	2/2/19/22	0/1/1/1
9	MAN	L	6	9	-	0/2/19/22	0/1/1/1
9	NAG	Y	1	9,5	-	1/6/23/26	0/1/1/1
9	NAG	Y	2	9	-	2/6/23/26	0/1/1/1
9	BMA	Y	3	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	4	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	5	9	-	1/2/19/22	0/1/1/1
9	MAN	Y	6	9	-	2/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	Y	5	MAN	O5-C1	-3.11	1.38	1.43
9	K	4	MAN	C1-C2	2.73	1.58	1.52
9	K	6	MAN	O5-C1	-2.32	1.39	1.43
9	L	6	MAN	O5-C1	-2.27	1.39	1.43
9	Y	4	MAN	C1-C2	2.22	1.57	1.52

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	4	MAN	C1-O5-C5	6.17	120.46	112.19
9	K	4	MAN	C1-C2-C3	3.49	114.73	109.64
9	K	4	MAN	O5-C5-C6	3.04	113.58	107.66
9	K	4	MAN	O5-C5-C4	2.89	117.86	110.83
9	K	3	BMA	C1-C2-C3	-2.79	105.58	109.64

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	L	2	NAG	O5-C5-C6-O6
9	K	2	NAG	O5-C5-C6-O6
9	Y	2	NAG	O5-C5-C6-O6
9	K	2	NAG	C4-C5-C6-O6
9	L	2	NAG	C4-C5-C6-O6

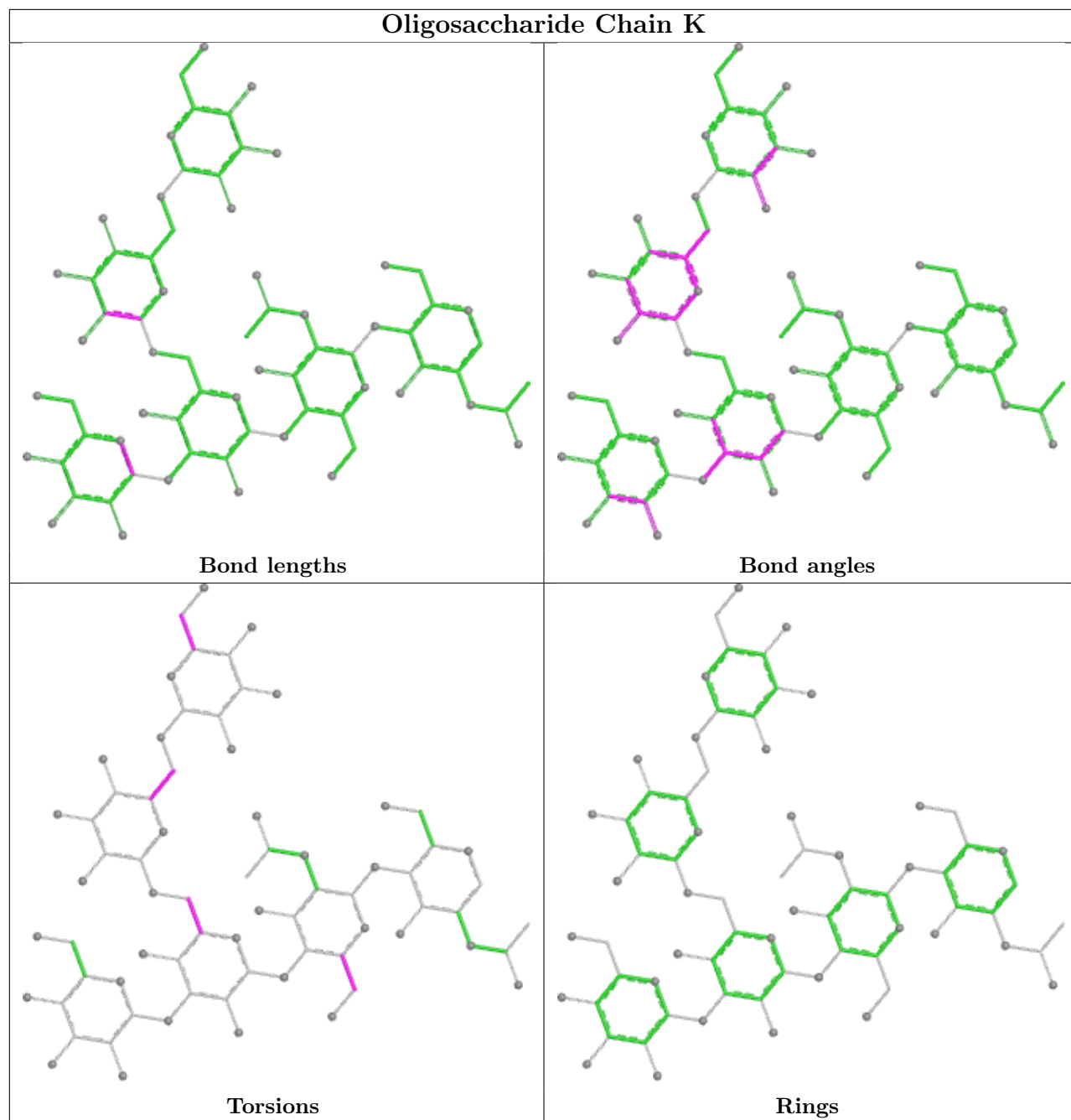
All (1) ring outliers are listed below:

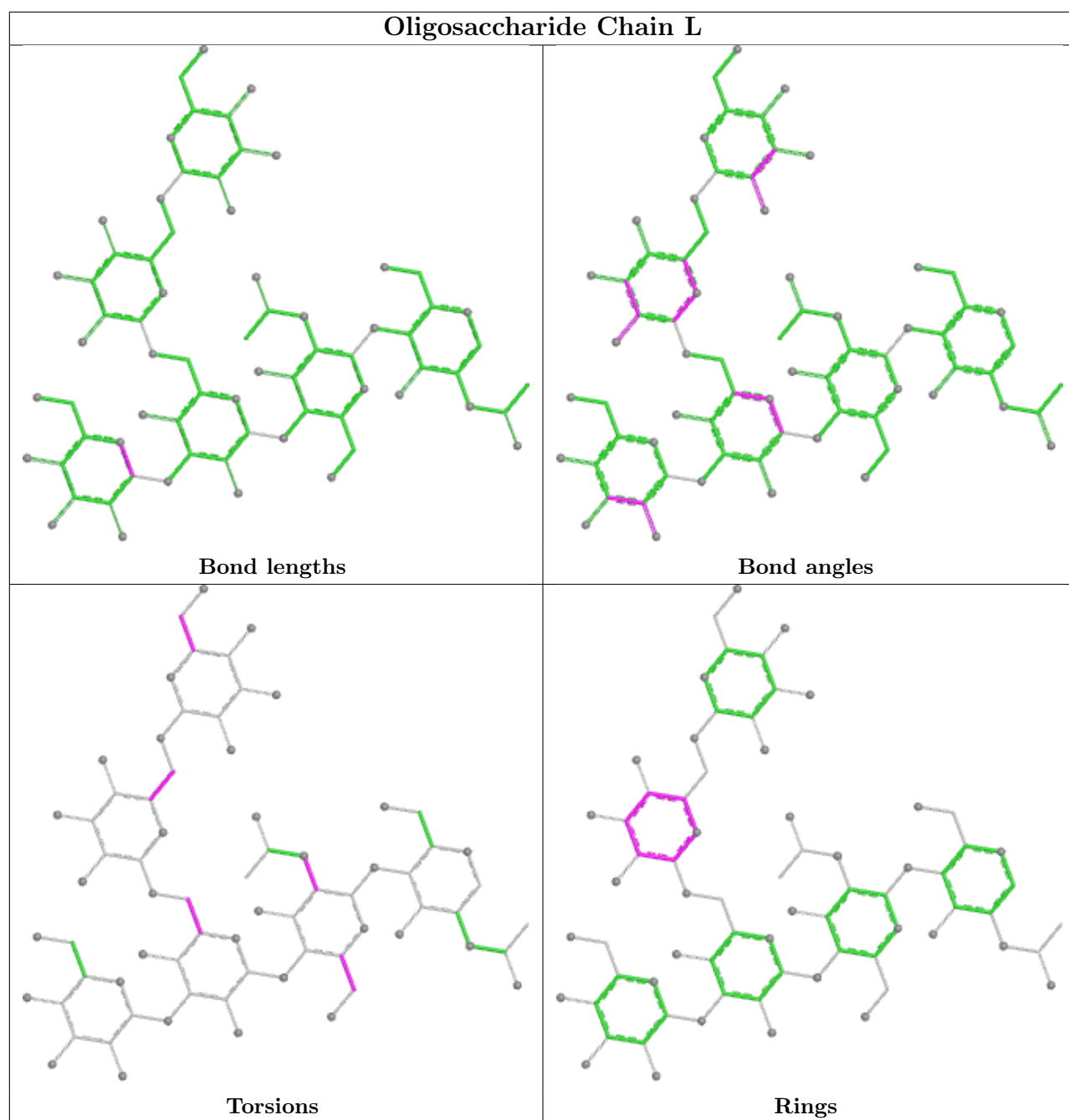
Mol	Chain	Res	Type	Atoms
9	L	4	MAN	C1-C2-C3-C4-C5-O5

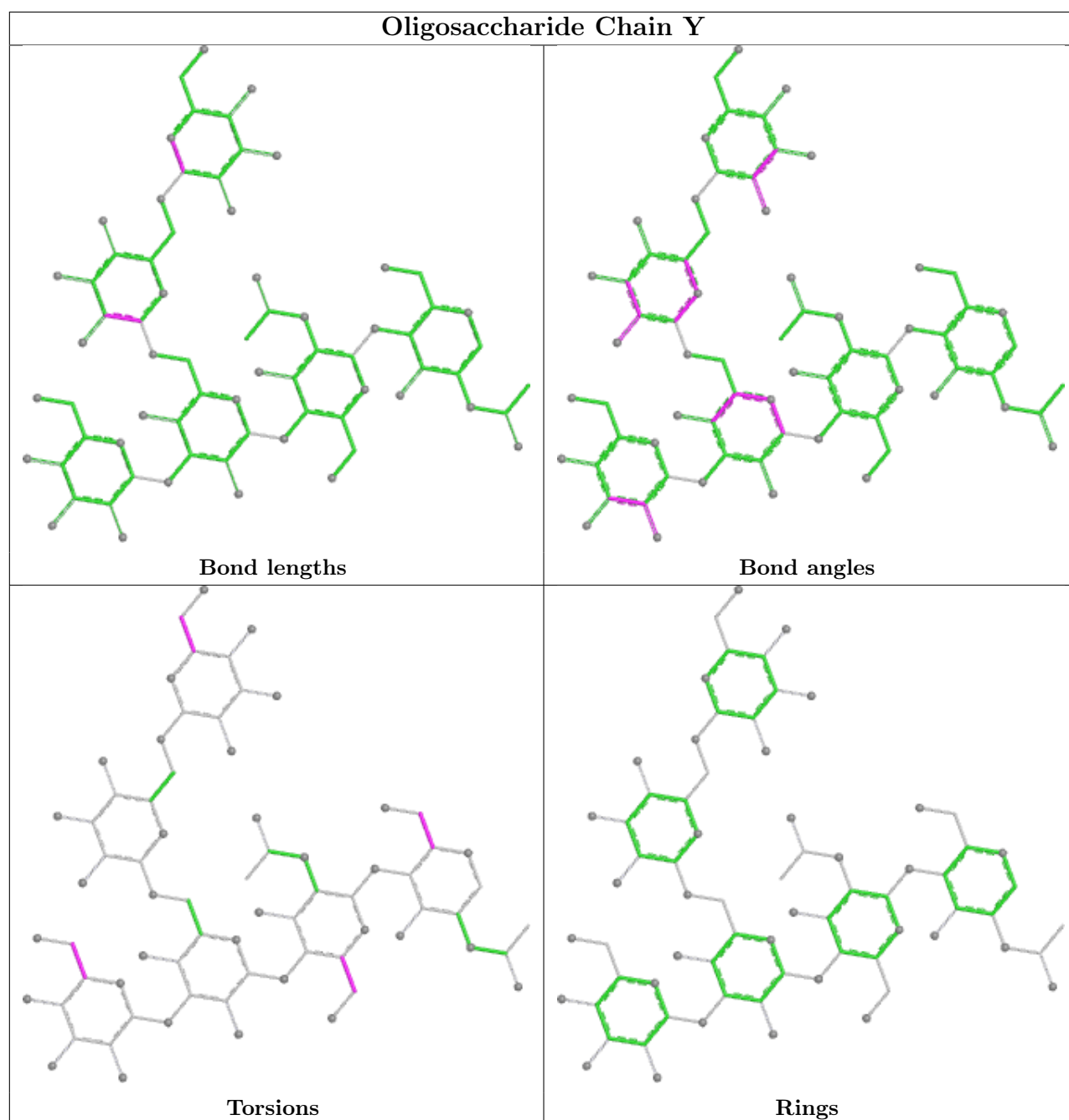
10 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	K	2	NAG	3	0
9	L	3	BMA	1	0
9	K	5	MAN	2	0
9	Y	2	NAG	2	0
9	Y	5	MAN	1	0
9	L	2	NAG	2	0
9	L	1	NAG	1	0
9	K	1	NAG	1	0
9	K	3	BMA	1	0
9	Y	1	NAG	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
10	NAG	U	601	2	14,14,15	0.27	0	17,19,21	0.40	0
10	NAG	T	602	2	14,14,15	0.32	0	17,19,21	0.46	0
10	NAG	U	603	2	14,14,15	0.28	0	17,19,21	0.53	0
10	NAG	S	401	2	14,14,15	0.21	0	17,19,21	0.40	0
10	NAG	U	602	2	14,14,15	0.23	0	17,19,21	0.52	0
10	NAG	T	603	2	14,14,15	0.58	0	17,19,21	0.48	0
10	NAG	T	601	2	14,14,15	0.20	0	17,19,21	0.54	0
10	NAG	S	402	2	14,14,15	0.30	0	17,19,21	0.41	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
10	NAG	U	601	2	-	2/6/23/26	0/1/1/1
10	NAG	T	602	2	-	0/6/23/26	0/1/1/1
10	NAG	U	603	2	-	3/6/23/26	0/1/1/1
10	NAG	S	401	2	-	0/6/23/26	0/1/1/1
10	NAG	U	602	2	-	0/6/23/26	0/1/1/1
10	NAG	T	603	2	-	1/6/23/26	0/1/1/1
10	NAG	T	601	2	-	2/6/23/26	0/1/1/1
10	NAG	S	402	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

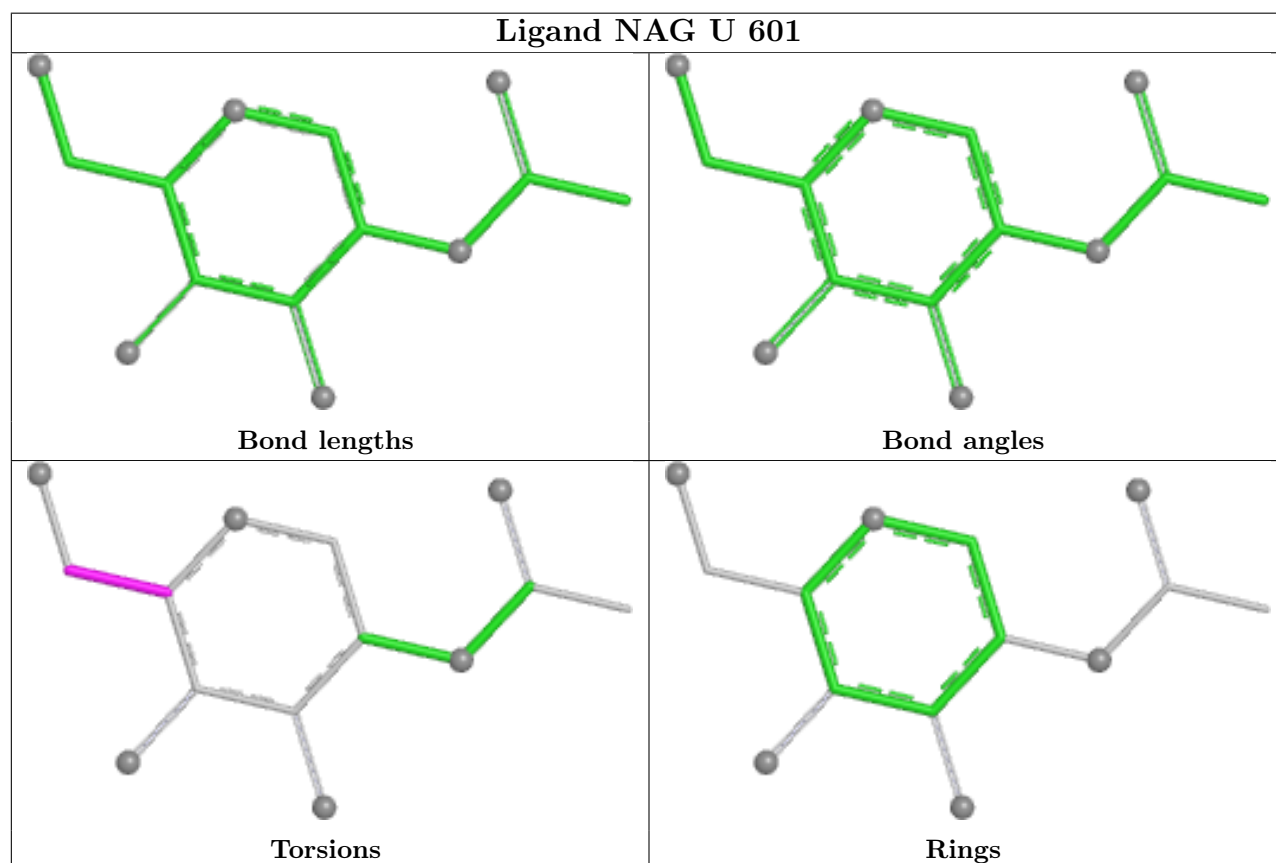
Mol	Chain	Res	Type	Atoms
10	T	601	NAG	C4-C5-C6-O6
10	T	601	NAG	O5-C5-C6-O6
10	U	601	NAG	C4-C5-C6-O6
10	U	603	NAG	O5-C5-C6-O6
10	U	601	NAG	O5-C5-C6-O6

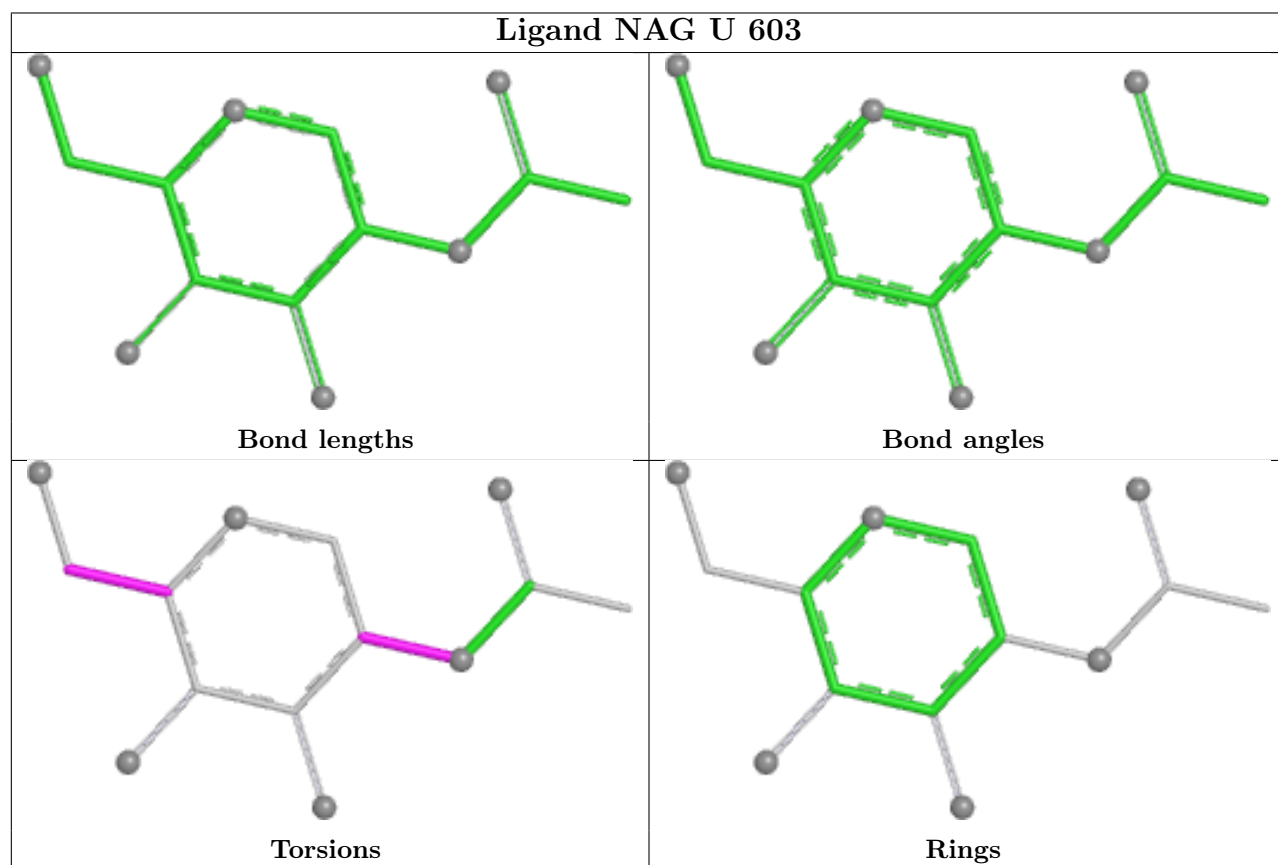
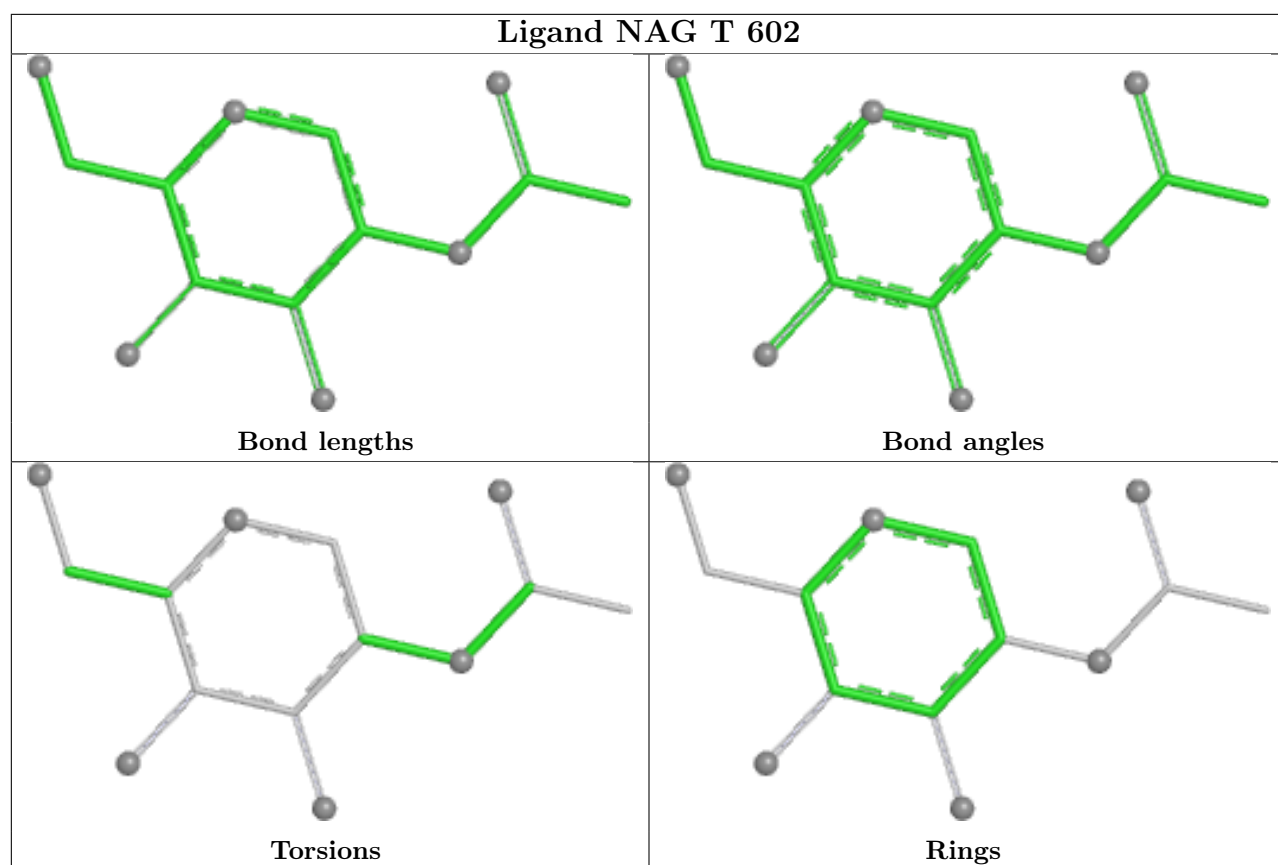
There are no ring outliers.

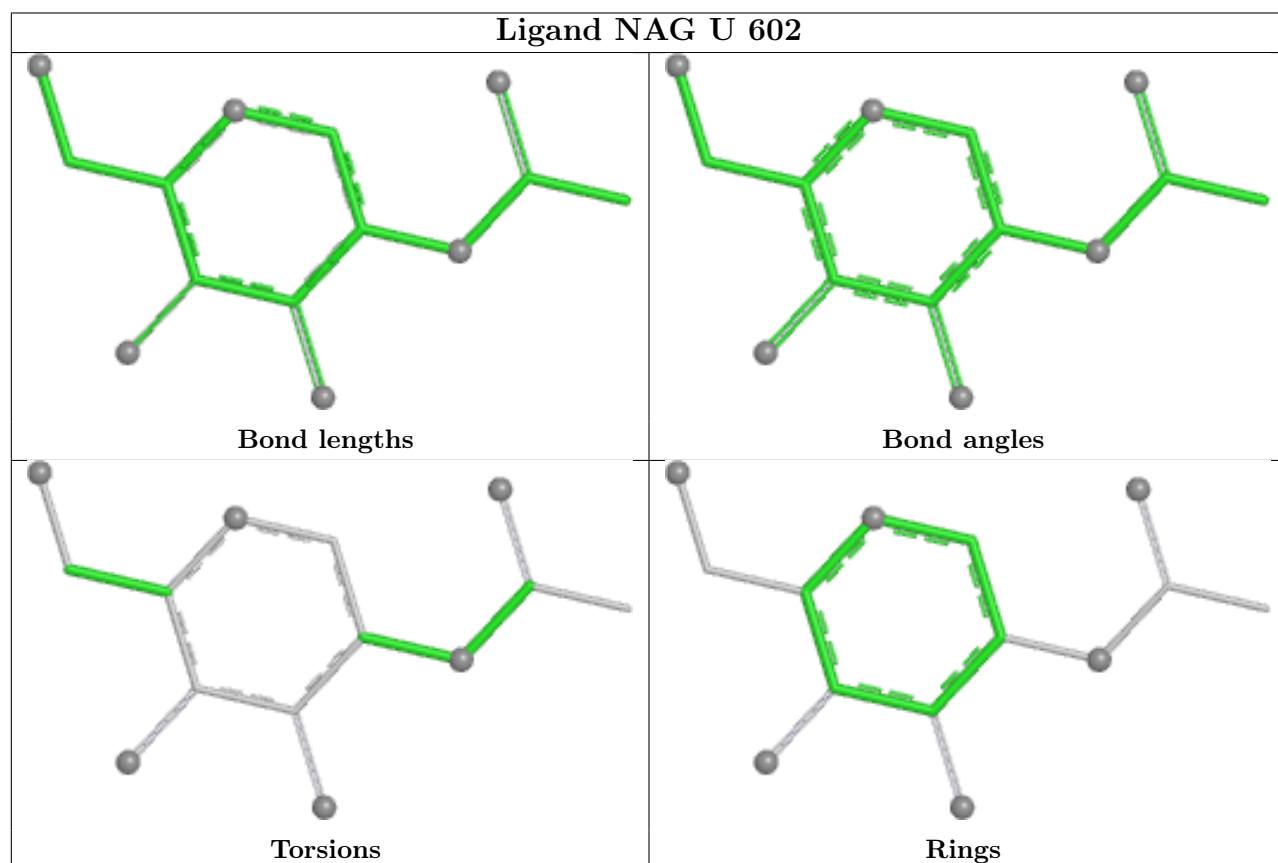
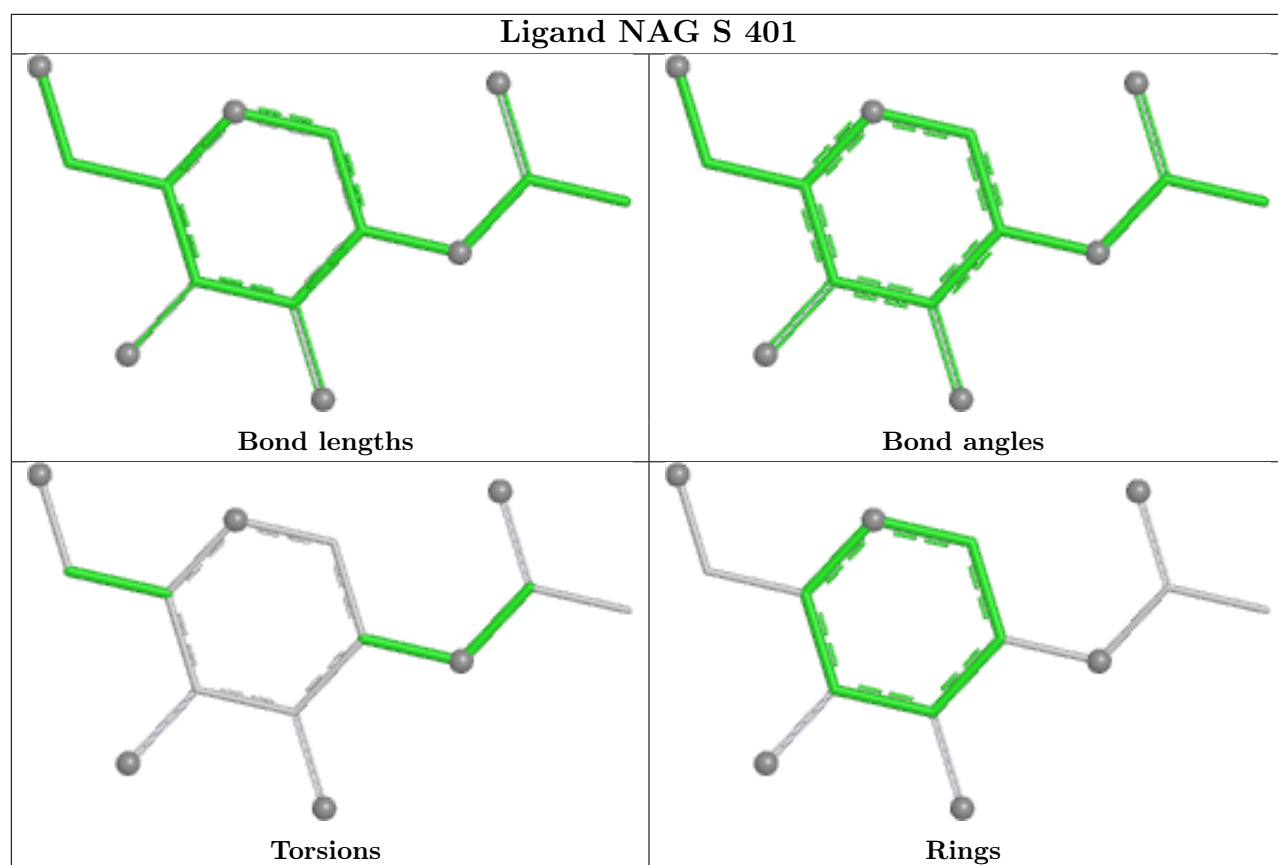
1 monomer is involved in 2 short contacts:

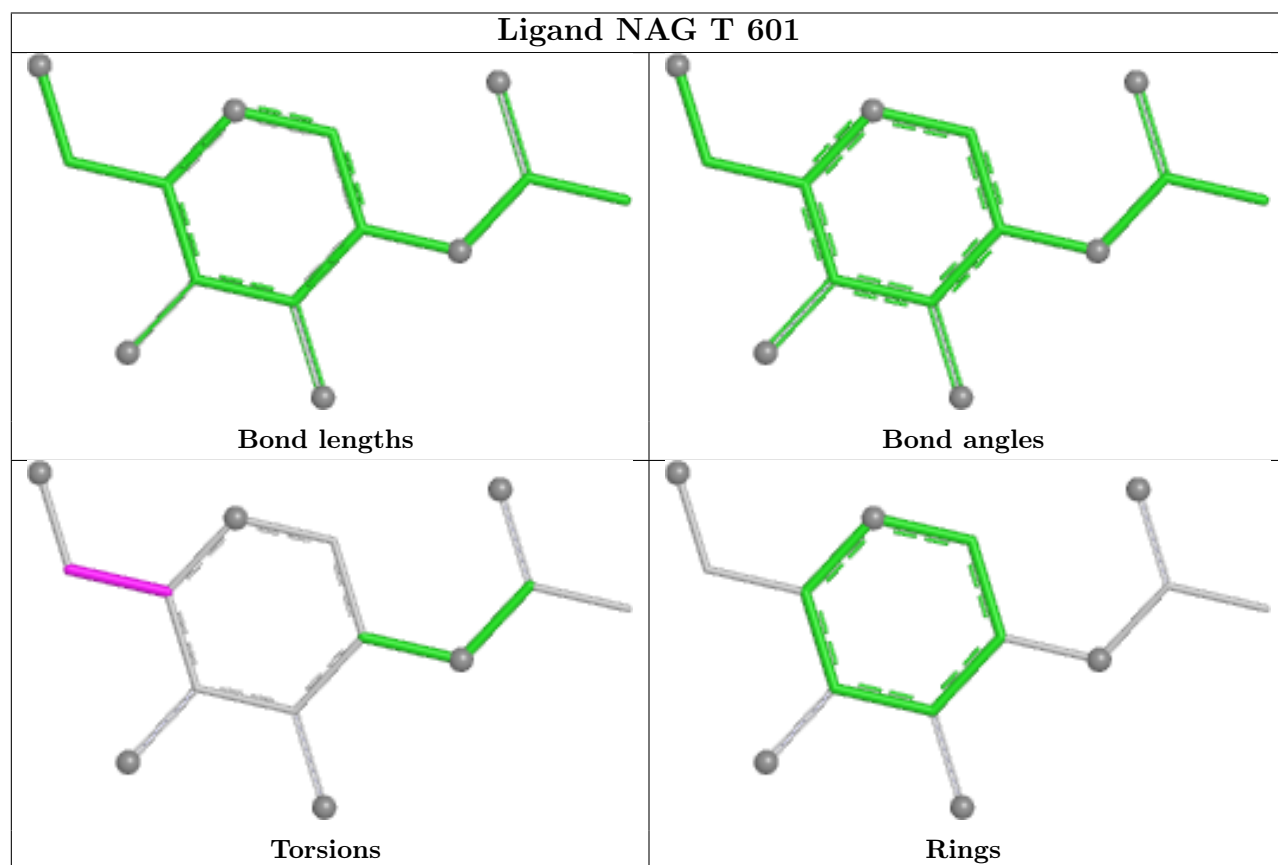
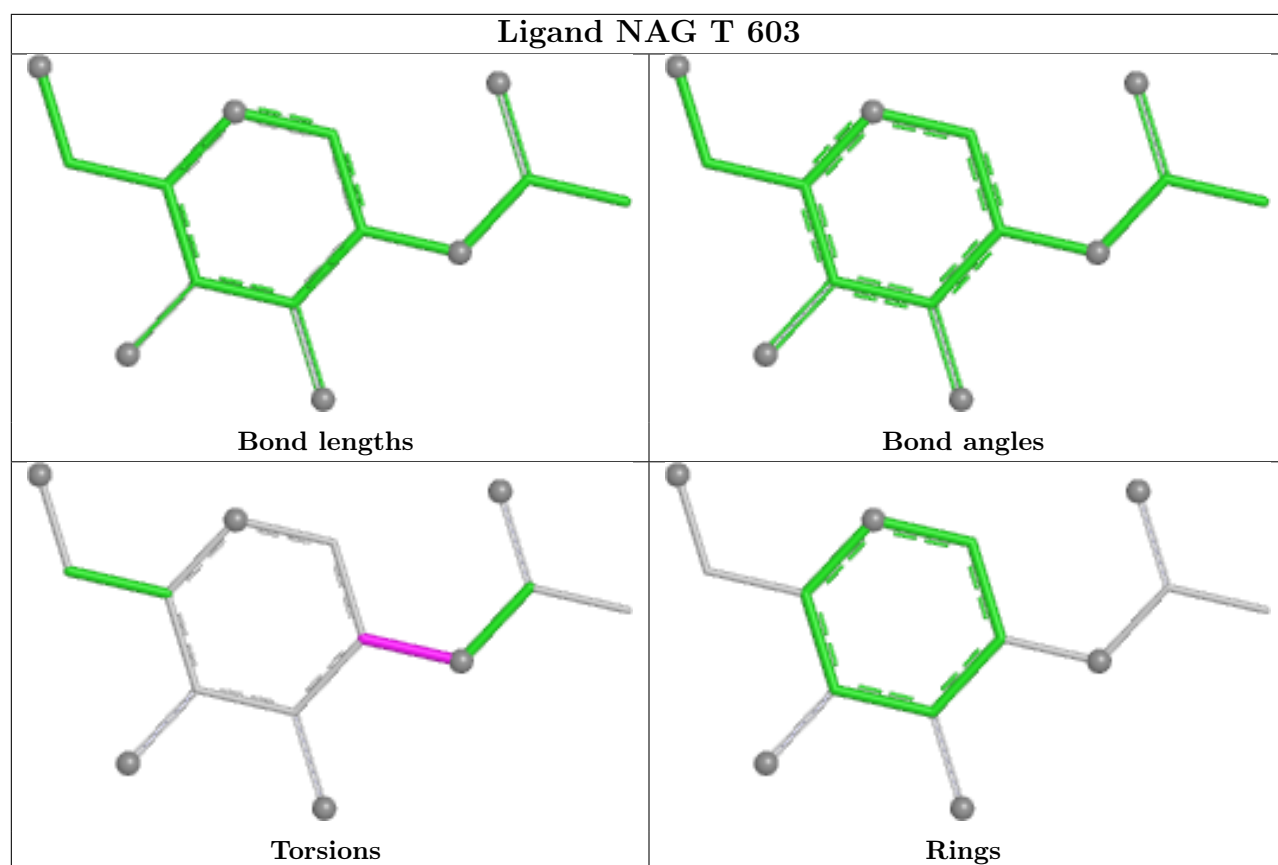
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	T	603	NAG	2	0

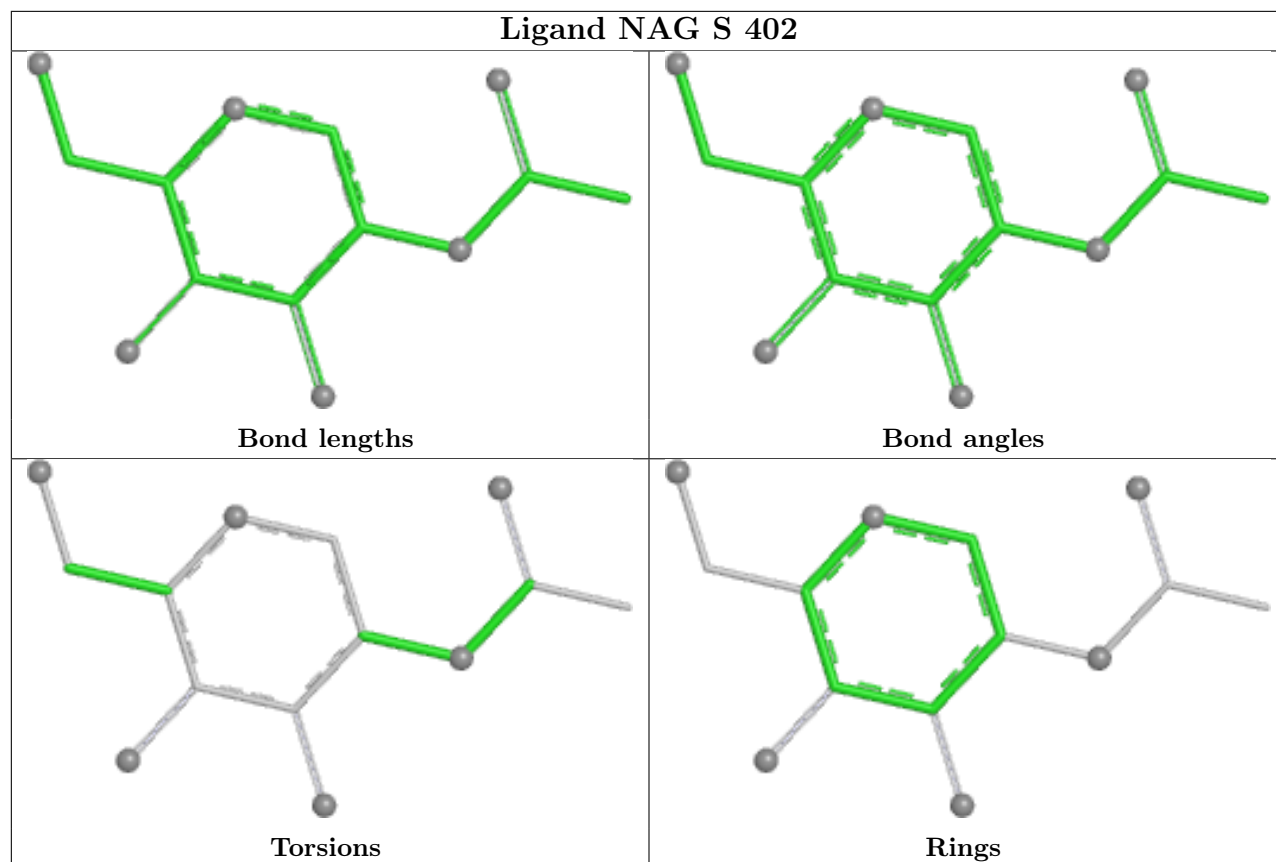
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	U	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U	311:VAL	C	312:ASN	N	3.22

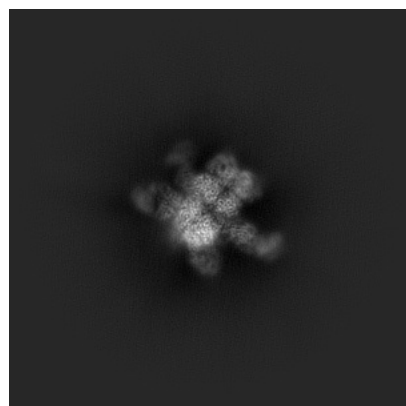
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26005. These allow visual inspection of the internal detail of the map and identification of artifacts.

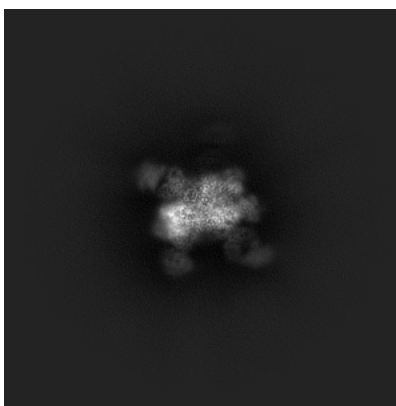
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

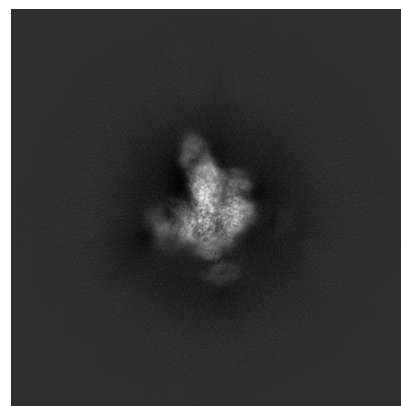
6.1.1 Primary map



X

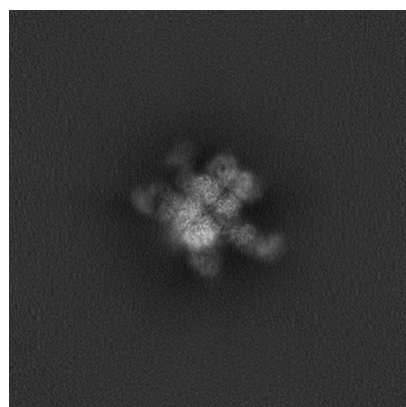


Y

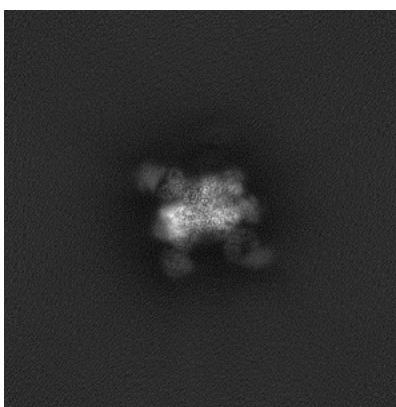


Z

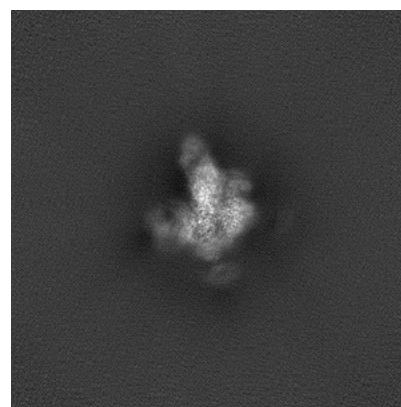
6.1.2 Raw map



X



Y

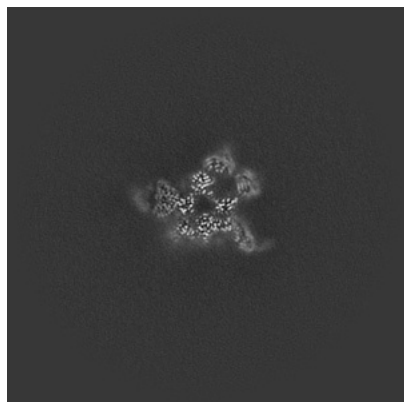


Z

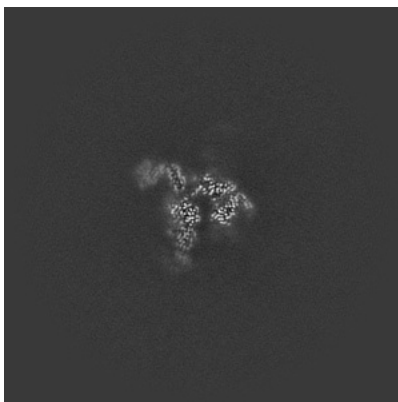
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

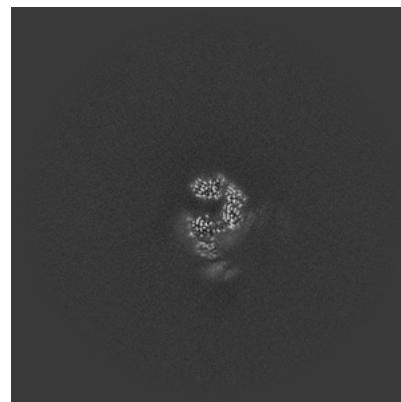
6.2.1 Primary map



X Index: 256

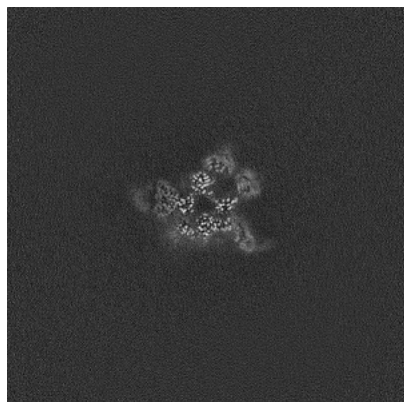


Y Index: 256



Z Index: 256

6.2.2 Raw map



X Index: 256



Y Index: 256

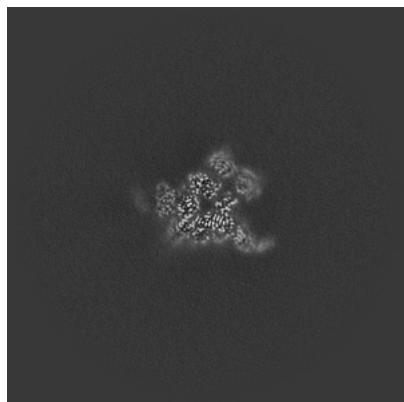


Z Index: 256

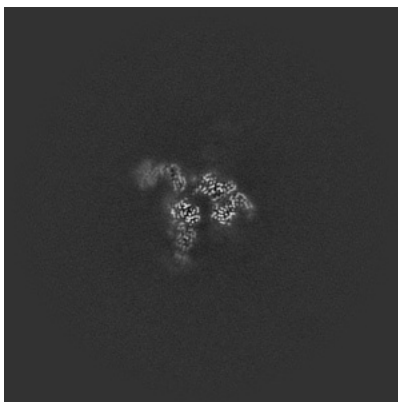
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 251

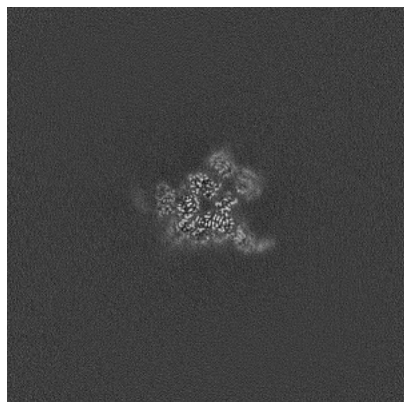


Y Index: 257

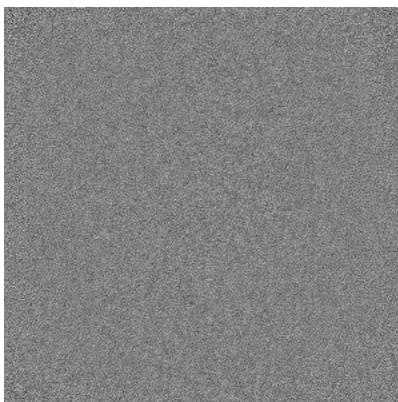


Z Index: 226

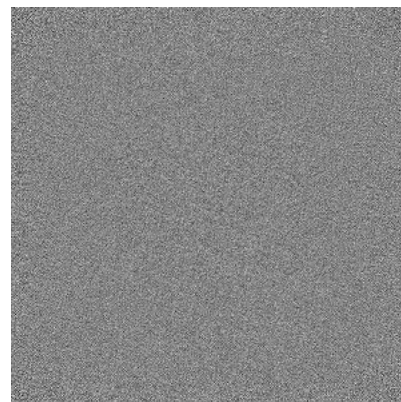
6.3.2 Raw map



X Index: 251



Y Index: 0

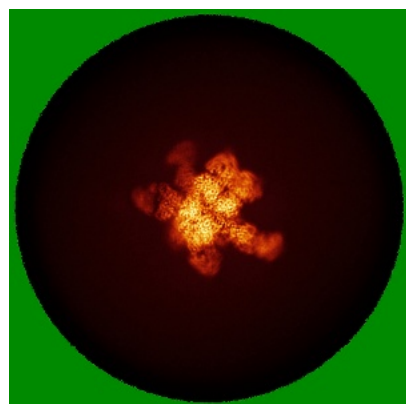


Z Index: 0

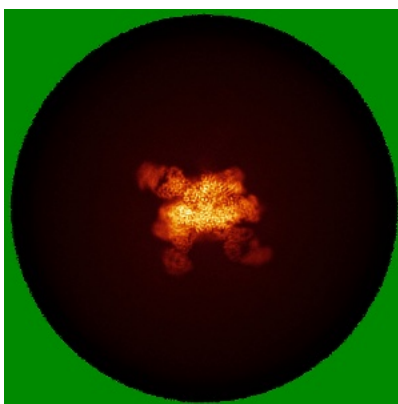
The images above show the largest variance slices of the map in three orthogonal directions.

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

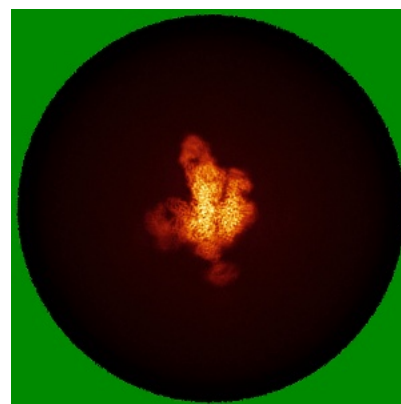
6.4.1 Primary map



X

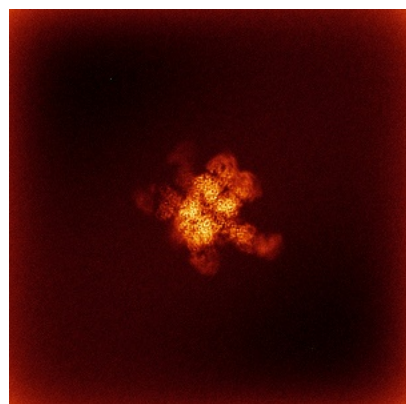


Y

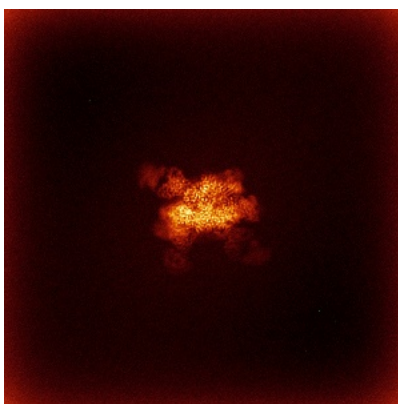


Z

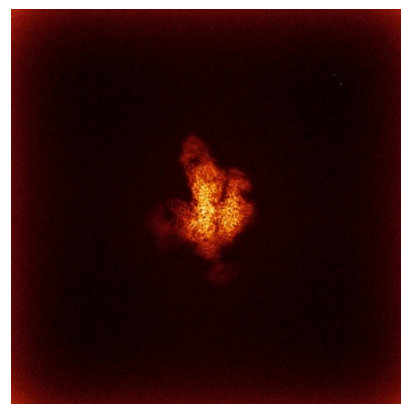
6.4.2 Raw map



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.

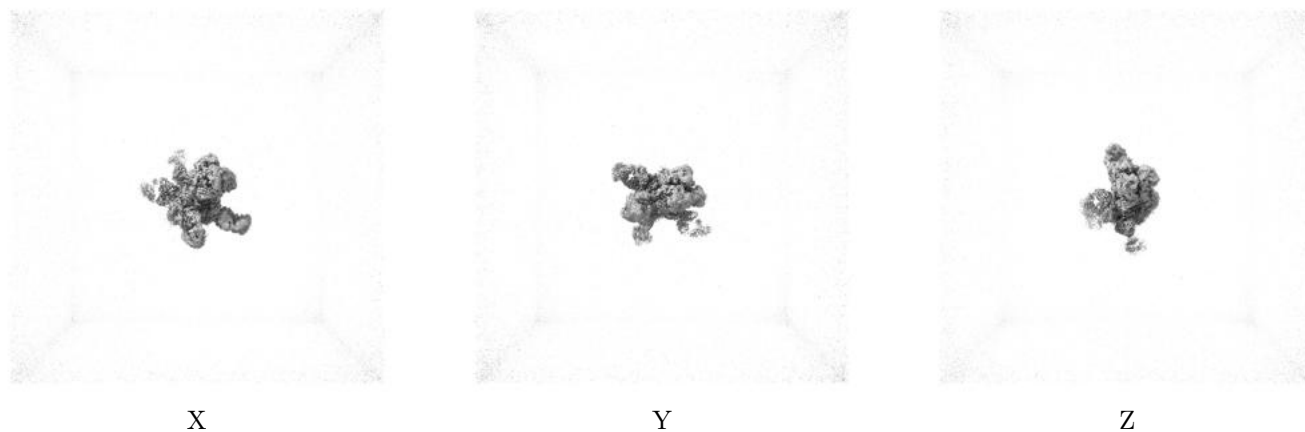
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

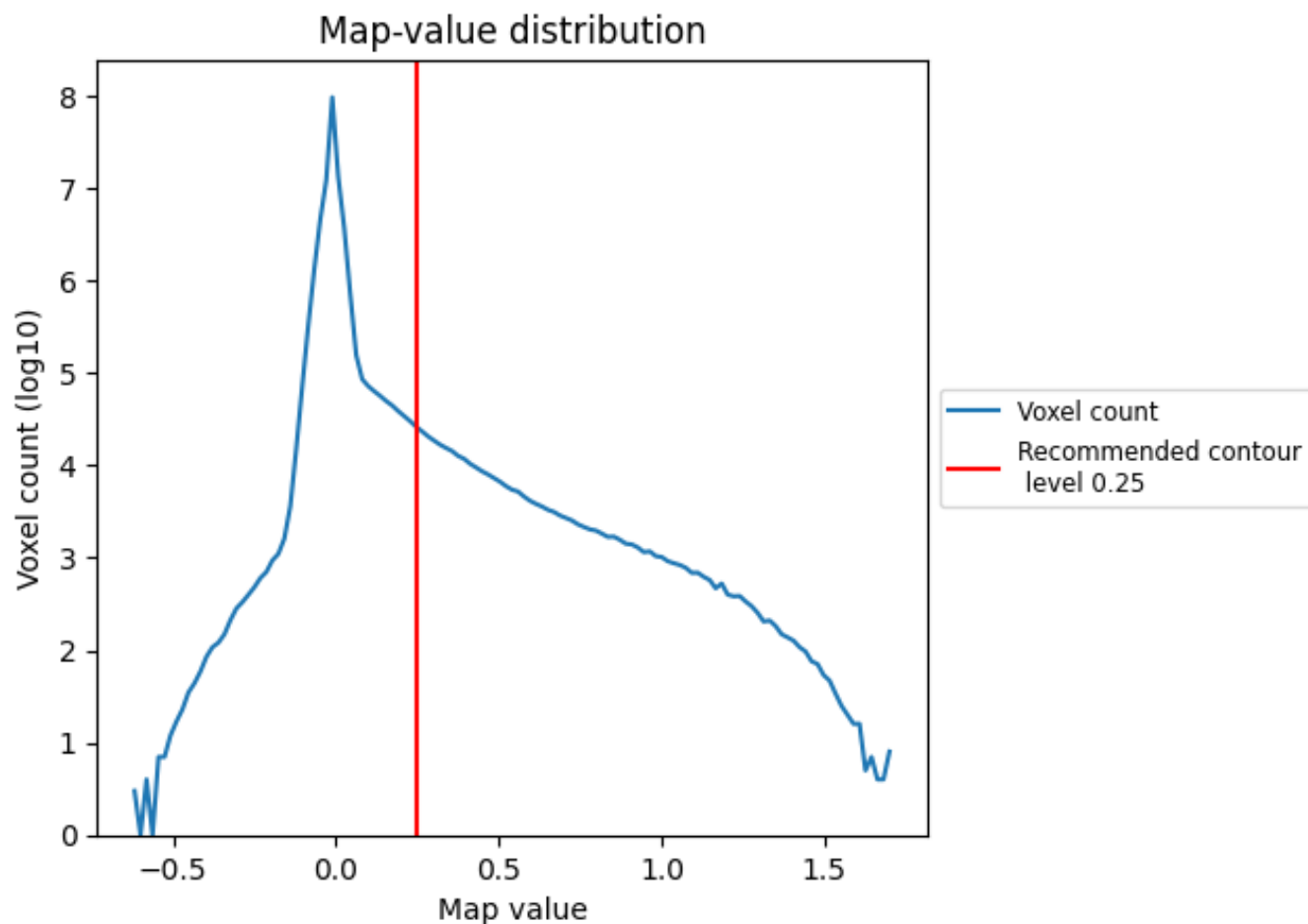
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

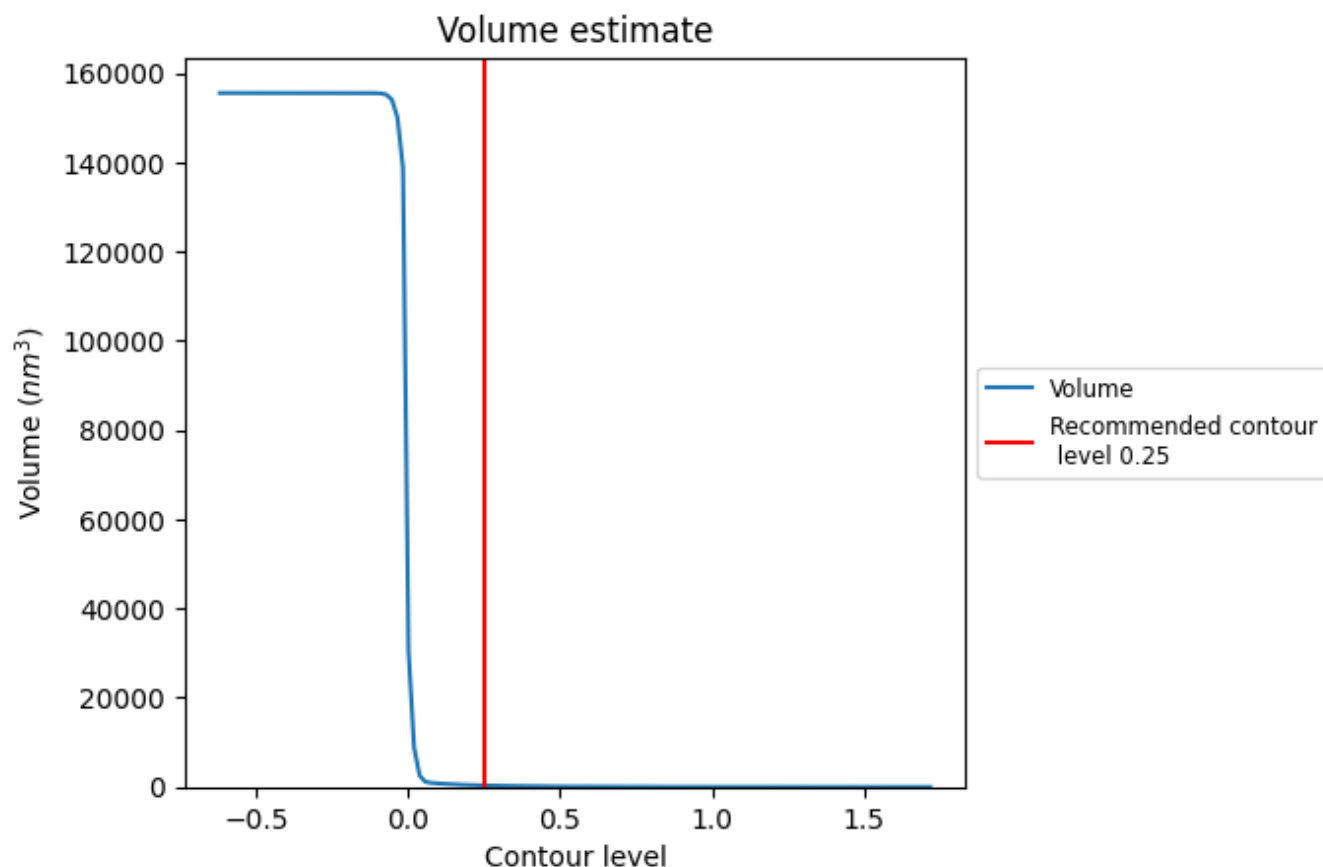
This section contains the results of statistical analysis of the map.

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.

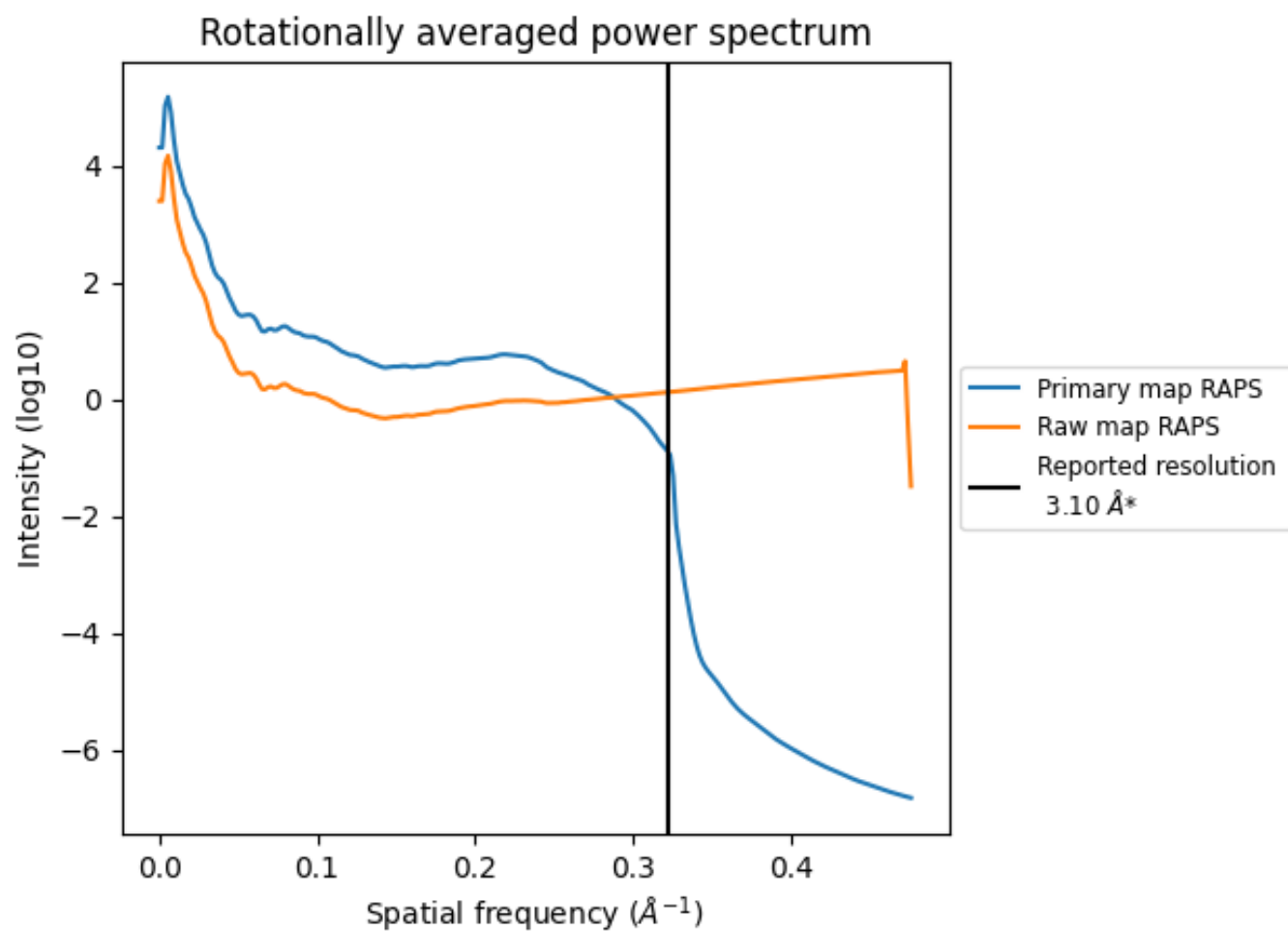
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm^3 ; this corresponds to an approximate mass of 300 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 ⓘ

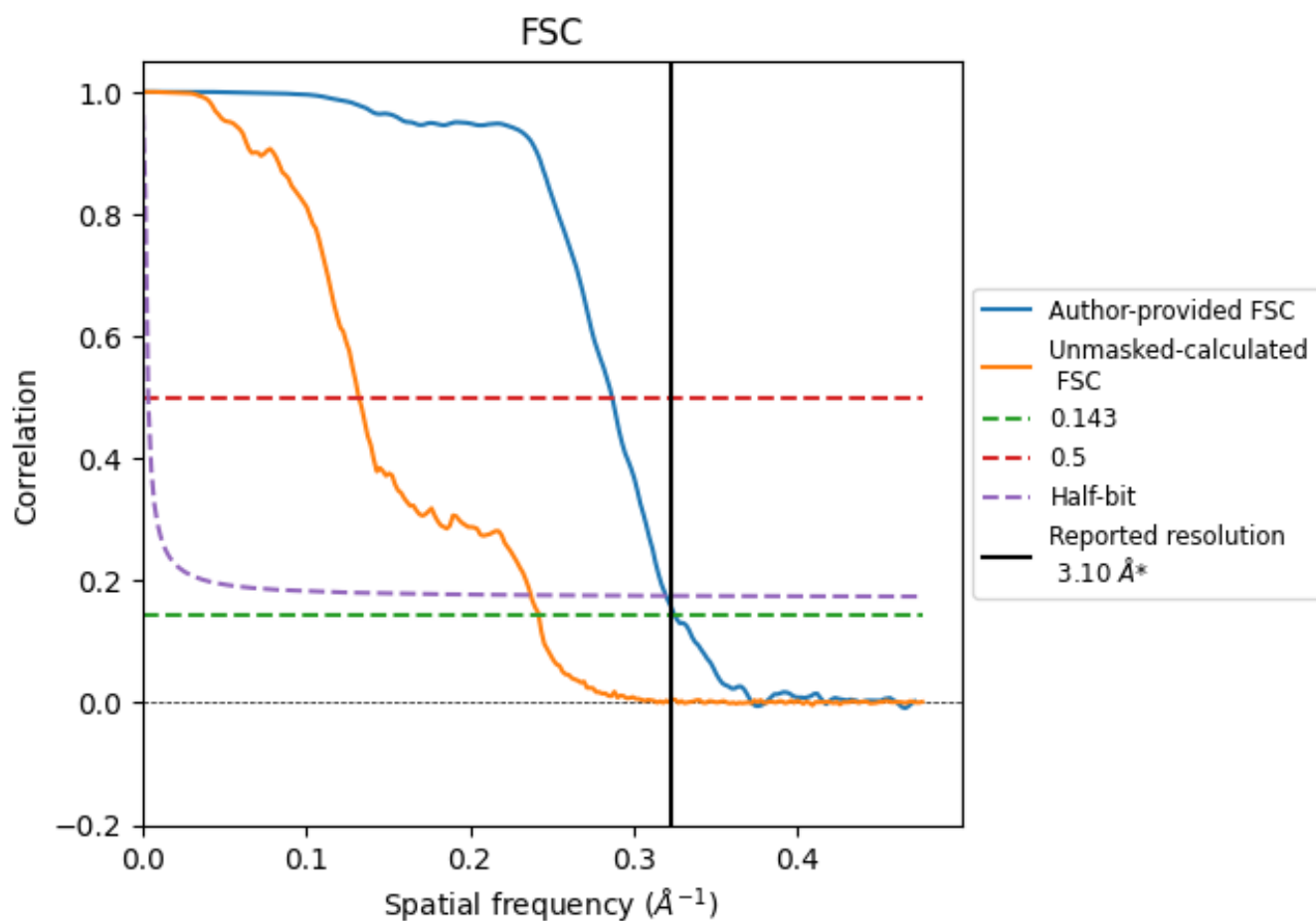


*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

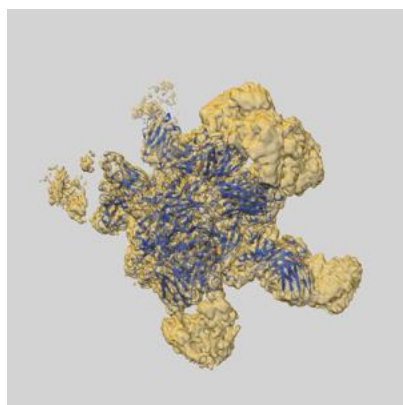
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.08	3.49	3.13
Unmasked-calculated*	4.13	7.56	4.22

*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 4.13 differs from the reported value 3.1 by more than 10 %

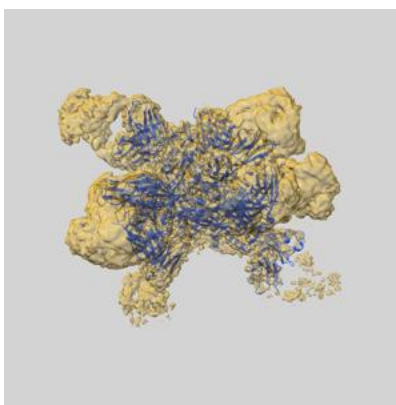
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26005 and PDB model 7TN9. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

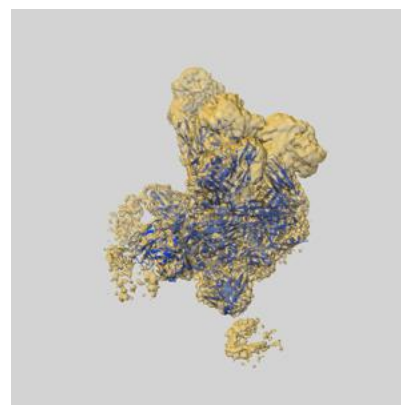
9.1 Map-model overlay [i](#)



X



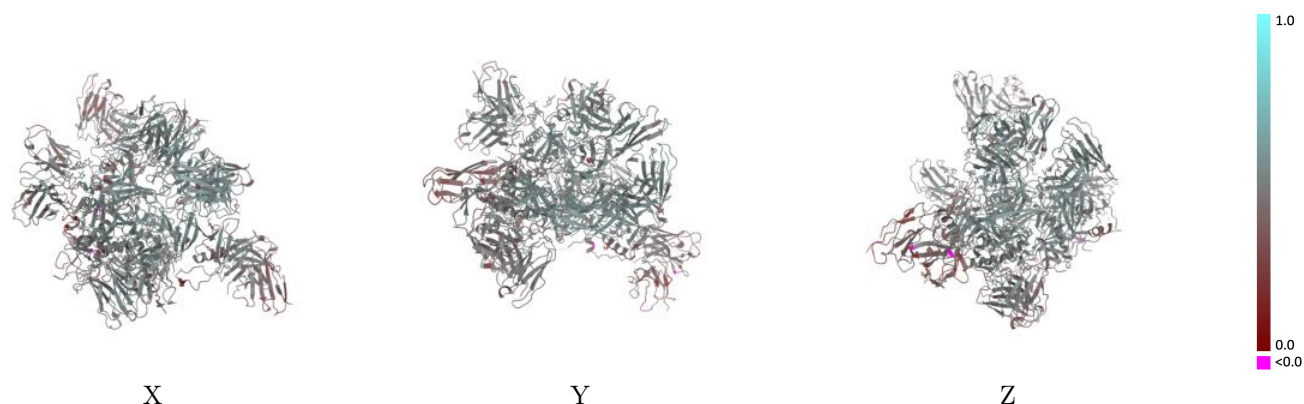
Y



Z

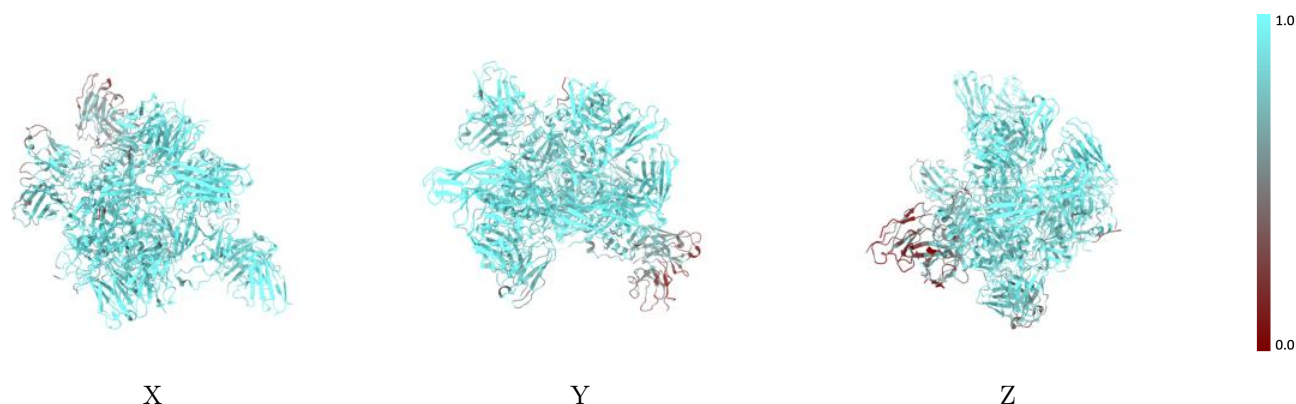
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



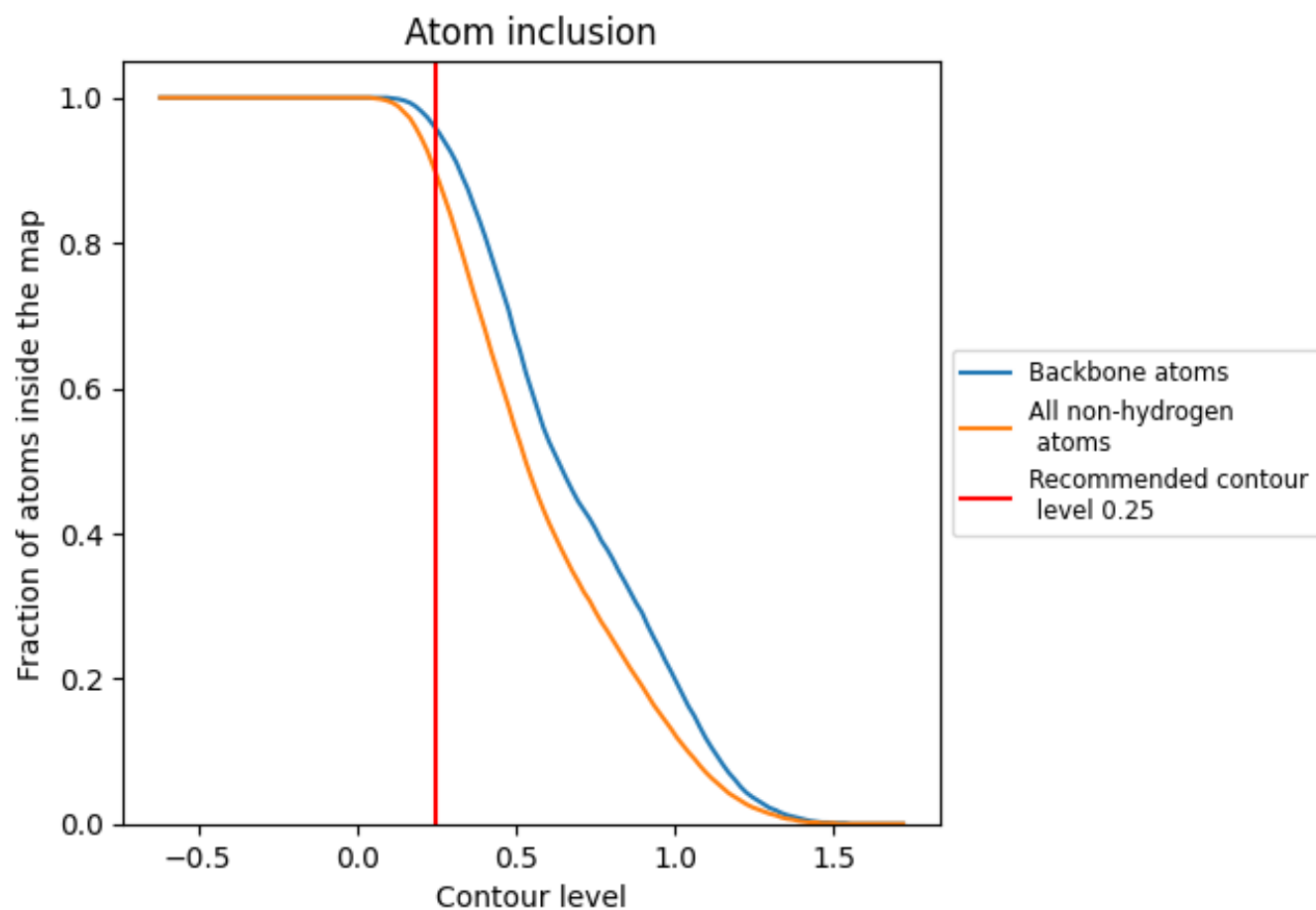
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 89% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8940	 0.4750
A	 0.9710	 0.5190
B	 0.9650	 0.5160
C	 0.9780	 0.5260
D	 0.9630	 0.5050
E	 0.9770	 0.5200
F	 0.9600	 0.5100
G	 0.9740	 0.4660
H	 0.9620	 0.4130
I	 0.5680	 0.3860
J	 0.3540	 0.3470
K	 0.9580	 0.4830
L	 0.9860	 0.5110
M	 0.8700	 0.4620
N	 0.8180	 0.4610
O	 0.8510	 0.4560
P	 0.7790	 0.4490
Q	 0.9540	 0.4850
R	 0.9350	 0.4820
S	 0.9080	 0.4920
T	 0.9540	 0.4920
U	 0.8870	 0.4830
V	 0.9290	 0.4540
W	 0.9360	 0.4640
X	 0.9610	 0.4690
Y	 0.9580	 0.5060

