



Full wwPDB EM Validation Report ⓘ

Oct 3, 2023 – 10:21 AM JST

PDB ID : 7Y0H
EMDB ID : EMD-33542
Title : Cryo-EM structure of human IgM-Fc in complex with the J chain and the P. falciparum VAR2CSA FCR3
Authors : Ji, C.; Xiao, J.
Deposited on : 2022-06-05
Resolution : 3.56 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:

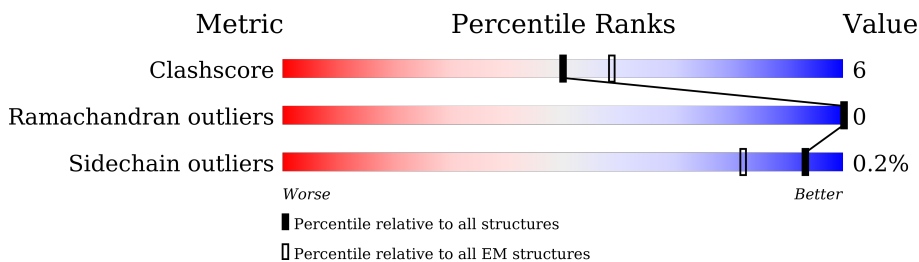
EMDB validation analysis : 0.0.1.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.56 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.



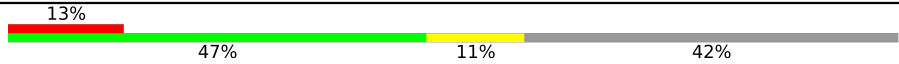
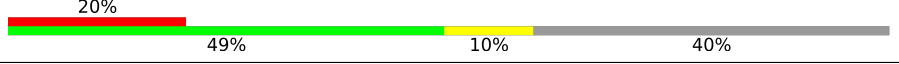
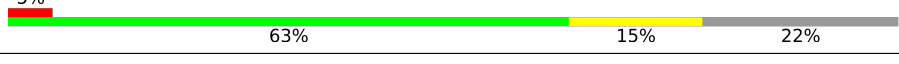
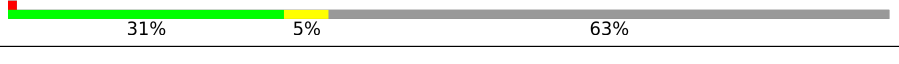
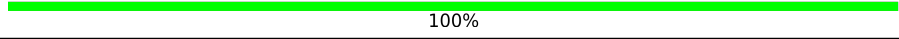
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	383	
1	B	383	
1	C	383	
1	D	383	
1	E	383	
1	F	383	
1	G	383	
1	H	383	

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Mol	Chain	Length	Quality of chain
1	K	383	
1	L	383	
2	J	136	
3	M	2636	
4	I	2	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 26470 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 Immunoglobulin heavy constant mu.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	231	Total 1786	C 1123	N 303	O 351	S 9	0	0
1	B	228	Total 1769	C 1114	N 300	O 347	S 8	0	0
1	C	229	Total 1772	C 1116	N 301	O 347	S 8	0	0
1	D	224	Total 1743	C 1100	N 296	O 339	S 8	0	0
1	E	224	Total 1743	C 1100	N 296	O 339	S 8	0	0
1	F	224	Total 1737	C 1095	N 295	O 339	S 8	0	0
1	G	224	Total 1742	C 1100	N 296	O 338	S 8	0	0
1	H	222	Total 1730	C 1092	N 293	O 337	S 8	0	0
1	K	223	Total 1737	C 1095	N 295	O 339	S 8	0	0
1	L	228	Total 1773	C 1116	N 299	O 349	S 9	0	0

There are 350 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	ALA	-	expression tag	UNP P01871
A	195	SER	-	expression tag	UNP P01871
A	196	ALA	-	expression tag	UNP P01871
A	197	TRP	-	expression tag	UNP P01871
A	198	SER	-	expression tag	UNP P01871
A	199	HIS	-	expression tag	UNP P01871
A	200	PRO	-	expression tag	UNP P01871
A	201	GLN	-	expression tag	UNP P01871
A	202	PHE	-	expression tag	UNP P01871
A	203	GLU	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
A	204	LYS	-	expression tag	UNP P01871
A	205	GLY	-	expression tag	UNP P01871
A	206	GLY	-	expression tag	UNP P01871
A	207	GLY	-	expression tag	UNP P01871
A	208	SER	-	expression tag	UNP P01871
A	209	GLY	-	expression tag	UNP P01871
A	210	GLY	-	expression tag	UNP P01871
A	211	GLY	-	expression tag	UNP P01871
A	212	SER	-	expression tag	UNP P01871
A	213	GLY	-	expression tag	UNP P01871
A	214	GLY	-	expression tag	UNP P01871
A	215	SER	-	expression tag	UNP P01871
A	216	ALA	-	expression tag	UNP P01871
A	217	TRP	-	expression tag	UNP P01871
A	218	SER	-	expression tag	UNP P01871
A	219	HIS	-	expression tag	UNP P01871
A	220	PRO	-	expression tag	UNP P01871
A	221	GLN	-	expression tag	UNP P01871
A	222	PHE	-	expression tag	UNP P01871
A	223	GLU	-	expression tag	UNP P01871
A	224	LYS	-	expression tag	UNP P01871
A	225	ILE	-	expression tag	UNP P01871
A	226	ASP	-	expression tag	UNP P01871
A	227	THR	-	expression tag	UNP P01871
A	228	THR	-	expression tag	UNP P01871
B	194	ALA	-	expression tag	UNP P01871
B	195	SER	-	expression tag	UNP P01871
B	196	ALA	-	expression tag	UNP P01871
B	197	TRP	-	expression tag	UNP P01871
B	198	SER	-	expression tag	UNP P01871
B	199	HIS	-	expression tag	UNP P01871
B	200	PRO	-	expression tag	UNP P01871
B	201	GLN	-	expression tag	UNP P01871
B	202	PHE	-	expression tag	UNP P01871
B	203	GLU	-	expression tag	UNP P01871
B	204	LYS	-	expression tag	UNP P01871
B	205	GLY	-	expression tag	UNP P01871
B	206	GLY	-	expression tag	UNP P01871
B	207	GLY	-	expression tag	UNP P01871
B	208	SER	-	expression tag	UNP P01871
B	209	GLY	-	expression tag	UNP P01871
B	210	GLY	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
B	211	GLY	-	expression tag	UNP P01871
B	212	SER	-	expression tag	UNP P01871
B	213	GLY	-	expression tag	UNP P01871
B	214	GLY	-	expression tag	UNP P01871
B	215	SER	-	expression tag	UNP P01871
B	216	ALA	-	expression tag	UNP P01871
B	217	TRP	-	expression tag	UNP P01871
B	218	SER	-	expression tag	UNP P01871
B	219	HIS	-	expression tag	UNP P01871
B	220	PRO	-	expression tag	UNP P01871
B	221	GLN	-	expression tag	UNP P01871
B	222	PHE	-	expression tag	UNP P01871
B	223	GLU	-	expression tag	UNP P01871
B	224	LYS	-	expression tag	UNP P01871
B	225	ILE	-	expression tag	UNP P01871
B	226	ASP	-	expression tag	UNP P01871
B	227	THR	-	expression tag	UNP P01871
B	228	THR	-	expression tag	UNP P01871
C	194	ALA	-	expression tag	UNP P01871
C	195	SER	-	expression tag	UNP P01871
C	196	ALA	-	expression tag	UNP P01871
C	197	TRP	-	expression tag	UNP P01871
C	198	SER	-	expression tag	UNP P01871
C	199	HIS	-	expression tag	UNP P01871
C	200	PRO	-	expression tag	UNP P01871
C	201	GLN	-	expression tag	UNP P01871
C	202	PHE	-	expression tag	UNP P01871
C	203	GLU	-	expression tag	UNP P01871
C	204	LYS	-	expression tag	UNP P01871
C	205	GLY	-	expression tag	UNP P01871
C	206	GLY	-	expression tag	UNP P01871
C	207	GLY	-	expression tag	UNP P01871
C	208	SER	-	expression tag	UNP P01871
C	209	GLY	-	expression tag	UNP P01871
C	210	GLY	-	expression tag	UNP P01871
C	211	GLY	-	expression tag	UNP P01871
C	212	SER	-	expression tag	UNP P01871
C	213	GLY	-	expression tag	UNP P01871
C	214	GLY	-	expression tag	UNP P01871
C	215	SER	-	expression tag	UNP P01871
C	216	ALA	-	expression tag	UNP P01871
C	217	TRP	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
C	218	SER	-	expression tag	UNP P01871
C	219	HIS	-	expression tag	UNP P01871
C	220	PRO	-	expression tag	UNP P01871
C	221	GLN	-	expression tag	UNP P01871
C	222	PHE	-	expression tag	UNP P01871
C	223	GLU	-	expression tag	UNP P01871
C	224	LYS	-	expression tag	UNP P01871
C	225	ILE	-	expression tag	UNP P01871
C	226	ASP	-	expression tag	UNP P01871
C	227	THR	-	expression tag	UNP P01871
C	228	THR	-	expression tag	UNP P01871
D	194	ALA	-	expression tag	UNP P01871
D	195	SER	-	expression tag	UNP P01871
D	196	ALA	-	expression tag	UNP P01871
D	197	TRP	-	expression tag	UNP P01871
D	198	SER	-	expression tag	UNP P01871
D	199	HIS	-	expression tag	UNP P01871
D	200	PRO	-	expression tag	UNP P01871
D	201	GLN	-	expression tag	UNP P01871
D	202	PHE	-	expression tag	UNP P01871
D	203	GLU	-	expression tag	UNP P01871
D	204	LYS	-	expression tag	UNP P01871
D	205	GLY	-	expression tag	UNP P01871
D	206	GLY	-	expression tag	UNP P01871
D	207	GLY	-	expression tag	UNP P01871
D	208	SER	-	expression tag	UNP P01871
D	209	GLY	-	expression tag	UNP P01871
D	210	GLY	-	expression tag	UNP P01871
D	211	GLY	-	expression tag	UNP P01871
D	212	SER	-	expression tag	UNP P01871
D	213	GLY	-	expression tag	UNP P01871
D	214	GLY	-	expression tag	UNP P01871
D	215	SER	-	expression tag	UNP P01871
D	216	ALA	-	expression tag	UNP P01871
D	217	TRP	-	expression tag	UNP P01871
D	218	SER	-	expression tag	UNP P01871
D	219	HIS	-	expression tag	UNP P01871
D	220	PRO	-	expression tag	UNP P01871
D	221	GLN	-	expression tag	UNP P01871
D	222	PHE	-	expression tag	UNP P01871
D	223	GLU	-	expression tag	UNP P01871
D	224	LYS	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
D	225	ILE	-	expression tag	UNP P01871
D	226	ASP	-	expression tag	UNP P01871
D	227	THR	-	expression tag	UNP P01871
D	228	THR	-	expression tag	UNP P01871
E	194	ALA	-	expression tag	UNP P01871
E	195	SER	-	expression tag	UNP P01871
E	196	ALA	-	expression tag	UNP P01871
E	197	TRP	-	expression tag	UNP P01871
E	198	SER	-	expression tag	UNP P01871
E	199	HIS	-	expression tag	UNP P01871
E	200	PRO	-	expression tag	UNP P01871
E	201	GLN	-	expression tag	UNP P01871
E	202	PHE	-	expression tag	UNP P01871
E	203	GLU	-	expression tag	UNP P01871
E	204	LYS	-	expression tag	UNP P01871
E	205	GLY	-	expression tag	UNP P01871
E	206	GLY	-	expression tag	UNP P01871
E	207	GLY	-	expression tag	UNP P01871
E	208	SER	-	expression tag	UNP P01871
E	209	GLY	-	expression tag	UNP P01871
E	210	GLY	-	expression tag	UNP P01871
E	211	GLY	-	expression tag	UNP P01871
E	212	SER	-	expression tag	UNP P01871
E	213	GLY	-	expression tag	UNP P01871
E	214	GLY	-	expression tag	UNP P01871
E	215	SER	-	expression tag	UNP P01871
E	216	ALA	-	expression tag	UNP P01871
E	217	TRP	-	expression tag	UNP P01871
E	218	SER	-	expression tag	UNP P01871
E	219	HIS	-	expression tag	UNP P01871
E	220	PRO	-	expression tag	UNP P01871
E	221	GLN	-	expression tag	UNP P01871
E	222	PHE	-	expression tag	UNP P01871
E	223	GLU	-	expression tag	UNP P01871
E	224	LYS	-	expression tag	UNP P01871
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E	226	ASP	-	expression tag	UNP P01871
E	227	THR	-	expression tag	UNP P01871
E	228	THR	-	expression tag	UNP P01871
F	194	ALA	-	expression tag	UNP P01871
F	195	SER	-	expression tag	UNP P01871
F	196	ALA	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
F	197	TRP	-	expression tag	UNP P01871
F	198	SER	-	expression tag	UNP P01871
F	199	HIS	-	expression tag	UNP P01871
F	200	PRO	-	expression tag	UNP P01871
F	201	GLN	-	expression tag	UNP P01871
F	202	PHE	-	expression tag	UNP P01871
F	203	GLU	-	expression tag	UNP P01871
F	204	LYS	-	expression tag	UNP P01871
F	205	GLY	-	expression tag	UNP P01871
F	206	GLY	-	expression tag	UNP P01871
F	207	GLY	-	expression tag	UNP P01871
F	208	SER	-	expression tag	UNP P01871
F	209	GLY	-	expression tag	UNP P01871
F	210	GLY	-	expression tag	UNP P01871
F	211	GLY	-	expression tag	UNP P01871
F	212	SER	-	expression tag	UNP P01871
F	213	GLY	-	expression tag	UNP P01871
F	214	GLY	-	expression tag	UNP P01871
F	215	SER	-	expression tag	UNP P01871
F	216	ALA	-	expression tag	UNP P01871
F	217	TRP	-	expression tag	UNP P01871
F	218	SER	-	expression tag	UNP P01871
F	219	HIS	-	expression tag	UNP P01871
F	220	PRO	-	expression tag	UNP P01871
F	221	GLN	-	expression tag	UNP P01871
F	222	PHE	-	expression tag	UNP P01871
F	223	GLU	-	expression tag	UNP P01871
F	224	LYS	-	expression tag	UNP P01871
F	225	ILE	-	expression tag	UNP P01871
F	226	ASP	-	expression tag	UNP P01871
F	227	THR	-	expression tag	UNP P01871
F	228	THR	-	expression tag	UNP P01871
G	194	ALA	-	expression tag	UNP P01871
G	195	SER	-	expression tag	UNP P01871
G	196	ALA	-	expression tag	UNP P01871
G	197	TRP	-	expression tag	UNP P01871
G	198	SER	-	expression tag	UNP P01871
G	199	HIS	-	expression tag	UNP P01871
G	200	PRO	-	expression tag	UNP P01871
G	201	GLN	-	expression tag	UNP P01871
G	202	PHE	-	expression tag	UNP P01871
G	203	GLU	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
G	204	LYS	-	expression tag	UNP P01871
G	205	GLY	-	expression tag	UNP P01871
G	206	GLY	-	expression tag	UNP P01871
G	207	GLY	-	expression tag	UNP P01871
G	208	SER	-	expression tag	UNP P01871
G	209	GLY	-	expression tag	UNP P01871
G	210	GLY	-	expression tag	UNP P01871
G	211	GLY	-	expression tag	UNP P01871
G	212	SER	-	expression tag	UNP P01871
G	213	GLY	-	expression tag	UNP P01871
G	214	GLY	-	expression tag	UNP P01871
G	215	SER	-	expression tag	UNP P01871
G	216	ALA	-	expression tag	UNP P01871
G	217	TRP	-	expression tag	UNP P01871
G	218	SER	-	expression tag	UNP P01871
G	219	HIS	-	expression tag	UNP P01871
G	220	PRO	-	expression tag	UNP P01871
G	221	GLN	-	expression tag	UNP P01871
G	222	PHE	-	expression tag	UNP P01871
G	223	GLU	-	expression tag	UNP P01871
G	224	LYS	-	expression tag	UNP P01871
G	225	ILE	-	expression tag	UNP P01871
G	226	ASP	-	expression tag	UNP P01871
G	227	THR	-	expression tag	UNP P01871
G	228	THR	-	expression tag	UNP P01871
H	194	ALA	-	expression tag	UNP P01871
H	195	SER	-	expression tag	UNP P01871
H	196	ALA	-	expression tag	UNP P01871
H	197	TRP	-	expression tag	UNP P01871
H	198	SER	-	expression tag	UNP P01871
H	199	HIS	-	expression tag	UNP P01871
H	200	PRO	-	expression tag	UNP P01871
H	201	GLN	-	expression tag	UNP P01871
H	202	PHE	-	expression tag	UNP P01871
H	203	GLU	-	expression tag	UNP P01871
H	204	LYS	-	expression tag	UNP P01871
H	205	GLY	-	expression tag	UNP P01871
H	206	GLY	-	expression tag	UNP P01871
H	207	GLY	-	expression tag	UNP P01871
H	208	SER	-	expression tag	UNP P01871
H	209	GLY	-	expression tag	UNP P01871
H	210	GLY	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
H	211	GLY	-	expression tag	UNP P01871
H	212	SER	-	expression tag	UNP P01871
H	213	GLY	-	expression tag	UNP P01871
H	214	GLY	-	expression tag	UNP P01871
H	215	SER	-	expression tag	UNP P01871
H	216	ALA	-	expression tag	UNP P01871
H	217	TRP	-	expression tag	UNP P01871
H	218	SER	-	expression tag	UNP P01871
H	219	HIS	-	expression tag	UNP P01871
H	220	PRO	-	expression tag	UNP P01871
H	221	GLN	-	expression tag	UNP P01871
H	222	PHE	-	expression tag	UNP P01871
H	223	GLU	-	expression tag	UNP P01871
H	224	LYS	-	expression tag	UNP P01871
H	225	ILE	-	expression tag	UNP P01871
H	226	ASP	-	expression tag	UNP P01871
H	227	THR	-	expression tag	UNP P01871
H	228	THR	-	expression tag	UNP P01871
K	194	ALA	-	expression tag	UNP P01871
K	195	SER	-	expression tag	UNP P01871
K	196	ALA	-	expression tag	UNP P01871
K	197	TRP	-	expression tag	UNP P01871
K	198	SER	-	expression tag	UNP P01871
K	199	HIS	-	expression tag	UNP P01871
K	200	PRO	-	expression tag	UNP P01871
K	201	GLN	-	expression tag	UNP P01871
K	202	PHE	-	expression tag	UNP P01871
K	203	GLU	-	expression tag	UNP P01871
K	204	LYS	-	expression tag	UNP P01871
K	205	GLY	-	expression tag	UNP P01871
K	206	GLY	-	expression tag	UNP P01871
K	207	GLY	-	expression tag	UNP P01871
K	208	SER	-	expression tag	UNP P01871
K	209	GLY	-	expression tag	UNP P01871
K	210	GLY	-	expression tag	UNP P01871
K	211	GLY	-	expression tag	UNP P01871
K	212	SER	-	expression tag	UNP P01871
K	213	GLY	-	expression tag	UNP P01871
K	214	GLY	-	expression tag	UNP P01871
K	215	SER	-	expression tag	UNP P01871
K	216	ALA	-	expression tag	UNP P01871
K	217	TRP	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
K	218	SER	-	expression tag	UNP P01871
K	219	HIS	-	expression tag	UNP P01871
K	220	PRO	-	expression tag	UNP P01871
K	221	GLN	-	expression tag	UNP P01871
K	222	PHE	-	expression tag	UNP P01871
K	223	GLU	-	expression tag	UNP P01871
K	224	LYS	-	expression tag	UNP P01871
K	225	ILE	-	expression tag	UNP P01871
K	226	ASP	-	expression tag	UNP P01871
K	227	THR	-	expression tag	UNP P01871
K	228	THR	-	expression tag	UNP P01871
L	194	ALA	-	expression tag	UNP P01871
L	195	SER	-	expression tag	UNP P01871
L	196	ALA	-	expression tag	UNP P01871
L	197	TRP	-	expression tag	UNP P01871
L	198	SER	-	expression tag	UNP P01871
L	199	HIS	-	expression tag	UNP P01871
L	200	PRO	-	expression tag	UNP P01871
L	201	GLN	-	expression tag	UNP P01871
L	202	PHE	-	expression tag	UNP P01871
L	203	GLU	-	expression tag	UNP P01871
L	204	LYS	-	expression tag	UNP P01871
L	205	GLY	-	expression tag	UNP P01871
L	206	GLY	-	expression tag	UNP P01871
L	207	GLY	-	expression tag	UNP P01871
L	208	SER	-	expression tag	UNP P01871
L	209	GLY	-	expression tag	UNP P01871
L	210	GLY	-	expression tag	UNP P01871
L	211	GLY	-	expression tag	UNP P01871
L	212	SER	-	expression tag	UNP P01871
L	213	GLY	-	expression tag	UNP P01871
L	214	GLY	-	expression tag	UNP P01871
L	215	SER	-	expression tag	UNP P01871
L	216	ALA	-	expression tag	UNP P01871
L	217	TRP	-	expression tag	UNP P01871
L	218	SER	-	expression tag	UNP P01871
L	219	HIS	-	expression tag	UNP P01871
L	220	PRO	-	expression tag	UNP P01871
L	221	GLN	-	expression tag	UNP P01871
L	222	PHE	-	expression tag	UNP P01871
L	223	GLU	-	expression tag	UNP P01871
L	224	LYS	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
L	225	ILE	-	expression tag	UNP P01871
L	226	ASP	-	expression tag	UNP P01871
L	227	THR	-	expression tag	UNP P01871
L	228	THR	-	expression tag	UNP P01871

- Molecule 2 is a protein called Immunoglobulin J chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	J	106	851	528	150	166	7	0	0

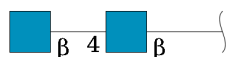
- Molecule 3 is a protein called Erythrocyte membrane protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	M	973	7919	5031	1332	1497	59	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	2629	HIS	-	expression tag	UNP Q6UDW7
M	2630	HIS	-	expression tag	UNP Q6UDW7
M	2631	HIS	-	expression tag	UNP Q6UDW7
M	2632	HIS	-	expression tag	UNP Q6UDW7
M	2633	HIS	-	expression tag	UNP Q6UDW7
M	2634	HIS	-	expression tag	UNP Q6UDW7
M	2635	HIS	-	expression tag	UNP Q6UDW7
M	2636	HIS	-	expression tag	UNP Q6UDW7

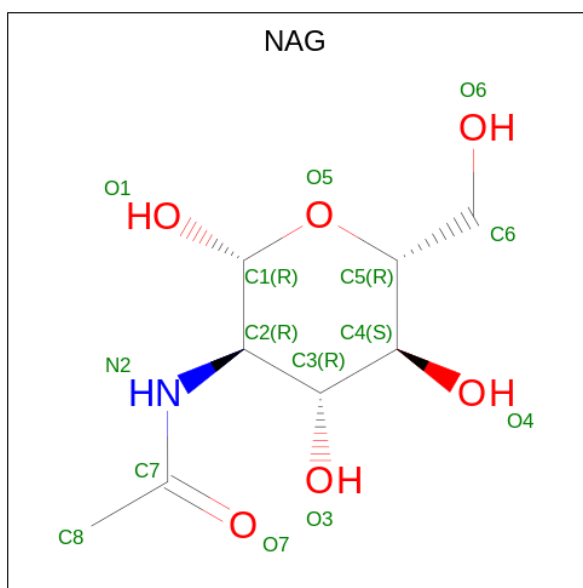
- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:

C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	A	1	Total 14	8	1	5	0
5	B	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	D	1	Total 14	8	1	5	0
5	E	1	Total 14	8	1	5	0
5	F	1	Total 14	8	1	5	0
5	G	1	Total 14	8	1	5	0
5	H	1	Total 14	8	1	5	0
5	K	1	Total 14	8	1	5	0
5	L	1	Total 14	8	1	5	0

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

TYR
ILE
LEU
THR
GLU
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THR
GLU
TYR
LEU
ILE
GLN
THR
ASN
LYS
TYR
ASP
ASN
GLU
PHE
LYS
ASN
LYS
SER
ASN
ASN
ASN
ASP
LYS
ASP
ALA
PRO
ASP
TYR
LEU
SER
LYS
GLU
CYS
LYS
CYS
ASN
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ASN
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ASN
ASN
PRO

TYR
GLU
THR
LEU
GLU
ASP
THR
PHE
LYS
SER
LYS
CYS
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HIS

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

Chain I:  100%

IMAGE
IMAGE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	690345	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.649	Depositor
Minimum map value	-1.117	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.12	Depositor
Map size (\AA)	342.40002, 342.40002, 342.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/1831	0.50	0/2508
1	B	0.27	0/1814	0.50	0/2485
1	C	0.27	0/1817	0.50	0/2488
1	D	0.26	0/1788	0.51	0/2449
1	E	0.26	0/1788	0.50	0/2449
1	F	0.27	0/1782	0.51	0/2442
1	G	0.26	0/1787	0.52	0/2447
1	H	0.25	0/1774	0.52	0/2430
1	K	0.25	0/1781	0.51	0/2437
1	L	0.25	0/1818	0.53	0/2490
2	J	0.26	0/864	0.55	0/1173
3	M	0.26	0/8086	0.47	1/10860 (0.0%)
All	All	0.26	0/26930	0.50	1/36658 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	2047	CYS	CA-CB-SG	5.35	123.64	114.00

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	1786	0	1744	20	0
1	B	1769	0	1729	18	0
1	C	1772	0	1732	30	0
1	D	1743	0	1708	35	0
1	E	1743	0	1710	19	0
1	F	1737	0	1690	19	0
1	G	1742	0	1708	21	0
1	H	1730	0	1691	22	0
1	K	1737	0	1698	29	0
1	L	1773	0	1722	34	0
2	J	851	0	844	15	0
3	M	7919	0	7542	92	0
4	I	28	0	25	0	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
5	E	14	0	13	0	0
5	F	14	0	13	1	0
5	G	14	0	13	1	0
5	H	14	0	13	0	0
5	K	14	0	13	0	0
5	L	14	0	13	0	0
All	All	26470	0	25673	315	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 6.

All (315) 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:F:535:THR:HG22	1:F:551:THR:HG22	1.56	0.86
1:D:471:THR:HG22	1:D:522:THR:HG22	1.62	0.81
1:F:373:THR:OG1	1:F:432:ASP:OD2	1.98	0.81
3:M:2105:ASP:OD2	3:M:2184:ARG:NH1	2.14	0.80
1:D:467:ARG:NH1	3:M:2057:ASN:O	2.15	0.80
3:M:1498:GLN:HE21	3:M:1498:GLN:N	1.80	0.79
1:L:380:ILE:HG21	1:L:408:VAL:HG23	1.64	0.78
1:D:525:GLU:OE1	3:M:2059:ARG:NH1	2.19	0.76
1:G:346:ARG:NH1	1:G:347:VAL:O	2.19	0.76
1:L:426:CYS:SG	1:L:439:GLN:NE2	2.59	0.76
1:C:567:VAL:HG12	1:D:567:VAL:HG13	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:1460:GLN:NE2	3:M:1464:GLU:OE2	2.20	0.75
1:K:489:MET:O	1:K:535:THR:OG1	2.05	0.74
1:E:564:VAL:HG21	1:F:564:VAL:HG21	1.68	0.74
1:A:550:ARG:NH1	1:B:462:GLU:OE1	2.22	0.73
1:F:381:SER:OG	1:F:427:THR:OG1	2.09	0.71
1:E:473:THR:HG22	1:E:520:ILE:HG22	1.71	0.71
3:M:1923:ASN:OD1	3:M:1924:LYS:N	2.23	0.71
1:C:380:ILE:HD12	1:C:428:VAL:HG12	1.72	0.71
1:D:490:GLN:NE2	1:D:532:GLU:OE1	2.24	0.71
3:M:2052:VAL:HG13	3:M:2068:ILE:HG21	1.73	0.70
1:G:363:THR:OG1	1:G:413:ILE:O	2.10	0.70
3:M:1161:ASP:OD1	3:M:1847:ASN:ND2	2.26	0.69
1:G:384:ARG:NH1	1:G:388:GLU:OE1	2.26	0.68
3:M:2186:ILE:HD12	3:M:2269:TYR:CE1	2.29	0.67
2:J:66:ASP:OD1	2:J:67:LEU:N	2.28	0.67
1:H:492:GLY:O	1:K:451:ARG:NH2	2.28	0.66
3:M:1465:ARG:NH2	3:M:1548:SER:O	2.28	0.66
1:C:345:ILE:N	1:C:371:ASP:O	2.29	0.65
1:A:419:ASN:O	1:A:443:ARG:NH2	2.30	0.65
1:L:456:LEU:HD11	1:L:552:VAL:HG11	1.77	0.65
3:M:2267:ASN:OD1	3:M:2271:ARG:NH1	2.29	0.65
3:M:1721:ASN:OD1	3:M:1738:ARG:NH2	2.30	0.65
1:L:366:THR:N	1:L:410:GLU:OE1	2.31	0.64
1:L:487:GLN:NE2	1:L:488:TRP:O	2.29	0.64
3:M:1710:ASP:OD1	3:M:1713:THR:HG22	1.98	0.64
3:M:2078:PHE:O	3:M:2083:TYR:N	2.29	0.64
1:C:535:THR:HG22	1:C:551:THR:HG22	1.80	0.64
1:A:385:GLN:OE1	1:A:423:ARG:NH1	2.31	0.62
1:A:490:GLN:NE2	1:A:532:GLU:OE1	2.33	0.61
1:D:353:SER:O	1:D:356:SER:OG	2.14	0.61
3:M:1414:ASP:OD1	3:M:1417:ARG:NH2	2.34	0.61
3:M:1666:ALA:HB2	3:M:1764:MET:SD	2.41	0.61
1:E:532:GLU:O	1:E:533:THR:OG1	2.16	0.61
1:K:490:GLN:NE2	1:K:532:GLU:OE1	2.34	0.61
1:G:473:THR:HG22	1:G:520:ILE:HG22	1.83	0.60
2:J:30:GLU:OE2	2:J:30:GLU:N	2.34	0.60
1:E:389:ALA:HB1	1:E:391:LYS:NZ	2.17	0.60
1:B:376:ASP:OD2	1:B:377:SER:N	2.34	0.60
1:D:348:PHE:N	1:D:368:LEU:O	2.33	0.60
1:F:559:PRO:O	1:F:560:THR:OG1	2.16	0.60
1:D:454:VAL:HG21	1:D:538:VAL:HG11	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:376:ASP:OD1	1:E:377:SER:N	2.33	0.59
1:F:384:ARG:NH2	1:F:386:ASN:OD1	2.34	0.59
3:M:1498:GLN:N	3:M:1498:GLN:NE2	2.51	0.58
1:B:553:ASP:OD1	1:B:554:LYS:N	2.35	0.58
1:L:367:CYS:SG	1:L:368:LEU:N	2.76	0.58
3:M:2014:THR:OG1	3:M:2017:ASP:OD2	2.21	0.58
1:D:537:VAL:HG12	1:D:549:GLU:HG2	1.85	0.58
1:H:530:THR:OG1	1:H:532:GLU:OE1	2.21	0.58
3:M:1765:GLN:NE2	3:M:1783:MET:O	2.37	0.57
1:C:566:LEU:HD21	1:D:566:LEU:HD23	1.84	0.57
1:G:567:VAL:HG23	1:H:567:VAL:HG13	1.86	0.57
1:L:355:ALA:HB1	1:L:485:PHE:HB2	1.86	0.57
3:M:1469:GLU:OE2	3:M:1473:ARG:NH2	2.36	0.57
3:M:2145:THR:HG22	3:M:2145:THR:O	2.04	0.57
3:M:2123:ILE:HG23	3:M:2124:LYS:HD2	1.85	0.57
1:K:430:HIS:ND1	1:K:432:ASP:OD1	2.38	0.57
1:C:567:VAL:HG12	1:D:567:VAL:CG1	2.33	0.56
3:M:2125:LEU:O	3:M:2129:LEU:HD13	2.06	0.56
1:D:384:ARG:NH2	1:D:388:GLU:OE1	2.39	0.56
1:D:456:LEU:HD11	1:D:488:TRP:CH2	2.41	0.56
1:K:419:ASN:O	1:K:445:LYS:NZ	2.32	0.56
1:L:380:ILE:CG2	1:L:408:VAL:HG23	2.32	0.56
1:H:486:VAL:HG22	1:H:538:VAL:HG12	1.86	0.56
1:K:541:GLU:OE1	1:K:541:GLU:N	2.39	0.56
1:D:454:VAL:HG21	1:D:538:VAL:CG1	2.37	0.55
3:M:1354:TYR:O	3:M:1358:ILE:HD12	2.06	0.55
1:L:472:ILE:HD12	1:L:488:TRP:CZ3	2.42	0.55
1:E:389:ALA:HB1	1:E:391:LYS:HZ1	1.72	0.54
3:M:1633:LEU:HD12	3:M:1636:LEU:HD23	1.87	0.54
1:A:356:SER:O	1:A:360:THR:OG1	2.25	0.54
1:D:553:ASP:OD2	1:D:555:SER:OG	2.20	0.54
1:F:475:LEU:HD21	1:F:477:THR:HG23	1.90	0.54
1:B:365:LEU:HD11	1:B:413:ILE:HD13	1.90	0.54
1:F:552:VAL:HG23	1:F:552:VAL:O	2.08	0.54
1:C:379:THR:OG1	1:C:429:THR:O	2.25	0.54
3:M:1637:PHE:HA	3:M:1640:ILE:HG22	1.90	0.53
3:M:2187:LYS:O	3:M:2190:GLY:N	2.41	0.53
1:A:442:SER:OG	1:A:445:LYS:NZ	2.41	0.53
1:C:566:LEU:HD13	1:H:564:VAL:HG11	1.90	0.53
3:M:1772:VAL:HG22	3:M:1777:GLU:O	2.08	0.53
3:M:1862:TYR:O	3:M:1866:ILE:HD12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:508:GLU:OE1	1:L:511:ALA:N	2.41	0.53
1:G:379:THR:OG1	1:G:429:THR:O	2.26	0.53
1:H:456:LEU:HD22	1:H:552:VAL:HB	1.91	0.52
3:M:1669:LEU:HD22	3:M:1691:ILE:HD13	1.91	0.52
3:M:2052:VAL:HG12	3:M:2058:LEU:HD11	1.91	0.52
3:M:1849:LEU:O	3:M:1849:LEU:HD23	2.09	0.52
1:A:543:LEU:HD11	1:A:548:THR:HG22	1.91	0.52
1:H:369:VAL:HG11	1:H:428:VAL:HG11	1.92	0.52
1:H:549:GLU:O	1:H:550:ARG:NH1	2.42	0.52
3:M:2051:ILE:HD12	3:M:2068:ILE:HD11	1.90	0.52
1:B:416:ASP:OD1	1:B:417:ASP:N	2.43	0.52
3:M:1700:ASP:OD2	3:M:1797:ARG:NH2	2.42	0.52
1:G:537:VAL:HG12	1:G:549:GLU:HG2	1.91	0.52
1:B:351:PRO:HG3	1:B:441:ILE:HG22	1.92	0.51
3:M:1696:TYR:O	3:M:1797:ARG:NH1	2.43	0.51
1:K:347:VAL:HG23	1:K:369:VAL:HA	1.91	0.51
1:E:439:GLN:OE1	1:E:440:THR:N	2.42	0.51
1:H:433:LEU:HB2	1:H:437:LEU:HD11	1.93	0.51
3:M:1781:LEU:HD23	3:M:1781:LEU:O	2.10	0.51
3:M:2204:VAL:HG22	3:M:2228:ILE:HG23	1.91	0.51
1:K:527:GLU:OE1	1:K:527:GLU:N	2.44	0.51
1:L:490:GLN:OE1	1:L:495:LEU:HD21	2.11	0.51
3:M:2064:PHE:O	3:M:2068:ILE:N	2.44	0.51
1:C:419:ASN:O	1:C:443:ARG:NH2	2.44	0.50
1:C:564:VAL:HG21	1:H:566:LEU:HD23	1.93	0.50
1:L:365:LEU:O	1:L:366:THR:HG23	2.11	0.50
3:M:2085:GLU:N	3:M:2085:GLU:OE1	2.44	0.50
1:A:456:LEU:HD21	1:A:552:VAL:HG12	1.92	0.50
3:M:2156:CYS:O	3:M:2160:LYS:N	2.44	0.50
1:C:566:LEU:CD1	1:H:564:VAL:HG11	2.40	0.50
1:F:537:VAL:HG12	1:F:549:GLU:HB3	1.93	0.50
1:B:472:ILE:HG21	1:B:552:VAL:HG11	1.93	0.50
1:D:456:LEU:HD12	1:D:474:CYS:HA	1.94	0.50
3:M:2061:LEU:N	3:M:2129:LEU:HD23	2.27	0.50
3:M:2189:TRP:CZ2	3:M:2266:ALA:HB1	2.47	0.50
1:F:475:LEU:HD21	1:F:477:THR:CG2	2.42	0.50
1:G:415:GLU:OE1	1:G:415:GLU:N	2.44	0.49
1:L:375:TYR:HB3	1:L:378:VAL:HG22	1.93	0.49
1:K:461:ARG:O	1:K:465:ASN:N	2.46	0.49
1:D:491:ARG:NH1	1:D:532:GLU:OE2	2.45	0.49
3:M:1405:TRP:NE1	3:M:1409:GLU:OE1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:566:LEU:HD23	1:C:566:LEU:H	1.77	0.49
1:F:425:THR:HG22	1:F:440:THR:HB	1.95	0.49
3:M:1038:TRP:NE1	3:M:1042:ILE:HD11	2.28	0.49
1:C:385:GLN:N	1:C:422:GLU:OE2	2.42	0.48
1:D:432:ASP:OD1	1:D:433:LEU:N	2.45	0.48
1:C:382:TRP:HB2	1:C:390:VAL:HG11	1.95	0.48
1:K:369:VAL:HG23	1:K:405:PHE:O	2.13	0.48
1:E:381:SER:O	1:E:427:THR:N	2.43	0.48
3:M:2079:LEU:HD22	3:M:2158:TYR:CE2	2.49	0.48
1:K:486:VAL:HG21	1:K:519:SER:HB2	1.94	0.48
3:M:2049:SER:HB3	3:M:2068:ILE:HG23	1.96	0.48
3:M:2121:ILE:O	3:M:2125:LEU:N	2.41	0.48
1:H:416:ASP:OD1	1:H:417:ASP:N	2.46	0.48
3:M:1796:ILE:HG23	3:M:1891:TYR:HE2	1.79	0.48
1:A:451:ARG:NH1	2:J:134:TYR:OH	2.46	0.48
1:E:371:ASP:OD1	1:E:402:ASN:ND2	2.46	0.48
2:J:8:VAL:HG11	2:J:67:LEU:HD13	1.96	0.48
1:K:416:ASP:OD2	1:K:420:SER:OG	2.32	0.48
1:A:522:THR:HG22	1:B:510:GLN:HE21	1.79	0.47
1:F:535:THR:CG2	1:F:551:THR:HG22	2.36	0.47
1:G:445:LYS:HE2	1:G:445:LYS:HA	1.96	0.47
2:J:129:THR:HG23	2:J:133:CYS:SG	2.54	0.47
1:A:567:VAL:HG23	1:B:567:VAL:HB	1.96	0.47
1:C:472:ILE:HD11	1:C:528:TRP:CD1	2.50	0.47
1:C:520:ILE:HD13	1:D:516:PHE:CE2	2.50	0.47
3:M:2193:VAL:HG23	3:M:2197:LYS:HE2	1.95	0.47
1:D:527:GLU:O	1:D:530:THR:OG1	2.31	0.47
1:H:476:VAL:HG12	1:H:479:PHE:CE1	2.50	0.47
1:C:488:TRP:NE1	1:C:519:SER:OG	2.41	0.47
3:M:2006:ASP:OD1	3:M:2007:ALA:N	2.47	0.47
1:G:357:ILE:O	1:G:361:LYS:N	2.46	0.46
1:H:560:THR:HG22	1:H:562:TYR:CE1	2.50	0.46
3:M:1038:TRP:CE2	3:M:1042:ILE:HD11	2.51	0.46
3:M:2019:LEU:O	3:M:2020:ASP:OD1	2.32	0.46
1:D:378:VAL:HG11	1:D:429:THR:OG1	2.16	0.46
1:D:454:VAL:CG2	1:D:538:VAL:HG11	2.45	0.46
1:K:559:PRO:O	1:K:560:THR:OG1	2.23	0.46
1:E:475:LEU:HD13	1:E:518:HIS:CE1	2.50	0.46
2:J:16:ARG:O	2:J:18:THR:HG23	2.14	0.46
3:M:1839:LYS:H	3:M:1839:LYS:HD2	1.81	0.46
3:M:1142:SER:OG	3:M:1187:GLY:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:456:LEU:HD21	1:H:472:ILE:CG2	2.46	0.46
1:K:400:HIS:CE1	1:K:402:ASN:HB3	2.51	0.46
3:M:2155:LEU:HD21	3:M:2174:PRO:HG2	1.98	0.46
1:B:383:THR:OG1	1:B:425:THR:OG1	2.32	0.45
1:C:564:VAL:HG21	1:H:566:LEU:CD2	2.47	0.45
1:K:538:VAL:O	1:K:538:VAL:HG13	2.16	0.45
3:M:2182:PHE:CB	3:M:2186:ILE:HD11	2.46	0.45
1:A:462:GLU:OE2	1:B:455:TYR:CD1	2.69	0.45
1:D:379:THR:OG1	1:D:380:ILE:N	2.49	0.45
1:F:380:ILE:HG23	1:F:428:VAL:HG22	1.97	0.45
3:M:1893:ASN:O	3:M:1894:LYS:HG2	2.15	0.45
3:M:2079:LEU:HD23	3:M:2162:GLY:HA3	1.98	0.45
1:G:567:VAL:CG2	1:H:567:VAL:HG13	2.47	0.45
1:K:523:VAL:HG21	1:K:534:TYR:OH	2.16	0.45
3:M:1412:MET:O	3:M:1415:ALA:HB3	2.16	0.45
1:G:489:MET:HE2	1:G:537:VAL:HG11	1.97	0.45
1:K:416:ASP:O	1:K:420:SER:N	2.42	0.45
3:M:2070:LYS:HE3	3:M:2151:TRP:HA	1.99	0.45
2:J:12:CYS:HB3	2:J:100:CYS:HA	1.97	0.45
1:B:559:PRO:O	1:C:560:THR:HG22	2.17	0.45
1:L:556:THR:HG22	1:L:556:THR:O	2.15	0.45
3:M:1239:ILE:O	3:M:1242:GLY:N	2.46	0.45
3:M:2093:LEU:CD2	3:M:2173:ILE:HD11	2.46	0.45
2:J:47:GLU:N	2:J:55:PRO:O	2.44	0.45
1:L:564:VAL:HG23	1:L:564:VAL:O	2.17	0.45
3:M:1454:PHE:CZ	3:M:1535:ALA:HB1	2.51	0.45
3:M:2013:LYS:HE2	3:M:2075:GLU:HA	1.98	0.45
3:M:2042:ARG:HA	3:M:2045:GLN:HG2	1.98	0.45
1:E:383:THR:HA	1:E:389:ALA:HB3	1.98	0.45
1:L:489:MET:N	1:L:535:THR:O	2.47	0.45
1:A:572:ALA:O	2:J:35:ARG:NE	2.50	0.44
1:F:427:THR:HG22	1:F:438:LYS:HG2	2.00	0.44
1:A:566:LEU:CD2	1:L:566:LEU:HD21	2.48	0.44
2:J:39:ILE:HB	1:L:566:LEU:HD12	1.99	0.44
1:G:565:SER:OG	5:G:601:NAG:H82	2.18	0.44
1:L:379:THR:O	1:L:380:ILE:HD13	2.18	0.44
1:D:384:ARG:NH2	1:D:389:ALA:O	2.45	0.44
1:L:382:TRP:CZ2	1:L:424:PHE:HB3	2.52	0.44
1:G:454:VAL:O	1:G:550:ARG:NH1	2.51	0.44
1:B:472:ILE:HD13	1:B:552:VAL:HG11	1.98	0.44
1:B:537:VAL:HG22	1:B:549:GLU:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:457:LEU:HD23	1:D:460:ALA:HB2	1.99	0.44
3:M:1139:VAL:N	3:M:1935:GLU:OE2	2.51	0.44
1:A:486:VAL:O	1:A:487:GLN:NE2	2.50	0.43
1:C:347:VAL:O	1:C:439:GLN:NE2	2.44	0.43
1:E:357:ILE:HG22	1:E:363:THR:HA	1.99	0.43
2:J:129:THR:HG23	2:J:129:THR:O	2.18	0.43
1:C:566:LEU:HD21	1:D:566:LEU:CD2	2.48	0.43
1:K:405:PHE:HE2	1:K:407:ALA:HB2	1.83	0.43
3:M:1700:ASP:O	3:M:1704:GLY:N	2.45	0.43
3:M:2143:TRP:CG	3:M:2143:TRP:O	2.72	0.43
1:H:527:GLU:O	1:H:530:THR:OG1	2.37	0.43
1:K:355:ALA:HB1	1:K:485:PHE:HB2	2.00	0.43
1:L:382:TRP:CE3	1:L:426:CYS:HB3	2.53	0.43
3:M:1639:ILE:HD13	3:M:1657:THR:CB	2.48	0.43
1:C:491:ARG:H	1:C:533:THR:HG1	1.63	0.43
3:M:2182:PHE:HB2	3:M:2186:ILE:HD11	2.01	0.43
1:C:460:ALA:HB2	1:D:457:LEU:HD23	2.01	0.43
1:F:564:VAL:O	5:F:601:NAG:H82	2.19	0.43
1:L:490:GLN:HB2	1:L:495:LEU:HD21	1.99	0.43
3:M:1454:PHE:CE2	3:M:1535:ALA:HB1	2.54	0.43
2:J:104:ASP:OD1	2:J:105:ARG:N	2.52	0.43
1:A:566:LEU:HD11	1:L:566:LEU:HD11	2.00	0.43
1:B:556:THR:HG23	1:B:557:GLY:N	2.34	0.43
1:L:456:LEU:HD11	1:L:552:VAL:CG1	2.48	0.43
3:M:1339:LEU:HD23	3:M:1343:PHE:HD2	1.84	0.42
1:F:477:THR:HG22	1:F:516:PHE:HB2	2.02	0.42
3:M:2066:GLU:OE1	3:M:2148:LYS:NZ	2.52	0.42
1:C:456:LEU:HD22	1:C:552:VAL:HB	2.00	0.42
1:G:462:GLU:OE1	1:G:462:GLU:N	2.48	0.42
1:K:400:HIS:CE1	1:K:402:ASN:CB	3.02	0.42
1:L:382:TRP:CE3	1:L:410:GLU:HG2	2.54	0.42
1:L:456:LEU:HD12	1:L:457:LEU:N	2.34	0.42
1:D:454:VAL:HG13	1:D:474:CYS:SG	2.59	0.42
1:F:552:VAL:HA	1:F:556:THR:HG21	2.01	0.42
1:K:471:THR:HG23	1:K:520:ILE:HG23	2.02	0.42
1:L:476:VAL:HG23	1:L:517:ALA:H	1.84	0.42
3:M:1502:LYS:O	3:M:1506:GLU:OE1	2.37	0.42
1:L:350:ILE:HG23	1:L:350:ILE:O	2.20	0.42
3:M:1708:VAL:O	3:M:1713:THR:HG21	2.20	0.42
1:B:567:VAL:HG22	1:C:567:VAL:HG22	2.02	0.42
3:M:1803:THR:HG21	3:M:1892:LEU:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:1866:ILE:O	3:M:1866:ILE:HG22	2.20	0.42
3:M:2182:PHE:CG	3:M:2186:ILE:HD11	2.54	0.42
1:D:564:VAL:HB	1:E:564:VAL:HG22	2.02	0.42
1:E:345:ILE:N	1:E:370:THR:O	2.52	0.42
1:B:365:LEU:HD13	1:B:424:PHE:HD2	1.85	0.41
1:G:516:PHE:CD2	1:H:520:ILE:HD12	2.55	0.41
3:M:1701:ILE:HD12	3:M:1701:ILE:H	1.84	0.41
3:M:1893:ASN:HA	3:M:1912:ILE:HD11	2.02	0.41
1:A:553:ASP:H	1:A:556:THR:HG22	1.85	0.41
1:C:470:ALA:N	1:C:523:VAL:O	2.50	0.41
1:D:456:LEU:HD23	1:D:552:VAL:HB	2.01	0.41
1:D:546:ARG:O	1:D:547:VAL:HG13	2.20	0.41
1:E:532:GLU:OE1	1:E:532:GLU:N	2.53	0.41
1:K:563:ASN:HD22	1:L:561:LEU:HD21	1.84	0.41
3:M:1639:ILE:HD13	3:M:1657:THR:OG1	2.19	0.41
3:M:2243:GLU:O	3:M:2246:SER:OG	2.30	0.41
1:A:396:ILE:HG23	1:A:407:ALA:HA	2.02	0.41
1:E:376:ASP:O	1:E:377:SER:OG	2.33	0.41
1:L:384:ARG:HH11	1:L:386:ASN:HB3	1.86	0.41
3:M:2020:ASP:HB3	3:M:2234:TRP:HZ2	1.86	0.41
1:A:509:PRO:HG3	1:B:501:VAL:HG23	2.02	0.41
1:D:560:THR:HG22	1:E:560:THR:O	2.20	0.41
1:H:537:VAL:HG21	1:K:545:ASN:HD22	1.85	0.41
1:K:454:VAL:O	1:K:550:ARG:NH1	2.53	0.41
1:K:470:ALA:N	1:K:523:VAL:O	2.46	0.41
2:J:20:ARG:NE	2:J:22:ILE:HD11	2.35	0.41
1:K:509:PRO:HG3	1:L:501:VAL:HG23	2.02	0.41
3:M:1552:ASP:OD1	3:M:1553:PHE:N	2.54	0.41
3:M:2014:THR:HG23	3:M:2082:TYR:HB2	2.02	0.41
1:F:535:THR:HG22	1:F:551:THR:CG2	2.40	0.41
2:J:8:VAL:HG12	2:J:10:ASN:H	1.85	0.41
1:D:545:ASN:ND2	1:E:537:VAL:HG11	2.35	0.41
1:G:541:GLU:N	1:G:541:GLU:OE2	2.54	0.41
1:K:525:GLU:OE1	1:K:529:ASN:ND2	2.54	0.41
1:L:382:TRP:CZ3	1:L:410:GLU:HG2	2.56	0.41
1:L:476:VAL:HG23	1:L:476:VAL:O	2.20	0.41
3:M:1641:ILE:HD13	3:M:1715:TYR:OH	2.20	0.41
3:M:1799:LEU:O	3:M:1803:THR:HG23	2.20	0.41
1:D:365:LEU:HD13	1:D:413:ILE:HD12	2.03	0.41
1:H:369:VAL:HG23	1:H:405:PHE:O	2.21	0.41
1:K:537:VAL:HG12	1:K:549:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:489:MET:SD	1:C:537:VAL:HG21	2.62	0.40
1:E:522:THR:HG21	1:F:510:GLN:HG3	2.03	0.40
1:G:369:VAL:HG21	1:G:372:LEU:HD22	2.03	0.40
1:K:453:ASP:OD1	1:K:453:ASP:O	2.39	0.40
3:M:1601:ASN:OD1	3:M:1672:GLN:NE2	2.43	0.40
3:M:2044:ARG:HB3	3:M:2044:ARG:CZ	2.51	0.40
1:C:463:GLN:OE1	1:C:471:THR:N	2.45	0.40
1:G:509:PRO:HG3	1:H:501:VAL:HG22	2.03	0.40
3:M:1854:ILE:HD12	3:M:1854:ILE:H	1.85	0.40
1:D:521:LEU:CD2	1:D:523:VAL:HG13	2.51	0.40
1:A:567:VAL:HG13	2:J:61:VAL:HA	2.04	0.40
1:G:445:LYS:HD3	1:G:446:GLY:H	1.86	0.40
1:L:488:TRP:HB3	1:L:495:LEU:HD12	2.03	0.40
1:C:365:LEU:HD11	1:C:413:ILE:HD13	2.04	0.40
1:G:391:LYS:HD3	1:G:392:THR:O	2.21	0.40
3:M:1772:VAL:O	3:M:1776:ASN:N	2.54	0.40
3:M:2271:ARG:NH1	3:M:2282:ASN:OD1	2.54	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	229/383 (60%)	224 (98%)	5 (2%)	0	100	100
1	B	226/383 (59%)	218 (96%)	8 (4%)	0	100	100
1	C	227/383 (59%)	221 (97%)	6 (3%)	0	100	100
1	D	222/383 (58%)	214 (96%)	8 (4%)	0	100	100
1	E	222/383 (58%)	213 (96%)	9 (4%)	0	100	100
1	F	222/383 (58%)	208 (94%)	14 (6%)	0	100	100
1	G	222/383 (58%)	218 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	218/383 (57%)	208 (95%)	10 (5%)	0	100	100
1	K	219/383 (57%)	208 (95%)	11 (5%)	0	100	100
1	L	224/383 (58%)	217 (97%)	7 (3%)	0	100	100
2	J	102/136 (75%)	89 (87%)	13 (13%)	0	100	100
3	M	937/2636 (36%)	879 (94%)	58 (6%)	0	100	100
All	All	3270/6602 (50%)	3117 (95%)	153 (5%)	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	205/331 (62%)	204 (100%)	1 (0%)	88	95
1	B	203/331 (61%)	203 (100%)	0	100	100
1	C	203/331 (61%)	202 (100%)	1 (0%)	88	95
1	D	200/331 (60%)	200 (100%)	0	100	100
1	E	200/331 (60%)	200 (100%)	0	100	100
1	F	198/331 (60%)	197 (100%)	1 (0%)	88	95
1	G	200/331 (60%)	200 (100%)	0	100	100
1	H	199/331 (60%)	199 (100%)	0	100	100
1	K	200/331 (60%)	200 (100%)	0	100	100
1	L	204/331 (62%)	203 (100%)	1 (0%)	88	95
2	J	100/128 (78%)	100 (100%)	0	100	100
3	M	838/2391 (35%)	835 (100%)	3 (0%)	91	97
All	All	2950/5829 (51%)	2943 (100%)	7 (0%)	93	98

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	546	ARG
1	C	391	LYS
1	F	346	ARG
1	L	395	ASN
3	M	1498	GLN
3	M	2015	LYS
3	M	2147	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	K	400	HIS
1	K	545	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

2 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	I	1	2,4	14,14,15	0.52	0	17,19,21	0.37	0
4	NAG	I	2	4	14,14,15	0.31	0	17,19,21	0.36	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
4	NAG	I	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

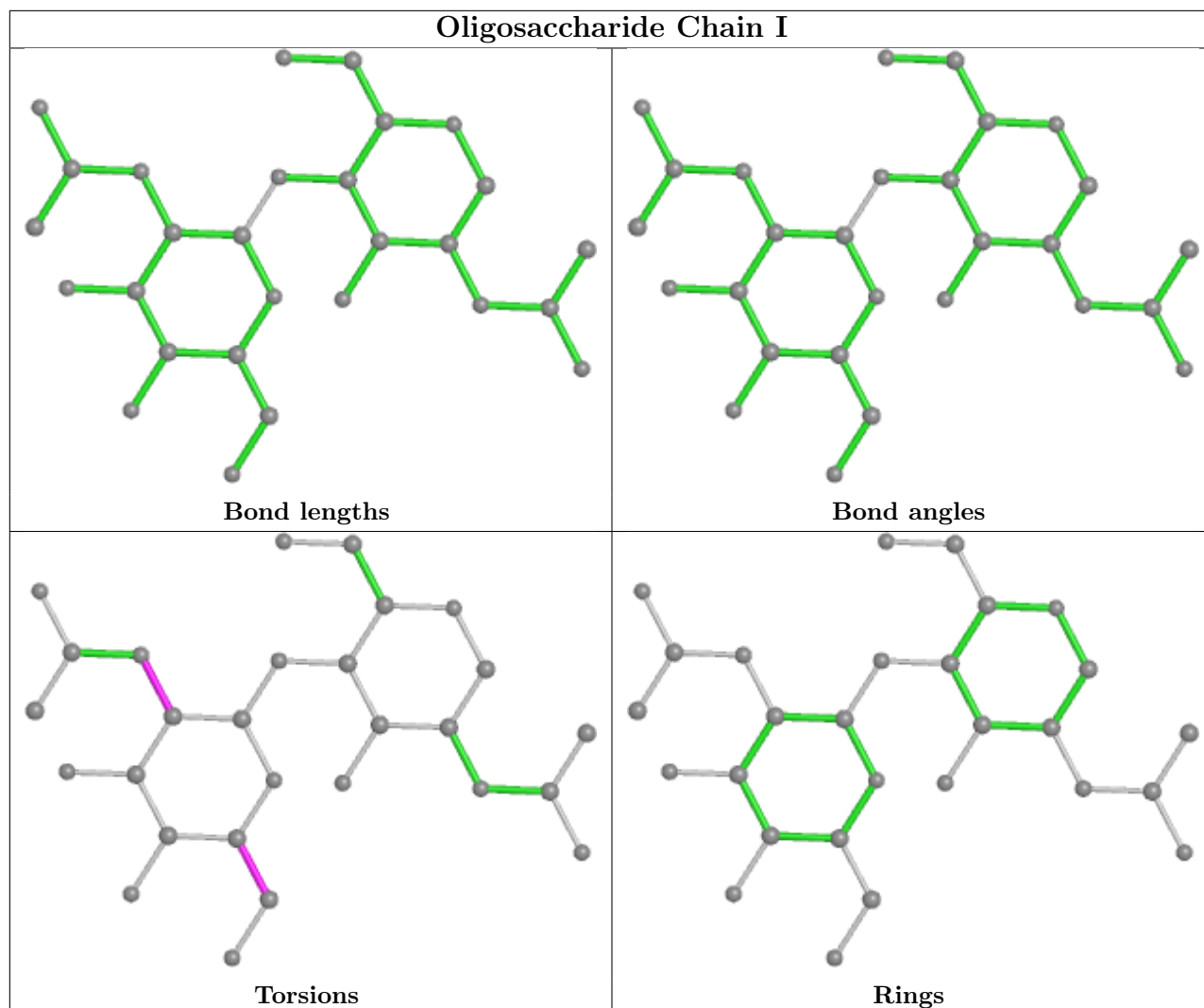
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	2	NAG	C4-C5-C6-O6
4	I	2	NAG	O5-C5-C6-O6
4	I	2	NAG	C1-C2-N2-C7
4	I	2	NAG	C3-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](#)

10 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	H	601	1	14,14,15	0.89	1 (7%)	17,19,21	1.13	1 (5%)
5	NAG	B	601	1	14,14,15	0.24	0	17,19,21	0.41	0
5	NAG	C	601	1	14,14,15	0.20	0	17,19,21	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	G	601	1	14,14,15	0.29	0	17,19,21	0.38	0
5	NAG	D	601	1	14,14,15	0.21	0	17,19,21	0.37	0
5	NAG	K	601	1	14,14,15	0.24	0	17,19,21	0.51	0
5	NAG	L	601	1	14,14,15	0.28	0	17,19,21	0.57	0
5	NAG	E	601	1	14,14,15	0.23	0	17,19,21	0.47	0
5	NAG	A	601	1	14,14,15	0.22	0	17,19,21	0.39	0
5	NAG	F	601	1	14,14,15	0.26	0	17,19,21	0.42	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	H	601	1	-	4/6/23/26	0/1/1/1
5	NAG	B	601	1	-	2/6/23/26	0/1/1/1
5	NAG	C	601	1	-	4/6/23/26	0/1/1/1
5	NAG	G	601	1	-	4/6/23/26	0/1/1/1
5	NAG	D	601	1	-	2/6/23/26	0/1/1/1
5	NAG	K	601	1	-	2/6/23/26	0/1/1/1
5	NAG	L	601	1	-	2/6/23/26	0/1/1/1
5	NAG	E	601	1	-	2/6/23/26	0/1/1/1
5	NAG	A	601	1	-	0/6/23/26	0/1/1/1
5	NAG	F	601	1	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	601	NAG	O5-C1	2.98	1.48	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	601	NAG	C1-O5-C5	4.35	118.09	112.19

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	601	NAG	C3-C2-N2-C7
5	E	601	NAG	C4-C5-C6-O6
5	B	601	NAG	O5-C5-C6-O6
5	L	601	NAG	O5-C5-C6-O6
5	E	601	NAG	O5-C5-C6-O6
5	F	601	NAG	O5-C5-C6-O6
5	D	601	NAG	O5-C5-C6-O6
5	L	601	NAG	C4-C5-C6-O6
5	G	601	NAG	O5-C5-C6-O6
5	C	601	NAG	O5-C5-C6-O6
5	C	601	NAG	C8-C7-N2-C2
5	C	601	NAG	O7-C7-N2-C2
5	K	601	NAG	C8-C7-N2-C2
5	K	601	NAG	O7-C7-N2-C2
5	C	601	NAG	C4-C5-C6-O6
5	B	601	NAG	C4-C5-C6-O6
5	G	601	NAG	C4-C5-C6-O6
5	F	601	NAG	C4-C5-C6-O6
5	G	601	NAG	C1-C2-N2-C7
5	D	601	NAG	C4-C5-C6-O6
5	H	601	NAG	C4-C5-C6-O6
5	H	601	NAG	O5-C5-C6-O6
5	F	601	NAG	C1-C2-N2-C7
5	H	601	NAG	C1-C2-N2-C7
5	G	601	NAG	C3-C2-N2-C7

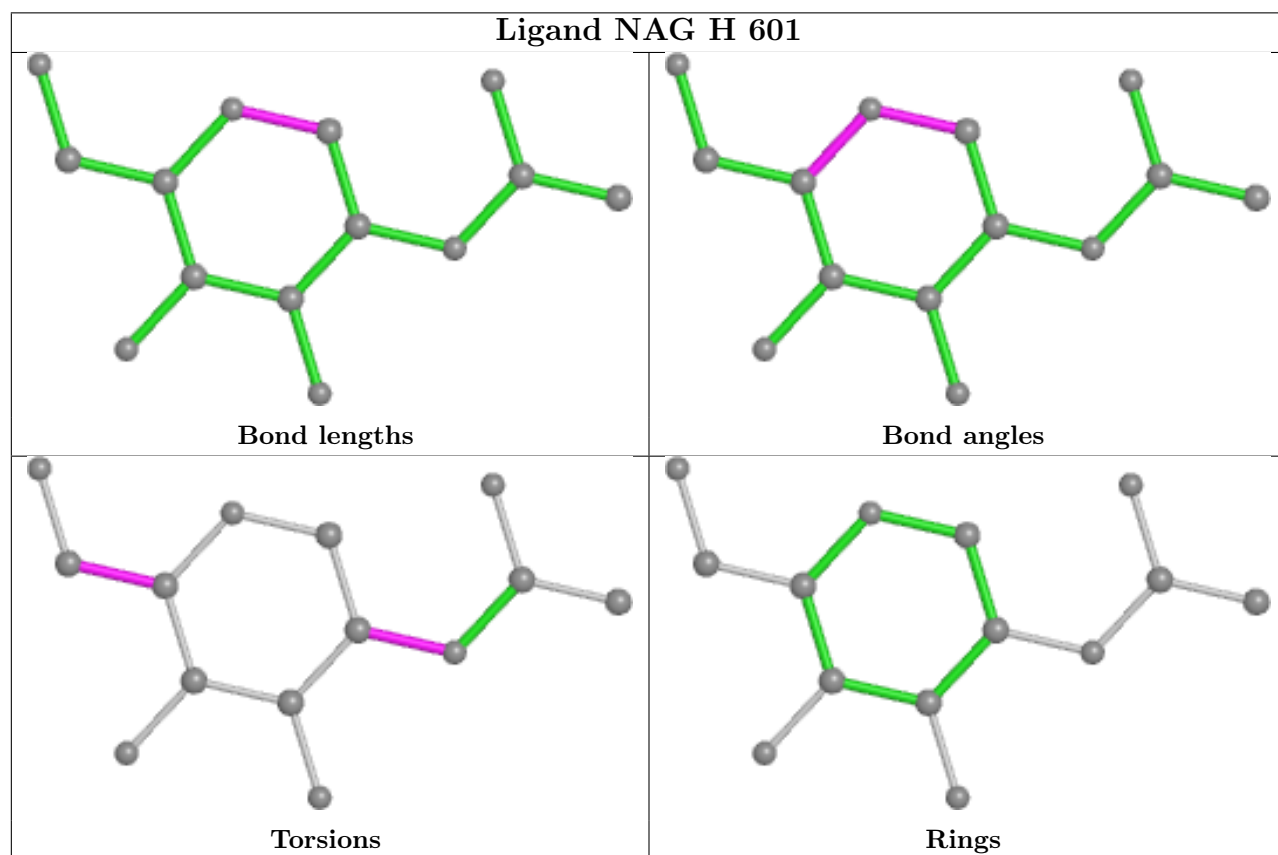
There are no ring outliers.

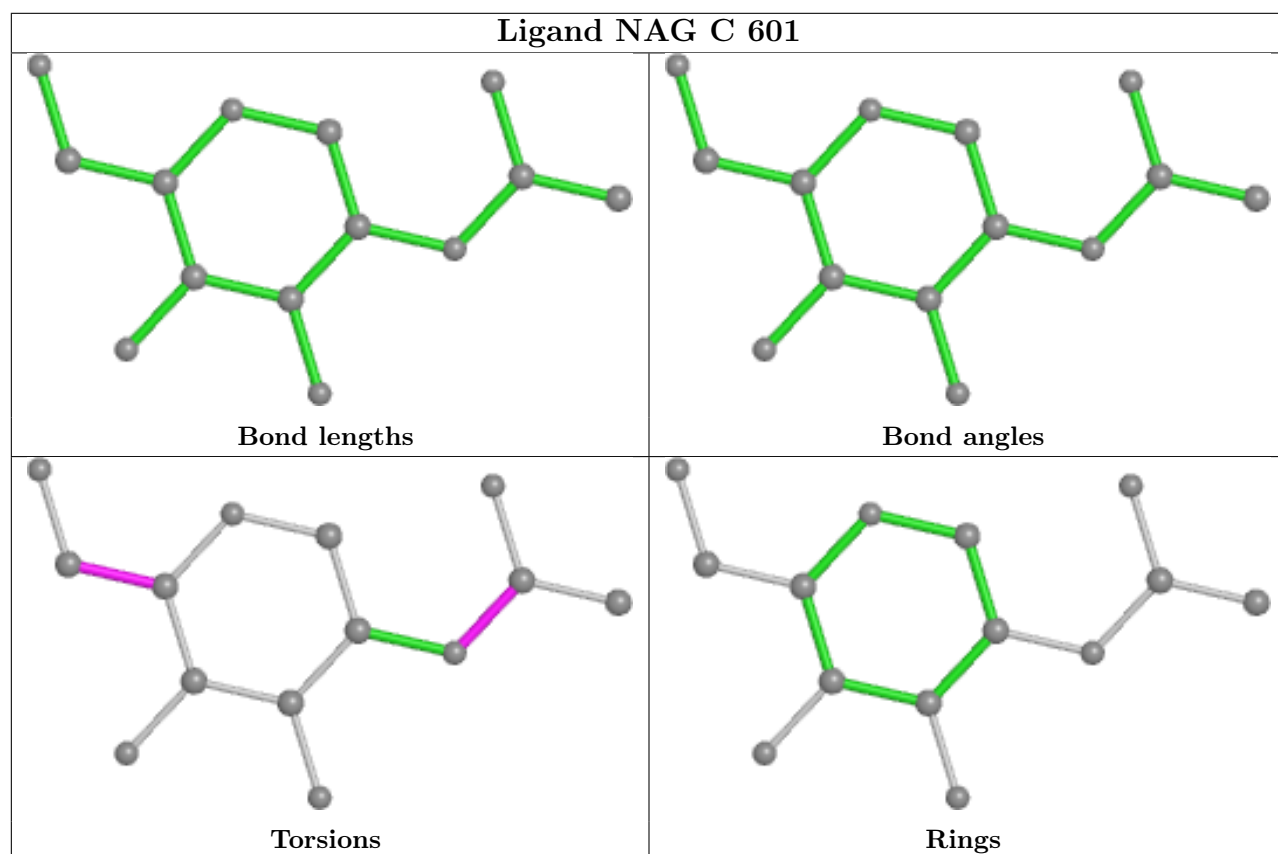
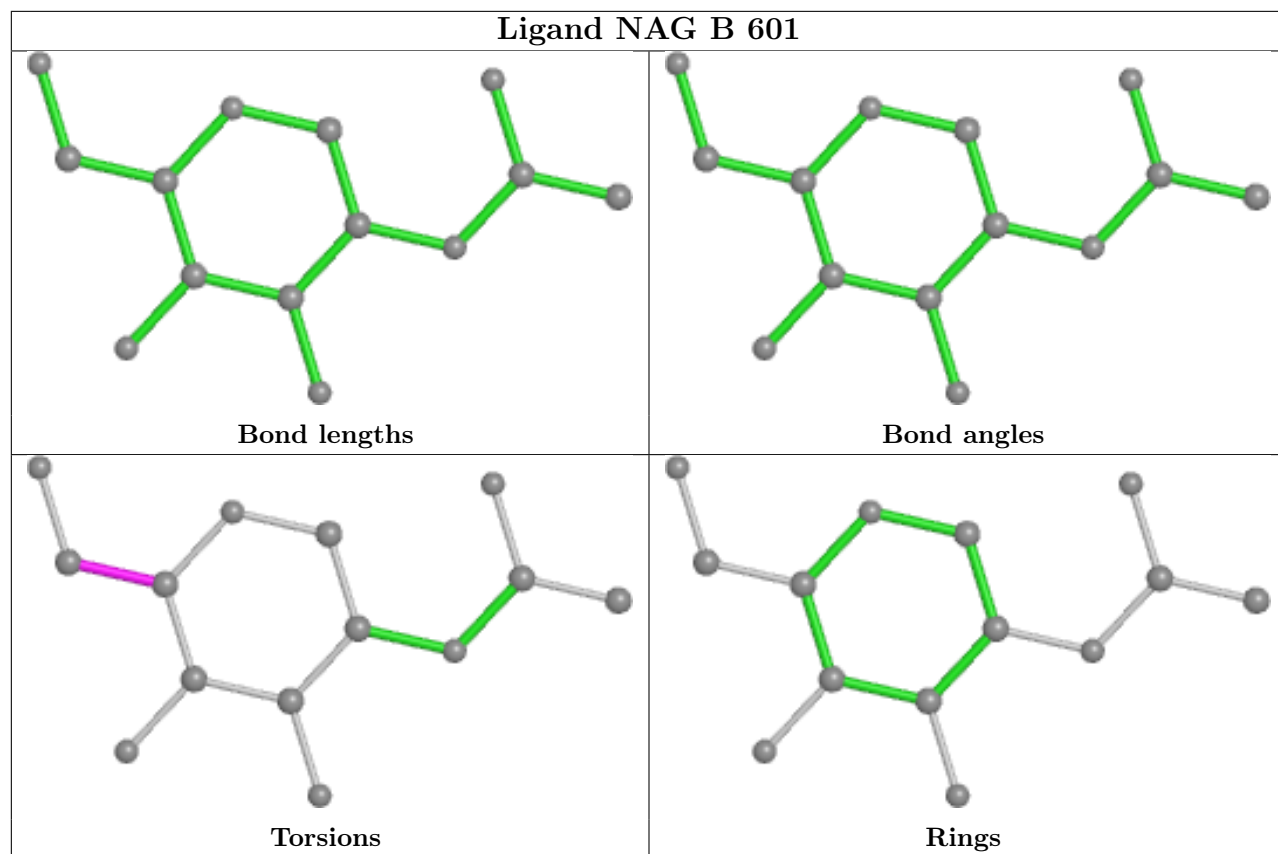
2 monomers are involved in 2 short contacts:

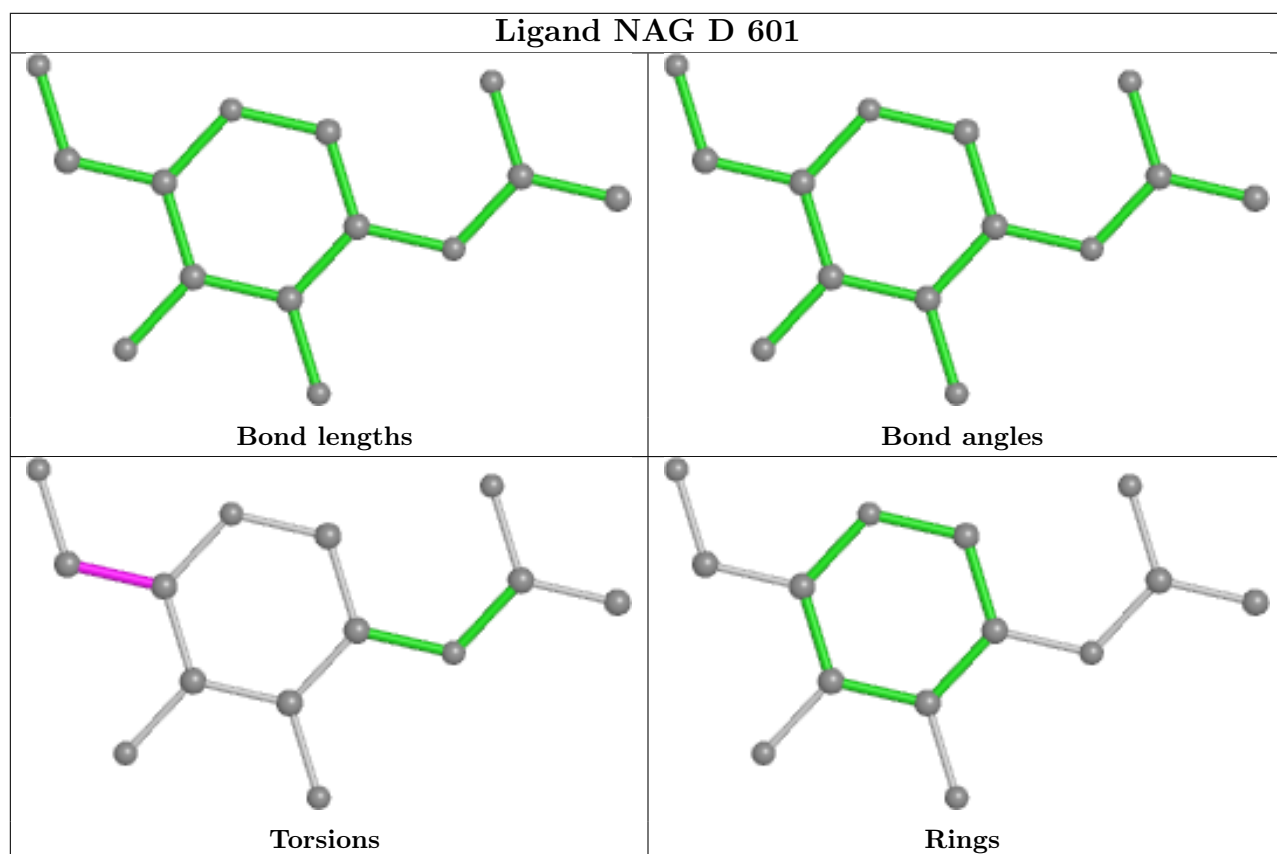
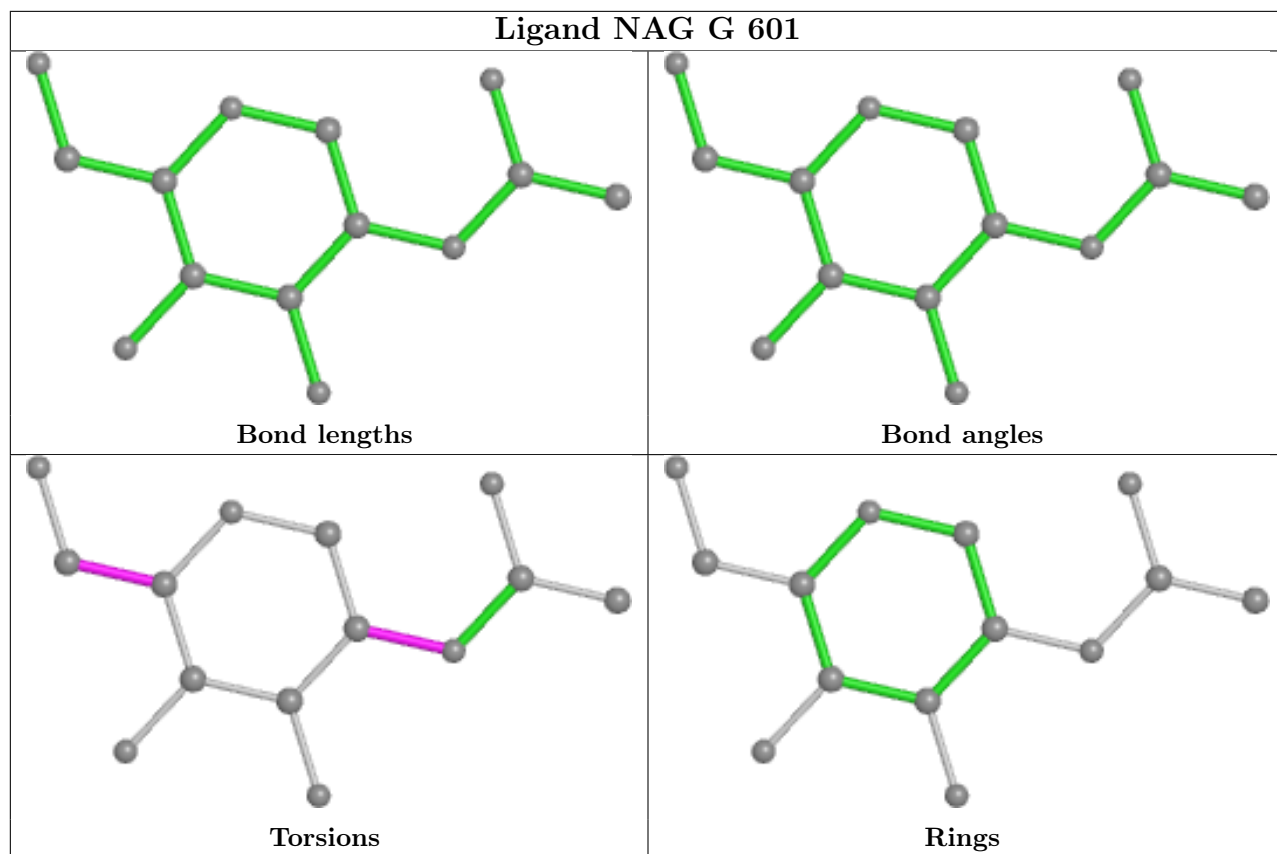
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	601	NAG	1	0
5	F	601	NAG	1	0

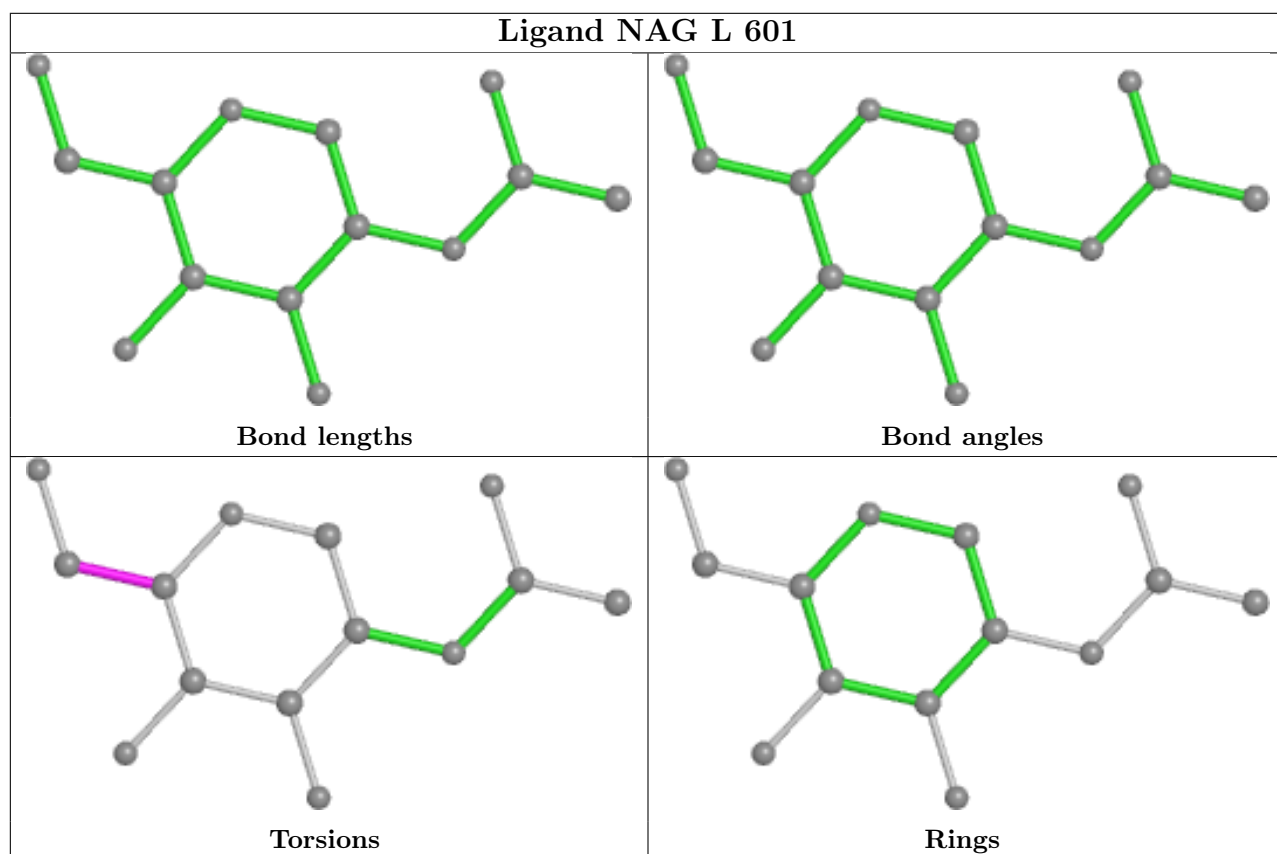
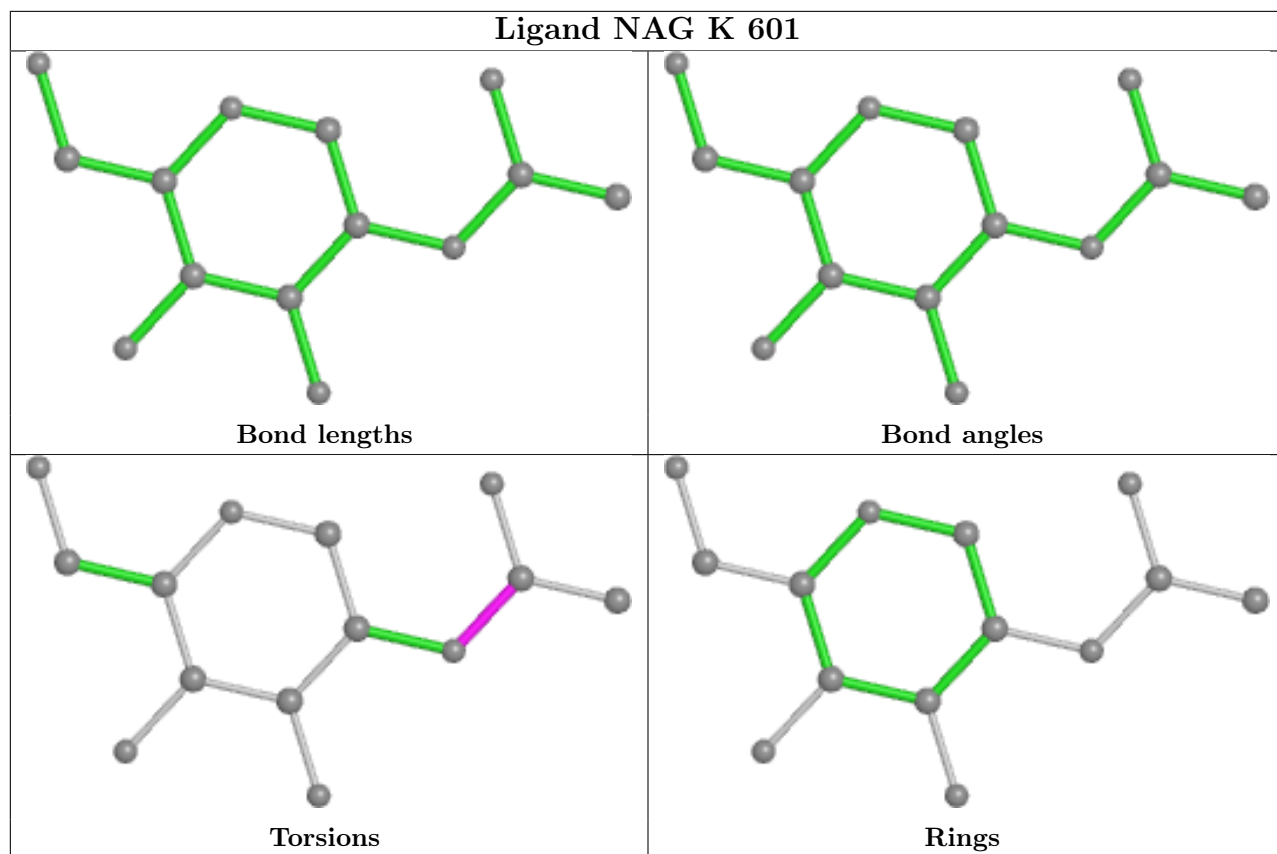
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

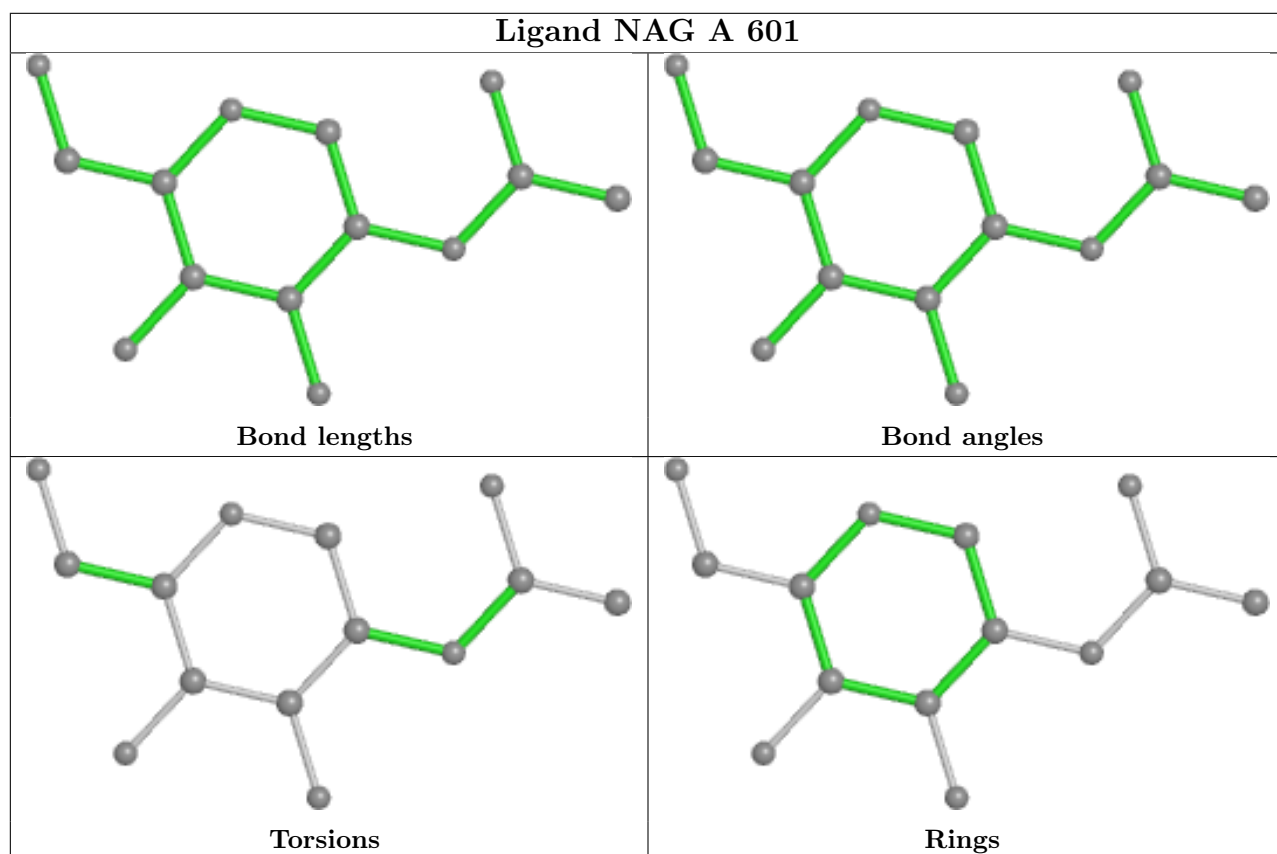
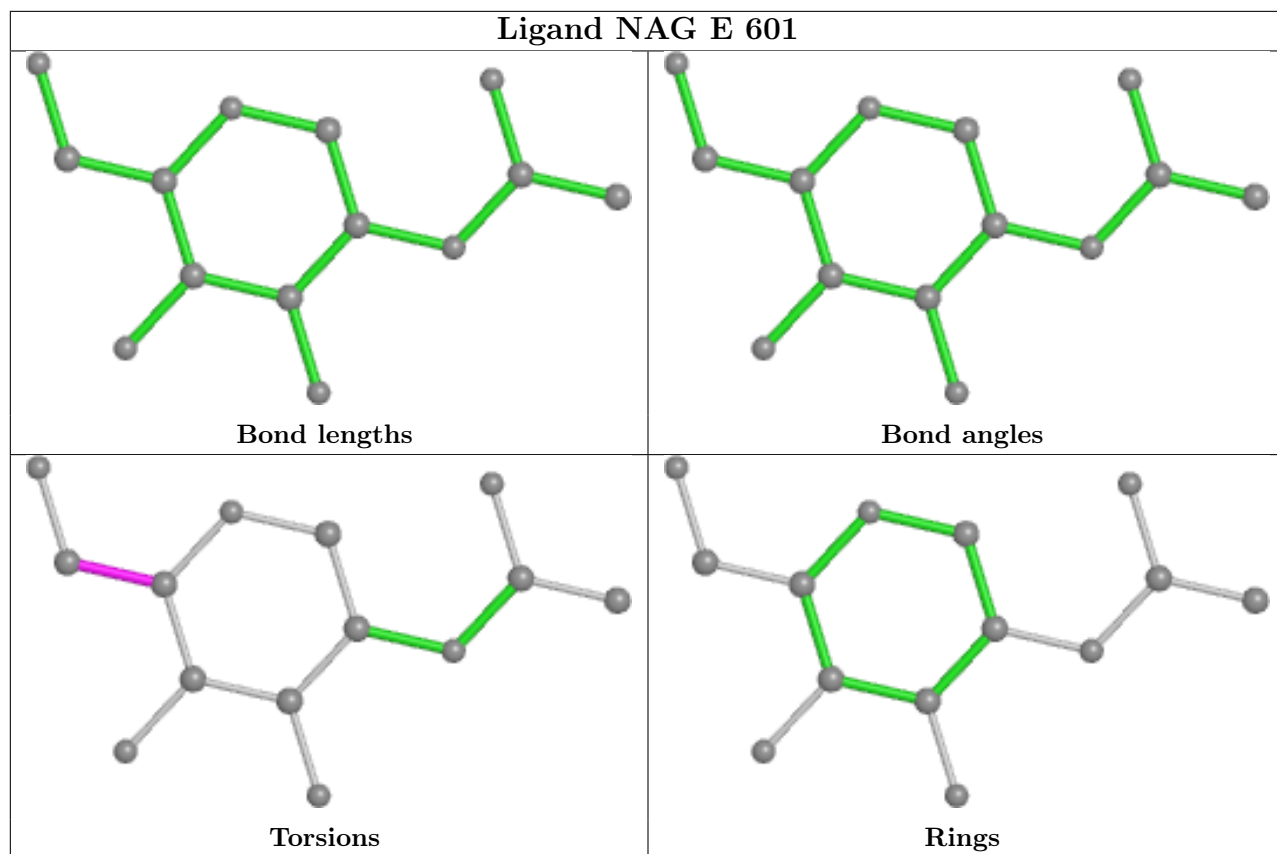
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

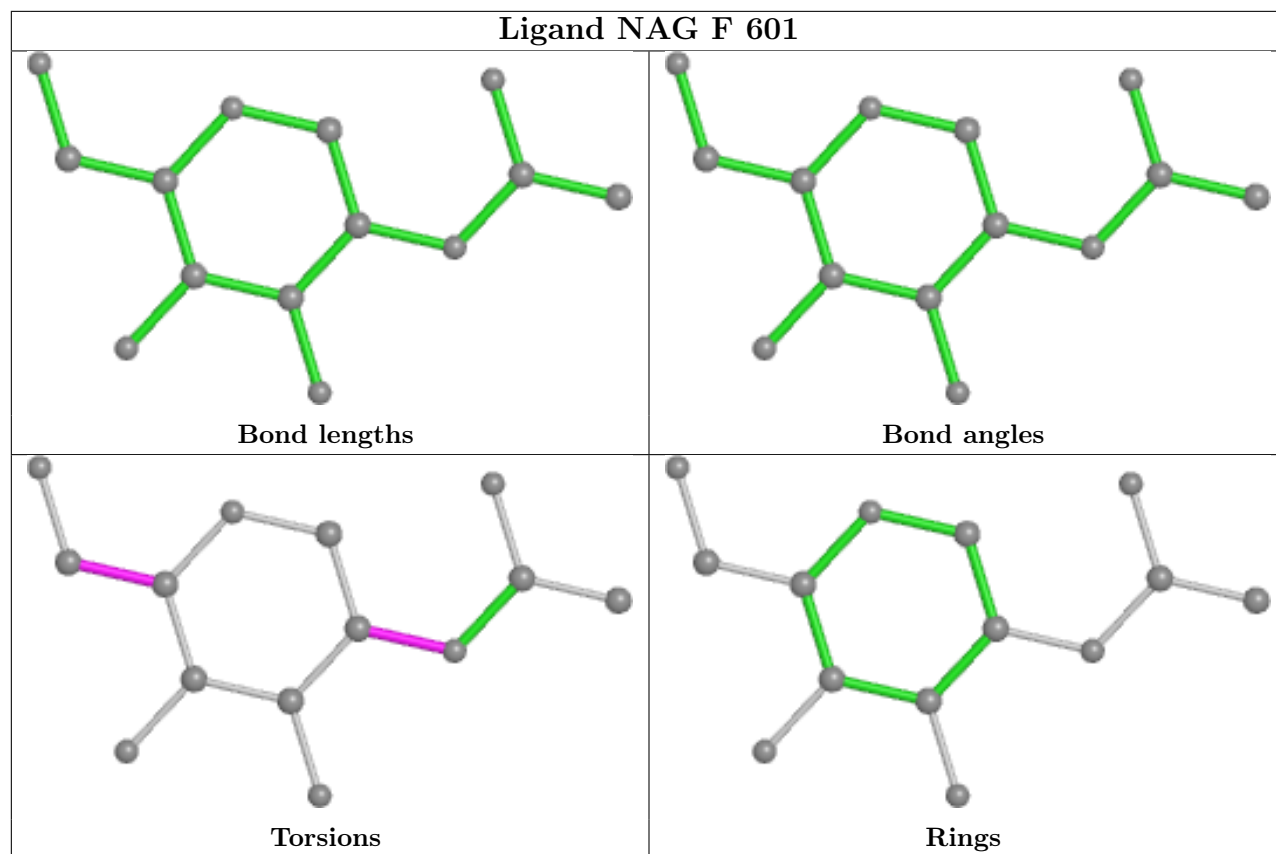












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

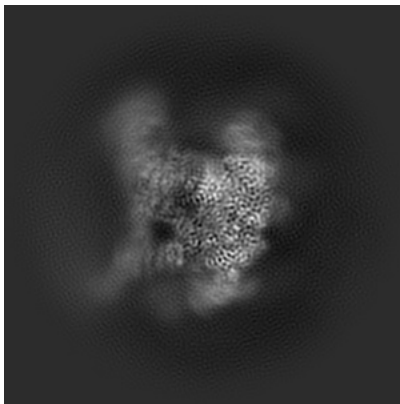
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33542. These allow visual inspection of the internal detail of the map and identification of artifacts.

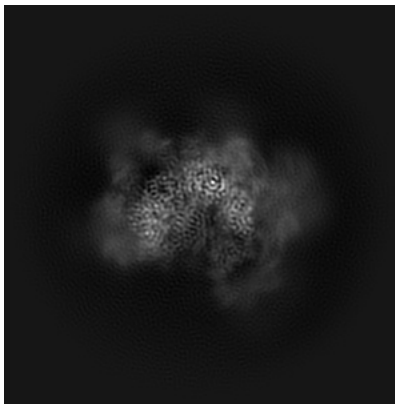
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

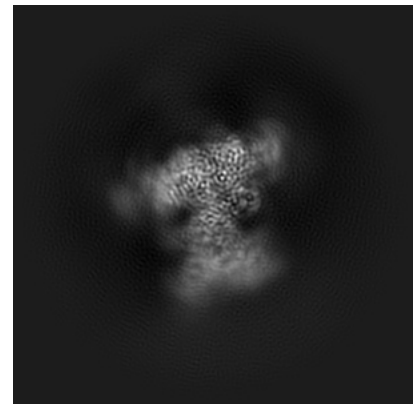
6.1.1 Primary map



X

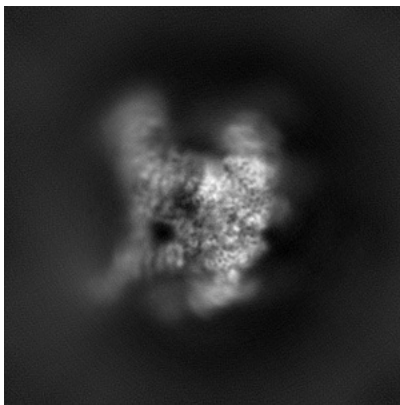


Y

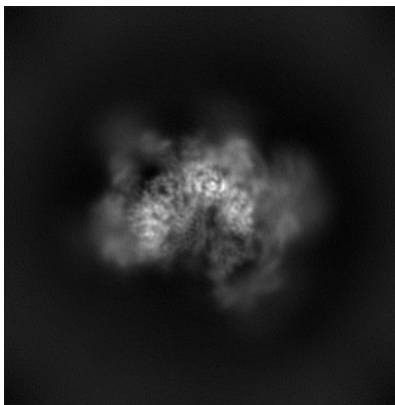


Z

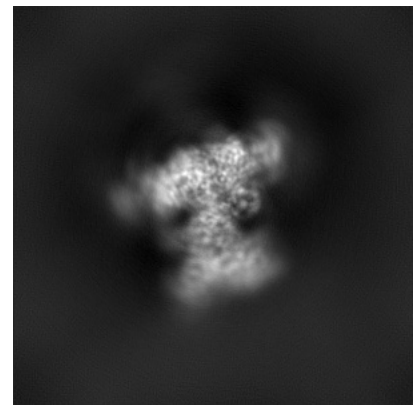
6.1.2 Raw map



X



Y

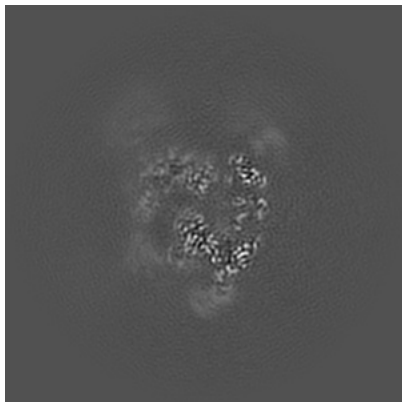


Z

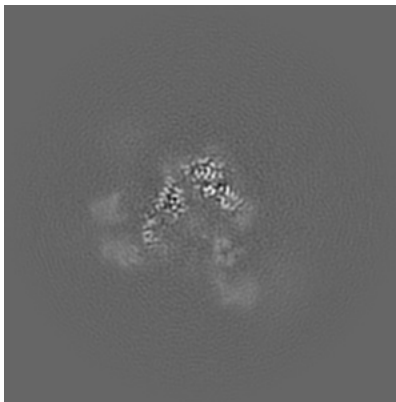
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

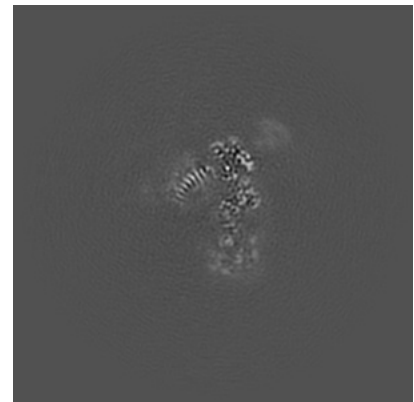
6.2.1 Primary map



X Index: 160

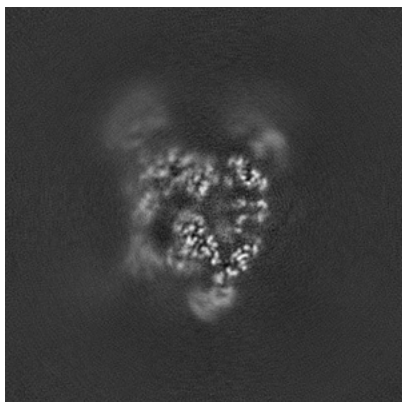


Y Index: 160

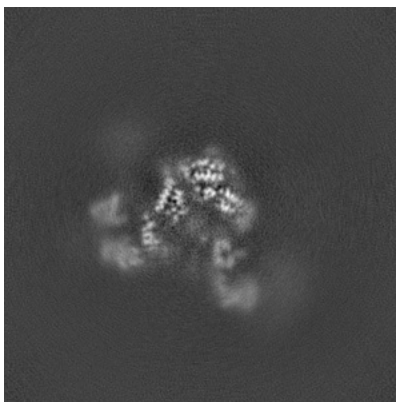


Z Index: 160

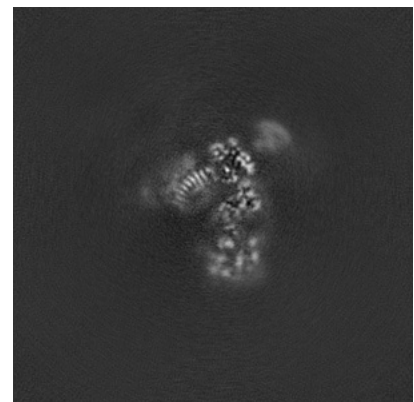
6.2.2 Raw map



X Index: 160



Y Index: 160

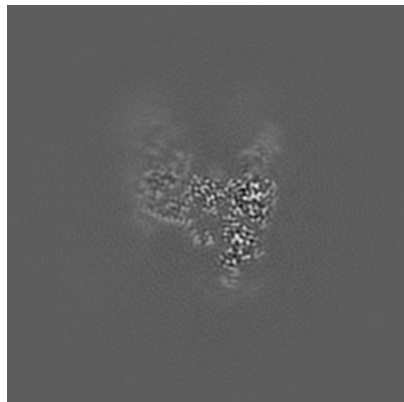


Z Index: 160

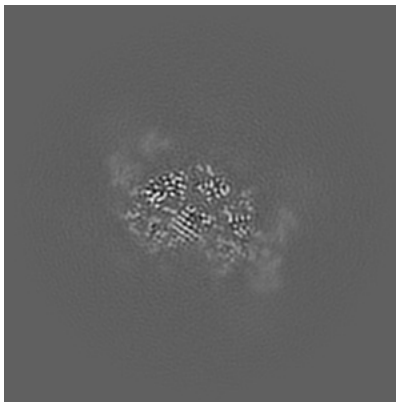
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

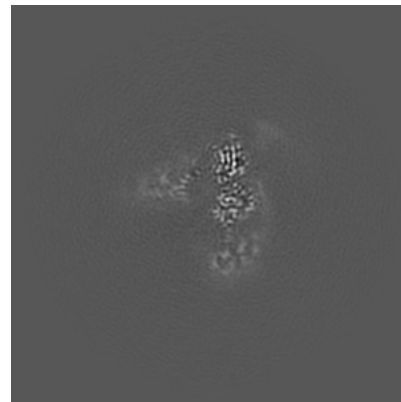
6.3.1 Primary map



X Index: 173

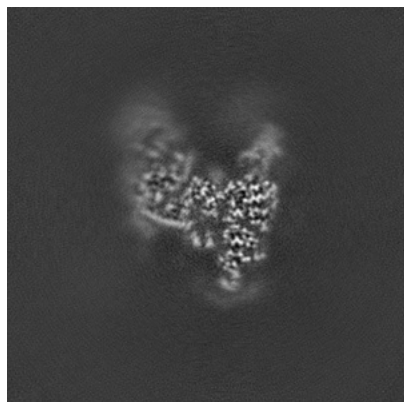


Y Index: 185

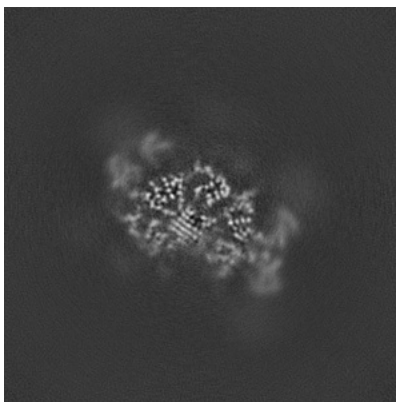


Z Index: 166

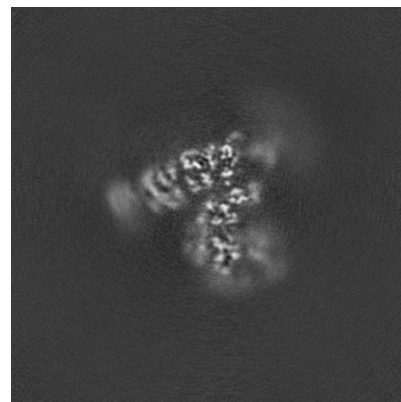
6.3.2 Raw map



X Index: 173



Y Index: 186

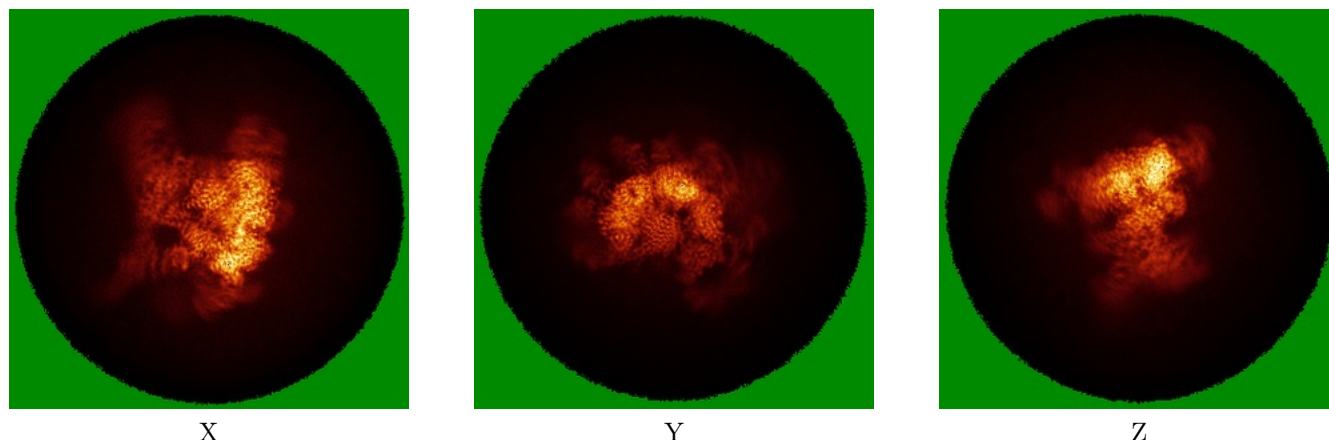


Z Index: 178

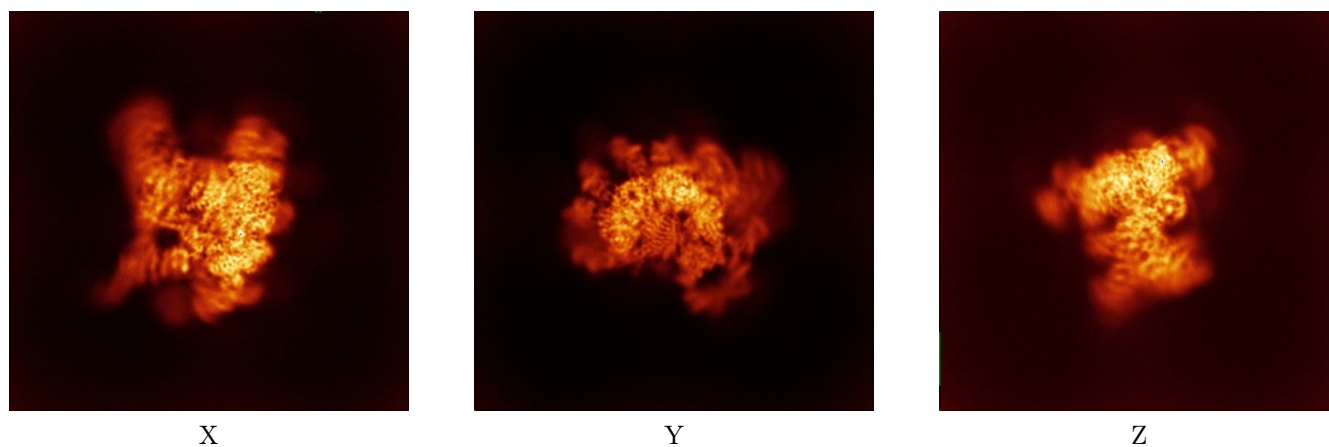
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



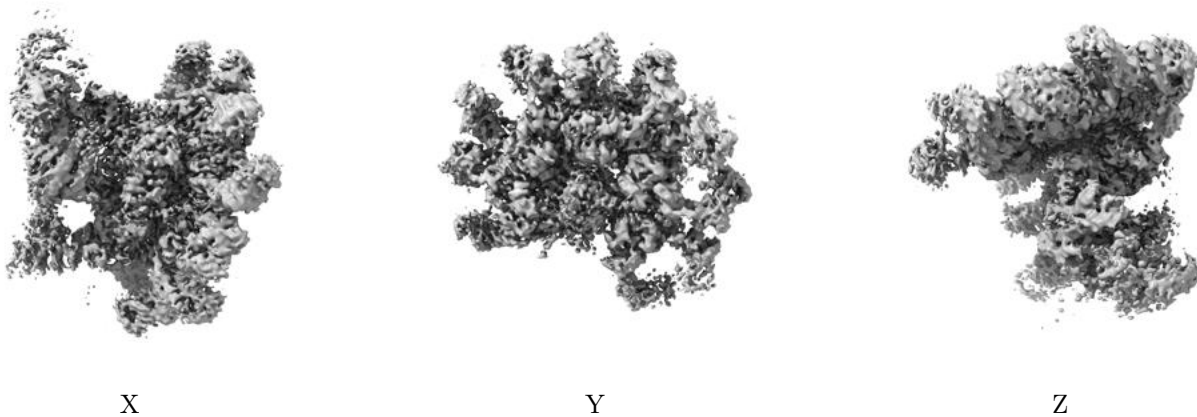
6.4.2 Raw map



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

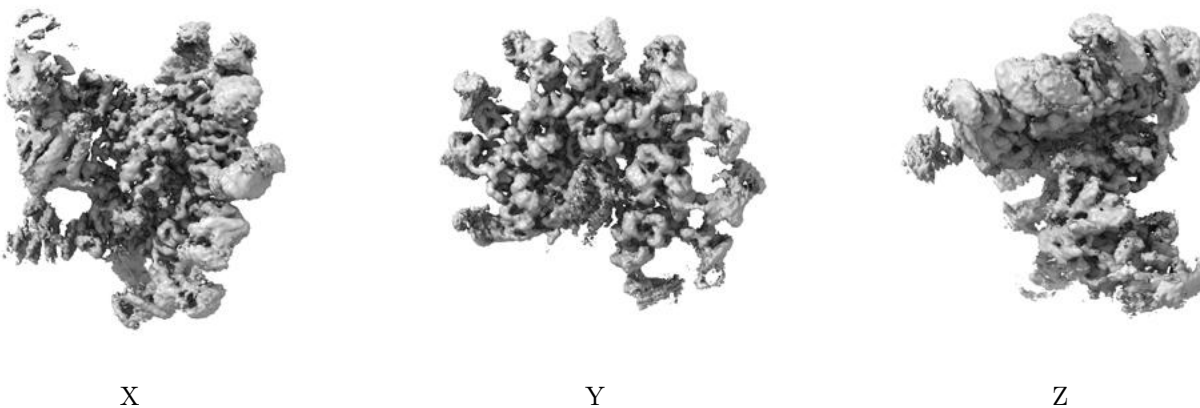
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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



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

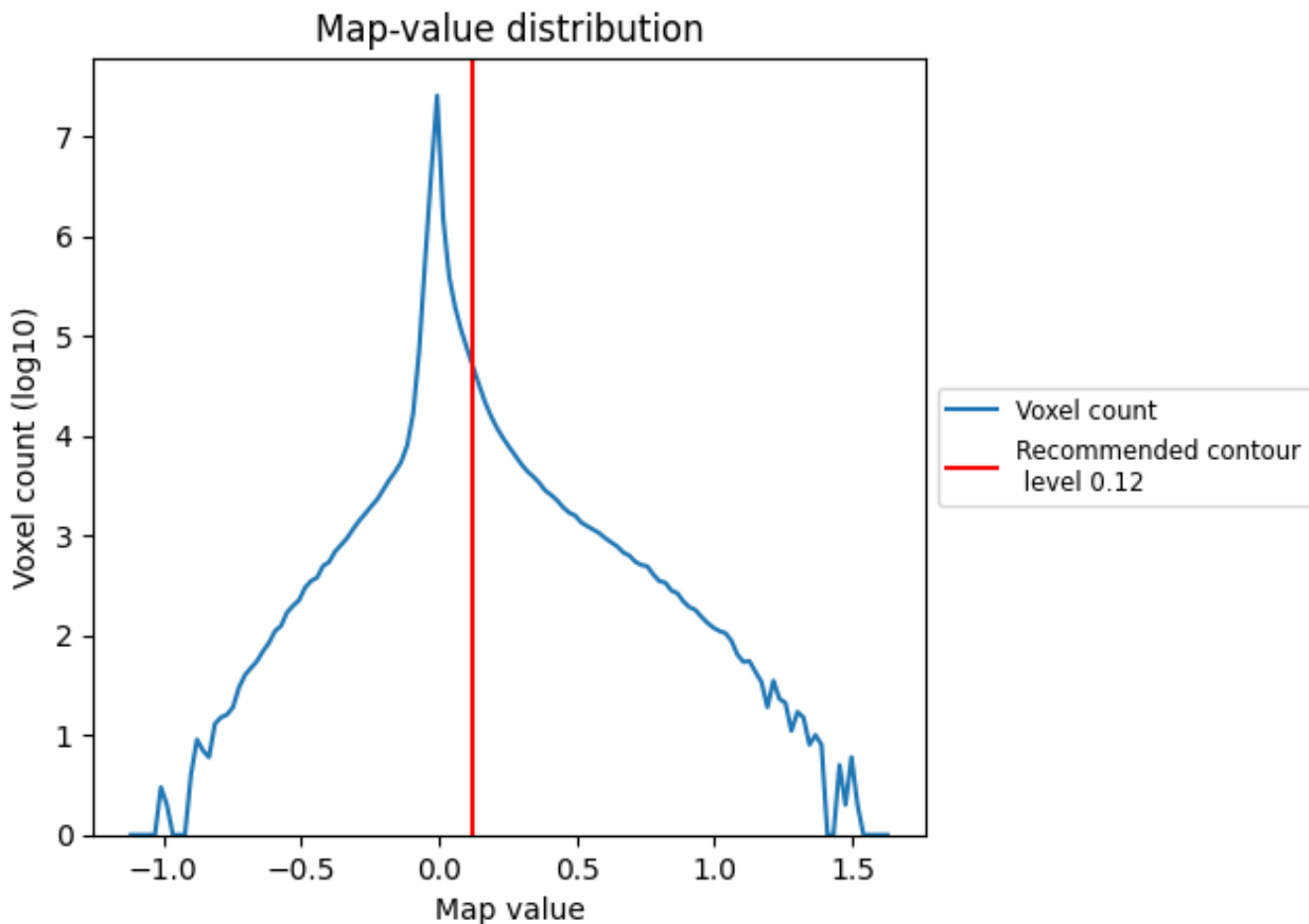
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

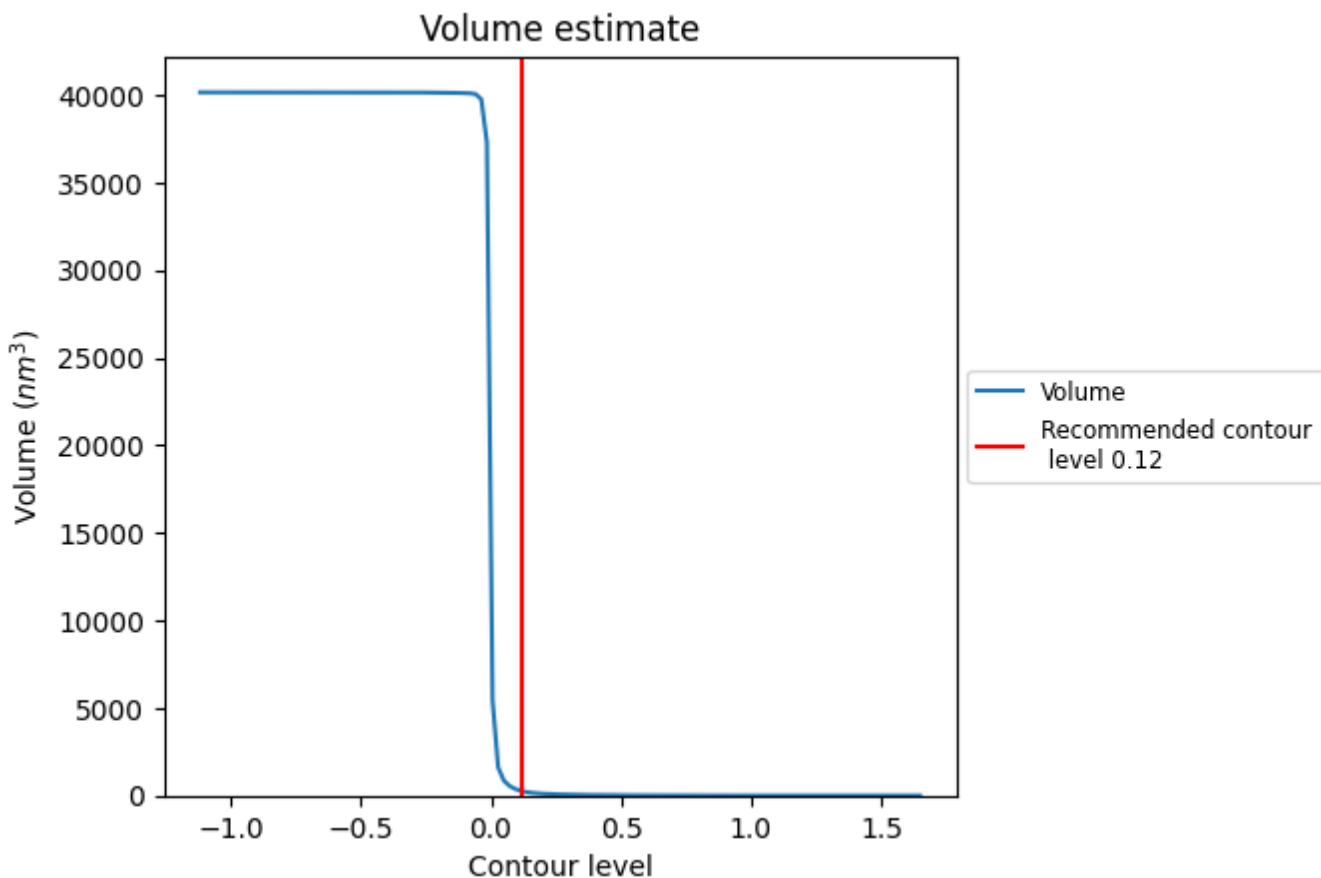
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

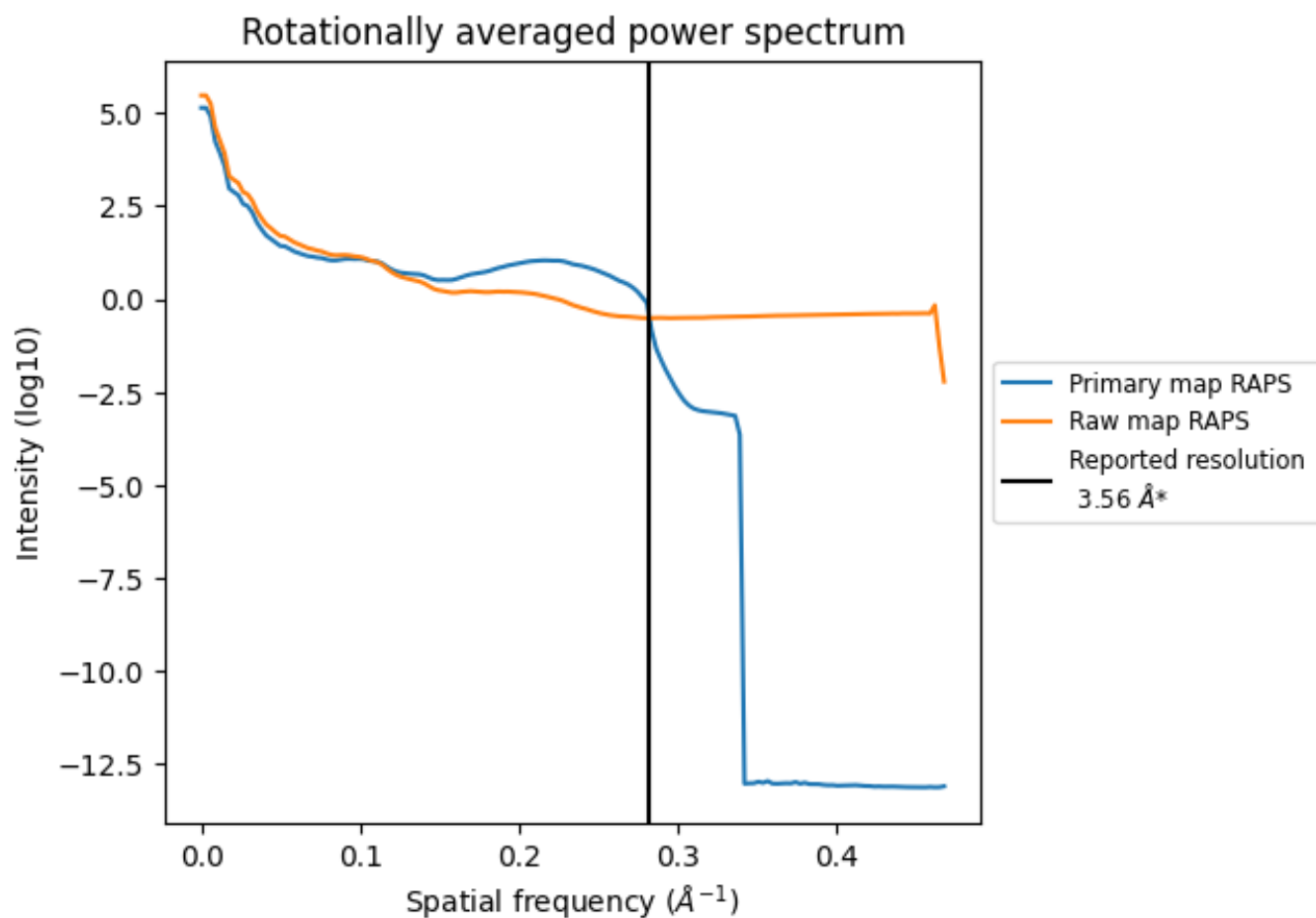
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 256 nm³; this corresponds to an approximate mass of 231 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 i

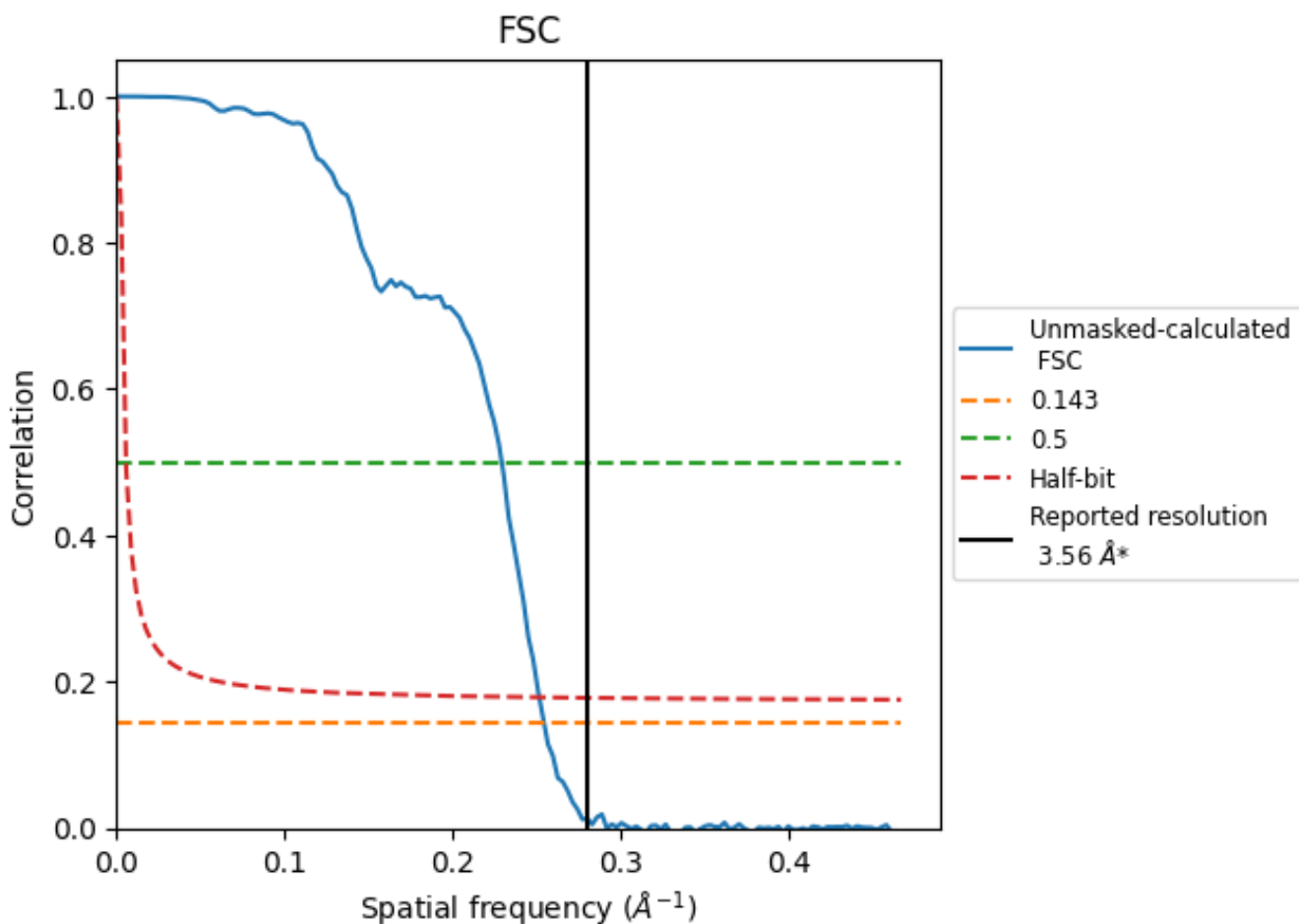


*Reported resolution corresponds to spatial frequency of 0.281 Å⁻¹

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 0.281 Å⁻¹

8.2 Resolution estimates [i](#)

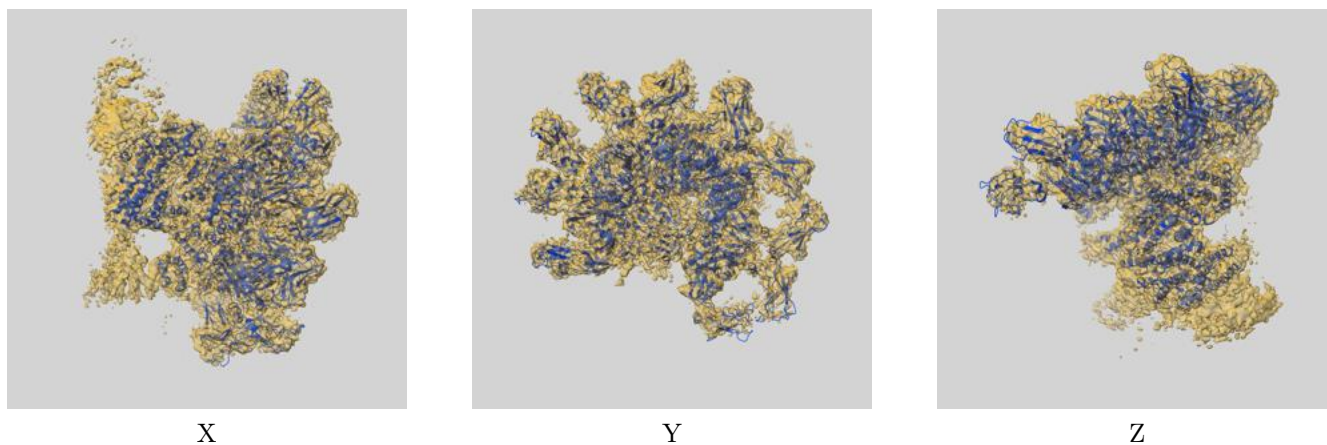
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.56	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.93	4.36	3.97

*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 3.93 differs from the reported value 3.56 by more than 10 %

9 Map-model fit [i](#)

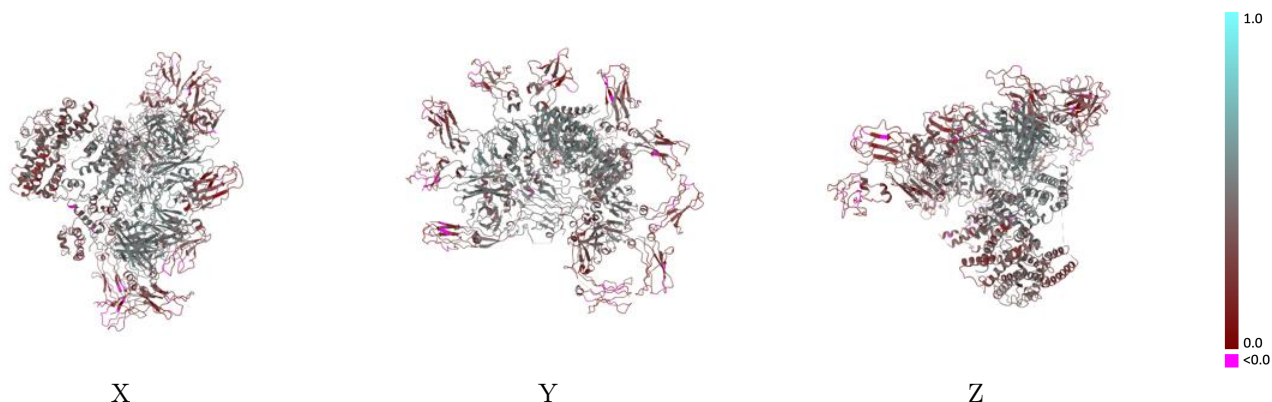
This section contains information regarding the fit between EMDB map EMD-33542 and PDB model 7Y0H. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



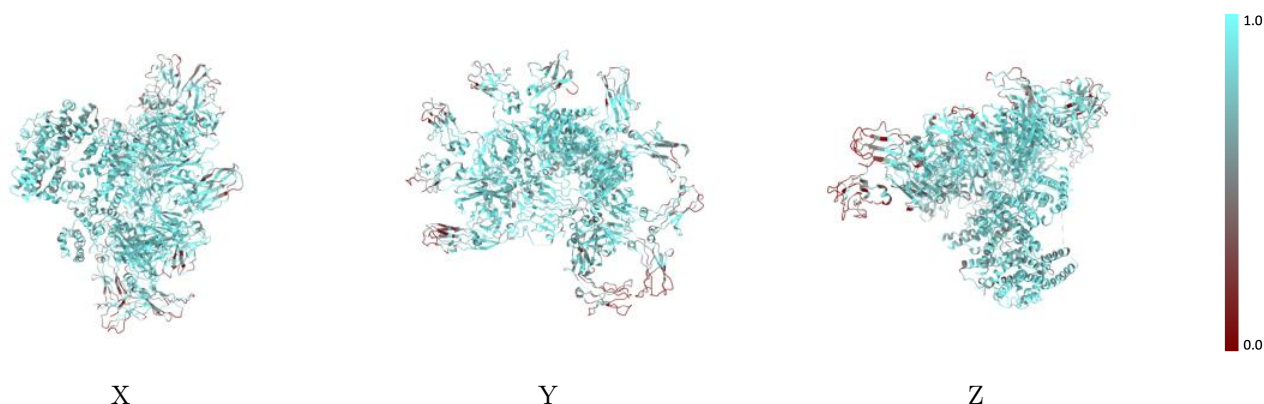
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



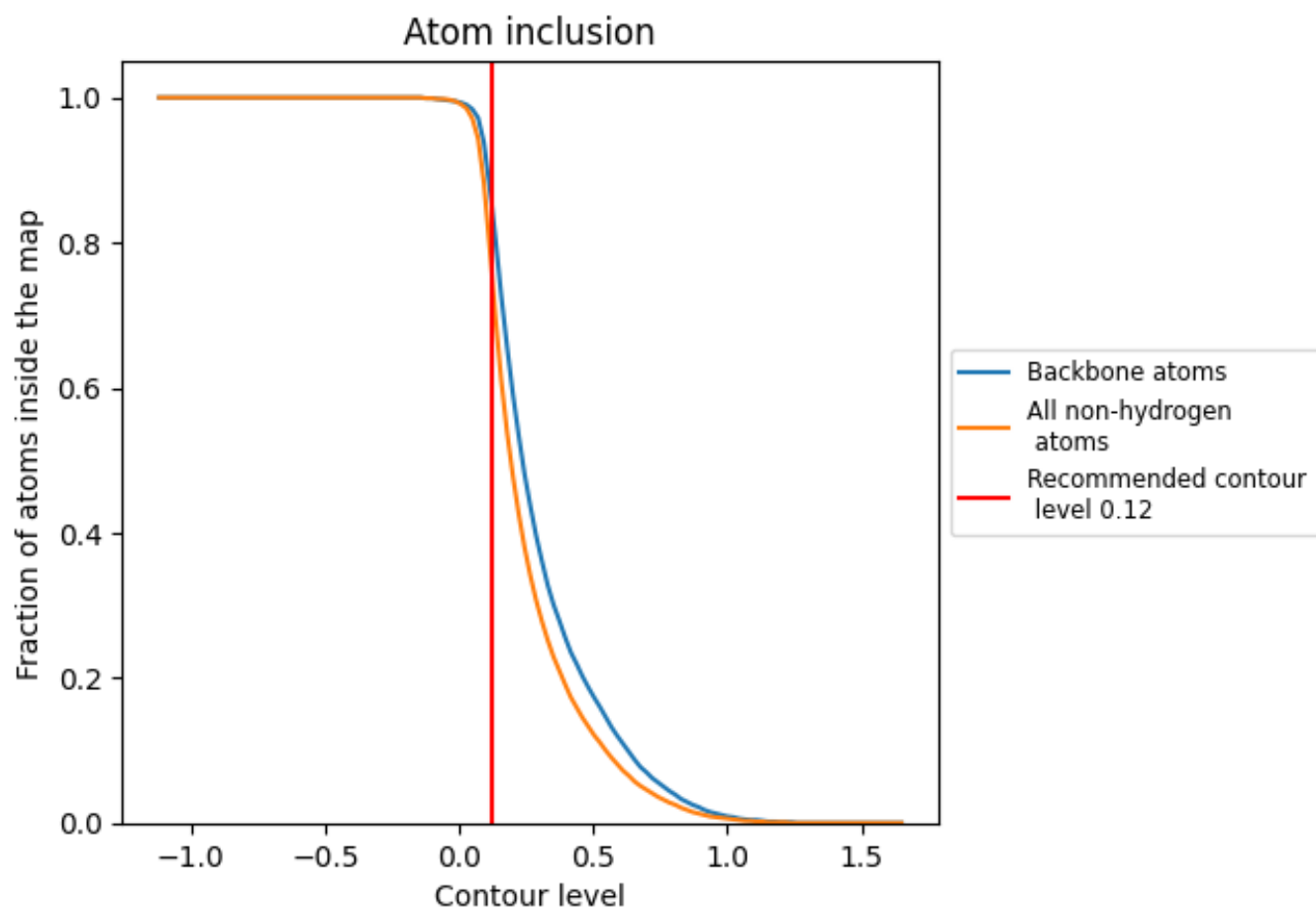
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 86% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

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	 0.7680	 0.3800
A	 0.7170	 0.3520
B	 0.7620	 0.3790
C	 0.7880	 0.4010
D	 0.8070	 0.4100
E	 0.8190	 0.4000
F	 0.8330	 0.4120
G	 0.7930	 0.3980
H	 0.7550	 0.3570
I	 0.6430	 0.3490
J	 0.8050	 0.4450
K	 0.6470	 0.3220
L	 0.5400	 0.2610
M	 0.8150	 0.3970

