



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 04:26 PM UTC

PDB ID : 7MY2 / pdb_00007my2
EMDB ID : EMD-24077
Title : CryoEM structure of neutralizing nanobody Nb30 in complex with SARS-CoV2 spike
Authors : Xu, K.; Kwong, P.D.
Deposited on : 2021-05-20
Resolution : 2.65 Å(reported)
Based on initial model : 6XKL

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:

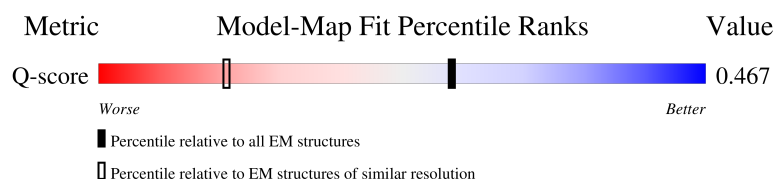
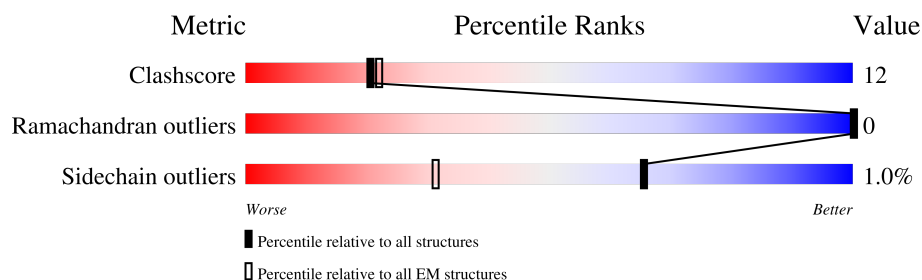
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 2.65 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	9050 (2.15 - 3.15)

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	B	1288	 5% 62% 18% 20%
1	C	1288	 9% 60% 20% 19%
1	E	1288	 62% 18% 19%
2	A	131	 22% 51% 40% 8%

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Mol	Chain	Length	Quality of chain
2	D	131	
2	H	131	
3	F	2	
3	I	2	
3	J	2	
3	K	2	
3	L	2	
3	M	2	
3	N	2	
3	O	2	
3	P	2	
3	Q	2	
3	T	2	
4	G	3	
4	S	3	
4	U	3	
4	V	3	
5	R	2	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 27884 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	B	1036	Total	C	N	O	S	0	0
			8062	5154	1339	1533	36		
1	C	1038	Total	C	N	O	S	0	0
			8083	5168	1344	1535	36		
1	E	1042	Total	C	N	O	S	0	0
			8114	5190	1348	1539	37		

There are 267 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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	817	PRO	PHE	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
B	1223	TYR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
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	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	SER	-	expression tag	UNP P0DTC2
B	1259	ALA	-	expression tag	UNP P0DTC2
B	1260	TRP	-	expression tag	UNP P0DTC2
B	1261	SER	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
B	1263	PRO	-	expression tag	UNP P0DTC2
B	1264	GLN	-	expression tag	UNP P0DTC2
B	1265	PHE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1266	GLU	-	expression tag	UNP P0DTC2
B	1267	LYS	-	expression tag	UNP P0DTC2
B	1268	GLY	-	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	GLY	-	expression tag	UNP P0DTC2
B	1273	GLY	-	expression tag	UNP P0DTC2
B	1274	GLY	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	SER	-	expression tag	UNP P0DTC2
B	1277	GLY	-	expression tag	UNP P0DTC2
B	1278	GLY	-	expression tag	UNP P0DTC2
B	1279	SER	-	expression tag	UNP P0DTC2
B	1280	ALA	-	expression tag	UNP P0DTC2
B	1281	TRP	-	expression tag	UNP P0DTC2
B	1282	SER	-	expression tag	UNP P0DTC2
B	1283	HIS	-	expression tag	UNP P0DTC2
B	1284	PRO	-	expression tag	UNP P0DTC2
B	1285	GLN	-	expression tag	UNP P0DTC2
B	1286	PHE	-	expression tag	UNP P0DTC2
B	1287	GLU	-	expression tag	UNP P0DTC2
B	1288	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	817	PRO	PHE	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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	HIS	-	expression tag	UNP P0DTC2
C	1251	HIS	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2
C	1257	HIS	-	expression tag	UNP P0DTC2
C	1258	SER	-	expression tag	UNP P0DTC2
C	1259	ALA	-	expression tag	UNP P0DTC2
C	1260	TRP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1261	SER	-	expression tag	UNP P0DTC2
C	1262	HIS	-	expression tag	UNP P0DTC2
C	1263	PRO	-	expression tag	UNP P0DTC2
C	1264	GLN	-	expression tag	UNP P0DTC2
C	1265	PHE	-	expression tag	UNP P0DTC2
C	1266	GLU	-	expression tag	UNP P0DTC2
C	1267	LYS	-	expression tag	UNP P0DTC2
C	1268	GLY	-	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	GLY	-	expression tag	UNP P0DTC2
C	1273	GLY	-	expression tag	UNP P0DTC2
C	1274	GLY	-	expression tag	UNP P0DTC2
C	1275	GLY	-	expression tag	UNP P0DTC2
C	1276	SER	-	expression tag	UNP P0DTC2
C	1277	GLY	-	expression tag	UNP P0DTC2
C	1278	GLY	-	expression tag	UNP P0DTC2
C	1279	SER	-	expression tag	UNP P0DTC2
C	1280	ALA	-	expression tag	UNP P0DTC2
C	1281	TRP	-	expression tag	UNP P0DTC2
C	1282	SER	-	expression tag	UNP P0DTC2
C	1283	HIS	-	expression tag	UNP P0DTC2
C	1284	PRO	-	expression tag	UNP P0DTC2
C	1285	GLN	-	expression tag	UNP P0DTC2
C	1286	PHE	-	expression tag	UNP P0DTC2
C	1287	GLU	-	expression tag	UNP P0DTC2
C	1288	LYS	-	expression tag	UNP P0DTC2
E	682	GLY	ARG	engineered mutation	UNP P0DTC2
E	683	SER	ARG	engineered mutation	UNP P0DTC2
E	685	SER	ARG	engineered mutation	UNP P0DTC2
E	817	PRO	PHE	engineered mutation	UNP P0DTC2
E	892	PRO	ALA	engineered mutation	UNP P0DTC2
E	899	PRO	ALA	engineered mutation	UNP P0DTC2
E	942	PRO	ALA	engineered mutation	UNP P0DTC2
E	986	PRO	LYS	engineered mutation	UNP P0DTC2
E	987	PRO	VAL	engineered mutation	UNP P0DTC2
E	1209	GLY	-	expression tag	UNP P0DTC2
E	1210	SER	-	expression tag	UNP P0DTC2
E	1211	GLY	-	expression tag	UNP P0DTC2
E	1212	TYR	-	expression tag	UNP P0DTC2
E	1213	ILE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1214	PRO	-	expression tag	UNP P0DTC2
E	1215	GLU	-	expression tag	UNP P0DTC2
E	1216	ALA	-	expression tag	UNP P0DTC2
E	1217	PRO	-	expression tag	UNP P0DTC2
E	1218	ARG	-	expression tag	UNP P0DTC2
E	1219	ASP	-	expression tag	UNP P0DTC2
E	1220	GLY	-	expression tag	UNP P0DTC2
E	1221	GLN	-	expression tag	UNP P0DTC2
E	1222	ALA	-	expression tag	UNP P0DTC2
E	1223	TYR	-	expression tag	UNP P0DTC2
E	1224	VAL	-	expression tag	UNP P0DTC2
E	1225	ARG	-	expression tag	UNP P0DTC2
E	1226	LYS	-	expression tag	UNP P0DTC2
E	1227	ASP	-	expression tag	UNP P0DTC2
E	1228	GLY	-	expression tag	UNP P0DTC2
E	1229	GLU	-	expression tag	UNP P0DTC2
E	1230	TRP	-	expression tag	UNP P0DTC2
E	1231	VAL	-	expression tag	UNP P0DTC2
E	1232	LEU	-	expression tag	UNP P0DTC2
E	1233	LEU	-	expression tag	UNP P0DTC2
E	1234	SER	-	expression tag	UNP P0DTC2
E	1235	THR	-	expression tag	UNP P0DTC2
E	1236	PHE	-	expression tag	UNP P0DTC2
E	1237	LEU	-	expression tag	UNP P0DTC2
E	1238	GLY	-	expression tag	UNP P0DTC2
E	1239	ARG	-	expression tag	UNP P0DTC2
E	1240	SER	-	expression tag	UNP P0DTC2
E	1241	LEU	-	expression tag	UNP P0DTC2
E	1242	GLU	-	expression tag	UNP P0DTC2
E	1243	VAL	-	expression tag	UNP P0DTC2
E	1244	LEU	-	expression tag	UNP P0DTC2
E	1245	PHE	-	expression tag	UNP P0DTC2
E	1246	GLN	-	expression tag	UNP P0DTC2
E	1247	GLY	-	expression tag	UNP P0DTC2
E	1248	PRO	-	expression tag	UNP P0DTC2
E	1249	GLY	-	expression tag	UNP P0DTC2
E	1250	HIS	-	expression tag	UNP P0DTC2
E	1251	HIS	-	expression tag	UNP P0DTC2
E	1252	HIS	-	expression tag	UNP P0DTC2
E	1253	HIS	-	expression tag	UNP P0DTC2
E	1254	HIS	-	expression tag	UNP P0DTC2
E	1255	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1256	HIS	-	expression tag	UNP P0DTC2
E	1257	HIS	-	expression tag	UNP P0DTC2
E	1258	SER	-	expression tag	UNP P0DTC2
E	1259	ALA	-	expression tag	UNP P0DTC2
E	1260	TRP	-	expression tag	UNP P0DTC2
E	1261	SER	-	expression tag	UNP P0DTC2
E	1262	HIS	-	expression tag	UNP P0DTC2
E	1263	PRO	-	expression tag	UNP P0DTC2
E	1264	GLN	-	expression tag	UNP P0DTC2
E	1265	PHE	-	expression tag	UNP P0DTC2
E	1266	GLU	-	expression tag	UNP P0DTC2
E	1267	LYS	-	expression tag	UNP P0DTC2
E	1268	GLY	-	expression tag	UNP P0DTC2
E	1269	GLY	-	expression tag	UNP P0DTC2
E	1270	GLY	-	expression tag	UNP P0DTC2
E	1271	SER	-	expression tag	UNP P0DTC2
E	1272	GLY	-	expression tag	UNP P0DTC2
E	1273	GLY	-	expression tag	UNP P0DTC2
E	1274	GLY	-	expression tag	UNP P0DTC2
E	1275	GLY	-	expression tag	UNP P0DTC2
E	1276	SER	-	expression tag	UNP P0DTC2
E	1277	GLY	-	expression tag	UNP P0DTC2
E	1278	GLY	-	expression tag	UNP P0DTC2
E	1279	SER	-	expression tag	UNP P0DTC2
E	1280	ALA	-	expression tag	UNP P0DTC2
E	1281	TRP	-	expression tag	UNP P0DTC2
E	1282	SER	-	expression tag	UNP P0DTC2
E	1283	HIS	-	expression tag	UNP P0DTC2
E	1284	PRO	-	expression tag	UNP P0DTC2
E	1285	GLN	-	expression tag	UNP P0DTC2
E	1286	PHE	-	expression tag	UNP P0DTC2
E	1287	GLU	-	expression tag	UNP P0DTC2
E	1288	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called Nanobody Nb30.

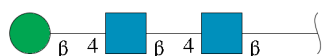
Mol	Chain	Residues	Atoms				AltConf	Trace
2	H	120	Total	C	N	O	S	
			910	571	157	176	6	0
2	A	120	Total	C	N	O	S	
			910	571	157	176	6	0
2	D	120	Total	C	N	O	S	
			910	571	157	176	6	0

- Molecule 3 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
3	F	2	Total	C	N	O	0	0
			28	16	2	10		
3	I	2	Total	C	N	O	0	0
			28	16	2	10		
3	J	2	Total	C	N	O	0	0
			28	16	2	10		
3	K	2	Total	C	N	O	0	0
			28	16	2	10		
3	L	2	Total	C	N	O	0	0
			28	16	2	10		
3	M	2	Total	C	N	O	0	0
			28	16	2	10		
3	N	2	Total	C	N	O	0	0
			28	16	2	10		
3	O	2	Total	C	N	O	0	0
			28	16	2	10		
3	P	2	Total	C	N	O	0	0
			28	16	2	10		
3	Q	2	Total	C	N	O	0	0
			28	16	2	10		
3	T	2	Total	C	N	O	0	0
			28	16	2	10		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	3	Total	C	N	O	0	0
			39	22	2	15		
4	S	3	Total	C	N	O	0	0
			39	22	2	15		

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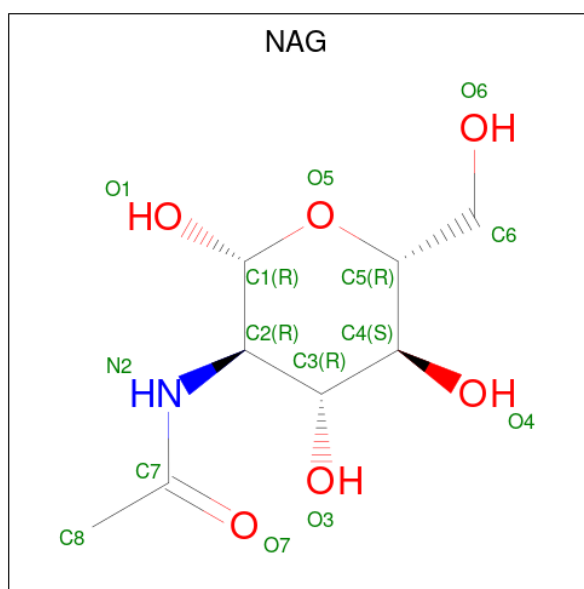
Mol	Chain	Residues	Atoms				AltConf	Trace
4	U	3	Total	C	N	O	0	0
			39	22	2	15		
4	V	3	Total	C	N	O	0	0
			39	22	2	15		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
5	R	2	Total	C	N	O	0	0
			25	14	1	10		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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

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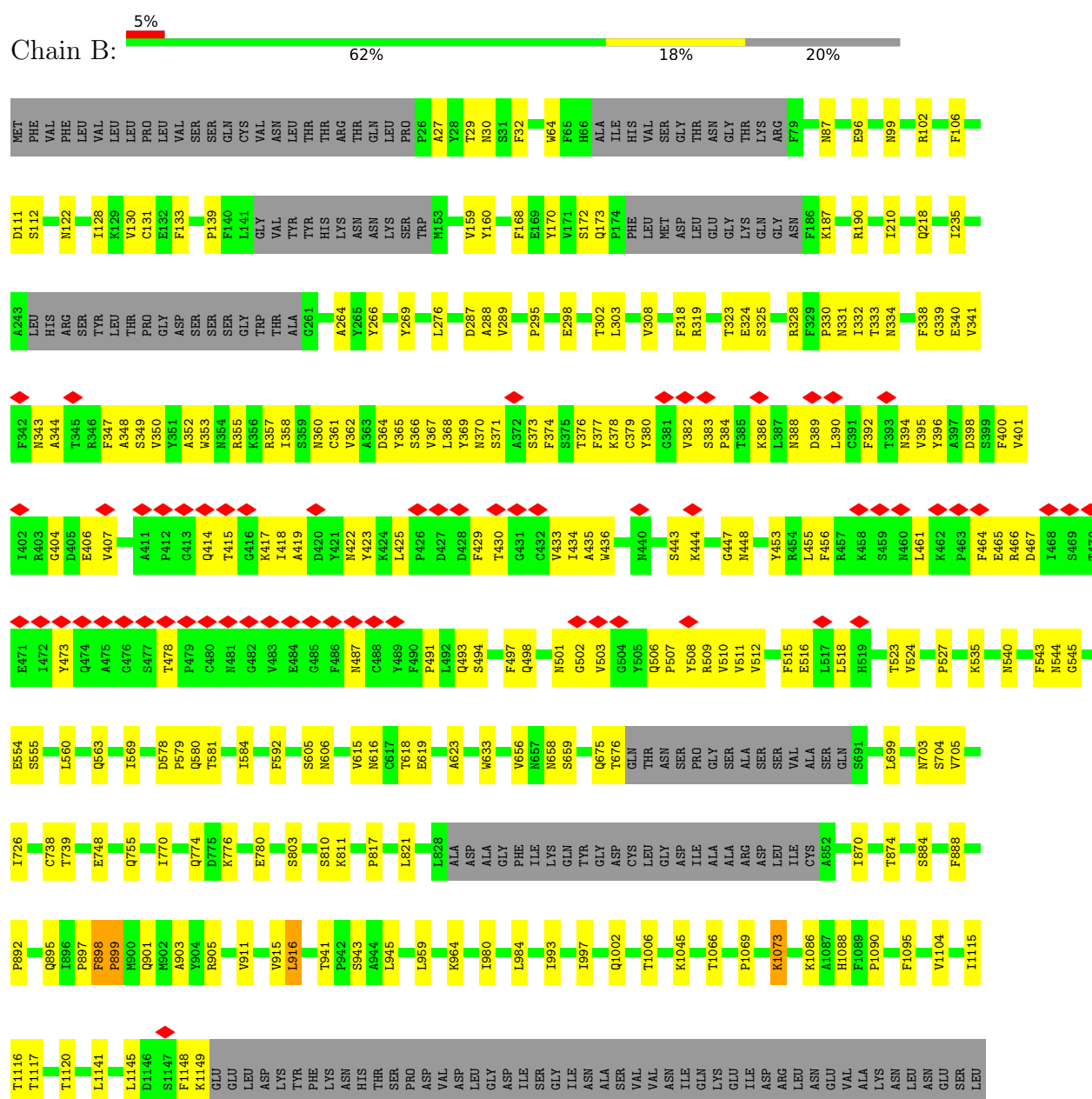
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Mol	Chain	Residues	Atoms				AltConf
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	

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



[illegible]

- Molecule 1: Spike glycoprotein



N87	PHE	VAL	VAL	LEU	VAL	LEU	PRO	VAL	SER	SER	GLN	CYS	VAL	ASN	LEU	THR	THR	THR	GLN	LEU	PRO	P26	P27	Y28	T29	T33	R34	D53	L54	F55	L56	P57	F58	M61	F65	H66	ALA	ILE	HIS	VAL	SER	GLY	THR	LYS	ARG	F79	V83	T84
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PHE	LEU	MET	ASP	LEU	GLU	GLY	LYS	GLN	GLY	ASN	F186	K187	M188	L189	R190	E191	I201	I203	Y204	S205			T208			L212	V213			Y227	D228	L229	P230	I231	G232	I233	P234	L235		Q239	T240	L241	L242	L243	L244	H245	R246	SER	TYR	LEU	THR	PRO	GLY	ASP	SER	SER	SER	GLY	THR	ALA	GLY
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A262	Y265	Y269	L270	Q271	R273	L276	Y289	L293	D294	E295	E298	T299	T302	L303	K304	T315	F318	R319	P322	S325	L326	V327	R328	F329	P330	N331	T332	L333	F338	G339	E340	V341	F342	N343	A344	T345	A348	S349	V350	F351	A352	N353	R354	R355	L356
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[illegible]

A419	D420	Y421	N422	Y423	Y424	L425	P426	D427	D428	F429	T430	V433	L434	A435	A436	Y437	S438	N439	M440	L441	D442	S443	K444	Y445	D446	D447	D447	M448	Y449	N450	Y451	L452	Y453	R454	L455	F456	R457	K458	S459	N460	L461	K462	P463	F464	E465	R466	D467	L468	S469	T470	E471	L472	Y473	Q474	A475	G476	S477	T478	D479
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C480	N481	G482	V483	E484	G485	F486	N487	C488	F489	F490	P491	L492	G493	S494	Y495	G496	F497	P498	P499	N501	N501	G502	F503	G504	F505	G506	P507	Y508	N509	V510	F511	V512	L513	S514	F515	E516	L517	L518	H519	A520	P521	A522	T523	V524	C525	G526	P527	K528	C538	V539	N542	F543	N544	G545	L546	S555
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L560
P561
F562
D578
P579
Q580
I584
S605
N606
C617
A623
D627
T632
W633
V642
T651
Q675
GLN THR
ASN THR
SER PRO
GLY SER
ALA SER
SER VAL
ALA SER
Q690
V729
M740
L752
Q755
L767
K776
E780
S803

P807	K314	R815	S816	P817	D820	L821	L828	ALA	ASP	ALA	GLY	PHE	ILE	LYS	GLN	TYR	GLY	ASP	CYS	LEU	GLY	ASP	ILE	ALA	ALA	ARG	ASP	LEU	ILE	CYS	A852	Q853	G857	I870	Y873	T874	T883	F888	P892	Q895	P897	F898	P899	M900	Q901	Y904	R905
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V915	L916	K921	T934	G935	D936	S937	L938	S939	S940	S943	A944	L945	L984	D985	P986	P987	E988	A989	T993	D994	T998	C1043	G1059	H1064	P1069	K1073	H1088	R1091	T1100	H1101	V1104	T1115	D1118	K1119	T1120	K1149	GLU	GLU	LEU	LEU
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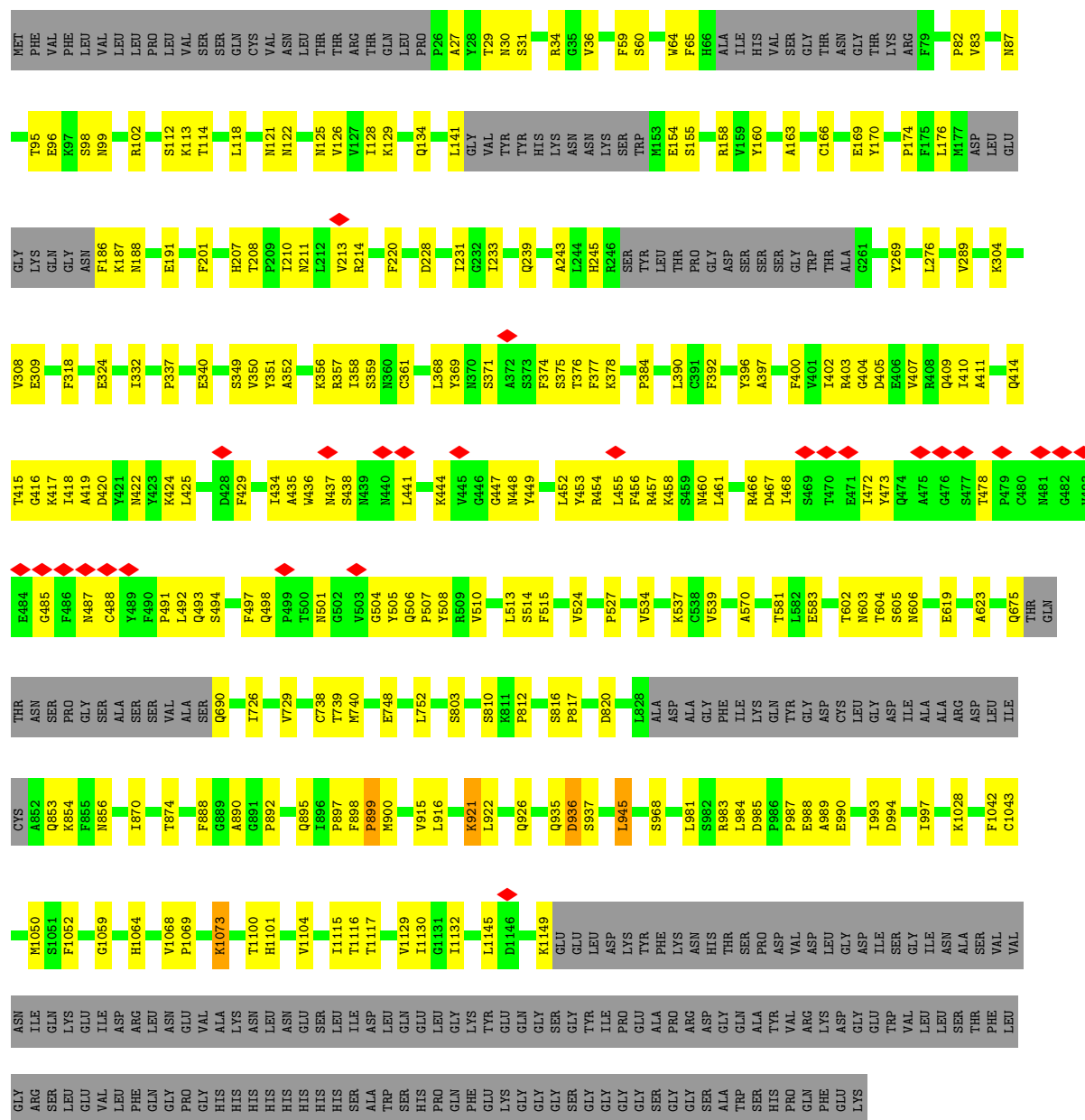
LYS	TYR	PHE	ASN	LYS	HIS	THR	SER	PRO	ASP	ASP	VAL	ASP	ASP	LEU	GLY	ASP	ALA	ASN	ILE	GLY	ILE	VAL	VAL	ASN	ASN	GLN	LYS	ILE	ILE	GLU	GLU	ASP	ARG	LEU	ASN	GLU	VAL	ALA	LYS	ASN	ASN	LEU	LEU	ASN	GLU	SER	LEU	ILE	ILE	ASP	GLY	GLN	TYR	GLU	GLN	GLY	SER	GLY	TYR
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PRO GLU ALA PRO ARG ASP GLY GLN TYR ALA VAL ARG LYS ASP GLY GLU TRP VAL LEU LEU SER SER THR THR PHE PHE LEU LEU GLY ARG SER SER LEU LEU VAL LEU PHE GLN GLY PRO PRO GLY HIS HIS HIS HIS HIS HIS HIS SER ALA TRP TRP SER HIS PRO GLN PHE PHE GLU GLY LYS GLY GLY GLY GLY

GLY
GLY
SER
GLY
GLY
SER
ALA
TRP
SER
HIS
PRO
GLN
PHE
GLU
LYS

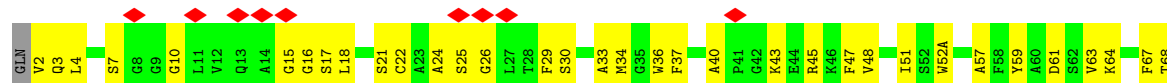
- Molecule 1: Spike glycoprotein

Chain E:  62% 18% 19%



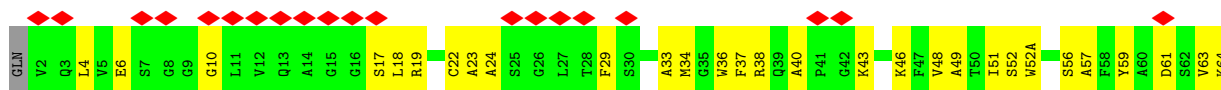
- Molecule 2: Nanobody Nb30

Chain H:  8% 47% 44% 8%

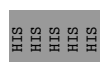
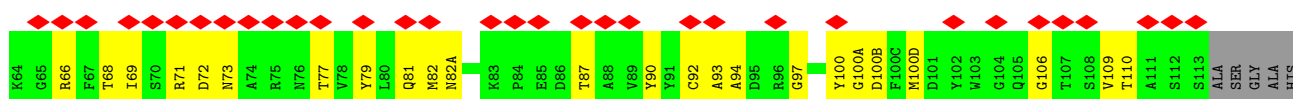




• Molecule 2: Nanobody Nb30



• Molecule 2: Nanobody Nb30



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  100%



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  50% 50%



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

Chain G:  100%



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

Chain S:  100%



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

Chain U:  100%



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

Chain V:  100%



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

Chain R:  100%

MOL
EMD

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	333232	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 ($e^-/\text{\AA}^2$)	40.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.098	Depositor
Minimum map value	-0.807	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	513.0, 513.0, 513.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	Depositor

5 Model quality

5.1 Standard geometry

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

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	B	0.43	8/8251 (0.1%)	0.53	2/11238 (0.0%)
1	C	0.47	10/8273 (0.1%)	0.57	3/11268 (0.0%)
1	E	0.46	9/8305 (0.1%)	0.54	4/11310 (0.0%)
2	A	0.15	0/930	0.41	0/1254
2	D	0.14	0/930	0.40	0/1254
2	H	0.15	0/930	0.46	0/1254
All	All	0.43	27/27619 (0.1%)	0.54	9/37578 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
All	All	0	2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	899	PRO	C-O	-7.52	1.14	1.24
1	E	897	PRO	C-O	-7.39	1.15	1.23
1	C	897	PRO	C-O	-7.36	1.15	1.23
1	C	899	PRO	C-O	-7.30	1.15	1.24
1	E	899	PRO	C-O	-7.16	1.15	1.24
1	E	1069	PRO	C-O	-6.62	1.16	1.23
1	E	816	SER	CA-CB	-6.60	1.44	1.53
1	C	892	PRO	C-O	-6.60	1.16	1.23
1	B	897	PRO	C-O	-6.56	1.14	1.23
1	E	892	PRO	C-O	-6.55	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1069	PRO	C-O	-6.46	1.16	1.23
1	B	1069	PRO	C-O	-6.44	1.16	1.23
1	C	803	SER	CA-CB	-5.86	1.44	1.53
1	B	892	PRO	C-O	-5.80	1.16	1.23
1	C	817	PRO	C-O	-5.80	1.16	1.24
1	E	817	PRO	C-O	-5.71	1.17	1.24
1	B	817	PRO	C-O	-5.71	1.17	1.24
1	B	803	SER	CA-CB	-5.65	1.44	1.53
1	E	803	SER	CA-CB	-5.43	1.44	1.53
1	E	1068	VAL	C-O	-5.24	1.18	1.24
1	C	898	PHE	C-O	-5.19	1.19	1.24
1	B	898	PHE	C-O	-5.16	1.19	1.24
1	C	816	SER	CA-CB	-5.16	1.45	1.53
1	C	901	GLN	C-O	-5.13	1.18	1.24
1	C	807	PRO	C-O	-5.09	1.18	1.23
1	B	903	ALA	CA-CB	-5.06	1.45	1.53
1	E	890	ALA	CA-CB	-5.05	1.47	1.54

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	941	THR	CB-CA-C	9.16	121.78	109.42
1	C	897	PRO	N-CA-CB	-7.75	96.41	103.31
1	C	904	TYR	CB-CA-C	-6.67	96.78	110.38
1	E	897	PRO	N-CA-CB	-6.04	97.93	103.31
1	C	888	PHE	CA-CB-CG	5.81	119.61	113.80
1	B	888	PHE	CA-CB-CG	5.59	119.39	113.80
1	E	888	PHE	CA-CB-CG	5.58	119.38	113.80
1	E	812	PRO	CB-CA-C	-5.22	102.94	111.56
1	E	899	PRO	CB-CA-C	5.03	120.91	112.62

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	122	ASN	Peptide
1	C	617	CYS	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	8062	0	7839	190	0
1	C	8083	0	7857	184	0
1	E	8114	0	7889	167	0
2	A	910	0	864	47	0
2	D	910	0	864	45	0
2	H	910	0	864	49	0
3	F	28	0	25	0	0
3	I	28	0	25	0	0
3	J	28	0	25	1	0
3	K	28	0	25	0	0
3	L	28	0	25	0	0
3	M	28	0	25	0	0
3	N	28	0	25	0	0
3	O	28	0	25	0	0
3	P	28	0	25	0	0
3	Q	28	0	25	0	0
3	T	28	0	25	1	0
4	G	39	0	34	0	0
4	S	39	0	34	0	0
4	U	39	0	34	0	0
4	V	39	0	34	0	0
5	R	25	0	22	0	0
6	B	140	0	130	1	0
6	C	140	0	130	3	0
6	E	126	0	117	0	0
All	All	27884	0	26987	665	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 12.

All (665) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:402:ILE:O	1:E:507:PRO:HA	1.49	1.11
2:D:90:TYR:O	2:D:106:GLY:HA2	1.58	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:434:ILE:O	1:B:510:VAL:HA	1.64	0.98
1:E:411:ALA:HB3	1:E:414:GLN:HB3	1.55	0.88
1:B:318:PHE:HZ	1:B:615:VAL:HG21	1.41	0.86
1:C:409:GLN:HE22	1:C:416:GLY:HA3	1.42	0.84
1:E:376:THR:HB	1:E:435:ALA:O	1.77	0.84
1:B:130:VAL:HG12	1:B:168:PHE:HB3	1.60	0.82
2:D:93:ALA:HB1	2:D:100(D):MET:HG3	1.61	0.82
1:C:448:ASN:H	1:C:497:PHE:H	1.28	0.81
1:C:65:PHE:O	1:C:265:TYR:HB3	1.80	0.80
2:A:87:THR:HG23	2:A:110:THR:HA	1.62	0.80
1:E:1100:THR:HG1	1:E:1101:HIS:HD1	1.30	0.79
1:E:375:SER:O	1:E:378:LYS:NZ	2.16	0.79
1:B:355:ARG:HD2	1:B:396:TYR:HB3	1.63	0.79
1:B:139:PRO:HB3	1:B:159:VAL:HG23	1.65	0.78
1:C:34:ARG:NH2	1:C:191:GLU:OE1	2.18	0.77
1:E:141:LEU:HB3	1:E:243:ALA:HA	1.68	0.74
1:E:752:LEU:HD21	1:E:990:GLU:HG3	1.68	0.74
1:B:401:VAL:HG12	1:B:507:PRO:HB2	1.68	0.73
1:B:1149:LYS:HG3	1:E:1145:LEU:HD21	1.70	0.73
1:B:478:THR:OG1	1:B:487:ASN:ND2	2.22	0.72
2:H:15:GLY:HA2	2:H:82(C):LEU:HB2	1.71	0.72
1:B:355:ARG:NE	1:B:398:ASP:OD1	2.24	0.71
1:E:357:ARG:NH2	1:E:358:ILE:O	2.23	0.71
1:E:96:GLU:OE2	1:E:186:PHE:N	2.24	0.70
1:C:97:LYS:HD3	1:C:186:PHE:HB3	1.72	0.70
1:B:159:VAL:HG13	1:B:160:TYR:HD1	1.55	0.70
1:C:356:LYS:NZ	1:C:357:ARG:O	2.24	0.70
1:E:155:SER:OG	1:E:158:ARG:NH2	2.24	0.70
1:E:1104:VAL:HG23	1:E:1115:ILE:HG12	1.74	0.70
2:A:29:PHE:O	2:A:71:ARG:NH2	2.24	0.70
1:C:369:TYR:HE2	1:C:388:ASN:HD21	1.38	0.70
1:B:365:TYR:HA	1:B:368:LEU:HD13	1.74	0.69
1:B:656:VAL:HG12	1:B:658:ASN:H	1.57	0.69
1:B:810:SER:OG	1:B:811:LYS:NZ	2.26	0.69
1:B:1104:VAL:HG23	1:B:1115:ILE:HG12	1.73	0.69
1:E:402:ILE:HB	1:E:510:VAL:HG11	1.73	0.69
1:B:64:TRP:HE1	1:B:264:ALA:HB1	1.56	0.69
1:B:433:VAL:HG12	1:B:512:VAL:HG22	1.74	0.69
2:H:29:PHE:HZ	2:H:78:VAL:HB	1.58	0.69
1:B:332:ILE:HG13	1:B:333:THR:H	1.57	0.69
1:C:65:PHE:HB2	1:C:265:TYR:HD2	1.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:TYR:OH	1:B:384:PRO:O	2.06	0.68
1:E:740:MET:HE2	1:E:856:ASN:HA	1.74	0.68
2:H:87:THR:HA	2:H:109:VAL:O	1.92	0.68
1:C:333:THR:HA	1:C:362:VAL:HG21	1.76	0.67
2:A:52:SER:HB3	2:A:56:SER:HB2	1.74	0.67
1:C:91:TYR:OH	1:C:191:GLU:OE2	2.13	0.67
1:C:409:GLN:HG2	1:C:418:ILE:HB	1.76	0.67
1:B:366:SER:HA	1:B:369:TYR:HD2	1.60	0.67
1:B:1148:PHE:HB3	1:B:1149:LYS:HZ2	1.59	0.66
1:C:364:ASP:HB2	1:C:527:PRO:HD2	1.77	0.66
1:B:776:LYS:NZ	1:B:780:GLU:OE2	2.24	0.66
1:B:535:LYS:NZ	1:B:554:GLU:OE2	2.24	0.66
1:C:212:LEU:HD12	1:C:213:VAL:H	1.61	0.66
1:C:329:PHE:O	1:C:580:GLN:NE2	2.26	0.66
1:C:1104:VAL:HG23	1:C:1115:ILE:HG12	1.77	0.66
1:E:498:GLN:O	1:E:501:ASN:ND2	2.27	0.66
1:B:323:THR:OG1	1:B:324:GLU:OE1	2.12	0.65
2:A:75:ARG:NH1	2:A:79:TYR:OH	2.29	0.65
1:C:406:GLU:O	1:C:409:GLN:HB3	1.96	0.65
1:E:738:CYS:SG	1:E:739:THR:N	2.68	0.65
2:D:32:TYR:HB3	2:D:94:ALA:HB1	1.77	0.65
1:B:404:GLY:HA2	1:B:407:VAL:HG23	1.78	0.65
1:C:134:GLN:HG2	1:C:161:SER:HB3	1.78	0.65
1:C:457:ARG:NH2	1:C:459:SER:OG	2.30	0.65
1:E:369:TYR:OH	1:E:384:PRO:O	2.09	0.65
1:C:325:SER:H	1:C:539:VAL:HG23	1.61	0.65
2:D:10:GLY:HA2	2:D:18:LEU:HD11	1.77	0.65
1:E:396:TYR:HB2	1:E:514:SER:HB3	1.79	0.64
1:E:472:ILE:HD12	1:E:488:CYS:HB3	1.77	0.64
2:A:37:PHE:HE2	2:A:100:TYR:HA	1.62	0.64
1:C:675:GLN:O	1:C:690:GLN:N	2.30	0.64
1:E:619:GLU:N	1:E:619:GLU:OE1	2.29	0.64
1:C:1043:CYS:HB2	1:C:1064:HIS:CE1	2.33	0.64
1:E:350:VAL:HA	1:E:400:PHE:HB2	1.79	0.63
1:E:452:LEU:HB3	1:E:492:LEU:HB3	1.79	0.63
1:B:414:GLN:NE2	1:B:415:THR:O	2.31	0.63
1:E:34:ARG:NH1	1:E:191:GLU:OE2	2.31	0.63
1:B:378:LYS:HD3	2:A:98:MET:HE2	1.81	0.63
1:B:430:THR:OG1	1:B:515:PHE:O	2.16	0.63
1:E:376:THR:CB	1:E:435:ALA:O	2.45	0.62
2:A:10:GLY:HA3	2:A:110:THR:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:738:CYS:SG	1:B:739:THR:N	2.72	0.62
1:E:378:LYS:NZ	2:H:100:TYR:HB3	2.14	0.62
1:E:434:ILE:O	1:E:510:VAL:HA	1.99	0.62
1:E:444:LYS:HD3	1:E:448:ASN:HD21	1.63	0.62
1:B:369:TYR:HE1	1:B:384:PRO:HB2	1.64	0.62
1:C:472:ILE:HD12	1:C:488:CYS:HB3	1.81	0.62
2:H:68:THR:HB	2:H:81:GLN:HB3	1.82	0.62
2:A:34:MET:HE1	2:A:78:VAL:HG11	1.82	0.62
1:B:443:SER:HA	1:B:448:ASN:HB2	1.81	0.62
1:C:188:ASN:HA	1:C:208:THR:O	2.00	0.62
1:C:729:VAL:HG22	1:C:1059:GLY:HA2	1.82	0.61
1:B:398:ASP:HB2	1:B:512:VAL:HB	1.82	0.61
1:B:367:VAL:O	1:B:371:SER:HB2	1.99	0.61
1:E:95:THR:O	1:E:98:SER:OG	2.17	0.61
1:E:409:GLN:OE1	1:E:418:ILE:N	2.33	0.61
1:B:456:PHE:HB2	1:B:491:PRO:HB3	1.83	0.61
1:E:853:GLN:NE2	1:E:854:LYS:O	2.33	0.61
1:E:396:TYR:O	1:E:513:LEU:HA	2.01	0.61
1:B:350:VAL:HB	1:B:400:PHE:CE2	2.36	0.61
1:E:726:ILE:HD13	1:E:945:LEU:HD13	1.83	0.61
1:C:391:CYS:O	1:C:523:THR:OG1	2.19	0.61
1:E:377:PHE:C	1:E:378:LYS:HD2	2.25	0.60
1:C:357:ARG:NH1	1:C:393:THR:OG1	2.34	0.60
1:B:99:ASN:O	1:B:102:ARG:NH2	2.34	0.60
1:B:357:ARG:HH12	1:B:395:VAL:HB	1.65	0.60
1:C:433:VAL:HG12	1:C:512:VAL:HG22	1.84	0.60
1:E:603:ASN:OD1	1:E:604:THR:N	2.34	0.60
2:D:34:MET:HE1	2:D:69:ILE:HG12	1.84	0.60
1:B:964:LYS:HE3	1:E:570:ALA:HA	1.84	0.59
2:D:6:GLU:HG3	2:D:106:GLY:H	1.67	0.59
2:D:30:SER:HA	2:D:71:ARG:HH22	1.67	0.59
2:D:62:SER:O	2:D:66:ARG:NH1	2.35	0.59
1:C:675:GLN:OE1	1:C:690:GLN:N	2.35	0.59
1:B:360:ASN:H	1:B:523:THR:HB	1.67	0.59
1:E:478:THR:OG1	1:E:487:ASN:ND2	2.31	0.59
1:E:309:GLU:N	1:E:309:GLU:OE1	2.35	0.59
1:C:355:ARG:NH1	1:C:398:ASP:OD2	2.35	0.59
1:C:276:LEU:HB3	1:C:289:VAL:HG22	1.85	0.59
2:D:87:THR:HG22	2:D:110:THR:HG23	1.84	0.59
1:C:106:PHE:HD1	1:C:235:ILE:HD11	1.68	0.58
2:D:3:GLN:H	2:D:26:GLY:HA3	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:61:ASP:OD1	2:A:64:LYS:NZ	2.32	0.58
1:E:420:ASP:OD1	1:E:460:ASN:ND2	2.37	0.58
1:E:424:LYS:HB3	1:E:461:LEU:HB2	1.85	0.58
1:B:339:GLY:O	1:B:343:ASN:N	2.35	0.58
2:H:71:ARG:HB3	2:H:78:VAL:HG23	1.86	0.58
2:A:40:ALA:HB3	2:A:43:LYS:HB2	1.85	0.58
1:B:376:THR:HB	1:B:435:ALA:HB3	1.86	0.58
1:C:475:ALA:HB3	1:C:487:ASN:HB2	1.84	0.58
1:C:418:ILE:HA	1:C:422:ASN:HB2	1.85	0.58
1:E:356:LYS:HB3	1:E:397:ALA:HB3	1.86	0.58
1:C:394:ASN:HD21	1:C:520:ALA:HB3	1.67	0.57
1:E:176:LEU:HD23	1:E:207:HIS:CD2	2.38	0.57
1:B:703:ASN:OD1	1:B:704:SER:N	2.37	0.57
1:B:357:ARG:NH1	1:B:358:ILE:O	2.30	0.57
1:B:380:TYR:HD2	1:B:429:PHE:HD1	1.50	0.57
1:C:113:LYS:HG3	1:C:114:THR:HG23	1.86	0.57
2:D:6:GLU:OE2	2:D:92:CYS:N	2.36	0.57
1:C:319:ARG:NH2	1:E:740:MET:SD	2.78	0.57
2:A:6:GLU:OE2	2:A:92:CYS:N	2.33	0.57
1:C:508:TYR:OH	2:D:100(B):ASP:OD2	2.23	0.57
1:C:1091:ARG:NH1	1:C:1118:ASP:O	2.37	0.57
1:C:1100:THR:HG1	1:C:1101:HIS:HD1	1.49	0.57
2:A:63:VAL:HB	2:A:67:PHE:HB2	1.87	0.57
1:B:347:PHE:CD2	1:B:509:ARG:HD3	2.40	0.57
1:E:456:PHE:HB3	1:E:473:TYR:CD2	2.40	0.57
2:D:72:ASP:HB2	2:D:77:THR:O	2.04	0.57
1:E:417:LYS:HD2	1:E:455:LEU:HD12	1.86	0.57
1:B:357:ARG:HH22	1:B:395:VAL:H	1.52	0.56
1:C:381:GLY:HA3	1:C:430:THR:HA	1.86	0.56
1:E:29:THR:HG22	1:E:30:ASN:H	1.70	0.56
1:E:324:GLU:OE2	1:E:537:LYS:NZ	2.39	0.56
1:E:400:PHE:HE2	1:E:402:ILE:HD13	1.71	0.56
2:A:36:TRP:HZ2	2:A:78:VAL:HG22	1.71	0.56
1:B:106:PHE:HD1	1:B:235:ILE:HD11	1.71	0.56
1:C:555:SER:OG	1:C:584:ILE:O	2.22	0.56
2:A:19:ARG:HE	2:A:79:TYR:HB3	1.70	0.56
1:B:349:SER:O	1:B:353:TRP:N	2.39	0.56
1:B:401:VAL:HG22	1:B:509:ARG:HG3	1.86	0.56
1:C:391:CYS:N	1:C:525:CYS:SG	2.79	0.56
1:B:395:VAL:HG11	1:B:524:VAL:HB	1.87	0.55
2:D:22:CYS:SG	2:D:23:ALA:N	2.80	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:68:THR:HB	2:D:81:GLN:HB3	1.87	0.55
1:B:407:VAL:HG21	1:B:508:TYR:HD2	1.70	0.55
1:C:355:ARG:HG2	1:C:396:TYR:HB3	1.87	0.55
1:C:936:ASP:O	1:C:937:SER:C	2.49	0.55
1:E:36:VAL:HG11	1:E:220:PHE:CZ	2.41	0.55
1:E:361:CYS:H	1:E:524:VAL:HG12	1.70	0.55
3:T:2:NAG:H83	3:T:2:NAG:H3	1.88	0.55
1:E:160:TYR:HE1	1:E:163:ALA:HB2	1.71	0.55
1:B:334:ASN:ND2	1:B:361:CYS:HA	2.22	0.55
1:B:699:LEU:HB3	1:C:873:TYR:HE1	1.71	0.55
1:C:338:PHE:HA	1:C:341:VAL:HG12	1.89	0.55
2:D:19:ARG:HH21	2:D:79:TYR:HB2	1.72	0.55
1:E:375:SER:H	1:E:436:TRP:HB3	1.72	0.55
2:D:10:GLY:HA3	2:D:110:THR:H	1.72	0.55
1:B:276:LEU:HB3	1:B:289:VAL:HG22	1.88	0.55
1:B:555:SER:OG	1:B:584:ILE:O	2.22	0.55
1:E:350:VAL:HG21	1:E:418:ILE:HD12	1.89	0.55
1:E:99:ASN:O	1:E:102:ARG:NH2	2.31	0.55
1:E:675:GLN:OE1	1:E:690:GLN:N	2.39	0.55
1:B:348:ALA:HB1	1:B:353:TRP:HA	1.90	0.54
1:C:65:PHE:HB2	1:C:265:TYR:CD2	2.40	0.54
1:C:405:ASP:N	1:C:504:GLY:O	2.39	0.54
1:B:436:TRP:CE2	1:B:509:ARG:HB3	2.42	0.54
2:H:52(A):TRP:O	2:H:71:ARG:NH2	2.41	0.54
2:A:59:TYR:HB3	2:A:63:VAL:HG23	1.90	0.54
1:C:448:ASN:HB2	1:C:497:PHE:HB2	1.89	0.54
2:H:7:SER:HB2	2:H:21:SER:HB2	1.89	0.54
1:B:498:GLN:H	1:B:501:ASN:ND2	2.06	0.54
1:E:113:LYS:HG3	1:E:114:THR:HG23	1.87	0.54
1:B:434:ILE:HD13	1:B:511:VAL:HG23	1.90	0.54
1:B:331:ASN:HD22	3:J:1:NAG:C7	2.21	0.54
1:E:154:GLU:HA	1:E:245:HIS:NE2	2.23	0.54
1:C:28:TYR:CD2	6:C:1306:NAG:H62	2.43	0.54
2:D:19:ARG:HE	2:D:79:TYR:HB3	1.73	0.54
1:C:395:VAL:HA	1:C:514:SER:O	2.08	0.54
1:E:96:GLU:HG2	1:E:213:VAL:HG22	1.90	0.54
2:H:10:GLY:HA3	2:H:109:VAL:HG13	1.90	0.54
2:A:4:LEU:HD21	2:A:93:ALA:HA	1.88	0.54
2:D:40:ALA:HB3	2:D:43:LYS:HB2	1.89	0.53
2:A:38:ARG:O	2:A:46:LYS:N	2.42	0.53
2:D:2:VAL:HG23	2:D:3:GLN:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:51:ILE:HD13	2:H:57:ALA:HB2	1.90	0.53
1:B:618:THR:OG1	1:B:619:GLU:OE1	2.27	0.53
1:C:154:GLU:HA	1:C:245:HIS:HE2	1.73	0.53
1:E:126:VAL:HG13	1:E:174:PRO:HA	1.91	0.53
1:E:456:PHE:HD2	1:E:491:PRO:HA	1.74	0.53
1:E:128:ILE:HD13	1:E:170:TYR:HD2	1.73	0.53
1:B:605:SER:OG	1:B:606:ASN:N	2.42	0.53
1:C:472:ILE:HG22	1:C:490:PHE:HA	1.91	0.53
2:H:95:ASP:HA	2:H:101:ASP:HB2	1.90	0.53
1:B:498:GLN:OE1	1:B:501:ASN:ND2	2.42	0.53
1:E:377:PHE:CD1	1:E:434:ILE:HG12	2.44	0.53
1:C:901:GLN:HE21	1:C:905:ARG:HE	1.57	0.52
1:B:368:LEU:HB3	1:B:374:PHE:HE2	1.74	0.52
1:B:705:VAL:HB	1:C:883:THR:HG21	1.90	0.52
1:C:125:ASN:HA	1:C:174:PRO:HD3	1.92	0.52
1:E:1043:CYS:HB2	1:E:1064:HIS:CE1	2.44	0.52
1:E:186:PHE:HA	1:E:210:ILE:O	2.10	0.52
1:B:1002:GLN:O	1:B:1006:THR:HG23	2.09	0.52
1:C:451:TYR:HB2	1:C:495:TYR:CD2	2.45	0.52
1:B:334:ASN:HB3	1:B:362:VAL:HG22	1.90	0.52
1:B:503:VAL:HG21	2:A:100:TYR:CE2	2.44	0.52
1:C:353:TRP:CD1	1:C:353:TRP:H	2.28	0.52
1:B:350:VAL:HG21	1:B:422:ASN:HB3	1.90	0.52
1:B:748:GLU:OE1	1:B:748:GLU:N	2.38	0.52
1:C:353:TRP:HZ3	1:C:355:ARG:HH11	1.58	0.52
1:C:441:LEU:HD11	1:C:509:ARG:NH1	2.23	0.52
1:B:770:ILE:O	1:B:774:GLN:HG2	2.09	0.52
1:B:456:PHE:HB3	1:B:473:TYR:CD1	2.45	0.52
1:C:457:ARG:NH1	1:C:467:ASP:OD2	2.43	0.52
1:E:403:ARG:HG2	1:E:505:TYR:HA	1.91	0.52
2:A:22:CYS:SG	2:A:23:ALA:N	2.83	0.52
1:E:870:ILE:O	1:E:874:THR:HG23	2.10	0.52
2:H:87:THR:HB	2:H:110:THR:HA	1.92	0.52
1:B:298:GLU:O	1:B:302:THR:HG23	2.11	0.51
1:B:1088:HIS:HB3	1:B:1120:THR:CG2	2.40	0.51
1:C:380:TYR:HE1	2:D:97:GLY:HA2	1.73	0.51
2:D:51:ILE:HG13	2:D:54:GLY:HA2	1.92	0.51
1:B:330:PRO:HA	1:B:579:PRO:HB2	1.91	0.51
1:C:350:VAL:HG21	1:C:418:ILE:HG23	1.92	0.51
1:C:393:THR:HB	1:C:523:THR:HA	1.93	0.51
1:E:118:LEU:O	1:E:128:ILE:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:870:ILE:O	1:C:874:THR:HG23	2.10	0.51
1:E:456:PHE:O	1:E:491:PRO:HB3	2.11	0.51
1:E:457:ARG:NH2	1:E:466:ARG:O	2.43	0.51
2:D:47:PHE:HB2	2:D:100:TYR:HE1	1.75	0.51
1:C:518:LEU:HD12	1:C:520:ALA:H	1.76	0.51
2:H:61:ASP:O	2:H:64:LYS:NZ	2.43	0.51
1:E:425:LEU:HD13	1:E:429:PHE:CD1	2.46	0.51
1:B:389:ASP:OD1	1:B:390:LEU:N	2.43	0.51
1:C:328:ARG:HG3	1:C:579:PRO:HD2	1.91	0.51
1:E:276:LEU:HB3	1:E:289:VAL:HG22	1.93	0.51
1:B:436:TRP:O	1:B:508:TYR:HA	2.11	0.51
1:B:506:GLN:OE1	1:B:507:PRO:HD2	2.11	0.51
1:C:339:GLY:O	1:C:344:ALA:N	2.44	0.51
1:E:186:PHE:CA	1:E:210:ILE:O	2.59	0.51
2:A:34:MET:CE	2:A:92:CYS:HB2	2.41	0.51
1:B:726:ILE:HD13	1:B:945:LEU:HD13	1.91	0.51
1:C:136:CYS:SG	1:C:161:SER:OG	2.49	0.51
1:E:452:LEU:HG	1:E:494:SER:HA	1.92	0.51
1:B:96:GLU:OE2	1:B:190:ARG:NH1	2.44	0.51
1:E:96:GLU:HA	1:E:187:LYS:HE3	1.92	0.51
1:E:378:LYS:HZ3	2:H:100:TYR:HB3	1.76	0.51
2:A:100(B):ASP:OD1	2:A:100(B):ASP:N	2.44	0.51
1:B:993:ILE:O	1:B:997:ILE:HG12	2.11	0.50
2:H:37:PHE:HE2	2:H:93:ALA:HB3	1.75	0.50
1:E:187:LYS:HD2	1:E:188:ASN:N	2.26	0.50
1:E:444:LYS:HD3	1:E:448:ASN:ND2	2.26	0.50
1:E:729:VAL:HG22	1:E:1059:GLY:HA2	1.92	0.50
2:A:37:PHE:CE2	2:A:100:TYR:HA	2.46	0.50
1:B:394:ASN:OD1	1:B:518:LEU:N	2.45	0.50
1:B:444:LYS:HG2	1:B:448:ASN:HA	1.94	0.50
1:B:569:ILE:HD12	1:B:569:ILE:H	1.77	0.50
1:B:870:ILE:O	1:B:874:THR:HG23	2.12	0.50
1:E:392:PHE:CE2	1:E:515:PHE:HB3	2.47	0.50
2:H:82:MET:HE2	2:H:82(C):LEU:HD22	1.93	0.50
1:C:169:GLU:CD	1:C:171:VAL:HG23	2.37	0.50
2:H:40:ALA:HB3	2:H:43:LYS:HB2	1.92	0.50
1:B:340:GLU:O	1:B:344:ALA:N	2.45	0.50
1:E:308:VAL:HG22	1:E:602:THR:HG23	1.92	0.50
1:E:376:THR:HA	1:E:378:LYS:NZ	2.27	0.50
1:B:497:PHE:CZ	1:B:507:PRO:HB3	2.47	0.50
1:B:916:LEU:O	1:B:916:LEU:HG	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:994:ASP:O	1:C:998:THR:HG23	2.11	0.50
1:B:325:SER:HA	1:B:540:ASN:HB3	1.93	0.49
1:B:497:PHE:CD1	1:B:507:PRO:HD3	2.47	0.49
1:B:377:PHE:HB2	1:B:434:ILE:HG23	1.93	0.49
1:B:658:ASN:OD1	1:B:659:SER:N	2.42	0.49
1:E:437:ASN:HA	1:E:508:TYR:CD1	2.47	0.49
1:B:382:VAL:HG21	1:B:390:LEU:HD11	1.94	0.49
1:C:271:GLN:HB2	1:C:272:PRO:HD2	1.94	0.49
1:C:1088:HIS:HB3	1:C:1120:THR:CG2	2.42	0.49
1:E:30:ASN:HA	1:E:60:SER:O	2.13	0.49
1:B:392:PHE:HB2	1:B:515:PHE:HB3	1.93	0.49
1:B:400:PHE:CG	1:B:401:VAL:N	2.81	0.49
1:C:448:ASN:OD1	1:C:450:ASN:ND2	2.46	0.49
1:B:374:PHE:HA	1:B:436:TRP:CB	2.42	0.49
1:B:456:PHE:HB3	1:B:473:TYR:CG	2.47	0.49
1:C:627:ASP:OD2	1:C:627:ASP:N	2.45	0.49
1:B:131:CYS:HB2	1:B:133:PHE:CE2	2.47	0.49
1:C:327:VAL:HG22	1:C:542:ASN:HB3	1.94	0.49
2:A:17:SER:HB3	2:A:82(A):ASN:HA	1.93	0.49
2:D:36:TRP:O	2:D:48:VAL:HB	2.12	0.49
1:E:1073:LYS:HE3	1:E:1073:LYS:HB3	1.39	0.49
2:D:28:THR:HG21	2:D:31:LYS:HB3	1.95	0.49
1:B:318:PHE:CD2	1:B:623:ALA:HB1	2.48	0.49
1:B:516:GLU:N	1:B:516:GLU:OE2	2.46	0.48
1:C:99:ASN:O	1:C:102:ARG:NE	2.29	0.48
1:C:293:LEU:O	1:C:632:THR:OG1	2.30	0.48
2:A:87:THR:HA	2:A:109:VAL:O	2.12	0.48
1:B:447:GLY:HA2	1:B:498:GLN:HA	1.96	0.48
1:C:295:PRO:HG3	1:C:633:TRP:CE3	2.48	0.48
1:E:985:ASP:N	1:E:988:GLU:OE2	2.40	0.48
1:B:395:VAL:HG13	1:B:515:PHE:CE2	2.49	0.48
1:C:642:VAL:HG22	1:C:651:ILE:HG12	1.94	0.48
1:E:112:SER:H	1:E:134:GLN:HG2	1.77	0.48
1:E:231:ILE:HG22	1:E:233:ILE:HG23	1.95	0.48
1:B:172:SER:OG	1:B:173:GLN:N	2.46	0.48
1:C:298:GLU:O	1:C:302:THR:HG23	2.13	0.48
1:C:424:LYS:HE2	1:C:461:LEU:HB2	1.95	0.48
1:C:28:TYR:HD2	6:C:1306:NAG:H62	1.78	0.48
1:C:329:PHE:CE2	1:C:528:LYS:HB2	2.48	0.48
1:B:498:GLN:O	1:B:506:GLN:NE2	2.46	0.48
1:E:452:LEU:CB	1:E:492:LEU:HB3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:29:PHE:HD2	2:H:73:ASN:HA	1.78	0.48
1:B:543:PHE:O	1:B:545:GLY:N	2.44	0.48
1:E:921:LYS:HB3	1:E:921:LYS:HE2	1.44	0.48
1:B:287:ASP:OD1	1:B:288:ALA:N	2.45	0.48
1:B:328:ARG:HH21	1:B:580:GLN:HB2	1.79	0.48
1:B:401:VAL:HA	1:B:509:ARG:HA	1.96	0.48
1:C:403:ARG:NH2	1:C:406:GLU:OE2	2.43	0.48
1:E:186:PHE:CD1	1:E:211:ASN:HB3	2.48	0.48
1:B:675:GLN:O	1:B:676:THR:OG1	2.26	0.48
1:E:351:TYR:HB2	1:E:454:ARG:HH21	1.79	0.48
2:A:48:VAL:HG13	2:A:63:VAL:HG11	1.96	0.48
1:B:453:TYR:HE2	1:B:455:LEU:HD13	1.78	0.47
1:E:1050:MET:HE2	1:E:1052:PHE:CZ	2.48	0.47
1:B:87:ASN:HB2	1:B:269:TYR:HD1	1.79	0.47
1:E:447:GLY:HA2	1:E:497:PHE:C	2.39	0.47
2:H:52(A):TRP:NE1	2:H:96:ARG:O	2.42	0.47
2:H:95:ASP:OD2	2:H:96:ARG:N	2.47	0.47
2:D:100(A):GLY:O	2:D:100(D):MET:HE2	2.15	0.47
2:D:51:ILE:CG1	2:D:54:GLY:HA2	2.45	0.47
1:B:303:LEU:HD12	1:B:308:VAL:HG12	1.96	0.47
1:C:353:TRP:CZ2	1:C:466:ARG:HB2	2.49	0.47
2:D:52:SER:HB3	2:D:56:SER:HB2	1.96	0.47
1:B:319:ARG:HD3	1:C:740:MET:HE2	1.95	0.47
1:B:560:LEU:HB2	1:B:563:GLN:OE1	2.14	0.47
1:E:64:TRP:CH2	1:E:214:ARG:HG2	2.49	0.47
1:E:1129:VAL:HB	1:E:1132:ILE:HD11	1.95	0.47
1:B:365:TYR:O	1:B:368:LEU:HB2	2.15	0.47
1:C:438:SER:OG	1:C:442:ASP:OD2	2.24	0.47
1:C:543:PHE:O	1:C:545:GLY:N	2.43	0.47
1:E:454:ARG:NH2	1:E:467:ASP:O	2.48	0.47
1:E:491:PRO:O	1:E:493:GLN:NE2	2.48	0.47
1:E:922:LEU:O	1:E:926:GLN:HG3	2.14	0.47
1:E:993:ILE:O	1:E:997:ILE:HG23	2.14	0.47
1:E:458:LYS:HA	1:E:473:TYR:HE1	1.79	0.47
1:B:187:LYS:HA	1:B:210:ILE:O	2.15	0.47
1:B:366:SER:O	1:B:370:ASN:ND2	2.48	0.47
1:C:203:ILE:HB	1:C:227:VAL:HG12	1.97	0.47
1:C:391:CYS:HB2	1:C:515:PHE:CE2	2.50	0.47
1:B:419:ALA:HA	1:B:423:TYR:O	2.14	0.46
1:B:578:ASP:OD1	1:B:578:ASP:N	2.48	0.46
1:C:338:PHE:O	1:C:342:PHE:N	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:380:TYR:CE1	2:D:97:GLY:HA2	2.49	0.46
1:C:442:ASP:O	1:C:507:PRO:HG2	2.15	0.46
1:C:419:ALA:HA	1:C:423:TYR:O	2.15	0.46
1:E:410:ILE:HD13	1:E:419:ALA:HB2	1.97	0.46
1:C:141:LEU:HB2	1:C:243:ALA:HA	1.97	0.46
1:C:172:SER:OG	1:C:173:GLN:N	2.49	0.46
1:E:356:LYS:O	1:E:396:TYR:HA	2.15	0.46
2:D:29:PHE:CE2	2:D:71:ARG:HB2	2.51	0.46
1:B:453:TYR:CZ	1:B:493:GLN:HB3	2.49	0.46
1:C:353:TRP:CD1	1:C:466:ARG:HD3	2.50	0.46
1:E:349:SER:HB2	1:E:352:ALA:HB3	1.98	0.46
2:H:34:MET:HG2	2:H:71:ARG:NH1	2.30	0.46
1:B:383:SER:H	1:B:386:LYS:HZ2	1.64	0.46
1:B:383:SER:HB2	1:B:386:LYS:HE3	1.96	0.46
1:B:884:SER:O	1:B:884:SER:OG	2.34	0.46
2:H:16:GLY:H	2:H:82(C):LEU:HG	1.81	0.46
1:B:748:GLU:H	1:B:748:GLU:CD	2.20	0.46
1:B:1073:LYS:HB3	1:B:1073:LYS:HE3	1.49	0.46
1:C:376:THR:HG21	1:C:407:VAL:CG1	2.45	0.46
1:C:1073:LYS:HB3	1:C:1073:LYS:HE3	1.57	0.46
1:E:318:PHE:CD2	1:E:623:ALA:HB1	2.50	0.46
1:B:406:GLU:OE1	1:B:418:ILE:HG12	2.16	0.46
1:C:130:VAL:CG1	1:C:168:PHE:HB3	2.46	0.46
1:C:330:PRO:HA	1:C:579:PRO:HB2	1.97	0.46
2:H:4:LEU:HD13	2:H:24:ALA:HB2	1.97	0.46
2:H:87:THR:HG22	2:H:111:ALA:HB3	1.96	0.46
1:C:986:PRO:N	1:C:987:PRO:HD2	2.30	0.46
1:C:1088:HIS:HB3	1:C:1120:THR:HG21	1.98	0.46
1:E:304:LYS:HE2	1:E:304:LYS:HB3	1.80	0.46
1:C:434:ILE:O	1:C:510:VAL:HA	2.16	0.46
1:E:437:ASN:OD1	1:E:438:SER:N	2.49	0.46
1:C:441:LEU:HD11	1:C:509:ARG:HH12	1.81	0.46
1:C:1100:THR:HG1	1:C:1101:HIS:CE1	2.33	0.46
1:E:407:VAL:HG21	1:E:508:TYR:CE2	2.51	0.46
1:B:394:ASN:HD21	1:B:518:LEU:HB3	1.80	0.45
1:B:394:ASN:ND2	1:B:396:TYR:OH	2.49	0.45
2:H:2:VAL:HG23	2:H:3:GLN:HG3	1.98	0.45
1:B:406:GLU:OE1	1:B:417:LYS:HB3	2.17	0.45
1:C:132:GLU:HB3	1:C:164:ASN:O	2.16	0.45
1:C:395:VAL:HG12	1:C:513:LEU:HD22	1.97	0.45
1:C:410:ILE:HG22	1:C:433:VAL:HG11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:59:TYR:HB2	2:H:64:LYS:HB3	1.97	0.45
1:B:911:VAL:HG12	1:B:915:VAL:HG21	1.97	0.45
1:E:415:THR:OG1	1:E:416:GLY:N	2.49	0.45
1:E:422:ASN:ND2	1:E:467:ASP:OD2	2.50	0.45
1:C:361:CYS:H	1:C:524:VAL:HG11	1.81	0.45
1:C:376:THR:HG23	1:C:378:LYS:HE2	1.99	0.45
2:D:52:SER:OG	2:D:55:ASP:N	2.49	0.45
1:B:380:TYR:HE1	2:A:52(A):TRP:CH2	2.34	0.45
1:C:304:LYS:HE2	1:C:304:LYS:HB3	1.79	0.45
1:E:352:ALA:HA	1:E:468:ILE:HD11	1.99	0.45
1:E:985:ASP:OD2	1:E:987:PRO:HD2	2.16	0.45
2:A:24:ALA:HB3	2:A:29:PHE:HD2	1.82	0.45
2:A:51:ILE:HD12	2:A:57:ALA:HB2	1.97	0.45
1:B:111:ASP:CG	1:B:112:SER:H	2.25	0.45
1:B:394:ASN:HB3	1:B:396:TYR:CE2	2.52	0.45
1:B:1141:LEU:HD23	1:B:1145:LEU:HB2	1.97	0.45
1:C:299:THR:HG22	1:C:315:THR:HG21	1.98	0.45
1:C:329:PHE:HE2	1:C:528:LYS:HD2	1.81	0.45
1:E:936:ASP:O	1:E:937:SER:C	2.59	0.45
2:H:2:VAL:N	2:H:26:GLY:HA3	2.32	0.45
2:D:21:SER:HA	2:D:79:TYR:HD1	1.81	0.45
2:D:29:PHE:O	2:D:71:ARG:NH2	2.50	0.45
2:D:72:ASP:OD2	2:D:77:THR:HG23	2.17	0.45
1:B:27:ALA:O	1:B:64:TRP:HB3	2.17	0.45
1:C:426:PRO:HA	1:C:463:PRO:HB3	1.99	0.45
1:C:33:THR:HG22	1:C:58:PHE:CD2	2.52	0.45
1:C:187:LYS:HD2	1:C:188:ASN:N	2.32	0.45
1:E:166:CYS:HB3	1:E:169:GLU:OE2	2.17	0.45
1:E:1116:THR:HG22	1:E:1117:THR:H	1.82	0.45
2:H:47:PHE:HB2	2:H:100:TYR:H	1.82	0.45
1:B:501:ASN:HB2	1:B:506:GLN:HG2	2.00	0.44
1:C:93:ALA:HB1	1:C:189:LEU:HD11	1.98	0.44
1:E:447:GLY:HA3	1:E:449:TYR:CE2	2.52	0.44
2:A:4:LEU:HD23	2:A:103:TRP:C	2.41	0.44
1:B:338:PHE:HA	1:B:341:VAL:HG12	1.98	0.44
1:C:129:LYS:HG2	1:C:169:GLU:HG2	2.00	0.44
1:C:351:TYR:CE1	1:C:452:LEU:HB2	2.52	0.44
1:C:457:ARG:NE	1:C:459:SER:O	2.43	0.44
1:C:467:ASP:OD1	1:C:467:ASP:N	2.50	0.44
1:E:96:GLU:HB2	1:E:187:LYS:HB3	2.00	0.44
1:E:125:ASN:HA	1:E:174:PRO:HD3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:581:THR:OG1	1:E:583:GLU:HG2	2.17	0.44
1:C:776:LYS:NZ	1:C:780:GLU:OE2	2.41	0.44
1:E:454:ARG:HH22	1:E:492:LEU:HD11	1.82	0.44
2:A:6:GLU:HG3	2:A:106:GLY:H	1.82	0.44
1:B:369:TYR:HE2	1:B:388:ASN:ND2	2.16	0.44
1:B:369:TYR:HE2	1:B:388:ASN:HD21	1.66	0.44
1:B:1090:PRO:HD3	1:B:1095:PHE:CE2	2.53	0.44
1:C:389:ASP:OD1	1:C:389:ASP:N	2.48	0.44
1:E:1130:ILE:O	1:E:1130:ILE:HG13	2.18	0.44
2:H:100(B):ASP:OD2	2:H:100(C):PHE:N	2.51	0.44
1:B:382:VAL:HG22	1:B:386:LYS:HG3	1.98	0.44
1:B:755:GLN:O	1:E:968:SER:OG	2.35	0.44
1:E:368:LEU:HA	1:E:374:PHE:HE2	1.83	0.44
1:E:425:LEU:HD13	1:E:429:PHE:HD1	1.83	0.44
1:E:454:ARG:HH11	1:E:491:PRO:HB2	1.81	0.44
1:E:514:SER:C	1:E:515:PHE:HD1	2.25	0.44
2:H:10:GLY:H	2:H:109:VAL:HA	1.83	0.44
1:B:425:LEU:HD23	1:B:425:LEU:HA	1.89	0.44
1:B:461:LEU:HD21	1:B:467:ASP:HB3	2.00	0.44
1:C:117:LEU:HD11	1:C:231:ILE:HG13	2.00	0.44
1:C:295:PRO:O	1:C:299:THR:HG23	2.17	0.44
1:C:374:PHE:HA	1:C:436:TRP:HB2	1.99	0.44
1:E:129:LYS:HB3	1:E:129:LYS:HE3	1.79	0.44
1:E:405:ASP:N	1:E:504:GLY:O	2.50	0.44
2:H:37:PHE:O	2:H:90:TYR:HA	2.18	0.44
1:B:379:CYS:HB2	1:B:384:PRO:HD3	1.99	0.44
1:C:344:ALA:O	1:C:509:ARG:NH1	2.50	0.44
1:C:466:ARG:HD2	1:C:468:ILE:HD11	1.99	0.44
2:A:48:VAL:HG13	2:A:63:VAL:HG21	1.99	0.44
1:B:901:GLN:HE21	1:B:905:ARG:HE	1.65	0.44
1:C:231:ILE:HG22	1:C:233:ILE:HG23	2.00	0.44
1:C:383:SER:HB3	1:C:386:LYS:HG2	1.99	0.44
2:D:33:ALA:HB2	2:D:52(A):TRP:HD1	1.82	0.44
1:B:959:LEU:HD23	1:B:959:LEU:HA	1.83	0.43
1:C:153:MET:O	1:C:245:HIS:NE2	2.47	0.43
1:C:228:ASP:OD1	1:C:229:LEU:N	2.51	0.43
2:H:3:GLN:NE2	2:H:25:SER:H	2.16	0.43
1:B:357:ARG:HH22	1:B:395:VAL:N	2.16	0.43
1:C:452:LEU:HG	1:C:494:SER:HA	2.00	0.43
1:E:485:GLY:N	1:E:488:CYS:SG	2.91	0.43
2:A:61:ASP:HA	2:A:64:LYS:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:ASP:HA	1:B:527:PRO:HD3	2.00	0.43
1:E:332:ILE:HG21	1:E:527:PRO:O	2.17	0.43
1:E:748:GLU:OE1	1:E:748:GLU:N	2.44	0.43
1:C:106:PHE:CD1	1:C:235:ILE:HD11	2.52	0.43
1:C:395:VAL:HG12	1:C:395:VAL:O	2.18	0.43
2:D:54:GLY:HA3	2:D:71:ARG:HD3	2.01	0.43
1:B:128:ILE:HD13	1:B:170:TYR:HD2	1.82	0.43
1:B:368:LEU:HB3	1:B:374:PHE:CE2	2.51	0.43
1:B:592:PHE:CE2	1:C:857:GLY:HA2	2.54	0.43
1:B:29:THR:HG22	1:B:30:ASN:H	1.84	0.43
1:B:365:TYR:HB2	1:B:388:ASN:HD21	1.84	0.43
1:B:502:GLY:O	1:B:506:GLN:HB2	2.19	0.43
1:B:1116:THR:HG22	1:B:1117:THR:N	2.34	0.43
1:C:96:GLU:O	1:C:187:LYS:HE3	2.19	0.43
1:C:102:ARG:HA	1:C:102:ARG:HD3	1.82	0.43
1:C:376:THR:HB	1:C:435:ALA:HB3	2.01	0.43
1:E:1028:LYS:NZ	1:E:1042:PHE:O	2.52	0.43
2:D:60:ALA:HB3	2:D:63:VAL:HG22	2.00	0.43
2:D:82:MET:SD	2:D:109:VAL:HG11	2.58	0.43
1:B:373:SER:O	1:B:436:TRP:HB2	2.18	0.43
1:B:453:TYR:CE2	1:B:455:LEU:HB2	2.54	0.43
1:C:83:VAL:HA	1:C:239:GLN:OE1	2.19	0.43
1:B:384:PRO:HD2	2:A:56:SER:OG	2.19	0.43
1:B:1116:THR:HG22	1:B:1117:THR:H	1.81	0.43
1:E:337:PRO:HB2	1:E:340:GLU:HG2	2.00	0.43
1:E:900:MET:HE3	1:E:900:MET:HB3	1.81	0.43
2:H:10:GLY:HA2	2:H:18:LEU:HD13	2.01	0.43
2:D:34:MET:O	2:D:51:ILE:HG22	2.19	0.43
2:D:73:ASN:N	2:D:73:ASN:OD1	2.52	0.43
1:C:376:THR:HA	2:D:100:TYR:O	2.19	0.43
2:H:36:TRP:O	2:H:48:VAL:HB	2.18	0.43
1:E:188:ASN:HA	1:E:208:THR:O	2.19	0.43
1:E:447:GLY:HA2	1:E:497:PHE:O	2.19	0.43
1:B:87:ASN:HB2	1:B:269:TYR:CD1	2.54	0.42
1:B:367:VAL:HG13	1:B:368:LEU:HD12	2.01	0.42
1:B:392:PHE:O	1:B:395:VAL:HG22	2.19	0.42
1:C:29:THR:O	1:C:61:ASN:HA	2.19	0.42
1:C:329:PHE:HB3	1:C:330:PRO:HD2	2.01	0.42
1:C:406:GLU:O	1:C:409:GLN:CB	2.66	0.42
1:E:461:LEU:HA	1:E:461:LEU:HD23	1.78	0.42
2:H:82(C):LEU:HB3	2:H:111:ALA:HB1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:PRO:HD3	1:B:544:ASN:HB3	2.01	0.42
1:E:1050:MET:HE2	1:E:1052:PHE:CE1	2.54	0.42
2:H:10:GLY:H	2:H:109:VAL:HG22	1.84	0.42
1:C:328:ARG:HD2	1:C:580:GLN:CG	2.49	0.42
1:C:473:TYR:N	1:C:488:CYS:O	2.52	0.42
1:C:989:ALA:O	1:C:993:ILE:HG12	2.18	0.42
1:E:453:TYR:O	1:E:492:LEU:HA	2.19	0.42
1:E:1145:LEU:O	1:E:1149:LYS:HA	2.20	0.42
2:H:17:SER:HA	2:H:82(A):ASN:HA	2.01	0.42
2:H:30:SER:HA	2:H:71:ARG:NH2	2.35	0.42
1:C:332:ILE:H	1:C:332:ILE:HD12	1.84	0.42
1:C:752:LEU:O	1:C:755:GLN:HG2	2.18	0.42
1:E:371:SER:O	1:E:371:SER:OG	2.34	0.42
2:H:45:ARG:HD3	2:H:103:TRP:CH2	2.54	0.42
2:A:33:ALA:HB1	2:A:98:MET:HB3	2.01	0.42
1:B:898:PHE:N	1:B:899:PRO:HD2	2.35	0.42
1:C:57:PRO:HG3	1:C:273:ARG:HD3	2.01	0.42
1:E:95:THR:OG1	1:E:96:GLU:N	2.52	0.42
1:E:357:ARG:CZ	1:E:359:SER:HB3	2.49	0.42
1:B:497:PHE:CE2	1:B:507:PRO:HB3	2.54	0.42
1:B:1045:LYS:O	1:B:1066:THR:HG21	2.20	0.42
1:C:444:LYS:HG2	1:C:448:ASN:HA	2.00	0.42
1:E:121:ASN:OD1	1:E:122:ASN:N	2.52	0.42
1:B:436:TRP:HZ3	1:B:511:VAL:HG22	1.85	0.42
1:C:111:ASP:C	1:C:134:GLN:HA	2.45	0.42
1:E:31:SER:O	1:E:59:PHE:HA	2.20	0.42
1:E:418:ILE:HD13	1:E:418:ILE:HA	1.88	0.42
1:E:472:ILE:HA	1:E:491:PRO:HD3	2.02	0.42
1:E:994:ASP:HA	1:E:997:ILE:HG12	2.01	0.42
2:H:67:PHE:CZ	2:H:82:MET:HG3	2.55	0.42
2:A:66:ARG:HG3	2:A:67:PHE:CD1	2.54	0.42
1:B:32:PHE:CG	1:B:218:GLN:HG2	2.55	0.42
1:B:616:ASN:HD22	6:B:1303:NAG:C7	2.32	0.42
1:C:392:PHE:H	1:C:515:PHE:HD2	1.66	0.42
1:E:27:ALA:O	1:E:64:TRP:HB3	2.19	0.42
2:H:59:TYR:HB3	2:H:63:VAL:HG23	2.02	0.42
2:A:82:MET:HB3	2:A:82(C):LEU:HD21	2.02	0.42
2:A:95:ASP:OD1	2:A:100(D):MET:HA	2.20	0.42
2:D:26:GLY:O	2:D:27:LEU:HD22	2.20	0.42
2:D:69:ILE:HG23	2:D:69:ILE:O	2.20	0.42
1:C:342:PHE:HB2	6:C:1309:NAG:H82	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:898:PHE:N	1:E:899:PRO:HD2	2.35	0.42
1:E:989:ALA:O	1:E:993:ILE:HG12	2.20	0.42
2:H:22:CYS:HB3	2:H:78:VAL:CG1	2.50	0.42
1:B:1086:LYS:HE3	1:B:1086:LYS:HB2	1.82	0.41
1:B:1088:HIS:HB3	1:B:1120:THR:HG21	2.01	0.41
1:C:87:ASN:HB2	1:C:269:TYR:HE1	1.85	0.41
1:C:241:LEU:HD23	1:C:241:LEU:HA	1.86	0.41
1:B:429:PHE:CE2	1:B:464:PHE:HZ	2.38	0.41
1:B:493:GLN:CD	1:B:494:SER:H	2.28	0.41
1:C:105:ILE:HD11	1:C:241:LEU:HD21	2.02	0.41
1:E:377:PHE:HD1	1:E:434:ILE:HG23	1.84	0.41
1:E:409:GLN:CD	1:E:417:LYS:H	2.28	0.41
1:E:748:GLU:HG3	1:E:981:LEU:HD21	2.02	0.41
2:H:33:ALA:HA	2:H:71:ARG:HH12	1.85	0.41
1:C:546:LEU:H	1:C:546:LEU:HD23	1.85	0.41
1:C:767:LEU:HD23	1:C:767:LEU:HA	1.88	0.41
1:C:985:ASP:HB3	1:C:987:PRO:HD2	2.02	0.41
1:E:983:ARG:O	1:E:984:LEU:HD22	2.21	0.41
2:A:34:MET:HG3	2:A:93:ALA:O	2.21	0.41
1:B:295:PRO:HG3	1:B:633:TRP:CZ3	2.55	0.41
1:B:374:PHE:HD1	1:B:436:TRP:HB3	1.86	0.41
1:C:105:ILE:HB	1:C:239:GLN:HB2	2.01	0.41
1:C:322:PRO:HA	1:C:538:CYS:O	2.20	0.41
1:E:466:ARG:NE	1:E:468:ILE:HD12	2.35	0.41
2:D:19:ARG:HA	2:D:19:ARG:HD2	1.92	0.41
1:B:980:ILE:O	1:B:984:LEU:HB2	2.20	0.41
1:C:331:ASN:HB2	1:C:580:GLN:HA	2.02	0.41
1:B:106:PHE:HB3	1:B:235:ILE:HD12	2.03	0.41
1:E:390:LEU:HD12	1:E:390:LEU:O	2.21	0.41
1:E:605:SER:OG	1:E:606:ASN:N	2.54	0.41
1:E:1116:THR:HG22	1:E:1117:THR:N	2.35	0.41
2:H:29:PHE:HE2	2:H:71:ARG:HB2	1.86	0.41
1:B:461:LEU:HD22	1:B:465:GLU:HB3	2.02	0.41
1:C:399:SER:HB2	1:C:511:VAL:HG12	2.03	0.41
1:C:921:LYS:HB3	1:C:921:LYS:HE3	1.31	0.41
2:A:49:ALA:HB1	2:A:69:ILE:HD12	2.02	0.41
1:B:395:VAL:O	1:B:395:VAL:HG12	2.21	0.41
1:C:134:GLN:CG	1:C:161:SER:HB3	2.50	0.41
1:E:418:ILE:HD11	1:E:453:TYR:HB2	2.02	0.41
1:E:441:LEU:O	1:E:444:LYS:NZ	2.29	0.41
1:B:383:SER:H	1:B:386:LYS:NZ	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:395:VAL:HG13	1:B:515:PHE:HE2	1.85	0.41
1:C:53:ASP:HB3	1:C:55:PHE:CE1	2.56	0.41
1:C:340:GLU:HA	1:C:344:ALA:HB2	2.03	0.41
1:C:405:ASP:OD1	1:C:406:GLU:HG3	2.20	0.41
1:C:578:ASP:HA	1:C:579:PRO:HD3	1.89	0.41
1:E:201:PHE:O	1:E:228:ASP:HA	2.20	0.41
1:E:537:LYS:HB3	1:E:537:LYS:HE2	1.75	0.41
2:H:37:PHE:CE2	2:H:93:ALA:HB3	2.56	0.41
2:A:96:ARG:HD2	2:A:96:ARG:HA	1.93	0.41
2:D:66:ARG:HB2	2:D:82(A):ASN:O	2.21	0.41
1:C:191:GLU:O	1:C:205:SER:HA	2.20	0.41
1:C:408:ARG:H	1:C:408:ARG:HD3	1.86	0.41
1:C:605:SER:OG	1:C:606:ASN:N	2.54	0.41
1:C:898:PHE:N	1:C:899:PRO:HD2	2.36	0.41
1:E:83:VAL:HG22	1:E:239:GLN:HG3	2.03	0.41
2:H:74:ALA:O	2:H:75:ARG:HG2	2.19	0.41
2:A:34:MET:SD	2:A:78:VAL:HG21	2.61	0.41
1:B:29:THR:HG22	1:B:30:ASN:N	2.36	0.40
1:B:506:GLN:CD	1:B:507:PRO:HD2	2.46	0.40
1:C:318:PHE:CD2	1:C:623:ALA:HB1	2.56	0.40
1:E:87:ASN:HB2	1:E:269:TYR:CE1	2.56	0.40
1:B:352:ALA:HA	1:B:466:ARG:HE	1.85	0.40
1:B:434:ILE:HG22	1:B:436:TRP:HE3	1.87	0.40
2:A:23:ALA:HB1	2:A:76:ASN:OD1	2.20	0.40
2:A:24:ALA:O	2:A:76:ASN:ND2	2.54	0.40
1:B:64:TRP:CD1	1:B:266:TYR:CE1	3.10	0.40
1:B:350:VAL:O	1:B:353:TRP:HD1	2.04	0.40
1:C:328:ARG:HD2	1:C:580:GLN:HG2	2.04	0.40
1:C:364:ASP:HA	1:C:526:GLY:HA3	2.02	0.40
1:E:404:GLY:H	1:E:506:GLN:N	2.19	0.40
2:A:51:ILE:HB	2:A:69:ILE:HD13	2.02	0.40
1:B:187:LYS:HA	1:B:187:LYS:HD2	1.90	0.40
1:B:323:THR:HG1	1:B:324:GLU:CD	2.19	0.40
1:C:369:TYR:HE1	1:C:377:PHE:CZ	2.39	0.40
1:C:405:ASP:O	1:C:408:ARG:NH2	2.54	0.40
1:C:453:TYR:O	1:C:492:LEU:HA	2.21	0.40
1:E:65:PHE:CE1	1:E:82:PRO:HG2	2.56	0.40
2:H:29:PHE:HB2	2:H:76:ASN:HA	2.03	0.40
2:H:67:PHE:CD2	2:H:80:LEU:HD21	2.56	0.40
2:A:18:LEU:HD23	2:A:19:ARG:N	2.37	0.40
1:B:578:ASP:OD2	1:B:581:THR:HB	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:560:LEU:O	1:C:562:PHE:N	2.55	0.40
1:C:984:LEU:HD13	1:C:988:GLU:OE1	2.22	0.40
1:E:186:PHE:N	1:E:210:ILE:O	2.55	0.40
1:E:534:VAL:HG23	1:E:539:VAL:HG21	2.02	0.40
2:H:40:ALA:HB3	2:H:43:LYS:H	1.86	0.40
2:A:6:GLU:HG3	2:A:106:GLY:N	2.37	0.40
2:A:24:ALA:C	2:A:76:ASN:HD21	2.30	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	B	1022/1288 (79%)	951 (93%)	71 (7%)	0	100	100
1	C	1024/1288 (80%)	947 (92%)	77 (8%)	0	100	100
1	E	1028/1288 (80%)	966 (94%)	62 (6%)	0	100	100
2	A	118/131 (90%)	106 (90%)	12 (10%)	0	100	100
2	D	118/131 (90%)	106 (90%)	12 (10%)	0	100	100
2	H	118/131 (90%)	112 (95%)	6 (5%)	0	100	100
All	All	3428/4257 (80%)	3188 (93%)	240 (7%)	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	B	898/1116 (80%)	893 (99%)	5 (1%)	78	88
1	C	900/1116 (81%)	884 (98%)	16 (2%)	51	72
1	E	903/1116 (81%)	893 (99%)	10 (1%)	65	80
2	A	92/100 (92%)	92 (100%)	0	100	100
2	D	92/100 (92%)	92 (100%)	0	100	100
2	H	92/100 (92%)	92 (100%)	0	100	100
All	All	2977/3648 (82%)	2946 (99%)	31 (1%)	65	81

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	821	LEU
1	B	895	GLN
1	B	916	LEU
1	B	943	SER
1	B	1073	LYS
1	C	814	LYS
1	C	820	ASP
1	C	821	LEU
1	C	853	GLN
1	C	895	GLN
1	C	915	VAL
1	C	916	LEU
1	C	921	LYS
1	C	934	ILE
1	C	936	ASP
1	C	937	SER
1	C	939	SER
1	C	940	SER
1	C	943	SER
1	C	945	LEU
1	C	1073	LYS
1	E	810	SER
1	E	820	ASP
1	E	895	GLN
1	E	915	VAL
1	E	916	LEU
1	E	921	LYS
1	E	935	GLN

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Mol	Chain	Res	Type
1	E	936	ASP
1	E	945	LEU
1	E	1073	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	414	GLN
1	B	501	ASN
1	B	564	GLN
1	B	655	HIS
1	B	804	GLN
1	B	1010	GLN
1	B	1011	GLN
1	C	30	ASN
1	C	66	HIS
1	C	394	ASN
1	C	409	GLN
1	C	506	GLN
1	C	804	GLN
1	C	856	ASN
1	C	901	GLN
1	C	1071	GLN
1	E	188	ASN
1	E	207	HIS
1	E	448	ASN
1	E	501	ASN
1	E	506	GLN
1	E	628	GLN
1	E	658	ASN
1	E	703	ASN
1	E	751	ASN
1	E	764	ASN
1	E	901	GLN
1	E	1011	GLN
2	D	76	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

36 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	F	1	3,1	14,14,15	0.21	0	17,19,21	0.53	0
3	NAG	F	2	3	14,14,15	0.20	0	17,19,21	0.45	0
4	NAG	G	1	4,1	14,14,15	0.23	0	17,19,21	0.51	0
4	NAG	G	2	4	14,14,15	0.24	0	17,19,21	0.48	0
4	BMA	G	3	4	11,11,12	0.56	0	15,15,17	0.64	0
3	NAG	I	1	3,1	14,14,15	0.24	0	17,19,21	0.47	0
3	NAG	I	2	3	14,14,15	0.20	0	17,19,21	0.47	0
3	NAG	J	1	3,1	14,14,15	0.43	0	17,19,21	0.46	0
3	NAG	J	2	3	14,14,15	0.30	0	17,19,21	0.53	0
3	NAG	K	1	3,1	14,14,15	0.17	0	17,19,21	0.45	0
3	NAG	K	2	3	14,14,15	0.19	0	17,19,21	0.48	0
3	NAG	L	1	3,1	14,14,15	0.25	0	17,19,21	0.54	0
3	NAG	L	2	3	14,14,15	0.19	0	17,19,21	0.43	0
3	NAG	M	1	3,1	14,14,15	0.21	0	17,19,21	0.51	0
3	NAG	M	2	3	14,14,15	0.20	0	17,19,21	0.45	0
3	NAG	N	1	3,1	14,14,15	0.24	0	17,19,21	0.50	0
3	NAG	N	2	3	14,14,15	0.19	0	17,19,21	0.51	0
3	NAG	O	1	3,1	14,14,15	0.16	0	17,19,21	0.48	0
3	NAG	O	2	3	14,14,15	0.22	0	17,19,21	0.46	0
3	NAG	P	1	3,1	14,14,15	0.33	0	17,19,21	0.61	0
3	NAG	P	2	3	14,14,15	0.29	0	17,19,21	0.53	0
3	NAG	Q	1	3,1	14,14,15	0.16	0	17,19,21	0.60	0
3	NAG	Q	2	3	14,14,15	0.20	0	17,19,21	0.44	0
5	NAG	R	1	5,1	14,14,15	0.29	0	17,19,21	0.49	0
5	BMA	R	2	5	11,11,12	0.58	0	15,15,17	0.62	0
4	NAG	S	1	4,1	14,14,15	0.26	0	17,19,21	0.50	0
4	NAG	S	2	4	14,14,15	0.26	0	17,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BMA	S	3	4	11,11,12	0.54	0	15,15,17	0.69	0
3	NAG	T	1	3,1	14,14,15	0.28	0	17,19,21	0.53	0
3	NAG	T	2	3	14,14,15	0.45	0	17,19,21	1.34	2 (11%)
4	NAG	U	1	4,1	14,14,15	0.22	0	17,19,21	0.52	0
4	NAG	U	2	4	14,14,15	0.18	0	17,19,21	0.47	0
4	BMA	U	3	4	11,11,12	0.56	0	15,15,17	0.73	0
4	NAG	V	1	4,1	14,14,15	0.35	0	17,19,21	0.51	0
4	NAG	V	2	4	14,14,15	0.22	0	17,19,21	0.45	0
4	BMA	V	3	4	11,11,12	0.65	0	15,15,17	0.97	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
4	NAG	G	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	NAG	J	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	NAG	K	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	2/6/23/26	0/1/1/1
3	NAG	L	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	L	2	3	-	2/6/23/26	0/1/1/1
3	NAG	M	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	2/6/23/26	0/1/1/1
3	NAG	N	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	0/6/23/26	0/1/1/1
3	NAG	O	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	O	2	3	-	0/6/23/26	0/1/1/1
3	NAG	P	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	P	2	3	-	3/6/23/26	0/1/1/1
3	NAG	Q	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	R	1	5,1	-	2/6/23/26	0/1/1/1
5	BMA	R	2	5	-	0/2/19/22	0/1/1/1
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	2/6/23/26	0/1/1/1
4	BMA	S	3	4	-	2/2/19/22	0/1/1/1
3	NAG	T	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	T	2	3	-	6/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1
4	BMA	U	3	4	-	2/2/19/22	0/1/1/1
4	NAG	V	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	V	2	4	-	1/6/23/26	0/1/1/1
4	BMA	V	3	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	2	NAG	C2-N2-C7	4.60	129.07	122.90
3	T	2	NAG	C1-C2-N2	2.11	113.77	110.43

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	J	1	NAG	C4-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
3	L	2	NAG	O5-C5-C6-O6
4	U	3	BMA	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
4	G	2	NAG	C4-C5-C6-O6
3	L	2	NAG	C4-C5-C6-O6
4	U	3	BMA	C4-C5-C6-O6
3	P	1	NAG	C8-C7-N2-C2
3	P	1	NAG	O7-C7-N2-C2
3	P	2	NAG	C8-C7-N2-C2
3	P	2	NAG	O7-C7-N2-C2
3	T	2	NAG	C8-C7-N2-C2
3	T	2	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	V	1	NAG	C4-C5-C6-O6
3	P	1	NAG	O5-C5-C6-O6
4	S	3	BMA	C4-C5-C6-O6
3	T	2	NAG	O5-C5-C6-O6
4	S	3	BMA	O5-C5-C6-O6
4	V	1	NAG	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	P	1	NAG	C4-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	O	1	NAG	C4-C5-C6-O6
3	O	1	NAG	O5-C5-C6-O6
3	P	2	NAG	O5-C5-C6-O6
3	F	1	NAG	C1-C2-N2-C7
3	L	1	NAG	C1-C2-N2-C7
3	Q	1	NAG	C1-C2-N2-C7
3	T	1	NAG	C1-C2-N2-C7
5	R	1	NAG	C1-C2-N2-C7
4	U	1	NAG	C4-C5-C6-O6
3	M	2	NAG	C4-C5-C6-O6
3	F	1	NAG	C3-C2-N2-C7
3	L	1	NAG	C3-C2-N2-C7
3	Q	1	NAG	C3-C2-N2-C7
3	T	1	NAG	C3-C2-N2-C7
5	R	1	NAG	C3-C2-N2-C7
3	K	2	NAG	C4-C5-C6-O6
4	S	2	NAG	C4-C5-C6-O6
3	M	2	NAG	O5-C5-C6-O6
3	J	1	NAG	C1-C2-N2-C7
3	T	2	NAG	C1-C2-N2-C7
3	T	2	NAG	C3-C2-N2-C7
4	S	2	NAG	O5-C5-C6-O6
3	T	2	NAG	C4-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
4	V	2	NAG	C4-C5-C6-O6
3	K	2	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

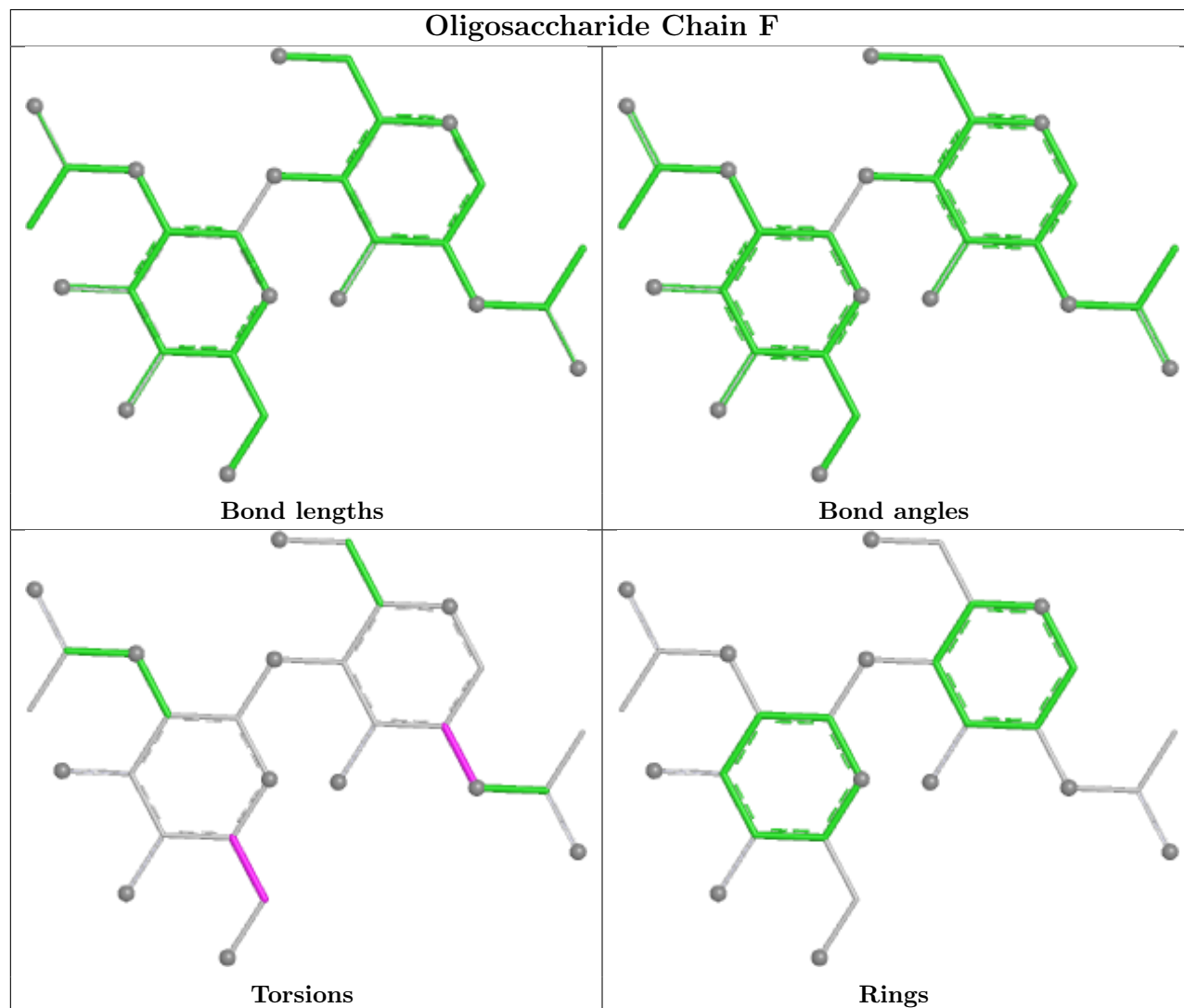
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	T	2	NAG	1	0

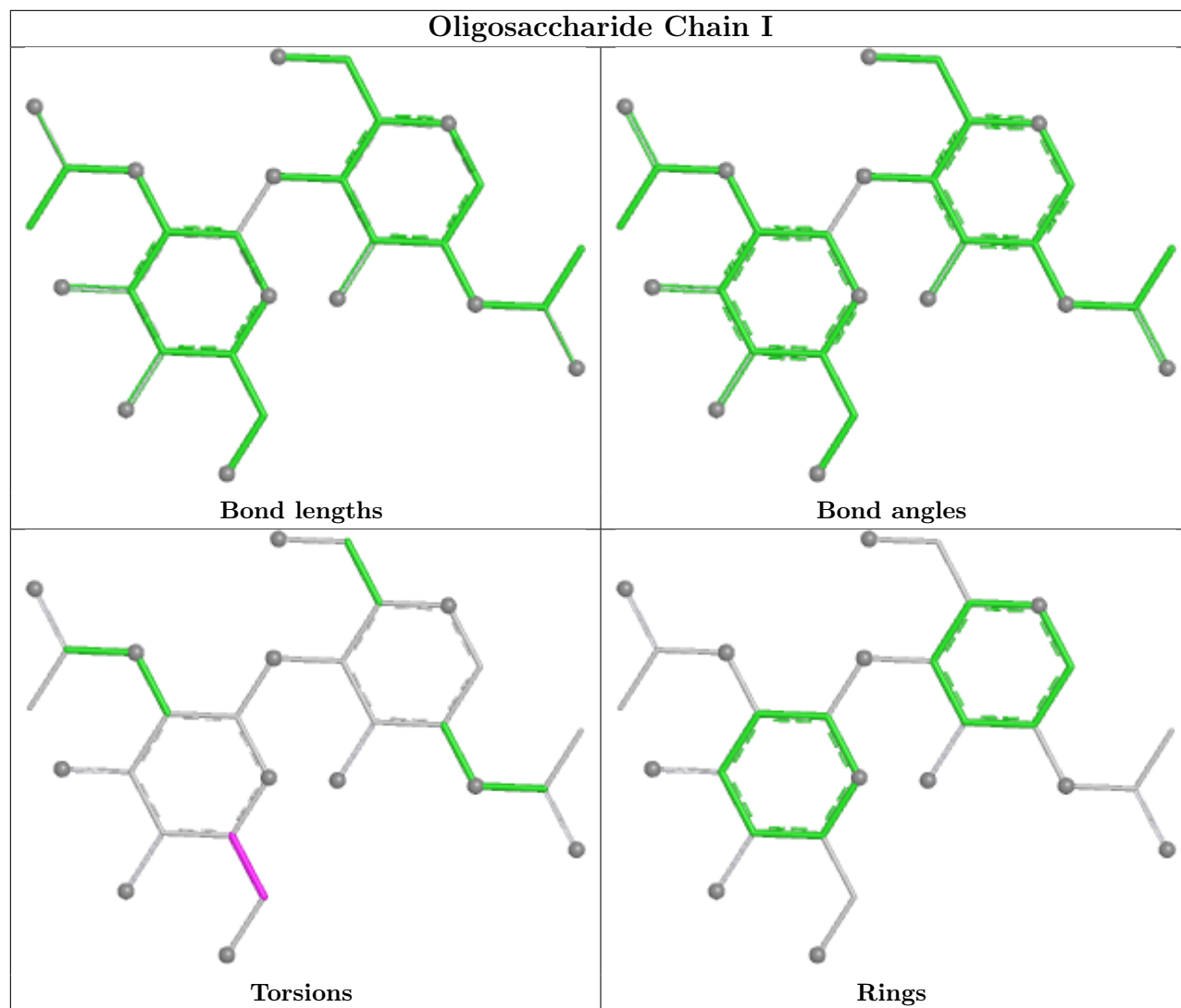
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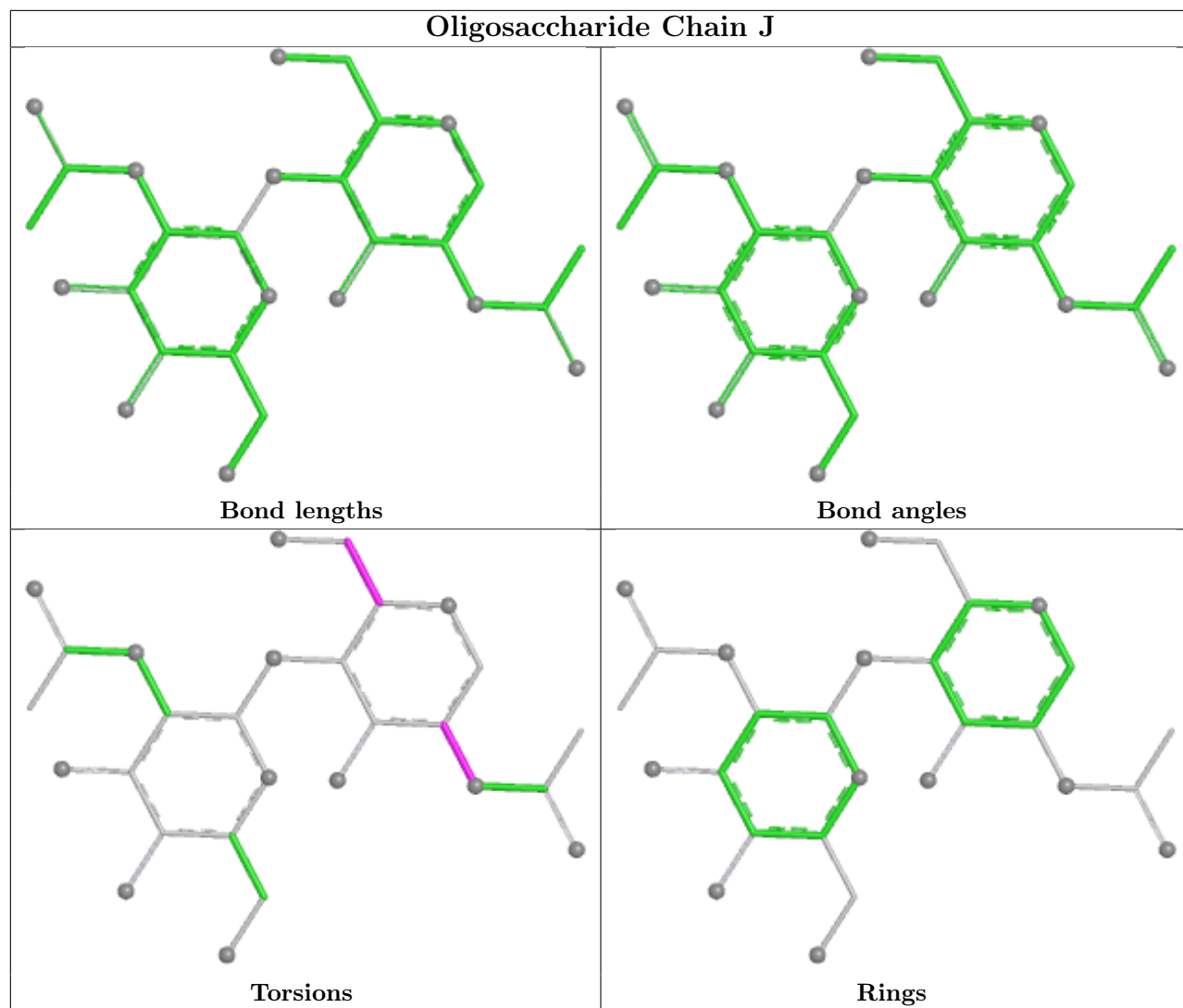
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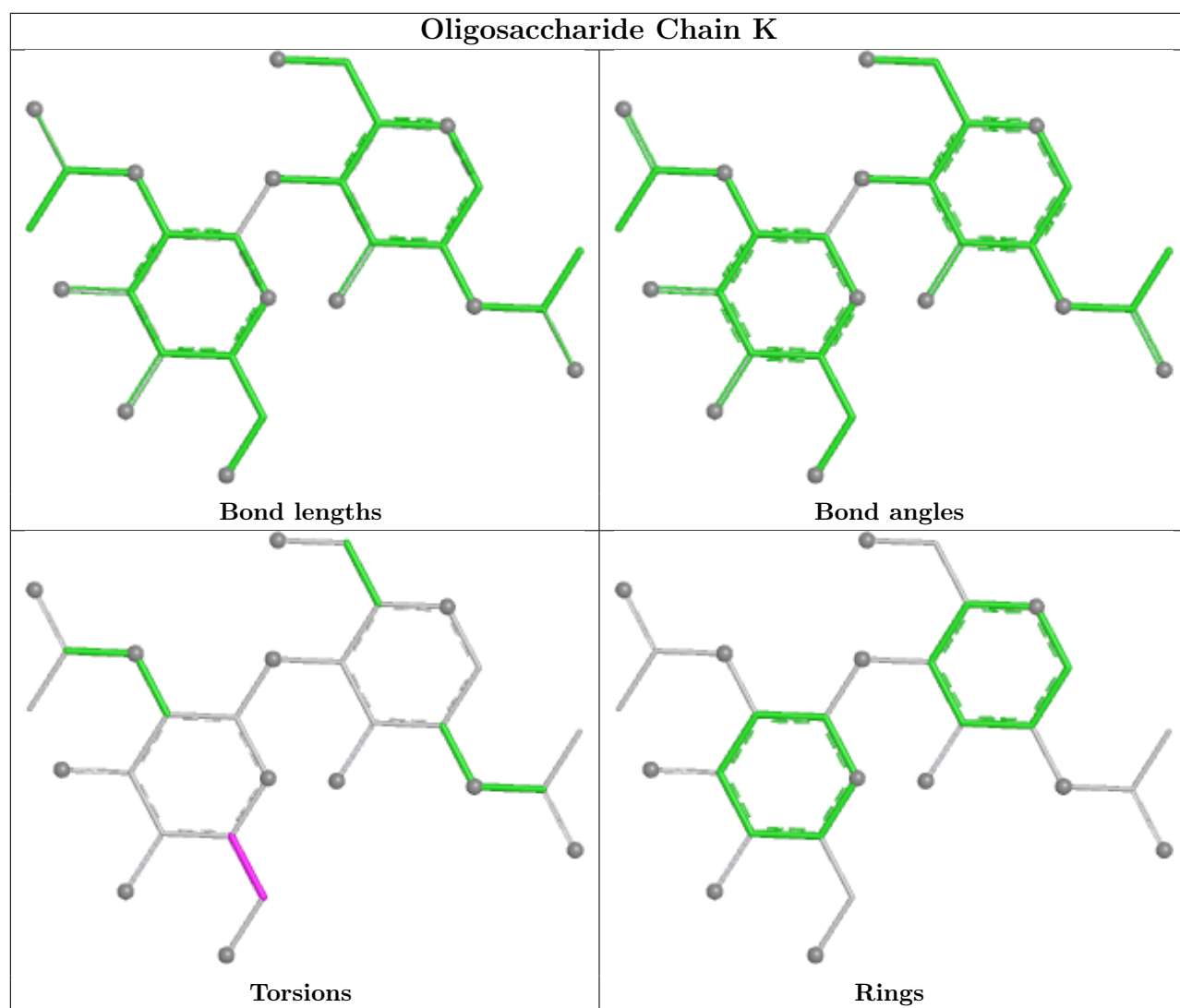
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	1	NAG	1	0

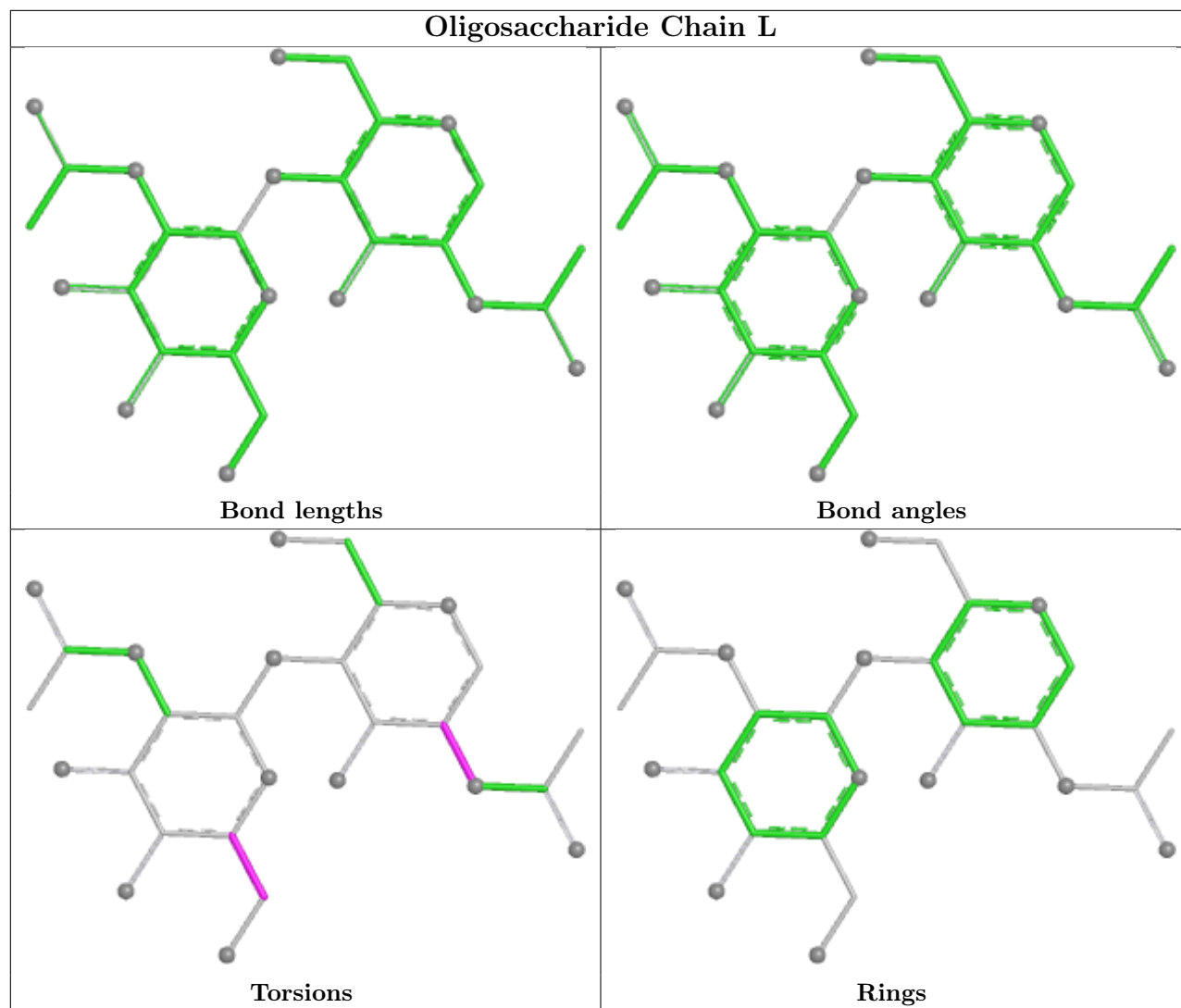
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

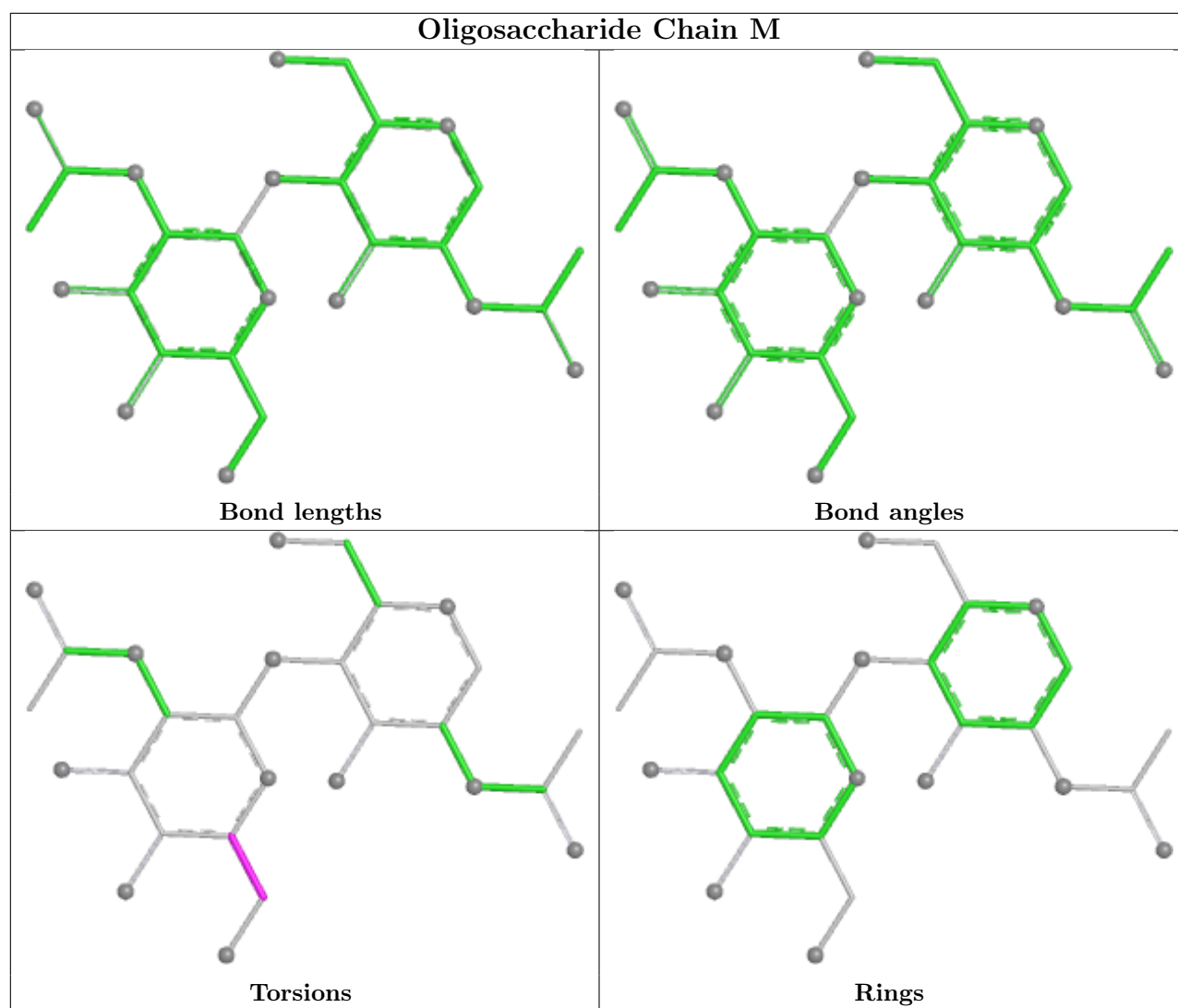


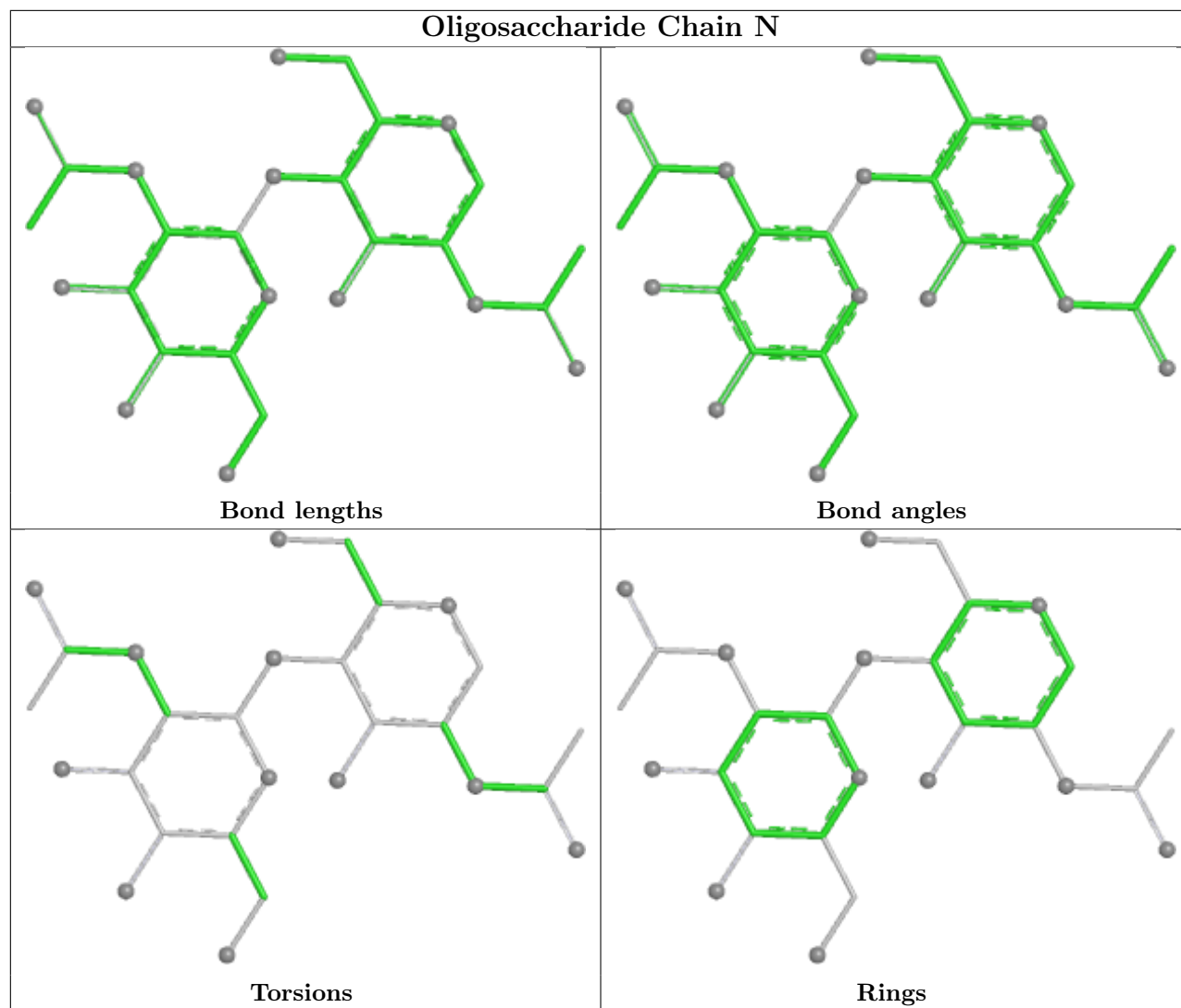


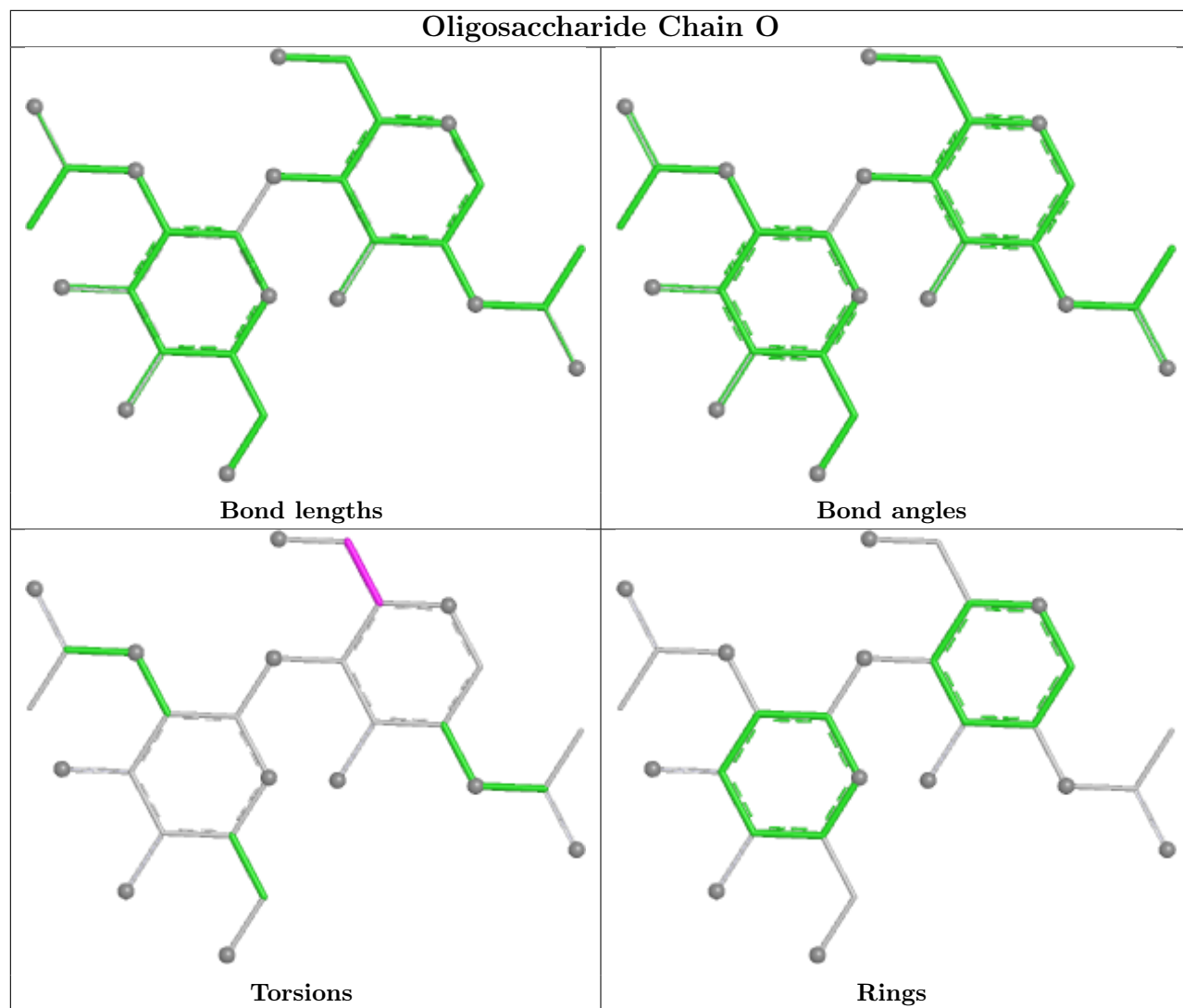


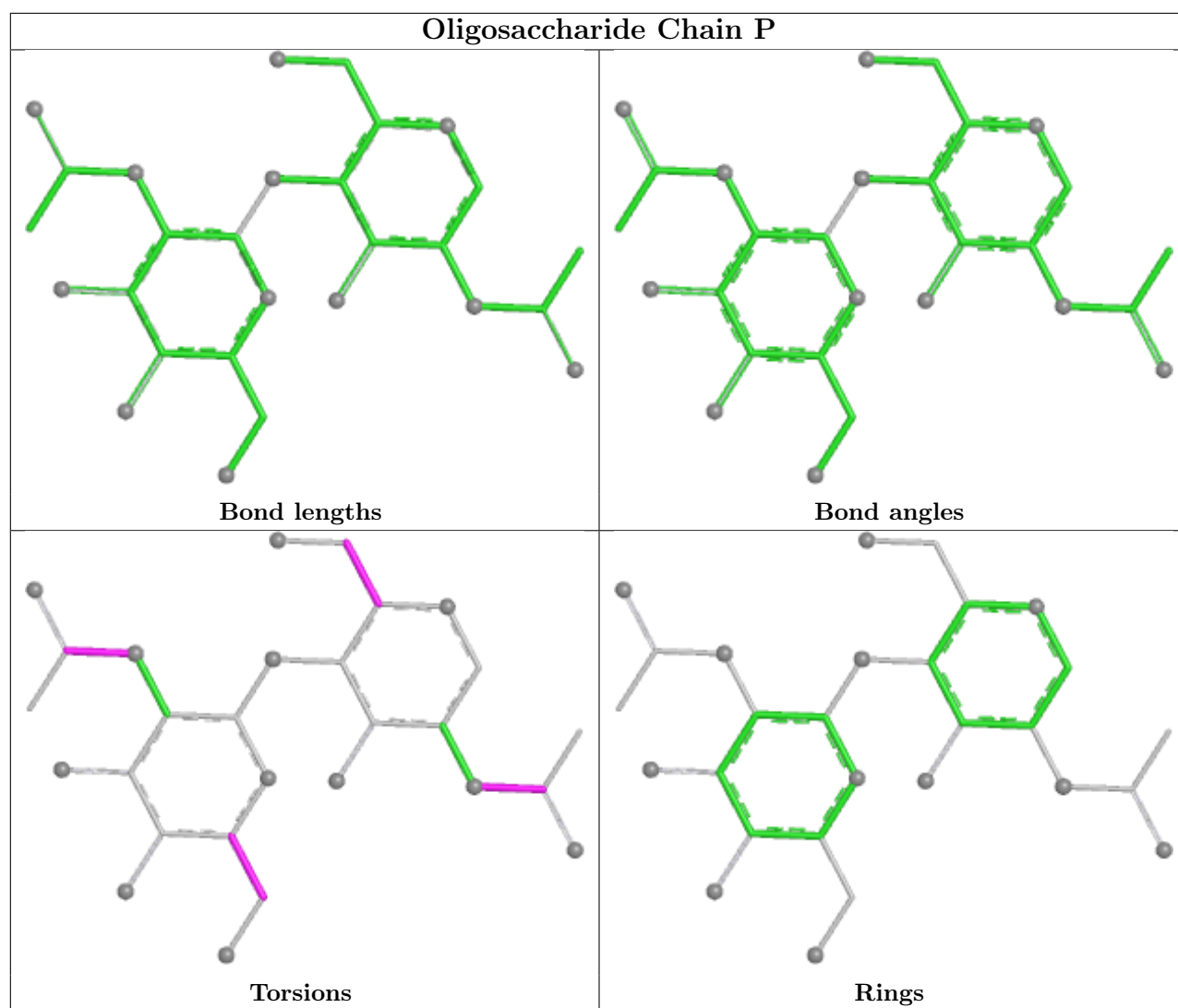


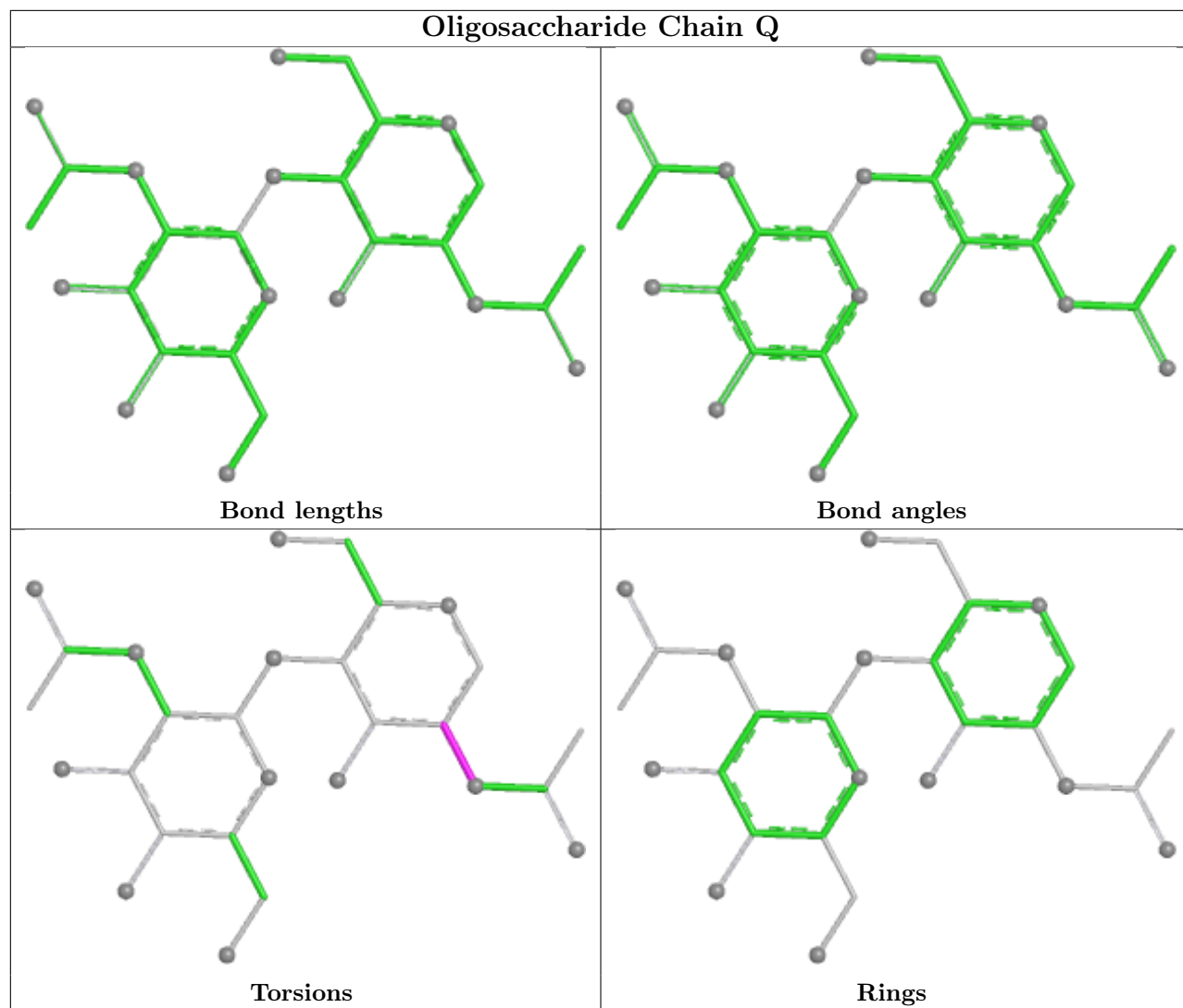


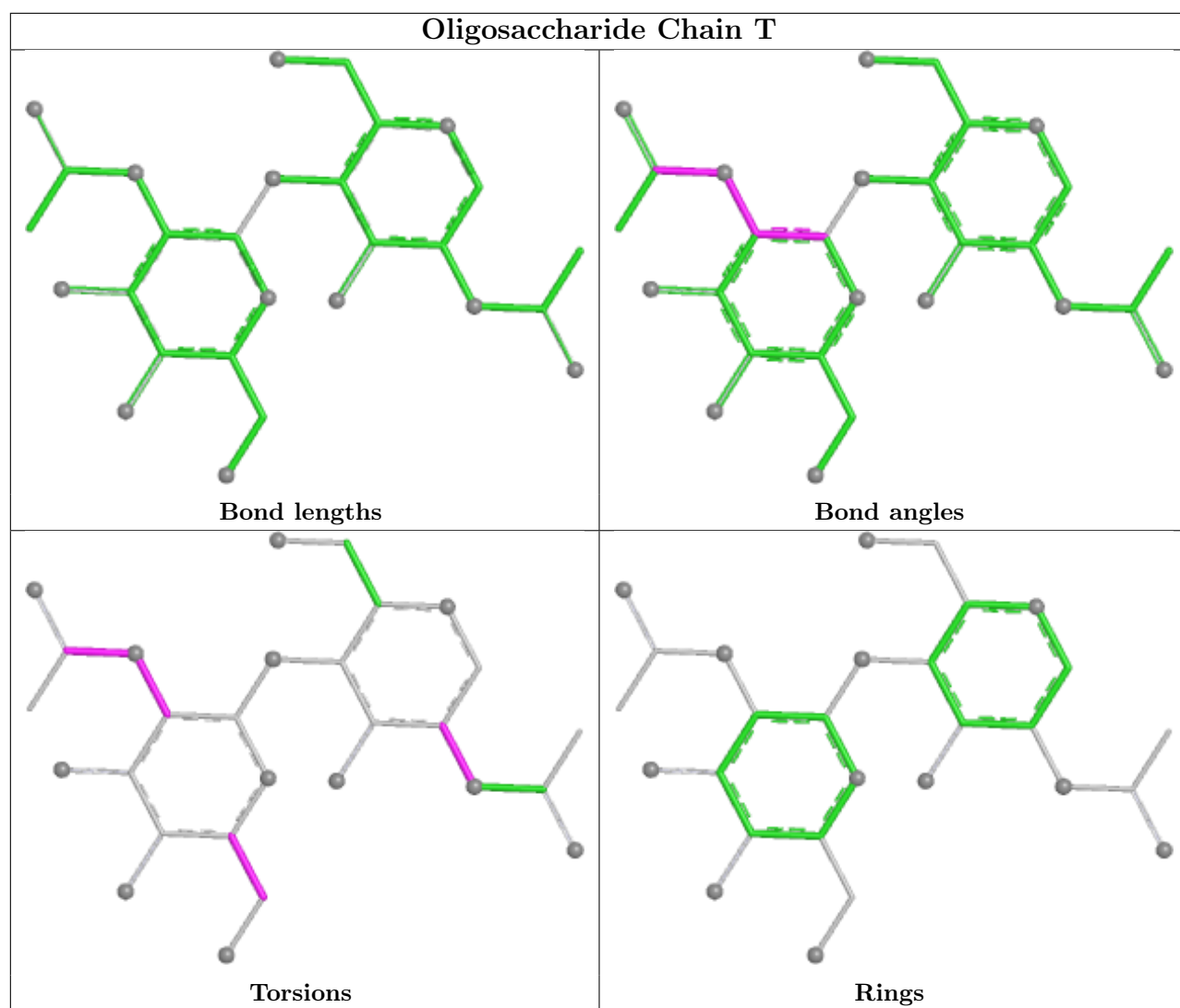


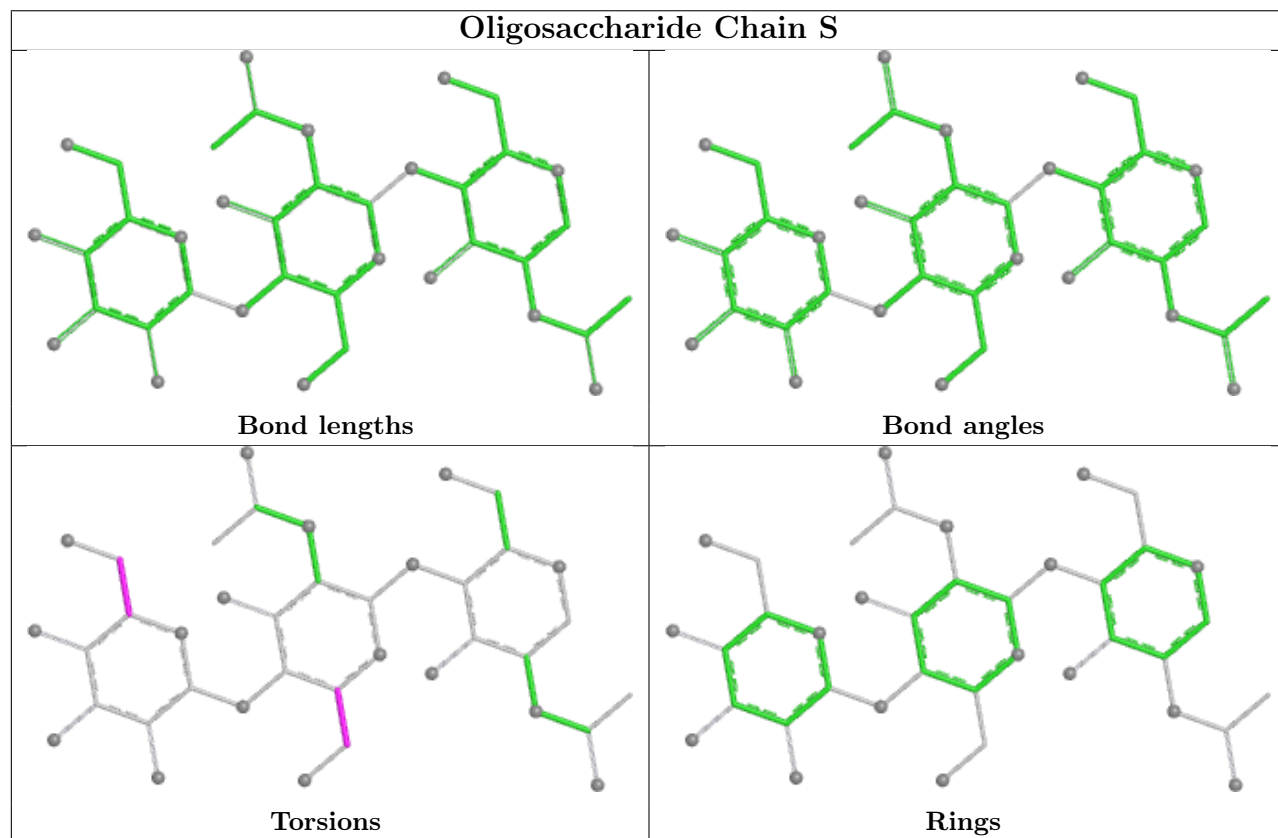
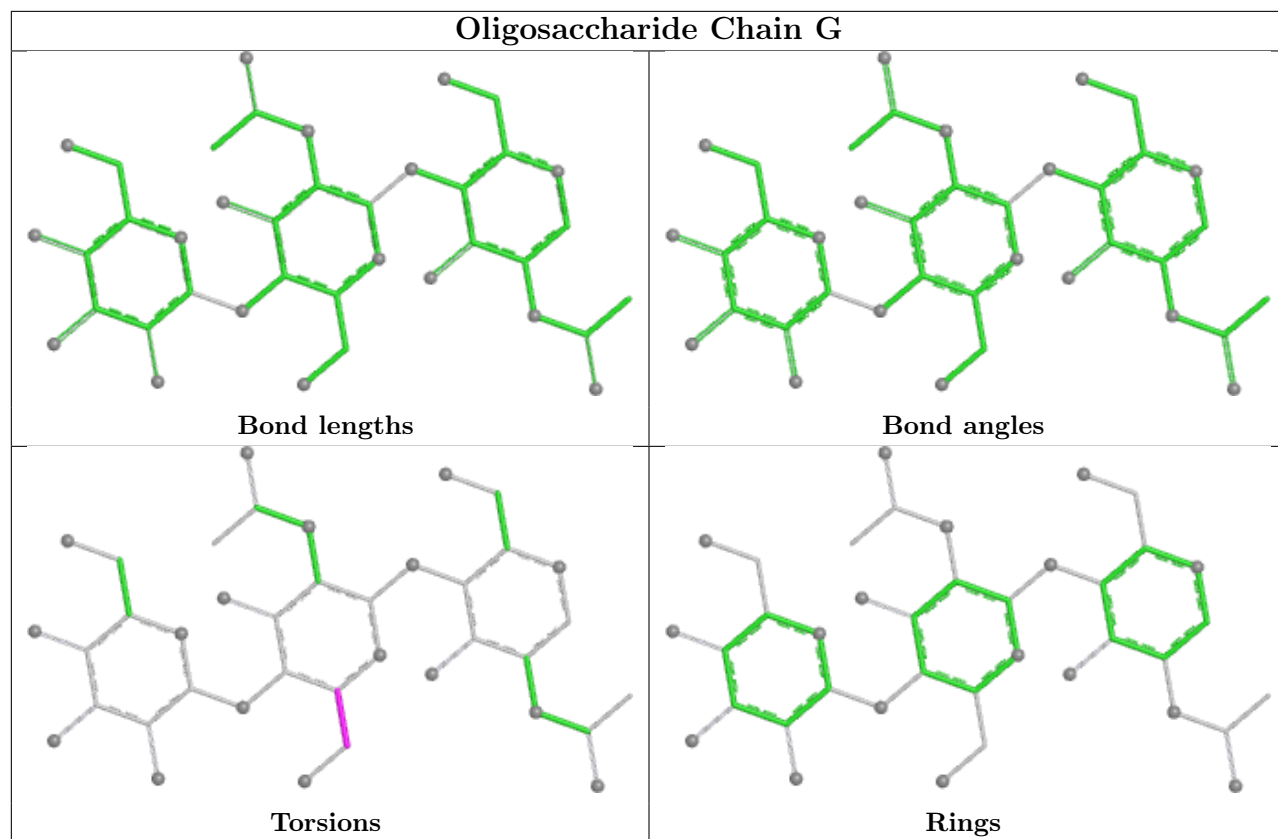


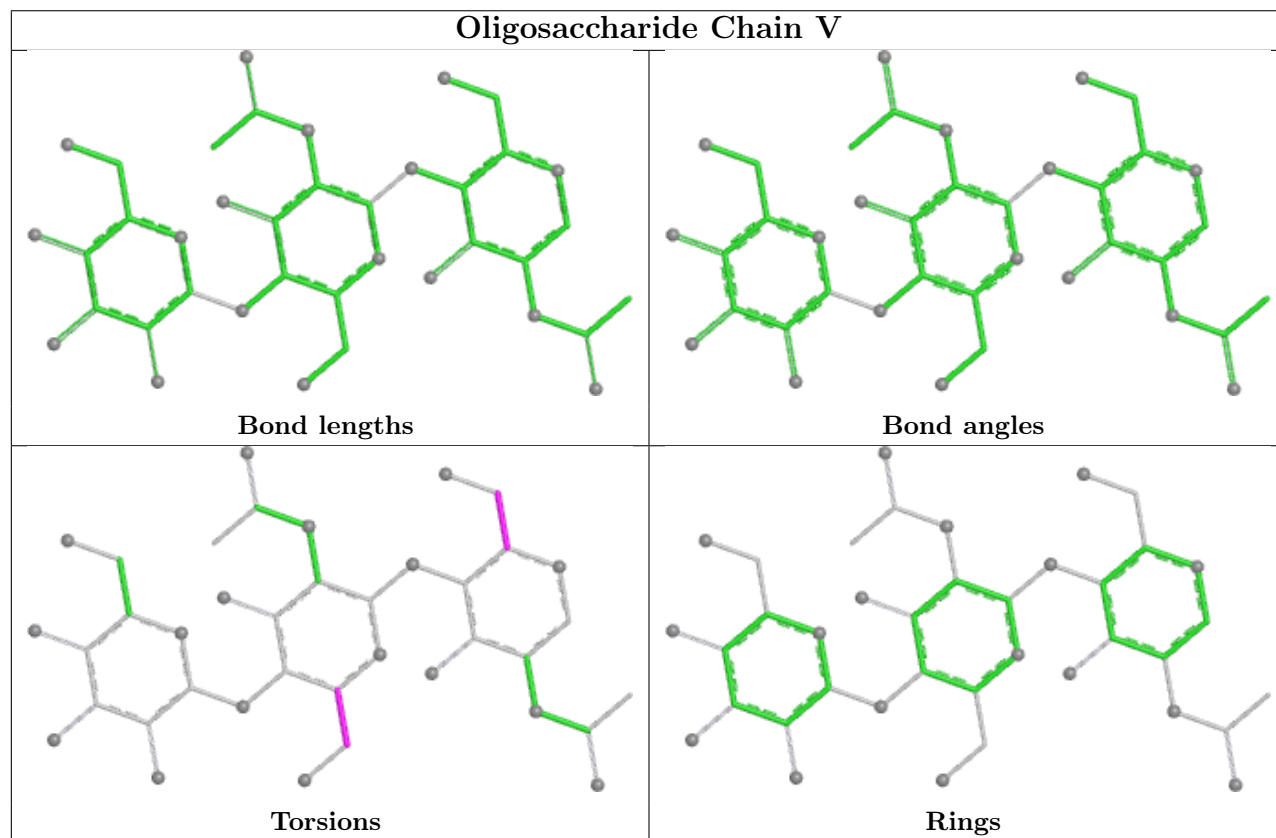
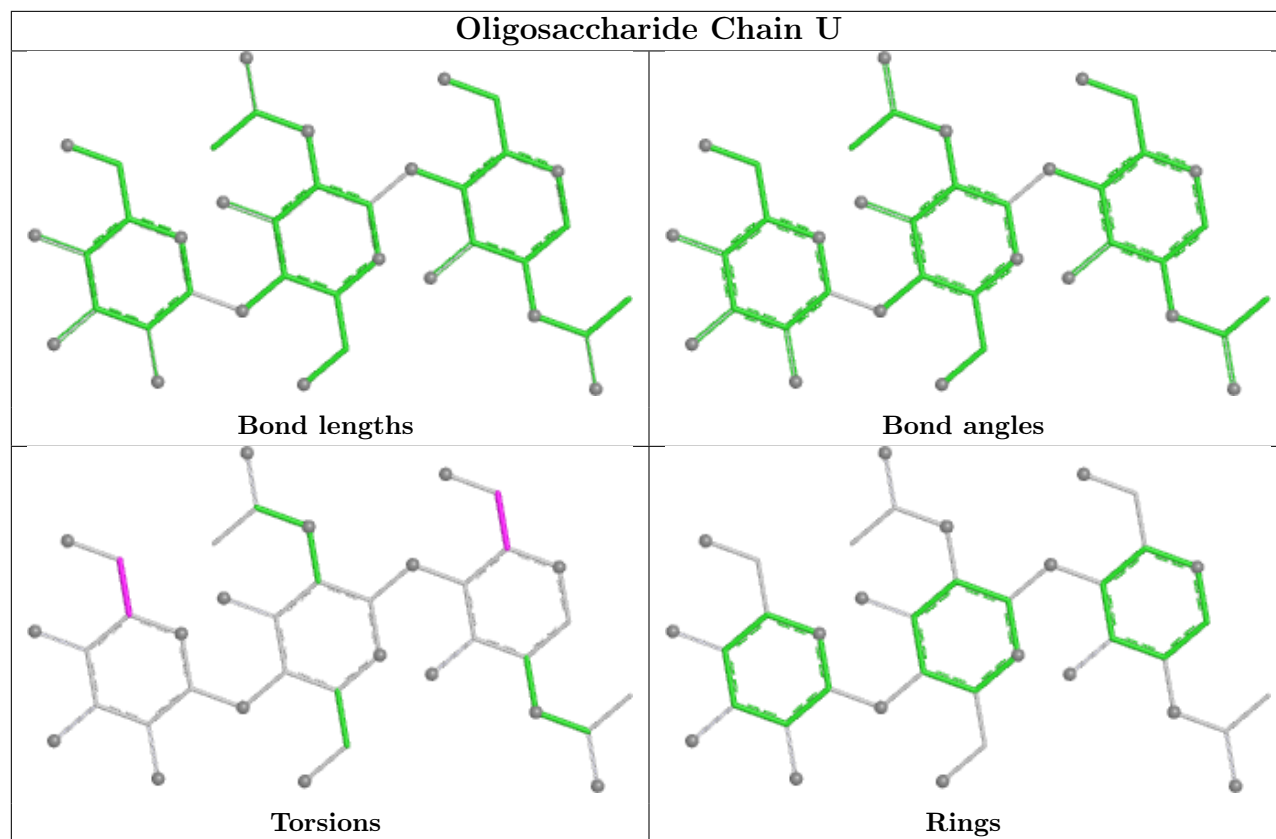


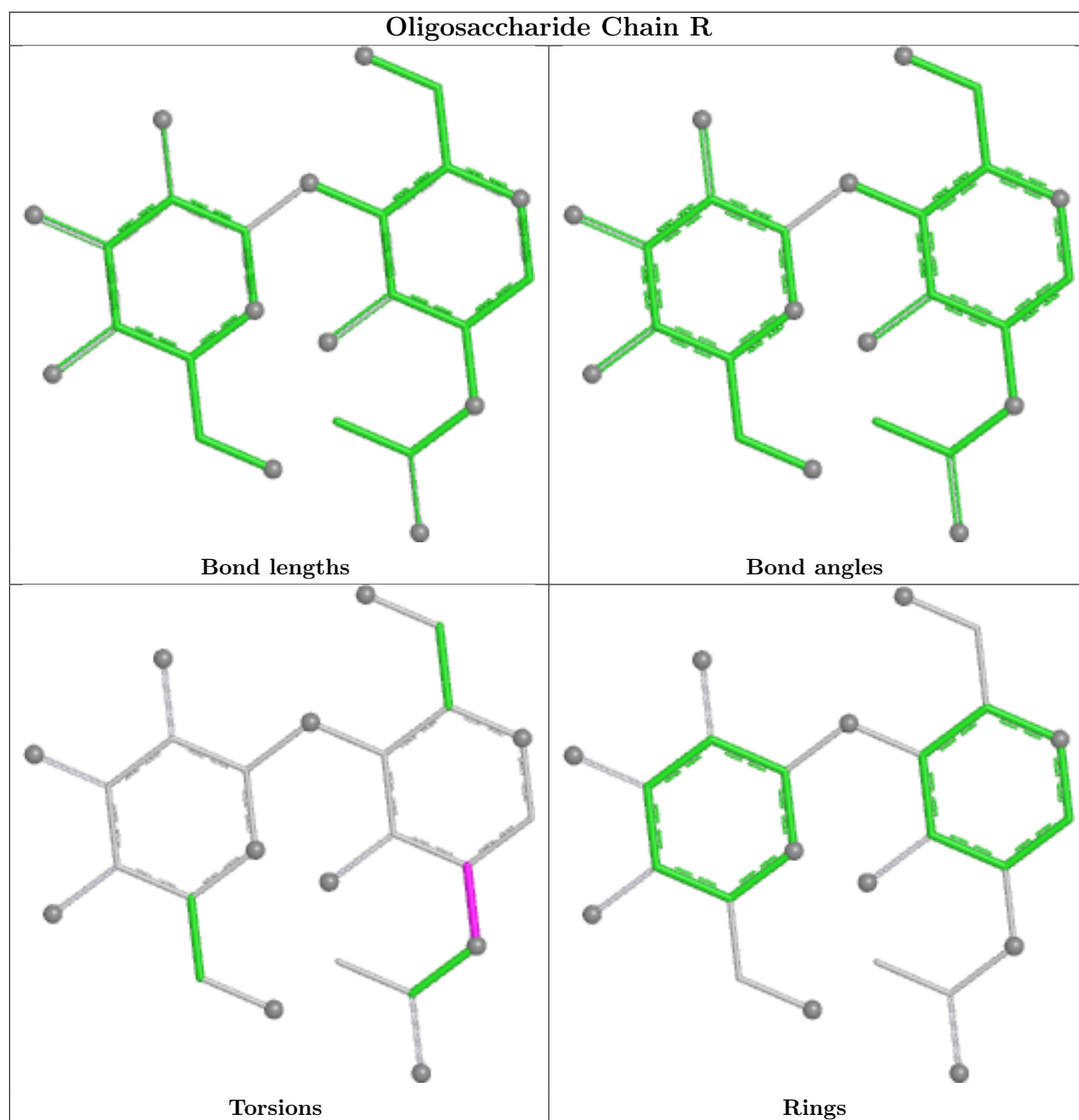












5.6 Ligand geometry [i](#)

29 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	C	1303	1	14,14,15	0.22	0	17,19,21	0.47	0
6	NAG	C	1302	1	14,14,15	0.19	0	17,19,21	0.53	0
6	NAG	C	1309	1	14,14,15	0.20	0	17,19,21	0.47	0
6	NAG	B	1302	1	14,14,15	0.15	0	17,19,21	0.57	0
6	NAG	B	1304	1	14,14,15	0.24	0	17,19,21	0.42	0
6	NAG	B	1305	1	14,14,15	0.20	0	17,19,21	0.47	0
6	NAG	C	1301	1	14,14,15	0.20	0	17,19,21	0.49	0
6	NAG	E	1308	1	14,14,15	0.29	0	17,19,21	1.11	2 (11%)
6	NAG	C	1304	1	14,14,15	0.20	0	17,19,21	0.44	0
6	NAG	E	1307	1	14,14,15	0.30	0	17,19,21	1.04	2 (11%)
6	NAG	C	1305	1	14,14,15	0.27	0	17,19,21	0.39	0
6	NAG	B	1306	1	14,14,15	0.41	0	17,19,21	0.52	0
6	NAG	E	1309	1	14,14,15	0.26	0	17,19,21	0.57	0
6	NAG	B	1310	1	14,14,15	0.28	0	17,19,21	0.54	0
6	NAG	C	1307	1	14,14,15	0.31	0	17,19,21	0.53	0
6	NAG	C	1308	1	14,14,15	0.21	0	17,19,21	0.44	0
6	NAG	B	1301	1	14,14,15	0.23	0	17,19,21	0.43	0
6	NAG	B	1303	1	14,14,15	0.32	0	17,19,21	0.48	0
6	NAG	E	1304	1	14,14,15	0.24	0	17,19,21	0.41	0
6	NAG	E	1306	1	14,14,15	0.38	0	17,19,21	1.13	3 (17%)
6	NAG	E	1302	1	14,14,15	0.21	0	17,19,21	0.57	0
6	NAG	E	1303	1	14,14,15	0.24	0	17,19,21	0.49	0
6	NAG	B	1307	1	14,14,15	0.42	0	17,19,21	0.76	0
6	NAG	E	1305	1	14,14,15	0.25	0	17,19,21	0.41	0
6	NAG	C	1306	1	14,14,15	0.27	0	17,19,21	0.37	0
6	NAG	E	1301	1	14,14,15	0.21	0	17,19,21	0.53	0
6	NAG	C	1310	1	14,14,15	0.26	0	17,19,21	0.48	0
6	NAG	B	1308	1	14,14,15	0.31	0	17,19,21	0.55	0
6	NAG	B	1309	1	14,14,15	0.26	0	17,19,21	0.45	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	C	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1302	1	-	4/6/23/26	0/1/1/1
6	NAG	C	1309	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1302	1	-	4/6/23/26	0/1/1/1
6	NAG	B	1304	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	E	1308	1	-	4/6/23/26	0/1/1/1
6	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1307	1	-	3/6/23/26	0/1/1/1
6	NAG	C	1305	1	-	3/6/23/26	0/1/1/1
6	NAG	B	1306	1	-	5/6/23/26	0/1/1/1
6	NAG	E	1309	1	-	4/6/23/26	0/1/1/1
6	NAG	B	1310	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1307	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
6	NAG	E	1304	1	-	3/6/23/26	0/1/1/1
6	NAG	E	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1302	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
6	NAG	E	1305	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
6	NAG	E	1301	1	-	4/6/23/26	0/1/1/1
6	NAG	C	1310	1	-	1/6/23/26	0/1/1/1
6	NAG	B	1308	1	-	4/6/23/26	0/1/1/1
6	NAG	B	1309	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1307	NAG	C1-O5-C5	-2.78	108.47	112.19
6	E	1308	NAG	O5-C1-C2	-2.33	107.68	111.29
6	E	1306	NAG	C1-O5-C5	-2.33	109.06	112.19
6	E	1308	NAG	C1-O5-C5	-2.28	109.13	112.19
6	E	1306	NAG	C2-N2-C7	-2.28	119.84	122.90
6	E	1307	NAG	C4-C3-C2	-2.14	107.89	111.02
6	E	1306	NAG	C4-C3-C2	-2.09	107.96	111.02

There are no chirality outliers.

All (63) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	1308	NAG	C8-C7-N2-C2
6	B	1308	NAG	O7-C7-N2-C2
6	C	1306	NAG	C4-C5-C6-O6
6	B	1310	NAG	O5-C5-C6-O6
6	E	1301	NAG	C4-C5-C6-O6
6	C	1306	NAG	O5-C5-C6-O6
6	E	1307	NAG	O5-C5-C6-O6
6	B	1301	NAG	C4-C5-C6-O6
6	B	1305	NAG	O5-C5-C6-O6
6	B	1307	NAG	O5-C5-C6-O6
6	B	1309	NAG	O5-C5-C6-O6
6	C	1309	NAG	O5-C5-C6-O6
6	E	1305	NAG	O5-C5-C6-O6
6	B	1303	NAG	C4-C5-C6-O6
6	B	1307	NAG	C4-C5-C6-O6
6	C	1301	NAG	O5-C5-C6-O6
6	E	1308	NAG	O5-C5-C6-O6
6	E	1305	NAG	C4-C5-C6-O6
6	C	1307	NAG	O5-C5-C6-O6
6	B	1310	NAG	C4-C5-C6-O6
6	E	1309	NAG	O5-C5-C6-O6
6	C	1308	NAG	C4-C5-C6-O6
6	B	1301	NAG	O5-C5-C6-O6
6	B	1308	NAG	C4-C5-C6-O6
6	C	1302	NAG	O5-C5-C6-O6
6	E	1301	NAG	O5-C5-C6-O6
6	B	1305	NAG	C4-C5-C6-O6
6	C	1309	NAG	C4-C5-C6-O6
6	B	1309	NAG	C4-C5-C6-O6
6	C	1307	NAG	C4-C5-C6-O6
6	E	1307	NAG	C4-C5-C6-O6
6	B	1303	NAG	O5-C5-C6-O6
6	C	1302	NAG	C4-C5-C6-O6
6	B	1302	NAG	C4-C5-C6-O6
6	C	1305	NAG	C8-C7-N2-C2
6	C	1305	NAG	O7-C7-N2-C2
6	E	1304	NAG	C8-C7-N2-C2
6	E	1304	NAG	O7-C7-N2-C2
6	E	1308	NAG	C8-C7-N2-C2
6	E	1308	NAG	O7-C7-N2-C2
6	C	1301	NAG	C4-C5-C6-O6
6	C	1308	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
6	B	1308	NAG	O5-C5-C6-O6
6	B	1302	NAG	O5-C5-C6-O6
6	B	1306	NAG	C8-C7-N2-C2
6	B	1306	NAG	O5-C5-C6-O6
6	E	1309	NAG	C4-C5-C6-O6
6	B	1306	NAG	C4-C5-C6-O6
6	E	1308	NAG	C4-C5-C6-O6
6	E	1304	NAG	O5-C5-C6-O6
6	C	1305	NAG	O5-C5-C6-O6
6	B	1306	NAG	O7-C7-N2-C2
6	B	1302	NAG	C1-C2-N2-C7
6	C	1302	NAG	C1-C2-N2-C7
6	E	1301	NAG	C1-C2-N2-C7
6	E	1309	NAG	C1-C2-N2-C7
6	C	1302	NAG	C3-C2-N2-C7
6	E	1309	NAG	C3-C2-N2-C7
6	C	1310	NAG	O5-C5-C6-O6
6	B	1306	NAG	C1-C2-N2-C7
6	E	1307	NAG	C1-C2-N2-C7
6	B	1302	NAG	C3-C2-N2-C7
6	E	1301	NAG	C3-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1309	NAG	1	0
6	B	1303	NAG	1	0
6	C	1306	NAG	2	0

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.

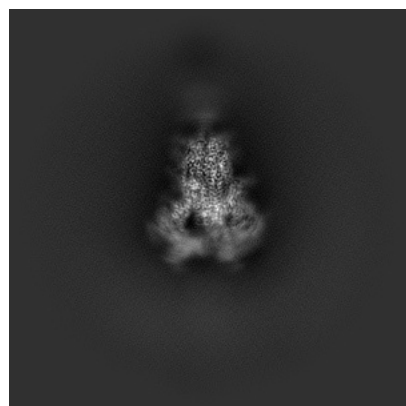
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24077. These allow visual inspection of the internal detail of the map and identification of artifacts.

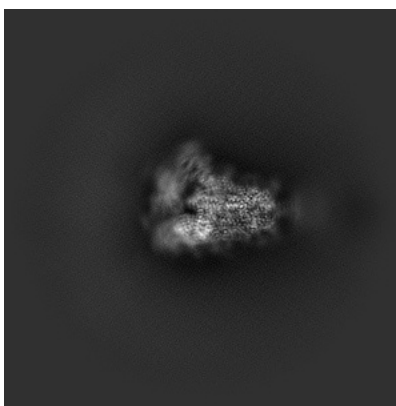
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

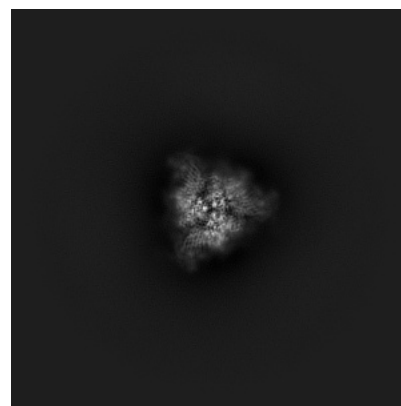
6.1.1 Primary map



X

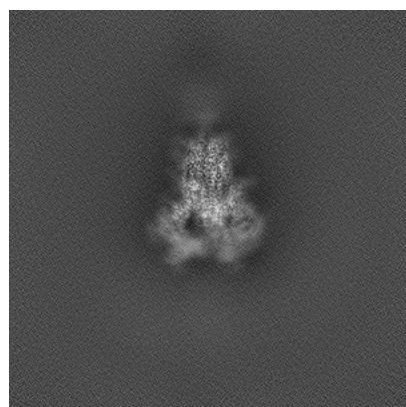


Y

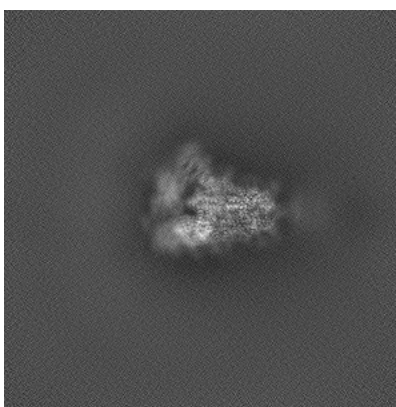


Z

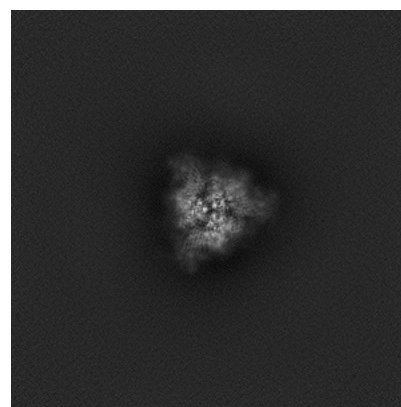
6.1.2 Raw map



X



Y

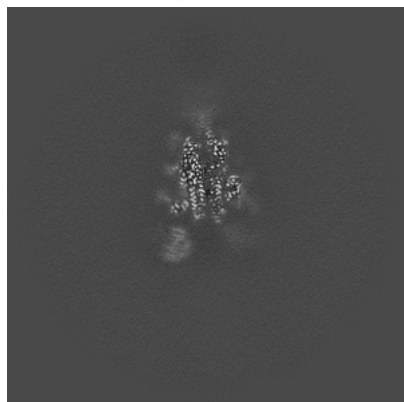


Z

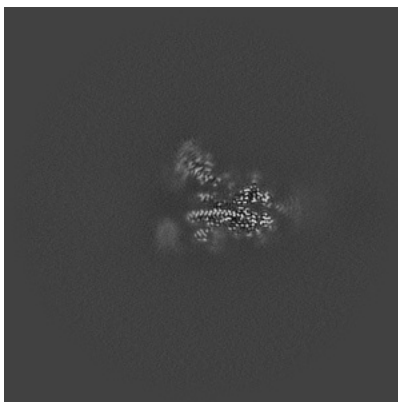
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

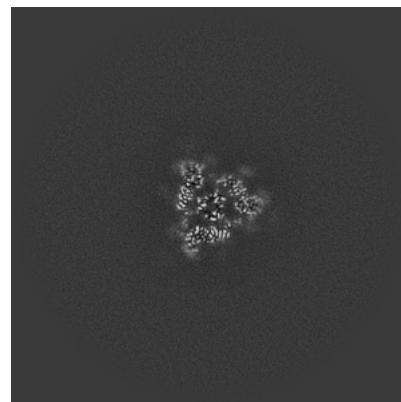
6.2.1 Primary map



X Index: 300

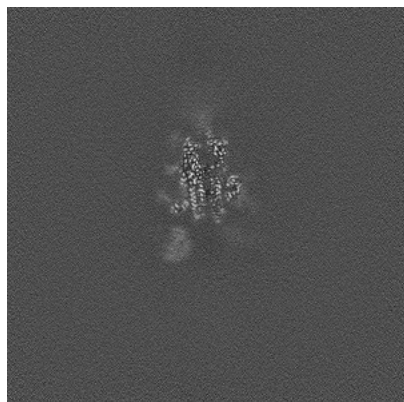


Y Index: 300

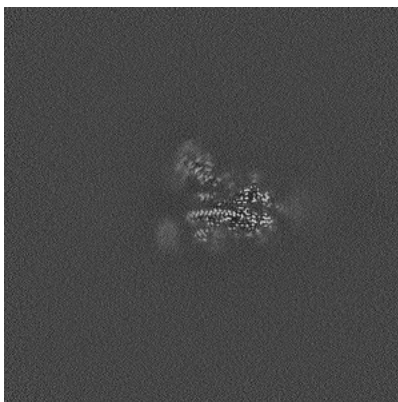


Z Index: 300

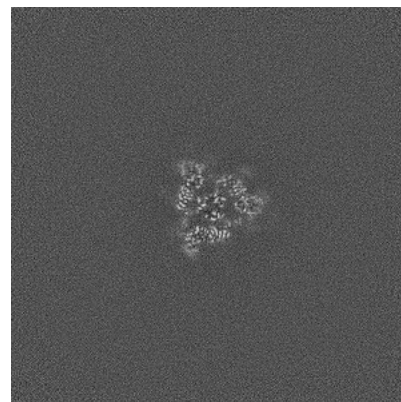
6.2.2 Raw map



X Index: 300



Y Index: 300

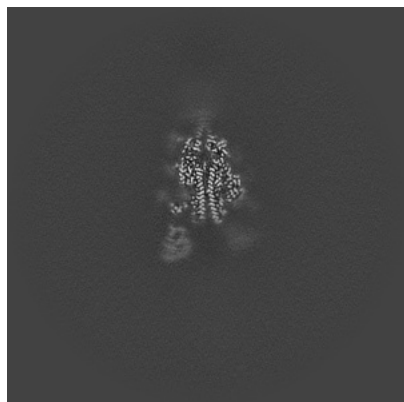


Z Index: 300

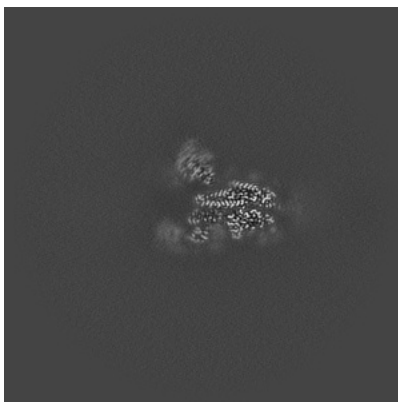
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

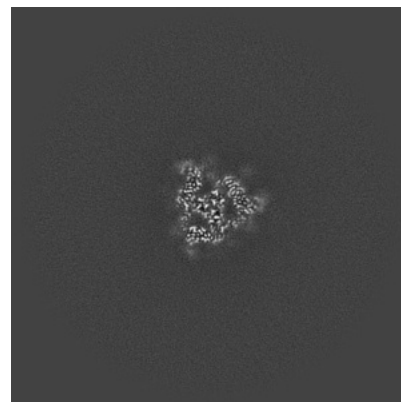
6.3.1 Primary map



X Index: 304

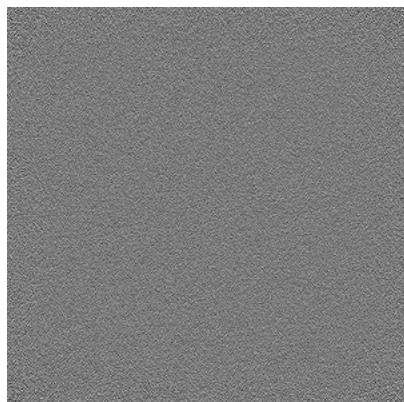


Y Index: 306

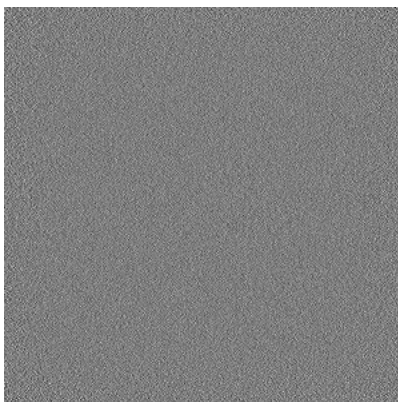


Z Index: 304

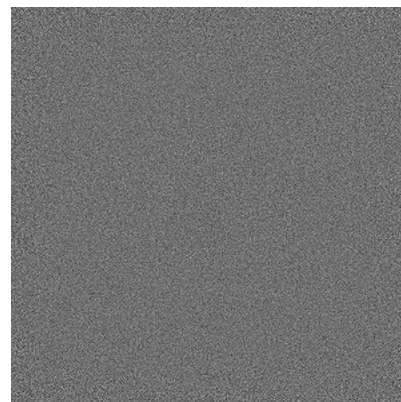
6.3.2 Raw map



X Index: 0



Y Index: 0

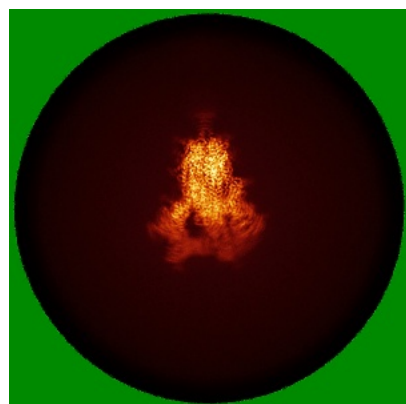


Z Index: 0

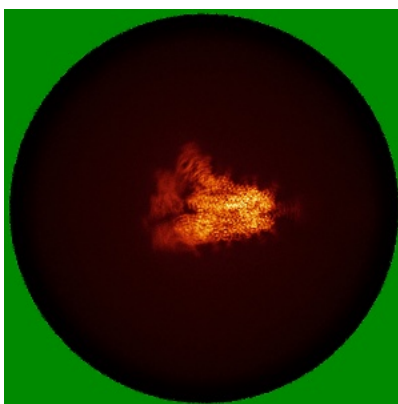
The images above show the largest variance slices of the map in three orthogonal directions.

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

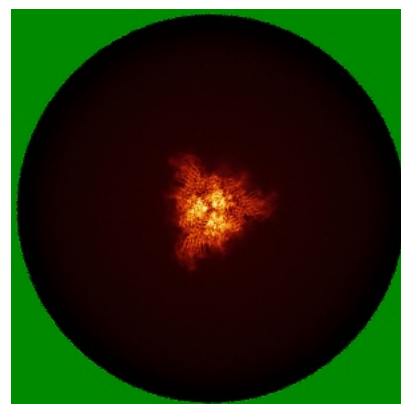
6.4.1 Primary map



X

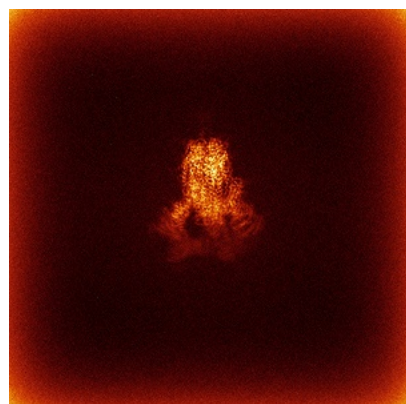


Y

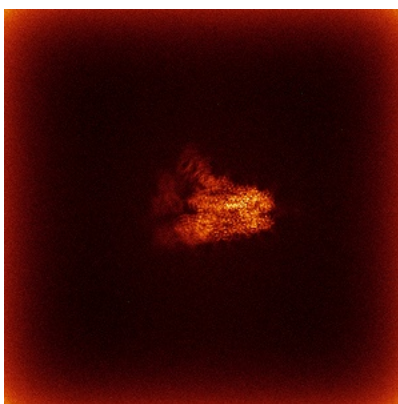


Z

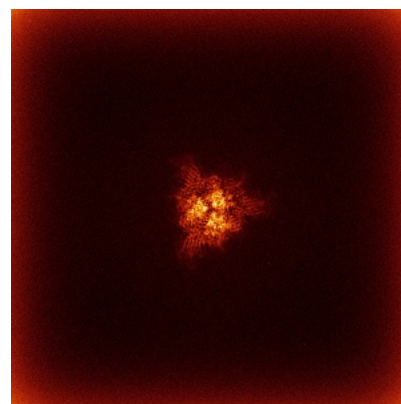
6.4.2 Raw map



X



Y



Z

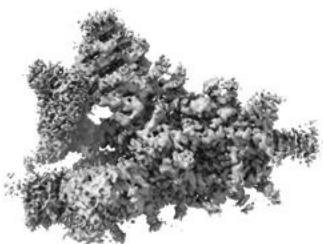
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

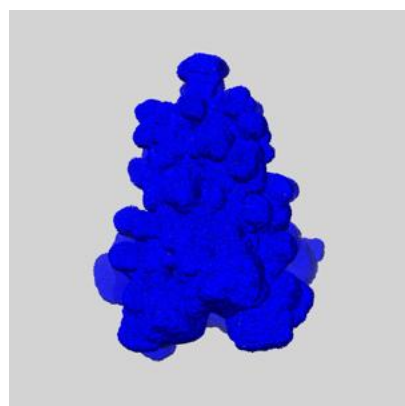
6.6 Mask visualisation [i](#)

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

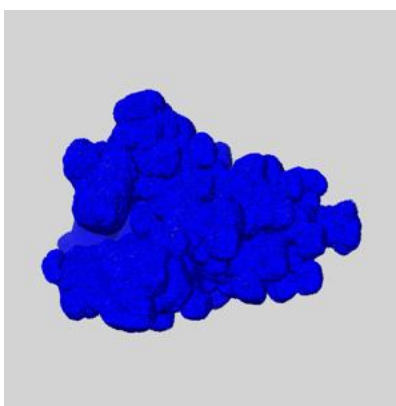
A mask typically either:

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

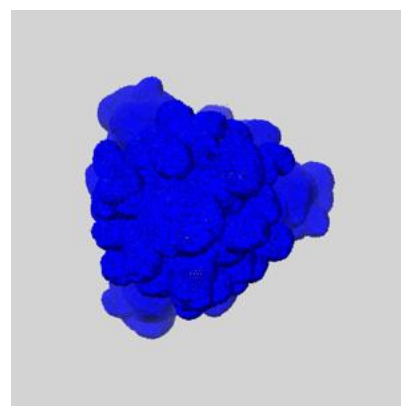
6.6.1 emd_24077_msk_1.map [i](#)



X



Y

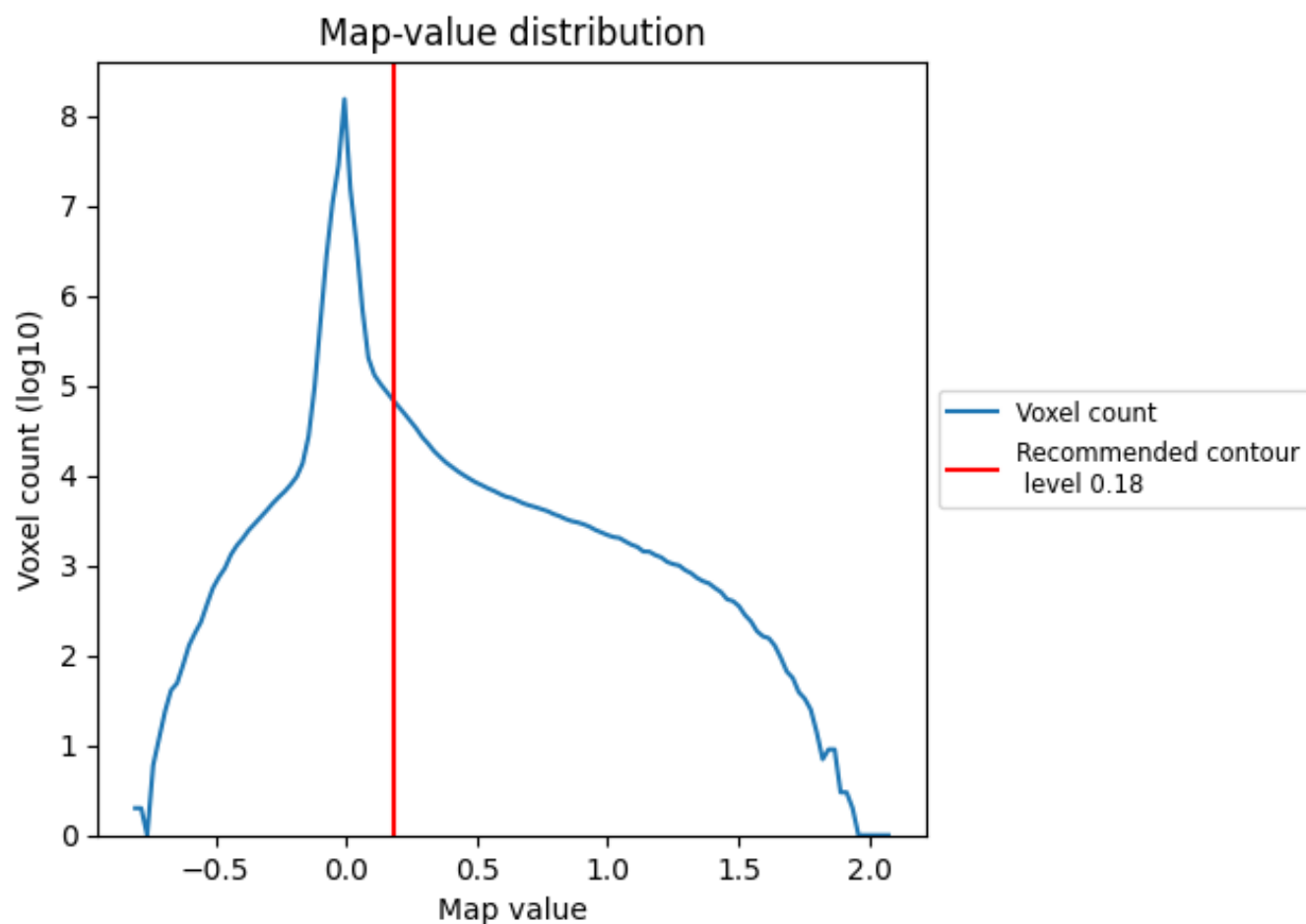


Z

7 Map analysis [i](#)

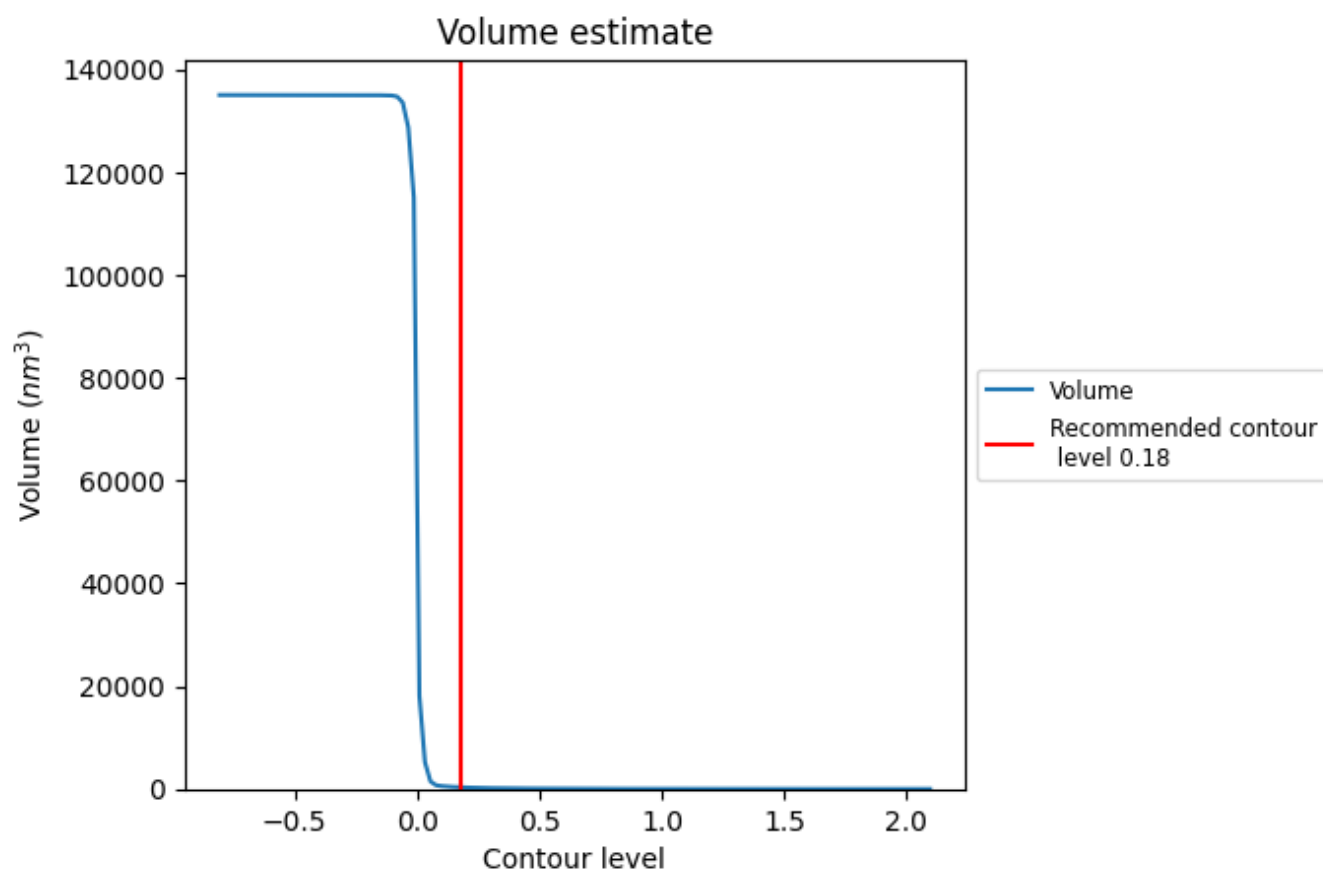
This section contains the results of statistical analysis of the map.

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.

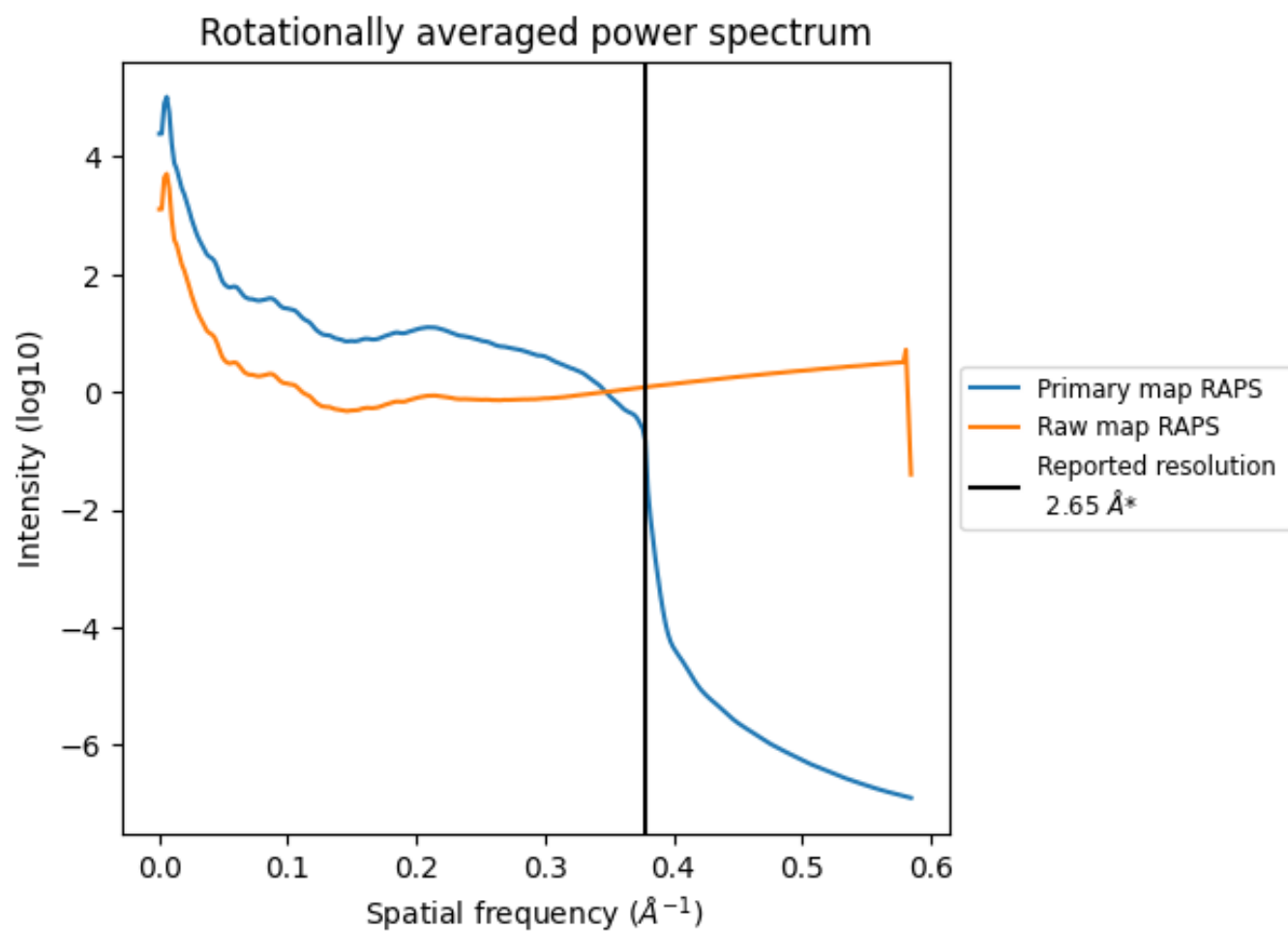
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 320 nm^3 ; this corresponds to an approximate mass of 289 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 ⓘ

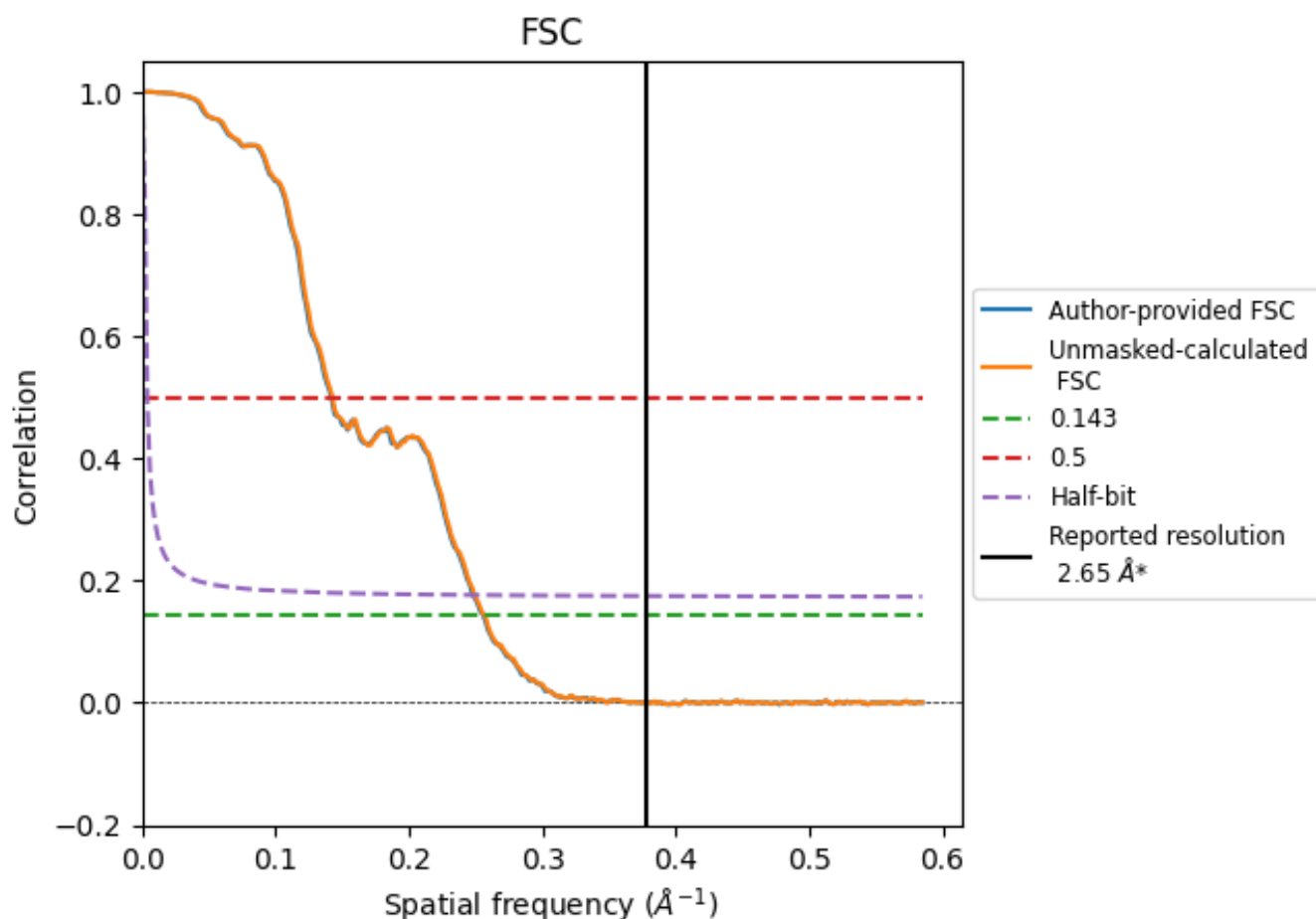


*Reported resolution corresponds to spatial frequency of 0.377 Å⁻¹

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 0.377 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	3.91	7.06	4.04
Unmasked-calculated*	3.90	7.01	4.01

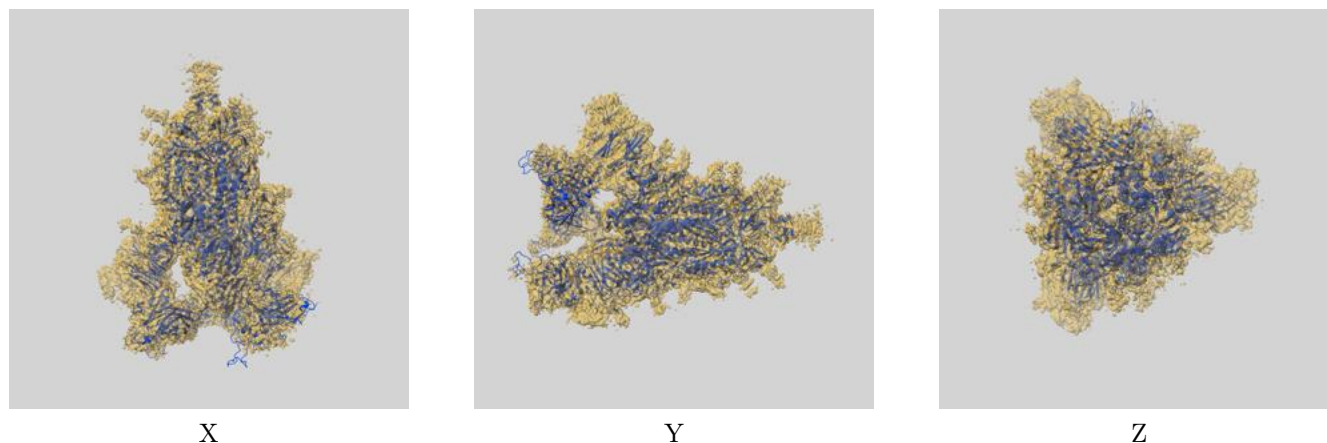
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.91 differs from the reported value 2.65 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.90 differs from the reported value 2.65 by more than 10 %

9 Map-model fit [i](#)

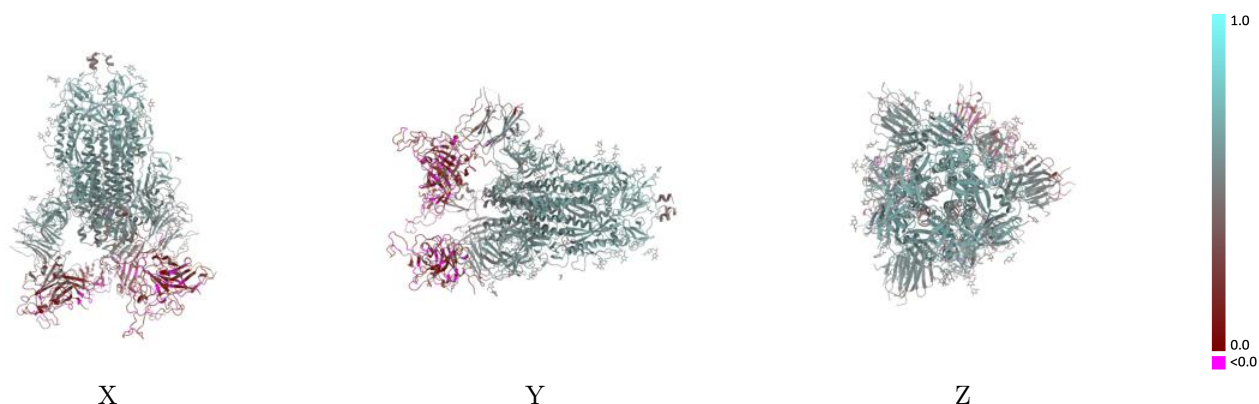
This section contains information regarding the fit between EMDB map EMD-24077 and PDB model 7MY2. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.18 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](#)

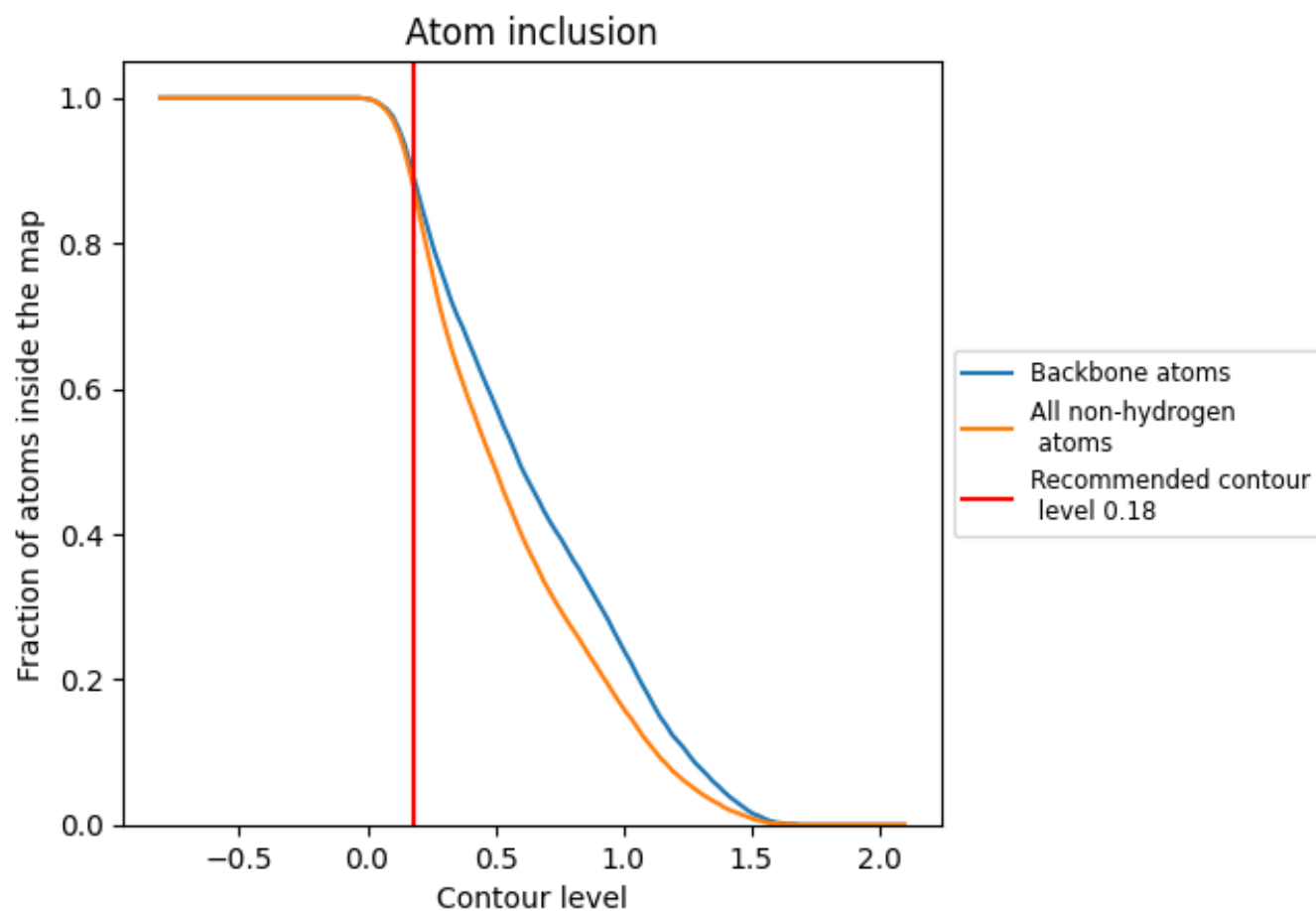


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 88% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8780	 0.4670
A	 0.6680	 0.2040
B	 0.9110	 0.4990
C	 0.8640	 0.4850
D	 0.3090	 0.1880
E	 0.9420	 0.5010
F	 1.0000	 0.5170
G	 1.0000	 0.5430
H	 0.8310	 0.2500
I	 1.0000	 0.5010
J	 0.9290	 0.4720
K	 1.0000	 0.5000
L	 1.0000	 0.5290
M	 1.0000	 0.5250
N	 1.0000	 0.5070
O	 0.9640	 0.5340
P	 0.9290	 0.3920
Q	 0.9640	 0.4880
R	 1.0000	 0.5400
S	 1.0000	 0.5490
T	 0.8930	 0.4630
U	 1.0000	 0.4870
V	 0.9740	 0.4860

