



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 06:59 PM UTC

PDB ID : 7S6L / pdb_00007s6l
EMDB ID : EMD-24879
Title : J08 fragment antigen binding in complex with SARS-CoV-2-6P-Mut7 S protein
(conformation 3)
Authors : Ozorowski, G.; Torres, J.L.; Ward, A.B.
Deposited on : 2021-09-14
Resolution : 4.00 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

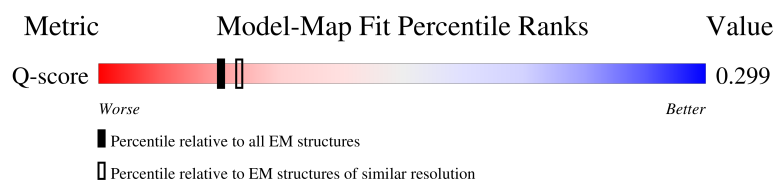
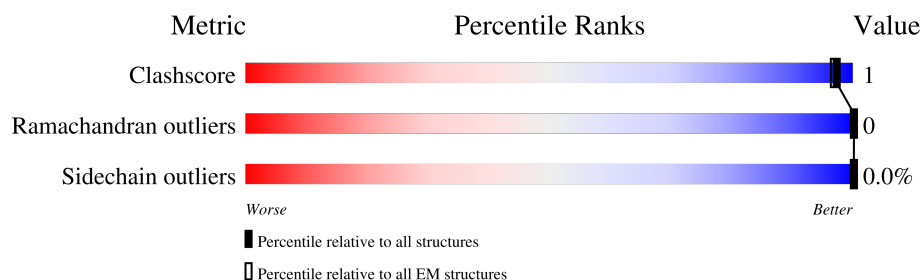
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

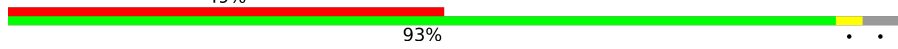
The reported resolution of this entry is 4.00 Å.

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.



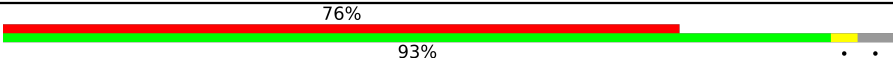
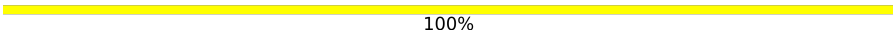
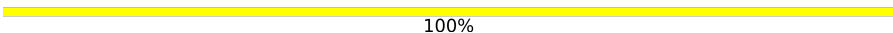
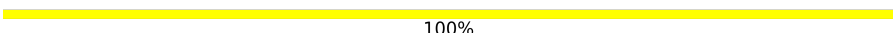
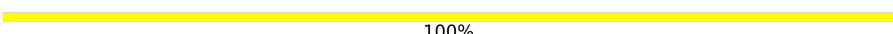
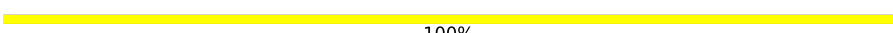
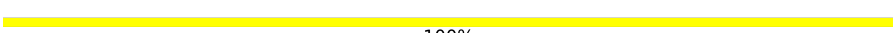
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	1280	
1	B	1280	
1	C	1280	
2	H	127	

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Mol	Chain	Length	Quality of chain
3	L	105	 76% 93%
4	D	2	 100%
4	E	2	 100%
4	F	2	 100%
4	G	2	 100%
4	I	2	 100%
4	J	2	 100%
4	K	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24755 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	984	Total	C	N	O	S	0	0
			7688	4911	1273	1467	37		
1	B	949	Total	C	N	O	S	0	0
			7436	4758	1235	1409	34		
1	C	961	Total	C	N	O	S	0	0
			7509	4794	1246	1434	35		

There are 249 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	705	CYS	VAL	engineered mutation	UNP P0DTC2
A	817	PRO	PHE	engineered mutation	UNP P0DTC2
A	883	CYS	THR	engineered mutation	UNP P0DTC2
A	892	PRO	ALA	engineered mutation	UNP P0DTC2
A	899	PRO	ALA	engineered mutation	UNP P0DTC2
A	942	PRO	ALA	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	TYR	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	GLU	-	expression tag	UNP P0DTC2
A	1216	ALA	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	ARG	-	expression tag	UNP P0DTC2
A	1219	ASP	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1222	ALA	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	VAL	-	expression tag	UNP P0DTC2
A	1225	ARG	-	expression tag	UNP P0DTC2
A	1226	LYS	-	expression tag	UNP P0DTC2
A	1227	ASP	-	expression tag	UNP P0DTC2
A	1228	GLY	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2
A	1230	TRP	-	expression tag	UNP P0DTC2
A	1231	VAL	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	SER	-	expression tag	UNP P0DTC2
A	1235	THR	-	expression tag	UNP P0DTC2
A	1236	PHE	-	expression tag	UNP P0DTC2
A	1237	LEU	-	expression tag	UNP P0DTC2
A	1238	GLY	-	expression tag	UNP P0DTC2
A	1239	ARG	-	expression tag	UNP P0DTC2
A	1240	SER	-	expression tag	UNP P0DTC2
A	1241	LEU	-	expression tag	UNP P0DTC2
A	1242	GLU	-	expression tag	UNP P0DTC2
A	1243	VAL	-	expression tag	UNP P0DTC2
A	1244	LEU	-	expression tag	UNP P0DTC2
A	1245	PHE	-	expression tag	UNP P0DTC2
A	1246	GLN	-	expression tag	UNP P0DTC2
A	1247	GLY	-	expression tag	UNP P0DTC2
A	1248	PRO	-	expression tag	UNP P0DTC2
A	1249	GLY	-	expression tag	UNP P0DTC2
A	1250	SER	-	expression tag	UNP P0DTC2
A	1251	ALA	-	expression tag	UNP P0DTC2
A	1252	TRP	-	expression tag	UNP P0DTC2
A	1253	SER	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	PRO	-	expression tag	UNP P0DTC2
A	1256	GLN	-	expression tag	UNP P0DTC2
A	1257	PHE	-	expression tag	UNP P0DTC2
A	1258	GLU	-	expression tag	UNP P0DTC2
A	1259	LYS	-	expression tag	UNP P0DTC2
A	1260	GLY	-	expression tag	UNP P0DTC2
A	1261	GLY	-	expression tag	UNP P0DTC2
A	1262	GLY	-	expression tag	UNP P0DTC2
A	1263	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1264	GLY	-	expression tag	UNP P0DTC2
A	1265	GLY	-	expression tag	UNP P0DTC2
A	1266	GLY	-	expression tag	UNP P0DTC2
A	1267	GLY	-	expression tag	UNP P0DTC2
A	1268	SER	-	expression tag	UNP P0DTC2
A	1269	GLY	-	expression tag	UNP P0DTC2
A	1270	GLY	-	expression tag	UNP P0DTC2
A	1271	SER	-	expression tag	UNP P0DTC2
A	1272	ALA	-	expression tag	UNP P0DTC2
A	1273	TRP	-	expression tag	UNP P0DTC2
A	1274	SER	-	expression tag	UNP P0DTC2
A	1275	HIS	-	expression tag	UNP P0DTC2
A	1276	PRO	-	expression tag	UNP P0DTC2
A	1277	GLN	-	expression tag	UNP P0DTC2
A	1278	PHE	-	expression tag	UNP P0DTC2
A	1279	GLU	-	expression tag	UNP P0DTC2
A	1280	LYS	-	expression tag	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	705	CYS	VAL	engineered mutation	UNP P0DTC2
B	817	PRO	PHE	engineered mutation	UNP P0DTC2
B	883	CYS	THR	engineered mutation	UNP P0DTC2
B	892	PRO	ALA	engineered mutation	UNP P0DTC2
B	899	PRO	ALA	engineered mutation	UNP P0DTC2
B	942	PRO	ALA	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLY	-	expression tag	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP P0DTC2
B	1240	SER	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2
B	1242	GLU	-	expression tag	UNP P0DTC2
B	1243	VAL	-	expression tag	UNP P0DTC2
B	1244	LEU	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	GLN	-	expression tag	UNP P0DTC2
B	1247	GLY	-	expression tag	UNP P0DTC2
B	1248	PRO	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	SER	-	expression tag	UNP P0DTC2
B	1251	ALA	-	expression tag	UNP P0DTC2
B	1252	TRP	-	expression tag	UNP P0DTC2
B	1253	SER	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	PRO	-	expression tag	UNP P0DTC2
B	1256	GLN	-	expression tag	UNP P0DTC2
B	1257	PHE	-	expression tag	UNP P0DTC2
B	1258	GLU	-	expression tag	UNP P0DTC2
B	1259	LYS	-	expression tag	UNP P0DTC2
B	1260	GLY	-	expression tag	UNP P0DTC2
B	1261	GLY	-	expression tag	UNP P0DTC2
B	1262	GLY	-	expression tag	UNP P0DTC2
B	1263	SER	-	expression tag	UNP P0DTC2
B	1264	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1265	GLY	-	expression tag	UNP P0DTC2
B	1266	GLY	-	expression tag	UNP P0DTC2
B	1267	GLY	-	expression tag	UNP P0DTC2
B	1268	SER	-	expression tag	UNP P0DTC2
B	1269	GLY	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	ALA	-	expression tag	UNP P0DTC2
B	1273	TRP	-	expression tag	UNP P0DTC2
B	1274	SER	-	expression tag	UNP P0DTC2
B	1275	HIS	-	expression tag	UNP P0DTC2
B	1276	PRO	-	expression tag	UNP P0DTC2
B	1277	GLN	-	expression tag	UNP P0DTC2
B	1278	PHE	-	expression tag	UNP P0DTC2
B	1279	GLU	-	expression tag	UNP P0DTC2
B	1280	LYS	-	expression tag	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	705	CYS	VAL	engineered mutation	UNP P0DTC2
C	817	PRO	PHE	engineered mutation	UNP P0DTC2
C	883	CYS	THR	engineered mutation	UNP P0DTC2
C	892	PRO	ALA	engineered mutation	UNP P0DTC2
C	899	PRO	ALA	engineered mutation	UNP P0DTC2
C	942	PRO	ALA	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2
C	1237	LEU	-	expression tag	UNP P0DTC2
C	1238	GLY	-	expression tag	UNP P0DTC2
C	1239	ARG	-	expression tag	UNP P0DTC2
C	1240	SER	-	expression tag	UNP P0DTC2
C	1241	LEU	-	expression tag	UNP P0DTC2
C	1242	GLU	-	expression tag	UNP P0DTC2
C	1243	VAL	-	expression tag	UNP P0DTC2
C	1244	LEU	-	expression tag	UNP P0DTC2
C	1245	PHE	-	expression tag	UNP P0DTC2
C	1246	GLN	-	expression tag	UNP P0DTC2
C	1247	GLY	-	expression tag	UNP P0DTC2
C	1248	PRO	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	SER	-	expression tag	UNP P0DTC2
C	1251	ALA	-	expression tag	UNP P0DTC2
C	1252	TRP	-	expression tag	UNP P0DTC2
C	1253	SER	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	PRO	-	expression tag	UNP P0DTC2
C	1256	GLN	-	expression tag	UNP P0DTC2
C	1257	PHE	-	expression tag	UNP P0DTC2
C	1258	GLU	-	expression tag	UNP P0DTC2
C	1259	LYS	-	expression tag	UNP P0DTC2
C	1260	GLY	-	expression tag	UNP P0DTC2
C	1261	GLY	-	expression tag	UNP P0DTC2
C	1262	GLY	-	expression tag	UNP P0DTC2
C	1263	SER	-	expression tag	UNP P0DTC2
C	1264	GLY	-	expression tag	UNP P0DTC2
C	1265	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1266	GLY	-	expression tag	UNP P0DTC2
C	1267	GLY	-	expression tag	UNP P0DTC2
C	1268	SER	-	expression tag	UNP P0DTC2
C	1269	GLY	-	expression tag	UNP P0DTC2
C	1270	GLY	-	expression tag	UNP P0DTC2
C	1271	SER	-	expression tag	UNP P0DTC2
C	1272	ALA	-	expression tag	UNP P0DTC2
C	1273	TRP	-	expression tag	UNP P0DTC2
C	1274	SER	-	expression tag	UNP P0DTC2
C	1275	HIS	-	expression tag	UNP P0DTC2
C	1276	PRO	-	expression tag	UNP P0DTC2
C	1277	GLN	-	expression tag	UNP P0DTC2
C	1278	PHE	-	expression tag	UNP P0DTC2
C	1279	GLU	-	expression tag	UNP P0DTC2
C	1280	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called J08 fragment antigen binding heavy chain variable domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	122	Total	C	N	O	S	0	0
			947	596	162	184	5		

- Molecule 3 is a protein called J08 fragment antigen binding light chain variable domain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	101	Total	C	N	O	S	0	0
			755	474	124	154	3		

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



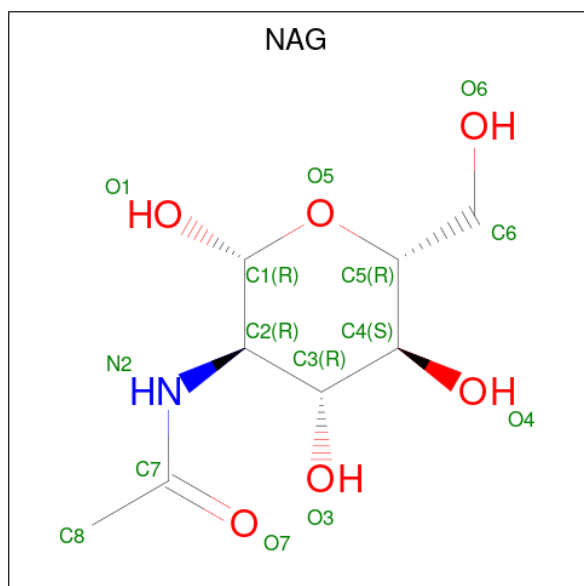
Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	2	Total	C	N	O		0	0
			28	16	2	10			
4	E	2	Total	C	N	O		0	0
			28	16	2	10			
4	F	2	Total	C	N	O		0	0
			28	16	2	10			

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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	J	2	Total	C	N	O	0	0
			28	16	2	10		
4	K	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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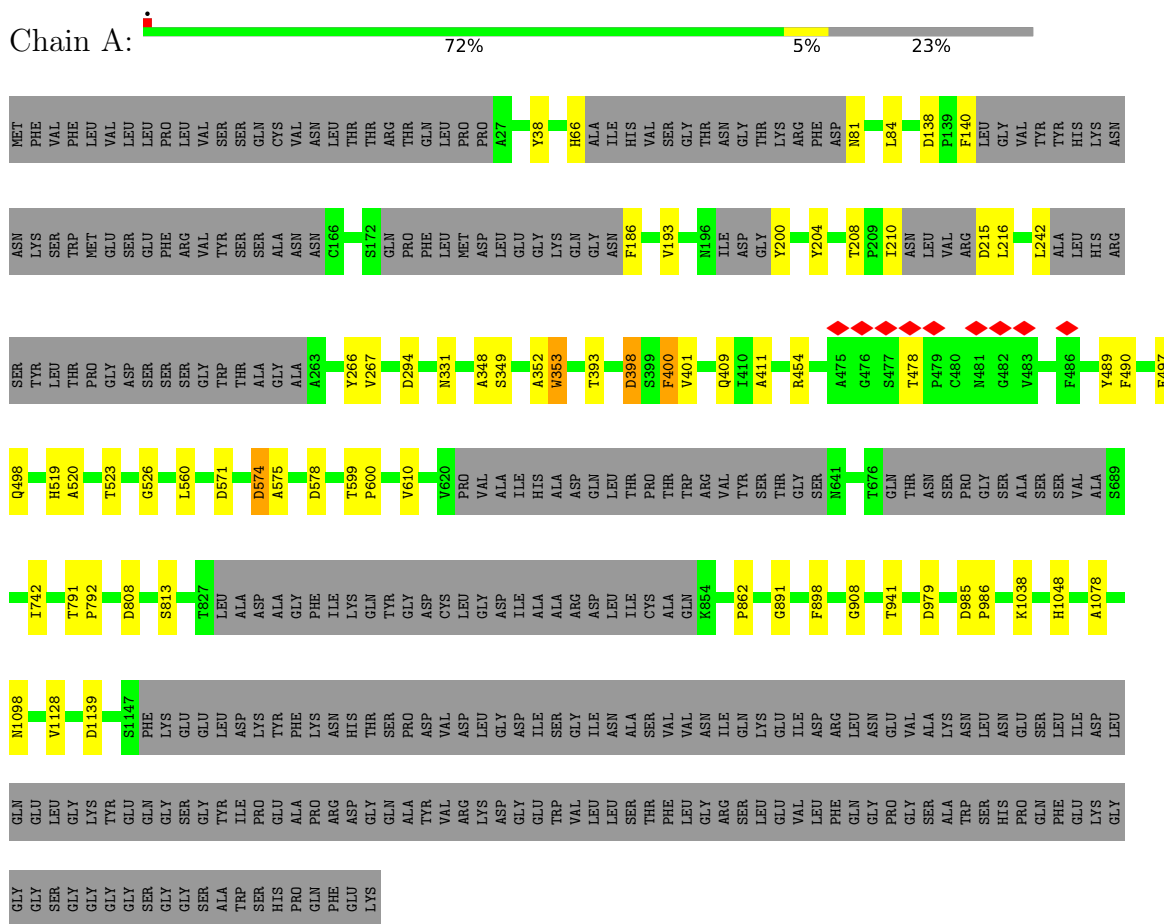
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Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C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

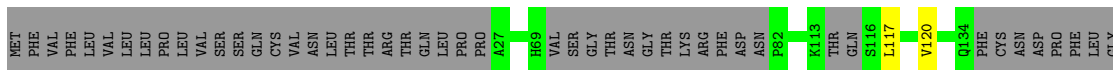
3 Residue-property plots

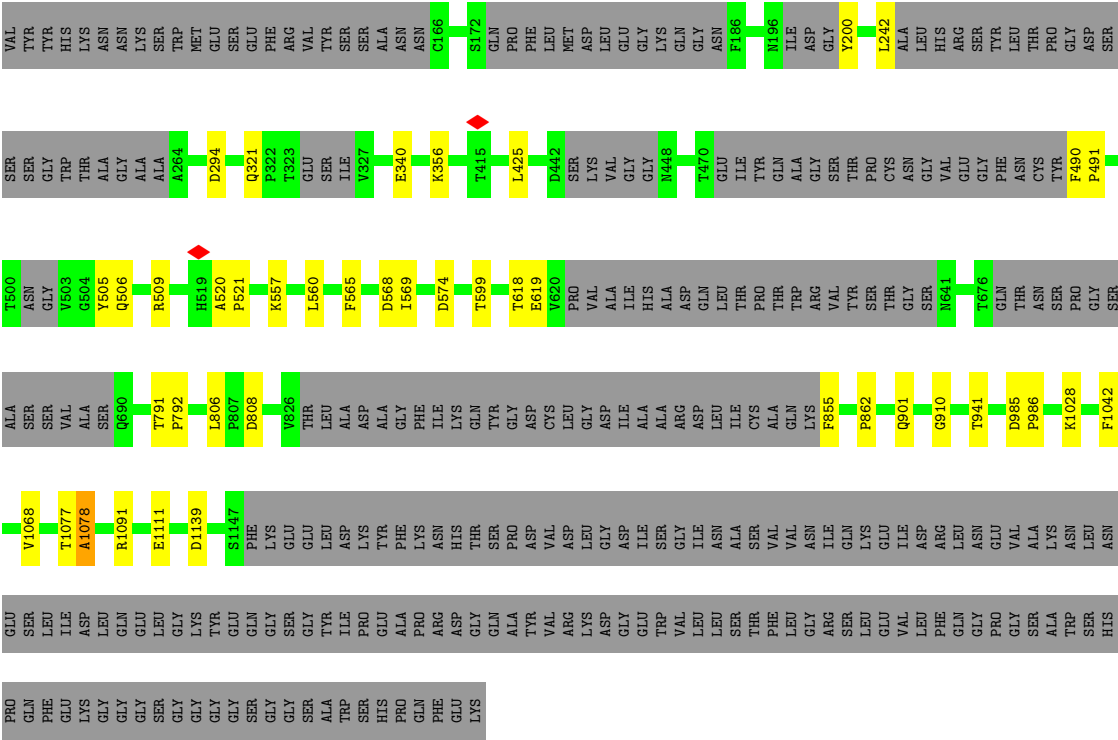
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Spike glycoprotein

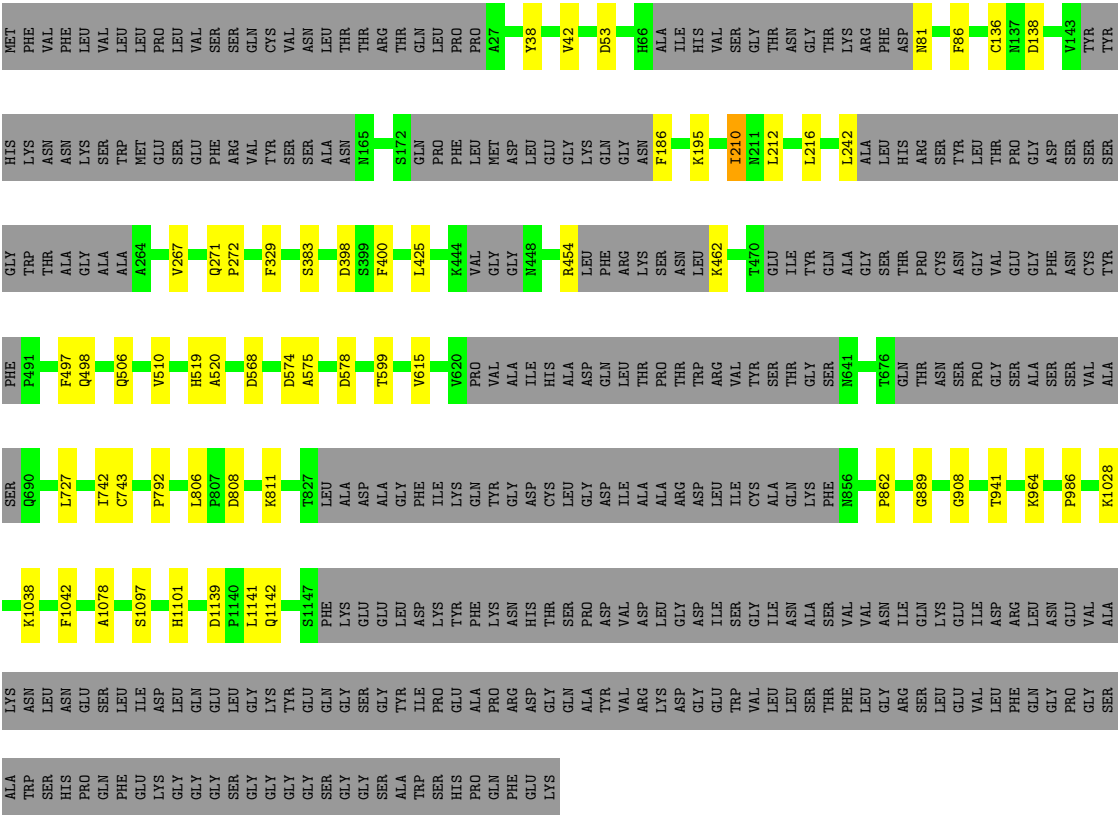


• Molecule 1: Spike glycoprotein

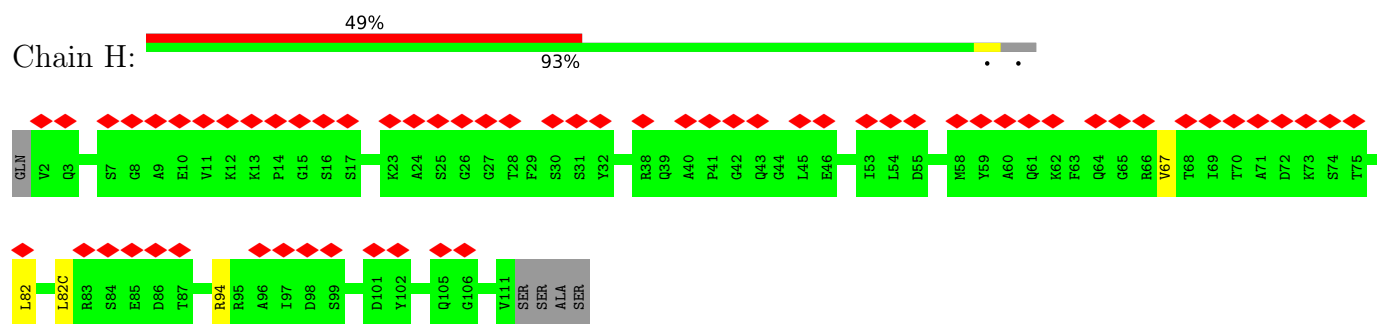




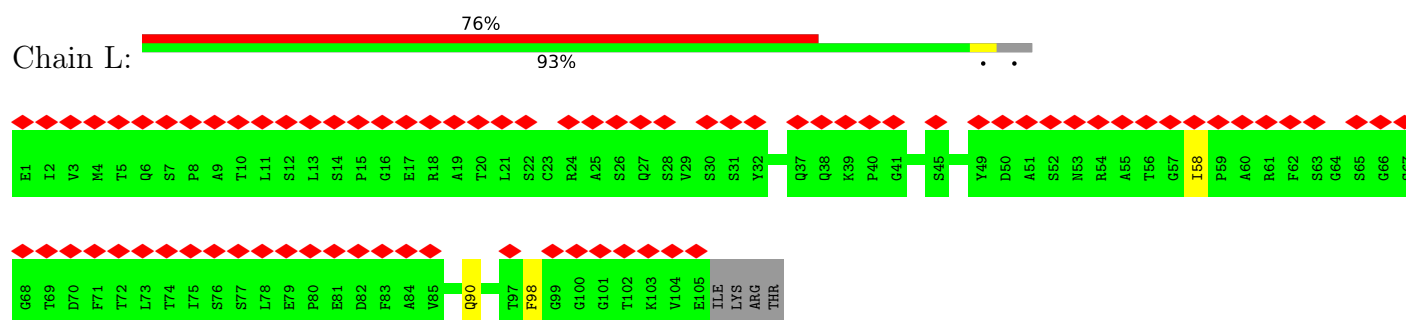
● Molecule 1: Spike glycoprotein



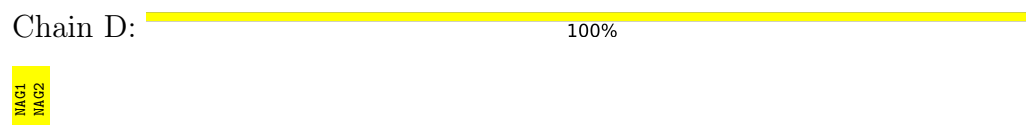
- Molecule 2: J08 fragment antigen binding heavy chain variable domain



- Molecule 3: J08 fragment antigen binding light chain variable domain



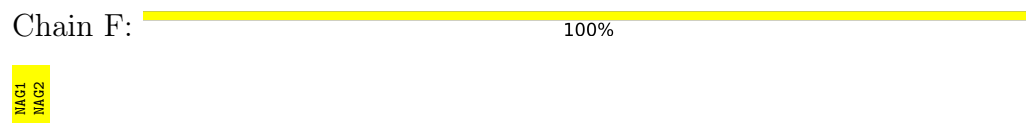
- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- 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



MAG1
MAG2

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

Chain I:  100%MAG1
MAG2

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

Chain J:  100%MAG1
MAG2

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

Chain K:  100%MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43511	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.821	Depositor
Minimum map value	-0.247	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	441.59998, 441.59998, 441.59998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.15, 1.15, 1.15	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1.01	10/7863 (0.1%)	1.29	74/10699 (0.7%)
1	B	1.01	3/7601 (0.0%)	1.24	46/10337 (0.4%)
1	C	1.00	5/7676 (0.1%)	1.26	63/10446 (0.6%)
2	H	0.95	0/966	1.13	2/1308 (0.2%)
3	L	0.87	0/772	1.27	4/1051 (0.4%)
All	All	1.00	18/24878 (0.1%)	1.26	189/33841 (0.6%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	242	LEU	CB-CG	6.12	1.65	1.53
1	A	242	LEU	CB-CG	6.07	1.65	1.53
1	A	200	TYR	CG-CD1	6.05	1.52	1.39
1	C	454	ARG	NE-CZ	5.96	1.39	1.33
1	B	200	TYR	CG-CD1	5.89	1.51	1.39
1	A	210	ILE	CB-CG1	5.87	1.65	1.53
1	C	242	LEU	CB-CG	5.71	1.64	1.53
1	C	462	LYS	C-N	5.71	1.40	1.33
1	A	1048	HIS	CB-CG	-5.64	1.42	1.50
1	A	66	HIS	CB-CG	5.46	1.57	1.50
1	C	81	ASN	C-N	5.46	1.40	1.33
1	C	186	PHE	CG-CD2	5.39	1.50	1.38
1	A	81	ASN	C-N	5.34	1.40	1.33
1	A	186	PHE	CG-CD1	5.15	1.49	1.38
1	A	186	PHE	CG-CD2	5.12	1.49	1.38
1	A	140	PHE	CG-CD2	5.11	1.49	1.38
1	B	855	PHE	CG-CD2	5.08	1.49	1.38
1	A	454	ARG	CD-NE	-5.03	1.39	1.46

All (189) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	792	PRO	CA-C-N	8.44	128.09	119.56
1	B	792	PRO	C-N-CA	8.44	128.09	119.56
1	A	1139	ASP	CA-C-N	8.30	128.03	119.56
1	A	1139	ASP	C-N-CA	8.30	128.03	119.56
1	C	811	LYS	CA-C-N	8.19	127.92	119.56
1	C	811	LYS	C-N-CA	8.19	127.92	119.56
3	L	98	PHE	CA-CB-CG	7.97	121.77	113.80
1	A	792	PRO	CA-C-N	7.65	127.29	119.56
1	A	792	PRO	C-N-CA	7.65	127.29	119.56
1	A	526	GLY	CA-C-N	7.60	127.53	119.85
1	A	526	GLY	C-N-CA	7.60	127.53	119.85
1	C	1139	ASP	CA-C-N	7.38	127.09	119.56
1	C	1139	ASP	C-N-CA	7.38	127.09	119.56
1	C	599	THR	CA-C-N	7.24	126.94	119.56
1	C	599	THR	C-N-CA	7.24	126.94	119.56
1	C	186	PHE	CA-CB-CG	7.20	121.00	113.80
1	B	490	PHE	CA-C-N	7.18	126.81	119.56
1	B	490	PHE	C-N-CA	7.18	126.81	119.56
1	B	120	VAL	N-CA-C	7.14	118.40	108.12
1	A	742	ILE	N-CA-C	7.07	118.71	111.00
1	A	578	ASP	CA-C-N	7.05	126.75	119.56
1	A	578	ASP	C-N-CA	7.05	126.75	119.56
1	A	862	PRO	CA-C-N	7.01	126.97	120.03
1	A	862	PRO	C-N-CA	7.01	126.97	120.03
1	C	400	PHE	N-CA-C	6.96	118.76	108.60
1	A	808	ASP	CA-C-N	6.93	126.62	119.56
1	A	808	ASP	C-N-CA	6.93	126.62	119.56
1	C	862	PRO	CA-C-N	6.85	126.81	120.03
1	C	862	PRO	C-N-CA	6.85	126.81	120.03
1	A	81	ASN	CA-C-N	6.81	126.78	120.03
1	A	81	ASN	C-N-CA	6.81	126.78	120.03
1	C	506	GLN	CA-C-N	6.80	126.72	119.85
1	C	506	GLN	C-N-CA	6.80	126.72	119.85
1	A	599	THR	CA-C-N	6.68	126.64	120.03
1	A	599	THR	C-N-CA	6.68	126.64	120.03
1	B	862	PRO	CA-C-N	6.59	126.55	120.03
1	B	862	PRO	C-N-CA	6.59	126.55	120.03
1	C	329	PHE	CA-C-N	6.58	126.55	120.03
1	C	329	PHE	C-N-CA	6.58	126.55	120.03
1	C	520	ALA	N-CA-C	-6.56	100.60	108.14
1	B	1139	ASP	CA-C-N	6.54	126.67	119.87
1	B	1139	ASP	C-N-CA	6.54	126.67	119.87
1	B	294	ASP	CA-C-N	6.50	126.19	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	294	ASP	C-N-CA	6.50	126.19	119.56
1	B	791	THR	CA-C-N	6.47	124.38	119.66
1	B	791	THR	C-N-CA	6.47	124.38	119.66
1	C	86	PHE	N-CA-C	-6.44	105.44	113.55
1	A	294	ASP	CA-C-N	6.43	126.11	119.56
1	A	294	ASP	C-N-CA	6.43	126.11	119.56
1	A	600	PRO	N-CA-C	-6.41	101.79	111.41
1	A	791	THR	CA-C-N	6.31	124.27	119.66
1	A	791	THR	C-N-CA	6.31	124.27	119.66
1	B	565	PHE	CA-CB-CG	6.27	120.07	113.80
1	A	941	THR	CA-C-N	6.25	125.87	119.56
1	A	941	THR	C-N-CA	6.25	125.87	119.56
1	B	321	GLN	CA-C-N	6.20	126.39	120.31
1	B	321	GLN	C-N-CA	6.20	126.39	120.31
1	A	489	TYR	N-CA-C	6.17	119.25	109.50
1	C	808	ASP	CA-C-N	6.17	126.29	119.87
1	C	808	ASP	C-N-CA	6.17	126.29	119.87
1	B	985	ASP	CA-C-N	6.16	126.72	120.38
1	B	985	ASP	C-N-CA	6.16	126.72	120.38
1	B	599	THR	CA-C-N	6.13	126.59	120.52
1	B	599	THR	C-N-CA	6.13	126.59	120.52
3	L	90	GLN	CB-CA-C	6.12	118.45	109.08
1	A	216	LEU	CA-C-N	6.11	126.30	120.31
1	A	216	LEU	C-N-CA	6.11	126.30	120.31
1	C	383	SER	CA-C-N	6.09	125.77	119.56
1	C	383	SER	C-N-CA	6.09	125.77	119.56
1	C	941	THR	CA-C-N	6.03	125.65	119.56
1	C	941	THR	C-N-CA	6.03	125.65	119.56
2	H	94	ARG	N-CA-C	6.02	119.36	109.72
1	B	1068	VAL	CA-C-N	6.02	125.98	119.78
1	B	1068	VAL	C-N-CA	6.02	125.98	119.78
1	C	425	LEU	CA-C-N	5.96	125.92	119.78
1	C	425	LEU	C-N-CA	5.96	125.92	119.78
1	C	792	PRO	CA-C-N	5.96	125.58	119.56
1	C	792	PRO	C-N-CA	5.96	125.58	119.56
1	A	519	HIS	N-CA-C	-5.95	107.01	114.56
3	L	58	ILE	CA-C-N	5.95	125.92	120.03
3	L	58	ILE	C-N-CA	5.95	125.92	120.03
1	C	216	LEU	CA-C-N	5.94	125.91	120.03
1	C	216	LEU	C-N-CA	5.94	125.91	120.03
1	C	727	LEU	CA-C-N	5.93	125.84	119.85
1	C	727	LEU	C-N-CA	5.93	125.84	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	619	GLU	N-CA-C	5.89	118.49	111.71
1	A	498	GLN	CA-C-N	5.89	125.57	119.56
1	A	498	GLN	C-N-CA	5.89	125.57	119.56
1	A	610	VAL	N-CA-C	5.84	116.29	108.11
1	A	560	LEU	N-CA-C	-5.81	102.06	110.08
1	C	498	GLN	CA-C-N	5.78	125.89	119.87
1	C	498	GLN	C-N-CA	5.78	125.89	119.87
1	B	986	PRO	N-CA-C	5.76	117.72	110.70
1	C	743	CYS	CA-C-N	-5.73	114.47	120.31
1	C	743	CYS	C-N-CA	-5.73	114.47	120.31
1	C	742	ILE	CB-CA-C	-5.72	104.55	112.04
1	C	210	ILE	N-CA-C	5.68	116.93	108.46
1	B	425	LEU	N-CA-C	-5.67	101.40	109.62
1	A	393	THR	N-CA-C	-5.67	105.18	111.36
1	A	490	PHE	N-CA-C	-5.64	101.20	109.50
1	B	901	GLN	N-CA-C	-5.60	105.26	111.36
1	A	574	ASP	CA-CB-CG	5.57	118.17	112.60
1	A	208	THR	CA-C-N	5.56	125.54	120.03
1	A	208	THR	C-N-CA	5.56	125.54	120.03
1	C	1097	SER	N-CA-C	5.53	117.48	109.07
1	C	510	VAL	N-CA-C	5.51	115.83	108.11
1	C	42	VAL	N-CA-C	5.51	116.52	108.58
1	C	136	CYS	N-CA-C	-5.49	102.16	110.28
1	C	578	ASP	CA-C-N	5.49	125.83	119.47
1	C	578	ASP	C-N-CA	5.49	125.83	119.47
1	B	941	THR	CA-C-N	5.48	125.15	119.56
1	B	941	THR	C-N-CA	5.48	125.15	119.56
1	A	1078	ALA	CA-C-N	5.47	125.09	119.56
1	A	1078	ALA	C-N-CA	5.47	125.09	119.56
1	A	401	VAL	N-CA-C	5.45	115.73	108.11
1	B	1078	ALA	CA-C-N	5.43	125.05	119.56
1	B	1078	ALA	C-N-CA	5.43	125.05	119.56
1	A	600	PRO	CA-C-N	-5.42	114.40	120.53
1	A	600	PRO	C-N-CA	-5.42	114.40	120.53
1	A	411	ALA	CA-C-N	5.42	125.34	119.76
1	A	411	ALA	C-N-CA	5.42	125.34	119.76
1	C	1101	HIS	N-CA-C	5.42	117.63	109.23
1	C	520	ALA	CA-C-O	-5.42	116.00	120.71
1	C	462	LYS	CA-C-N	5.41	125.68	119.83
1	C	462	LYS	C-N-CA	5.41	125.68	119.83
1	C	519	HIS	CA-C-N	5.41	129.85	122.07
1	C	519	HIS	C-N-CA	5.41	129.85	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	910	GLY	CA-C-N	-5.39	116.08	123.14
1	B	910	GLY	C-N-CA	-5.39	116.08	123.14
1	A	400	PHE	N-CA-C	5.38	116.45	108.60
1	A	478	THR	CA-C-N	5.37	125.27	119.85
1	A	478	THR	C-N-CA	5.37	125.27	119.85
1	B	806	LEU	CA-C-N	5.37	125.31	119.78
1	B	806	LEU	C-N-CA	5.37	125.31	119.78
1	C	986	PRO	N-CA-C	5.36	117.24	110.70
1	A	38	TYR	CA-C-N	5.34	125.81	120.04
1	A	38	TYR	C-N-CA	5.34	125.81	120.04
1	A	520	ALA	CA-C-N	5.33	125.31	120.03
1	A	520	ALA	C-N-CA	5.33	125.31	120.03
1	A	349	SER	N-CA-C	-5.33	103.86	110.41
1	C	138	ASP	CA-C-N	5.32	125.23	119.85
1	C	138	ASP	C-N-CA	5.32	125.23	119.85
1	C	806	LEU	CA-C-N	5.32	125.24	119.76
1	C	806	LEU	C-N-CA	5.32	125.24	119.76
1	A	138	ASP	CA-C-N	5.31	125.25	119.78
1	A	138	ASP	C-N-CA	5.31	125.25	119.78
1	A	267	VAL	N-CA-C	5.30	115.61	107.77
1	B	491	PRO	N-CA-C	5.28	120.46	113.86
1	C	267	VAL	N-CA-C	5.26	115.70	108.12
1	A	891	GLY	CA-C-N	5.26	125.17	119.85
1	A	891	GLY	C-N-CA	5.26	125.17	119.85
1	C	1078	ALA	CA-C-N	5.25	124.86	119.56
1	C	1078	ALA	C-N-CA	5.25	124.86	119.56
1	B	808	ASP	CA-C-N	5.24	124.86	119.56
1	B	808	ASP	C-N-CA	5.24	124.86	119.56
1	B	560	LEU	CA-C-N	5.23	126.38	119.84
1	B	560	LEU	C-N-CA	5.23	126.38	119.84
1	B	1111	GLU	CA-C-N	5.23	124.99	119.76
1	B	1111	GLU	C-N-CA	5.23	124.99	119.76
1	A	985	ASP	CA-C-N	5.22	125.76	120.38
1	A	985	ASP	C-N-CA	5.22	125.76	120.38
1	A	523	THR	N-CA-C	-5.21	107.60	114.31
1	B	618	THR	CA-C-N	5.16	127.72	120.28
1	B	618	THR	C-N-CA	5.16	127.72	120.28
2	H	67	VAL	N-CA-C	5.16	115.33	108.11
1	A	353	TRP	N-CA-CB	-5.14	102.08	109.83
1	A	409	GLN	CA-C-N	-5.14	116.82	121.65
1	A	409	GLN	C-N-CA	-5.14	116.82	121.65
1	C	889	GLY	N-CA-C	-5.13	106.28	112.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	813	SER	CB-CA-C	-5.11	110.66	116.54
1	B	509	ARG	N-CA-C	-5.11	101.63	109.76
1	C	615	VAL	CA-C-N	5.11	128.81	121.50
1	C	615	VAL	C-N-CA	5.11	128.81	121.50
1	A	898	PHE	CA-CB-CG	-5.11	108.69	113.80
1	A	186	PHE	CA-CB-CG	5.09	118.89	113.80
1	C	38	TYR	CA-C-N	5.07	125.52	120.04
1	C	38	TYR	C-N-CA	5.07	125.52	120.04
1	A	84	LEU	CA-C-N	5.07	125.05	120.03
1	A	84	LEU	C-N-CA	5.07	125.05	120.03
1	A	979	ASP	CA-CB-CG	5.06	117.66	112.60
1	C	81	ASN	CA-C-N	5.05	125.03	120.03
1	C	81	ASN	C-N-CA	5.05	125.03	120.03
1	B	117	LEU	CB-CA-C	-5.05	102.01	110.19
1	A	986	PRO	N-CA-C	5.04	116.84	110.70
1	A	1098	ASN	CA-CB-CG	5.04	117.64	112.60
1	A	1128	VAL	N-CA-C	5.04	117.34	111.05
1	A	497	PHE	CA-CB-CG	5.03	118.83	113.80
1	A	398	ASP	CA-CB-CG	5.02	117.62	112.60
1	B	1091	ARG	N-CA-C	-5.01	106.01	111.82

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	7688	0	7491	9	0
1	B	7436	0	7277	7	0
1	C	7509	0	7335	12	0
2	H	947	0	929	4	0
3	L	755	0	730	0	0
4	D	28	0	25	0	0
4	E	28	0	25	0	0
4	F	28	0	25	0	0
4	G	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	K	28	0	25	0	0
5	A	98	0	91	0	0
5	B	70	0	64	0	0
5	C	56	0	52	0	0
All	All	24755	0	24144	31	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 1.

All (31) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:82:LEU:HD22	2:H:82(C):LEU:HD23	1.25	1.09
2:H:82:LEU:HD22	2:H:82(C):LEU:CD2	1.90	1.00
2:H:82:LEU:CD2	2:H:82(C):LEU:HD23	2.12	0.77
1:A:193:VAL:HG12	1:A:204:TYR:HB2	1.84	0.58
1:B:505:TYR:O	1:B:506:GLN:C	2.49	0.56
1:B:557:LYS:NZ	1:B:574:ASP:OD2	2.40	0.56
1:A:571:ASP:OD2	1:C:964:LYS:NZ	2.43	0.52
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.45	0.50
1:B:340:GLU:OE1	1:B:356:LYS:NZ	2.45	0.49
1:B:568:ASP:OD1	1:B:569:ILE:N	2.46	0.48
1:C:497:PHE:CD1	1:C:497:PHE:N	2.85	0.45
1:A:400:PHE:CD1	1:A:400:PHE:N	2.85	0.44
1:B:520:ALA:HB3	1:B:521:PRO:HD3	1.98	0.44
1:A:348:ALA:HB1	1:A:352:ALA:O	2.18	0.44
1:C:398:ASP:OD1	1:C:398:ASP:C	2.61	0.44
1:C:574:ASP:OD1	1:C:575:ALA:N	2.51	0.44
1:C:1028:LYS:NZ	1:C:1042:PHE:O	2.50	0.44
1:A:574:ASP:OD1	1:A:575:ALA:N	2.51	0.43
1:C:210:ILE:CG2	1:C:212:LEU:H	2.32	0.42
1:A:353:TRP:CH2	1:A:400:PHE:CE1	3.06	0.42
1:A:353:TRP:HE1	1:A:398:ASP:CG	2.27	0.42
1:C:908:GLY:O	1:C:1038:LYS:NZ	2.52	0.42
1:C:568:ASP:OD1	1:C:568:ASP:C	2.63	0.41
1:B:1077:THR:OG1	1:B:1078:ALA:N	2.54	0.41
1:A:908:GLY:O	1:A:1038:LYS:NZ	2.54	0.41
1:C:53:ASP:OD2	1:C:195:LYS:NZ	2.54	0.41
1:C:210:ILE:HG23	1:C:212:LEU:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:82:LEU:HD22	2:H:82(C):LEU:CG	2.50	0.40
1:C:271:GLN:HB2	1:C:272:PRO:HD2	2.03	0.40
1:A:215:ASP:N	1:A:266:TYR:HH	2.19	0.40
1:C:1141:LEU:O	1:C:1142:GLN:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	964/1280 (75%)	945 (98%)	19 (2%)	0	100	100
1	B	921/1280 (72%)	892 (97%)	29 (3%)	0	100	100
1	C	939/1280 (73%)	923 (98%)	16 (2%)	0	100	100
2	H	120/127 (94%)	120 (100%)	0	0	100	100
3	L	99/105 (94%)	97 (98%)	2 (2%)	0	100	100
All	All	3043/4072 (75%)	2977 (98%)	66 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	865/1108 (78%)	864 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	837/1108 (76%)	837 (100%)	0	100	100
1	C	847/1108 (76%)	847 (100%)	0	100	100
2	H	103/107 (96%)	103 (100%)	0	100	100
3	L	83/87 (95%)	83 (100%)	0	100	100
All	All	2735/3518 (78%)	2734 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	331	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	282	ASN
1	A	450	ASN
1	A	856	ASN
3	L	89	GLN
1	B	314	GLN
1	B	439	ASN
1	B	540	ASN
1	B	564	GLN
1	B	613	GLN
1	B	690	GLN
1	B	804	GLN
1	C	66	HIS
1	C	115	GLN
1	C	196	ASN
1	C	343	ASN
1	C	690	GLN
1	C	913	GLN

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 ⓘ

14 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	D	1	4,1	14,14,15	2.06	6 (42%)	17,19,21	1.07	1 (5%)
4	NAG	D	2	4	14,14,15	2.09	6 (42%)	17,19,21	1.09	2 (11%)
4	NAG	E	1	4,1	14,14,15	2.17	7 (50%)	17,19,21	1.27	1 (5%)
4	NAG	E	2	4	14,14,15	2.01	6 (42%)	17,19,21	1.00	2 (11%)
4	NAG	F	1	4,1	14,14,15	2.17	6 (42%)	17,19,21	0.95	1 (5%)
4	NAG	F	2	4	14,14,15	2.06	5 (35%)	17,19,21	0.98	1 (5%)
4	NAG	G	1	4,1	14,14,15	2.16	5 (35%)	17,19,21	1.15	2 (11%)
4	NAG	G	2	4	14,14,15	2.00	6 (42%)	17,19,21	0.94	1 (5%)
4	NAG	I	1	4,1	14,14,15	2.15	6 (42%)	17,19,21	1.03	1 (5%)
4	NAG	I	2	4	14,14,15	2.08	6 (42%)	17,19,21	0.98	1 (5%)
4	NAG	J	1	4,1	14,14,15	2.10	6 (42%)	17,19,21	1.00	1 (5%)
4	NAG	J	2	4	14,14,15	2.06	5 (35%)	17,19,21	0.87	1 (5%)
4	NAG	K	1	4,1	14,14,15	2.18	4 (28%)	17,19,21	1.28	1 (5%)
4	NAG	K	2	4	14,14,15	2.02	6 (42%)	17,19,21	0.94	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	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	NAG	F	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
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
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	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

All (80) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	1	NAG	C1-C2	5.79	1.60	1.52
4	G	1	NAG	C1-C2	5.72	1.60	1.52
4	F	1	NAG	C1-C2	5.54	1.59	1.52
4	I	1	NAG	C1-C2	5.33	1.59	1.52
4	E	1	NAG	C1-C2	5.24	1.59	1.52
4	J	1	NAG	C1-C2	5.17	1.59	1.52
4	J	2	NAG	C1-C2	5.00	1.59	1.52
4	D	1	NAG	C1-C2	4.91	1.59	1.52
4	F	2	NAG	C1-C2	4.83	1.58	1.52
4	D	2	NAG	C1-C2	4.83	1.58	1.52
4	I	2	NAG	C1-C2	4.75	1.58	1.52
4	K	2	NAG	C1-C2	4.74	1.58	1.52
4	E	2	NAG	C1-C2	4.67	1.58	1.52
4	G	2	NAG	C1-C2	4.48	1.58	1.52
4	G	2	NAG	O5-C5	3.29	1.49	1.43
4	I	1	NAG	O5-C5	3.27	1.49	1.43
4	I	2	NAG	O5-C5	3.25	1.49	1.43
4	K	2	NAG	O5-C5	3.23	1.49	1.43
4	D	2	NAG	O5-C5	3.22	1.49	1.43
4	K	1	NAG	O5-C5	3.20	1.49	1.43
4	G	1	NAG	O5-C5	3.18	1.49	1.43
4	E	1	NAG	O5-C5	3.16	1.49	1.43
4	J	2	NAG	O5-C5	3.10	1.49	1.43
4	D	1	NAG	O5-C5	3.10	1.49	1.43
4	F	2	NAG	O5-C5	3.09	1.49	1.43
4	E	2	NAG	O5-C5	3.08	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	NAG	O5-C5	2.98	1.49	1.43
4	J	1	NAG	O5-C5	2.93	1.49	1.43
4	E	2	NAG	C3-C2	2.79	1.58	1.52
4	I	2	NAG	C2-N2	2.65	1.50	1.46
4	K	1	NAG	C4-C5	2.64	1.58	1.53
4	J	2	NAG	C3-C2	2.57	1.57	1.52
4	D	2	NAG	C2-N2	2.56	1.50	1.46
4	D	2	NAG	C3-C2	2.56	1.57	1.52
4	G	1	NAG	O5-C1	2.54	1.48	1.43
4	I	2	NAG	C3-C2	2.53	1.57	1.52
4	G	2	NAG	C4-C5	2.51	1.58	1.53
4	D	1	NAG	C4-C5	2.51	1.58	1.53
4	F	1	NAG	O5-C1	2.50	1.47	1.43
4	F	2	NAG	C2-N2	2.48	1.50	1.46
4	F	2	NAG	C3-C2	2.45	1.57	1.52
4	I	1	NAG	C4-C5	2.44	1.58	1.53
4	G	2	NAG	C3-C2	2.41	1.57	1.52
4	E	1	NAG	C4-C5	2.37	1.58	1.53
4	F	1	NAG	C4-C5	2.36	1.58	1.53
4	K	2	NAG	C3-C2	2.35	1.57	1.52
4	E	1	NAG	O5-C1	2.34	1.47	1.43
4	J	1	NAG	C3-C2	2.32	1.57	1.52
4	I	1	NAG	O5-C1	2.31	1.47	1.43
4	K	2	NAG	C4-C5	2.30	1.57	1.53
4	J	1	NAG	C4-C5	2.28	1.57	1.53
4	E	1	NAG	C4-C3	2.28	1.58	1.52
4	J	2	NAG	C4-C5	2.28	1.57	1.53
4	F	2	NAG	C4-C5	2.25	1.57	1.53
4	D	2	NAG	C4-C5	2.24	1.57	1.53
4	I	2	NAG	C4-C5	2.23	1.57	1.53
4	E	2	NAG	C4-C5	2.21	1.57	1.53
4	G	1	NAG	C3-C2	2.20	1.57	1.52
4	D	1	NAG	O5-C1	2.20	1.47	1.43
4	J	1	NAG	O5-C1	2.19	1.47	1.43
4	G	2	NAG	C2-N2	2.16	1.49	1.46
4	K	2	NAG	C2-N2	2.13	1.49	1.46
4	G	2	NAG	C4-C3	2.13	1.57	1.52
4	K	1	NAG	O5-C1	2.13	1.47	1.43
4	F	1	NAG	C3-C2	2.12	1.57	1.52
4	D	2	NAG	C4-C3	2.10	1.57	1.52
4	J	1	NAG	C4-C3	2.10	1.57	1.52
4	E	1	NAG	C2-N2	2.09	1.49	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	2	NAG	C2-N2	2.09	1.49	1.46
4	I	1	NAG	C3-C2	2.09	1.56	1.52
4	E	1	NAG	C3-C2	2.08	1.56	1.52
4	D	1	NAG	C3-C2	2.08	1.56	1.52
4	D	1	NAG	C4-C3	2.08	1.57	1.52
4	I	1	NAG	C4-C3	2.07	1.57	1.52
4	K	2	NAG	C4-C3	2.07	1.57	1.52
4	E	2	NAG	C4-C3	2.07	1.57	1.52
4	E	2	NAG	C2-N2	2.04	1.49	1.46
4	G	1	NAG	C4-C5	2.04	1.57	1.53
4	F	1	NAG	C4-C3	2.03	1.57	1.52
4	I	2	NAG	C4-C3	2.03	1.57	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	1	NAG	O4-C4-C3	-3.62	101.83	110.38
4	D	2	NAG	C8-C7-N2	3.15	121.33	116.12
4	E	1	NAG	C2-N2-C7	3.06	127.00	122.90
4	I	2	NAG	C8-C7-N2	2.84	120.83	116.12
4	F	2	NAG	C8-C7-N2	2.75	120.67	116.12
4	D	1	NAG	C8-C7-N2	2.33	119.97	116.12
4	G	1	NAG	C1-C2-N2	-2.25	106.89	110.43
4	E	2	NAG	C8-C7-N2	2.22	119.79	116.12
4	I	1	NAG	C8-C7-N2	2.21	119.78	116.12
4	G	2	NAG	C8-C7-N2	2.20	119.76	116.12
4	F	1	NAG	C8-C7-N2	2.16	119.70	116.12
4	J	1	NAG	C8-C7-N2	2.16	119.69	116.12
4	E	2	NAG	C1-O5-C5	2.11	115.02	112.19
4	J	2	NAG	C8-C7-N2	2.08	119.58	116.12
4	D	2	NAG	O7-C7-C8	-2.08	118.34	122.05
4	G	1	NAG	O4-C4-C3	-2.06	105.52	110.38
4	K	2	NAG	C8-C7-N2	2.02	119.47	116.12

There are no chirality outliers.

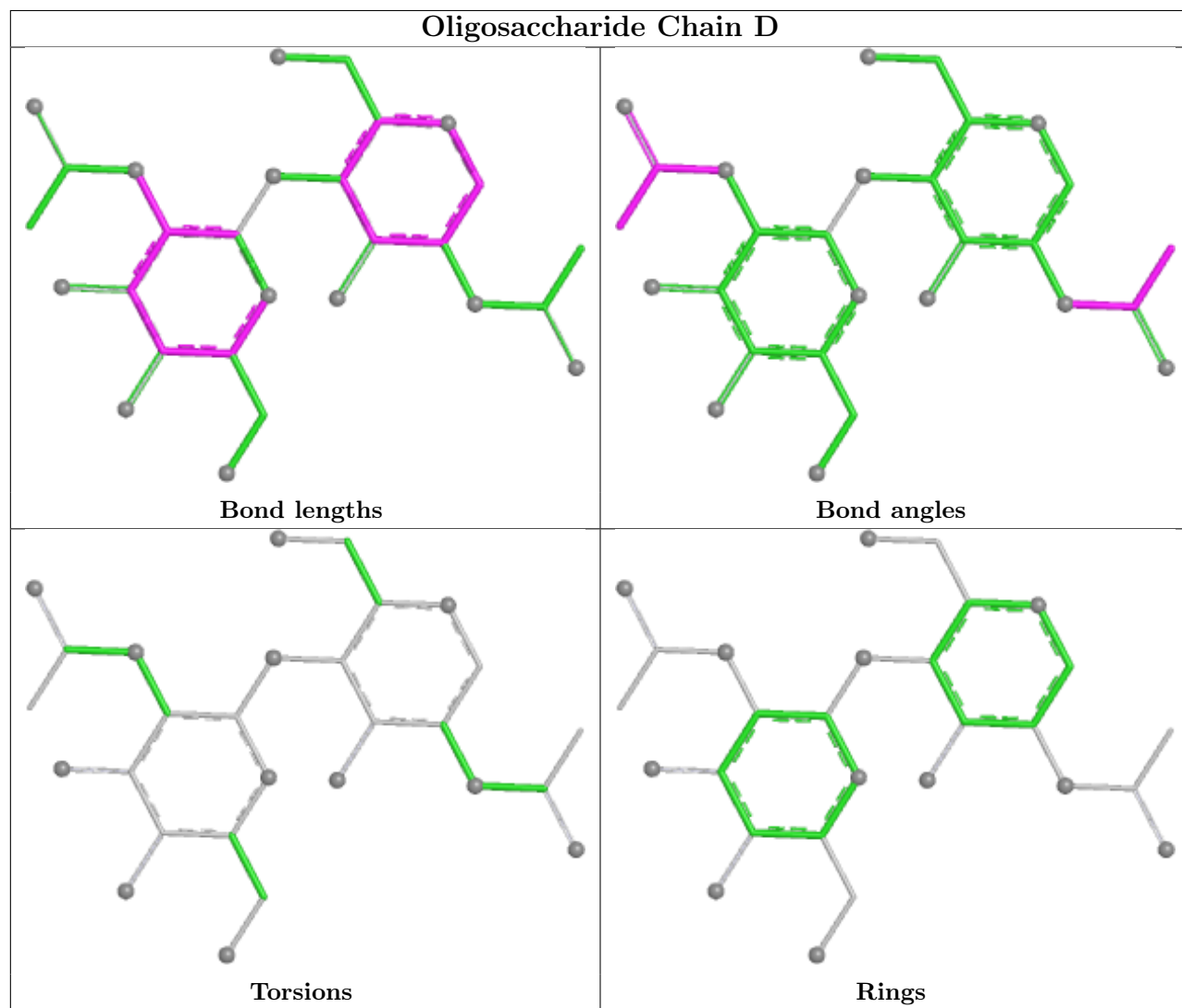
All (4) torsion outliers are listed below:

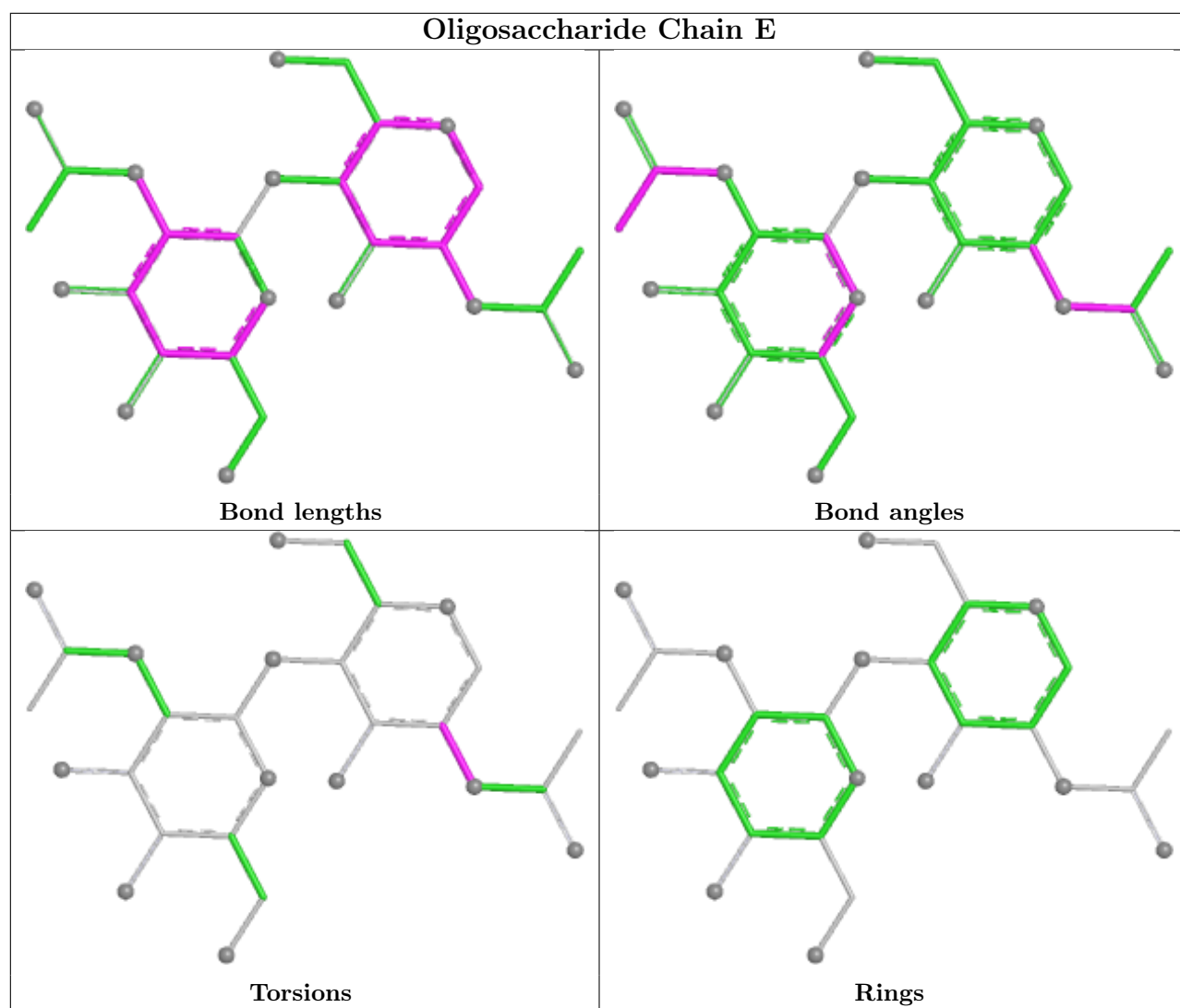
Mol	Chain	Res	Type	Atoms
4	G	2	NAG	O5-C5-C6-O6
4	E	1	NAG	C1-C2-N2-C7
4	E	1	NAG	C3-C2-N2-C7
4	F	1	NAG	C1-C2-N2-C7

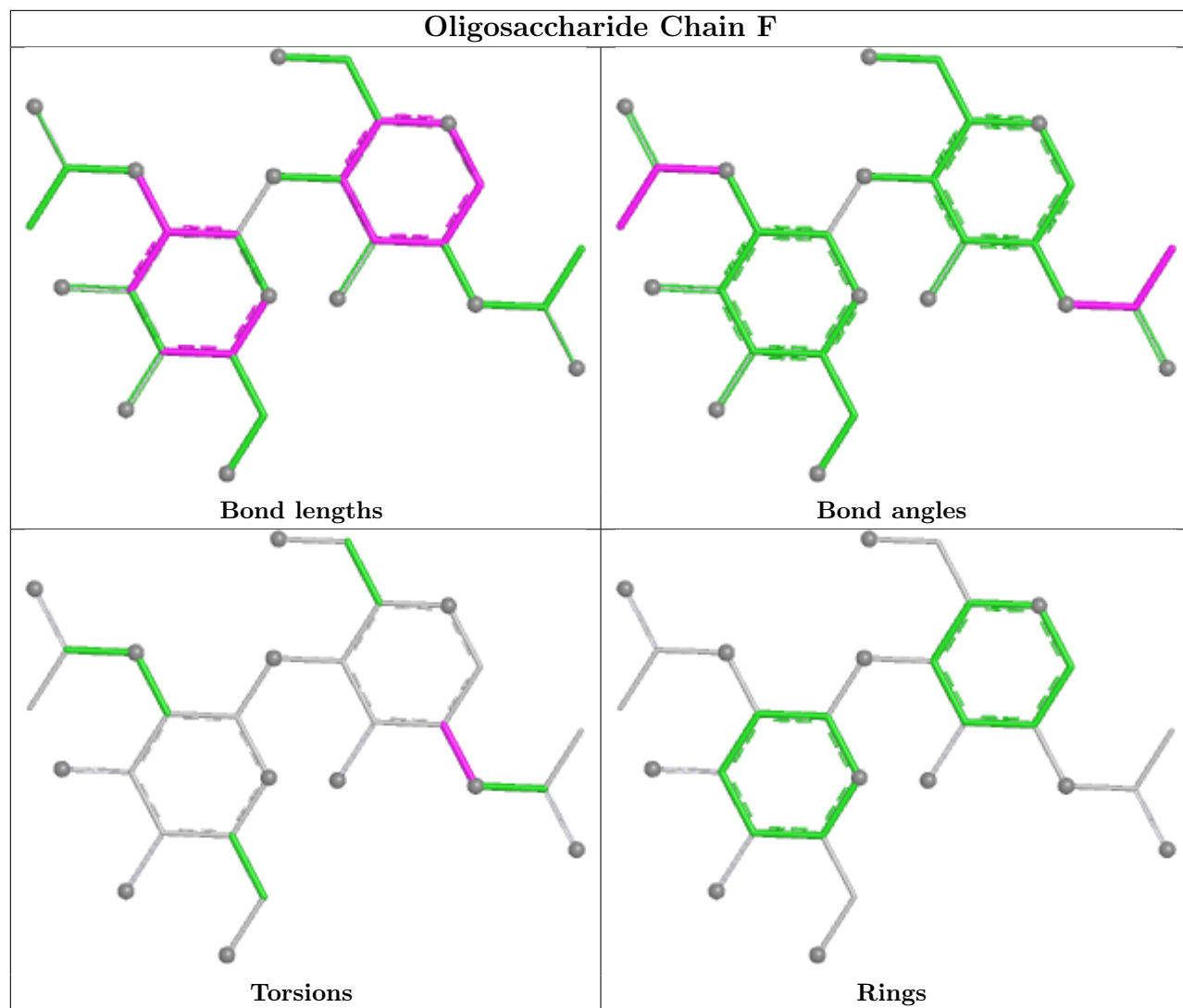
There are no ring outliers.

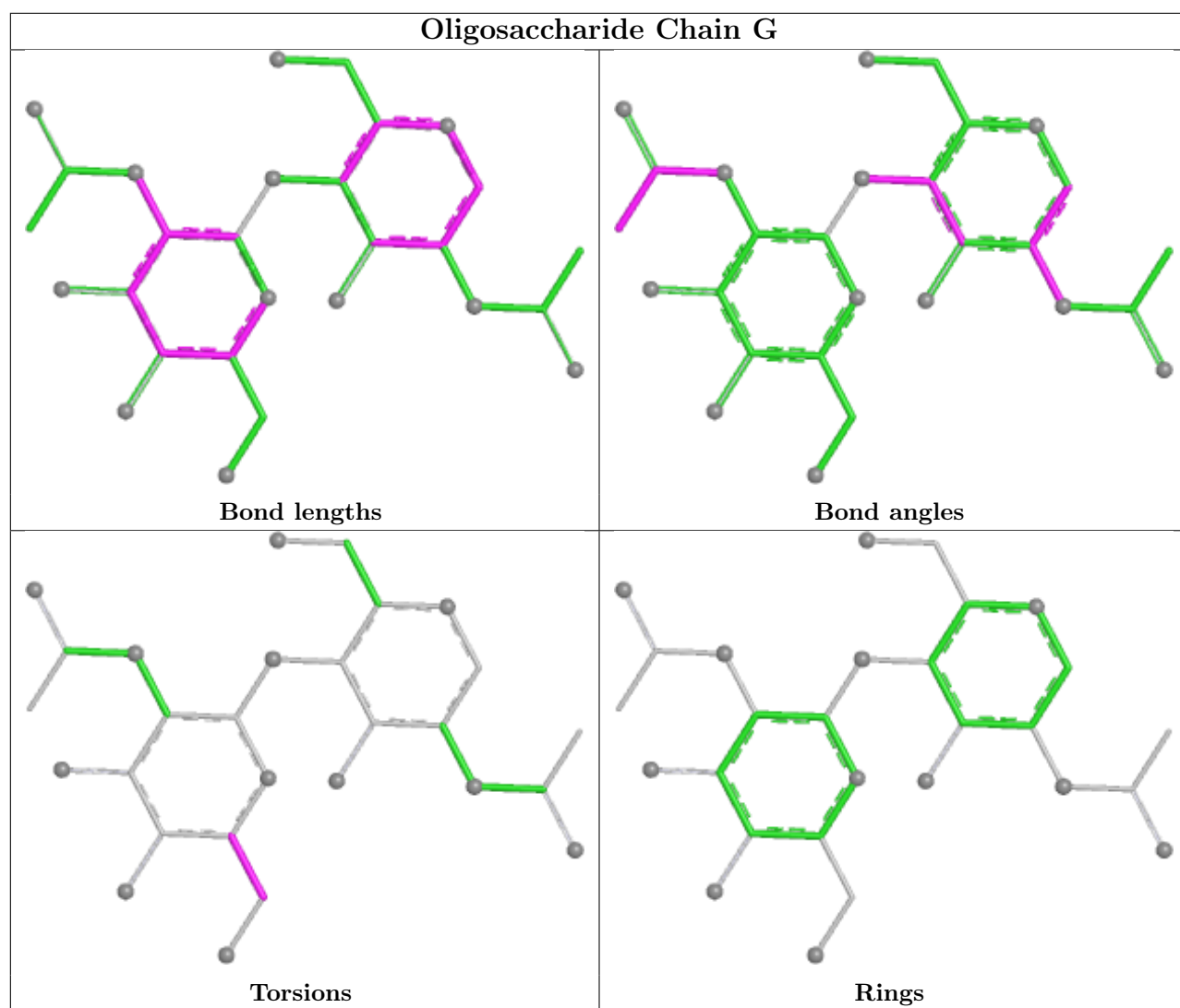
No monomer is involved in short contacts.

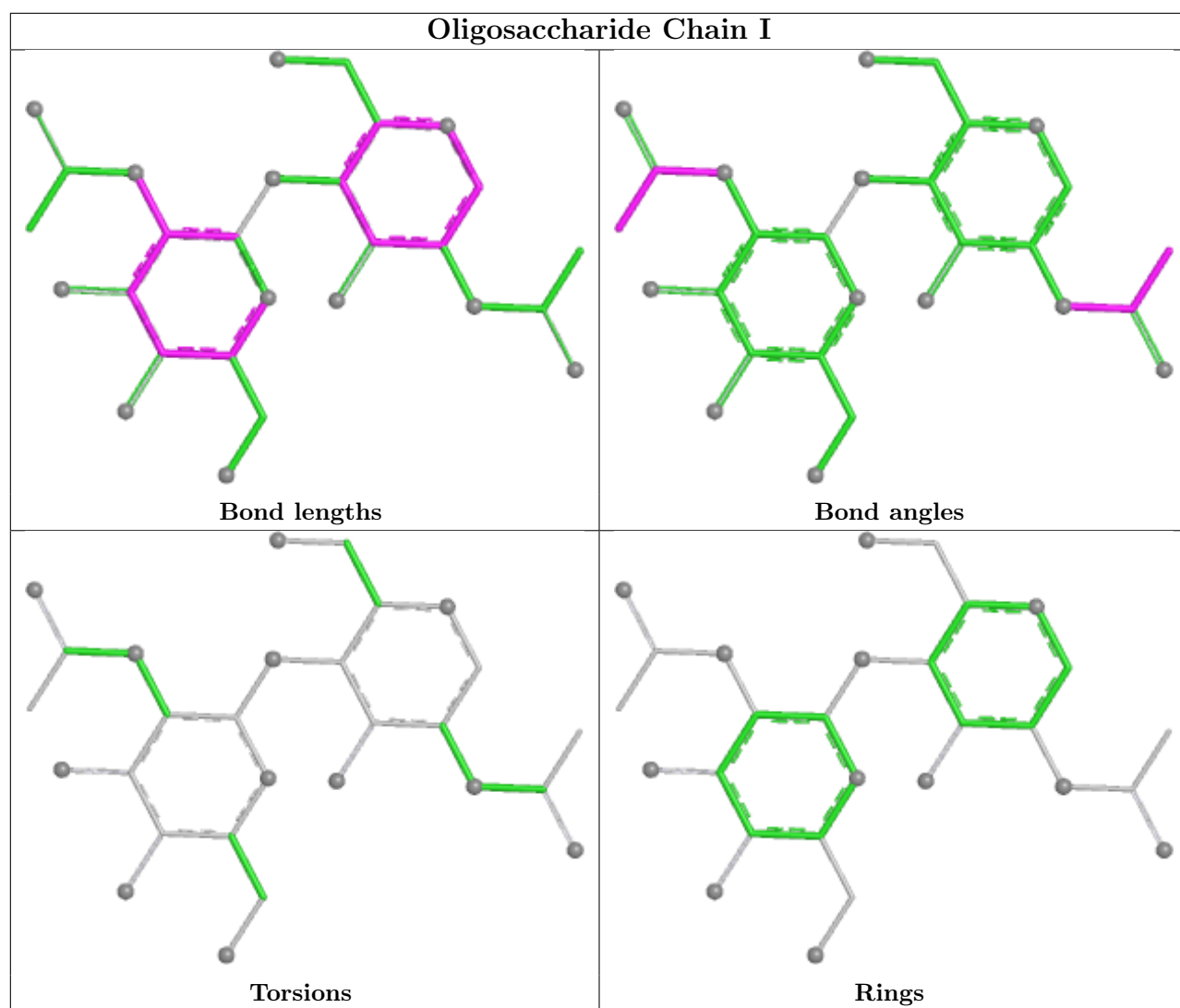
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

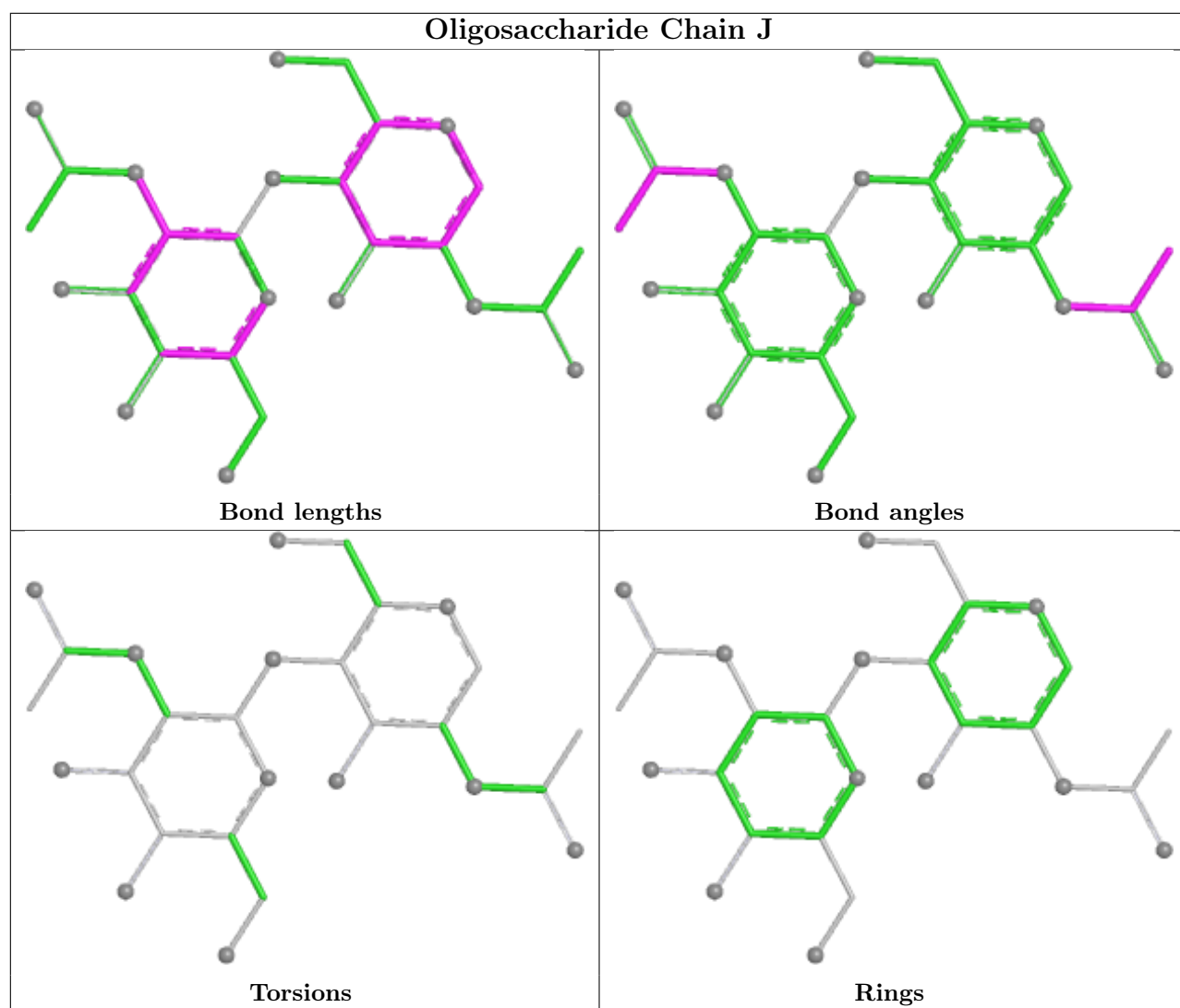


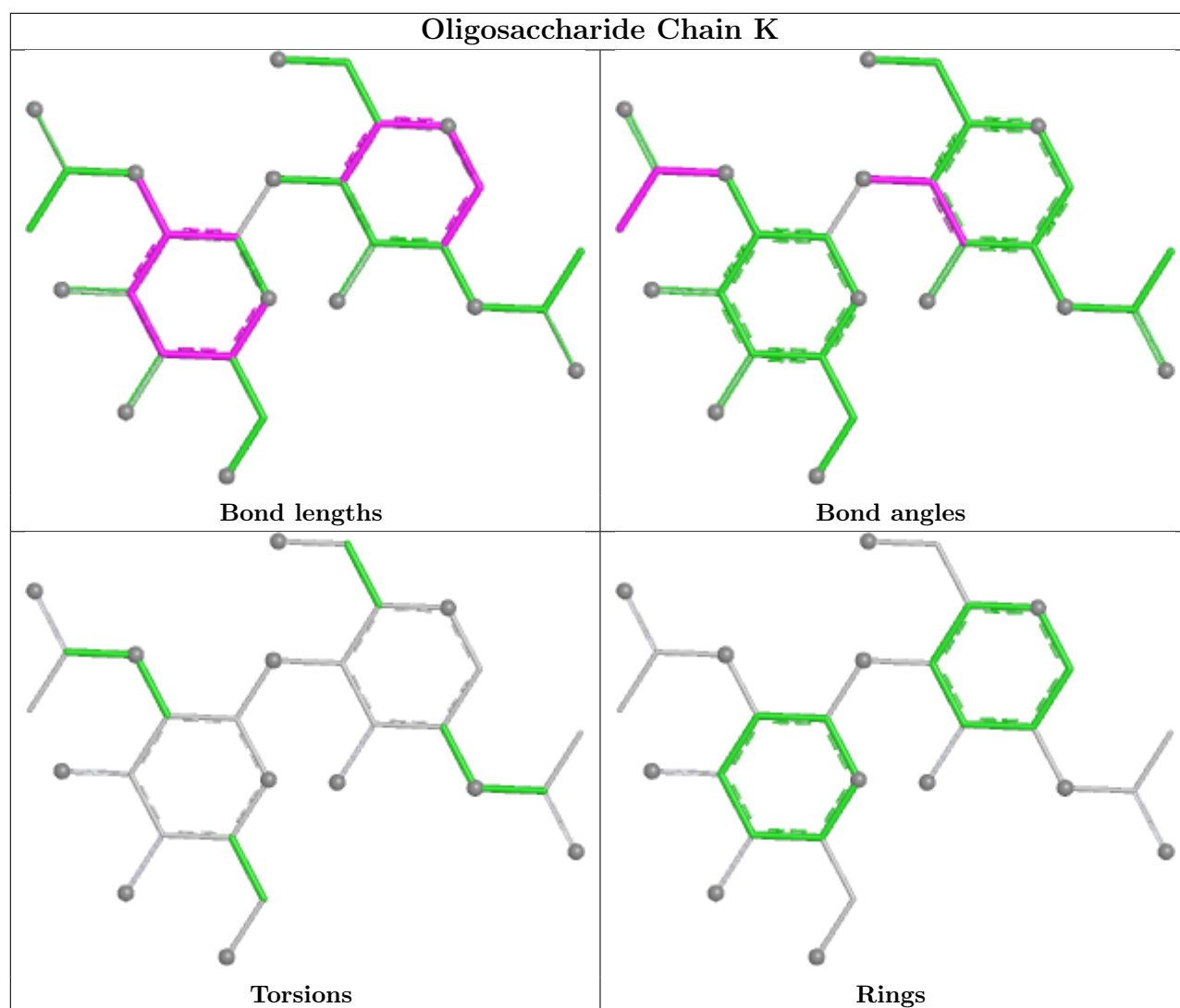












5.6 Ligand geometry [i](#)

16 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	$\# Z > 2$
5	NAG	B	1302	1	14,14,15	2.12	5 (35%)	17,19,21	7.09	3 (17%)
5	NAG	C	1301	1	14,14,15	2.27	5 (35%)	17,19,21	0.99	1 (5%)
5	NAG	A	1306	1	14,14,15	2.20	5 (35%)	17,19,21	1.12	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	B	1304	1	14,14,15	2.20	6 (42%)	17,19,21	1.10	2 (11%)
5	NAG	A	1307	1	14,14,15	2.18	6 (42%)	17,19,21	1.15	1 (5%)
5	NAG	A	1303	1	14,14,15	2.19	6 (42%)	17,19,21	1.01	2 (11%)
5	NAG	B	1305	1	14,14,15	2.28	6 (42%)	17,19,21	0.90	1 (5%)
5	NAG	B	1303	1	14,14,15	2.18	5 (35%)	17,19,21	1.13	2 (11%)
5	NAG	C	1302	1	14,14,15	2.19	5 (35%)	17,19,21	0.96	1 (5%)
5	NAG	C	1303	1	14,14,15	2.30	7 (50%)	17,19,21	0.98	1 (5%)
5	NAG	A	1305	1	14,14,15	2.28	5 (35%)	17,19,21	0.94	0
5	NAG	A	1302	1	14,14,15	2.23	6 (42%)	17,19,21	1.21	2 (11%)
5	NAG	A	1301	1	14,14,15	2.38	5 (35%)	17,19,21	1.07	2 (11%)
5	NAG	A	1304	1	14,14,15	2.15	6 (42%)	17,19,21	0.97	1 (5%)
5	NAG	C	1304	1	14,14,15	2.18	5 (35%)	17,19,21	1.11	2 (11%)
5	NAG	B	1301	1	14,14,15	2.26	6 (42%)	17,19,21	1.04	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	1302	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1301	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1306	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1303	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1302	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1301	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1304	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1301	1	-	0/6/23/26	0/1/1/1

All (89) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1301	NAG	C1-C2	6.50	1.61	1.52
5	C	1301	NAG	C1-C2	6.21	1.60	1.52
5	B	1305	NAG	C1-C2	5.99	1.60	1.52
5	A	1305	NAG	C1-C2	5.90	1.60	1.52
5	C	1303	NAG	C1-C2	5.87	1.60	1.52
5	B	1304	NAG	C1-C2	5.72	1.60	1.52
5	B	1302	NAG	C1-C2	5.70	1.60	1.52
5	B	1301	NAG	C1-C2	5.68	1.60	1.52
5	C	1302	NAG	C1-C2	5.61	1.60	1.52
5	A	1306	NAG	C1-C2	5.61	1.60	1.52
5	A	1304	NAG	C1-C2	5.53	1.59	1.52
5	C	1304	NAG	C1-C2	5.51	1.59	1.52
5	A	1303	NAG	C1-C2	5.44	1.59	1.52
5	B	1303	NAG	C1-C2	5.43	1.59	1.52
5	A	1307	NAG	C1-C2	5.41	1.59	1.52
5	A	1302	NAG	C1-C2	5.40	1.59	1.52
5	A	1305	NAG	O5-C5	3.34	1.49	1.43
5	B	1301	NAG	O5-C5	3.34	1.49	1.43
5	A	1302	NAG	O5-C5	3.32	1.49	1.43
5	B	1305	NAG	O5-C5	3.32	1.49	1.43
5	C	1304	NAG	O5-C5	3.30	1.49	1.43
5	C	1303	NAG	O5-C5	3.29	1.49	1.43
5	B	1303	NAG	O5-C5	3.22	1.49	1.43
5	A	1304	NAG	O5-C5	3.22	1.49	1.43
5	A	1306	NAG	O5-C5	3.21	1.49	1.43
5	B	1304	NAG	O5-C5	3.21	1.49	1.43
5	A	1301	NAG	O5-C5	3.20	1.49	1.43
5	C	1302	NAG	O5-C5	3.18	1.49	1.43
5	A	1303	NAG	O5-C5	3.11	1.49	1.43
5	C	1301	NAG	O5-C5	3.10	1.49	1.43
5	A	1307	NAG	O5-C5	3.08	1.49	1.43
5	B	1302	NAG	O5-C5	3.05	1.49	1.43
5	A	1302	NAG	O5-C1	2.85	1.48	1.43
5	A	1301	NAG	O5-C1	2.76	1.48	1.43
5	A	1305	NAG	O5-C1	2.74	1.48	1.43
5	B	1301	NAG	O5-C1	2.73	1.48	1.43
5	C	1303	NAG	O5-C1	2.70	1.48	1.43
5	A	1306	NAG	O5-C1	2.68	1.48	1.43
5	C	1304	NAG	O5-C1	2.66	1.48	1.43
5	A	1303	NAG	O5-C1	2.65	1.48	1.43
5	B	1304	NAG	O5-C1	2.63	1.48	1.43
5	B	1303	NAG	C2-N2	2.61	1.50	1.46
5	B	1305	NAG	O5-C1	2.57	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1303	NAG	O5-C1	2.57	1.48	1.43
5	A	1307	NAG	C3-C2	2.55	1.57	1.52
5	C	1301	NAG	O5-C1	2.54	1.48	1.43
5	A	1304	NAG	O5-C1	2.52	1.47	1.43
5	A	1302	NAG	C2-N2	2.50	1.50	1.46
5	C	1301	NAG	C3-C2	2.50	1.57	1.52
5	C	1302	NAG	O5-C1	2.50	1.47	1.43
5	A	1307	NAG	O5-C1	2.49	1.47	1.43
5	A	1301	NAG	C3-C2	2.45	1.57	1.52
5	C	1302	NAG	C3-C2	2.37	1.57	1.52
5	A	1307	NAG	C2-N2	2.37	1.50	1.46
5	C	1303	NAG	C2-N2	2.34	1.50	1.46
5	B	1301	NAG	C2-N2	2.33	1.50	1.46
5	C	1304	NAG	C3-C2	2.33	1.57	1.52
5	A	1303	NAG	C2-N2	2.31	1.50	1.46
5	A	1303	NAG	C3-C2	2.31	1.57	1.52
5	A	1306	NAG	C3-C2	2.31	1.57	1.52
5	B	1302	NAG	O5-C1	2.30	1.47	1.43
5	C	1303	NAG	C3-C2	2.30	1.57	1.52
5	B	1305	NAG	C3-C2	2.28	1.57	1.52
5	A	1305	NAG	C3-C2	2.28	1.57	1.52
5	B	1302	NAG	C4-C5	2.25	1.57	1.53
5	B	1301	NAG	C4-C5	2.25	1.57	1.53
5	A	1302	NAG	C3-C2	2.24	1.57	1.52
5	B	1304	NAG	C3-C2	2.23	1.57	1.52
5	B	1301	NAG	C3-C2	2.23	1.57	1.52
5	A	1306	NAG	C4-C5	2.22	1.57	1.53
5	C	1303	NAG	C4-C5	2.20	1.57	1.53
5	A	1303	NAG	C4-C5	2.20	1.57	1.53
5	B	1305	NAG	C4-C5	2.19	1.57	1.53
5	B	1302	NAG	C3-C2	2.18	1.57	1.52
5	C	1302	NAG	C4-C5	2.18	1.57	1.53
5	A	1302	NAG	C4-C5	2.17	1.57	1.53
5	A	1305	NAG	C4-C5	2.17	1.57	1.53
5	B	1303	NAG	C4-C5	2.16	1.57	1.53
5	A	1304	NAG	C3-C2	2.15	1.57	1.52
5	A	1301	NAG	C2-N2	2.15	1.49	1.46
5	C	1303	NAG	C4-C3	2.11	1.57	1.52
5	C	1304	NAG	C4-C5	2.11	1.57	1.53
5	A	1307	NAG	C4-C5	2.10	1.57	1.53
5	A	1304	NAG	C4-C5	2.10	1.57	1.53
5	B	1304	NAG	C4-C5	2.09	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1301	NAG	C4-C5	2.06	1.57	1.53
5	B	1305	NAG	C2-N2	2.05	1.49	1.46
5	A	1304	NAG	C2-N2	2.02	1.49	1.46
5	B	1304	NAG	C2-N2	2.00	1.49	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1302	NAG	C2-N2-C7	28.38	160.94	122.90
5	B	1302	NAG	C8-C7-N2	5.22	124.78	116.12
5	A	1302	NAG	C8-C7-N2	3.41	121.77	116.12
5	B	1302	NAG	O7-C7-N2	-3.33	116.10	121.98
5	B	1303	NAG	C8-C7-N2	3.12	121.30	116.12
5	A	1302	NAG	O7-C7-C8	-2.70	117.25	122.05
5	B	1301	NAG	C8-C7-N2	2.65	120.51	116.12
5	A	1303	NAG	C8-C7-N2	2.61	120.44	116.12
5	B	1304	NAG	C8-C7-N2	2.60	120.43	116.12
5	A	1307	NAG	C8-C7-N2	2.60	120.43	116.12
5	A	1306	NAG	C8-C7-N2	2.54	120.33	116.12
5	A	1306	NAG	O7-C7-C8	-2.42	117.74	122.05
5	C	1304	NAG	C8-C7-N2	2.41	120.12	116.12
5	C	1303	NAG	C8-C7-N2	2.40	120.09	116.12
5	C	1304	NAG	O7-C7-C8	-2.37	117.84	122.05
5	C	1302	NAG	C8-C7-N2	2.36	120.04	116.12
5	A	1301	NAG	O7-C7-C8	-2.31	117.93	122.05
5	A	1304	NAG	C8-C7-N2	2.22	119.81	116.12
5	C	1301	NAG	C1-O5-C5	2.22	115.16	112.19
5	B	1304	NAG	O7-C7-C8	-2.21	118.11	122.05
5	A	1301	NAG	C8-C7-N2	2.17	119.71	116.12
5	A	1303	NAG	O7-C7-C8	-2.08	118.34	122.05
5	B	1303	NAG	O7-C7-C8	-2.06	118.39	122.05
5	B	1301	NAG	O7-C7-C8	-2.04	118.42	122.05
5	B	1305	NAG	C8-C7-N2	2.03	119.49	116.12

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1302	NAG	C8-C7-N2-C2
5	B	1302	NAG	O7-C7-N2-C2
5	A	1304	NAG	O5-C5-C6-O6
5	A	1306	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	B	1302	NAG	C3-C2-N2-C7
5	A	1301	NAG	C1-C2-N2-C7
5	A	1303	NAG	C1-C2-N2-C7
5	B	1302	NAG	C1-C2-N2-C7

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.

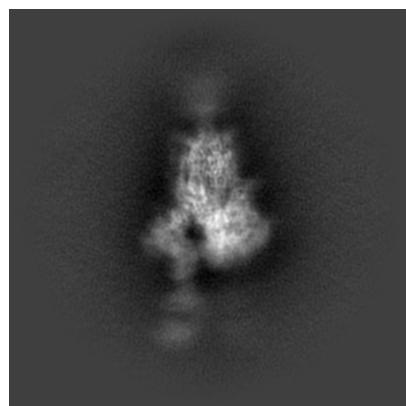
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24879. These allow visual inspection of the internal detail of the map and identification of artifacts.

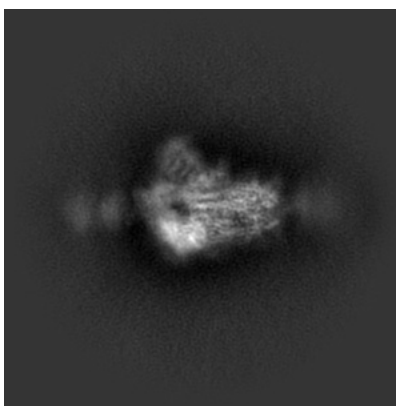
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

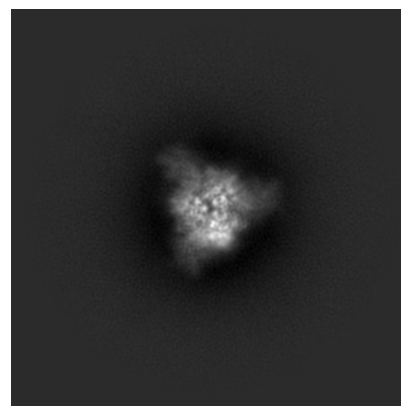
6.1.1 Primary map



X

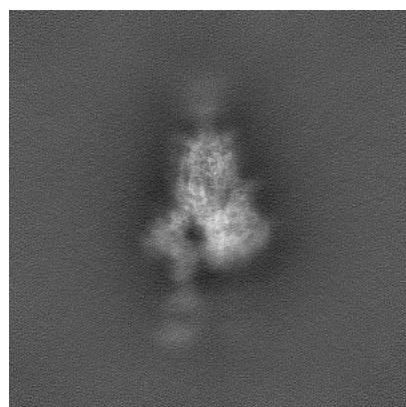


Y

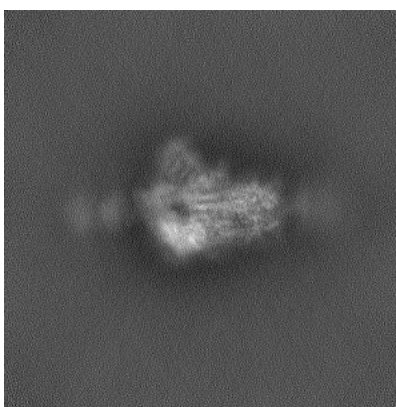


Z

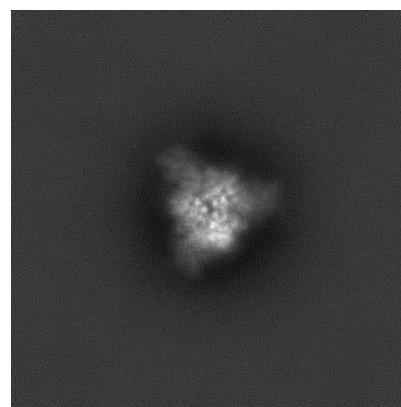
6.1.2 Raw map



X



Y

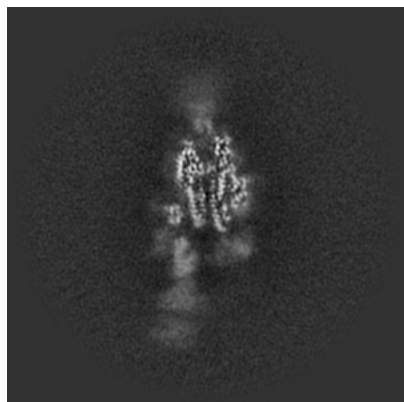


Z

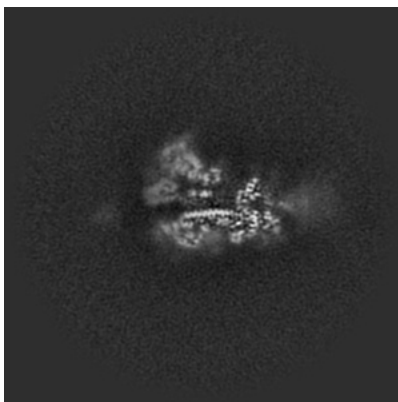
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

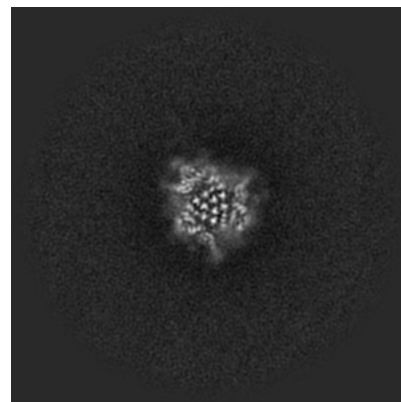
6.2.1 Primary map



X Index: 192



Y Index: 192

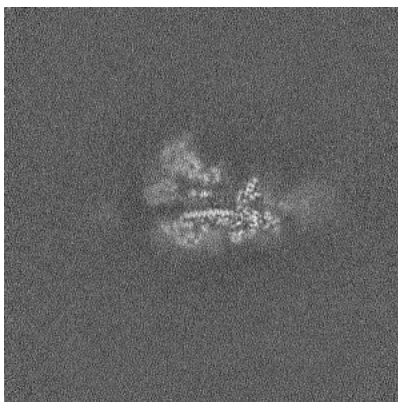


Z Index: 192

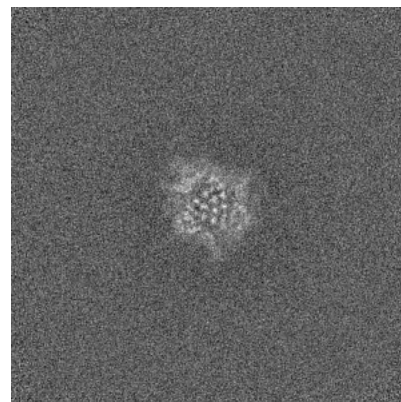
6.2.2 Raw map



X Index: 192



Y Index: 192

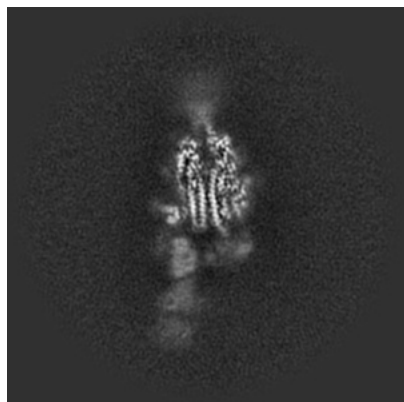


Z Index: 192

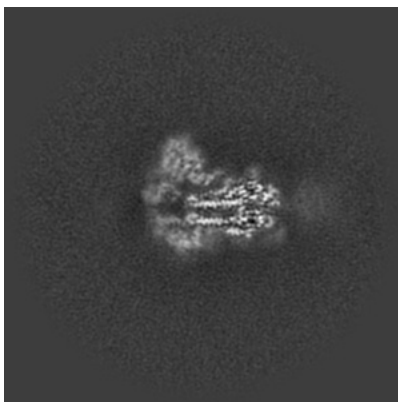
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

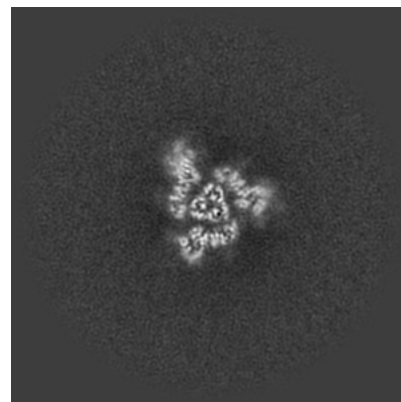
6.3.1 Primary map



X Index: 194

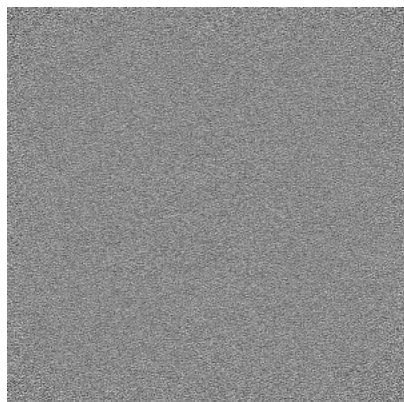


Y Index: 198

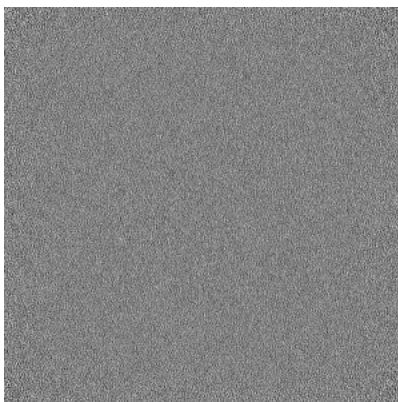


Z Index: 180

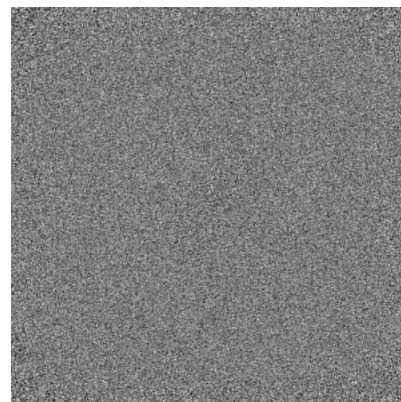
6.3.2 Raw map



X Index: 0



Y Index: 0

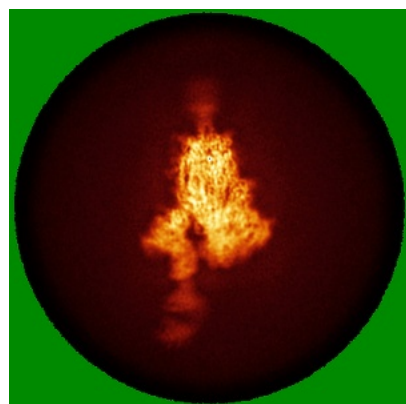


Z Index: 0

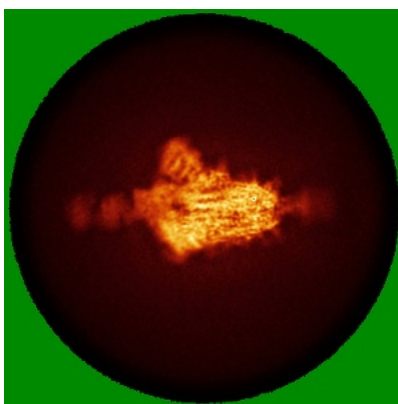
The images above show the largest variance slices of the map in three orthogonal directions.

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

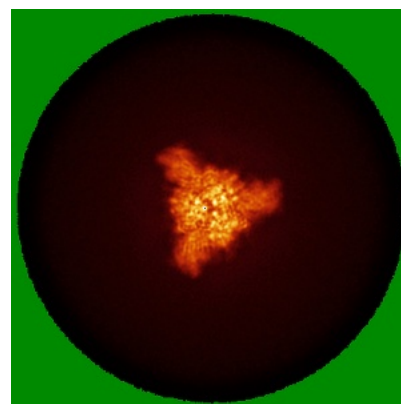
6.4.1 Primary map



X

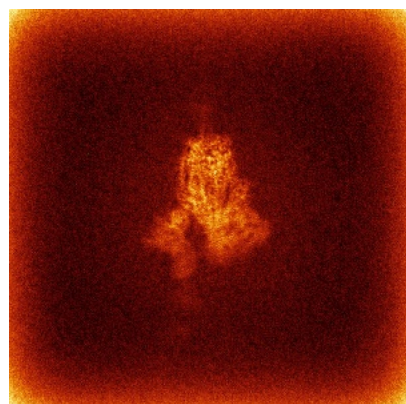


Y

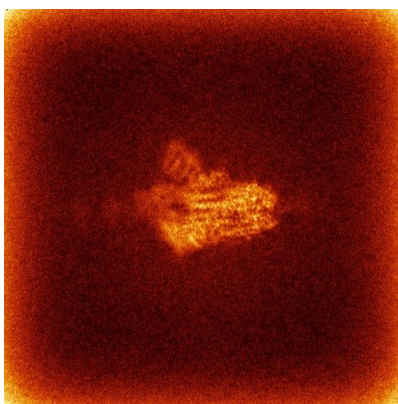


Z

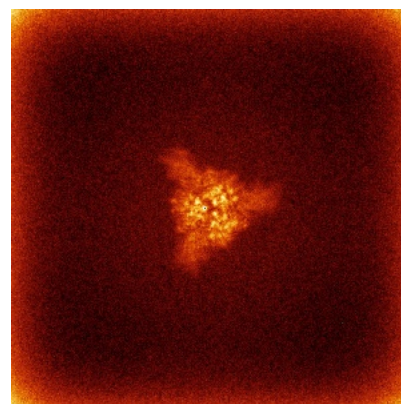
6.4.2 Raw map



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](#)

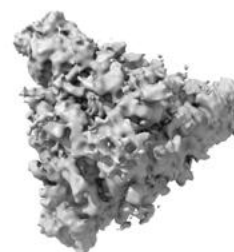
6.5.1 Primary map



X



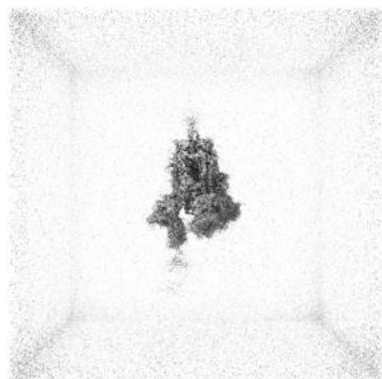
Y



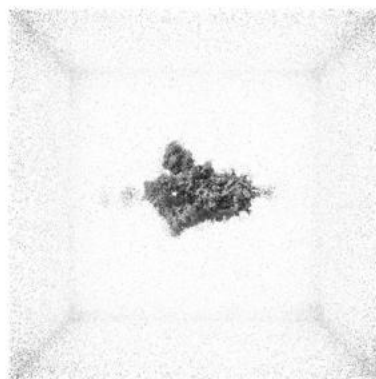
Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

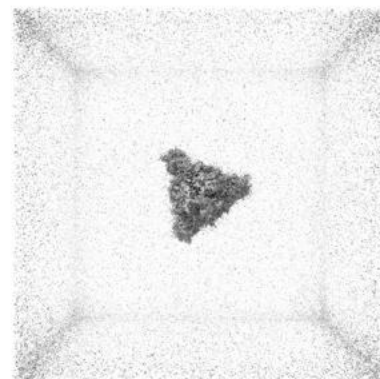
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

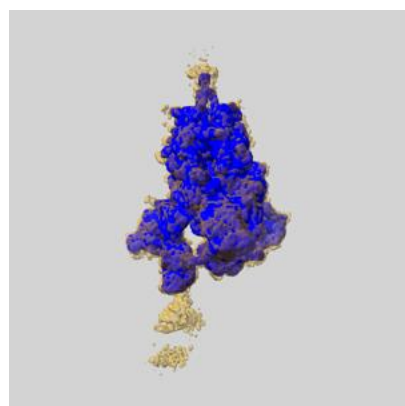
6.6 Mask visualisation [i](#)

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

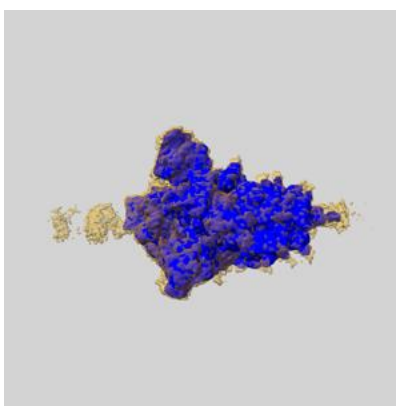
A mask typically either:

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

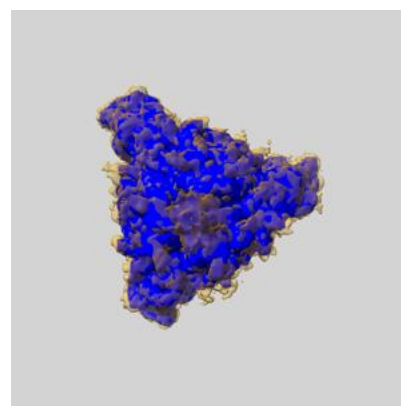
6.6.1 emd_24879_msk_1.map [i](#)



X



Y

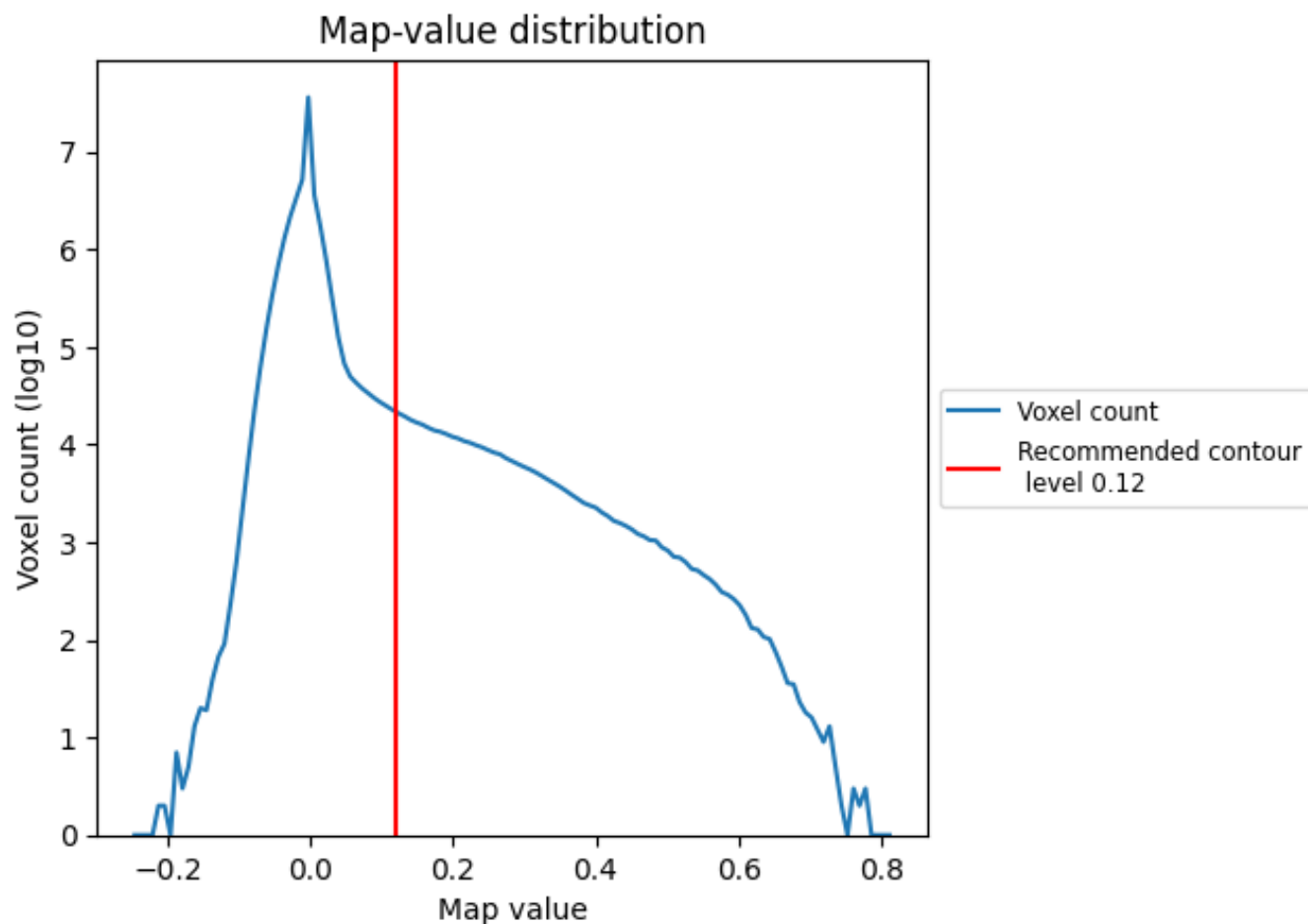


Z

7 Map analysis [i](#)

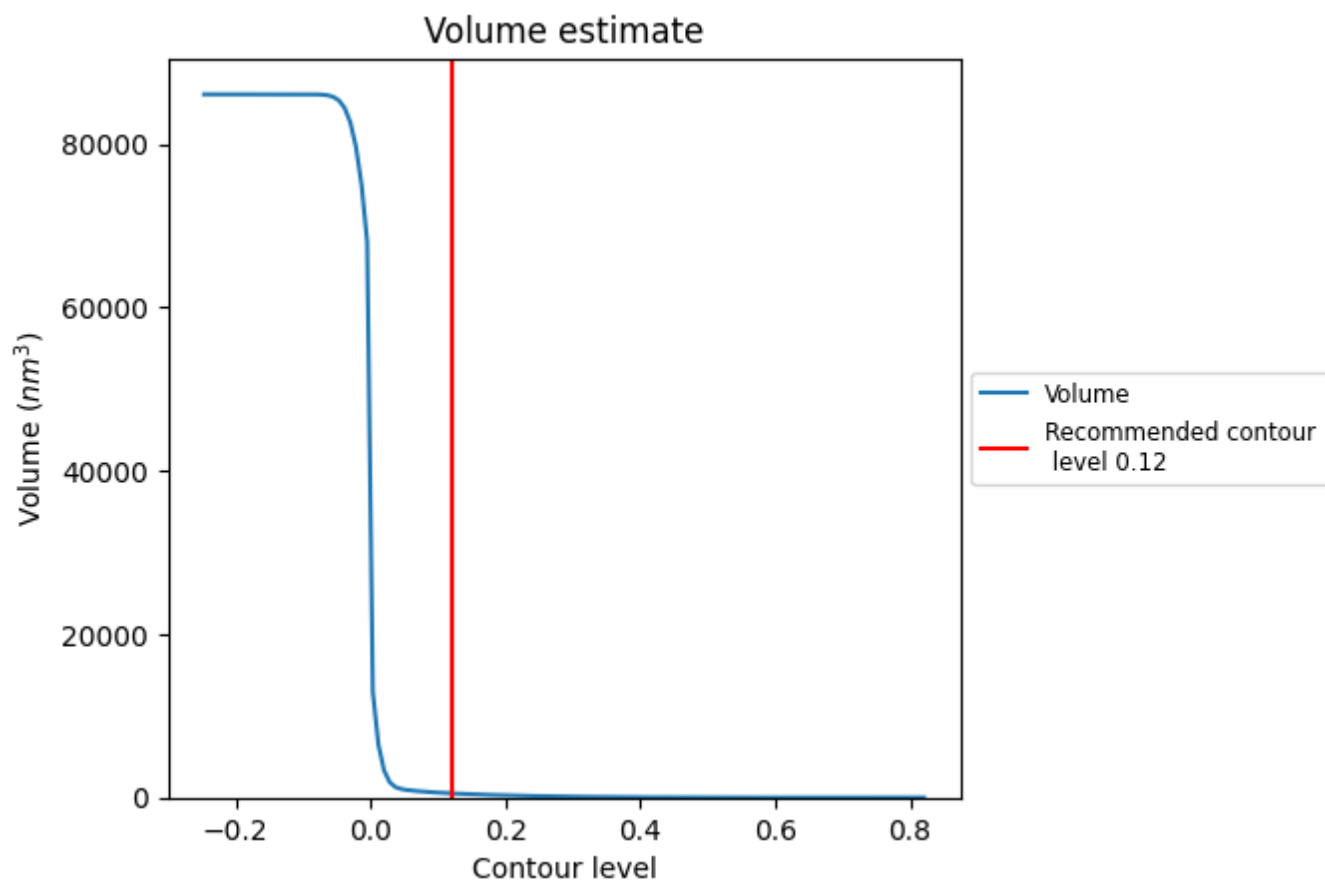
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

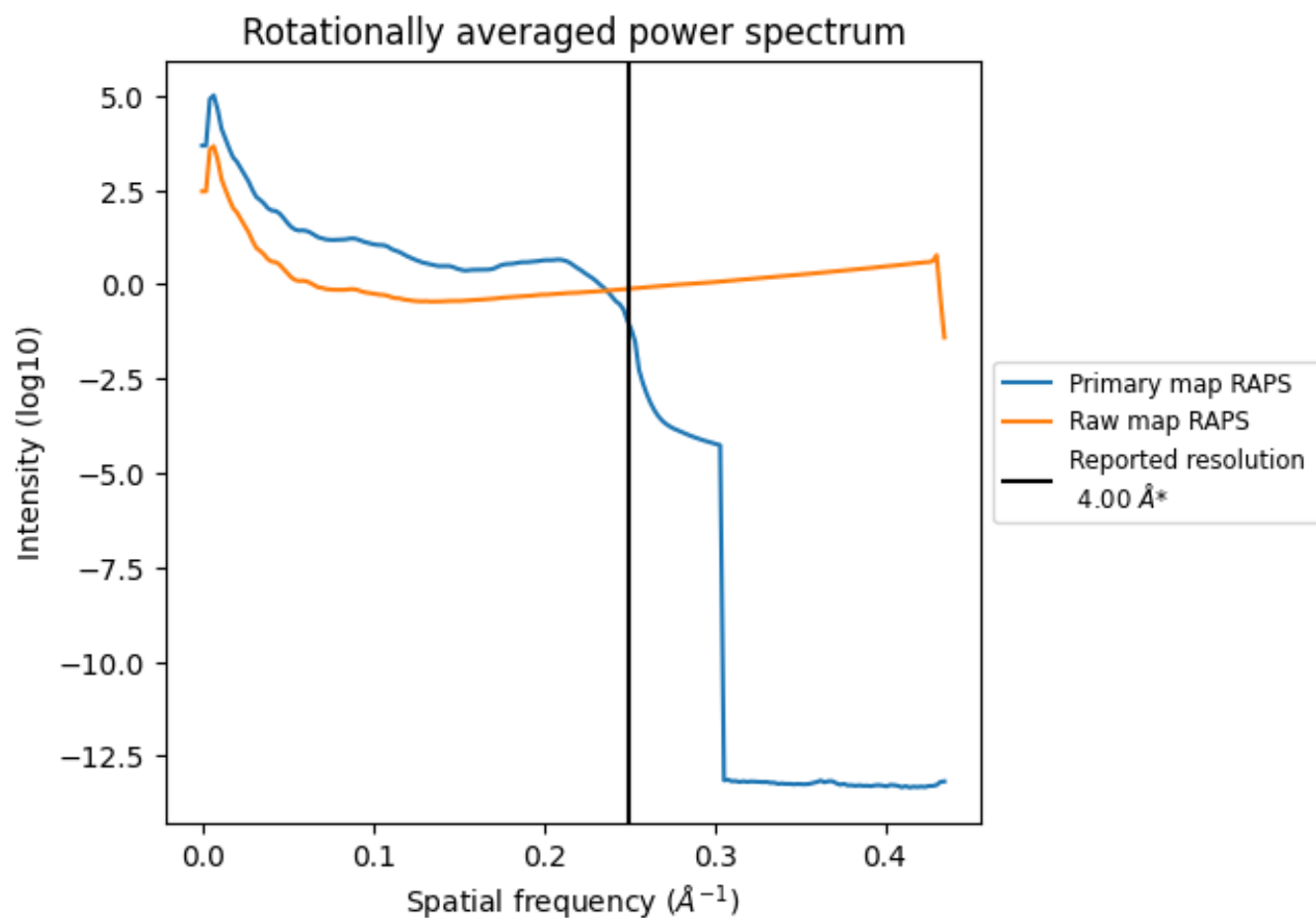
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 511 nm³; this corresponds to an approximate mass of 462 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 ⓘ

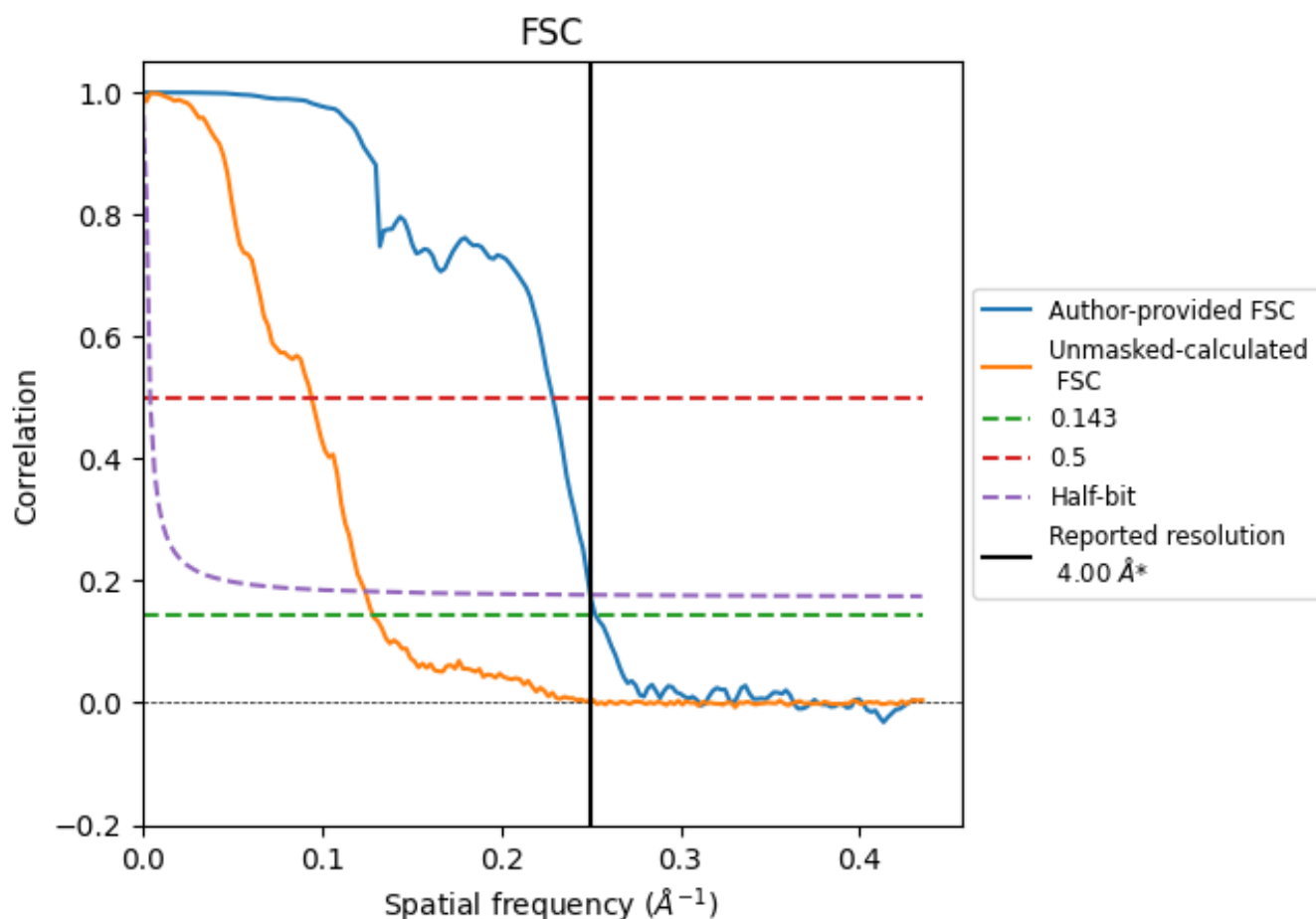


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

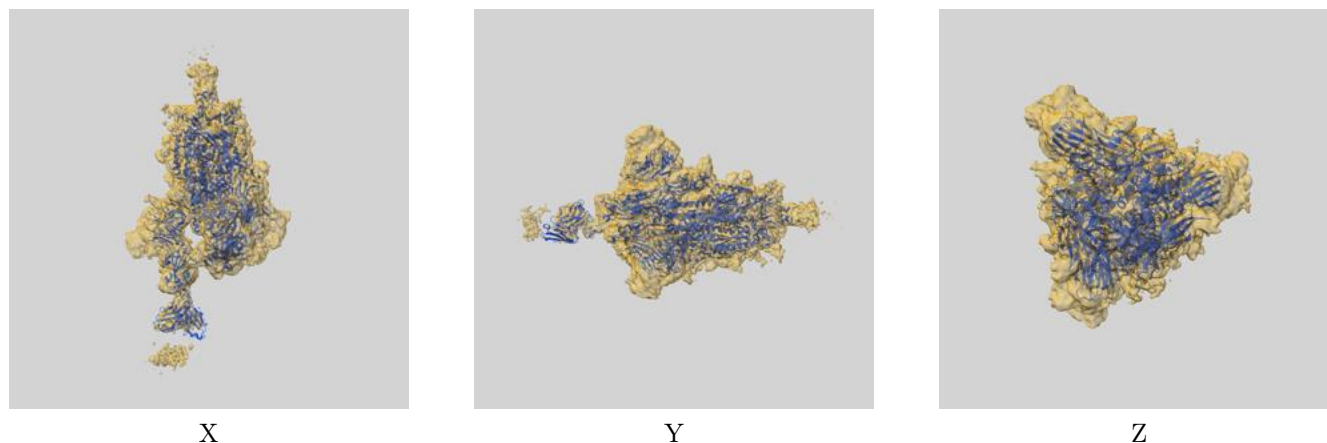
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.96	4.37	4.00
Unmasked-calculated*	7.77	10.59	8.04

*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 7.77 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24879 and PDB model 7S6L. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



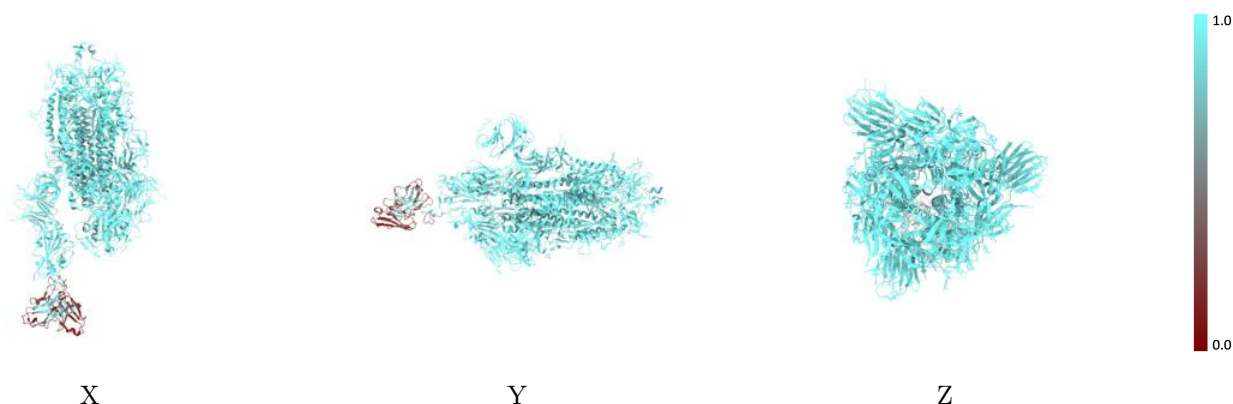
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



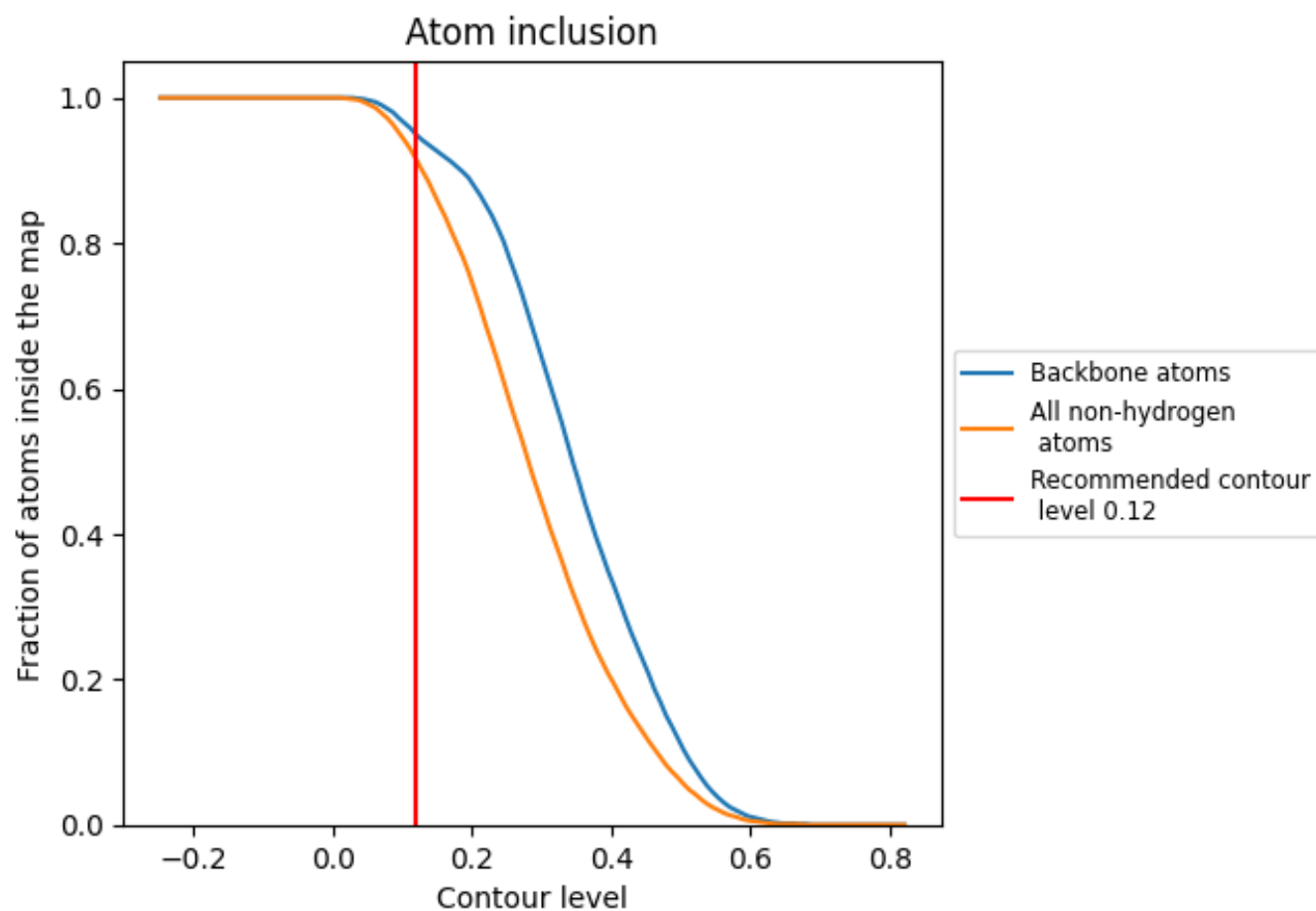
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9150	0.2990
A	0.9550	0.3080
B	0.9550	0.3170
C	0.9670	0.3240
D	0.8930	0.3300
E	0.8570	0.2630
F	0.9290	0.3820
G	1.0000	0.3950
H	0.4140	0.0760
I	0.9290	0.4120
J	0.9640	0.3280
K	1.0000	0.3510
L	0.2080	0.0280

1.0

0.0

<0.0