



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 08:57 PM UTC

PDB ID : 8XM5 / pdb_00008xm5
EMDB ID : EMD-38463
Title : Cryo-EM structure of SARS-CoV-2 Omicron EG.5 spike protein(6P), RBD-closed state
Authors : Li, L.J.; Gu, Y.H.; Shi, K.Y.; Qi, J.X.; Gao, G.F.
Deposited on : 2023-12-27
Resolution : 2.61 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

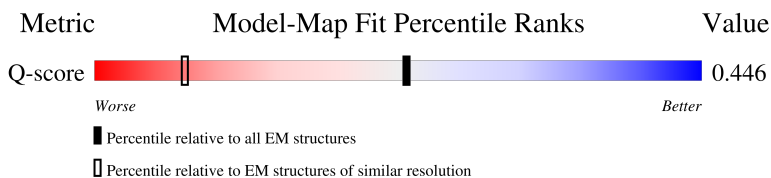
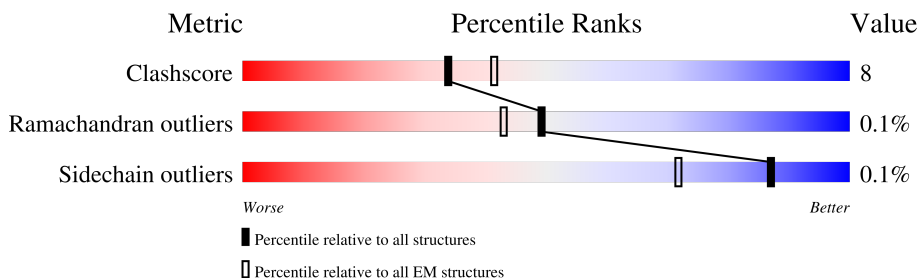
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.61 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	8735 (2.11 - 3.11)

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	1271	10% 66% 14% 20%
1	B	1271	9% 65% 14% 21%
1	C	1271	8% 63% 17% 20%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24226 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1021	Total	C	N	O	S	0	0
			7992	5112	1333	1511	36		
1	B	1008	Total	C	N	O	S	0	0
			7894	5052	1314	1492	36		
1	C	1018	Total	C	N	O	S	0	0
			7962	5096	1327	1503	36		

There are 405 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP P0DTC2
A	-14	GLY	-	expression tag	UNP P0DTC2
A	-13	ILE	-	expression tag	UNP P0DTC2
A	-12	LEU	-	expression tag	UNP P0DTC2
A	-11	PRO	-	expression tag	UNP P0DTC2
A	-10	SER	-	expression tag	UNP P0DTC2
A	-9	PRO	-	expression tag	UNP P0DTC2
A	-8	GLY	-	expression tag	UNP P0DTC2
A	-7	MET	-	expression tag	UNP P0DTC2
A	-6	PRO	-	expression tag	UNP P0DTC2
A	-5	ALA	-	expression tag	UNP P0DTC2
A	-4	LEU	-	expression tag	UNP P0DTC2
A	-3	LEU	-	expression tag	UNP P0DTC2
A	-2	SER	-	expression tag	UNP P0DTC2
A	-1	LEU	-	expression tag	UNP P0DTC2
A	0	VAL	-	expression tag	UNP P0DTC2
A	1	SER	-	expression tag	UNP P0DTC2
A	2	LEU	-	expression tag	UNP P0DTC2
A	3	LEU	-	expression tag	UNP P0DTC2
A	4	SER	-	expression tag	UNP P0DTC2
A	5	VAL	-	expression tag	UNP P0DTC2
A	6	LEU	-	expression tag	UNP P0DTC2
A	7	LEU	-	expression tag	UNP P0DTC2
A	8	MET	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	expression tag	UNP P0DTC2
A	10	CYS	-	expression tag	UNP P0DTC2
A	11	VAL	-	expression tag	UNP P0DTC2
A	12	ALA	-	expression tag	UNP P0DTC2
A	13	GLU	-	expression tag	UNP P0DTC2
A	14	THR	-	expression tag	UNP P0DTC2
A	15	GLY	-	expression tag	UNP P0DTC2
A	16	THR	-	expression tag	UNP P0DTC2
A	17	GLN	-	expression tag	UNP P0DTC2
A	18	CYS	-	expression tag	UNP P0DTC2
A	19	VAL	-	expression tag	UNP P0DTC2
A	20	ASN	-	expression tag	UNP P0DTC2
A	21	LEU	-	expression tag	UNP P0DTC2
A	22	ILE	-	expression tag	UNP P0DTC2
A	23	THR	-	expression tag	UNP P0DTC2
A	24	ARG	-	expression tag	UNP P0DTC2
A	25	THR	-	expression tag	UNP P0DTC2
A	26	GLN	-	expression tag	UNP P0DTC2
A	27	SER	-	expression tag	UNP P0DTC2
A	83	ALA	VAL	variant	UNP P0DTC2
A	142	ASP	GLY	variant	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	146	GLN	HIS	variant	UNP P0DTC2
A	183	GLU	GLN	variant	UNP P0DTC2
A	213	GLU	VAL	variant	UNP P0DTC2
A	252	VAL	GLY	variant	UNP P0DTC2
A	339	HIS	GLY	variant	UNP P0DTC2
A	346	THR	ARG	variant	UNP P0DTC2
A	368	ILE	LEU	variant	UNP P0DTC2
A	371	PHE	SER	variant	UNP P0DTC2
A	373	PRO	SER	variant	UNP P0DTC2
A	375	PHE	SER	variant	UNP P0DTC2
A	376	ALA	THR	variant	UNP P0DTC2
A	405	ASN	ASP	variant	UNP P0DTC2
A	408	SER	ARG	variant	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	440	LYS	ASN	variant	UNP P0DTC2
A	445	PRO	VAL	variant	UNP P0DTC2
A	446	SER	GLY	variant	UNP P0DTC2
A	456	LEU	PHE	variant	UNP P0DTC2
A	460	LYS	ASN	variant	UNP P0DTC2
A	477	ASN	SER	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	478	LYS	THR	variant	UNP P0DTC2
A	484	ALA	GLU	variant	UNP P0DTC2
A	486	PRO	PHE	variant	UNP P0DTC2
A	490	SER	PHE	variant	UNP P0DTC2
A	498	ARG	GLN	variant	UNP P0DTC2
A	501	TYR	ASN	variant	UNP P0DTC2
A	505	HIS	TYR	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	655	TYR	HIS	variant	UNP P0DTC2
A	679	LYS	ASN	variant	UNP P0DTC2
A	681	HIS	PRO	variant	UNP P0DTC2
A	764	LYS	ASN	variant	UNP P0DTC2
A	796	TYR	ASP	variant	UNP P0DTC2
A	817	PRO	PHE	engineered mutation	UNP P0DTC2
A	892	PRO	ALA	engineered mutation	UNP P0DTC2
A	899	PRO	ALA	engineered mutation	UNP P0DTC2
A	942	PRO	ALA	engineered mutation	UNP P0DTC2
A	954	HIS	GLN	variant	UNP P0DTC2
A	969	LYS	ASN	variant	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	TYR	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	GLU	-	expression tag	UNP P0DTC2
A	1216	ALA	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	ARG	-	expression tag	UNP P0DTC2
A	1219	ASP	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	ALA	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	VAL	-	expression tag	UNP P0DTC2
A	1225	ARG	-	expression tag	UNP P0DTC2
A	1226	LYS	-	expression tag	UNP P0DTC2
A	1227	ASP	-	expression tag	UNP P0DTC2
A	1228	GLY	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1230	TRP	-	expression tag	UNP P0DTC2
A	1231	VAL	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	SER	-	expression tag	UNP P0DTC2
A	1235	THR	-	expression tag	UNP P0DTC2
A	1236	PHE	-	expression tag	UNP P0DTC2
A	1237	LEU	-	expression tag	UNP P0DTC2
A	1238	GLY	-	expression tag	UNP P0DTC2
A	1239	SER	-	expression tag	UNP P0DTC2
A	1240	ALA	-	expression tag	UNP P0DTC2
A	1241	TRP	-	expression tag	UNP P0DTC2
A	1242	SER	-	expression tag	UNP P0DTC2
A	1243	HIS	-	expression tag	UNP P0DTC2
A	1244	PRO	-	expression tag	UNP P0DTC2
A	1245	GLN	-	expression tag	UNP P0DTC2
A	1246	PHE	-	expression tag	UNP P0DTC2
A	1247	GLU	-	expression tag	UNP P0DTC2
A	1248	LYS	-	expression tag	UNP P0DTC2
A	1249	HIS	-	expression tag	UNP P0DTC2
A	1250	HIS	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2
B	-15	MET	-	initiating methionine	UNP P0DTC2
B	-14	GLY	-	expression tag	UNP P0DTC2
B	-13	ILE	-	expression tag	UNP P0DTC2
B	-12	LEU	-	expression tag	UNP P0DTC2
B	-11	PRO	-	expression tag	UNP P0DTC2
B	-10	SER	-	expression tag	UNP P0DTC2
B	-9	PRO	-	expression tag	UNP P0DTC2
B	-8	GLY	-	expression tag	UNP P0DTC2
B	-7	MET	-	expression tag	UNP P0DTC2
B	-6	PRO	-	expression tag	UNP P0DTC2
B	-5	ALA	-	expression tag	UNP P0DTC2
B	-4	LEU	-	expression tag	UNP P0DTC2
B	-3	LEU	-	expression tag	UNP P0DTC2
B	-2	SER	-	expression tag	UNP P0DTC2
B	-1	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	VAL	-	expression tag	UNP P0DTC2
B	1	SER	-	expression tag	UNP P0DTC2
B	2	LEU	-	expression tag	UNP P0DTC2
B	3	LEU	-	expression tag	UNP P0DTC2
B	4	SER	-	expression tag	UNP P0DTC2
B	5	VAL	-	expression tag	UNP P0DTC2
B	6	LEU	-	expression tag	UNP P0DTC2
B	7	LEU	-	expression tag	UNP P0DTC2
B	8	MET	-	expression tag	UNP P0DTC2
B	9	GLY	-	expression tag	UNP P0DTC2
B	10	CYS	-	expression tag	UNP P0DTC2
B	11	VAL	-	expression tag	UNP P0DTC2
B	12	ALA	-	expression tag	UNP P0DTC2
B	13	GLU	-	expression tag	UNP P0DTC2
B	14	THR	-	expression tag	UNP P0DTC2
B	15	GLY	-	expression tag	UNP P0DTC2
B	16	THR	-	expression tag	UNP P0DTC2
B	17	GLN	-	expression tag	UNP P0DTC2
B	18	CYS	-	expression tag	UNP P0DTC2
B	19	VAL	-	expression tag	UNP P0DTC2
B	20	ASN	-	expression tag	UNP P0DTC2
B	21	LEU	-	expression tag	UNP P0DTC2
B	22	ILE	-	expression tag	UNP P0DTC2
B	23	THR	-	expression tag	UNP P0DTC2
B	24	ARG	-	expression tag	UNP P0DTC2
B	25	THR	-	expression tag	UNP P0DTC2
B	26	GLN	-	expression tag	UNP P0DTC2
B	27	SER	-	expression tag	UNP P0DTC2
B	83	ALA	VAL	variant	UNP P0DTC2
B	142	ASP	GLY	variant	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	146	GLN	HIS	variant	UNP P0DTC2
B	183	GLU	GLN	variant	UNP P0DTC2
B	213	GLU	VAL	variant	UNP P0DTC2
B	252	VAL	GLY	variant	UNP P0DTC2
B	339	HIS	GLY	variant	UNP P0DTC2
B	346	THR	ARG	variant	UNP P0DTC2
B	368	ILE	LEU	variant	UNP P0DTC2
B	371	PHE	SER	variant	UNP P0DTC2
B	373	PRO	SER	variant	UNP P0DTC2
B	375	PHE	SER	variant	UNP P0DTC2
B	376	ALA	THR	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	405	ASN	ASP	variant	UNP P0DTC2
B	408	SER	ARG	variant	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	440	LYS	ASN	variant	UNP P0DTC2
B	445	PRO	VAL	variant	UNP P0DTC2
B	446	SER	GLY	variant	UNP P0DTC2
B	456	LEU	PHE	variant	UNP P0DTC2
B	460	LYS	ASN	variant	UNP P0DTC2
B	477	ASN	SER	variant	UNP P0DTC2
B	478	LYS	THR	variant	UNP P0DTC2
B	484	ALA	GLU	variant	UNP P0DTC2
B	486	PRO	PHE	variant	UNP P0DTC2
B	490	SER	PHE	variant	UNP P0DTC2
B	498	ARG	GLN	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	505	HIS	TYR	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	655	TYR	HIS	variant	UNP P0DTC2
B	679	LYS	ASN	variant	UNP P0DTC2
B	681	HIS	PRO	variant	UNP P0DTC2
B	764	LYS	ASN	variant	UNP P0DTC2
B	796	TYR	ASP	variant	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	954	HIS	GLN	variant	UNP P0DTC2
B	969	LYS	ASN	variant	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

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLY	-	expression tag	UNP P0DTC2
B	1239	SER	-	expression tag	UNP P0DTC2
B	1240	ALA	-	expression tag	UNP P0DTC2
B	1241	TRP	-	expression tag	UNP P0DTC2
B	1242	SER	-	expression tag	UNP P0DTC2
B	1243	HIS	-	expression tag	UNP P0DTC2
B	1244	PRO	-	expression tag	UNP P0DTC2
B	1245	GLN	-	expression tag	UNP P0DTC2
B	1246	PHE	-	expression tag	UNP P0DTC2
B	1247	GLU	-	expression tag	UNP P0DTC2
B	1248	LYS	-	expression tag	UNP P0DTC2
B	1249	HIS	-	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
C	-15	MET	-	initiating methionine	UNP P0DTC2
C	-14	GLY	-	expression tag	UNP P0DTC2
C	-13	ILE	-	expression tag	UNP P0DTC2
C	-12	LEU	-	expression tag	UNP P0DTC2
C	-11	PRO	-	expression tag	UNP P0DTC2
C	-10	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	PRO	-	expression tag	UNP P0DTC2
C	-8	GLY	-	expression tag	UNP P0DTC2
C	-7	MET	-	expression tag	UNP P0DTC2
C	-6	PRO	-	expression tag	UNP P0DTC2
C	-5	ALA	-	expression tag	UNP P0DTC2
C	-4	LEU	-	expression tag	UNP P0DTC2
C	-3	LEU	-	expression tag	UNP P0DTC2
C	-2	SER	-	expression tag	UNP P0DTC2
C	-1	LEU	-	expression tag	UNP P0DTC2
C	0	VAL	-	expression tag	UNP P0DTC2
C	1	SER	-	expression tag	UNP P0DTC2
C	2	LEU	-	expression tag	UNP P0DTC2
C	3	LEU	-	expression tag	UNP P0DTC2
C	4	SER	-	expression tag	UNP P0DTC2
C	5	VAL	-	expression tag	UNP P0DTC2
C	6	LEU	-	expression tag	UNP P0DTC2
C	7	LEU	-	expression tag	UNP P0DTC2
C	8	MET	-	expression tag	UNP P0DTC2
C	9	GLY	-	expression tag	UNP P0DTC2
C	10	CYS	-	expression tag	UNP P0DTC2
C	11	VAL	-	expression tag	UNP P0DTC2
C	12	ALA	-	expression tag	UNP P0DTC2
C	13	GLU	-	expression tag	UNP P0DTC2
C	14	THR	-	expression tag	UNP P0DTC2
C	15	GLY	-	expression tag	UNP P0DTC2
C	16	THR	-	expression tag	UNP P0DTC2
C	17	GLN	-	expression tag	UNP P0DTC2
C	18	CYS	-	expression tag	UNP P0DTC2
C	19	VAL	-	expression tag	UNP P0DTC2
C	20	ASN	-	expression tag	UNP P0DTC2
C	21	LEU	-	expression tag	UNP P0DTC2
C	22	ILE	-	expression tag	UNP P0DTC2
C	23	THR	-	expression tag	UNP P0DTC2
C	24	ARG	-	expression tag	UNP P0DTC2
C	25	THR	-	expression tag	UNP P0DTC2
C	26	GLN	-	expression tag	UNP P0DTC2
C	27	SER	-	expression tag	UNP P0DTC2
C	83	ALA	VAL	variant	UNP P0DTC2
C	142	ASP	GLY	variant	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	146	GLN	HIS	variant	UNP P0DTC2
C	183	GLU	GLN	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	213	GLU	VAL	variant	UNP P0DTC2
C	252	VAL	GLY	variant	UNP P0DTC2
C	339	HIS	GLY	variant	UNP P0DTC2
C	346	THR	ARG	variant	UNP P0DTC2
C	368	ILE	LEU	variant	UNP P0DTC2
C	371	PHE	SER	variant	UNP P0DTC2
C	373	PRO	SER	variant	UNP P0DTC2
C	375	PHE	SER	variant	UNP P0DTC2
C	376	ALA	THR	variant	UNP P0DTC2
C	405	ASN	ASP	variant	UNP P0DTC2
C	408	SER	ARG	variant	UNP P0DTC2
C	417	ASN	LYS	variant	UNP P0DTC2
C	440	LYS	ASN	variant	UNP P0DTC2
C	445	PRO	VAL	variant	UNP P0DTC2
C	446	SER	GLY	variant	UNP P0DTC2
C	456	LEU	PHE	variant	UNP P0DTC2
C	460	LYS	ASN	variant	UNP P0DTC2
C	477	ASN	SER	variant	UNP P0DTC2
C	478	LYS	THR	variant	UNP P0DTC2
C	484	ALA	GLU	variant	UNP P0DTC2
C	486	PRO	PHE	variant	UNP P0DTC2
C	490	SER	PHE	variant	UNP P0DTC2
C	498	ARG	GLN	variant	UNP P0DTC2
C	501	TYR	ASN	variant	UNP P0DTC2
C	505	HIS	TYR	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	655	TYR	HIS	variant	UNP P0DTC2
C	679	LYS	ASN	variant	UNP P0DTC2
C	681	HIS	PRO	variant	UNP P0DTC2
C	764	LYS	ASN	variant	UNP P0DTC2
C	796	TYR	ASP	variant	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	954	HIS	GLN	variant	UNP P0DTC2
C	969	LYS	ASN	variant	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

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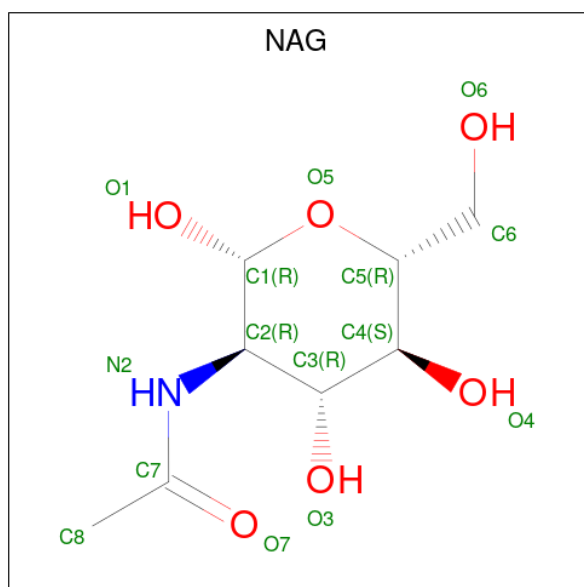
Chain	Residue	Modelled	Actual	Comment	Reference
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
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	SER	-	expression tag	UNP P0DTC2
C	1240	ALA	-	expression tag	UNP P0DTC2
C	1241	TRP	-	expression tag	UNP P0DTC2
C	1242	SER	-	expression tag	UNP P0DTC2
C	1243	HIS	-	expression tag	UNP P0DTC2
C	1244	PRO	-	expression tag	UNP P0DTC2
C	1245	GLN	-	expression tag	UNP P0DTC2
C	1246	PHE	-	expression tag	UNP P0DTC2
C	1247	GLU	-	expression tag	UNP P0DTC2
C	1248	LYS	-	expression tag	UNP P0DTC2
C	1249	HIS	-	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

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



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

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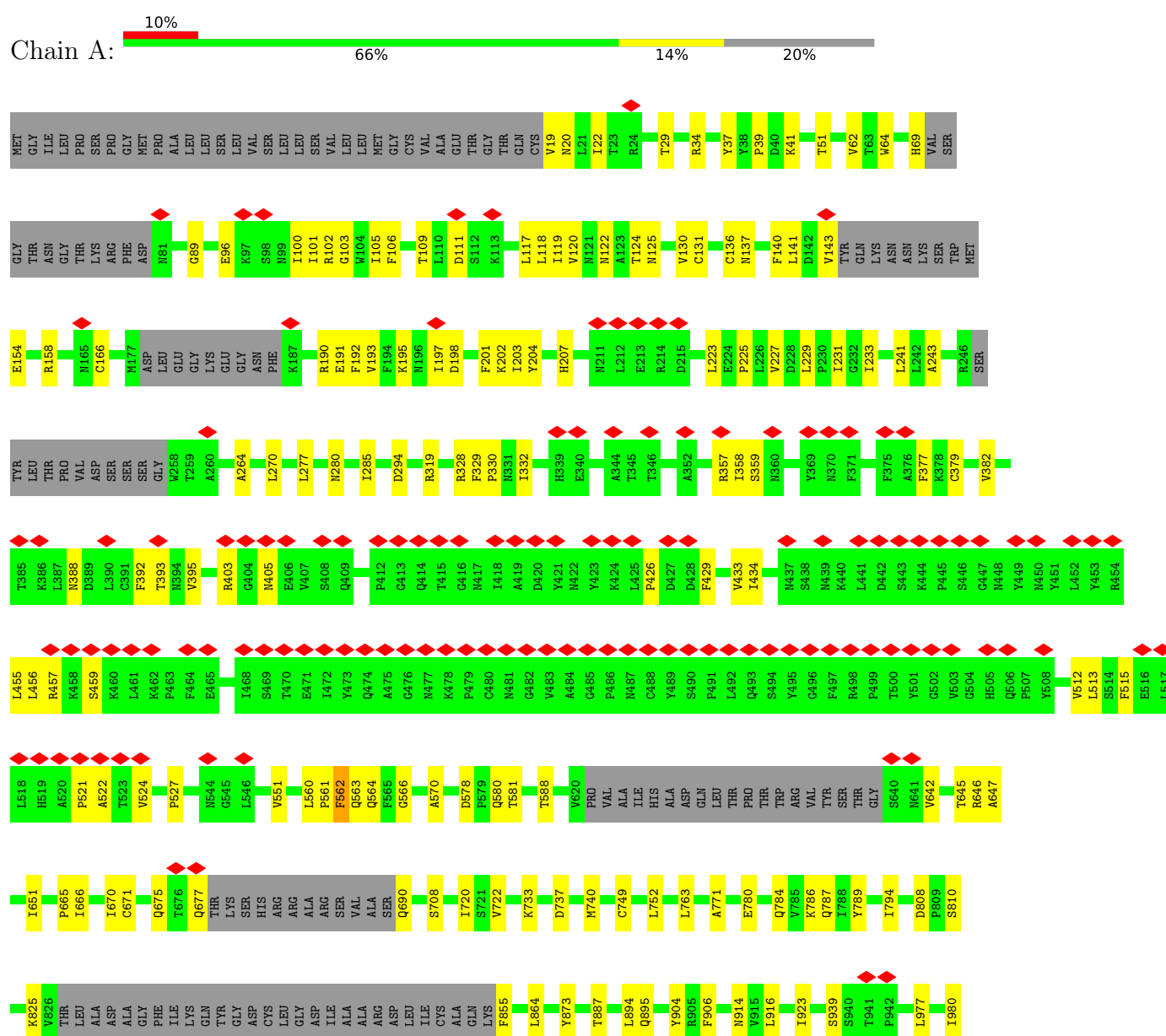
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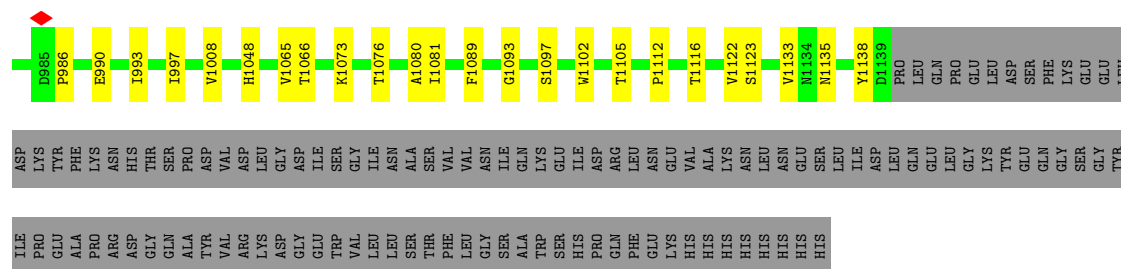
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2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

3 Residue-property plots

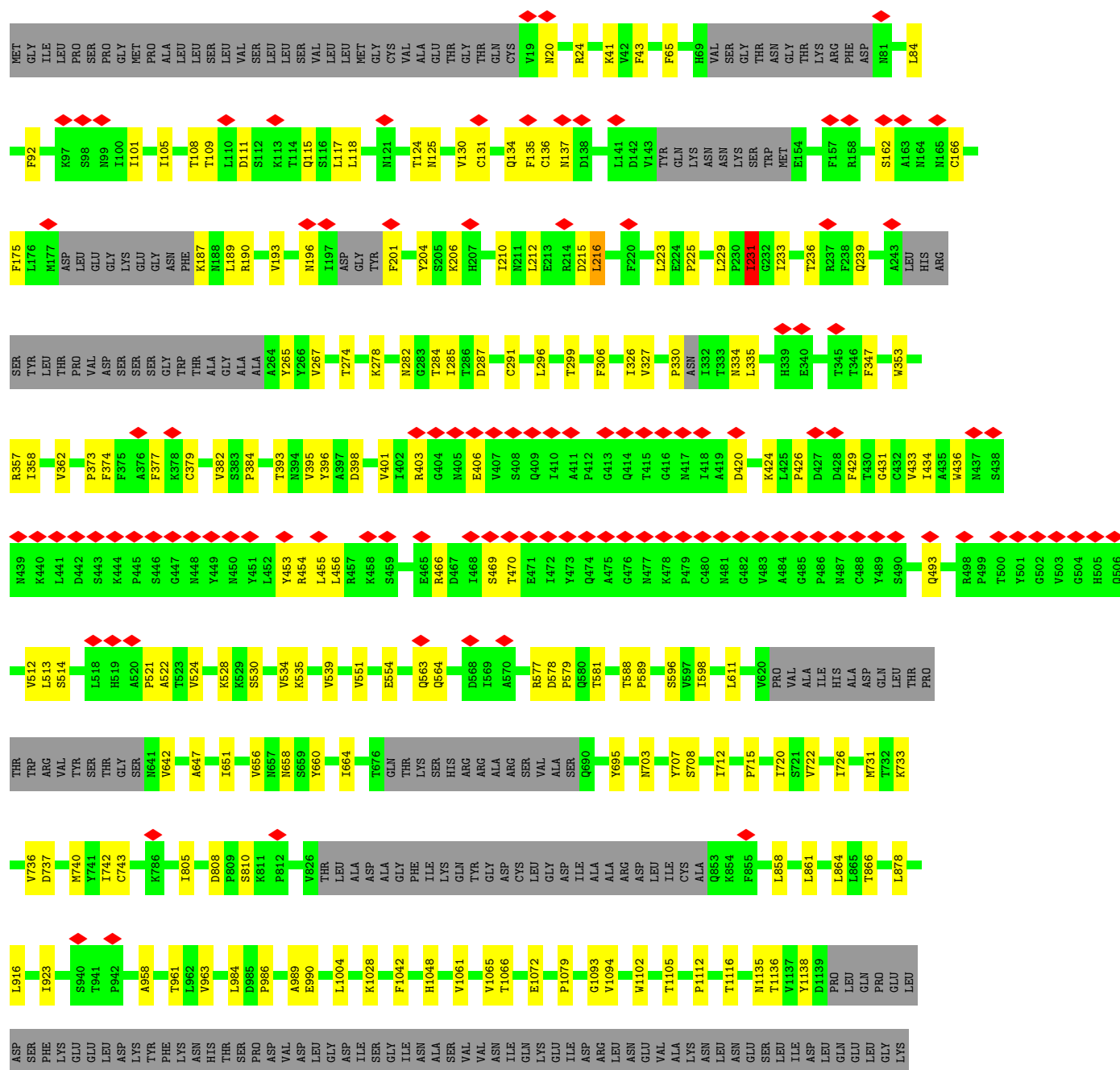
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Spike glycoprotein





• Molecule 1: Spike glycoprotein



TYR	GLY	GLN	GLY	PRO	SER	GLY	TYR	PRO	GLY	PRO	PRO	ALA	ALA	ARG	ASP	GLY	GLN	ALA	TYR	VAL	VAL	LEU	LEU	SER	GLY	THR	PHE	LEU	GLY	SER	ALA	ALA	TRP	SER	HIS	PRO	GLN	GLY	LYS	HIS	HIS	HIS	HIS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

● Molecule 1: Spike glycoprotein



VAL	ARG	GLY	LEU	LEU	THR	THR	PHE	VAL	VAL	ASN	ILE	ALA	GLN	GLY	THR	LEU	LEU	VAL	VAL	CYS	V19	N20	L21	I22	T23	R24	S27	Y28	Y37	Y38	P39	D40	K41	R44	V47	T51	A67	I68	H69	VAL												
SER	GLY	THR	ASN	GLY	THR	LYS	ARG	ASP	ASP	N81	P82	A93	K97	S98	T108	T109	L110	D111	T114	L118	I119	V120	N121	N122	A123	T124	N125	V130	Q134	N137	D138	P139	F140	L141	V143	TYR	GLN	LYS	ASN	LYS	SER	TRP	MET	E154	F157	R158	V159	I160				
S161	S162	F168	F175	L176	M177	ASP	LEU	GLY	GLY	LYS	GLY	GLY	ASN	PHE	K187	N188	L189	R190	V193	F194	K195	N196	I197	D198	G199	Y200	F201	K202	I203	Y204	K206	H207	T208	P209	L210	ASN	LEU	GLY	ARG	ASP	L216	F220	L223	L226	V227	D228	N229	P230	T231	G232	I233	H234
I235	T240	R246	SER	TYR	LEU	THR	THR	VAL	ASP	SER	SER	SER	GLY	W258	T259	A260	G261	A262	A263	A264	Y265	Y266	D287	A288	F306	T307	S316	N317	V327	R328	F329	N330	N331	I332	H339	F342	N343	A344	T345	T346	F347	A352	W353	N354	R355	I358	N370	F371				
A372	P373	F374	C379	P384	D389	T393	N394	V395	S399	F400	V401	L402	R403	G404	N405	I410	G413	N417	N422	Y423	K424	L425	P426	D427	G431	C432	V433	I434	A435	W436	N437	S438	N439	K440	G502	V503	G504	H505	Q506	R509	V512	L513	S514	F515	E516	L517	L518	H519	A520	F521		
L456	R457	K458	S459	K460	L461	R466	D467	L468	S469	T470	E471	L472	Y473	Q474	A475	G476	N477	K478	N481	G482	Y483	A484	G485	P486	N487	C488	Y489	S490	P491	S494	Y495	G496	F497	R498	P499	T500	G502	V503	G504	H505	Q506	R509	V512	L513	S514	F515	E516	L517	L518	H519	A520	F521
K528	T531	N532	L533	V534	K535	N540	T549	E554	N555	N556	K557	F558	L560	P561	F562	O563	N564	F565	R566	R567	T573	R577	D578	T581	L582	C590	S591	F592	T602	V620	PRO	VAL	ALA	ILE	HIS	ALA	ASP	GLN	LEU	THR	PRO	THR	TRP	ARG	VAL	TYR	SER	THR				
GLY	SER	N641	N642	F643	Q644	T645	T651	C662	D663	I664	P665	C671	T676	GLN	THR	LYS	SER	HIS	ARG	ARG	ALA	ALA	GLY	PHE	ILE	LYS	GLN	TYR	GLY	ASP	LEU	ILE	ALA	ALA	ARG	ASP	LEU	ILE	CYS	A852	F855	L858	P862	L865	M869	L878						
F759	L763	A766	I770	A771	Y789	P792	F793	I794	I805	L821	L822	Y826	THR	LEU	ALA	ASP	ALA	ALA	GLY	ILE	LYS	GLN	TYR	GLY	ASP	CYS	LEU	GLY	ASP	ILE	ALA	ALA	ARG	ASP	LEU	ILE	CYS	A852	F855	L858	P862	L865	M869	L878								
S884	T887	A903	Y904	Q913	L916	Y917	I923	A930	I934	Q935	T941	P942	S943	A944	L945	N955	K969	S975	D979	I980	R983	L984	D985	E988	A989	E990	I993	T997	T998	R1000	L1001	Q1002	S1003	L1004	V1008	Q1011	L1012	K1028														
F1042	H1048	V1061	F1062	L1063	H1064	V1065	T1066	C1082	G1093	V1094	W1102	T1105	Q1106	R1107	P1112	T1116	V1122	S1123	I1132	N1135	T1136	V1137	I1138	D1139	PRO	LEU	GLN	GLY	ILE	PRO	GLY	LYS	ASP	GLY	GLY	TYR	ILE	ASP	PRO	ALA	PRO	PRO	ASP	GLY	GLN	ALA	ASP					
VAL	ASP	LYS	GLY	ILE	TRP	VAL	GLY	ILE	ALA	SER	THR	PHE	VAL	VAL	ASN	ILE	LYS	GLY	ILE	PRO	GLN	ARG	PHE	GLU	ASN	GLY	VAL	GLY	LEU	ASP	GLY	GLY	TRP	ALA	ASP	GLY	GLY	TRP	ALA	PRO	PRO	ASP	GLY	GLN	ALA	ASP						
VAL	ARG	LYS	ASP	GLY	TRP	VAL	GLY	ILE	ALA	SER	THR	PHE	VAL	VAL	ASN	ILE	LYS	GLY	ILE	PRO	GLN	ARG	PHE	GLU	ASN	GLY	VAL	GLY	LEU	ASP	GLY	GLY	TRP	ALA	ASP	GLY	GLY	TRP	ALA	PRO	PRO	ASP	GLY	GLN	ALA	ASP						
VAL	ARG	LYS	ASP	GLY	TRP	VAL	GLY	ILE	ALA	SER	THR	PHE	VAL	VAL	ASN	ILE	LYS	GLY	ILE	PRO	GLN	ARG	PHE	GLU	ASN	GLY	VAL	GLY	LEU	ASP	GLY	GLY	TRP	ALA	ASP	GLY	GLY	TRP	ALA	PRO	PRO	ASP	GLY	GLN	ALA	ASP						

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	473611	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.922	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	413.696, 413.696, 413.696	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.808, 0.808, 0.808	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.18	0/8180	0.40	5/11134 (0.0%)
1	B	0.19	0/8076	0.38	1/10987 (0.0%)
1	C	0.22	0/8149	0.41	0/11090
All	All	0.20	0/24405	0.39	6/33211 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	524	VAL	CA-C-N	-8.90	110.96	121.64
1	A	524	VAL	C-N-CA	-8.90	110.96	121.64
1	B	231	ILE	CB-CA-C	-7.80	102.72	111.45
1	A	122	ASN	CA-CB-CG	6.34	118.94	112.60
1	A	562	PHE	CA-CB-CG	6.05	119.85	113.80
1	A	561	PRO	CB-CA-C	5.36	121.21	112.26

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7992	0	7816	128	0
1	B	7894	0	7738	132	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	7962	0	7793	181	0
2	A	154	0	143	3	0
2	B	98	0	91	1	0
2	C	126	0	117	1	0
All	All	24226	0	23698	395	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 8.

All (395) 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:C:190:ARG:HH12	1:C:207:HIS:CE1	1.48	1.30
1:A:562:PHE:CE1	1:B:41:LYS:HE2	1.81	1.15
1:C:190:ARG:NH1	1:C:207:HIS:CE1	2.24	1.06
1:C:175:PHE:HB3	1:C:190:ARG:HH22	1.33	0.89
1:A:562:PHE:CE1	1:B:41:LYS:CE	2.56	0.88
1:C:37:TYR:HB2	1:C:206:LYS:HD3	1.57	0.87
1:C:175:PHE:HB3	1:C:190:ARG:NH2	1.91	0.84
1:C:168:PHE:CE2	1:C:229:LEU:HD12	2.16	0.81
1:A:562:PHE:CZ	1:B:41:LYS:HE2	2.16	0.81
1:C:190:ARG:NH1	1:C:207:HIS:NE2	2.31	0.79
1:C:433:VAL:HG22	1:C:512:VAL:HG22	1.65	0.78
1:C:67:ALA:H	1:C:263:ALA:HB3	1.48	0.77
1:A:562:PHE:CE2	1:B:41:LYS:HG2	2.19	0.77
1:A:562:PHE:CZ	1:B:41:LYS:CE	2.67	0.77
1:B:124:THR:O	1:B:125:ASN:OD1	2.03	0.76
1:B:563:GLN:HG3	1:C:41:LYS:HD3	1.68	0.75
1:A:124:THR:O	1:A:125:ASN:OD1	2.05	0.74
1:B:330:PRO:HG3	1:B:579:PRO:HB2	1.68	0.74
1:C:189:LEU:O	1:C:190:ARG:HG3	1.88	0.74
1:C:732:THR:OG1	1:C:955:ASN:ND2	2.22	0.72
1:A:329:PHE:O	1:A:580:GLN:NE2	2.22	0.72
1:C:93:ALA:HB3	1:C:266:TYR:HB2	1.72	0.72
1:C:37:TYR:CD1	1:C:206:LYS:HE2	2.25	0.71
1:C:742:ILE:HD13	1:C:1001:LEU:HD22	1.70	0.71
1:B:455:LEU:HD12	1:B:456:LEU:HG	1.73	0.70
1:C:455:LEU:HD12	1:C:456:LEU:HG	1.73	0.70
1:A:645:THR:HG23	1:A:670:ILE:HD13	1.72	0.70
1:A:231:ILE:HD12	1:A:233:ILE:HG12	1.74	0.70
1:B:115:GLN:HB2	1:B:233:ILE:HG12	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:563:GLN:CG	1:C:41:LYS:HD3	2.22	0.69
1:B:658:ASN:ND2	1:B:660:TYR:OH	2.24	0.69
1:C:1116:THR:HG22	1:C:1138:TYR:HB3	1.74	0.69
1:C:168:PHE:HE2	1:C:229:LEU:HD12	1.55	0.69
1:B:20:ASN:ND2	1:B:137:ASN:OD1	2.20	0.69
1:B:108:THR:HA	1:B:236:THR:HG22	1.74	0.69
1:A:562:PHE:CD1	1:B:41:LYS:HE2	2.26	0.69
1:C:227:VAL:CG2	1:C:229:LEU:HD23	2.23	0.68
1:A:393:THR:HA	1:A:522:ALA:HA	1.75	0.68
1:B:1102:TRP:HB2	1:B:1135:ASN:HD22	1.59	0.68
1:C:535:LYS:NZ	1:C:554:GLU:OE2	2.25	0.67
1:A:642:VAL:HG12	1:A:651:ILE:HG22	1.77	0.67
1:C:227:VAL:HB	1:C:229:LEU:HD22	1.76	0.67
1:A:319:ARG:HH22	1:B:740:MET:HB2	1.59	0.67
1:B:326:ILE:HD11	1:B:534:VAL:HG22	1.76	0.67
1:A:37:TYR:OH	1:A:195:LYS:NZ	2.27	0.66
1:C:139:PRO:HB3	1:C:159:VAL:HG13	1.77	0.66
1:A:319:ARG:NH1	1:B:740:MET:SD	2.68	0.66
1:B:454:ARG:NH2	1:B:469:SER:O	2.29	0.66
1:C:347:PHE:HB2	1:C:401:VAL:HG23	1.78	0.66
1:A:1122:VAL:HG23	1:A:1123:SER:H	1.61	0.66
1:C:124:THR:O	1:C:125:ASN:OD1	2.13	0.66
1:B:1116:THR:HG22	1:B:1138:TYR:HB3	1.79	0.65
1:B:1102:TRP:HB2	1:B:1135:ASN:ND2	2.12	0.65
1:C:353:TRP:O	1:C:466:ARG:NH2	2.30	0.65
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.30	0.64
1:C:168:PHE:HE2	1:C:229:LEU:CD1	2.10	0.64
1:C:227:VAL:CG2	1:C:229:LEU:CD2	2.75	0.64
1:A:330:PRO:HG2	1:A:332:ILE:HD11	1.79	0.64
1:C:457:ARG:NH1	1:C:459:SER:O	2.28	0.64
1:C:766:ALA:HB1	1:C:1012:LEU:HD11	1.81	0.63
1:C:456:LEU:HB2	1:C:491:PRO:HB3	1.81	0.63
1:B:426:PRO:HG2	1:B:429:PHE:HB2	1.81	0.63
1:B:564:GLN:HB2	1:B:577:ARG:H	1.62	0.63
1:C:1122:VAL:HG23	1:C:1123:SER:H	1.62	0.63
1:B:353:TRP:O	1:B:466:ARG:NH2	2.32	0.62
1:A:96:GLU:O	1:A:190:ARG:NH1	2.33	0.62
1:B:65:PHE:HB2	1:B:265:TYR:HB3	1.82	0.62
1:C:189:LEU:O	1:C:190:ARG:CG	2.47	0.62
1:C:187:LYS:O	1:C:209:PRO:HA	2.00	0.61
1:B:374:PHE:HD1	1:B:436:TRP:HB3	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:770:ILE:HD11	1:C:1012:LEU:HD12	1.82	0.61
1:A:914:ASN:ND2	1:C:1123:SER:OG	2.32	0.61
1:C:37:TYR:HB2	1:C:206:LYS:CD	2.28	0.61
1:A:358:ILE:HB	1:A:395:VAL:HB	1.82	0.61
1:C:642:VAL:HG12	1:C:651:ILE:HG12	1.83	0.61
1:A:873:TYR:HE1	1:C:699:LEU:HB3	1.66	0.61
1:B:134:GLN:NE2	1:B:162:SER:OG	2.34	0.61
1:B:722:VAL:HG22	1:B:1065:VAL:HG22	1.83	0.61
1:C:1105:THR:HG22	1:C:1112:PRO:HA	1.83	0.61
1:A:328:ARG:NH2	1:A:578:ASP:OD2	2.32	0.61
1:A:64:TRP:HE1	1:A:264:ALA:HB1	1.66	0.60
1:A:433:VAL:HG22	1:A:512:VAL:HG22	1.83	0.60
1:A:564:GLN:OE1	1:B:41:LYS:HD3	2.00	0.60
1:C:194:PHE:CZ	1:C:235:ILE:HG13	2.37	0.60
1:A:562:PHE:CZ	1:B:41:LYS:HE3	2.35	0.60
1:A:403:ARG:HH12	1:A:405:ASN:HD21	1.50	0.60
1:B:206:LYS:HD2	1:B:225:PRO:HG3	1.83	0.59
1:B:403:ARG:NH2	1:B:406:GLU:OE2	2.36	0.59
1:C:189:LEU:C	1:C:190:ARG:HG3	2.27	0.59
1:B:327:VAL:HG13	1:B:530:SER:HA	1.83	0.59
1:C:37:TYR:HD1	1:C:206:LYS:HE2	1.65	0.59
1:C:540:ASN:HA	1:C:549:THR:HA	1.85	0.59
1:A:195:LYS:HG2	1:A:202:LYS:HB2	1.84	0.58
1:C:884:SER:OG	1:C:887:THR:OG1	2.21	0.58
1:A:570:ALA:HB1	1:B:963:VAL:HG11	1.86	0.58
1:C:722:VAL:HG22	1:C:1065:VAL:HG22	1.84	0.58
1:B:379:CYS:HB2	1:B:384:PRO:HG3	1.86	0.58
1:C:194:PHE:CZ	1:C:203:ILE:HD12	2.38	0.57
1:A:455:LEU:HD12	1:A:456:LEU:HG	1.85	0.57
1:C:190:ARG:NH1	1:C:207:HIS:CD2	2.71	0.57
1:C:403:ARG:HH12	1:C:405:ASN:HD21	1.49	0.57
1:A:1081:ILE:HD13	1:A:1133:VAL:HG23	1.87	0.57
1:C:24:ARG:NH1	1:C:82:PRO:O	2.37	0.57
1:C:742:ILE:HG23	1:C:1000:ARG:HB2	1.87	0.57
1:B:708:SER:HA	2:B:1303:NAG:H61	1.87	0.56
1:A:106:PHE:HB2	1:A:117:LEU:HB3	1.87	0.56
1:C:220:PHE:HE1	1:C:288:ALA:HB3	1.70	0.56
1:C:227:VAL:HB	1:C:229:LEU:CD2	2.36	0.56
1:B:454:ARG:HH22	1:B:470:THR:HA	1.70	0.56
1:B:274:THR:HG23	1:B:291:CYS:HB2	1.86	0.56
1:C:227:VAL:HG21	1:C:229:LEU:CD2	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:645:THR:HG22	1:A:647:ALA:H	1.70	0.56
1:C:187:LYS:HA	1:C:210:ILE:HG23	1.87	0.56
1:C:201:PHE:HD2	1:C:232:GLY:HA2	1.70	0.56
1:C:726:ILE:HG12	1:C:1061:VAL:HG22	1.88	0.56
1:B:215:ASP:O	1:B:216:LEU:C	2.49	0.55
1:C:194:PHE:HB3	1:C:201:PHE:CZ	2.41	0.55
1:B:707:TYR:HB3	1:C:792:PRO:HG2	1.87	0.55
1:A:143:VAL:HB	1:A:154:GLU:HA	1.88	0.55
1:A:1105:THR:HG22	1:A:1112:PRO:HA	1.89	0.55
1:B:189:LEU:HB3	1:B:223:LEU:HD21	1.88	0.55
1:A:201:PHE:HB2	1:A:231:ILE:HG12	1.88	0.55
1:C:916:LEU:HD12	1:C:923:ILE:HD13	1.89	0.55
1:A:225:PRO:HB2	1:C:562:PHE:HZ	1.70	0.55
1:A:675:GLN:HG3	1:A:677:GLN:HG3	1.88	0.55
1:A:763:LEU:HG	1:A:1008:VAL:HG21	1.88	0.55
1:C:307:THR:HA	1:C:602:THR:HG21	1.88	0.55
1:C:821:LEU:HD22	1:C:935:GLN:HG3	1.88	0.54
1:C:749:CYS:SG	1:C:997:ILE:HD11	2.47	0.54
1:C:1082:CYS:HB2	1:C:1132:ILE:HG12	1.90	0.54
1:A:319:ARG:NH2	1:B:737:ASP:OD2	2.41	0.54
1:B:206:LYS:HB3	1:B:223:LEU:HB3	1.89	0.54
1:C:567:ARG:HG2	1:C:573:THR:HA	1.90	0.54
1:A:201:PHE:HD2	1:A:203:ILE:HD11	1.72	0.54
1:A:192:PHE:HA	1:A:204:TYR:O	2.08	0.54
1:C:109:THR:OG1	1:C:111:ASP:OD1	2.22	0.54
1:C:130:VAL:HG11	1:C:231:ILE:HD11	1.90	0.54
1:C:903:ALA:HB1	1:C:913:GLN:HB2	1.90	0.53
1:C:563:GLN:O	1:C:577:ARG:NH2	2.32	0.53
1:A:203:ILE:HD13	1:A:227:VAL:HG23	1.90	0.53
1:B:398:ASP:HB2	1:B:512:VAL:HB	1.89	0.53
1:C:168:PHE:CE2	1:C:229:LEU:CD1	2.86	0.53
1:A:20:ASN:OD1	1:A:137:ASN:ND2	2.40	0.53
1:A:89:GLY:HA3	1:A:270:LEU:HD12	1.91	0.53
1:A:562:PHE:CE2	1:B:41:LYS:CG	2.91	0.53
1:A:722:VAL:HG22	1:A:1065:VAL:HG22	1.91	0.53
1:B:193:VAL:HG12	1:B:204:TYR:HB2	1.90	0.52
1:C:37:TYR:CD1	1:C:206:LYS:CE	2.93	0.52
1:C:993:ILE:O	1:C:997:ILE:HG12	2.10	0.52
1:A:578:ASP:HB3	1:A:581:THR:O	2.08	0.52
1:A:675:GLN:O	1:A:690:GLN:NE2	2.43	0.52
1:B:118:LEU:HD12	1:B:135:PHE:HE1	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:535:LYS:HZ1	1:B:554:GLU:HG2	1.75	0.52
1:C:228:ASP:O	1:C:229:LEU:C	2.53	0.52
1:A:1116:THR:HG22	1:A:1138:TYR:HB3	1.92	0.52
1:C:190:ARG:HA	1:C:206:LYS:O	2.09	0.52
1:C:227:VAL:HG21	1:C:229:LEU:HD23	1.90	0.52
1:C:980:ILE:HG23	1:C:984:LEU:HD12	1.91	0.52
1:C:203:ILE:CG2	1:C:229:LEU:HB2	2.39	0.52
1:A:749:CYS:HB2	1:A:993:ILE:HD11	1.93	0.51
1:C:316:SER:OG	1:C:317:ASN:N	2.41	0.51
1:C:999:GLY:O	1:C:1002:GLN:HG3	2.11	0.51
1:A:456:LEU:HD21	1:B:373:PRO:HG3	1.93	0.51
1:A:646:ARG:HH22	1:B:866:THR:HG21	1.76	0.51
1:A:388:ASN:OD1	1:A:527:PRO:HG2	2.11	0.51
1:A:665:PRO:HB3	1:B:864:LEU:HD13	1.92	0.51
1:B:534:VAL:HG21	1:B:539:VAL:HG11	1.92	0.51
1:B:1048:HIS:HA	1:B:1066:THR:HG22	1.92	0.51
1:C:930:ALA:O	1:C:934:ILE:HG12	2.11	0.51
1:A:906:PHE:CD2	1:A:916:LEU:HB2	2.46	0.51
1:C:122:ASN:OD1	1:C:125:ASN:N	2.42	0.51
1:B:808:ASP:OD2	1:B:810:SER:OG	2.29	0.50
1:C:822:LEU:HD23	1:C:945:LEU:HD11	1.93	0.50
1:C:1048:HIS:HA	1:C:1066:THR:HG22	1.92	0.50
1:A:105:ILE:HD12	1:A:241:LEU:HD11	1.94	0.50
1:A:521:PRO:HG3	1:B:41:LYS:HZ2	1.76	0.50
1:A:752:LEU:HD22	1:A:997:ILE:HD12	1.92	0.50
1:C:227:VAL:HG23	1:C:229:LEU:HD23	1.93	0.50
1:C:644:GLN:NE2	1:C:645:THR:O	2.41	0.50
1:A:873:TYR:CE1	1:C:699:LEU:HB3	2.46	0.50
1:B:598:ILE:HG23	1:B:664:ILE:HG21	1.92	0.50
1:C:190:ARG:NH1	1:C:207:HIS:ND1	2.58	0.50
1:B:712:ILE:HD13	1:B:1094:VAL:HG11	1.93	0.50
1:B:656:VAL:HG23	1:B:695:TYR:HB3	1.93	0.50
1:B:393:THR:HA	1:B:522:ALA:HA	1.93	0.50
1:C:208:THR:OG1	1:C:223:LEU:HA	2.12	0.50
1:C:39:PRO:HG3	1:C:51:THR:HG21	1.92	0.49
1:A:130:VAL:HG12	1:A:130:VAL:O	2.13	0.49
1:C:676:THR:HA	1:C:690:GLN:HA	1.93	0.49
1:C:736:VAL:HG22	1:C:858:LEU:HD22	1.95	0.49
1:C:452:LEU:HD23	1:C:494:SER:HA	1.95	0.49
1:A:377:PHE:CD1	1:A:434:ILE:HG12	2.48	0.49
1:C:379:CYS:HB2	1:C:384:PRO:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:LYS:NZ	1:A:939:SER:HA	2.28	0.49
1:B:396:TYR:HB2	1:B:514:SER:HB3	1.95	0.49
1:C:374:PHE:HD1	1:C:436:TRP:HB3	1.76	0.49
1:A:136:CYS:SG	1:A:137:ASN:N	2.85	0.49
1:B:433:VAL:HG22	1:B:512:VAL:HG22	1.94	0.49
1:C:805:ILE:HD12	1:C:878:LEU:HD22	1.95	0.49
1:C:328:ARG:HE	1:C:533:LEU:HB2	1.78	0.49
1:A:521:PRO:CG	1:B:41:LYS:HZ2	2.26	0.49
1:A:1122:VAL:HG23	1:A:1123:SER:N	2.27	0.49
1:C:40:ASP:OD1	1:C:44:ARG:NH1	2.44	0.49
1:C:403:ARG:HG2	1:C:497:PHE:HE1	1.78	0.49
1:C:578:ASP:HB3	1:C:581:THR:O	2.13	0.49
1:C:201:PHE:CD2	1:C:232:GLY:HA2	2.48	0.48
1:C:358:ILE:HB	1:C:395:VAL:HB	1.95	0.48
1:C:662:CYS:HB2	1:C:671:CYS:HB3	1.66	0.48
1:C:770:ILE:HD13	1:C:1011:GLN:HG3	1.95	0.48
1:B:358:ILE:HB	1:B:395:VAL:HB	1.95	0.48
1:A:895:GLN:HG2	1:C:713:ALA:HB2	1.95	0.48
1:B:420:ASP:HA	1:B:424:LYS:HE2	1.95	0.48
1:C:1135:ASN:OD1	1:C:1136:THR:N	2.46	0.48
1:A:382:VAL:HG11	1:A:392:PHE:HZ	1.78	0.48
1:C:794:ILE:HG13	1:C:794:ILE:O	2.14	0.48
1:A:22:ILE:HD13	1:A:69:HIS:HB3	1.94	0.48
1:A:560:LEU:HB2	1:A:563:GLN:OE1	2.14	0.48
1:B:958:ALA:O	1:B:961:THR:HG22	2.14	0.48
1:A:1073:LYS:HA	2:A:1306:NAG:H82	1.96	0.48
1:A:34:ARG:NH2	1:A:191:GLU:OE2	2.46	0.48
1:A:986:PRO:O	1:A:990:GLU:HG2	2.14	0.47
1:A:562:PHE:CD2	1:B:41:LYS:HG2	2.49	0.47
1:A:1102:TRP:HB2	1:A:1135:ASN:HD22	1.79	0.47
1:B:1135:ASN:OD1	1:B:1136:THR:N	2.43	0.47
1:C:979:ASP:O	1:C:983:ARG:HB3	2.14	0.47
1:C:342:PHE:HB2	1:C:371:PHE:HE2	1.79	0.47
1:A:377:PHE:HD1	1:A:434:ILE:HG12	1.78	0.47
1:B:131:CYS:HA	1:B:166:CYS:HA	1.97	0.47
1:B:984:LEU:HB3	1:B:989:ALA:HB2	1.95	0.47
1:A:426:PRO:HG2	1:A:429:PHE:HB2	1.94	0.47
1:A:1080:ALA:HB2	1:A:1089:PHE:CE1	2.49	0.47
1:A:887:THR:HB	1:A:894:LEU:HD12	1.97	0.47
1:B:377:PHE:HD1	1:B:434:ILE:HG12	1.80	0.47
1:B:736:VAL:HG22	1:B:858:LEU:HG	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:220:PHE:CE1	1:C:288:ALA:HB3	2.50	0.47
1:B:92:PHE:HB3	1:B:190:ARG:HB2	1.97	0.46
1:B:175:PHE:HB3	1:B:190:ARG:NH2	2.30	0.46
1:C:287:ASP:HB3	1:C:306:PHE:CE2	2.50	0.46
1:C:1102:TRP:CD1	1:C:1135:ASN:HD22	2.33	0.46
1:A:392:PHE:CD1	1:A:515:PHE:HB3	2.49	0.46
1:A:737:ASP:HB3	1:A:740:MET:HB3	1.95	0.46
1:B:1094:VAL:HG22	1:C:904:TYR:OH	2.15	0.46
1:C:108:THR:HB	1:C:114:THR:HG21	1.98	0.46
1:B:130:VAL:HG11	1:B:231:ILE:HG23	1.97	0.46
1:B:382:VAL:HA	1:C:983:ARG:O	2.15	0.46
1:B:589:PRO:HG3	1:C:855:PHE:CG	2.50	0.46
1:A:109:THR:OG1	1:A:111:ASP:OD1	2.23	0.46
1:A:708:SER:HA	2:A:1305:NAG:H82	1.98	0.46
1:A:195:LYS:HE2	1:A:197:ILE:HG13	1.98	0.46
1:A:1076:THR:HB	1:A:1097:SER:HB3	1.97	0.46
1:B:327:VAL:HG21	1:B:528:LYS:HD2	1.98	0.46
1:B:805:ILE:HD12	1:B:878:LEU:HD22	1.98	0.46
1:C:425:LEU:HD21	1:C:512:VAL:HG11	1.98	0.46
1:C:979:ASP:O	1:C:983:ARG:CB	2.64	0.46
1:A:357:ARG:NH1	1:A:359:SER:OG	2.49	0.45
1:A:808:ASP:OD2	1:A:810:SER:OG	2.27	0.45
1:A:733:LYS:HD2	1:A:771:ALA:HB1	1.99	0.45
1:A:864:LEU:HD13	1:C:665:PRO:HB3	1.98	0.45
1:C:44:ARG:HB3	1:C:47:VAL:HG11	1.98	0.45
1:B:736:VAL:HG11	1:B:1004:LEU:HD21	1.98	0.45
1:B:347:PHE:HB2	1:B:401:VAL:HG23	1.97	0.45
1:B:377:PHE:CD1	1:B:434:ILE:HG12	2.51	0.45
1:B:731:MET:HE3	1:B:731:MET:HB2	1.83	0.45
1:A:140:PHE:CE1	1:A:158:ARG:HG2	2.51	0.45
1:C:752:LEU:HD11	1:C:990:GLU:CD	2.42	0.45
1:A:551:VAL:HG22	1:A:588:THR:O	2.17	0.45
1:A:1048:HIS:HA	1:A:1066:THR:HG22	1.97	0.45
1:B:1093:GLY:HA3	1:B:1105:THR:O	2.16	0.45
1:C:130:VAL:O	1:C:130:VAL:HG12	2.17	0.45
1:A:131:CYS:HA	1:A:166:CYS:HA	1.99	0.45
1:C:563:GLN:NE2	1:C:565:PHE:O	2.49	0.45
1:C:733:LYS:HG2	1:C:771:ALA:HA	1.99	0.45
1:A:521:PRO:CG	1:B:41:LYS:NZ	2.80	0.44
1:A:780:GLU:O	1:A:784:GLN:NE2	2.49	0.44
1:C:353:TRP:HZ3	1:C:355:ARG:HH11	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:ASP:HB3	1:B:306:PHE:HE2	1.81	0.44
1:B:563:GLN:HG2	1:C:41:LYS:HD3	1.97	0.44
1:C:431:GLY:HA2	1:C:515:PHE:CD2	2.53	0.44
1:C:752:LEU:O	1:C:755:GLN:HG3	2.17	0.44
1:B:187:LYS:HB2	1:B:210:ILE:O	2.18	0.44
1:B:715:PRO:HA	1:B:1072:GLU:HA	1.99	0.44
1:B:563:GLN:HG3	1:C:41:LYS:CD	2.45	0.44
1:B:578:ASP:HB3	1:B:581:THR:O	2.17	0.44
1:C:532:ASN:OD1	1:C:533:LEU:N	2.50	0.44
1:A:193:VAL:HG23	1:A:223:LEU:HD22	2.00	0.43
1:A:977:LEU:O	1:A:980:ILE:HG22	2.17	0.43
1:C:22:ILE:HD13	1:C:69:HIS:HA	2.00	0.43
1:C:469:SER:OG	1:C:471:GLU:OE2	2.33	0.43
1:A:39:PRO:HG3	1:A:51:THR:HG21	2.00	0.43
1:A:102:ARG:HD2	1:A:141:LEU:HD23	2.00	0.43
1:A:143:VAL:C	1:A:243:ALA:HB1	2.43	0.43
1:A:666:ILE:HG12	1:A:671:CYS:HA	2.01	0.43
1:A:96:GLU:OE1	1:A:100:ILE:HB	2.18	0.43
1:A:118:LEU:HD21	1:A:120:VAL:HG23	2.00	0.43
1:B:92:PHE:HZ	1:B:101:ILE:HD13	1.83	0.43
1:C:231:ILE:HD12	1:C:231:ILE:HA	1.85	0.43
1:C:327:VAL:O	1:C:531:THR:N	2.52	0.43
1:A:786:LYS:HG3	1:A:787:GLN:HG3	1.99	0.43
1:B:109:THR:OG1	1:B:111:ASP:OD1	2.32	0.43
1:B:334:ASN:O	1:B:362:VAL:N	2.39	0.43
1:A:19:VAL:HG22	1:A:158:ARG:HD3	2.01	0.43
1:A:566:GLY:HA2	1:B:43:PHE:HB3	1.99	0.43
1:B:24:ARG:HH12	1:B:84:LEU:HG	1.83	0.43
1:C:240:THR:HG21	1:C:265:TYR:CZ	2.54	0.43
1:A:229:LEU:HB3	1:A:231:ILE:HG23	2.00	0.43
1:A:457:ARG:NH1	1:A:459:SER:OG	2.48	0.43
1:B:84:LEU:HD13	1:B:267:VAL:HG21	2.01	0.43
1:B:282:ASN:HB3	1:B:284:THR:HG23	2.00	0.43
1:A:855:PHE:HA	1:C:592:PHE:HZ	1.84	0.43
1:C:190:ARG:HH11	1:C:207:HIS:CD2	2.37	0.43
1:C:193:VAL:CG1	1:C:204:TYR:HB2	2.49	0.43
1:A:190:ARG:HG2	1:A:207:HIS:ND1	2.33	0.42
1:A:379:CYS:HB3	1:A:382:VAL:O	2.19	0.42
1:C:190:ARG:NH1	1:C:207:HIS:CG	2.87	0.42
1:C:435:ALA:HA	1:C:509:ARG:O	2.19	0.42
1:C:560:LEU:HB2	1:C:563:GLN:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:ASN:ND2	2:A:1303:NAG:O7	2.52	0.42
1:A:1093:GLY:HA3	1:A:1105:THR:O	2.18	0.42
1:B:551:VAL:HB	1:B:588:THR:HG23	2.02	0.42
1:B:647:ALA:HA	1:C:862:PRO:HG2	2.01	0.42
1:A:103:GLY:HA3	1:A:119:ILE:O	2.19	0.42
1:B:278:LYS:O	1:B:285:ILE:HA	2.18	0.42
1:C:393:THR:HB	1:C:516:GLU:O	2.20	0.42
1:C:1122:VAL:HG23	1:C:1123:SER:N	2.31	0.42
1:C:118:LEU:HD21	1:C:120:VAL:HG23	2.01	0.42
1:C:431:GLY:HA3	1:C:513:LEU:O	2.19	0.42
1:C:520:ALA:HB3	1:C:521:PRO:HD3	2.01	0.42
1:C:763:LEU:HD22	1:C:1008:VAL:HG21	2.01	0.42
1:A:720:ILE:HG13	1:A:923:ILE:HG23	2.01	0.42
1:B:742:ILE:HG22	1:B:743:CYS:SG	2.59	0.42
1:B:522:ALA:C	1:B:524:VAL:H	2.28	0.42
1:B:357:ARG:NH1	1:C:230:PRO:HB2	2.35	0.42
1:B:596:SER:OG	1:B:611:LEU:HB3	2.20	0.42
1:B:986:PRO:O	1:B:990:GLU:HG2	2.20	0.42
1:B:130:VAL:HG12	1:B:130:VAL:O	2.19	0.42
1:C:97:LYS:HE2	1:C:97:LYS:HB2	1.88	0.42
1:C:227:VAL:CB	1:C:229:LEU:CD2	2.98	0.42
1:C:720:ILE:CD1	1:C:923:ILE:HG23	2.50	0.42
1:B:229:LEU:HB2	1:B:231:ILE:HD11	2.02	0.42
1:B:642:VAL:HG22	1:B:651:ILE:HG22	2.01	0.42
1:C:724:THR:HG22	1:C:1063:LEU:HD23	2.02	0.42
1:A:29:THR:HG22	1:A:62:VAL:O	2.20	0.41
1:B:196:ASN:HA	1:B:201:PHE:N	2.35	0.41
1:B:726:ILE:HG13	1:B:1061:VAL:HG22	2.02	0.41
1:C:742:ILE:HG22	1:C:997:ILE:HD13	2.01	0.41
1:A:294:ASP:N	1:A:294:ASP:OD1	2.53	0.41
1:A:794:ILE:O	1:A:794:ILE:HG13	2.20	0.41
1:B:117:LEU:HD11	1:B:231:ILE:HD13	2.02	0.41
1:C:37:TYR:CG	1:C:206:LYS:HD2	2.55	0.41
1:C:453:TYR:CE2	1:C:455:LEU:HB3	2.55	0.41
1:C:865:LEU:HA	1:C:869:MET:HE3	2.02	0.41
1:C:759:PHE:O	1:C:763:LEU:HG	2.20	0.41
1:C:969:LYS:HZ3	1:C:975:SER:H	1.69	0.41
1:B:720:ILE:HG13	1:B:923:ILE:HG23	2.01	0.41
1:C:27:SER:OG	1:C:28:TYR:N	2.53	0.41
1:A:513:LEU:HD23	1:A:513:LEU:HA	1.97	0.41
1:A:789:TYR:HA	1:C:703:ASN:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:VAL:HG11	1:B:528:LYS:HG2	2.03	0.41
1:B:431:GLY:HA3	1:B:513:LEU:O	2.21	0.41
1:B:589:PRO:HG3	1:C:855:PHE:CD1	2.56	0.41
1:C:287:ASP:HB3	1:C:306:PHE:HE2	1.85	0.41
1:A:873:TYR:CZ	1:C:699:LEU:HD22	2.55	0.41
1:A:904:TYR:OH	1:C:1094:VAL:HG11	2.21	0.41
1:B:136:CYS:SG	1:B:137:ASN:N	2.93	0.41
1:C:742:ILE:HD11	1:C:1004:LEU:HD12	2.03	0.41
1:A:277:LEU:HD13	1:A:285:ILE:HD13	2.03	0.41
1:B:703:ASN:O	1:C:789:TYR:HA	2.21	0.41
1:C:134:GLN:OE1	1:C:162:SER:OG	2.38	0.41
1:C:330:PRO:O	1:C:332:ILE:HG12	2.21	0.41
1:A:96:GLU:OE1	1:A:101:ILE:HG13	2.21	0.41
1:B:105:ILE:HB	1:B:239:GLN:HB3	2.03	0.41
1:C:216:LEU:HD23	1:C:216:LEU:HA	1.90	0.41
1:C:327:VAL:HG11	1:C:528:LYS:HE3	2.02	0.41
1:C:345:THR:HA	1:C:509:ARG:HH22	1.86	0.41
1:C:720:ILE:HD11	1:C:923:ILE:HG23	2.03	0.41
1:C:1028:LYS:NZ	1:C:1042:PHE:O	2.54	0.41
2:C:1309:NAG:H83	2:C:1309:NAG:H2	1.91	0.41
1:A:41:LYS:HE3	1:C:562:PHE:CZ	2.56	0.41
1:B:216:LEU:HD23	1:B:216:LEU:HA	1.91	0.41
1:B:1079:PRO:HB3	1:C:917:TYR:CE1	2.56	0.41
1:B:521:PRO:HG3	1:B:563:GLN:CD	2.45	0.40
1:B:563:GLN:HB2	1:C:41:LYS:HB3	2.02	0.40
1:A:41:LYS:HD2	1:C:563:GLN:HA	2.04	0.40
1:B:453:TYR:CE1	1:B:493:GLN:HB3	2.56	0.40
1:B:564:GLN:OE1	1:B:564:GLN:N	2.54	0.40
1:B:916:LEU:HD12	1:B:923:ILE:HD12	2.04	0.40
1:C:353:TRP:CZ3	1:C:355:ARG:HD2	2.56	0.40
1:A:749:CYS:CB	1:A:993:ILE:HD11	2.52	0.40
1:B:733:LYS:HE2	1:B:861:LEU:HD11	2.03	0.40
1:B:1105:THR:HG22	1:B:1112:PRO:HA	2.03	0.40
1:A:197:ILE:HG22	1:A:198:ASP:OD1	2.22	0.40
1:C:141:LEU:HD12	1:C:141:LEU:HA	1.96	0.40
1:C:1093:GLY:HA2	1:C:1107:ARG:HD2	2.03	0.40
1:B:296:LEU:O	1:B:299:THR:HG22	2.22	0.40
1:B:335:LEU:HD23	1:B:362:VAL:HB	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	1005/1271 (79%)	966 (96%)	39 (4%)	0	100	100
1	B	988/1271 (78%)	943 (95%)	44 (4%)	1 (0%)	48	69
1	C	1000/1271 (79%)	951 (95%)	47 (5%)	2 (0%)	43	64
All	All	2993/3813 (78%)	2860 (96%)	130 (4%)	3 (0%)	49	69

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	226	LEU
1	B	216	LEU
1	C	229	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	894/1107 (81%)	894 (100%)	0	100	100
1	B	886/1107 (80%)	884 (100%)	2 (0%)	87	95
1	C	890/1107 (80%)	889 (100%)	1 (0%)	88	96
All	All	2670/3321 (80%)	2667 (100%)	3 (0%)	87	96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	212	LEU
1	B	231	ILE
1	C	233	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	HIS
1	A	81	ASN
1	A	334	ASN
1	A	658	ASN
1	A	751	ASN
1	A	762	GLN
1	A	935	GLN
1	B	69	HIS
1	B	121	ASN
1	B	317	ASN
1	B	321	GLN
1	B	422	ASN
1	B	448	ASN
1	B	658	ASN
1	B	710	ASN
1	B	717	ASN
1	B	1002	GLN
1	B	1054	GLN
1	C	81	ASN
1	C	121	ASN
1	C	207	HIS
1	C	439	ASN
1	C	448	ASN
1	C	506	GLN
1	C	563	GLN
1	C	607	GLN
1	C	751	ASN
1	C	777	ASN
1	C	784	GLN
1	C	856	ASN
1	C	955	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

27 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	$\# Z > 2$
2	NAG	B	1301	1	14,14,15	0.28	0	17,19,21	0.53	0
2	NAG	A	1309	1	14,14,15	0.23	0	17,19,21	0.45	0
2	NAG	B	1303	1	14,14,15	0.38	0	17,19,21	0.47	0
2	NAG	B	1302	1	14,14,15	0.39	0	17,19,21	0.44	0
2	NAG	C	1305	1	14,14,15	0.27	0	17,19,21	0.37	0
2	NAG	C	1306	1	14,14,15	0.24	0	17,19,21	0.49	0
2	NAG	A	1303	1	14,14,15	0.39	0	17,19,21	0.65	0
2	NAG	A	1302	1	14,14,15	0.39	0	17,19,21	0.62	0
2	NAG	A	1311	1	14,14,15	0.40	0	17,19,21	0.96	3 (17%)
2	NAG	C	1307	1	14,14,15	0.42	0	17,19,21	0.43	0
2	NAG	C	1302	1	14,14,15	0.21	0	17,19,21	0.45	0
2	NAG	C	1308	1	14,14,15	0.22	0	17,19,21	0.49	0
2	NAG	B	1304	1	14,14,15	0.38	0	17,19,21	0.59	0
2	NAG	B	1306	1	14,14,15	0.40	0	17,19,21	0.59	0
2	NAG	C	1304	1	14,14,15	0.25	0	17,19,21	0.56	0
2	NAG	B	1307	1	14,14,15	0.37	0	17,19,21	0.41	0
2	NAG	C	1309	1	14,14,15	0.39	0	17,19,21	0.65	0
2	NAG	B	1305	1	14,14,15	0.27	0	17,19,21	0.54	0
2	NAG	A	1308	1	14,14,15	0.21	0	17,19,21	0.38	0
2	NAG	A	1301	1	14,14,15	0.38	0	17,19,21	0.53	0
2	NAG	A	1310	1	14,14,15	0.37	0	17,19,21	0.60	0
2	NAG	C	1301	1	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
2	NAG	A	1305	1	14,14,15	0.46	0	17,19,21	0.52	0
2	NAG	A	1304	1	14,14,15	0.38	0	17,19,21	0.55	0
2	NAG	A	1306	1	14,14,15	0.20	0	17,19,21	0.51	0
2	NAG	C	1303	1	14,14,15	0.27	0	17,19,21	0.49	0
2	NAG	A	1307	1	14,14,15	0.20	0	17,19,21	0.47	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
2	NAG	B	1301	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1309	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1302	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1303	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1311	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1307	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1302	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1304	1	-	4/6/23/26	0/1/1/1
2	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1304	1	-	4/6/23/26	0/1/1/1
2	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1309	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1305	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1301	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1310	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1306	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1303	1	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1307	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1311	NAG	C1-O5-C5	2.13	115.04	112.19
2	A	1311	NAG	C1-C2-N2	2.06	113.68	110.43
2	A	1311	NAG	O5-C1-C2	-2.03	108.14	111.29

There are no chirality outliers.

All (62) torsion outliers are listed below:

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

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Mol	Chain	Res	Type	Atoms
2	C	1308	NAG	C4-C5-C6-O6
2	C	1304	NAG	O5-C5-C6-O6
2	A	1307	NAG	O5-C5-C6-O6
2	C	1304	NAG	C4-C5-C6-O6
2	C	1306	NAG	O5-C5-C6-O6
2	C	1308	NAG	O5-C5-C6-O6
2	B	1304	NAG	C4-C5-C6-O6
2	C	1305	NAG	C4-C5-C6-O6
2	A	1309	NAG	O5-C5-C6-O6
2	A	1311	NAG	C8-C7-N2-C2
2	A	1311	NAG	O7-C7-N2-C2
2	B	1305	NAG	C8-C7-N2-C2
2	B	1305	NAG	O7-C7-N2-C2
2	C	1303	NAG	C8-C7-N2-C2
2	C	1303	NAG	O7-C7-N2-C2
2	C	1307	NAG	C8-C7-N2-C2
2	C	1307	NAG	O7-C7-N2-C2
2	A	1303	NAG	O5-C5-C6-O6
2	B	1301	NAG	O5-C5-C6-O6
2	B	1301	NAG	C4-C5-C6-O6
2	C	1306	NAG	C4-C5-C6-O6
2	A	1306	NAG	O5-C5-C6-O6
2	B	1303	NAG	C4-C5-C6-O6
2	C	1302	NAG	O5-C5-C6-O6
2	B	1302	NAG	O5-C5-C6-O6
2	B	1306	NAG	C4-C5-C6-O6
2	A	1303	NAG	C4-C5-C6-O6
2	A	1308	NAG	C4-C5-C6-O6
2	C	1304	NAG	C1-C2-N2-C7
2	C	1303	NAG	O5-C5-C6-O6
2	B	1306	NAG	O5-C5-C6-O6
2	B	1301	NAG	C3-C2-N2-C7
2	C	1304	NAG	C3-C2-N2-C7
2	B	1301	NAG	C1-C2-N2-C7
2	A	1308	NAG	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 5 short contacts:

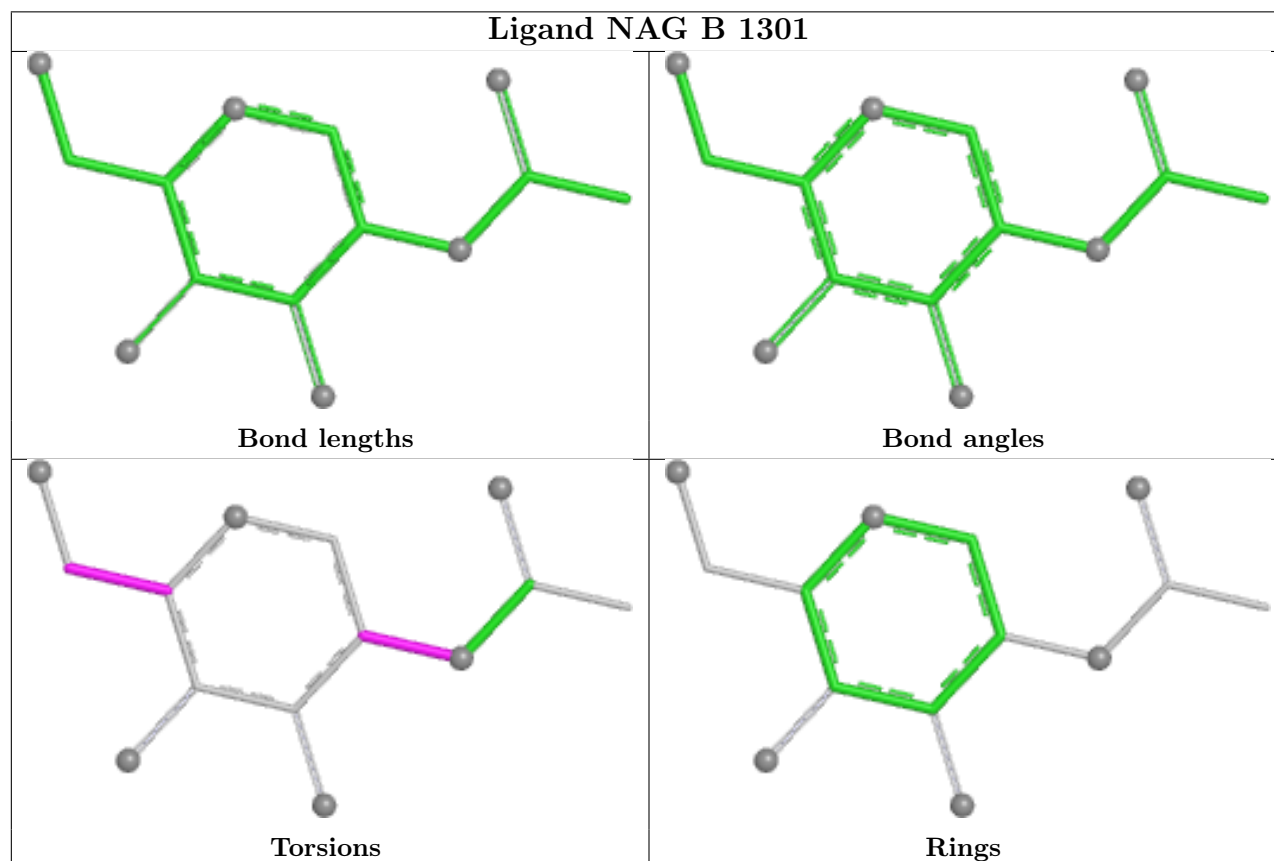
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1303	NAG	1	0
2	A	1303	NAG	1	0

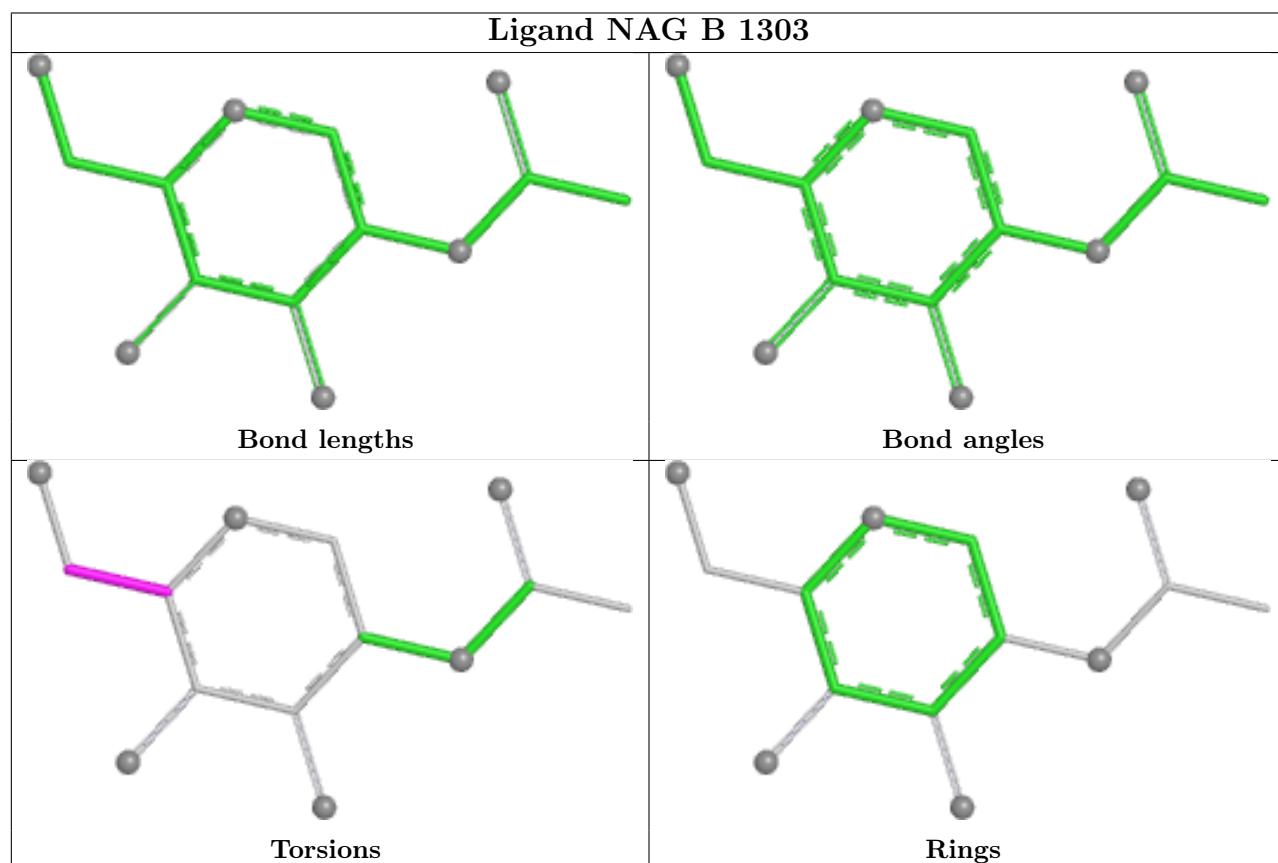
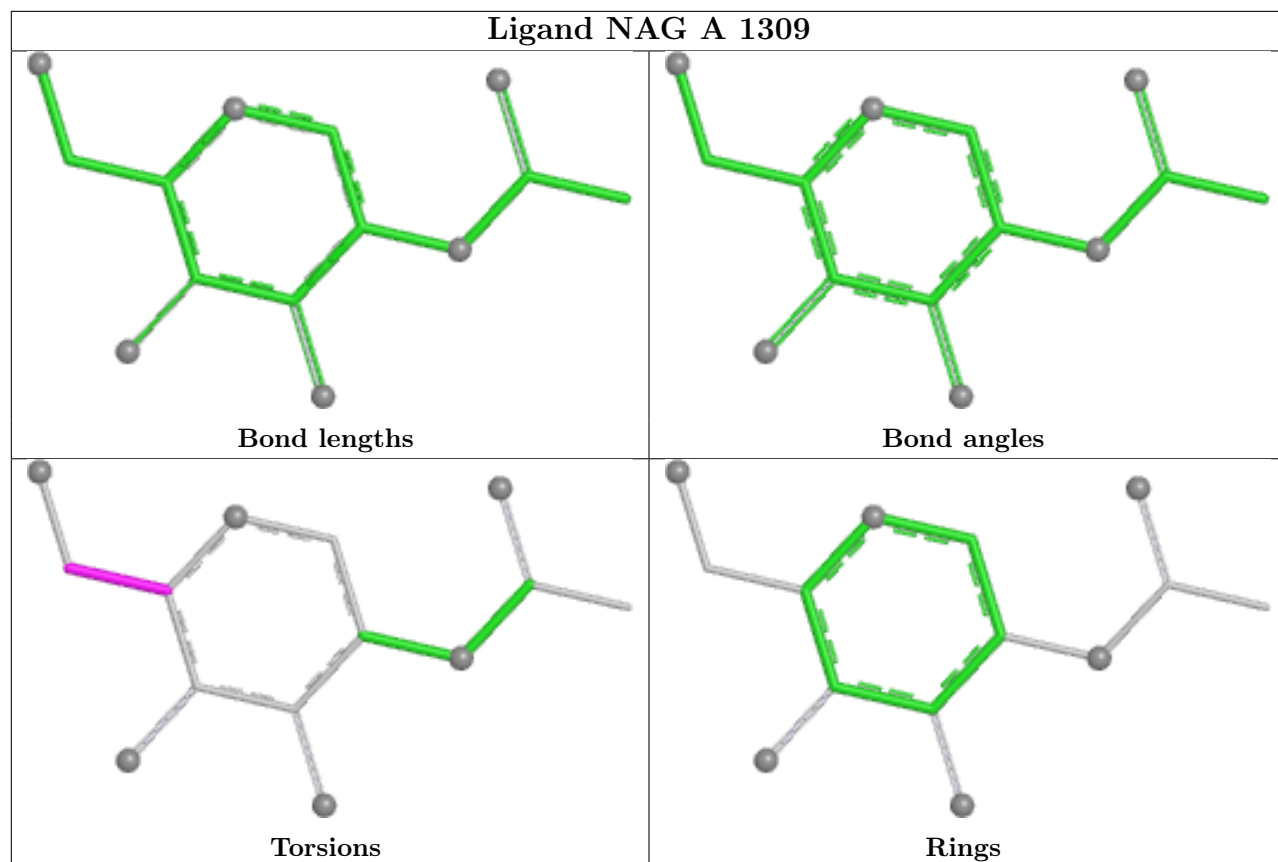
Continued on next page...

Continued from previous page...

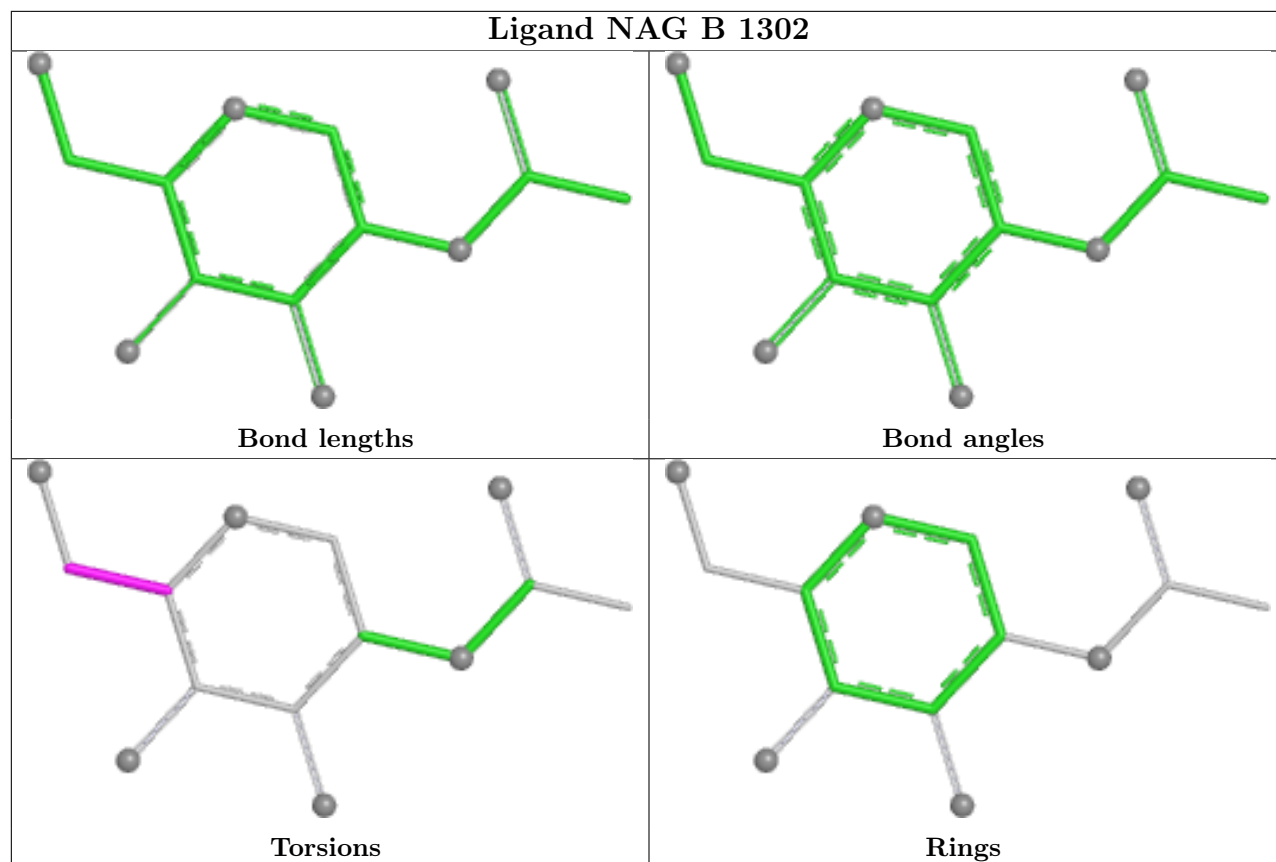
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1309	NAG	1	0
2	A	1305	NAG	1	0
2	A	1306	NAG	1	0

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.

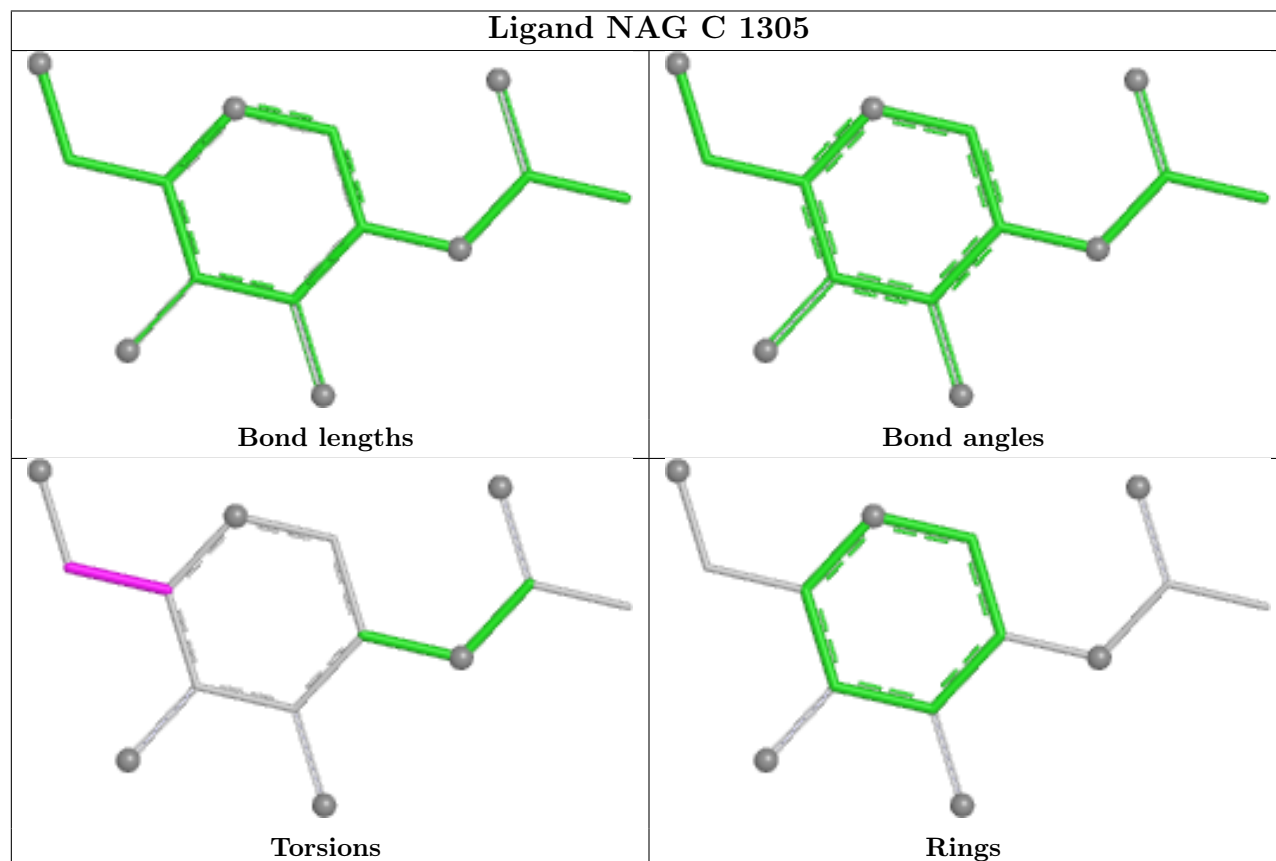




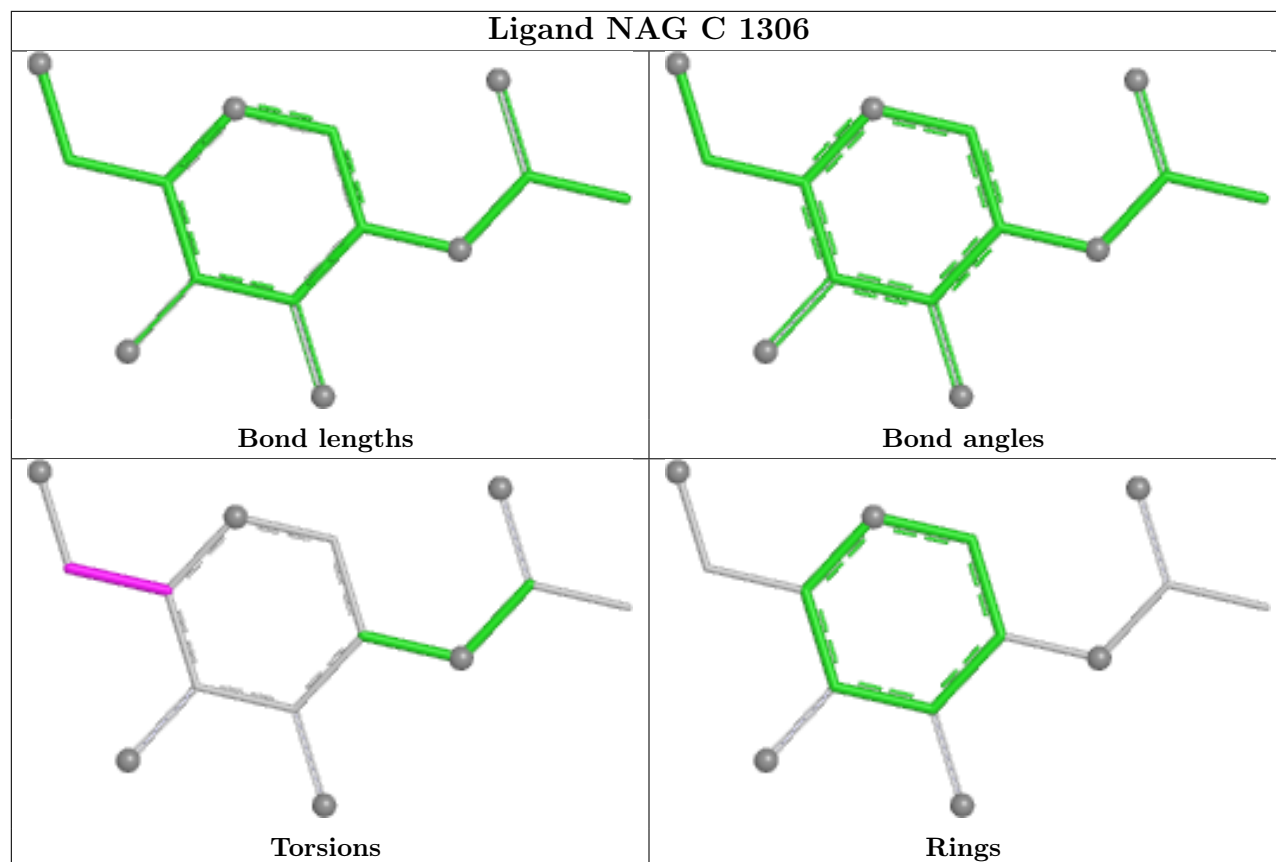
Ligand NAG B 1302



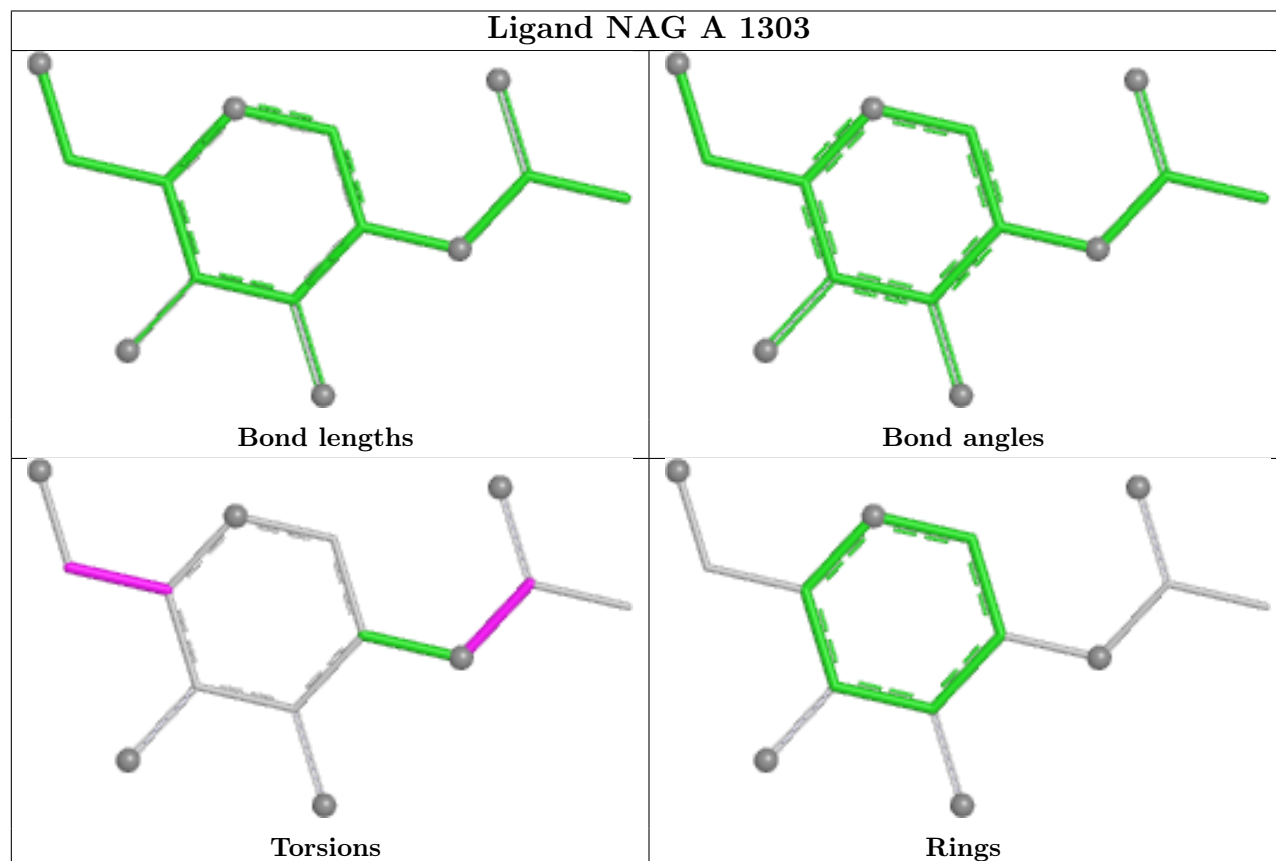
Ligand NAG C 1305



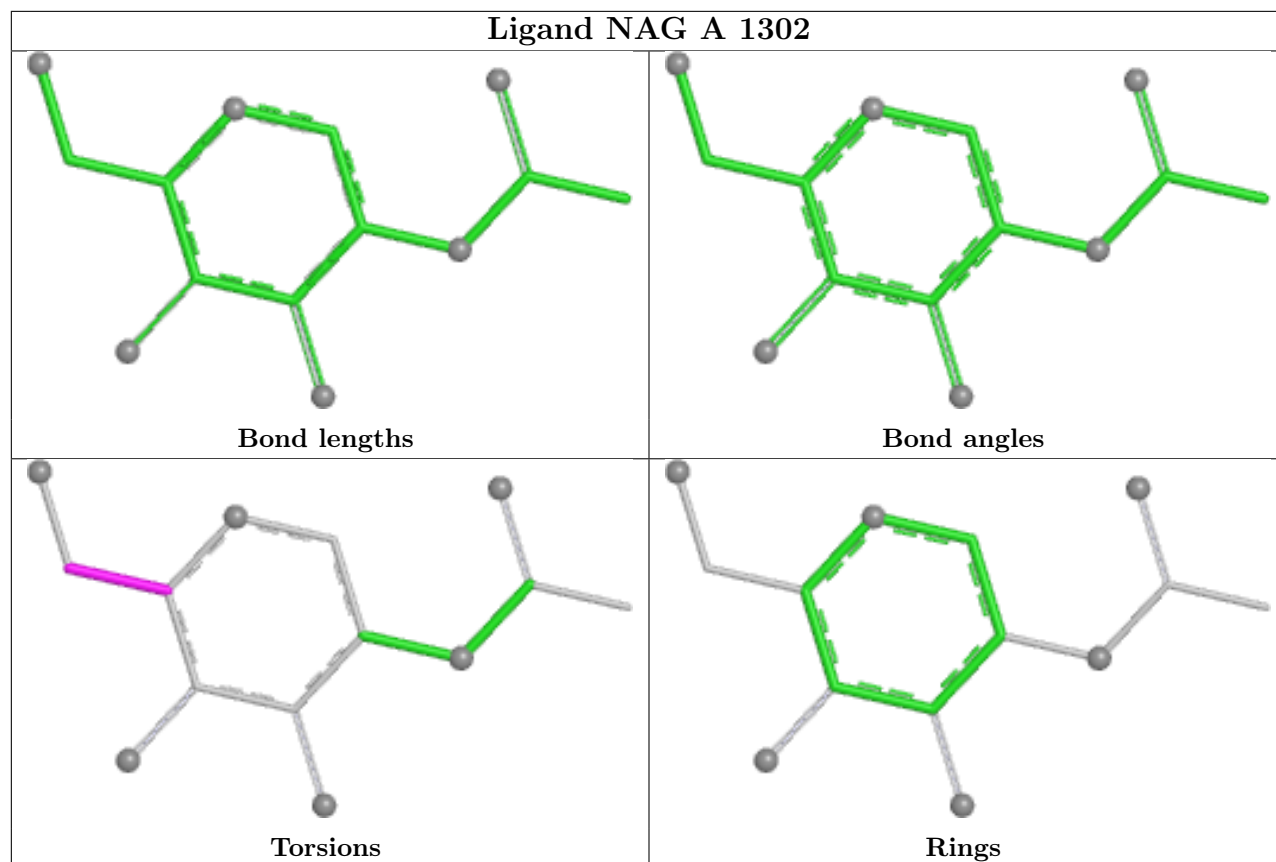
Ligand NAG C 1306



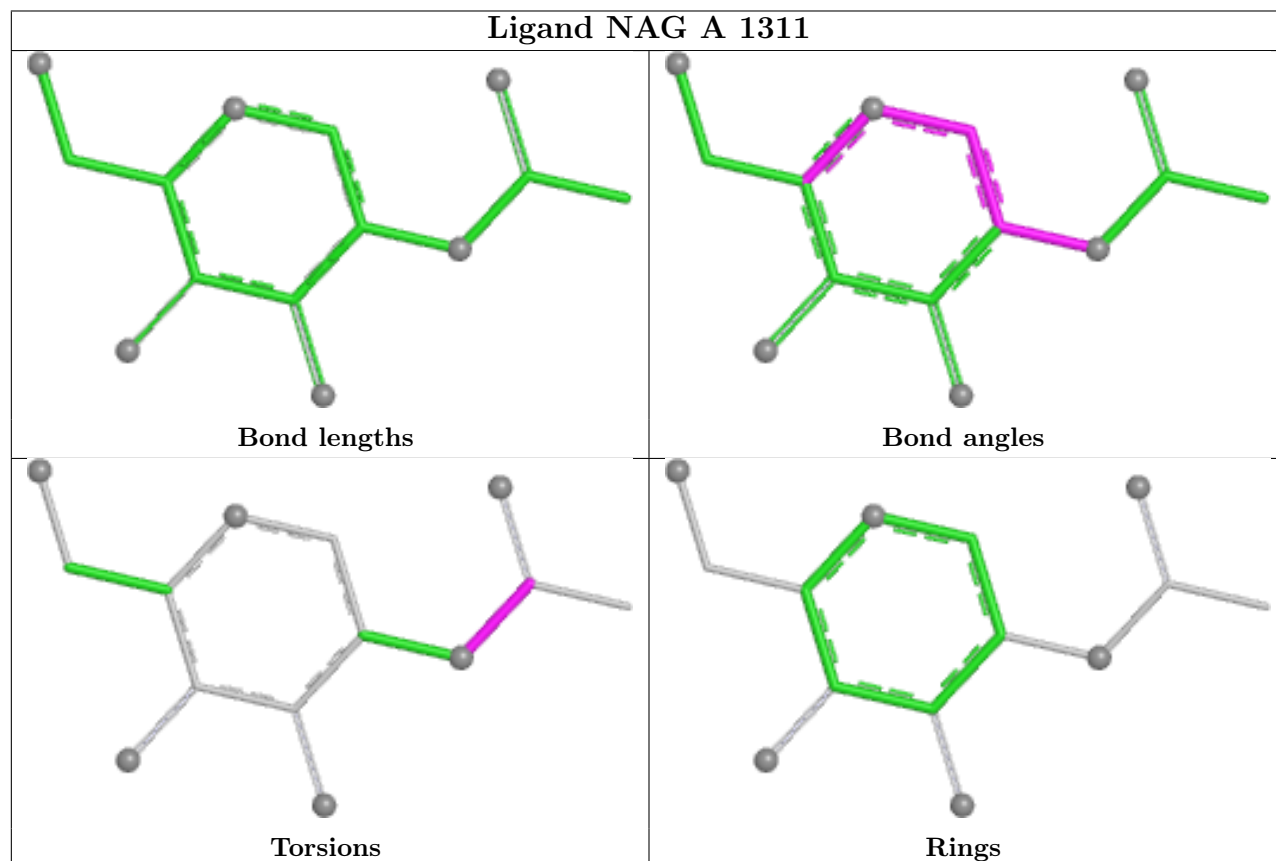
Ligand NAG A 1303

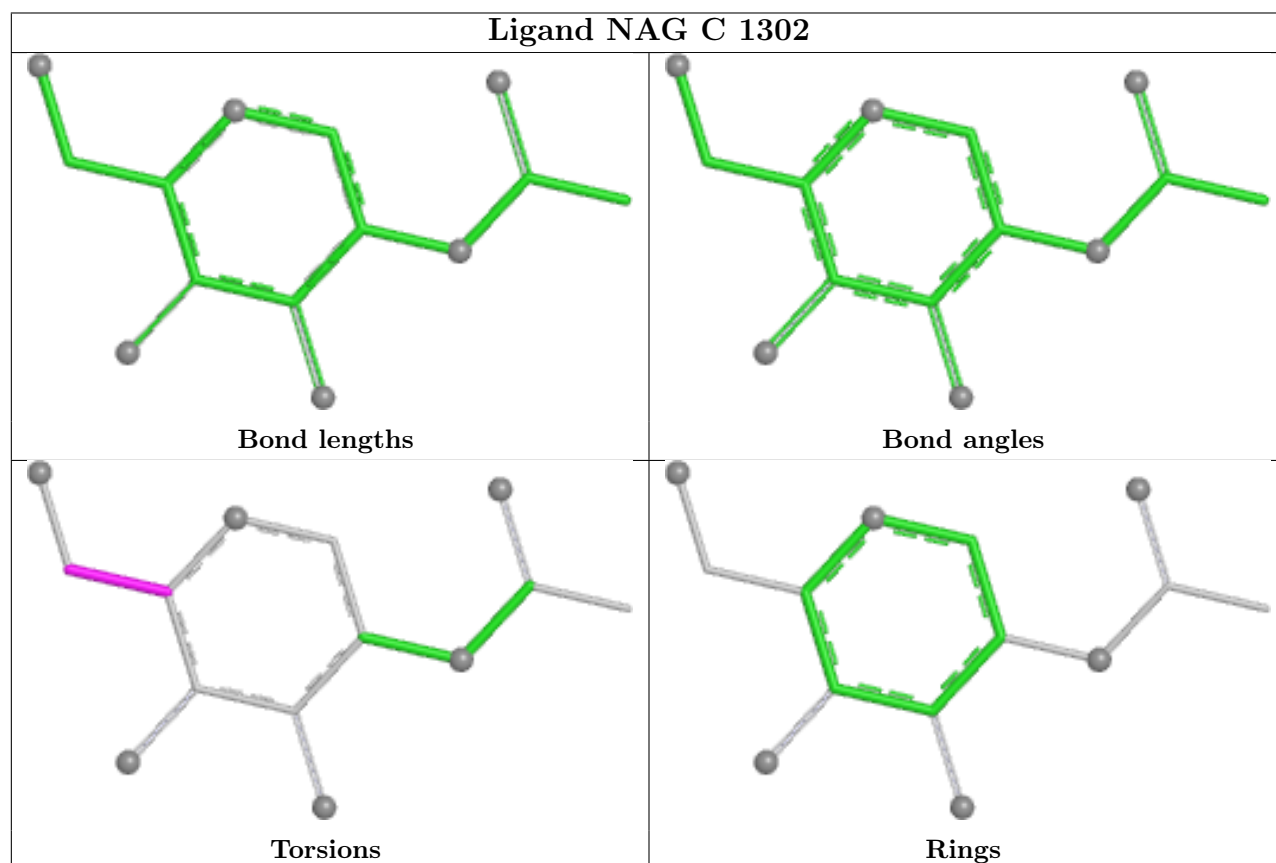
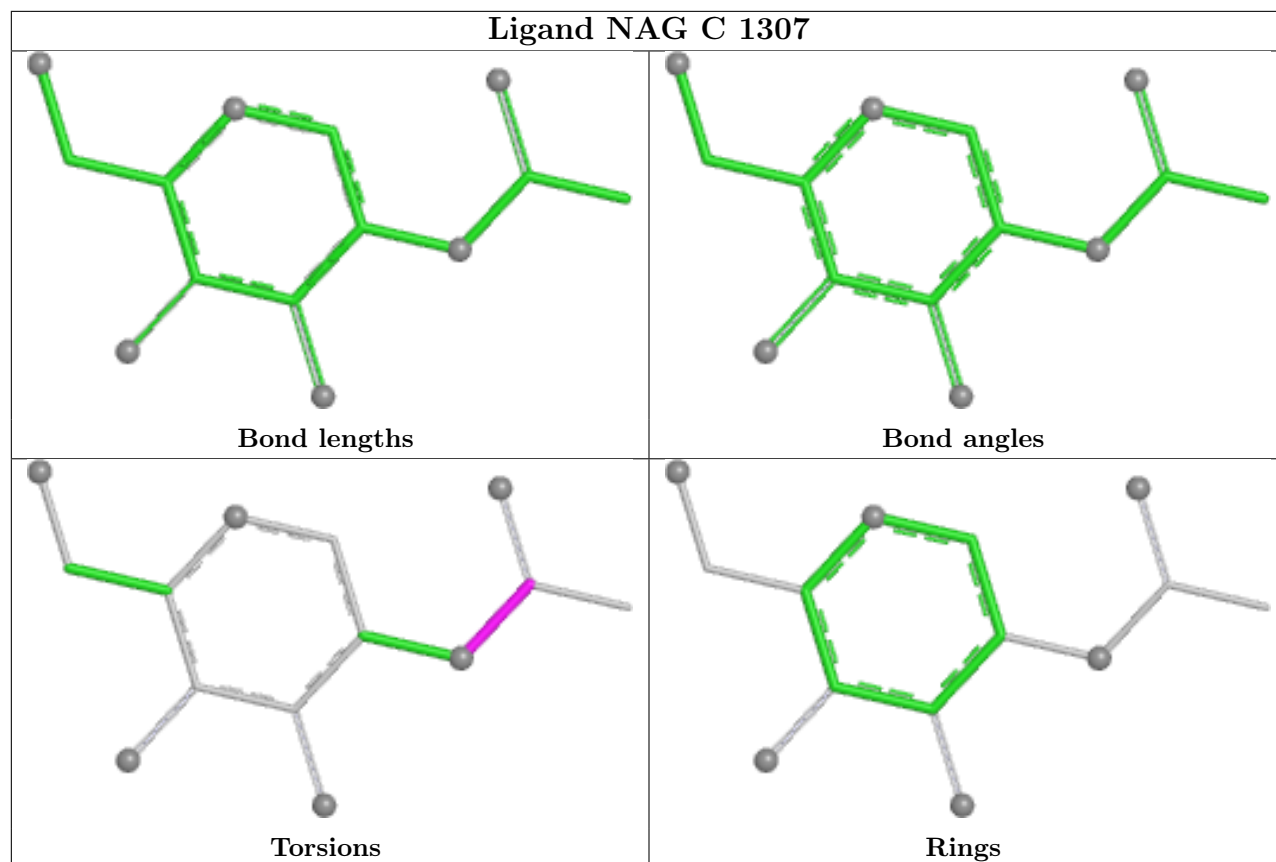


Ligand NAG A 1302

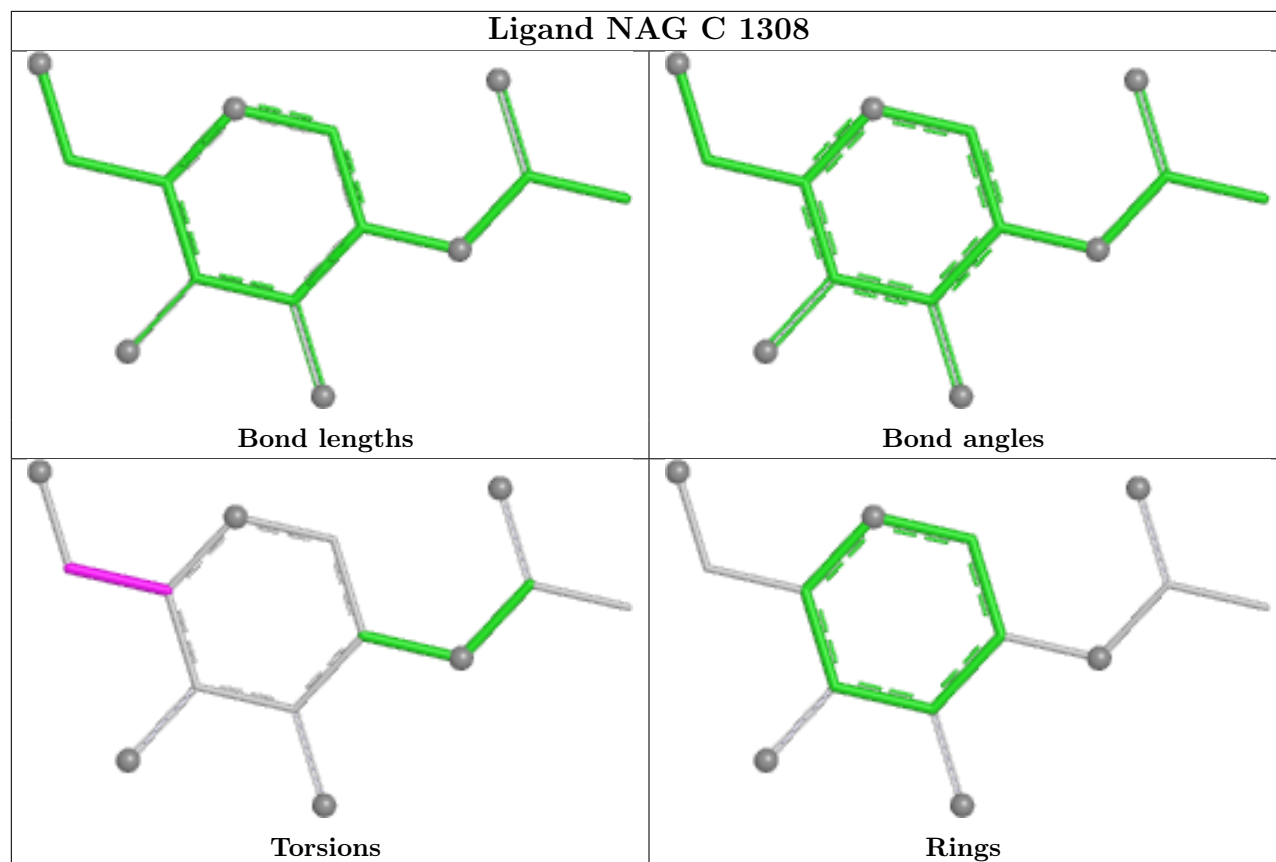


Ligand NAG A 1311

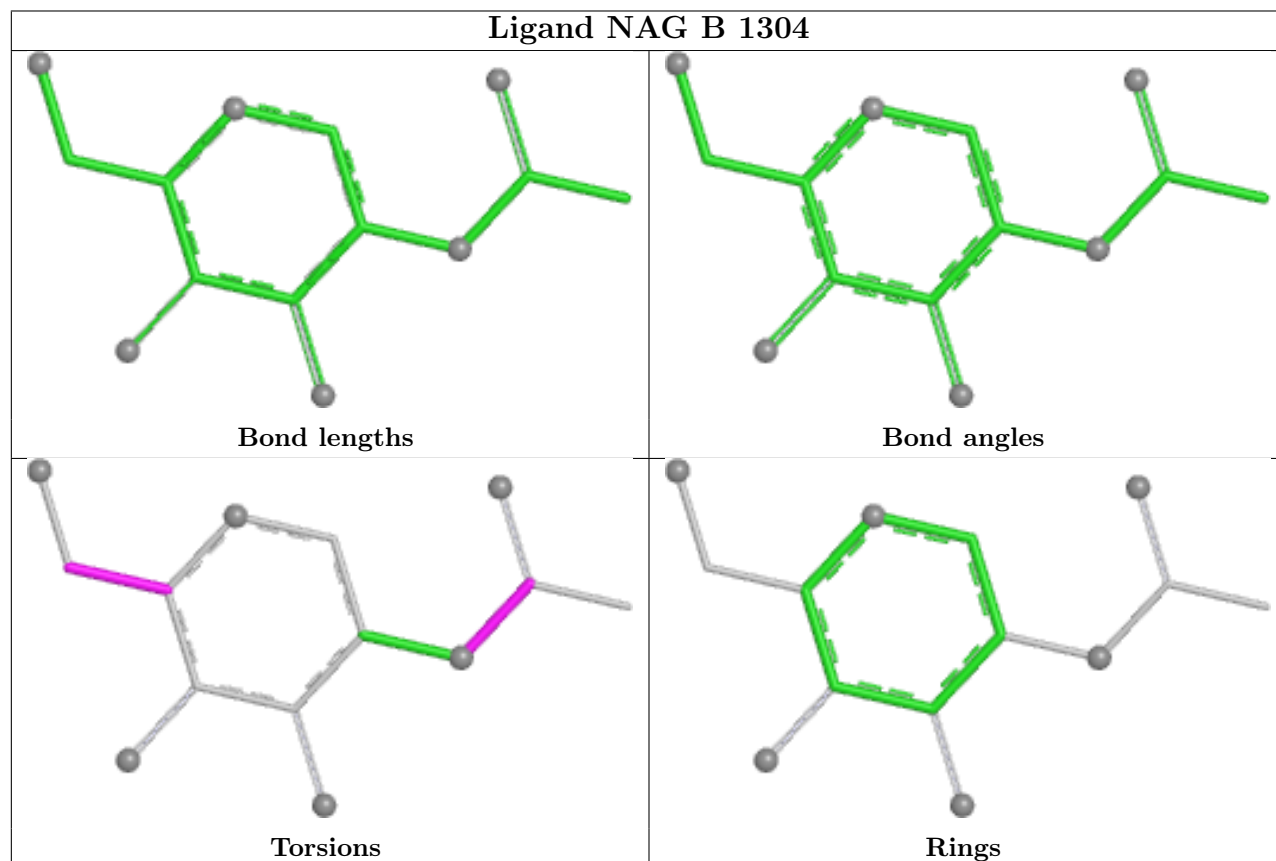


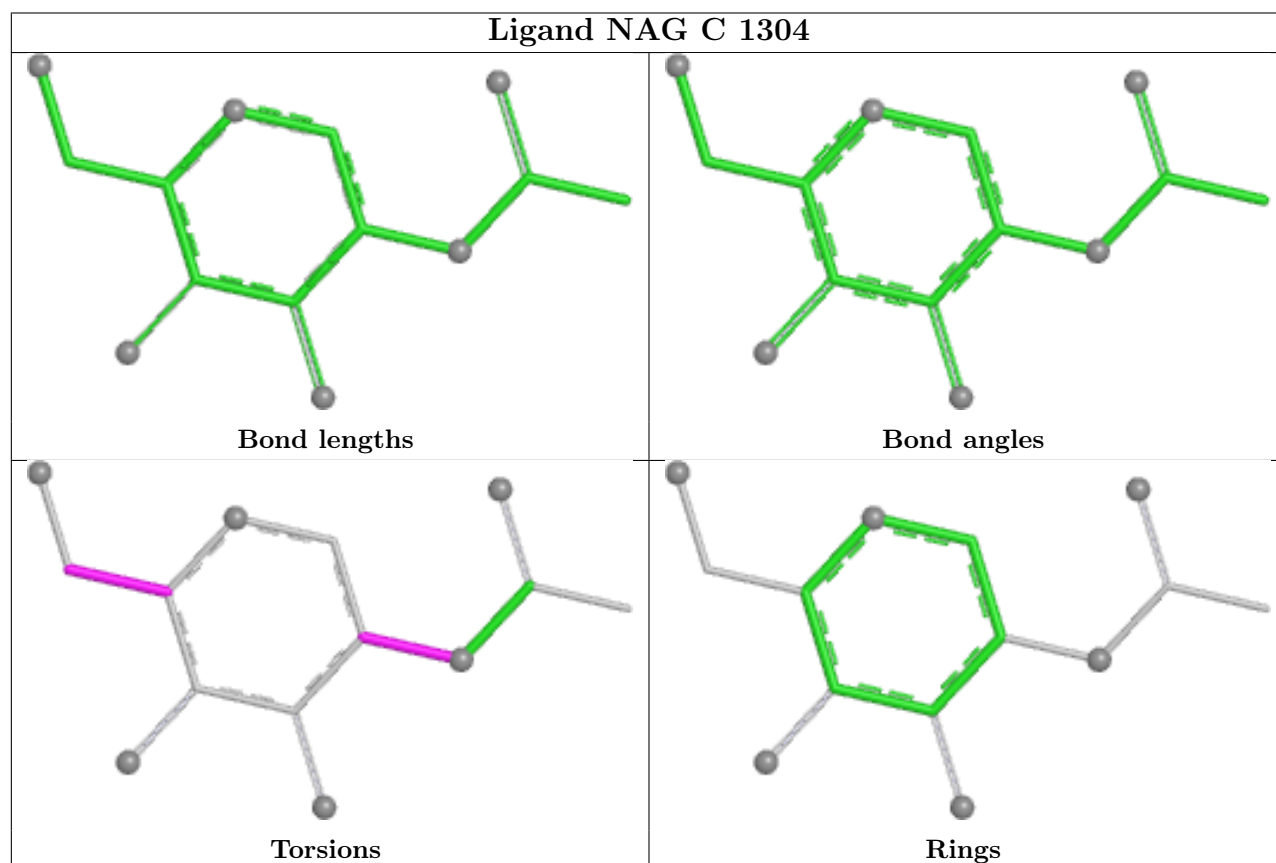
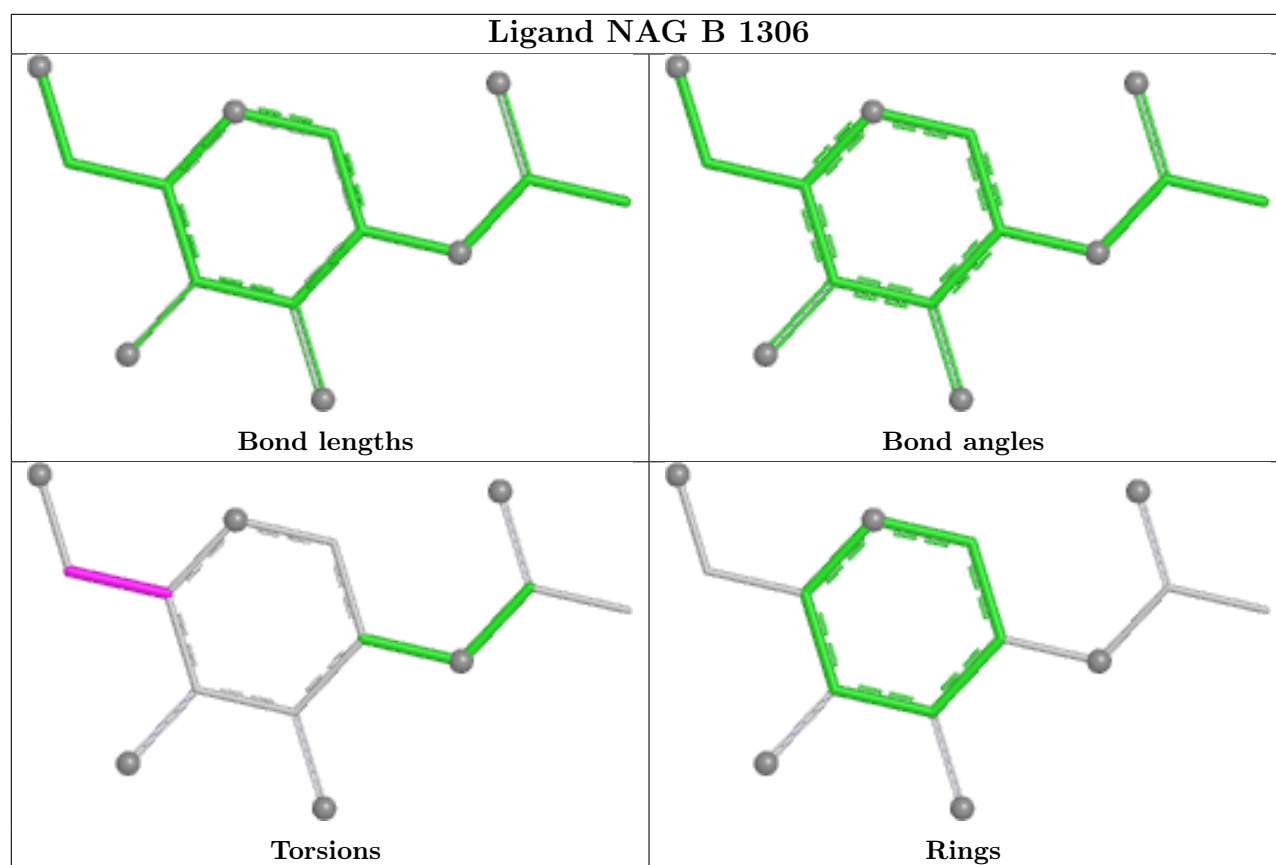


Ligand NAG C 1308

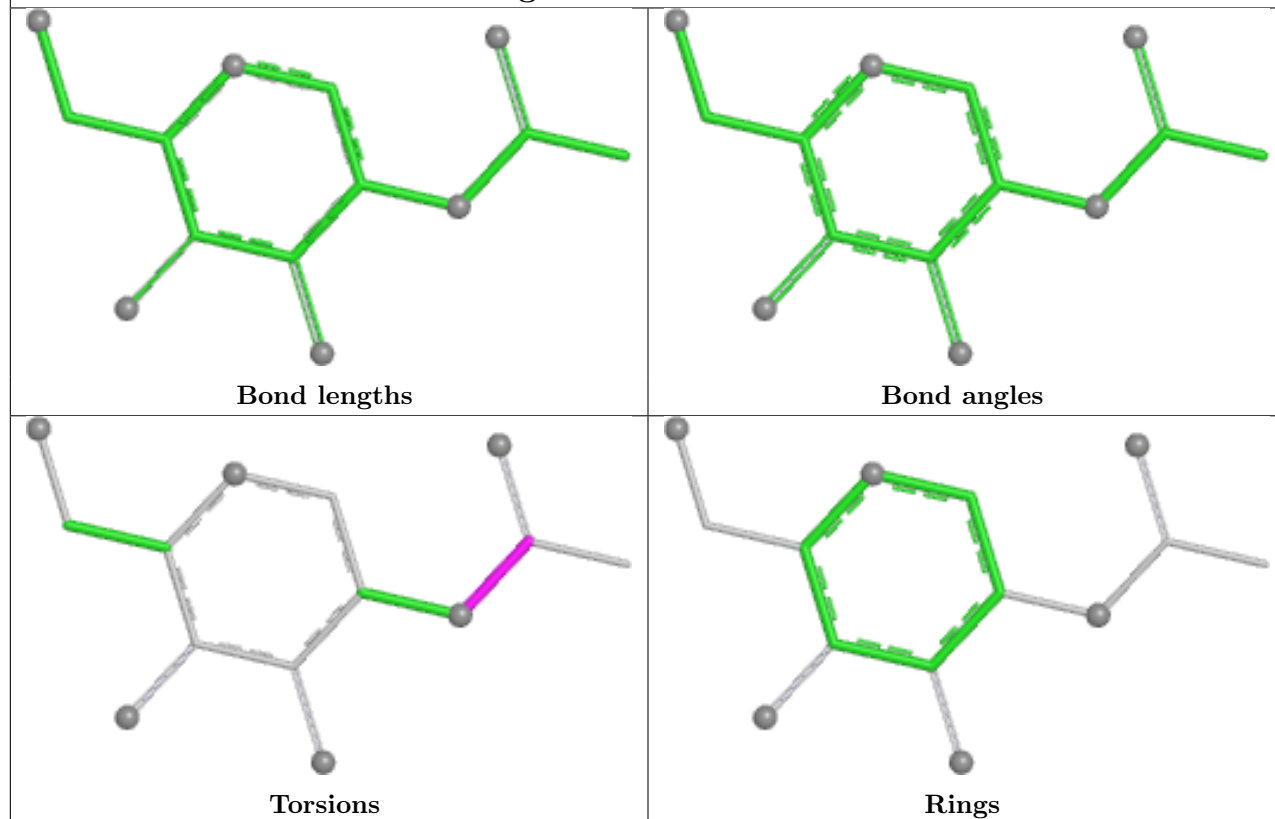


Ligand NAG B 1304

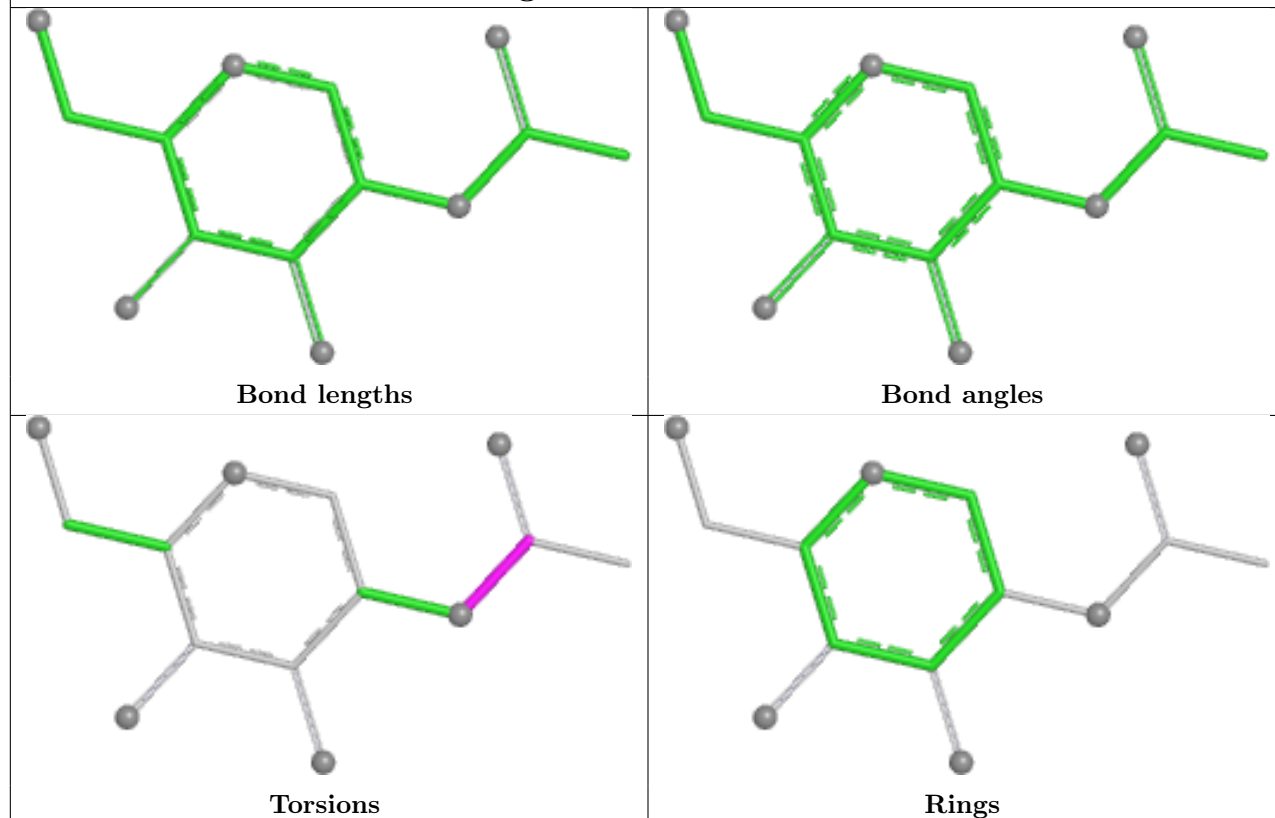




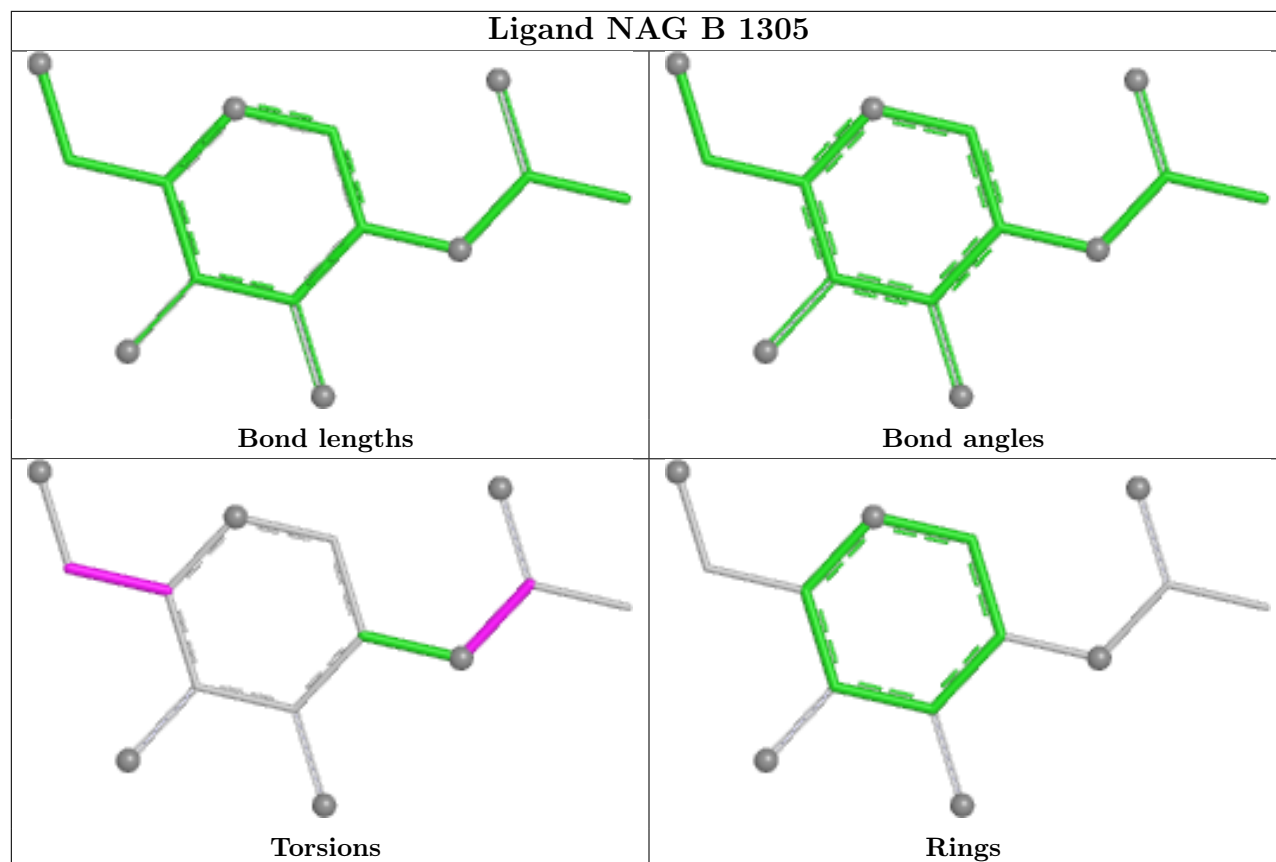
Ligand NAG B 1307



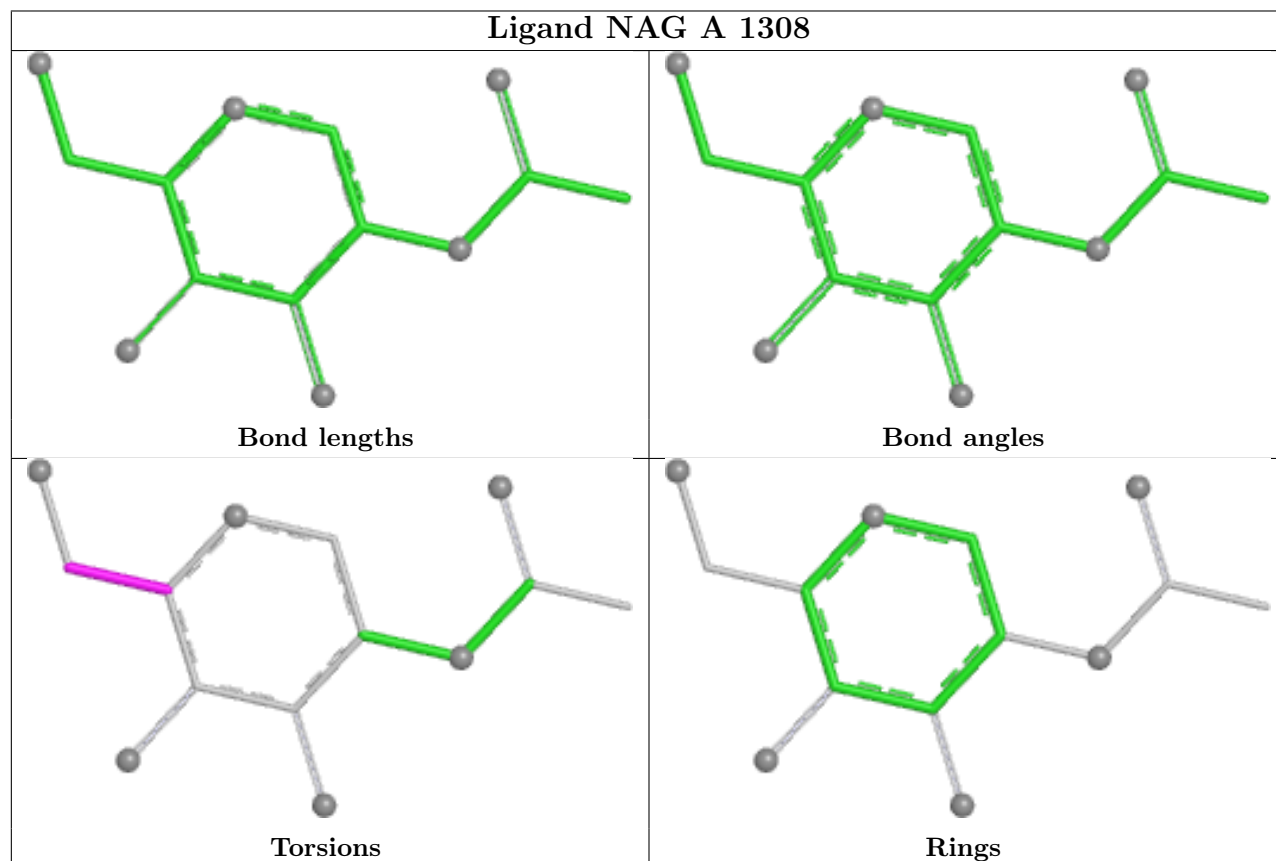
Ligand NAG C 1309

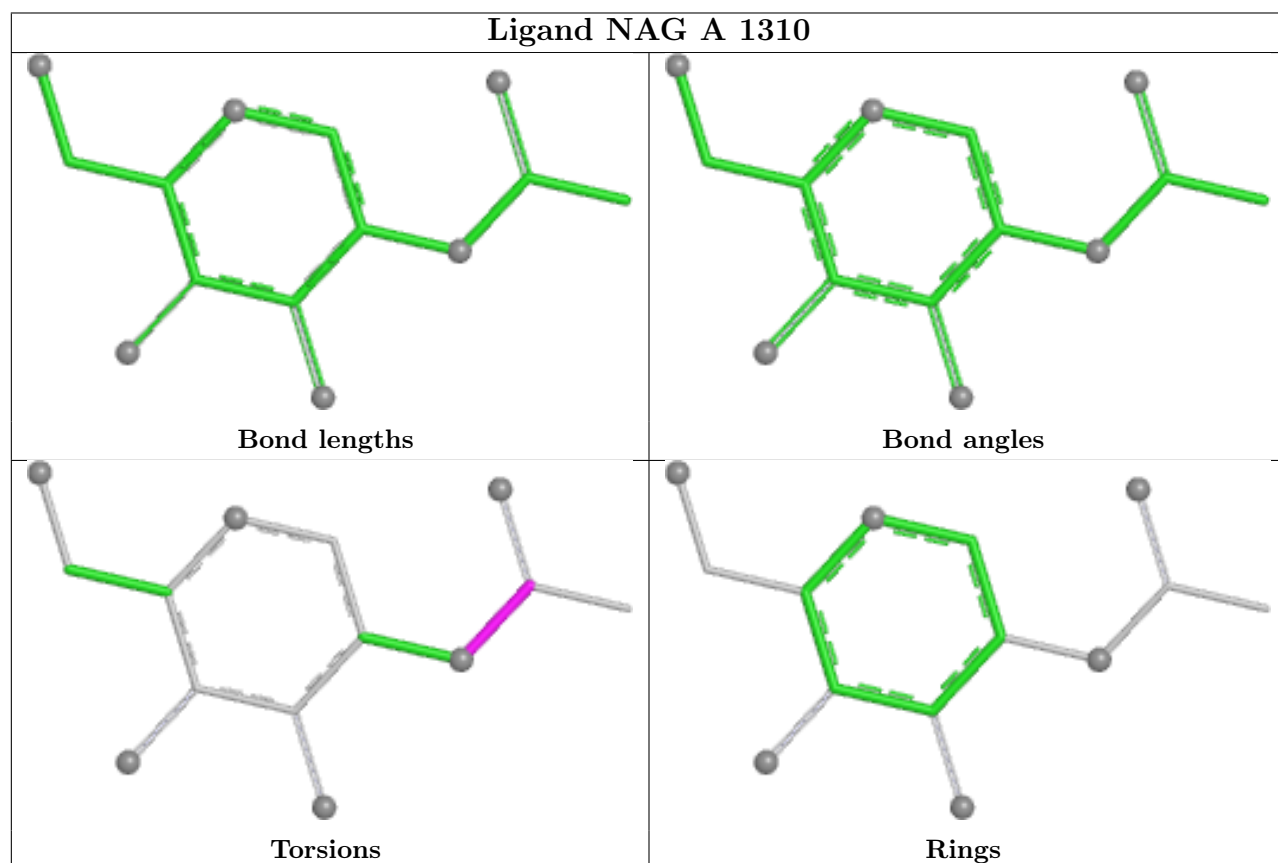
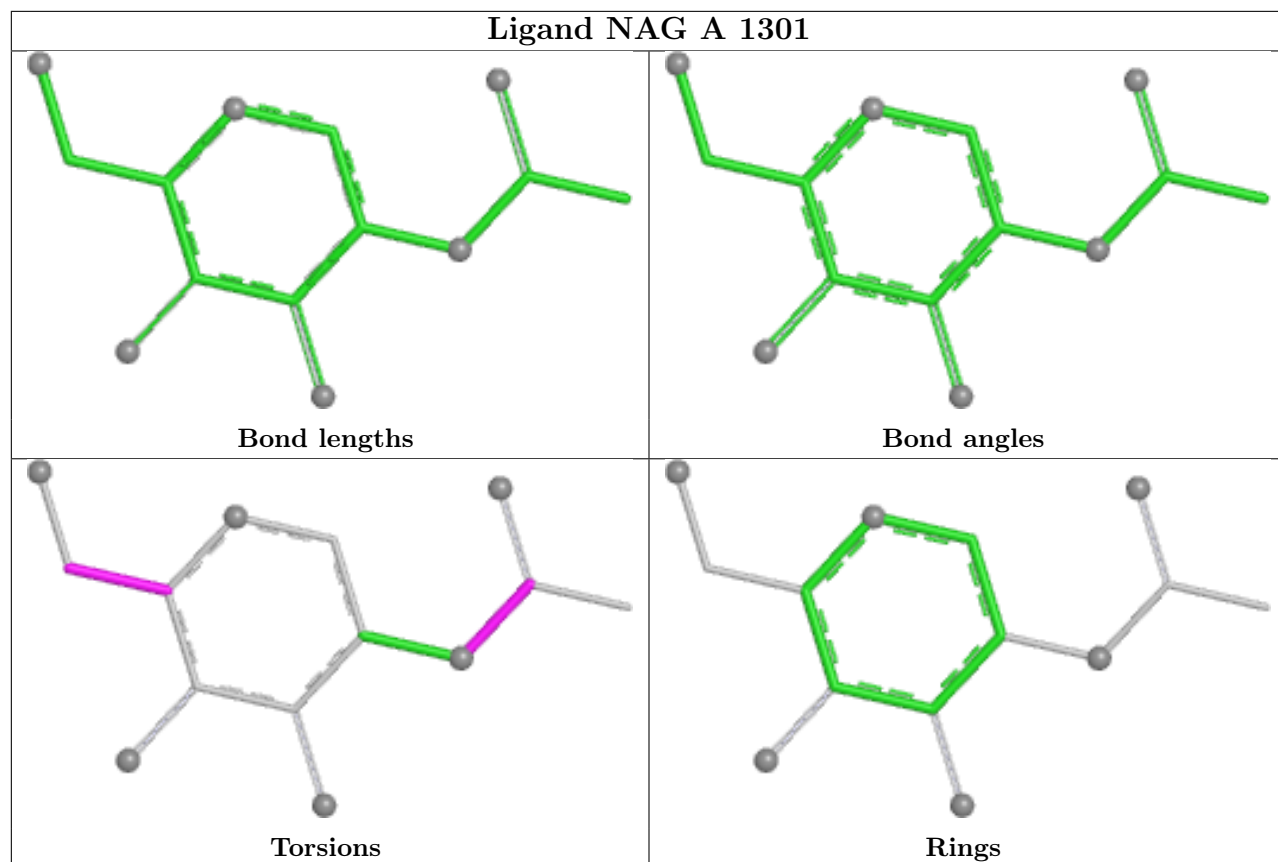


Ligand NAG B 1305

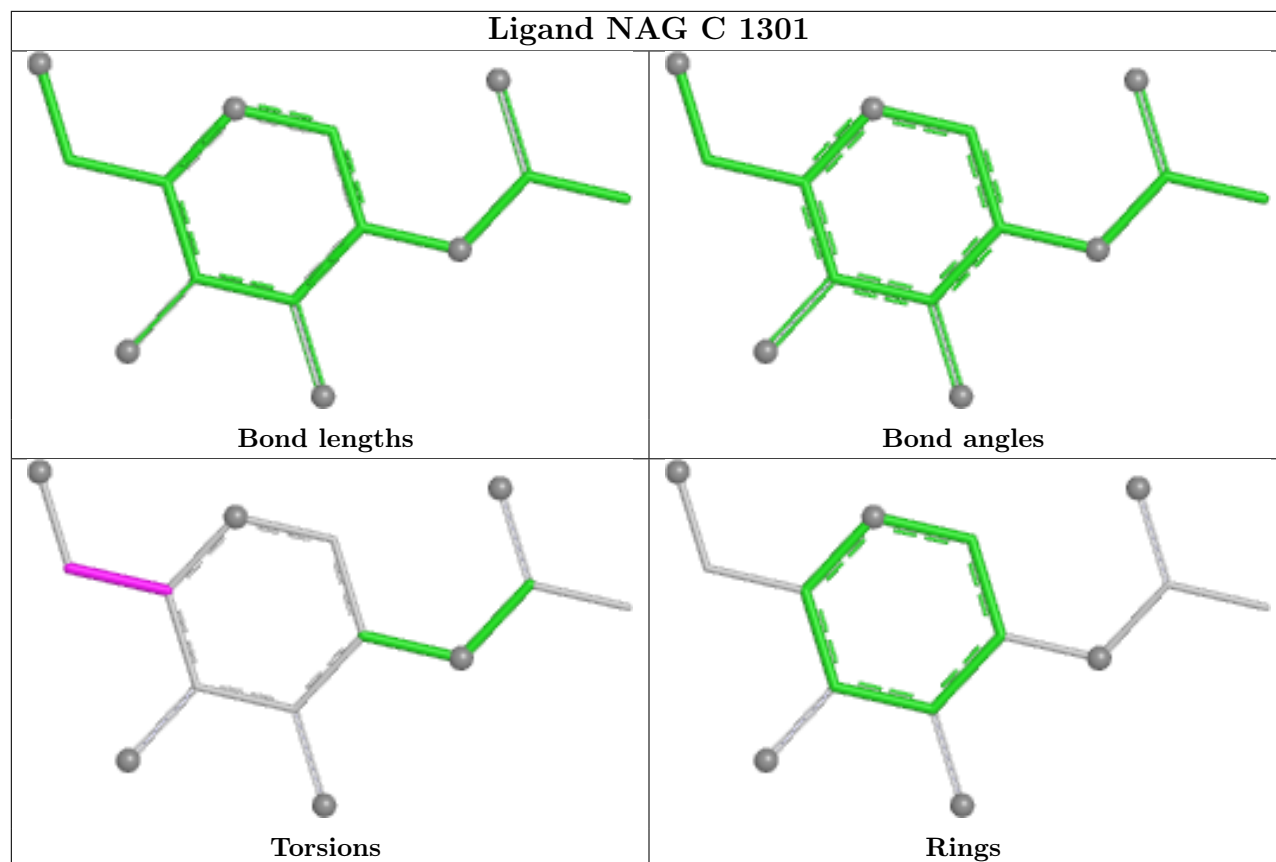


Ligand NAG A 1308

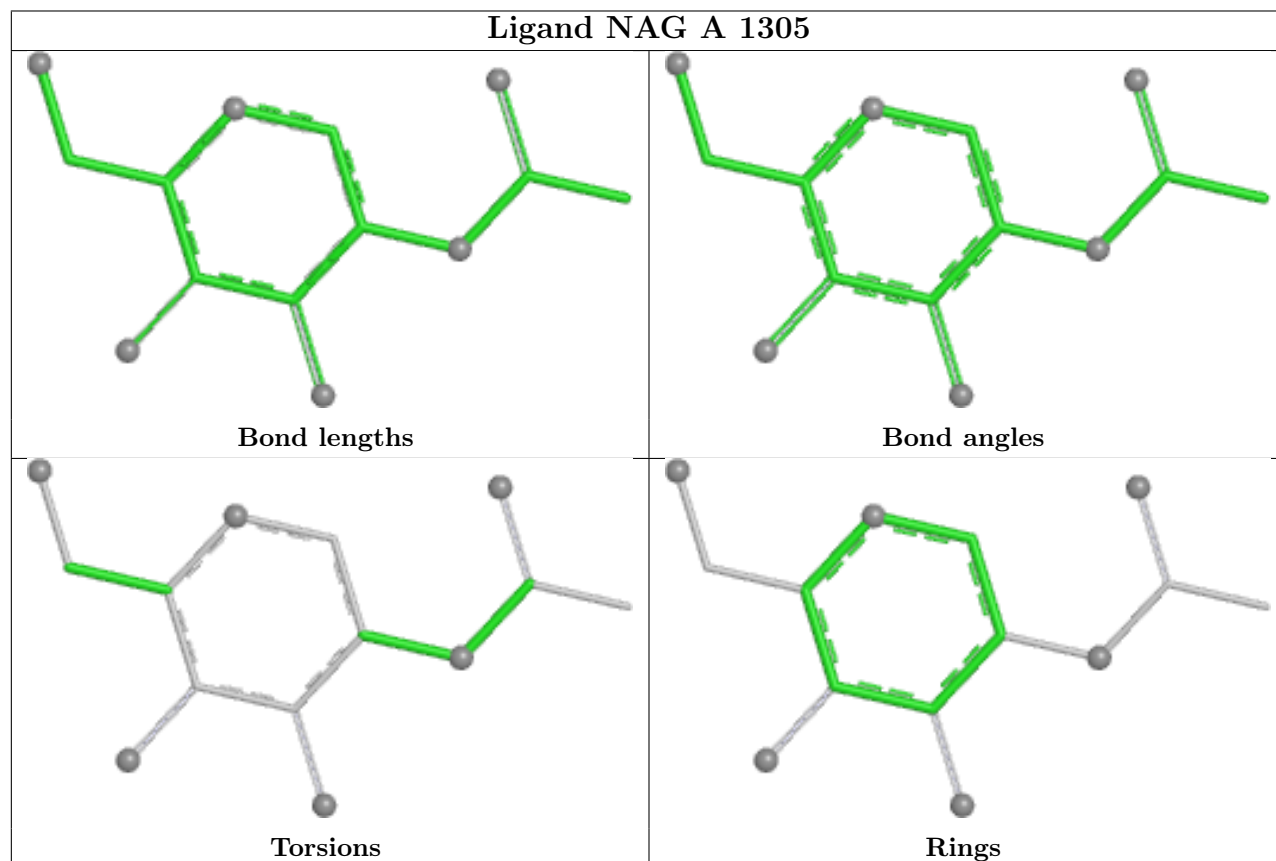




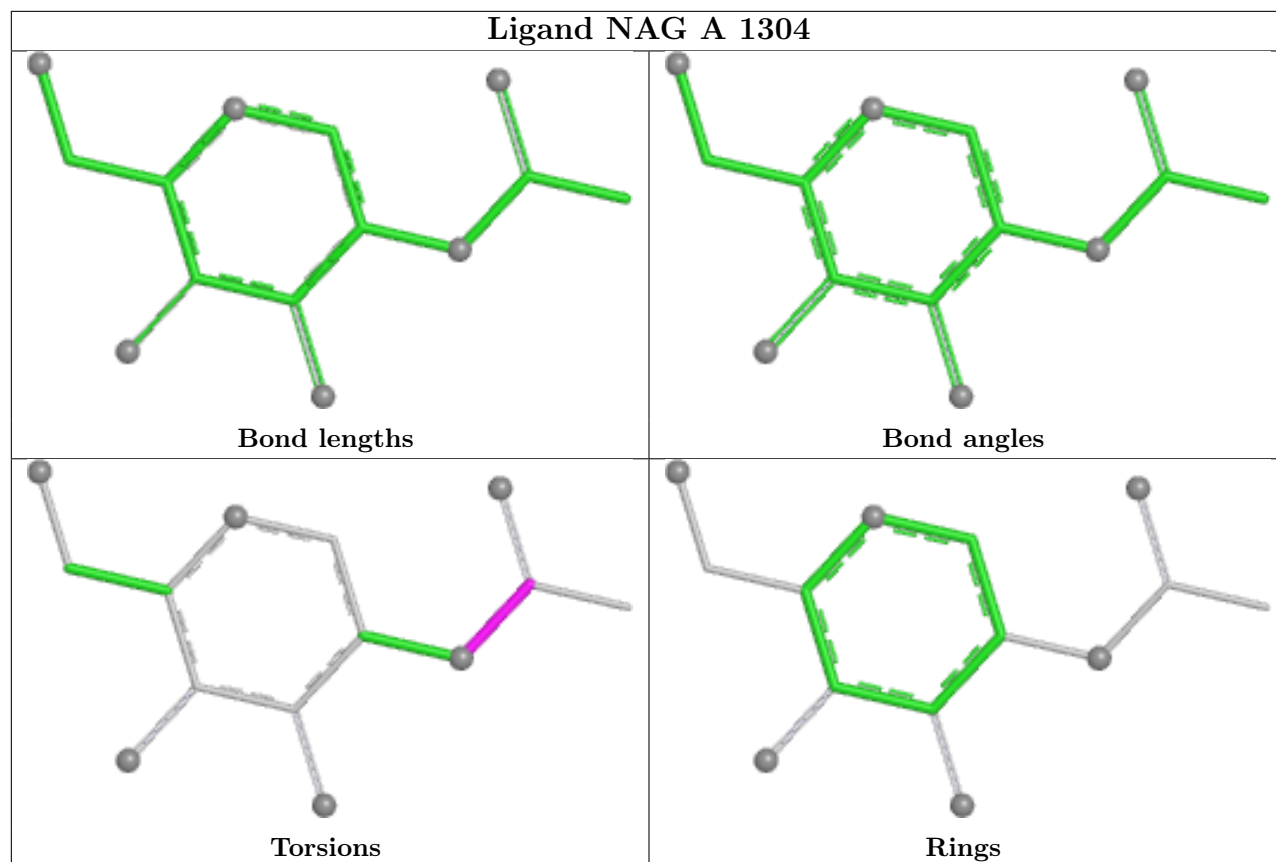
Ligand NAG C 1301



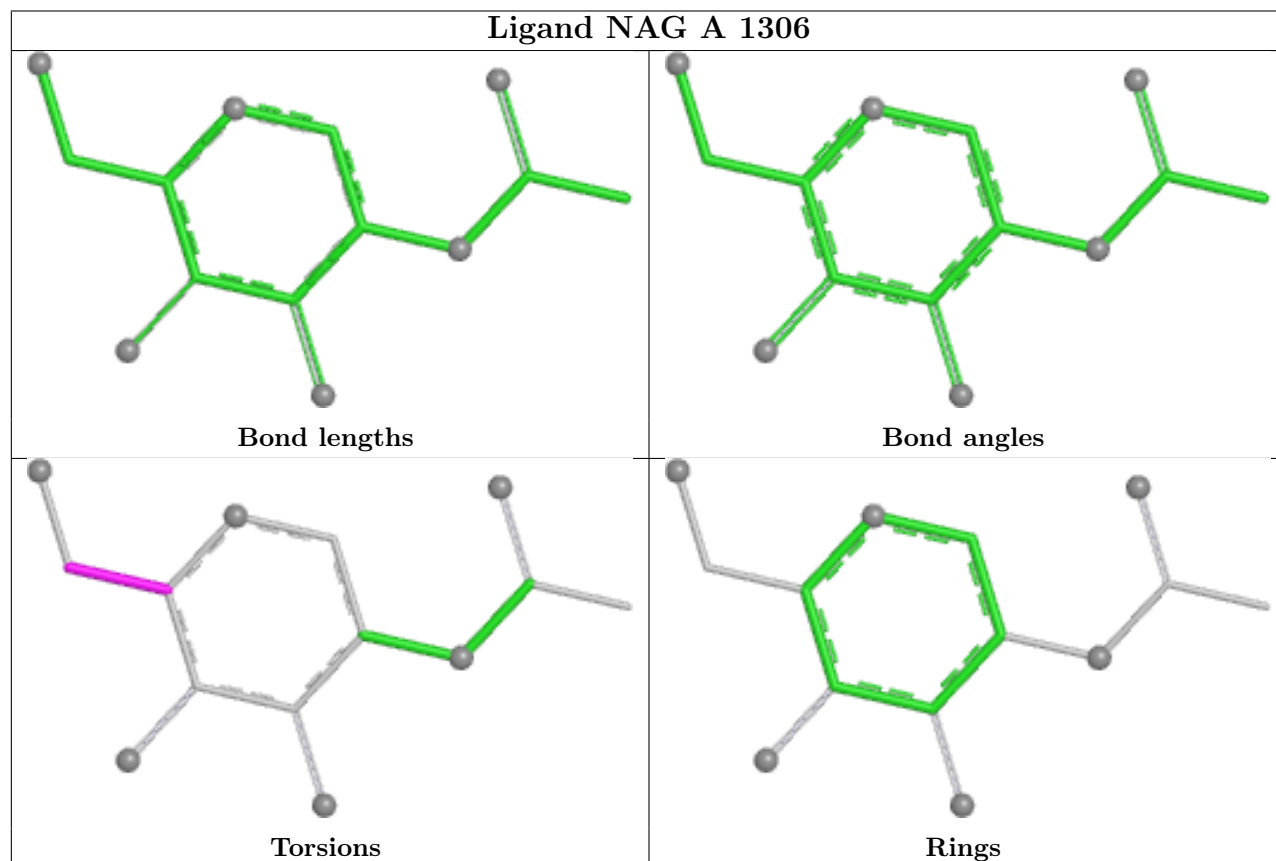
Ligand NAG A 1305



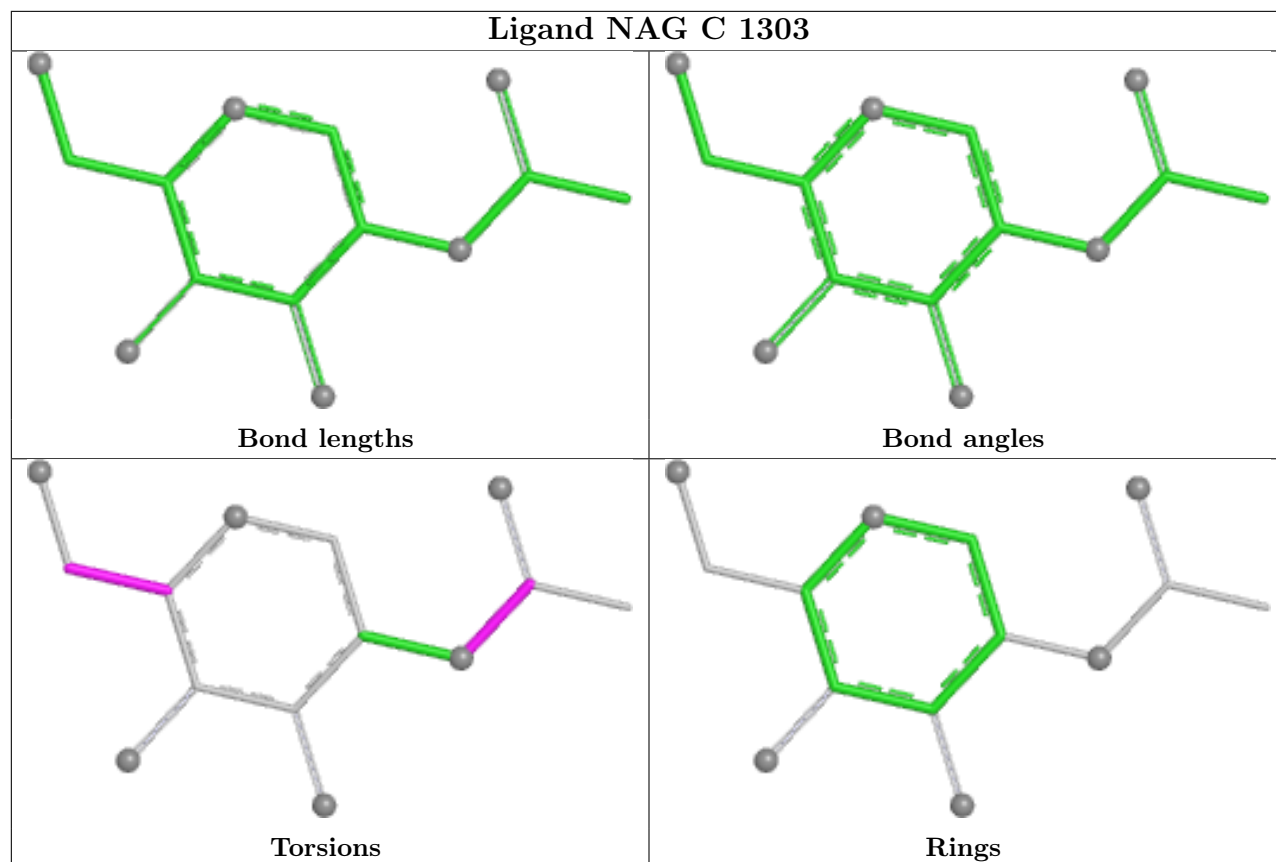
Ligand NAG A 1304



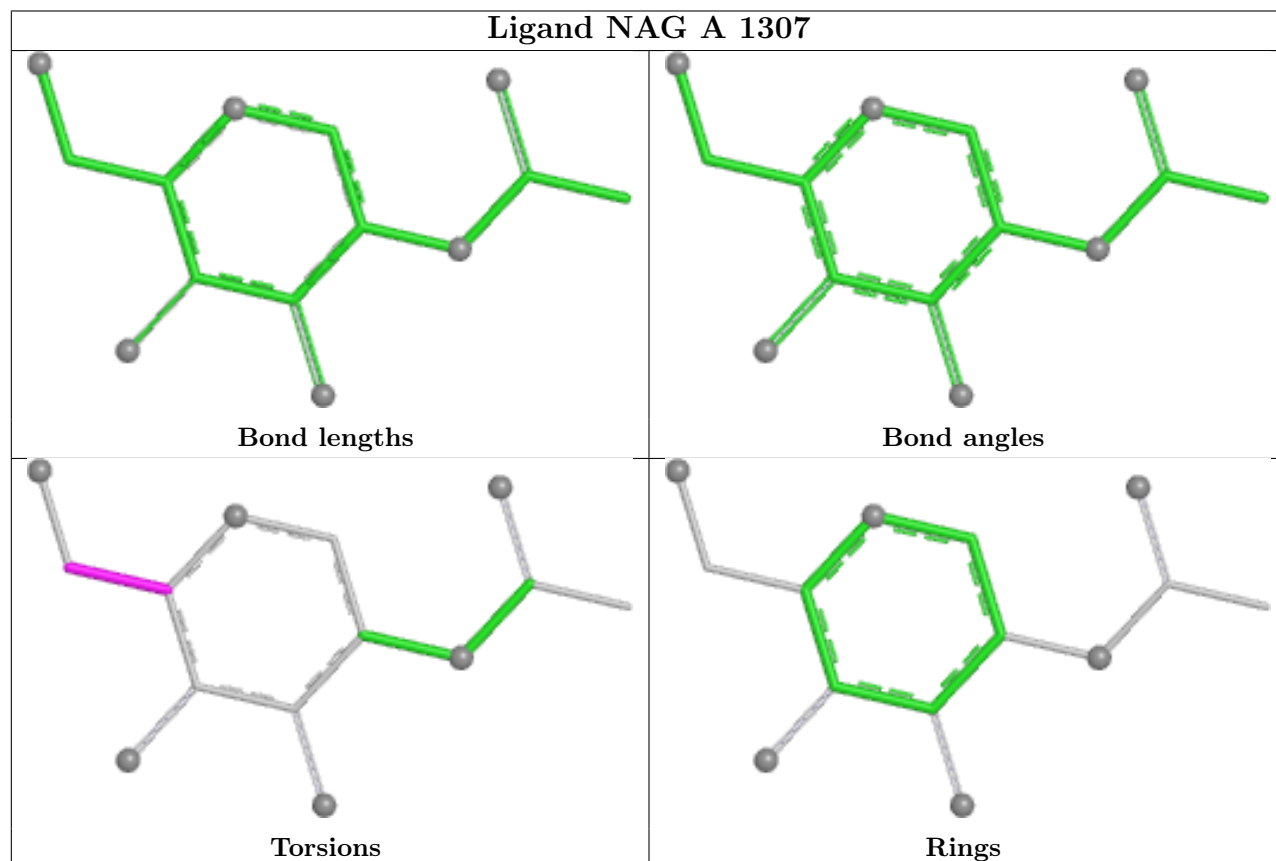
Ligand NAG A 1306



Ligand NAG C 1303



Ligand NAG A 1307



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

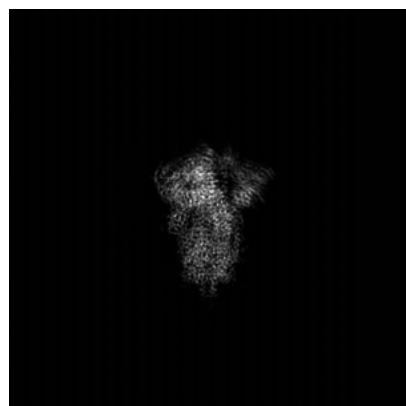
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38463. These allow visual inspection of the internal detail of the map and identification of artifacts.

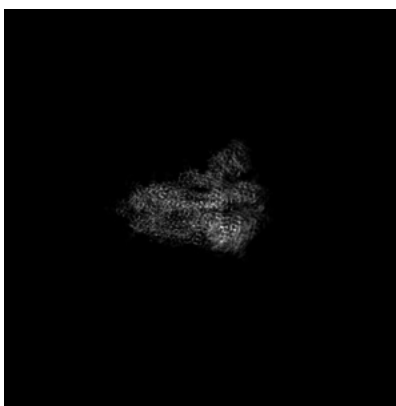
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

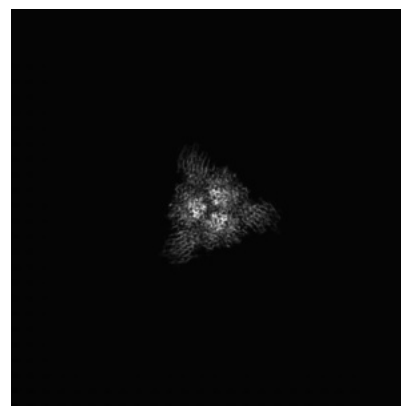
6.1.1 Primary map



X

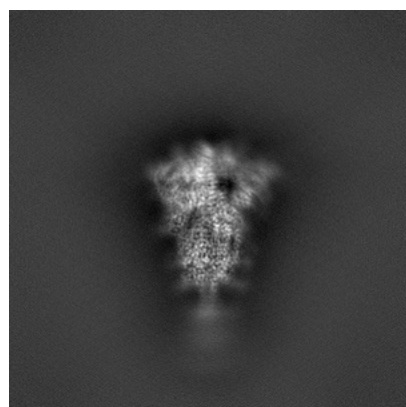


Y

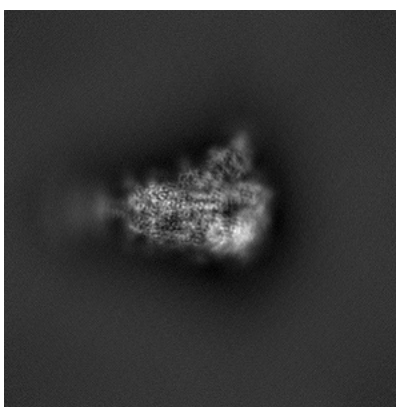


Z

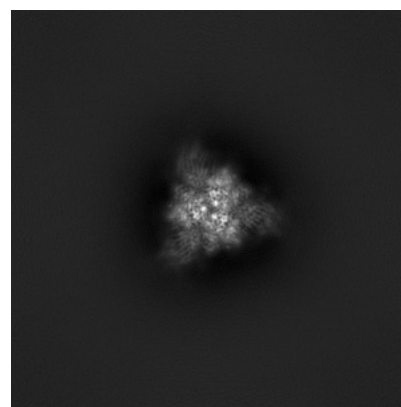
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

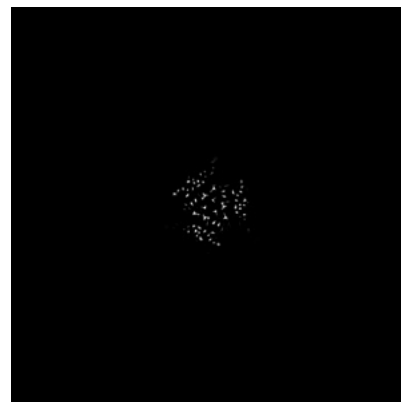
6.2.1 Primary map



X Index: 256



Y Index: 256

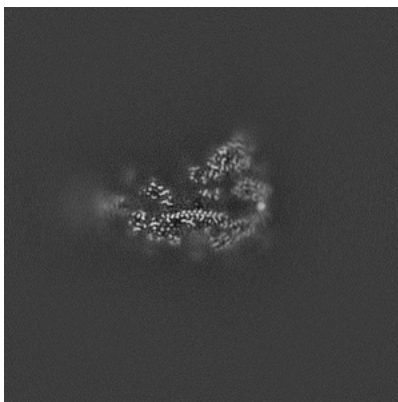


Z Index: 256

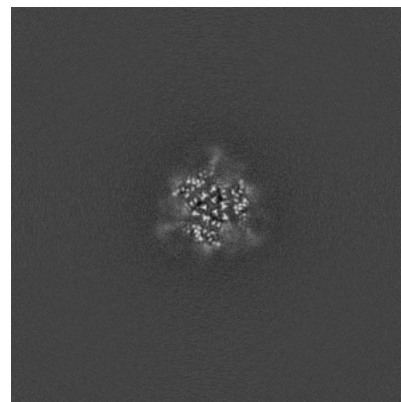
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 262



Y Index: 247

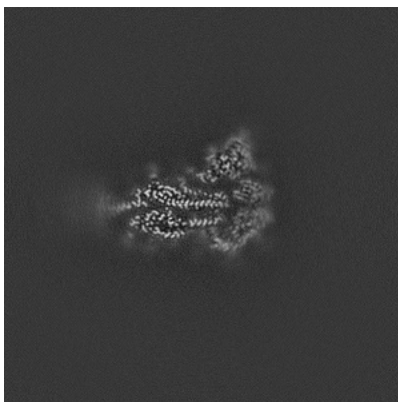


Z Index: 277

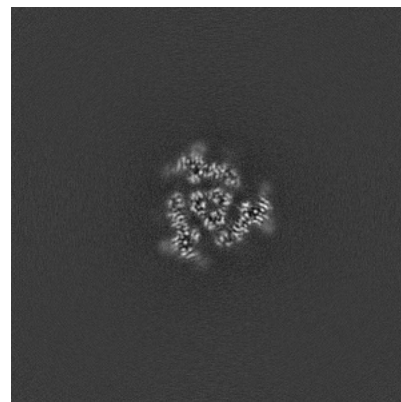
6.3.2 Raw map



X Index: 262



Y Index: 247

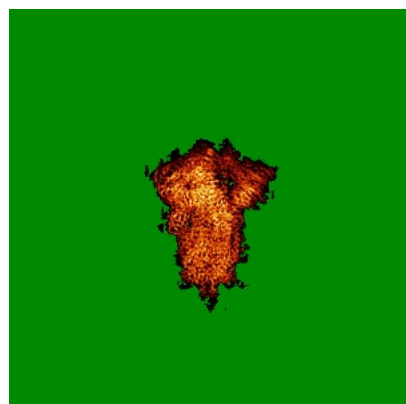


Z Index: 277

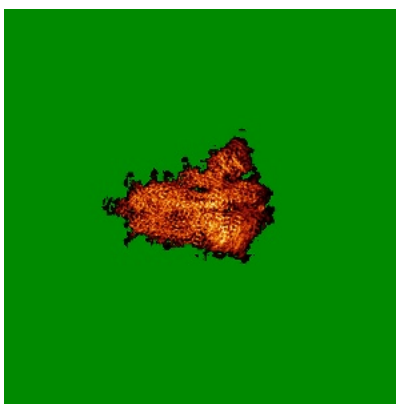
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

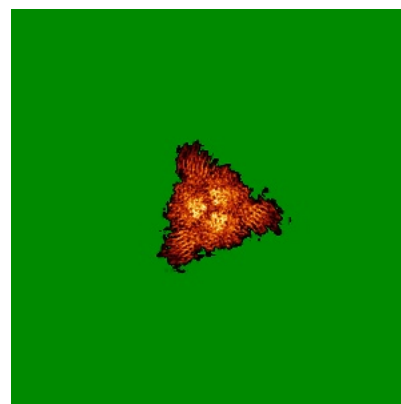
6.4.1 Primary map



X

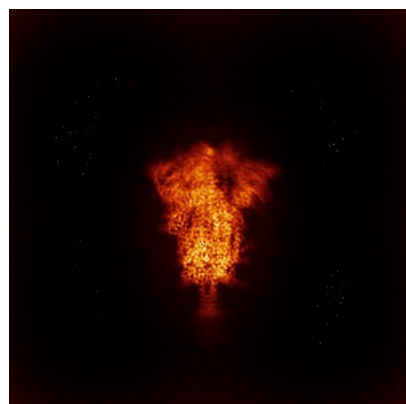


Y

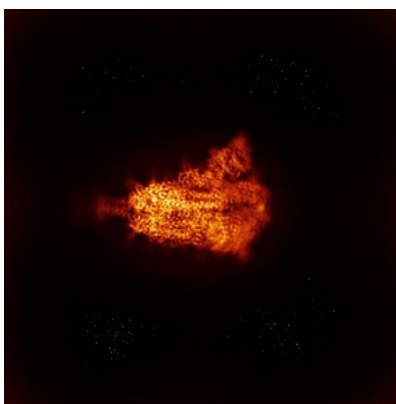


Z

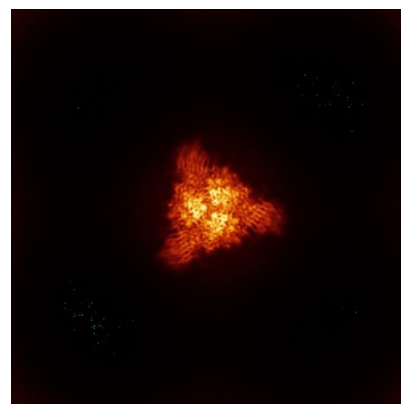
6.4.2 Raw map



X



Y

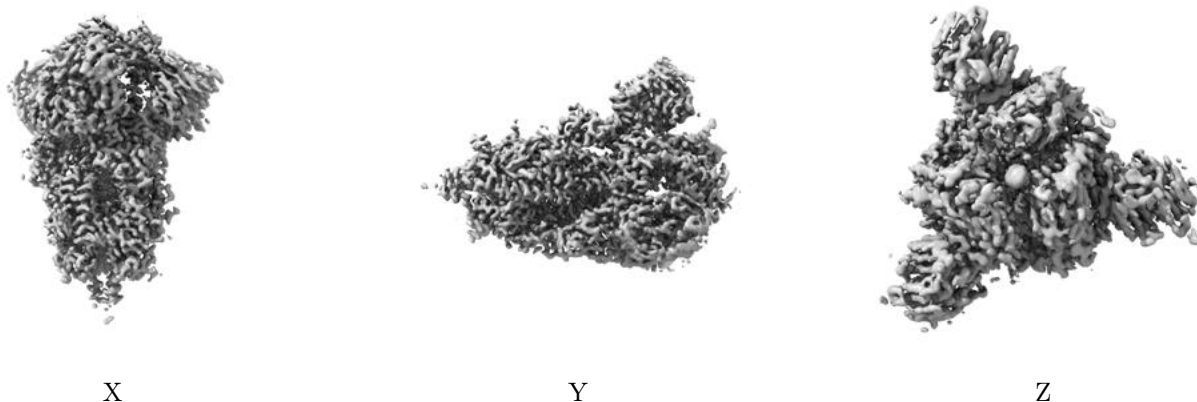


Z

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

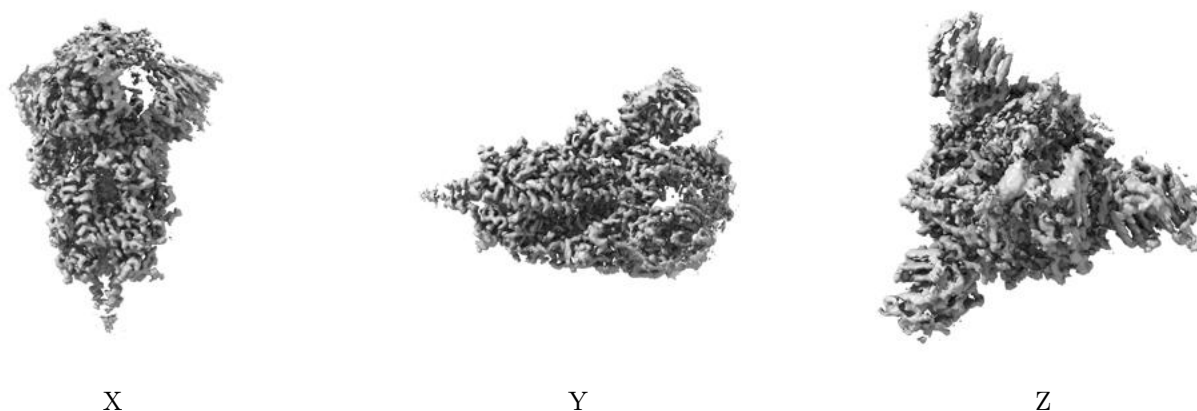
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

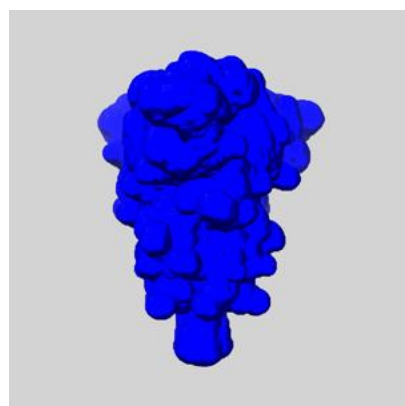
6.6 Mask visualisation [i](#)

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

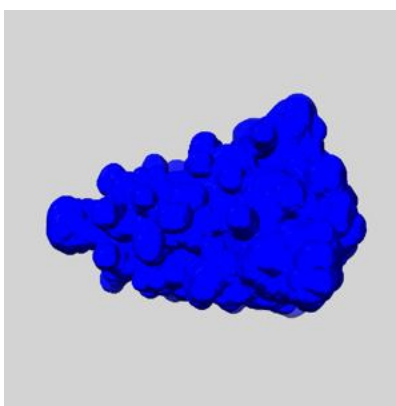
A mask typically either:

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

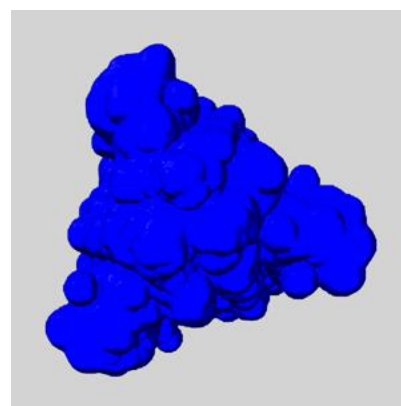
6.6.1 emd_38463_msk_1.map [i](#)



X



Y

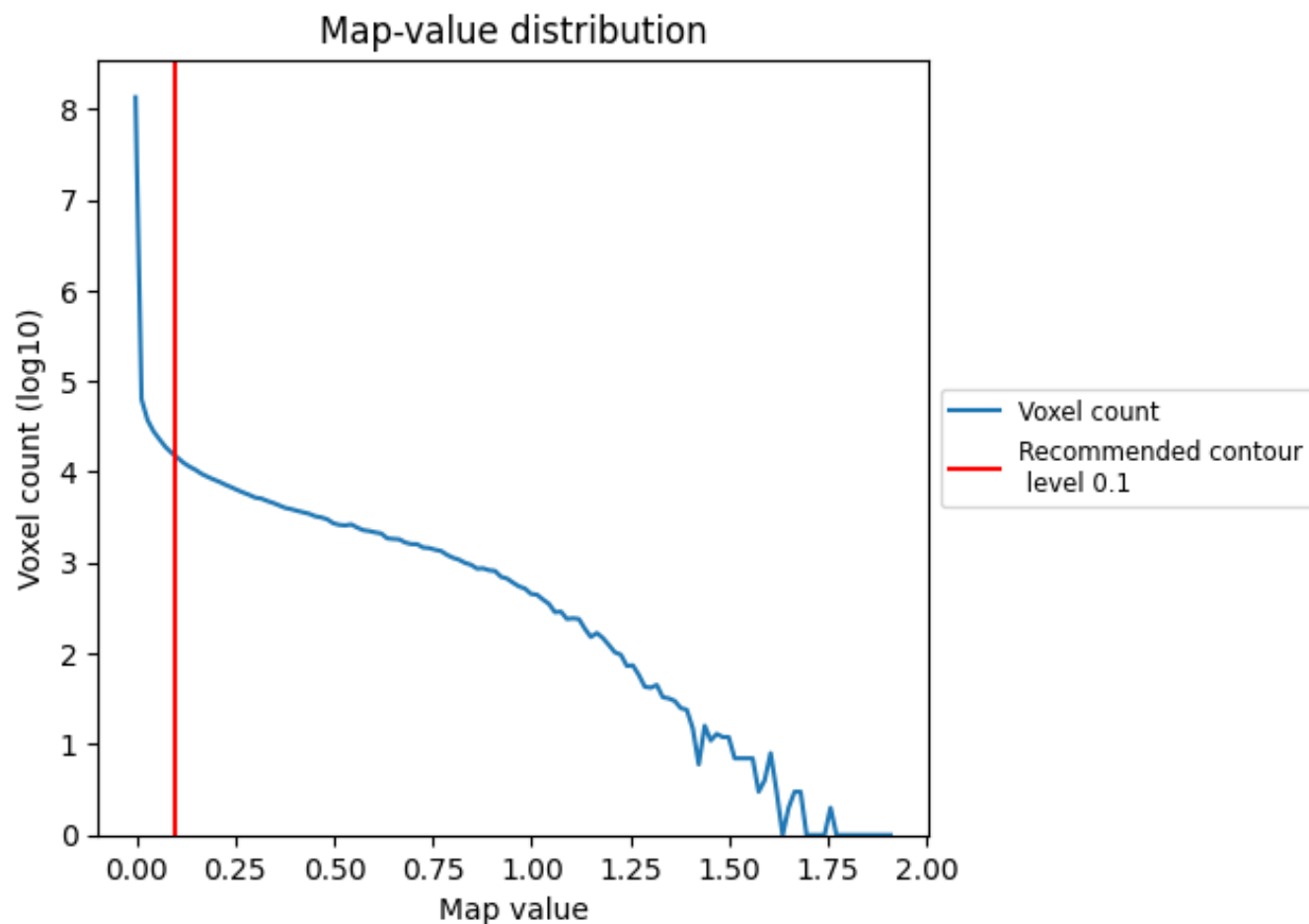


Z

7 Map analysis [i](#)

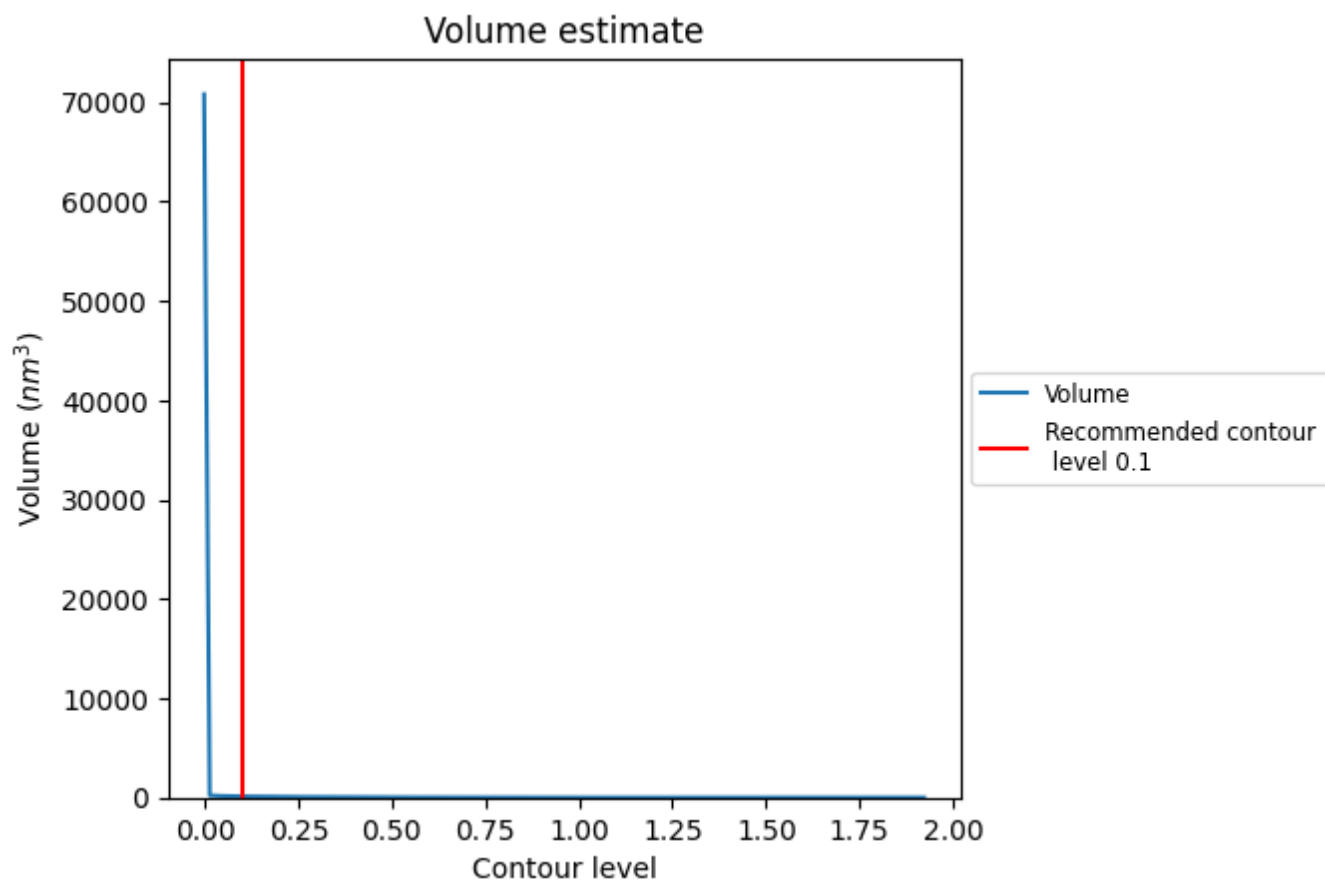
This section contains the results of statistical analysis of the map.

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.

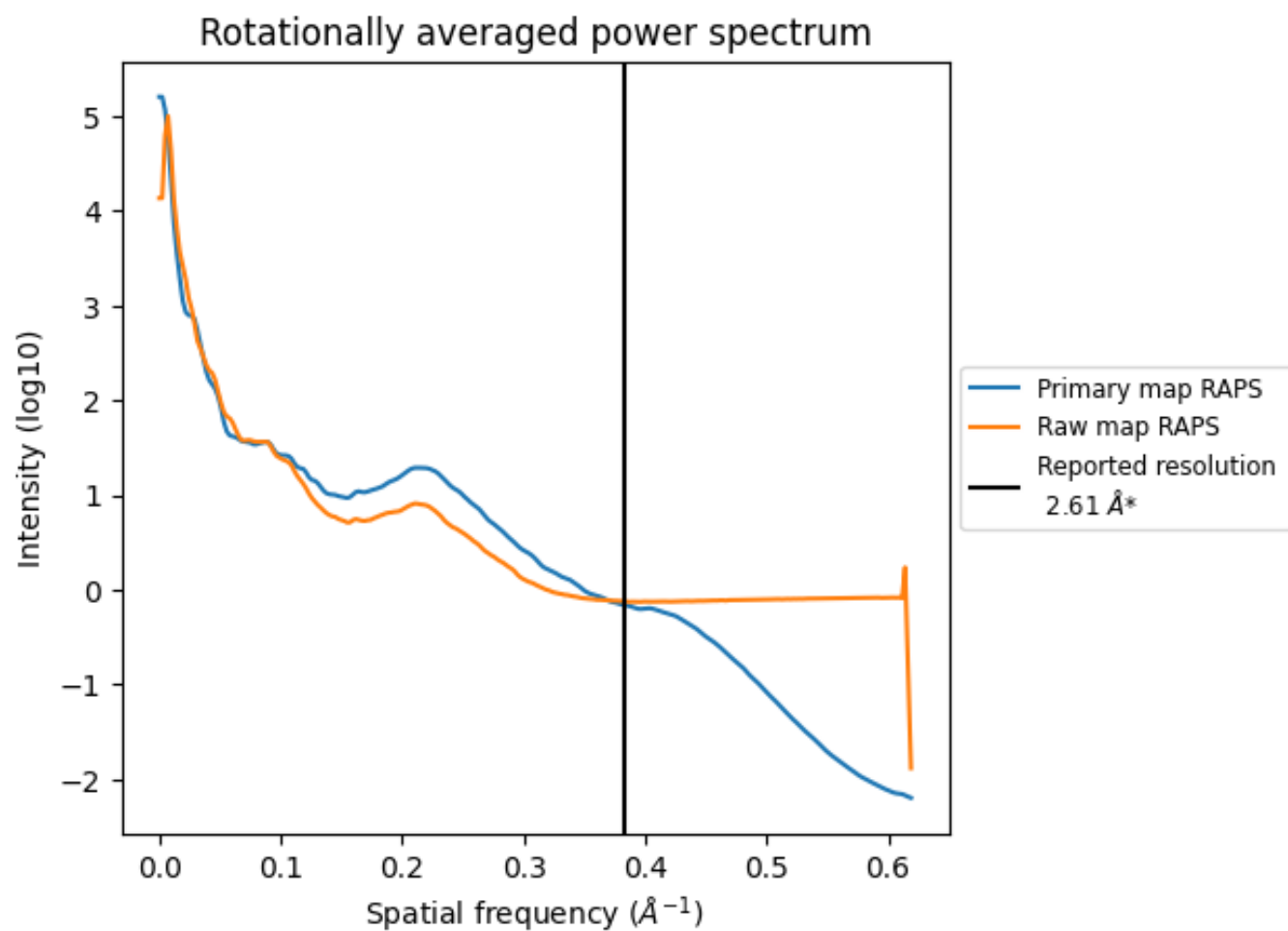
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 119 nm³; this corresponds to an approximate mass of 108 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](#)

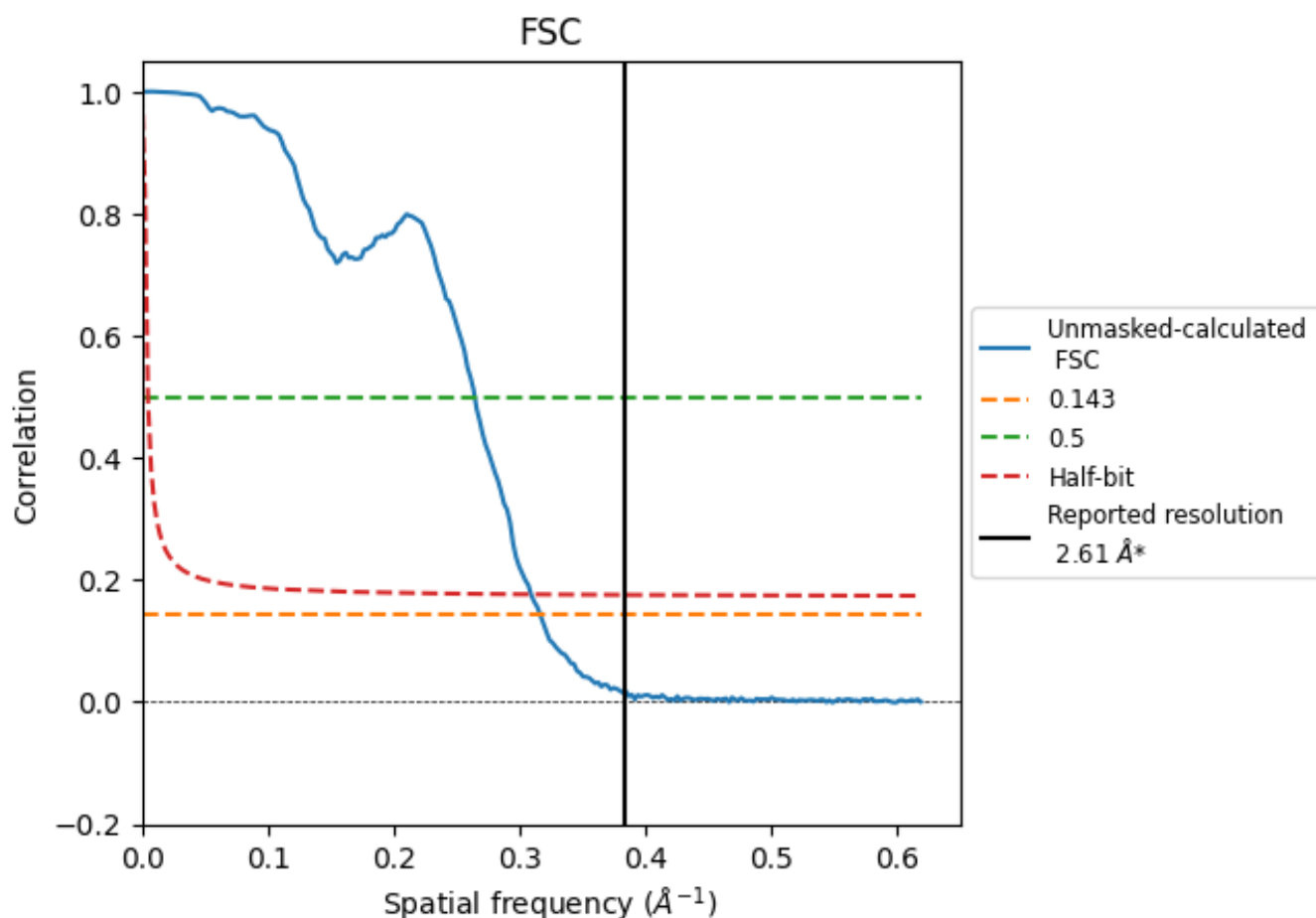


*Reported resolution corresponds to spatial frequency of 0.383 Å⁻¹

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 0.383 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

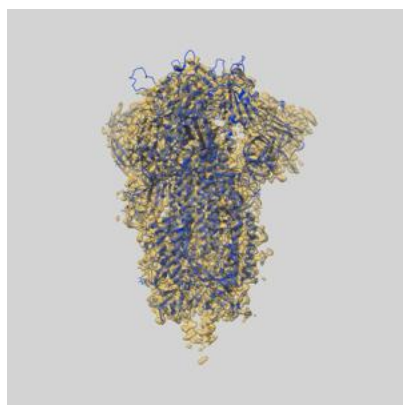
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.61	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	3.78	3.23

*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 3.16 differs from the reported value 2.61 by more than 10 %

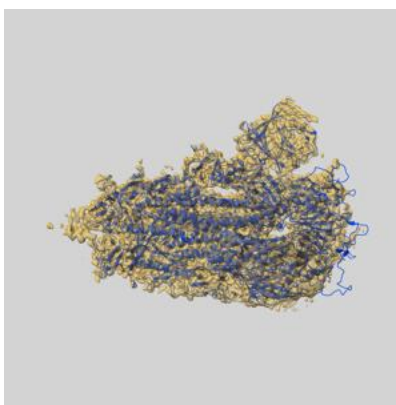
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38463 and PDB model 8XM5. Per-residue inclusion information can be found in section 3 on page 15.

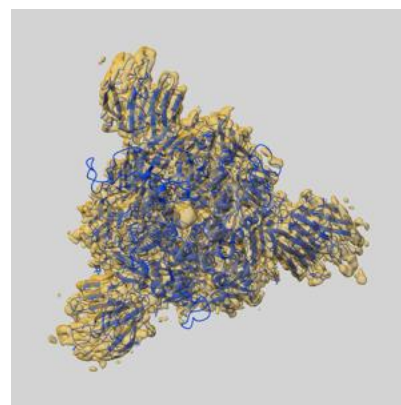
9.1 Map-model overlay [i](#)



X



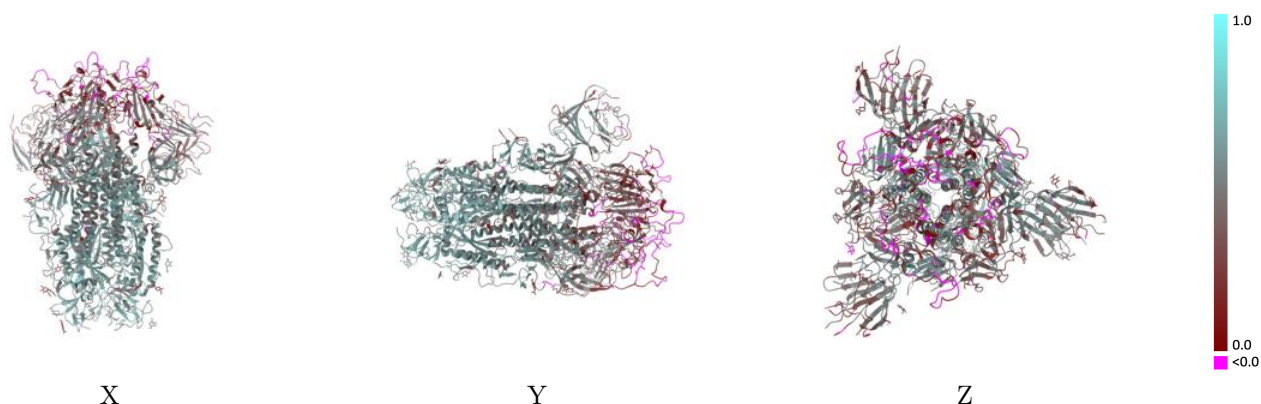
Y



Z

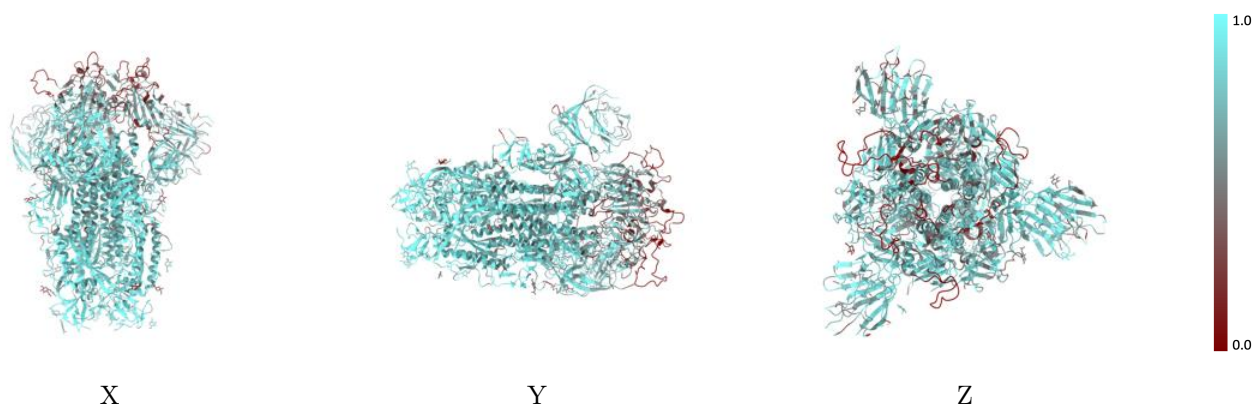
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



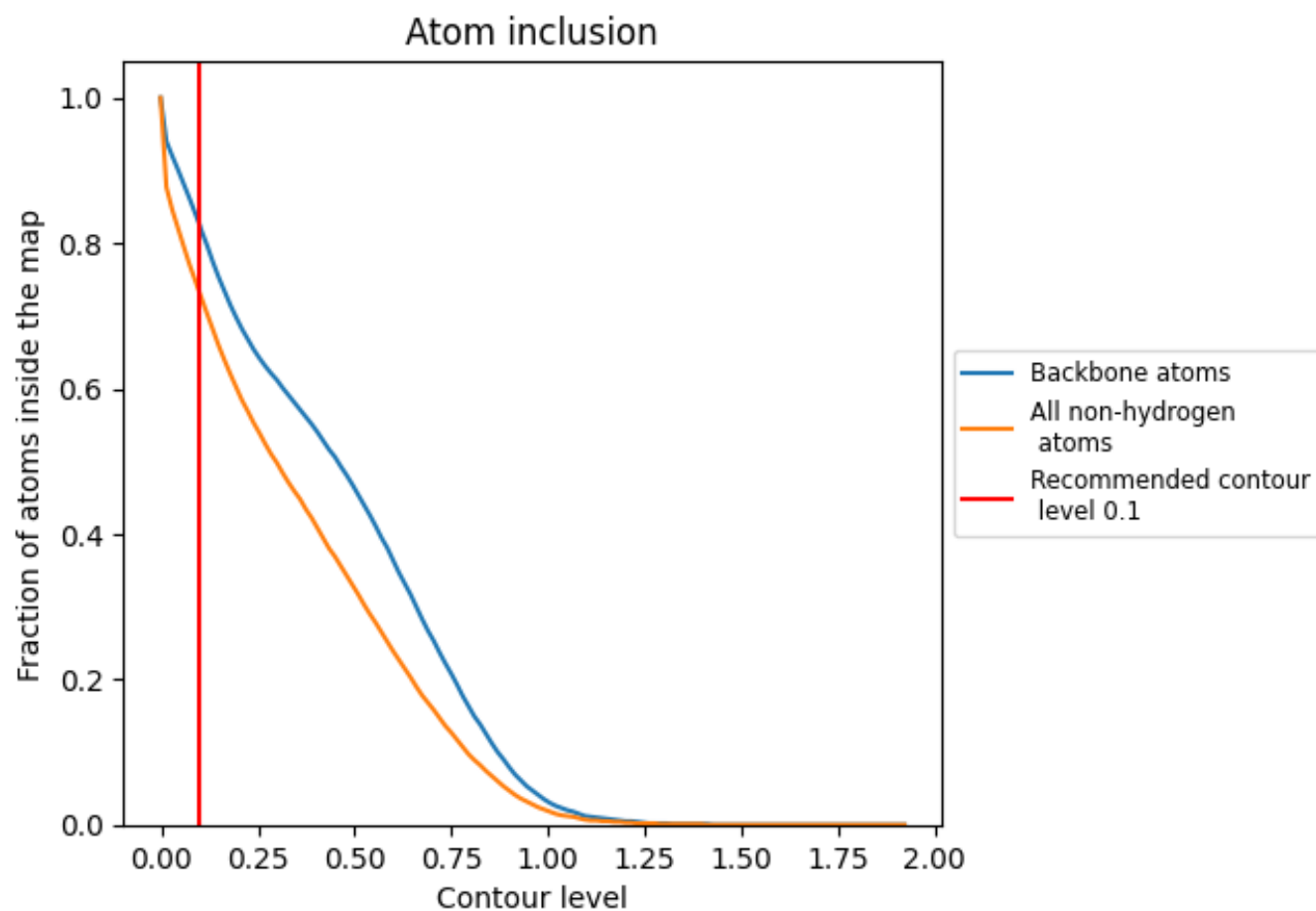
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 73% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7300	0.4460
A	0.7200	0.4450
B	0.7240	0.4420
C	0.7460	0.4500

