Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 09:29 AM UTC

PDB ID	:	7JVC / pdb_00007jvc
EMDB ID	:	EMD-22506
Title	:	SARS-CoV-2 spike in complex with the S2A4 neutralizing antibody Fab fragment
Authors	:	Park, Y.J.; Tortorici, M.A.; Walls, A.C.; Czudnochowski, N.; Seattle Structural Genomics Center for Infectious Disease (SSGCID); Snell, G.; Veesler, D.
Deposited on	:	2020-08-20
Resolution	:	3.30 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:

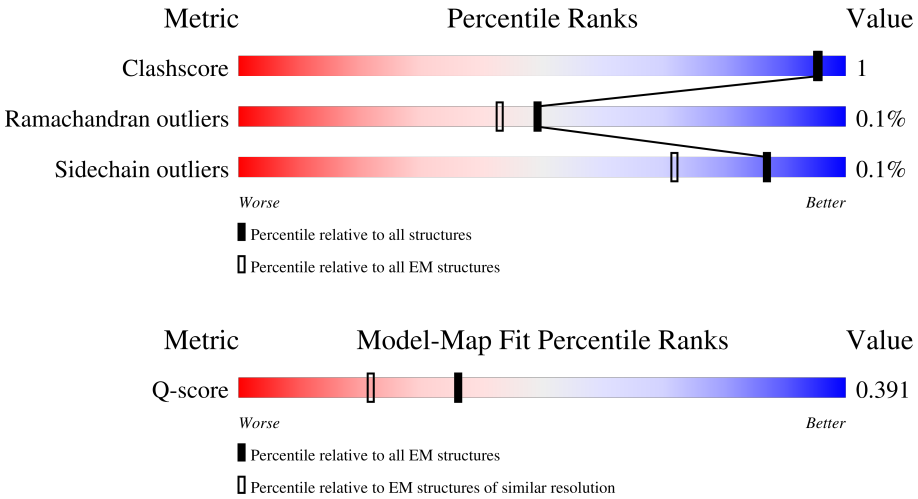
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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 3.30 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	15087 (2.80 - 3.80)

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 <=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	1281	7% 73% · 23%
1	B	1281	7% 73% · 23%
1	E	1281	7% 73% · 23%

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Mol	Chain	Length	Quality of chain
2	C	228	80% 93%
2	F	228	79% 93%
2	H	228	79% 93%
3	D	217	87% 92% 6%
3	G	217	88% 92% 6%
3	L	217	87% 92% 6%
4	I	2	100%
4	J	2	50% 100%
4	M	2	100%
4	N	2	50% 100%
4	O	2	100%
4	P	2	50% 100%
4	R	2	100%
4	S	2	50% 100%
4	T	2	100%
4	U	2	50% 100%
4	W	2	100%
4	X	2	50% 100%
5	K	3	100% 100%
5	Q	3	100% 100%
5	V	3	100% 100%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 29562 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	990	Total	C	N	O	S	0	0
			7354	4704	1242	1373	35		
1	B	990	Total	C	N	O	S	0	0
			7353	4704	1242	1372	35		
1	E	990	Total	C	N	O	S	0	0
			7353	4704	1242	1372	35		

There are 264 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	expression tag	UNP P0DTC2
A	-17	GLY	-	expression tag	UNP P0DTC2
A	-16	ILE	-	expression tag	UNP P0DTC2
A	-15	LEU	-	expression tag	UNP P0DTC2
A	-14	PRO	-	expression tag	UNP P0DTC2
A	-13	SER	-	expression tag	UNP P0DTC2
A	-12	PRO	-	expression tag	UNP P0DTC2
A	-11	GLY	-	expression tag	UNP P0DTC2
A	-10	MET	-	expression tag	UNP P0DTC2
A	-9	PRO	-	expression tag	UNP P0DTC2
A	-8	ALA	-	expression tag	UNP P0DTC2
A	-7	LEU	-	expression tag	UNP P0DTC2
A	-6	LEU	-	expression tag	UNP P0DTC2
A	-5	SER	-	expression tag	UNP P0DTC2
A	-4	LEU	-	expression tag	UNP P0DTC2
A	-3	VAL	-	expression tag	UNP P0DTC2
A	-2	SER	-	expression tag	UNP P0DTC2
A	-1	LEU	-	expression tag	UNP P0DTC2
A	0	LEU	-	expression tag	UNP P0DTC2
A	1	SER	-	expression tag	UNP P0DTC2
A	2	VAL	-	expression tag	UNP P0DTC2
A	3	LEU	-	expression tag	UNP P0DTC2
A	4	LEU	-	expression tag	UNP P0DTC2
A	5	MET	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	6	GLY	-	expression tag	UNP P0DTC2
A	7	CYS	-	expression tag	UNP P0DTC2
A	8	VAL	-	expression tag	UNP P0DTC2
A	9	ALA	-	expression tag	UNP P0DTC2
A	10	GLU	-	expression tag	UNP P0DTC2
A	11	THR	-	expression tag	UNP P0DTC2
A	12	GLY	-	expression tag	UNP P0DTC2
A	13	THR	-	expression tag	UNP P0DTC2
A	682	SER	ARG	engineered mutation	UNP P0DTC2
A	683	GLY	ARG	engineered mutation	UNP P0DTC2
A	685	GLY	ARG	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1212	GLY	-	expression tag	UNP P0DTC2
A	1213	SER	-	expression tag	UNP P0DTC2
A	1214	GLY	-	expression tag	UNP P0DTC2
A	1215	ARG	-	expression tag	UNP P0DTC2
A	1216	GLU	-	expression tag	UNP P0DTC2
A	1217	ASN	-	expression tag	UNP P0DTC2
A	1218	LEU	-	expression tag	UNP P0DTC2
A	1219	TYR	-	expression tag	UNP P0DTC2
A	1220	PHE	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	GLY	-	expression tag	UNP P0DTC2
A	1223	GLY	-	expression tag	UNP P0DTC2
A	1224	GLY	-	expression tag	UNP P0DTC2
A	1225	GLY	-	expression tag	UNP P0DTC2
A	1226	SER	-	expression tag	UNP P0DTC2
A	1227	GLY	-	expression tag	UNP P0DTC2
A	1228	TYR	-	expression tag	UNP P0DTC2
A	1229	ILE	-	expression tag	UNP P0DTC2
A	1230	PRO	-	expression tag	UNP P0DTC2
A	1231	GLU	-	expression tag	UNP P0DTC2
A	1232	ALA	-	expression tag	UNP P0DTC2
A	1233	PRO	-	expression tag	UNP P0DTC2
A	1234	ARG	-	expression tag	UNP P0DTC2
A	1235	ASP	-	expression tag	UNP P0DTC2
A	1236	GLY	-	expression tag	UNP P0DTC2
A	1237	GLN	-	expression tag	UNP P0DTC2
A	1238	ALA	-	expression tag	UNP P0DTC2
A	1239	TYR	-	expression tag	UNP P0DTC2
A	1240	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1241	ARG	-	expression tag	UNP P0DTC2
A	1242	LYS	-	expression tag	UNP P0DTC2
A	1243	ASP	-	expression tag	UNP P0DTC2
A	1244	GLY	-	expression tag	UNP P0DTC2
A	1245	GLU	-	expression tag	UNP P0DTC2
A	1246	TRP	-	expression tag	UNP P0DTC2
A	1247	VAL	-	expression tag	UNP P0DTC2
A	1248	LEU	-	expression tag	UNP P0DTC2
A	1249	LEU	-	expression tag	UNP P0DTC2
A	1250	SER	-	expression tag	UNP P0DTC2
A	1251	THR	-	expression tag	UNP P0DTC2
A	1252	PHE	-	expression tag	UNP P0DTC2
A	1253	LEU	-	expression tag	UNP P0DTC2
A	1254	GLY	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	HIS	-	expression tag	UNP P0DTC2
A	1257	HIS	-	expression tag	UNP P0DTC2
A	1258	HIS	-	expression tag	UNP P0DTC2
A	1259	HIS	-	expression tag	UNP P0DTC2
A	1260	HIS	-	expression tag	UNP P0DTC2
A	1261	HIS	-	expression tag	UNP P0DTC2
A	1262	HIS	-	expression tag	UNP P0DTC2
B	-18	MET	-	expression tag	UNP P0DTC2
B	-17	GLY	-	expression tag	UNP P0DTC2
B	-16	ILE	-	expression tag	UNP P0DTC2
B	-15	LEU	-	expression tag	UNP P0DTC2
B	-14	PRO	-	expression tag	UNP P0DTC2
B	-13	SER	-	expression tag	UNP P0DTC2
B	-12	PRO	-	expression tag	UNP P0DTC2
B	-11	GLY	-	expression tag	UNP P0DTC2
B	-10	MET	-	expression tag	UNP P0DTC2
B	-9	PRO	-	expression tag	UNP P0DTC2
B	-8	ALA	-	expression tag	UNP P0DTC2
B	-7	LEU	-	expression tag	UNP P0DTC2
B	-6	LEU	-	expression tag	UNP P0DTC2
B	-5	SER	-	expression tag	UNP P0DTC2
B	-4	LEU	-	expression tag	UNP P0DTC2
B	-3	VAL	-	expression tag	UNP P0DTC2
B	-2	SER	-	expression tag	UNP P0DTC2
B	-1	LEU	-	expression tag	UNP P0DTC2
B	0	LEU	-	expression tag	UNP P0DTC2
B	1	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2	VAL	-	expression tag	UNP P0DTC2
B	3	LEU	-	expression tag	UNP P0DTC2
B	4	LEU	-	expression tag	UNP P0DTC2
B	5	MET	-	expression tag	UNP P0DTC2
B	6	GLY	-	expression tag	UNP P0DTC2
B	7	CYS	-	expression tag	UNP P0DTC2
B	8	VAL	-	expression tag	UNP P0DTC2
B	9	ALA	-	expression tag	UNP P0DTC2
B	10	GLU	-	expression tag	UNP P0DTC2
B	11	THR	-	expression tag	UNP P0DTC2
B	12	GLY	-	expression tag	UNP P0DTC2
B	13	THR	-	expression tag	UNP P0DTC2
B	682	SER	ARG	engineered mutation	UNP P0DTC2
B	683	GLY	ARG	engineered mutation	UNP P0DTC2
B	685	GLY	ARG	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1212	GLY	-	expression tag	UNP P0DTC2
B	1213	SER	-	expression tag	UNP P0DTC2
B	1214	GLY	-	expression tag	UNP P0DTC2
B	1215	ARG	-	expression tag	UNP P0DTC2
B	1216	GLU	-	expression tag	UNP P0DTC2
B	1217	ASN	-	expression tag	UNP P0DTC2
B	1218	LEU	-	expression tag	UNP P0DTC2
B	1219	TYR	-	expression tag	UNP P0DTC2
B	1220	PHE	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	GLY	-	expression tag	UNP P0DTC2
B	1223	GLY	-	expression tag	UNP P0DTC2
B	1224	GLY	-	expression tag	UNP P0DTC2
B	1225	GLY	-	expression tag	UNP P0DTC2
B	1226	SER	-	expression tag	UNP P0DTC2
B	1227	GLY	-	expression tag	UNP P0DTC2
B	1228	TYR	-	expression tag	UNP P0DTC2
B	1229	ILE	-	expression tag	UNP P0DTC2
B	1230	PRO	-	expression tag	UNP P0DTC2
B	1231	GLU	-	expression tag	UNP P0DTC2
B	1232	ALA	-	expression tag	UNP P0DTC2
B	1233	PRO	-	expression tag	UNP P0DTC2
B	1234	ARG	-	expression tag	UNP P0DTC2
B	1235	ASP	-	expression tag	UNP P0DTC2
B	1236	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1237	GLN	-	expression tag	UNP P0DTC2
B	1238	ALA	-	expression tag	UNP P0DTC2
B	1239	TYR	-	expression tag	UNP P0DTC2
B	1240	VAL	-	expression tag	UNP P0DTC2
B	1241	ARG	-	expression tag	UNP P0DTC2
B	1242	LYS	-	expression tag	UNP P0DTC2
B	1243	ASP	-	expression tag	UNP P0DTC2
B	1244	GLY	-	expression tag	UNP P0DTC2
B	1245	GLU	-	expression tag	UNP P0DTC2
B	1246	TRP	-	expression tag	UNP P0DTC2
B	1247	VAL	-	expression tag	UNP P0DTC2
B	1248	LEU	-	expression tag	UNP P0DTC2
B	1249	LEU	-	expression tag	UNP P0DTC2
B	1250	SER	-	expression tag	UNP P0DTC2
B	1251	THR	-	expression tag	UNP P0DTC2
B	1252	PHE	-	expression tag	UNP P0DTC2
B	1253	LEU	-	expression tag	UNP P0DTC2
B	1254	GLY	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
B	1259	HIS	-	expression tag	UNP P0DTC2
B	1260	HIS	-	expression tag	UNP P0DTC2
B	1261	HIS	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
E	-18	MET	-	expression tag	UNP P0DTC2
E	-17	GLY	-	expression tag	UNP P0DTC2
E	-16	ILE	-	expression tag	UNP P0DTC2
E	-15	LEU	-	expression tag	UNP P0DTC2
E	-14	PRO	-	expression tag	UNP P0DTC2
E	-13	SER	-	expression tag	UNP P0DTC2
E	-12	PRO	-	expression tag	UNP P0DTC2
E	-11	GLY	-	expression tag	UNP P0DTC2
E	-10	MET	-	expression tag	UNP P0DTC2
E	-9	PRO	-	expression tag	UNP P0DTC2
E	-8	ALA	-	expression tag	UNP P0DTC2
E	-7	LEU	-	expression tag	UNP P0DTC2
E	-6	LEU	-	expression tag	UNP P0DTC2
E	-5	SER	-	expression tag	UNP P0DTC2
E	-4	LEU	-	expression tag	UNP P0DTC2
E	-3	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	SER	-	expression tag	UNP P0DTC2
E	-1	LEU	-	expression tag	UNP P0DTC2
E	0	LEU	-	expression tag	UNP P0DTC2
E	1	SER	-	expression tag	UNP P0DTC2
E	2	VAL	-	expression tag	UNP P0DTC2
E	3	LEU	-	expression tag	UNP P0DTC2
E	4	LEU	-	expression tag	UNP P0DTC2
E	5	MET	-	expression tag	UNP P0DTC2
E	6	GLY	-	expression tag	UNP P0DTC2
E	7	CYS	-	expression tag	UNP P0DTC2
E	8	VAL	-	expression tag	UNP P0DTC2
E	9	ALA	-	expression tag	UNP P0DTC2
E	10	GLU	-	expression tag	UNP P0DTC2
E	11	THR	-	expression tag	UNP P0DTC2
E	12	GLY	-	expression tag	UNP P0DTC2
E	13	THR	-	expression tag	UNP P0DTC2
E	682	SER	ARG	engineered mutation	UNP P0DTC2
E	683	GLY	ARG	engineered mutation	UNP P0DTC2
E	685	GLY	ARG	engineered mutation	UNP P0DTC2
E	986	PRO	LYS	engineered mutation	UNP P0DTC2
E	987	PRO	VAL	engineered mutation	UNP P0DTC2
E	1212	GLY	-	expression tag	UNP P0DTC2
E	1213	SER	-	expression tag	UNP P0DTC2
E	1214	GLY	-	expression tag	UNP P0DTC2
E	1215	ARG	-	expression tag	UNP P0DTC2
E	1216	GLU	-	expression tag	UNP P0DTC2
E	1217	ASN	-	expression tag	UNP P0DTC2
E	1218	LEU	-	expression tag	UNP P0DTC2
E	1219	TYR	-	expression tag	UNP P0DTC2
E	1220	PHE	-	expression tag	UNP P0DTC2
E	1221	GLN	-	expression tag	UNP P0DTC2
E	1222	GLY	-	expression tag	UNP P0DTC2
E	1223	GLY	-	expression tag	UNP P0DTC2
E	1224	GLY	-	expression tag	UNP P0DTC2
E	1225	GLY	-	expression tag	UNP P0DTC2
E	1226	SER	-	expression tag	UNP P0DTC2
E	1227	GLY	-	expression tag	UNP P0DTC2
E	1228	TYR	-	expression tag	UNP P0DTC2
E	1229	ILE	-	expression tag	UNP P0DTC2
E	1230	PRO	-	expression tag	UNP P0DTC2
E	1231	GLU	-	expression tag	UNP P0DTC2
E	1232	ALA	-	expression tag	UNP P0DTC2

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

- Molecule 2 is a protein called S2A4 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	220	Total	C	N	O	S	0	0
			1105	661	220	220	4		
2	C	220	Total	C	N	O	S	0	0
			1105	661	220	220	4		
2	F	220	Total	C	N	O	S	0	0
			1105	661	220	220	4		

- Molecule 3 is a protein called S2A4 Fab light chain.

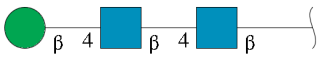
Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	214	Total	C	N	O	S	0	0
			1094	660	215	215	4		
3	D	214	Total	C	N	O	S	0	0
			1088	656	214	214	4		
3	G	214	Total	C	N	O	S	0	0
			1090	658	214	214	4		

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



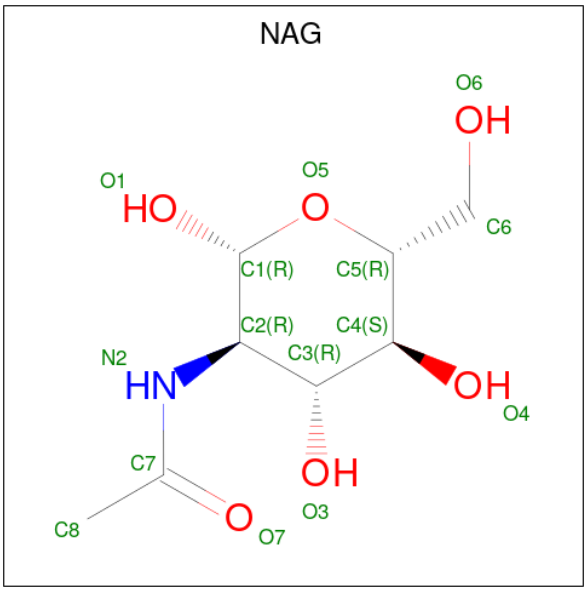
Mol	Chain	Residues	Atoms				AltConf	Trace
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	J	2	Total	C	N	O	0	0
			28	16	2	10		
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	S	2	Total	C	N	O	0	0
			28	16	2	10		
4	T	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		
4	W	2	Total	C	N	O	0	0
			28	16	2	10		
4	X	2	Total	C	N	O	0	0
			28	16	2	10		

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



Mol	Chain	Residues	Atoms	AltConf	Trace
5	K	3	Total C N O 39 22 2 15	0	0
5	Q	3	Total C N O 39 22 2 15	0	0
5	V	3	Total C N O 39 22 2 15	0	0

- Molecule 6 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
6	A	1	Total C N O 14 8 1 5	0
6	A	1	Total C N O 14 8 1 5	0
6	A	1	Total C N O 14 8 1 5	0
6	A	1	Total C N O 14 8 1 5	0
6	A	1	Total C N O 14 8 1 5	0
6	A	1	Total C N O 14 8 1 5	0

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

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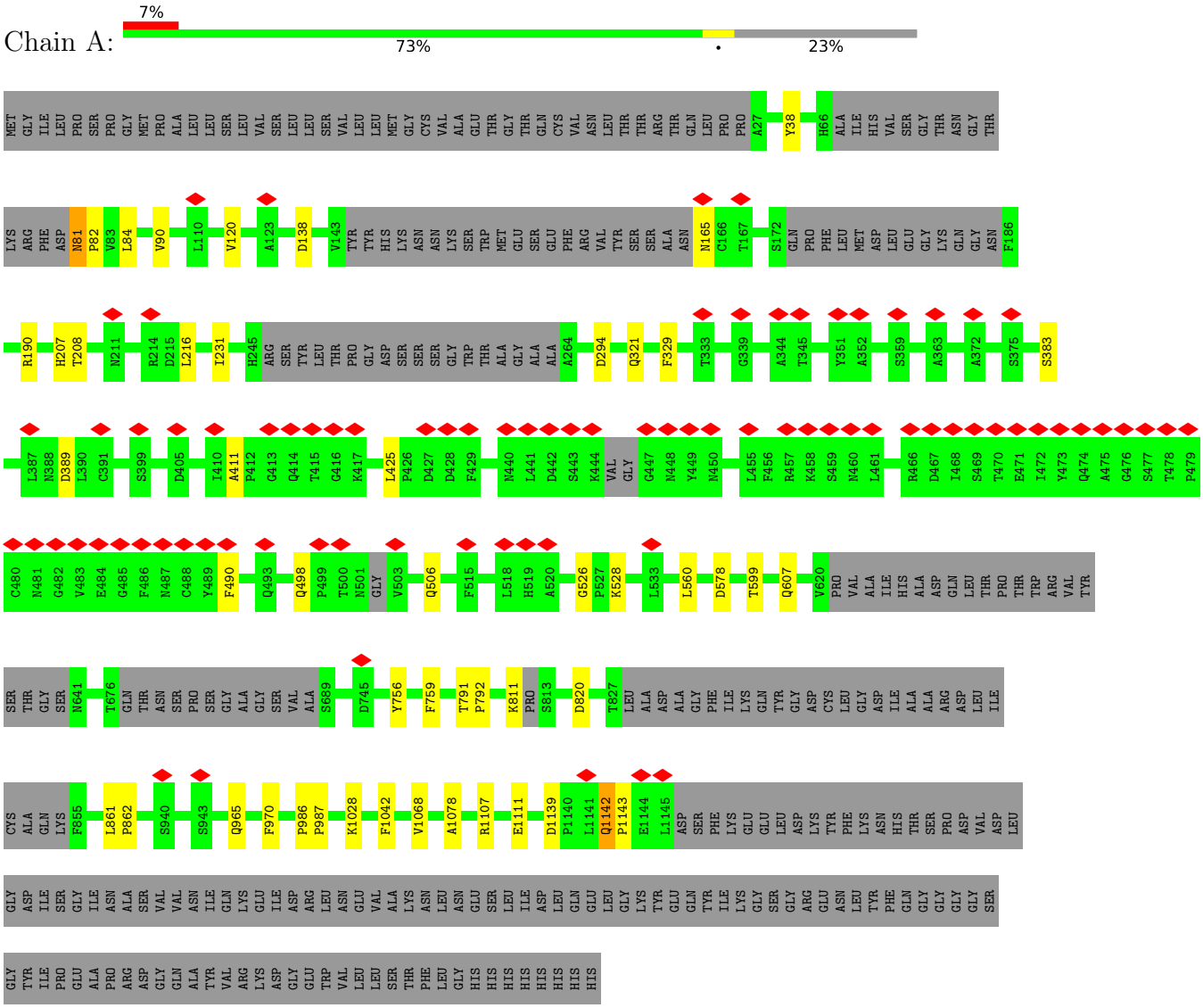
Mol	Chain	Residues	Atoms				AltConf
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	

3 Residue-property plots (i)

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

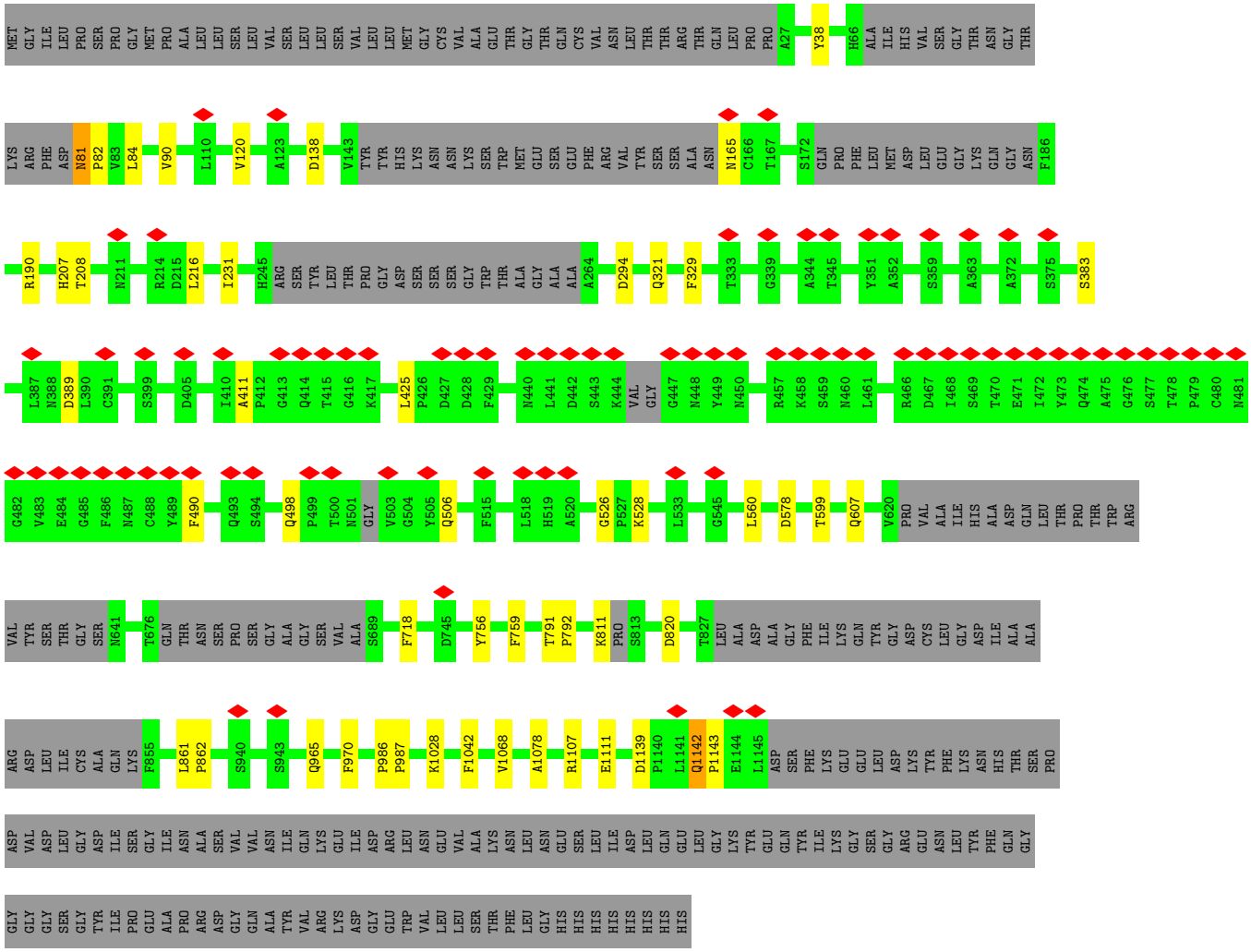
Chain A:



• Molecule 1: Spike glycoprotein

Chain B:

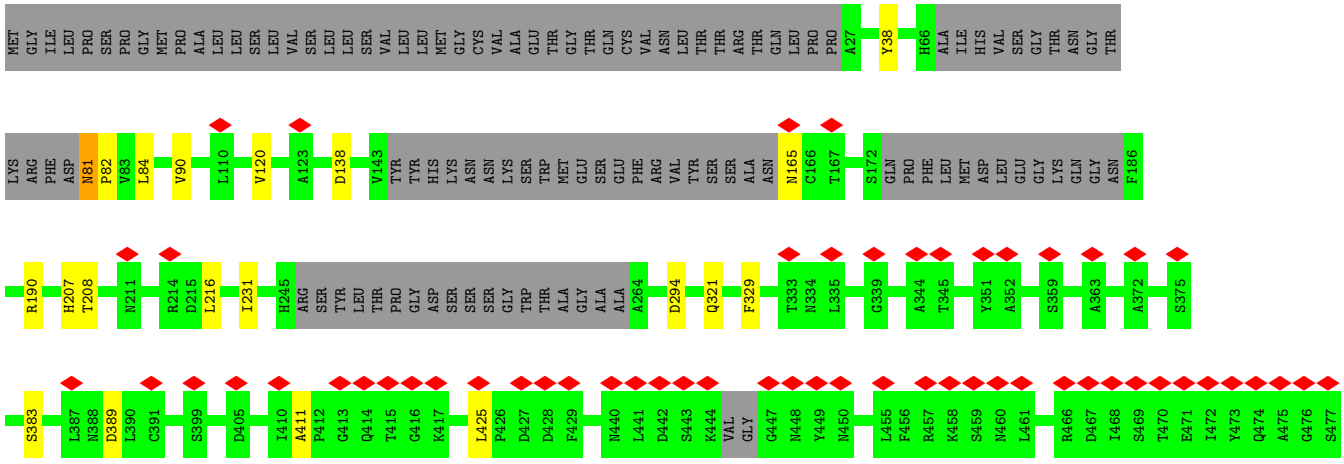


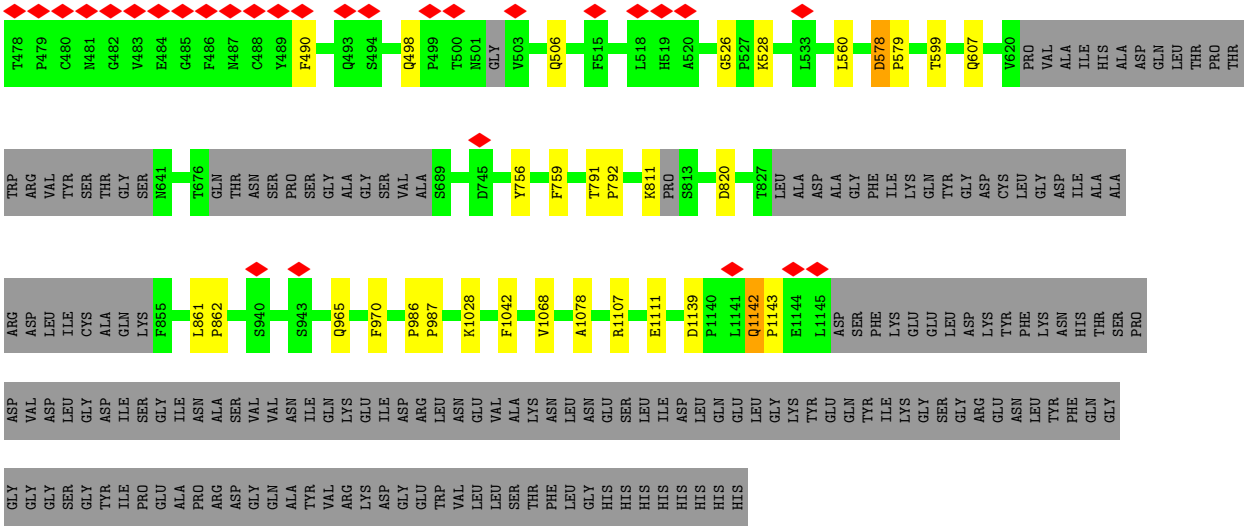


• Molecule 1: Spike glycoprotein

Chain E:

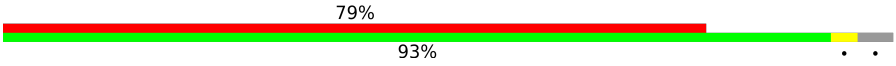


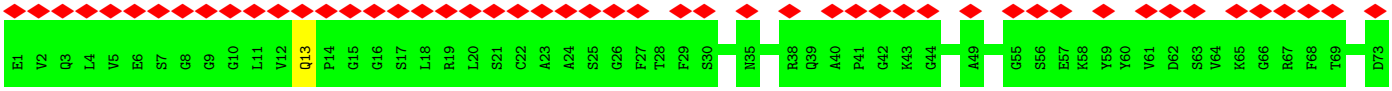


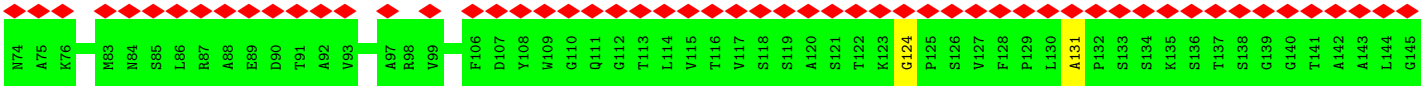


• Molecule 2: S2A4 Fab heavy chain

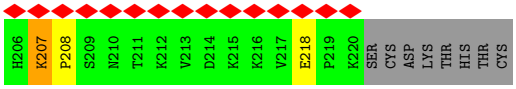
Chain H:





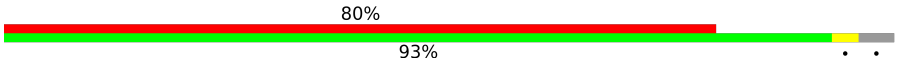


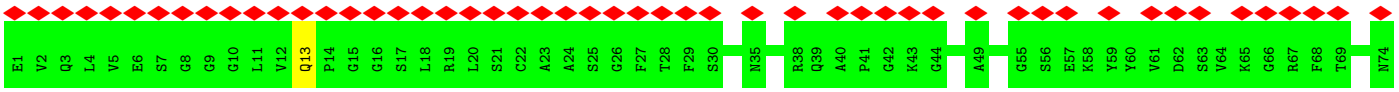




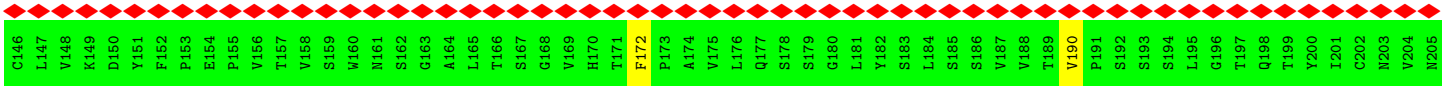
• Molecule 2: S2A4 Fab heavy chain

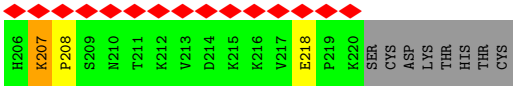
Chain C:



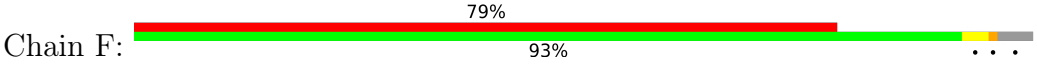


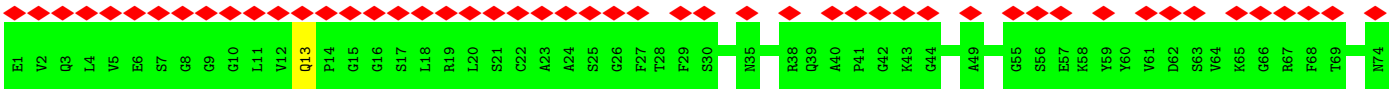




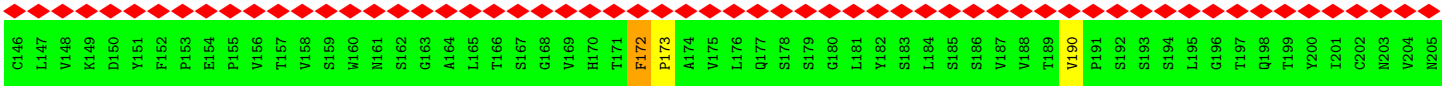


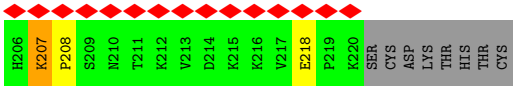
• Molecule 2: S2A4 Fab heavy chain



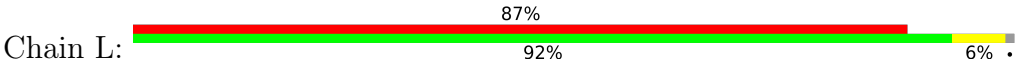


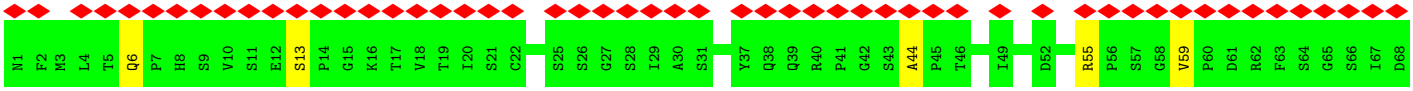


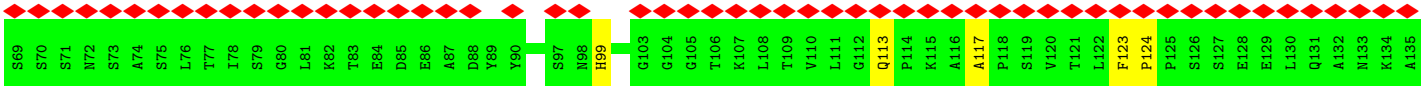


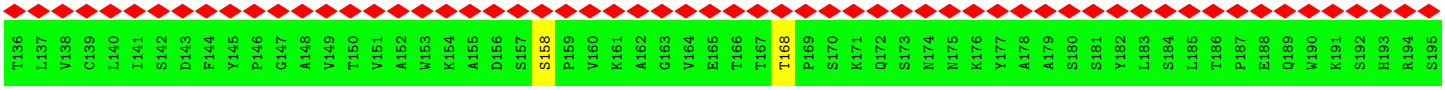


• Molecule 3: S2A4 Fab light chain



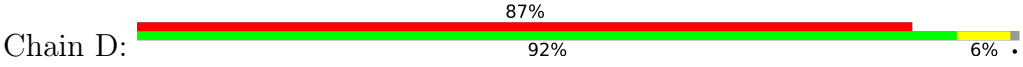


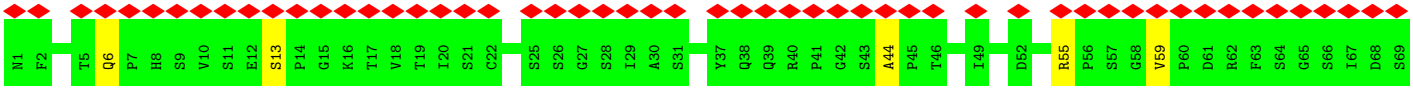


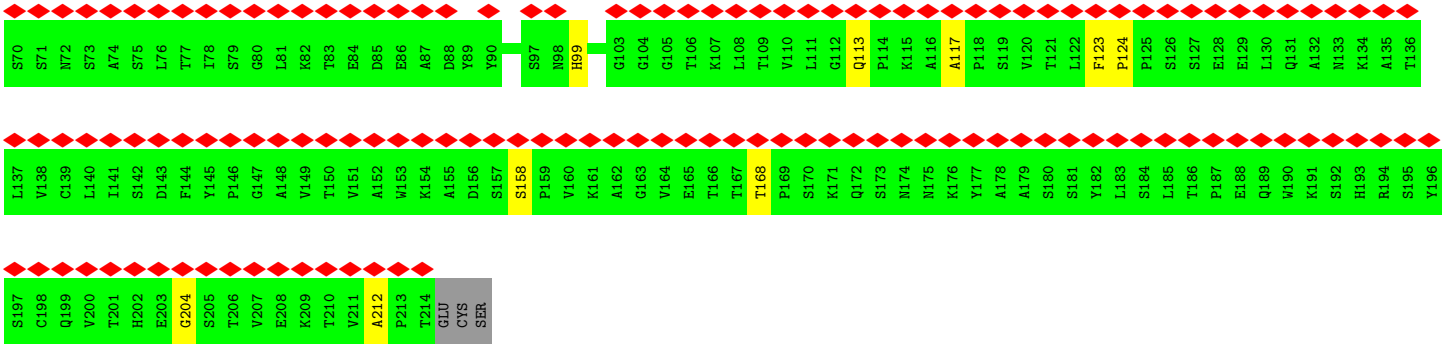




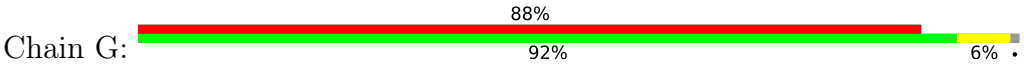
• Molecule 3: S2A4 Fab light chain

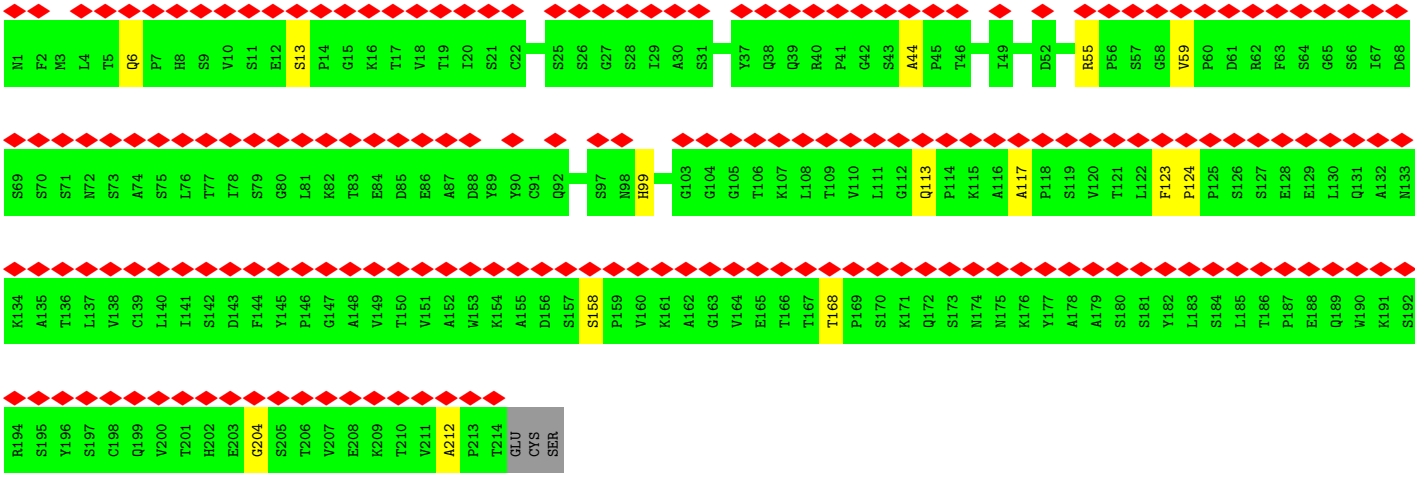




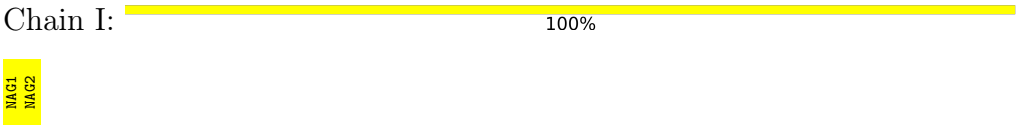


• Molecule 3: S2A4 Fab light chain

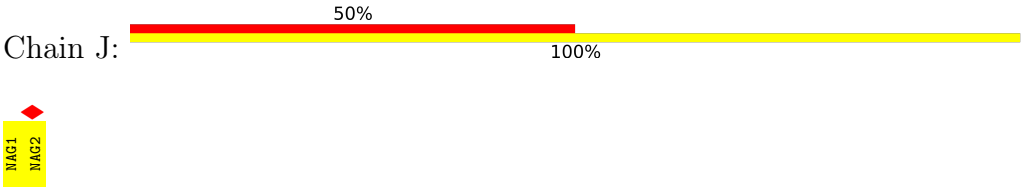




• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



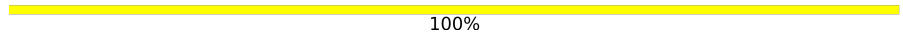


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



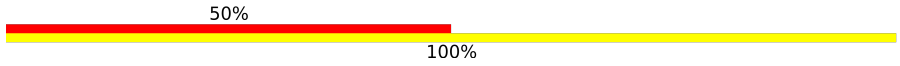


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



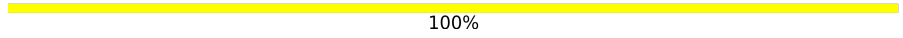


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





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



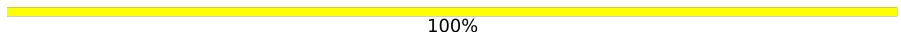


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



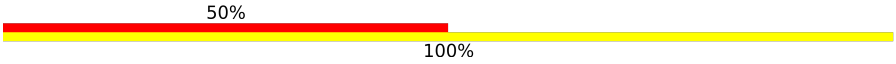


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





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



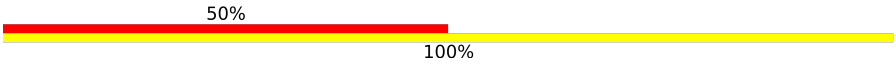


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





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





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



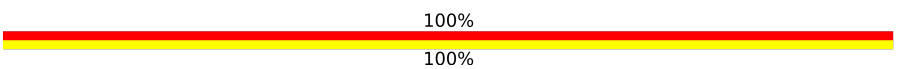


• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





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




NAG1
NAG2
BMA3

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	28599	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 ($e^-/Å^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.254	Depositor
Minimum map value	-2.103	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.72	1/7509 (0.0%)	1.02	60/10246 (0.6%)
1	B	0.72	1/7508 (0.0%)	1.02	60/10245 (0.6%)
1	E	0.72	1/7508 (0.0%)	1.02	60/10245 (0.6%)
2	C	0.54	0/1115	1.18	14/1554 (0.9%)
2	F	0.54	0/1115	1.18	14/1554 (0.9%)
2	H	0.54	0/1115	1.18	14/1554 (0.9%)
3	D	0.53	0/1101	1.26	24/1541 (1.6%)
3	G	0.53	0/1104	1.26	24/1546 (1.6%)
3	L	0.52	0/1108	1.26	24/1551 (1.5%)
All	All	0.68	3/29183 (0.0%)	1.07	294/40036 (0.7%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	607	GLN	CD-NE2	-6.05	1.20	1.33
1	A	607	GLN	CD-NE2	-6.05	1.20	1.33
1	E	607	GLN	CD-NE2	-6.03	1.20	1.33

All (294) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	861	LEU	CA-C-N	7.60	125.14	119.66
1	A	861	LEU	C-N-CA	7.60	125.14	119.66
1	E	861	LEU	CA-C-N	7.57	125.11	119.66
1	E	861	LEU	C-N-CA	7.57	125.11	119.66
1	B	861	LEU	CA-C-N	7.57	125.11	119.66
1	B	861	LEU	C-N-CA	7.57	125.11	119.66
1	B	862	PRO	CA-C-N	7.53	127.49	120.03
1	B	862	PRO	C-N-CA	7.53	127.49	120.03
1	A	1139	ASP	CA-C-N	7.52	127.23	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1139	ASP	C-N-CA	7.52	127.23	119.56
1	E	1139	ASP	CA-C-N	7.51	127.22	119.56
1	E	1139	ASP	C-N-CA	7.51	127.22	119.56
1	B	1139	ASP	CA-C-N	7.50	127.21	119.56
1	B	1139	ASP	C-N-CA	7.50	127.21	119.56
1	E	862	PRO	CA-C-N	7.50	127.45	120.03
1	E	862	PRO	C-N-CA	7.50	127.45	120.03
1	A	862	PRO	CA-C-N	7.48	127.44	120.03
1	A	862	PRO	C-N-CA	7.48	127.44	120.03
2	H	124	GLY	CA-C-N	7.33	127.25	119.85
2	H	124	GLY	C-N-CA	7.33	127.25	119.85
2	C	124	GLY	CA-C-N	7.33	127.25	119.85
2	C	124	GLY	C-N-CA	7.33	127.25	119.85
2	F	124	GLY	CA-C-N	7.32	127.24	119.85
2	F	124	GLY	C-N-CA	7.32	127.24	119.85
1	B	791	THR	CA-C-N	6.99	124.69	119.66
1	B	791	THR	C-N-CA	6.99	124.69	119.66
1	E	792	PRO	CA-C-N	6.98	126.61	119.56
1	E	792	PRO	C-N-CA	6.98	126.61	119.56
1	B	792	PRO	CA-C-N	6.96	126.59	119.56
1	B	792	PRO	C-N-CA	6.96	126.59	119.56
1	E	791	THR	CA-C-N	6.96	124.67	119.66
1	E	791	THR	C-N-CA	6.96	124.67	119.66
1	A	791	THR	CA-C-N	6.92	124.64	119.66
1	A	791	THR	C-N-CA	6.92	124.64	119.66
1	A	792	PRO	CA-C-N	6.92	126.55	119.56
1	A	792	PRO	C-N-CA	6.92	126.55	119.56
1	A	1111	GLU	CA-C-N	6.83	126.59	119.76
1	A	1111	GLU	C-N-CA	6.83	126.59	119.76
1	B	1111	GLU	CA-C-N	6.79	126.55	119.76
1	B	1111	GLU	C-N-CA	6.79	126.55	119.76
1	E	1111	GLU	CA-C-N	6.78	126.54	119.76
1	E	1111	GLU	C-N-CA	6.78	126.54	119.76
2	F	218	GLU	CA-C-N	6.67	126.59	119.85
2	F	218	GLU	C-N-CA	6.67	126.59	119.85
2	H	218	GLU	CA-C-N	6.67	126.58	119.85
2	H	218	GLU	C-N-CA	6.67	126.58	119.85
2	C	218	GLU	CA-C-N	6.65	126.57	119.85
2	C	218	GLU	C-N-CA	6.65	126.57	119.85
1	B	498	GLN	CA-C-N	6.52	126.22	119.56
1	B	498	GLN	C-N-CA	6.52	126.22	119.56
1	A	498	GLN	CA-C-N	6.51	126.20	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	498	GLN	C-N-CA	6.51	126.20	119.56
1	E	498	GLN	CA-C-N	6.49	126.18	119.56
1	E	498	GLN	C-N-CA	6.49	126.18	119.56
3	L	55	ARG	CA-C-N	6.47	126.65	120.31
3	L	55	ARG	C-N-CA	6.47	126.65	120.31
3	D	55	ARG	CA-C-N	6.47	126.65	120.31
3	D	55	ARG	C-N-CA	6.47	126.65	120.31
1	E	578	ASP	CA-C-N	6.46	126.96	119.47
1	E	578	ASP	C-N-CA	6.46	126.96	119.47
1	A	578	ASP	CA-C-N	6.46	126.96	119.47
1	A	578	ASP	C-N-CA	6.46	126.96	119.47
3	G	59	VAL	CA-C-N	6.45	126.41	120.21
3	G	59	VAL	C-N-CA	6.45	126.41	120.21
3	G	55	ARG	CA-C-N	6.45	126.63	120.31
3	G	55	ARG	C-N-CA	6.45	126.63	120.31
1	B	578	ASP	CA-C-N	6.43	126.92	119.47
1	B	578	ASP	C-N-CA	6.43	126.92	119.47
3	D	59	VAL	CA-C-N	6.42	126.38	120.21
3	D	59	VAL	C-N-CA	6.42	126.38	120.21
3	L	59	VAL	CA-C-N	6.41	126.36	120.21
3	L	59	VAL	C-N-CA	6.41	126.36	120.21
1	A	526	GLY	CA-C-N	6.40	126.31	119.85
1	A	526	GLY	C-N-CA	6.40	126.31	119.85
1	E	526	GLY	CA-C-N	6.39	126.31	119.85
1	E	526	GLY	C-N-CA	6.39	126.31	119.85
3	L	123	PHE	CA-C-N	6.37	126.94	120.38
3	L	123	PHE	C-N-CA	6.37	126.94	120.38
3	G	123	PHE	CA-C-N	6.36	126.94	120.38
3	G	123	PHE	C-N-CA	6.36	126.94	120.38
1	B	526	GLY	CA-C-N	6.36	126.28	119.85
1	B	526	GLY	C-N-CA	6.36	126.28	119.85
1	E	425	LEU	CA-C-N	6.36	126.27	119.85
1	E	425	LEU	C-N-CA	6.36	126.27	119.85
1	A	425	LEU	CA-C-N	6.35	126.26	119.85
1	A	425	LEU	C-N-CA	6.35	126.26	119.85
3	D	123	PHE	CA-C-N	6.33	126.90	120.38
3	D	123	PHE	C-N-CA	6.33	126.90	120.38
1	B	425	LEU	CA-C-N	6.33	126.24	119.85
1	B	425	LEU	C-N-CA	6.33	126.24	119.85
3	D	124	PRO	CA-C-N	6.28	126.23	119.76
3	D	124	PRO	C-N-CA	6.28	126.23	119.76
3	L	124	PRO	CA-C-N	6.25	126.20	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	124	PRO	C-N-CA	6.25	126.20	119.76
3	G	124	PRO	CA-C-N	6.24	126.19	119.76
3	G	124	PRO	C-N-CA	6.24	126.19	119.76
1	A	599	THR	CA-C-N	6.18	126.15	120.03
1	A	599	THR	C-N-CA	6.18	126.15	120.03
1	E	599	THR	CA-C-N	6.18	126.15	120.03
1	E	599	THR	C-N-CA	6.18	126.15	120.03
1	B	599	THR	CA-C-N	6.16	126.13	120.03
1	B	599	THR	C-N-CA	6.16	126.13	120.03
1	B	321	GLN	CA-C-N	6.15	126.10	119.76
1	B	321	GLN	C-N-CA	6.15	126.10	119.76
1	A	321	GLN	CA-C-N	6.14	126.09	119.76
1	A	321	GLN	C-N-CA	6.14	126.09	119.76
1	E	321	GLN	CA-C-N	6.14	126.09	119.76
1	E	321	GLN	C-N-CA	6.14	126.09	119.76
3	D	113	GLN	CA-C-N	6.12	126.08	119.78
3	D	113	GLN	C-N-CA	6.12	126.08	119.78
1	E	329	PHE	CA-C-N	6.12	126.09	120.03
1	E	329	PHE	C-N-CA	6.12	126.09	120.03
3	G	6	GLN	CA-C-N	6.11	125.86	119.76
3	G	6	GLN	C-N-CA	6.11	125.86	119.76
3	G	212	ALA	CA-C-N	6.10	126.05	119.76
3	G	212	ALA	C-N-CA	6.10	126.05	119.76
3	L	212	ALA	CA-C-N	6.09	126.03	119.76
3	L	212	ALA	C-N-CA	6.09	126.03	119.76
1	B	1078	ALA	CA-C-N	6.09	125.71	119.56
1	B	1078	ALA	C-N-CA	6.09	125.71	119.56
3	L	113	GLN	CA-C-N	6.08	126.05	119.78
3	L	113	GLN	C-N-CA	6.08	126.05	119.78
1	A	329	PHE	CA-C-N	6.08	126.05	120.03
1	A	329	PHE	C-N-CA	6.08	126.05	120.03
3	D	6	GLN	CA-C-N	6.08	125.84	119.76
3	D	6	GLN	C-N-CA	6.08	125.84	119.76
1	B	208	THR	CA-C-N	6.08	125.84	119.76
1	B	208	THR	C-N-CA	6.08	125.84	119.76
3	G	113	GLN	CA-C-N	6.07	126.03	119.78
3	G	113	GLN	C-N-CA	6.07	126.03	119.78
1	E	208	THR	CA-C-N	6.07	125.83	119.76
1	E	208	THR	C-N-CA	6.07	125.83	119.76
1	B	329	PHE	CA-C-N	6.06	126.03	120.03
1	B	329	PHE	C-N-CA	6.06	126.03	120.03
3	D	212	ALA	CA-C-N	6.06	126.00	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	212	ALA	C-N-CA	6.06	126.00	119.76
1	A	208	THR	CA-C-N	6.05	125.81	119.76
1	A	208	THR	C-N-CA	6.05	125.81	119.76
1	A	1078	ALA	CA-C-N	6.05	125.67	119.56
1	A	1078	ALA	C-N-CA	6.05	125.67	119.56
1	E	1078	ALA	CA-C-N	6.04	125.67	119.56
1	E	1078	ALA	C-N-CA	6.04	125.67	119.56
3	L	6	GLN	CA-C-N	6.04	125.80	119.76
3	L	6	GLN	C-N-CA	6.04	125.80	119.76
1	B	560	LEU	CA-C-N	6.03	126.47	119.47
1	B	560	LEU	C-N-CA	6.03	126.47	119.47
1	A	560	LEU	CA-C-N	6.02	126.45	119.47
1	A	560	LEU	C-N-CA	6.02	126.45	119.47
1	E	560	LEU	CA-C-N	6.01	126.44	119.47
1	E	560	LEU	C-N-CA	6.01	126.44	119.47
1	A	231	ILE	N-CA-C	5.95	116.99	111.45
1	E	231	ILE	N-CA-C	5.95	116.98	111.45
1	B	231	ILE	N-CA-C	5.94	116.97	111.45
1	A	38	TYR	CA-C-N	5.88	125.50	119.56
1	A	38	TYR	C-N-CA	5.88	125.50	119.56
1	B	38	TYR	CA-C-N	5.88	125.50	119.56
1	B	38	TYR	C-N-CA	5.88	125.50	119.56
2	C	172	PHE	CA-C-N	5.88	125.83	119.78
2	C	172	PHE	C-N-CA	5.88	125.83	119.78
2	F	172	PHE	CA-C-N	5.88	125.83	119.78
2	F	172	PHE	C-N-CA	5.88	125.83	119.78
2	H	172	PHE	CA-C-N	5.87	125.83	119.78
2	H	172	PHE	C-N-CA	5.87	125.83	119.78
1	E	38	TYR	CA-C-N	5.87	125.49	119.56
1	E	38	TYR	C-N-CA	5.87	125.49	119.56
1	A	216	LEU	CA-C-N	5.87	125.82	119.78
1	A	216	LEU	C-N-CA	5.87	125.82	119.78
1	B	216	LEU	CA-C-N	5.86	125.82	119.78
1	B	216	LEU	C-N-CA	5.86	125.82	119.78
2	C	190	VAL	CA-C-N	5.83	125.77	119.76
2	C	190	VAL	C-N-CA	5.83	125.77	119.76
1	E	1142	GLN	CA-C-N	5.82	125.44	119.56
1	E	1142	GLN	C-N-CA	5.82	125.44	119.56
1	E	216	LEU	CA-C-N	5.82	125.77	119.78
1	E	216	LEU	C-N-CA	5.82	125.77	119.78
1	B	1142	GLN	CA-C-N	5.81	125.43	119.56
1	B	1142	GLN	C-N-CA	5.81	125.43	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	190	VAL	CA-C-N	5.81	125.75	119.76
2	H	190	VAL	C-N-CA	5.81	125.75	119.76
2	F	190	VAL	CA-C-N	5.76	125.70	119.76
2	F	190	VAL	C-N-CA	5.76	125.70	119.76
1	A	138	ASP	CA-C-N	5.76	125.67	119.85
1	A	138	ASP	C-N-CA	5.76	125.67	119.85
1	A	1142	GLN	CA-C-N	5.76	125.43	119.56
1	A	1142	GLN	C-N-CA	5.76	125.43	119.56
1	B	138	ASP	CA-C-N	5.74	125.65	119.85
1	B	138	ASP	C-N-CA	5.74	125.65	119.85
1	A	383	SER	CA-C-N	5.73	127.00	119.84
1	A	383	SER	C-N-CA	5.73	127.00	119.84
1	E	138	ASP	CA-C-N	5.73	125.64	119.85
1	E	138	ASP	C-N-CA	5.73	125.64	119.85
1	E	383	SER	CA-C-N	5.73	127.00	119.84
1	E	383	SER	C-N-CA	5.73	127.00	119.84
1	B	383	SER	CA-C-N	5.72	127.00	119.84
1	B	383	SER	C-N-CA	5.72	127.00	119.84
3	D	44	ALA	CA-C-N	5.72	125.48	119.76
3	D	44	ALA	C-N-CA	5.72	125.48	119.76
1	E	294	ASP	CA-C-N	5.70	125.37	119.56
1	E	294	ASP	C-N-CA	5.70	125.37	119.56
1	B	294	ASP	CA-C-N	5.69	125.37	119.56
1	B	294	ASP	C-N-CA	5.69	125.37	119.56
3	G	44	ALA	CA-C-N	5.69	125.45	119.76
3	G	44	ALA	C-N-CA	5.69	125.45	119.76
3	L	44	ALA	CA-C-N	5.69	125.45	119.76
3	L	44	ALA	C-N-CA	5.69	125.45	119.76
1	A	294	ASP	CA-C-N	5.68	125.35	119.56
1	A	294	ASP	C-N-CA	5.68	125.35	119.56
1	A	81	ASN	CA-C-N	5.65	126.11	120.52
1	A	81	ASN	C-N-CA	5.65	126.11	120.52
1	E	81	ASN	CA-C-N	5.65	126.11	120.52
1	E	81	ASN	C-N-CA	5.65	126.11	120.52
1	B	81	ASN	CA-C-N	5.64	126.10	120.52
1	B	81	ASN	C-N-CA	5.64	126.10	120.52
1	E	84	LEU	CA-C-N	5.58	125.52	119.78
1	E	84	LEU	C-N-CA	5.58	125.52	119.78
1	B	120	VAL	N-CA-C	5.56	116.13	108.12
1	E	120	VAL	N-CA-C	5.55	116.12	108.12
1	A	120	VAL	N-CA-C	5.54	116.09	108.12
3	L	168	THR	CA-C-N	5.54	125.46	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	168	THR	C-N-CA	5.54	125.46	119.76
2	C	207	LYS	CA-C-N	5.53	125.20	119.56
2	C	207	LYS	C-N-CA	5.53	125.20	119.56
1	B	84	LEU	CA-C-N	5.53	125.47	119.78
1	B	84	LEU	C-N-CA	5.53	125.47	119.78
1	B	90	VAL	N-CA-C	5.53	116.08	108.12
1	A	90	VAL	N-CA-C	5.52	116.07	108.12
1	A	84	LEU	CA-C-N	5.52	125.47	119.78
1	A	84	LEU	C-N-CA	5.52	125.47	119.78
2	F	207	LYS	CA-C-N	5.52	125.19	119.56
2	F	207	LYS	C-N-CA	5.52	125.19	119.56
1	E	90	VAL	N-CA-C	5.51	116.05	108.12
2	H	207	LYS	CA-C-N	5.51	125.18	119.56
2	H	207	LYS	C-N-CA	5.51	125.18	119.56
3	G	117	ALA	CA-C-N	5.50	125.41	119.85
3	G	117	ALA	C-N-CA	5.50	125.41	119.85
3	D	117	ALA	CA-C-N	5.50	125.40	119.85
3	D	117	ALA	C-N-CA	5.50	125.40	119.85
3	D	168	THR	CA-C-N	5.48	125.41	119.76
3	D	168	THR	C-N-CA	5.48	125.41	119.76
3	G	168	THR	CA-C-N	5.46	125.38	119.76
3	G	168	THR	C-N-CA	5.46	125.38	119.76
3	L	117	ALA	CA-C-N	5.45	125.36	119.85
3	L	117	ALA	C-N-CA	5.45	125.36	119.85
1	A	411	ALA	CA-C-N	5.43	125.36	119.76
1	A	411	ALA	C-N-CA	5.43	125.36	119.76
1	E	411	ALA	CA-C-N	5.42	125.34	119.76
1	E	411	ALA	C-N-CA	5.42	125.34	119.76
1	B	411	ALA	CA-C-N	5.41	125.34	119.76
1	B	411	ALA	C-N-CA	5.41	125.34	119.76
1	B	490	PHE	CA-C-N	5.40	125.07	119.56
1	B	490	PHE	C-N-CA	5.40	125.07	119.56
1	E	1107	ARG	N-CA-C	5.40	117.24	111.36
1	B	1107	ARG	N-CA-C	5.39	117.24	111.36
1	A	490	PHE	CA-C-N	5.39	125.06	119.56
1	A	490	PHE	C-N-CA	5.39	125.06	119.56
1	A	1107	ARG	N-CA-C	5.38	117.23	111.36
1	E	490	PHE	CA-C-N	5.36	125.03	119.56
1	E	490	PHE	C-N-CA	5.36	125.03	119.56
1	E	1068	VAL	CA-C-N	5.36	125.37	119.90
1	E	1068	VAL	C-N-CA	5.36	125.37	119.90
1	A	1068	VAL	CA-C-N	5.35	125.35	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1068	VAL	C-N-CA	5.35	125.35	119.90
1	B	1068	VAL	CA-C-N	5.31	125.31	119.90
1	B	1068	VAL	C-N-CA	5.31	125.31	119.90
3	L	13	SER	CA-C-N	5.29	125.21	119.76
3	L	13	SER	C-N-CA	5.29	125.21	119.76
2	F	131	ALA	CA-C-N	5.28	125.19	119.85
2	F	131	ALA	C-N-CA	5.28	125.19	119.85
3	G	13	SER	CA-C-N	5.28	125.19	119.76
3	G	13	SER	C-N-CA	5.28	125.19	119.76
2	H	131	ALA	CA-C-N	5.27	125.17	119.85
2	H	131	ALA	C-N-CA	5.27	125.17	119.85
3	D	13	SER	CA-C-N	5.25	125.17	119.76
3	D	13	SER	C-N-CA	5.25	125.17	119.76
2	C	131	ALA	CA-C-N	5.24	125.14	119.85
2	C	131	ALA	C-N-CA	5.24	125.14	119.85
1	A	506	GLN	CA-C-N	5.18	124.94	119.76
1	A	506	GLN	C-N-CA	5.18	124.94	119.76
1	E	506	GLN	CA-C-N	5.18	124.94	119.76
1	E	506	GLN	C-N-CA	5.18	124.94	119.76
3	D	158	SER	CA-C-N	5.18	125.08	119.85
3	D	158	SER	C-N-CA	5.18	125.08	119.85
2	H	13	GLN	CA-C-N	5.18	125.42	119.83
2	H	13	GLN	C-N-CA	5.18	125.42	119.83
1	B	506	GLN	CA-C-N	5.17	124.93	119.76
1	B	506	GLN	C-N-CA	5.17	124.93	119.76
3	L	158	SER	CA-C-N	5.17	125.07	119.85
3	L	158	SER	C-N-CA	5.17	125.07	119.85
3	G	158	SER	CA-C-N	5.17	125.07	119.85
3	G	158	SER	C-N-CA	5.17	125.07	119.85
2	F	13	GLN	CA-C-N	5.10	125.34	119.83
2	F	13	GLN	C-N-CA	5.10	125.34	119.83
2	C	13	GLN	CA-C-N	5.07	125.36	119.93
2	C	13	GLN	C-N-CA	5.07	125.36	119.93

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	7354	0	6908	23	0
1	B	7353	0	6905	23	0
1	E	7353	0	6905	23	0
2	C	1105	0	568	1	0
2	F	1105	0	568	2	0
2	H	1105	0	568	1	0
3	D	1088	0	566	0	0
3	G	1090	0	572	0	0
3	L	1094	0	578	0	0
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	M	28	0	25	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	R	28	0	25	0	0
4	S	28	0	25	0	0
4	T	28	0	25	0	0
4	U	28	0	25	0	0
4	W	28	0	25	0	0
4	X	28	0	25	0	0
5	K	39	0	34	0	0
5	Q	39	0	34	0	0
5	V	39	0	34	0	0
6	A	154	0	143	0	0
6	B	154	0	143	0	0
6	E	154	0	143	0	0
All	All	29562	0	24969	53	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (53) 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:B:965:GLN:NE2	1:E:759:PHE:CD1	2.52	0.78
1:A:965:GLN:NE2	1:B:759:PHE:CD1	2.51	0.77
1:A:759:PHE:CD1	1:E:965:GLN:NE2	2.55	0.75
1:B:970:PHE:HE2	1:E:759:PHE:CE1	2.10	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:759:PHE:CE1	1:E:970:PHE:HE2	2.09	0.69
1:A:970:PHE:HE2	1:B:759:PHE:CE1	2.10	0.69
1:E:756:TYR:O	1:E:759:PHE:HD1	1.78	0.67
1:B:756:TYR:O	1:B:759:PHE:HD1	1.78	0.67
1:A:756:TYR:O	1:A:759:PHE:HD1	1.78	0.66
1:A:965:GLN:NE2	1:B:759:PHE:CE1	2.64	0.66
1:B:965:GLN:NE2	1:E:759:PHE:CE1	2.64	0.64
1:A:759:PHE:CE1	1:E:965:GLN:NE2	2.67	0.62
1:A:970:PHE:HE2	1:B:759:PHE:HE1	1.52	0.57
1:B:970:PHE:HE2	1:E:759:PHE:HE1	1.52	0.56
1:B:965:GLN:HE22	1:E:759:PHE:HD1	1.53	0.56
1:A:759:PHE:HE1	1:E:970:PHE:HE2	1.50	0.55
1:A:965:GLN:HE22	1:B:759:PHE:HD1	1.53	0.55
1:A:759:PHE:HD1	1:E:965:GLN:HE22	1.56	0.54
1:E:811:LYS:NZ	1:E:820:ASP:OD2	2.43	0.52
1:A:759:PHE:HE1	1:E:970:PHE:CE2	2.28	0.51
1:B:811:LYS:NZ	1:B:820:ASP:OD2	2.43	0.51
1:A:811:LYS:NZ	1:A:820:ASP:OD2	2.43	0.51
1:B:970:PHE:CE2	1:E:759:PHE:HE1	2.29	0.51
1:A:970:PHE:CE2	1:B:759:PHE:HE1	2.29	0.50
1:A:1028:LYS:NZ	1:A:1042:PHE:O	2.44	0.50
1:A:389:ASP:OD1	1:A:528:LYS:NZ	2.45	0.50
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.44	0.50
1:E:1028:LYS:NZ	1:E:1042:PHE:O	2.44	0.50
1:B:389:ASP:OD1	1:B:528:LYS:NZ	2.45	0.49
1:B:1142:GLN:N	1:B:1143:PRO:CD	2.76	0.49
1:A:1142:GLN:N	1:A:1143:PRO:CD	2.76	0.48
1:E:1142:GLN:N	1:E:1143:PRO:CD	2.76	0.47
1:E:389:ASP:OD1	1:E:528:LYS:NZ	2.45	0.47
1:A:970:PHE:CE2	1:B:759:PHE:CE1	2.98	0.46
2:H:207:LYS:N	2:H:208:PRO:CD	2.79	0.46
2:C:207:LYS:N	2:C:208:PRO:CD	2.79	0.45
1:B:756:TYR:O	1:B:759:PHE:CD1	2.66	0.45
2:F:207:LYS:N	2:F:208:PRO:CD	2.79	0.45
1:E:578:ASP:HA	1:E:579:PRO:HD3	1.89	0.42
1:E:756:TYR:O	1:E:759:PHE:CD1	2.66	0.42
1:A:759:PHE:CE1	1:E:970:PHE:CE2	2.98	0.41
1:A:986:PRO:HB2	1:A:987:PRO:HD3	2.03	0.41
1:B:986:PRO:HB2	1:B:987:PRO:HD3	2.03	0.41
1:E:190:ARG:HH11	1:E:207:HIS:CE1	2.38	0.41
1:A:190:ARG:HH11	1:A:207:HIS:CE1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:81:ASN:N	1:E:82:PRO:CD	2.84	0.41
1:E:986:PRO:HB2	1:E:987:PRO:HD3	2.03	0.41
1:A:81:ASN:N	1:A:82:PRO:CD	2.84	0.40
1:B:81:ASN:N	1:B:82:PRO:CD	2.84	0.40
1:A:756:TYR:O	1:A:759:PHE:CD1	2.66	0.40
1:B:190:ARG:HH11	1:B:207:HIS:CE1	2.38	0.40
1:B:718:PHE:CD1	1:B:718:PHE:C	3.00	0.40
2:F:172:PHE:HA	2:F:173:PRO:HD3	1.96	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	968/1281 (76%)	940 (97%)	28 (3%)	0	100	100
1	B	968/1281 (76%)	940 (97%)	28 (3%)	0	100	100
1	E	968/1281 (76%)	940 (97%)	28 (3%)	0	100	100
2	C	218/228 (96%)	218 (100%)	0	0	100	100
2	F	218/228 (96%)	218 (100%)	0	0	100	100
2	H	218/228 (96%)	218 (100%)	0	0	100	100
3	D	212/217 (98%)	206 (97%)	4 (2%)	2 (1%)	14	43
3	G	212/217 (98%)	206 (97%)	4 (2%)	2 (1%)	14	43
3	L	212/217 (98%)	206 (97%)	4 (2%)	2 (1%)	14	43
All	All	4194/5178 (81%)	4092 (98%)	96 (2%)	6 (0%)	49	75

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	204	GLY
3	D	204	GLY
3	G	204	GLY
3	L	99	HIS
3	D	99	HIS
3	G	99	HIS

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	755/1107 (68%)	754 (100%)	1 (0%)	88 90
1	B	754/1107 (68%)	753 (100%)	1 (0%)	88 90
1	E	754/1107 (68%)	753 (100%)	1 (0%)	88 90
2	C	15/193 (8%)	15 (100%)	0	100 100
2	F	15/193 (8%)	15 (100%)	0	100 100
2	H	15/193 (8%)	15 (100%)	0	100 100
3	D	18/188 (10%)	18 (100%)	0	100 100
3	G	19/188 (10%)	19 (100%)	0	100 100
3	L	20/188 (11%)	20 (100%)	0	100 100
All	All	2365/4464 (53%)	2362 (100%)	3 (0%)	87 90

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

Mol	Chain	Res	Type
1	A	165	ASN
1	B	165	ASN
1	E	165	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	207	HIS

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Mol	Chain	Res	Type
1	A	394	ASN
1	A	607	GLN
1	A	1010	GLN
1	B	207	HIS
1	B	394	ASN
1	B	607	GLN
1	B	690	GLN
1	B	1010	GLN
1	E	207	HIS
1	E	394	ASN
1	E	607	GLN
1	E	955	ASN
1	E	1010	GLN
1	E	1011	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

33 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	4,1	14,14,15	1.53	2 (14%)	17,19,21	0.95	1 (5%)
4	NAG	I	2	4	14,14,15	1.42	2 (14%)	17,19,21	0.90	1 (5%)
4	NAG	J	1	4,1	14,14,15	1.62	2 (14%)	17,19,21	0.92	1 (5%)
4	NAG	J	2	4	14,14,15	1.53	2 (14%)	17,19,21	0.90	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	NAG	K	1	1,5	14,14,15	1.62	2 (14%)	17,19,21	1.03	1 (5%)
5	NAG	K	2	5	14,14,15	1.81	2 (14%)	17,19,21	1.02	1 (5%)
5	BMA	K	3	5	11,11,12	1.38	3 (27%)	15,15,17	0.60	0
4	NAG	M	1	4,1	14,14,15	1.59	2 (14%)	17,19,21	1.01	1 (5%)
4	NAG	M	2	4	14,14,15	1.49	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	N	1	4,1	14,14,15	1.47	2 (14%)	17,19,21	1.05	1 (5%)
4	NAG	N	2	4	14,14,15	1.45	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	O	1	4,1	14,14,15	1.51	2 (14%)	17,19,21	0.95	1 (5%)
4	NAG	O	2	4	14,14,15	1.42	2 (14%)	17,19,21	0.89	1 (5%)
4	NAG	P	1	4,1	14,14,15	1.62	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	P	2	4	14,14,15	1.54	2 (14%)	17,19,21	0.90	1 (5%)
5	NAG	Q	1	1,5	14,14,15	1.62	2 (14%)	17,19,21	1.03	1 (5%)
5	NAG	Q	2	5	14,14,15	1.81	2 (14%)	17,19,21	1.02	1 (5%)
5	BMA	Q	3	5	11,11,12	1.39	3 (27%)	15,15,17	0.61	0
4	NAG	R	1	4,1	14,14,15	1.58	2 (14%)	17,19,21	1.01	1 (5%)
4	NAG	R	2	4	14,14,15	1.49	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	S	1	4,1	14,14,15	1.46	2 (14%)	17,19,21	1.06	1 (5%)
4	NAG	S	2	4	14,14,15	1.45	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	T	1	4,1	14,14,15	1.51	2 (14%)	17,19,21	0.94	1 (5%)
4	NAG	T	2	4	14,14,15	1.42	2 (14%)	17,19,21	0.89	1 (5%)
4	NAG	U	1	4,1	14,14,15	1.62	2 (14%)	17,19,21	0.92	1 (5%)
4	NAG	U	2	4	14,14,15	1.53	2 (14%)	17,19,21	0.90	1 (5%)
5	NAG	V	1	1,5	14,14,15	1.62	2 (14%)	17,19,21	1.03	1 (5%)
5	NAG	V	2	5	14,14,15	1.81	2 (14%)	17,19,21	1.02	1 (5%)
5	BMA	V	3	5	11,11,12	1.39	3 (27%)	15,15,17	0.60	0
4	NAG	W	1	4,1	14,14,15	1.59	2 (14%)	17,19,21	1.01	1 (5%)
4	NAG	W	2	4	14,14,15	1.49	2 (14%)	17,19,21	0.93	1 (5%)
4	NAG	X	1	4,1	14,14,15	1.46	2 (14%)	17,19,21	1.06	1 (5%)
4	NAG	X	2	4	14,14,15	1.46	2 (14%)	17,19,21	0.93	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1
5	NAG	K	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	K	2	5	-	0/6/23/26	0/1/1/1
5	BMA	K	3	5	-	0/2/19/22	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
5	NAG	Q	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	0/6/23/26	0/1/1/1
5	BMA	Q	3	5	-	0/2/19/22	0/1/1/1
4	NAG	R	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	R	2	4	-	0/6/23/26	0/1/1/1
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	0/6/23/26	0/1/1/1
4	NAG	T	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	T	2	4	-	0/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1
5	NAG	V	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	V	2	5	-	0/6/23/26	0/1/1/1
5	BMA	V	3	5	-	0/2/19/22	0/1/1/1
4	NAG	W	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	W	2	4	-	0/6/23/26	0/1/1/1
4	NAG	X	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	X	2	4	-	0/6/23/26	0/1/1/1

All (69) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Q	2	NAG	C1-C2	5.22	1.59	1.52
5	K	2	NAG	C1-C2	5.22	1.59	1.52
5	V	2	NAG	C1-C2	5.20	1.59	1.52
4	U	1	NAG	C1-C2	4.57	1.58	1.52
4	J	1	NAG	C1-C2	4.56	1.58	1.52
4	P	1	NAG	C1-C2	4.56	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	2	NAG	C1-C2	4.34	1.58	1.52
4	J	2	NAG	C1-C2	4.34	1.58	1.52
4	U	2	NAG	C1-C2	4.32	1.58	1.52
5	V	1	NAG	C1-C2	4.26	1.58	1.52
5	K	1	NAG	C1-C2	4.24	1.58	1.52
5	Q	1	NAG	C1-C2	4.21	1.58	1.52
4	W	1	NAG	C1-C2	4.13	1.58	1.52
4	M	1	NAG	C1-C2	4.09	1.57	1.52
4	R	1	NAG	C1-C2	4.08	1.57	1.52
4	S	1	NAG	C1-C2	4.01	1.57	1.52
4	N	1	NAG	C1-C2	3.99	1.57	1.52
4	X	1	NAG	C1-C2	3.97	1.57	1.52
4	I	1	NAG	C1-C2	3.94	1.57	1.52
4	T	1	NAG	C1-C2	3.92	1.57	1.52
4	O	1	NAG	C1-C2	3.89	1.57	1.52
4	R	2	NAG	C1-C2	3.85	1.57	1.52
4	M	2	NAG	C1-C2	3.85	1.57	1.52
4	W	2	NAG	C1-C2	3.85	1.57	1.52
4	X	2	NAG	C1-C2	3.79	1.57	1.52
4	S	2	NAG	C1-C2	3.77	1.57	1.52
4	N	2	NAG	C1-C2	3.76	1.57	1.52
4	I	2	NAG	C1-C2	3.64	1.57	1.52
4	T	2	NAG	C1-C2	3.59	1.57	1.52
4	O	2	NAG	C1-C2	3.57	1.57	1.52
4	M	1	NAG	O5-C5	2.77	1.48	1.43
4	R	1	NAG	O5-C5	2.76	1.48	1.43
4	W	1	NAG	O5-C5	2.76	1.48	1.43
4	I	1	NAG	O5-C5	2.49	1.48	1.43
4	T	1	NAG	O5-C5	2.46	1.48	1.43
5	K	2	NAG	O5-C5	2.46	1.48	1.43
4	O	1	NAG	O5-C5	2.45	1.48	1.43
5	Q	2	NAG	O5-C5	2.44	1.48	1.43
5	V	2	NAG	O5-C5	2.43	1.48	1.43
4	W	2	NAG	O5-C5	2.42	1.48	1.43
4	R	2	NAG	O5-C5	2.42	1.48	1.43
4	M	2	NAG	O5-C5	2.39	1.48	1.43
5	V	3	BMA	O5-C5	2.27	1.47	1.43
5	Q	3	BMA	O5-C5	2.25	1.47	1.43
5	K	3	BMA	C1-C2	2.24	1.57	1.52
5	K	3	BMA	O5-C5	2.23	1.47	1.43
5	V	3	BMA	C1-C2	2.22	1.57	1.52
4	J	1	NAG	O5-C5	2.22	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Q	3	BMA	C1-C2	2.21	1.57	1.52
4	X	2	NAG	O5-C5	2.19	1.47	1.43
4	T	2	NAG	O5-C5	2.19	1.47	1.43
4	U	1	NAG	O5-C5	2.19	1.47	1.43
4	P	1	NAG	O5-C5	2.19	1.47	1.43
5	Q	3	BMA	C2-C3	2.18	1.55	1.52
5	K	3	BMA	C2-C3	2.17	1.55	1.52
4	N	2	NAG	O5-C5	2.17	1.47	1.43
5	V	3	BMA	C2-C3	2.16	1.55	1.52
4	S	2	NAG	O5-C5	2.15	1.47	1.43
4	O	2	NAG	O5-C5	2.15	1.47	1.43
4	I	2	NAG	O5-C5	2.15	1.47	1.43
4	N	1	NAG	O5-C5	2.14	1.47	1.43
4	X	1	NAG	O5-C5	2.13	1.47	1.43
4	S	1	NAG	O5-C5	2.10	1.47	1.43
5	K	1	NAG	O5-C5	2.09	1.47	1.43
5	V	1	NAG	O5-C5	2.08	1.47	1.43
4	J	2	NAG	O5-C5	2.08	1.47	1.43
5	Q	1	NAG	O5-C5	2.08	1.47	1.43
4	U	2	NAG	O5-C5	2.06	1.47	1.43
4	P	2	NAG	O5-C5	2.05	1.47	1.43

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	K	2	NAG	C8-C7-N2	2.56	120.36	116.12
5	Q	2	NAG	C8-C7-N2	2.54	120.33	116.12
5	V	2	NAG	C8-C7-N2	2.54	120.33	116.12
5	K	1	NAG	C8-C7-N2	2.53	120.31	116.12
5	V	1	NAG	C8-C7-N2	2.52	120.30	116.12
5	Q	1	NAG	C8-C7-N2	2.52	120.30	116.12
4	N	2	NAG	C8-C7-N2	2.48	120.23	116.12
4	X	2	NAG	C8-C7-N2	2.48	120.22	116.12
4	S	2	NAG	C8-C7-N2	2.46	120.19	116.12
4	I	2	NAG	C8-C7-N2	2.45	120.18	116.12
4	T	2	NAG	C8-C7-N2	2.45	120.17	116.12
4	O	2	NAG	C8-C7-N2	2.43	120.15	116.12
4	X	1	NAG	C8-C7-N2	2.40	120.11	116.12
4	N	1	NAG	C8-C7-N2	2.40	120.09	116.12
4	U	2	NAG	C8-C7-N2	2.39	120.08	116.12
4	S	1	NAG	C8-C7-N2	2.39	120.08	116.12
4	M	2	NAG	C8-C7-N2	2.38	120.07	116.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	P	2	NAG	C8-C7-N2	2.38	120.06	116.12
4	R	2	NAG	C8-C7-N2	2.37	120.05	116.12
4	J	2	NAG	C8-C7-N2	2.36	120.02	116.12
4	W	2	NAG	C8-C7-N2	2.35	120.02	116.12
4	O	1	NAG	C8-C7-N2	2.35	120.02	116.12
4	I	1	NAG	C8-C7-N2	2.33	119.99	116.12
4	T	1	NAG	C8-C7-N2	2.32	119.97	116.12
4	P	1	NAG	C8-C7-N2	2.32	119.97	116.12
4	J	1	NAG	C8-C7-N2	2.31	119.95	116.12
4	R	1	NAG	C8-C7-N2	2.30	119.93	116.12
4	U	1	NAG	C8-C7-N2	2.30	119.93	116.12
4	W	1	NAG	C8-C7-N2	2.29	119.92	116.12
4	M	1	NAG	C8-C7-N2	2.28	119.89	116.12

There are no chirality outliers.

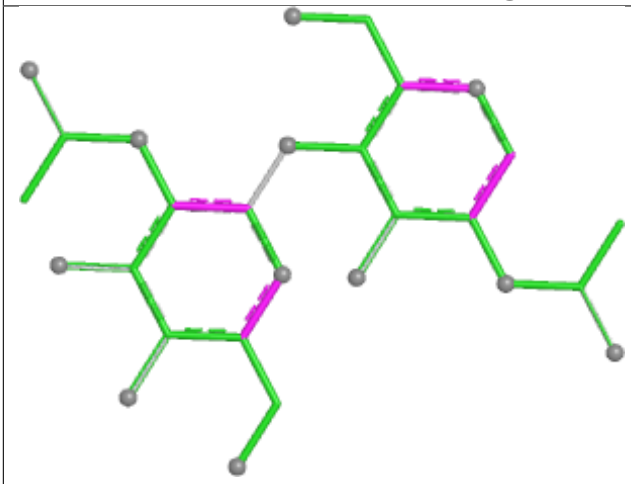
There are no torsion outliers.

There are no ring outliers.

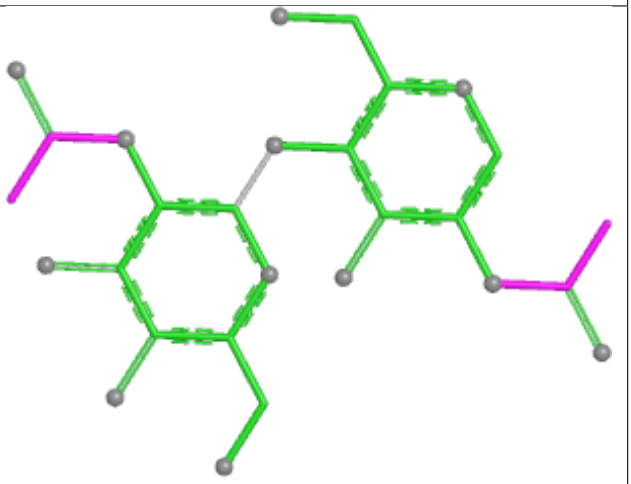
No monomer is involved in short contacts.

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

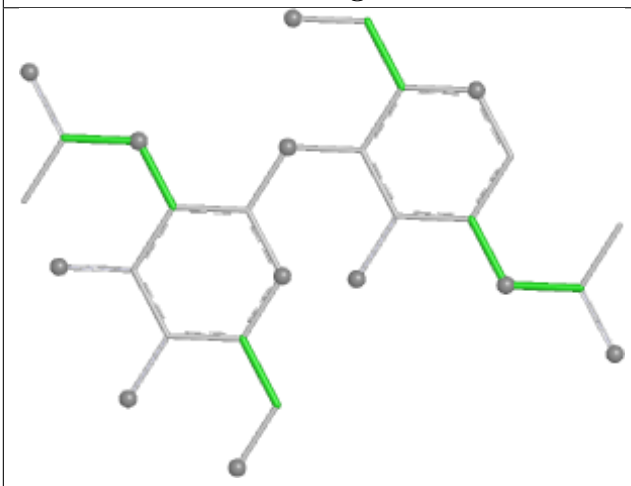
Oligosaccharide Chain I



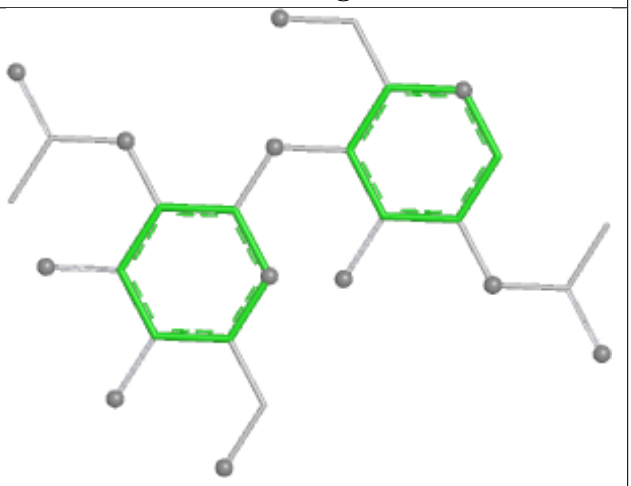
Bond lengths



Bond angles

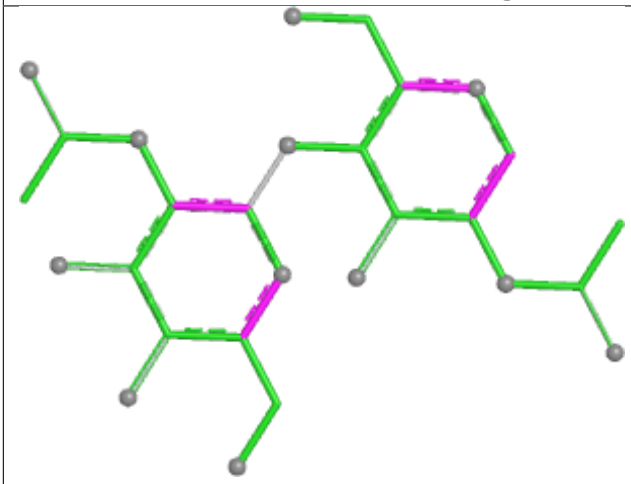


Torsions

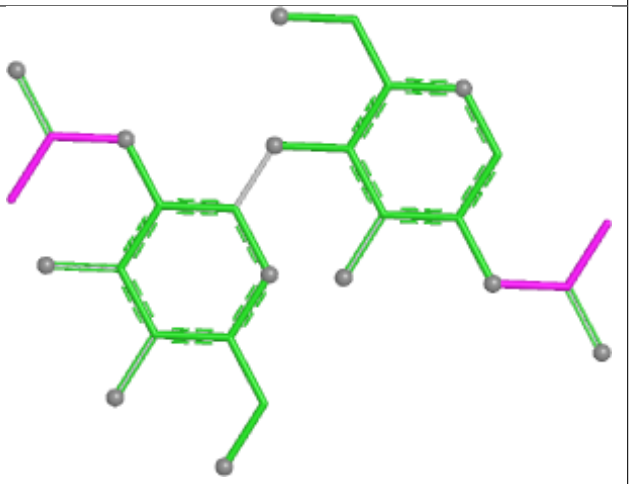


Rings

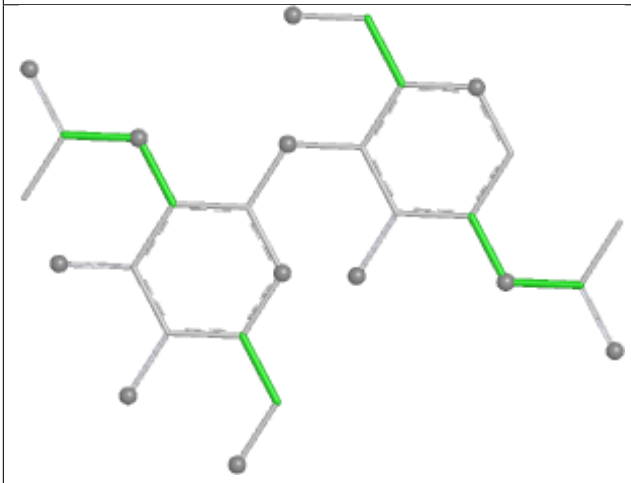
Oligosaccharide Chain J



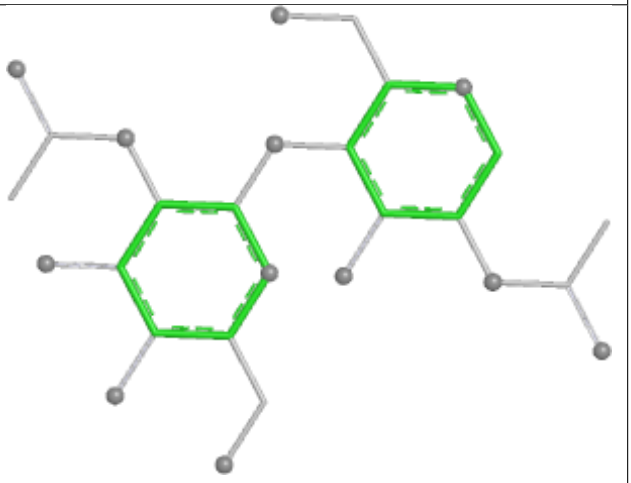
Bond lengths



Bond angles

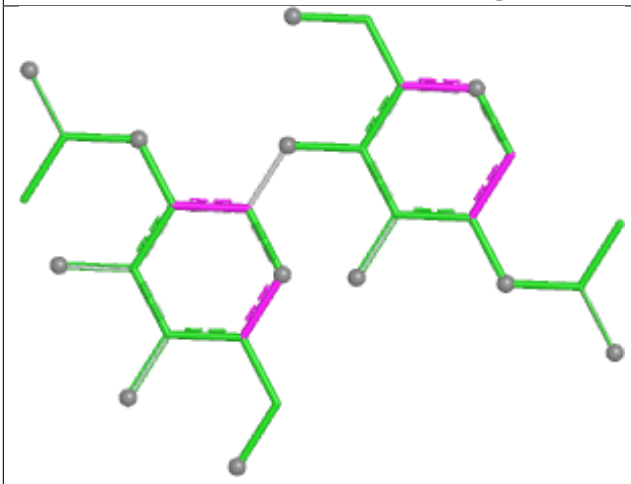


Torsions

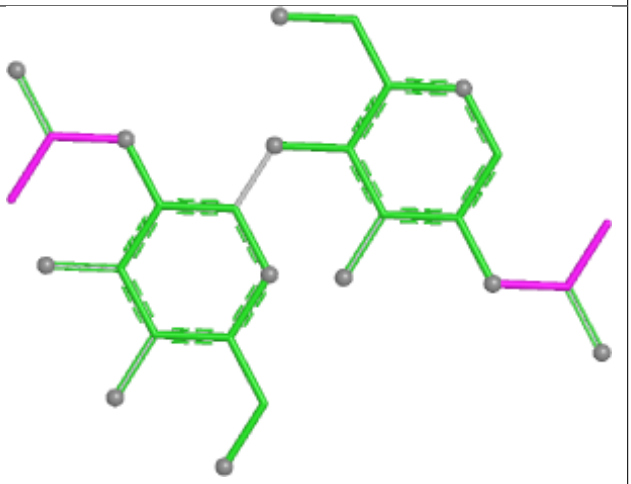


Rings

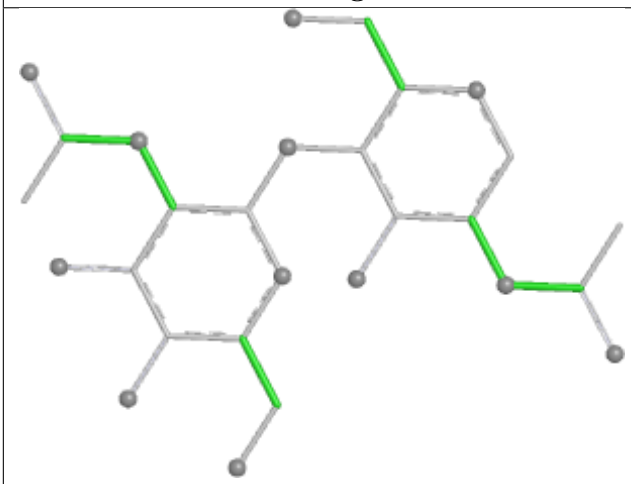
Oligosaccharide Chain M



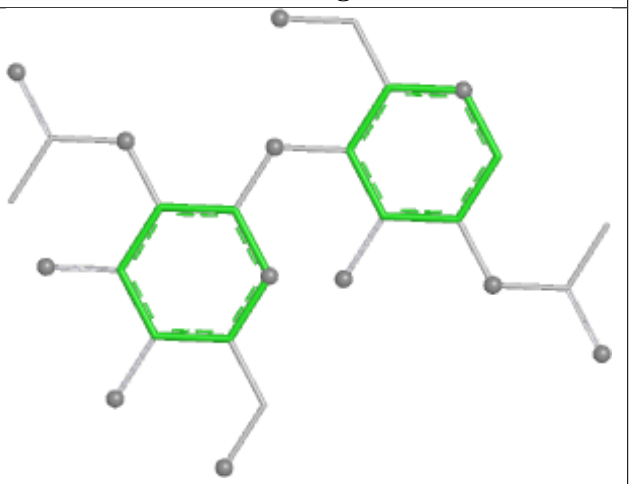
Bond lengths



Bond angles

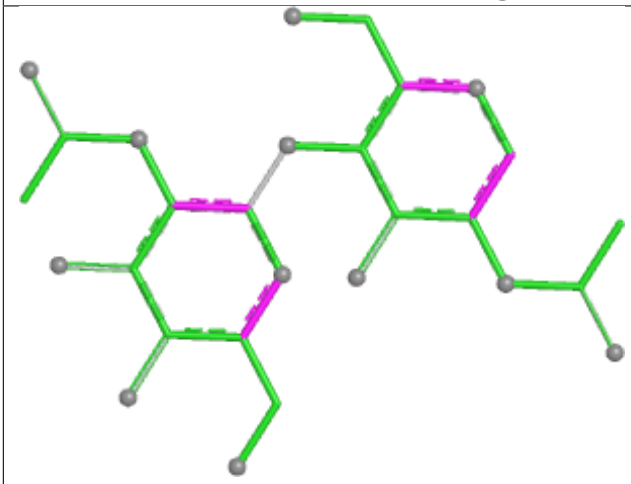


Torsions

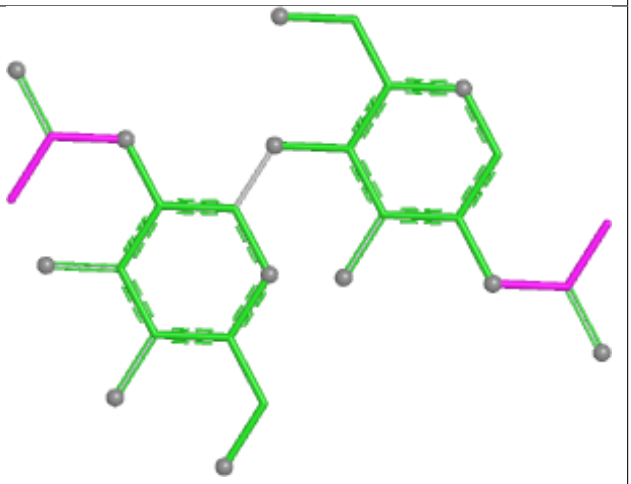


Rings

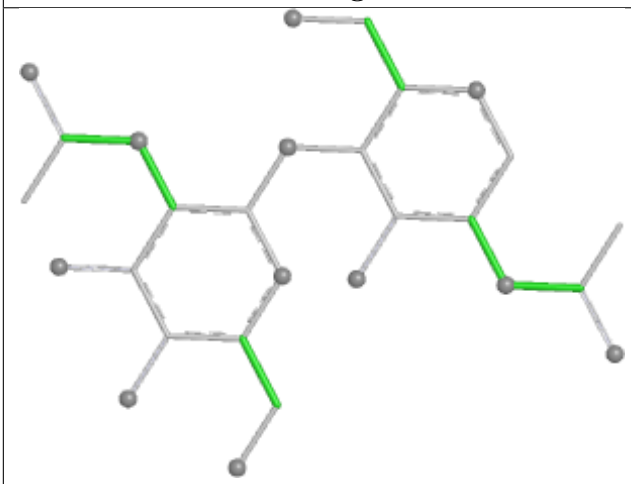
Oligosaccharide Chain N



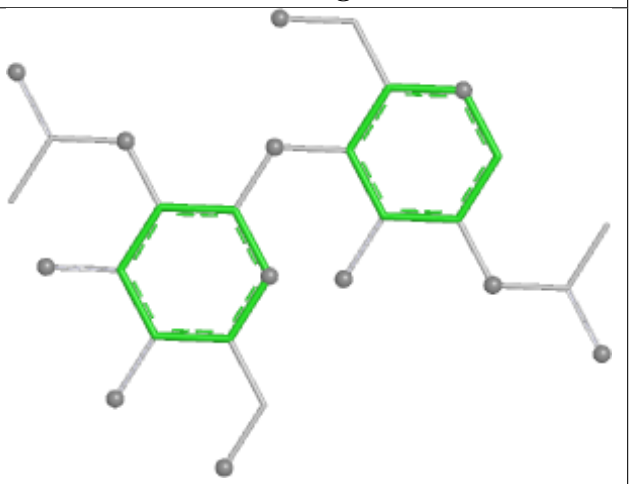
Bond lengths



Bond angles

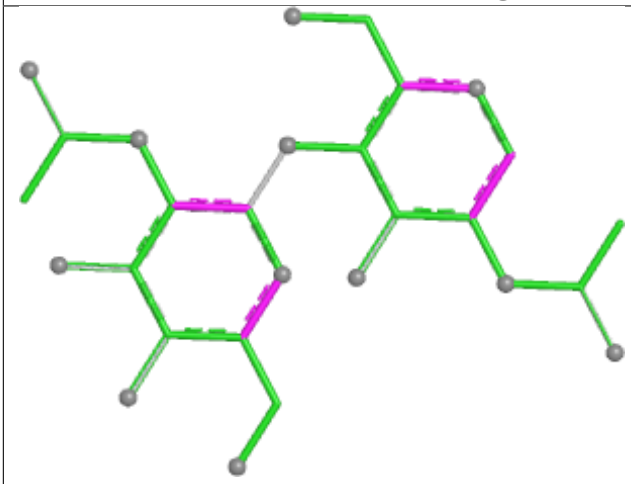


Torsions

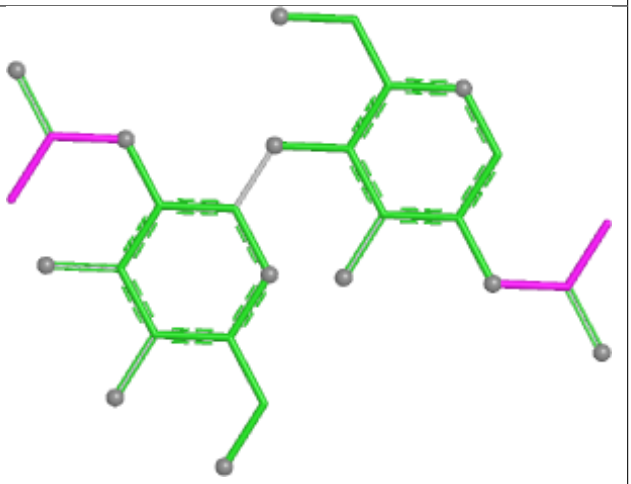


Rings

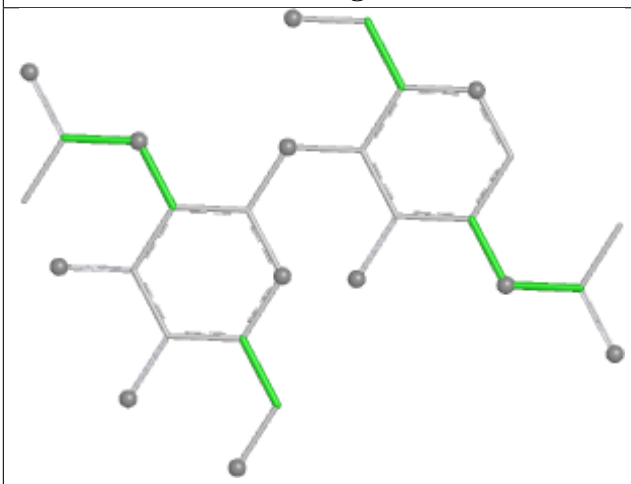
Oligosaccharide Chain O



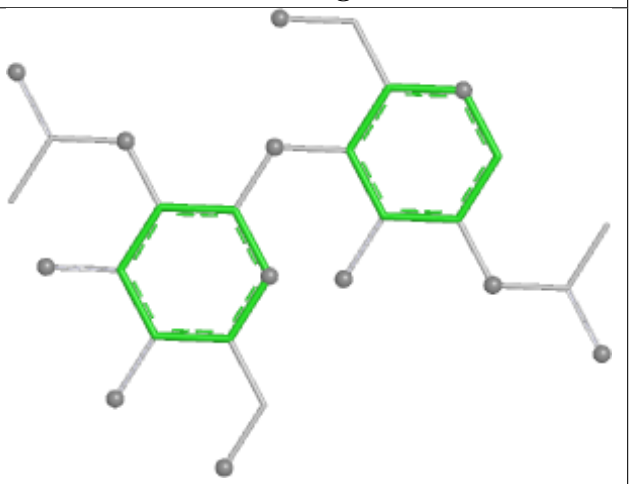
Bond lengths



Bond angles

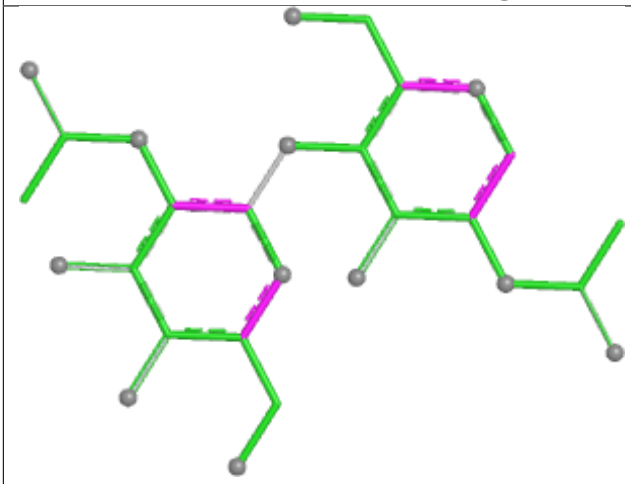


Torsions

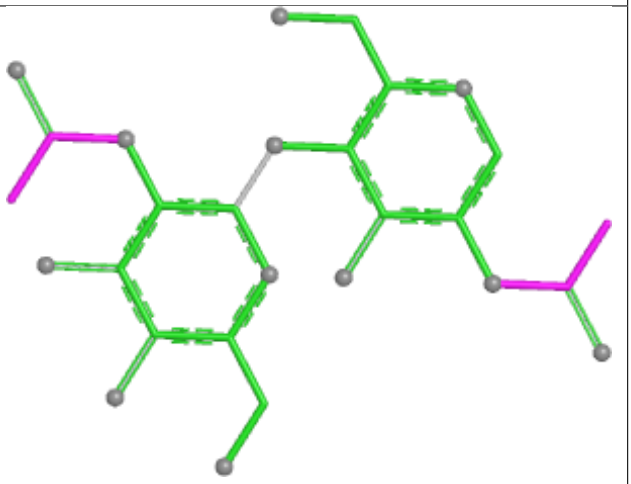


Rings

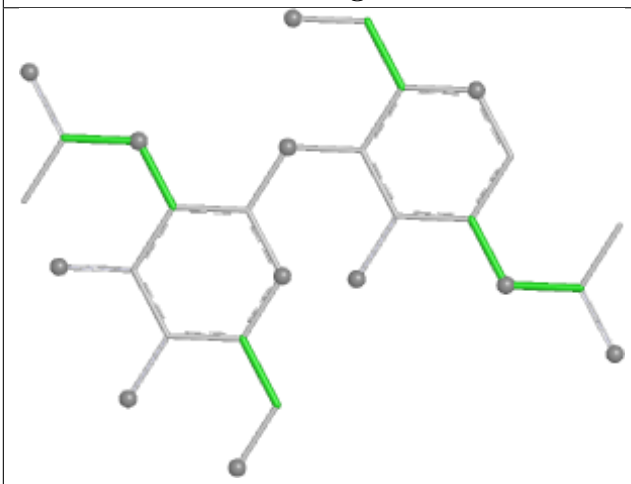
Oligosaccharide Chain P



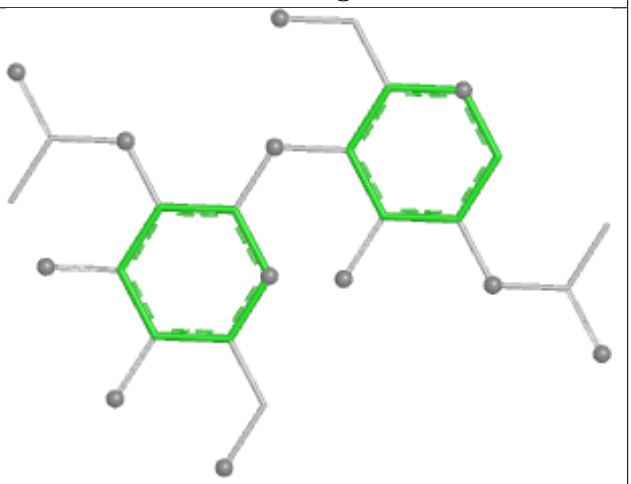
Bond lengths



Bond angles

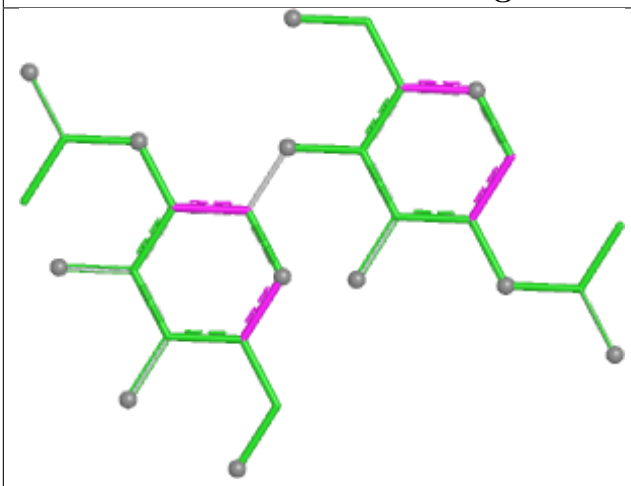


Torsions

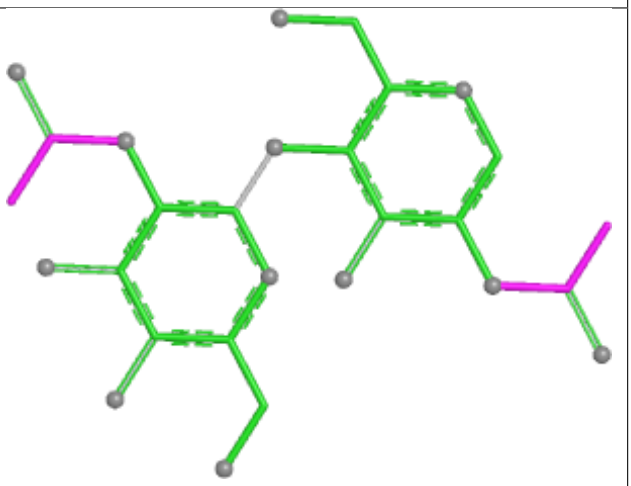


Rings

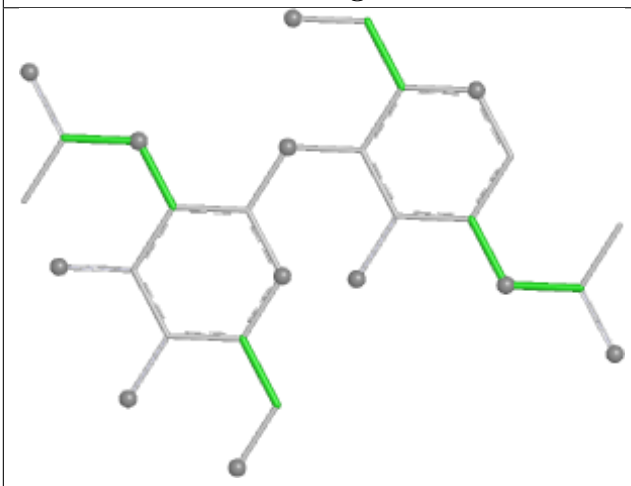
Oligosaccharide Chain R



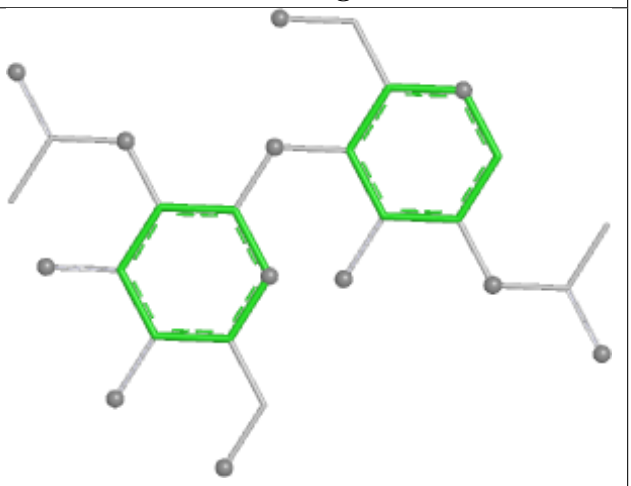
Bond lengths



Bond angles

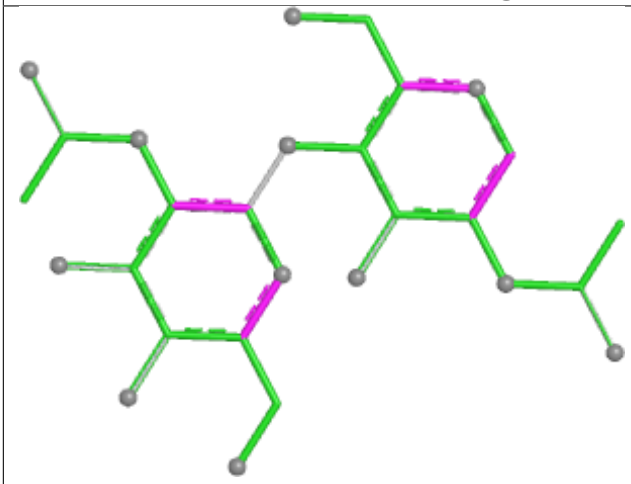


Torsions

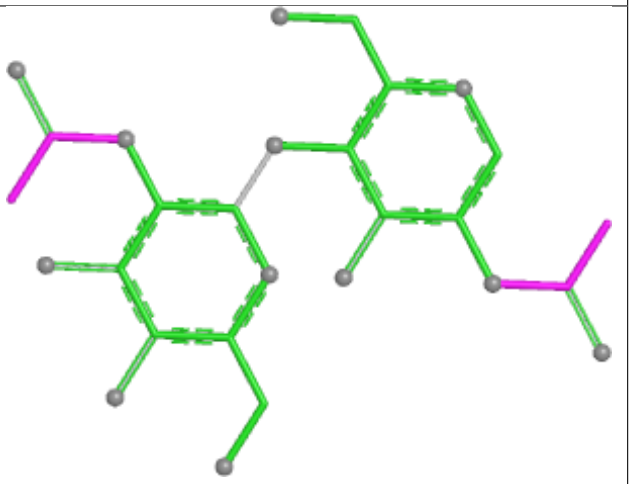


Rings

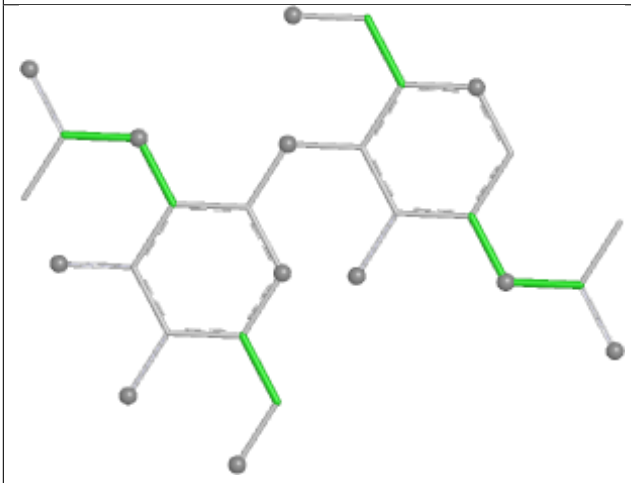
Oligosaccharide Chain S



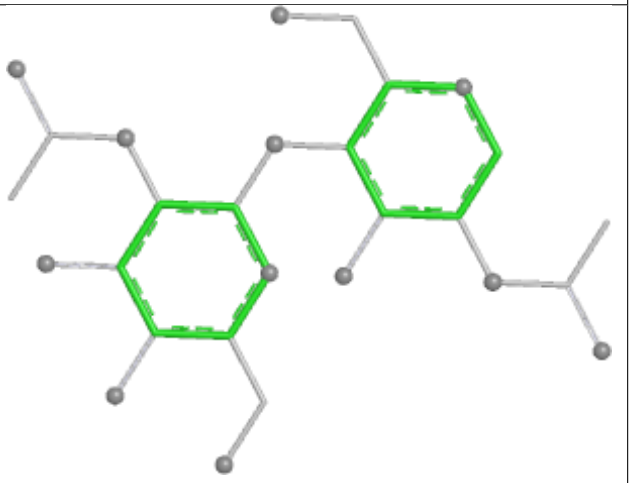
Bond lengths



Bond angles

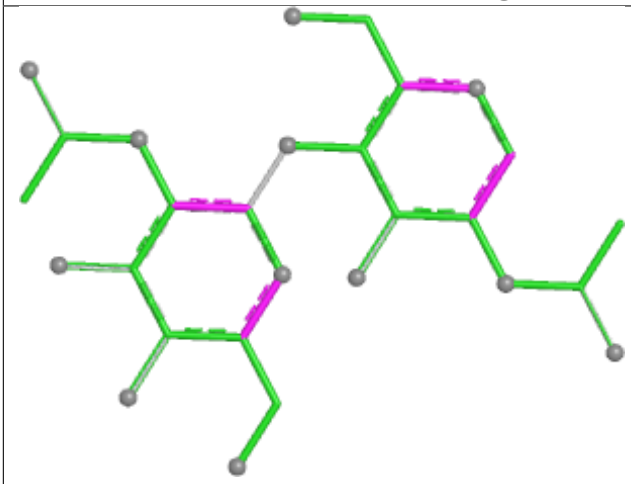


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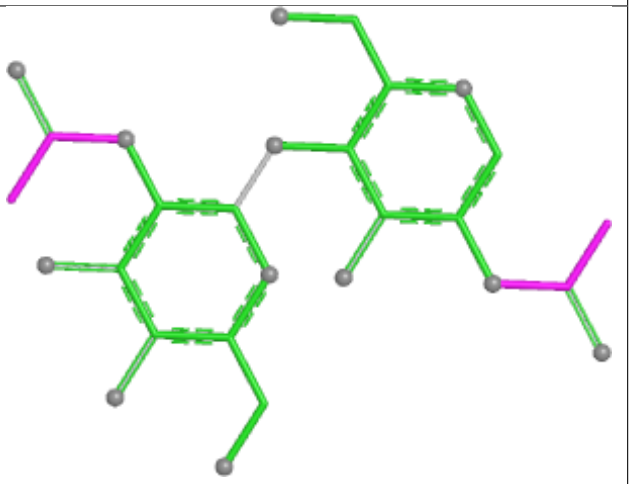


Rings

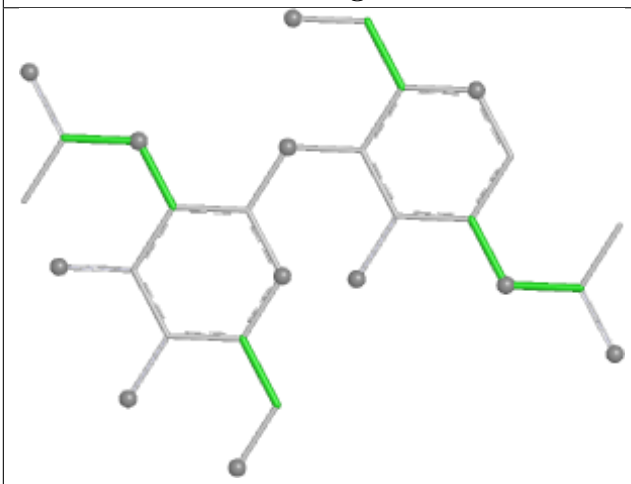
Oligosaccharide Chain T



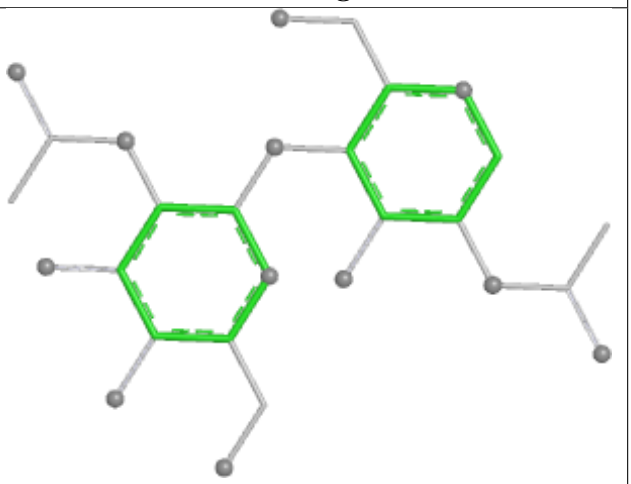
Bond lengths



Bond angles

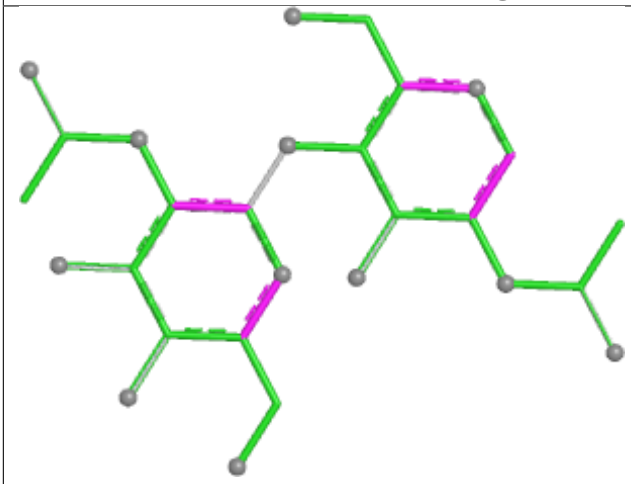


Torsions

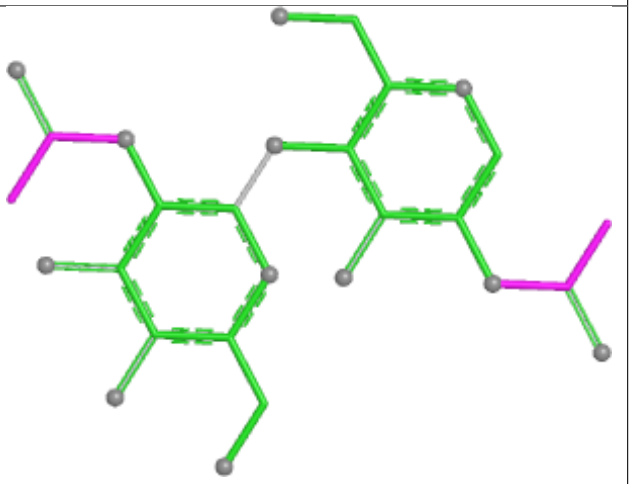


Rings

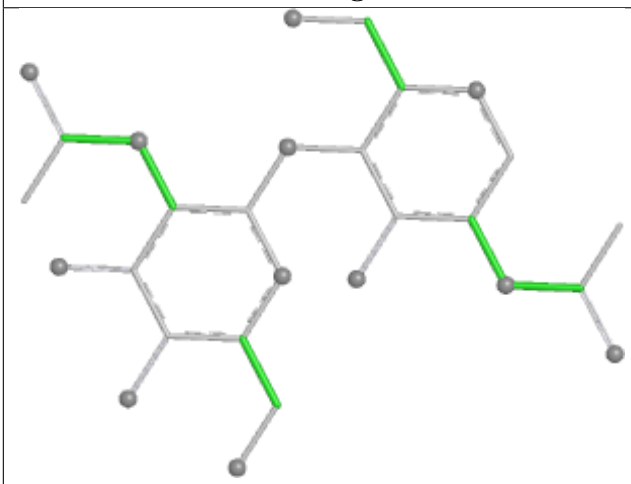
Oligosaccharide Chain U



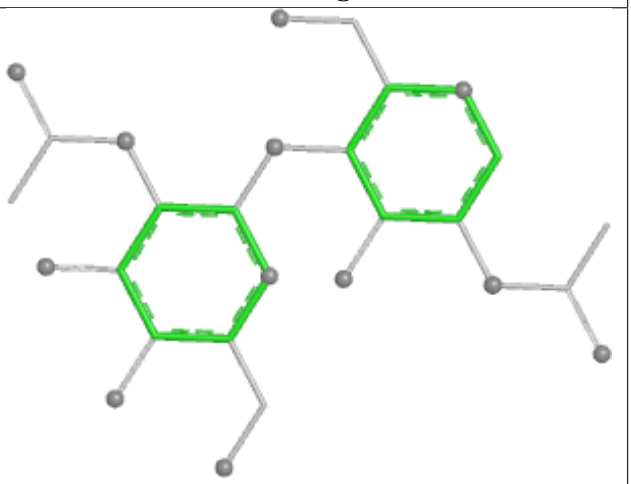
Bond lengths



Bond angles

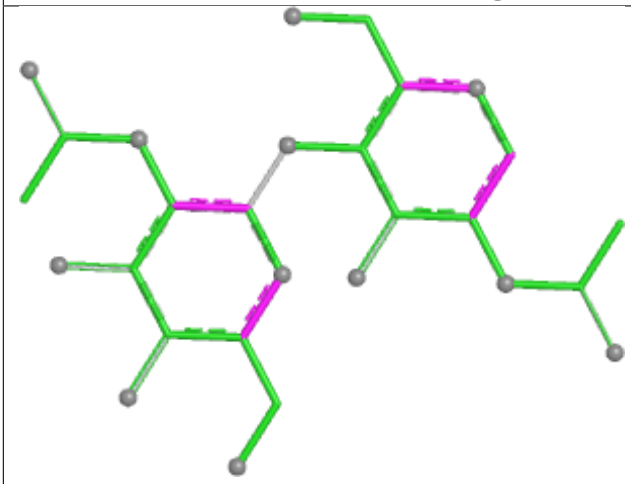


Torsions

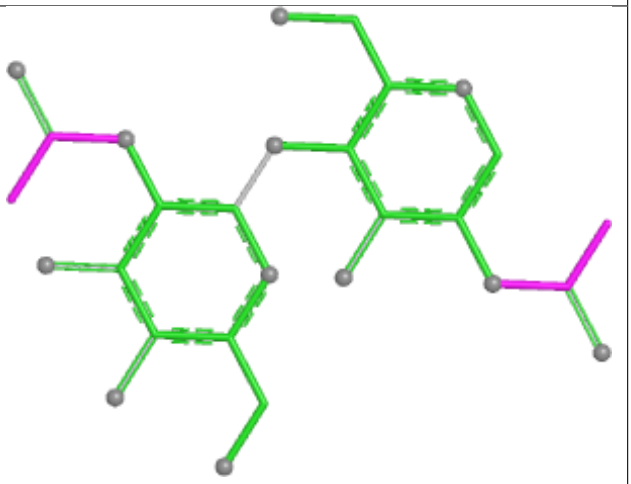


Rings

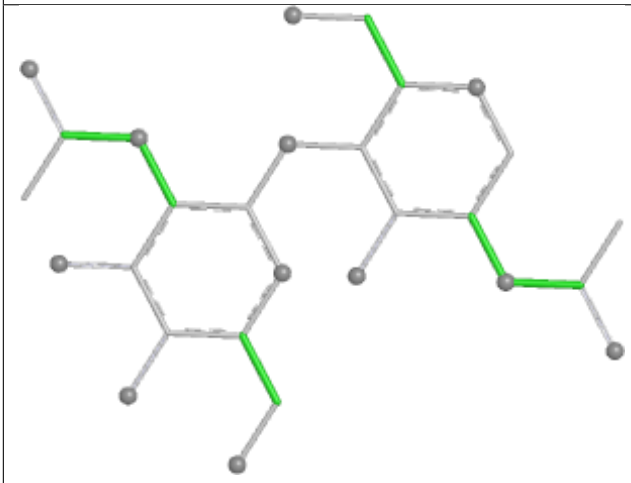
Oligosaccharide Chain W



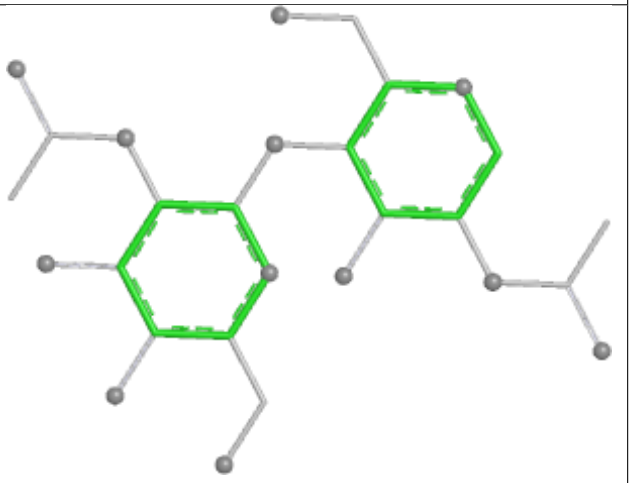
Bond lengths



Bond angles

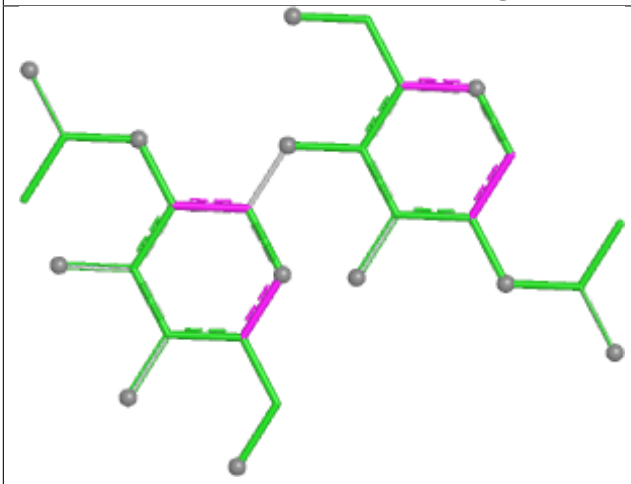


Torsions

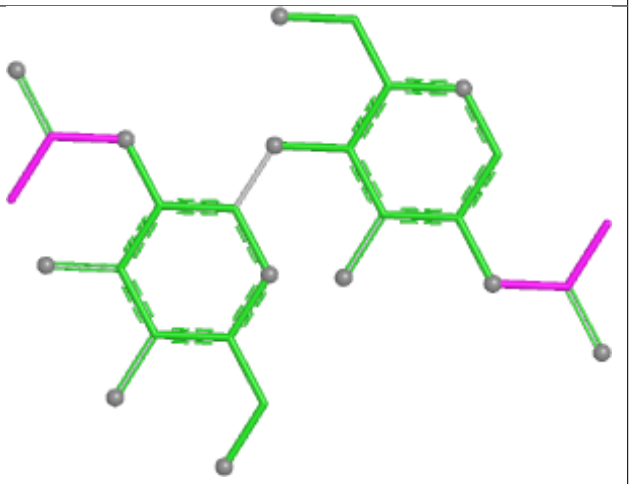


Rings

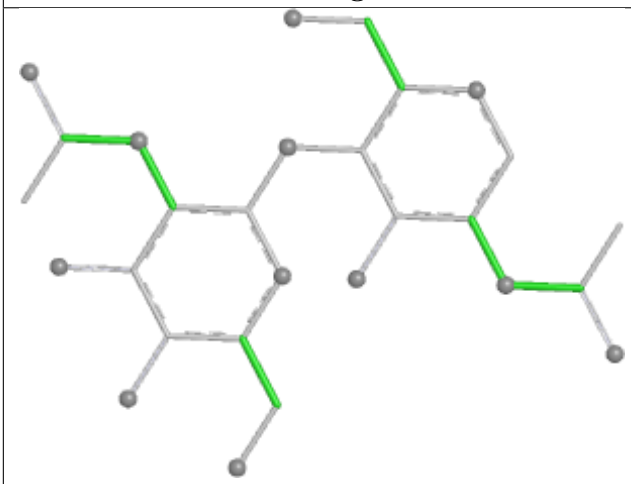
Oligosaccharide Chain X



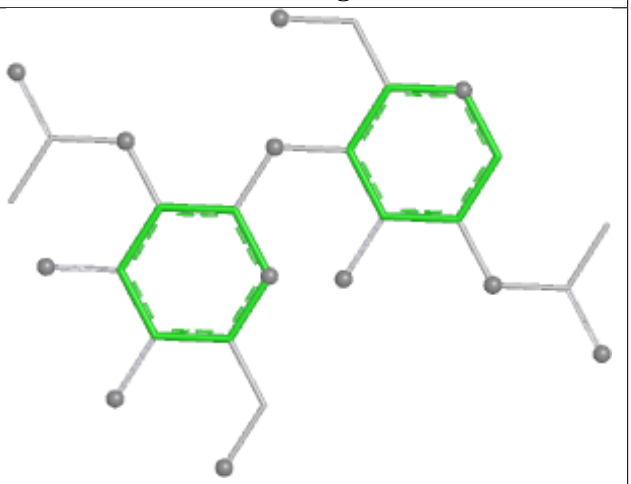
Bond lengths



Bond angles

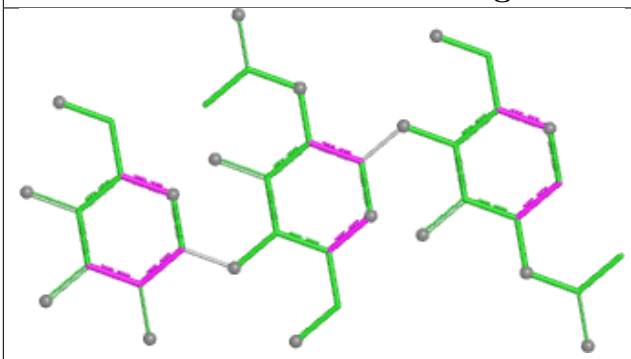


Torsions

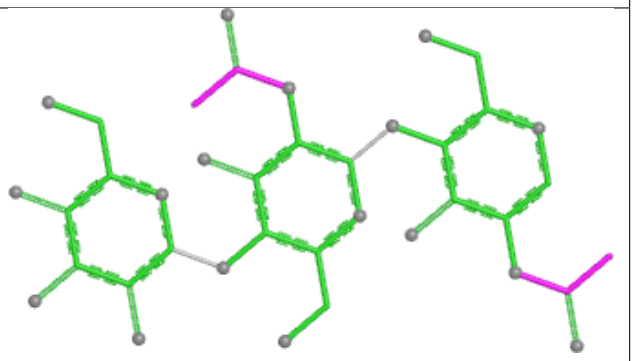


Rings

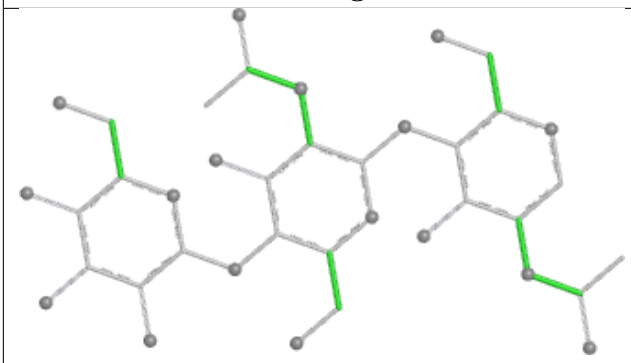
Oligosaccharide Chain K



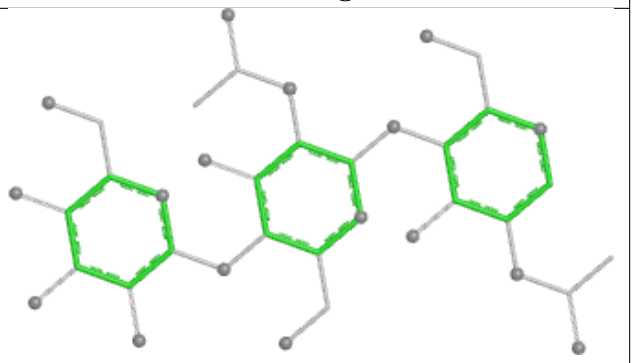
Bond lengths



Bond angles

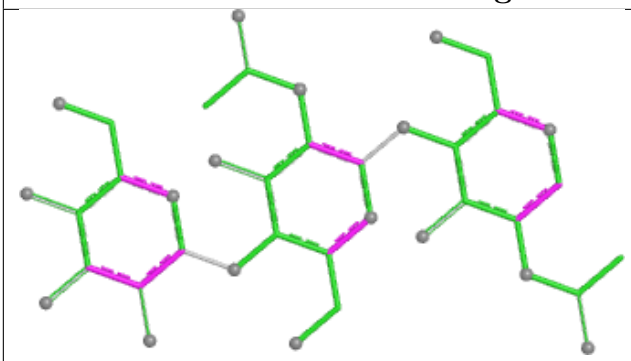


Torsions

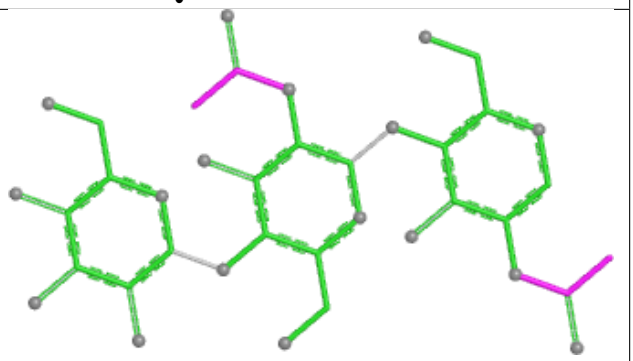


Rings

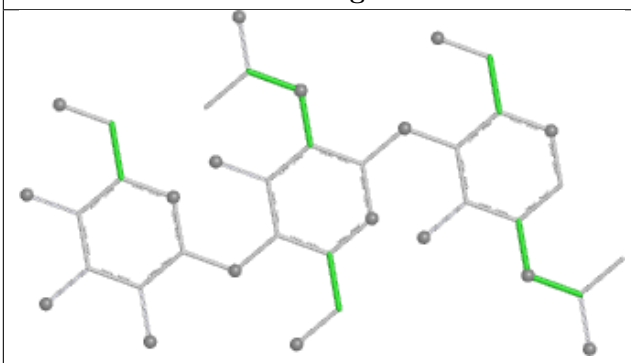
Oligosaccharide Chain Q



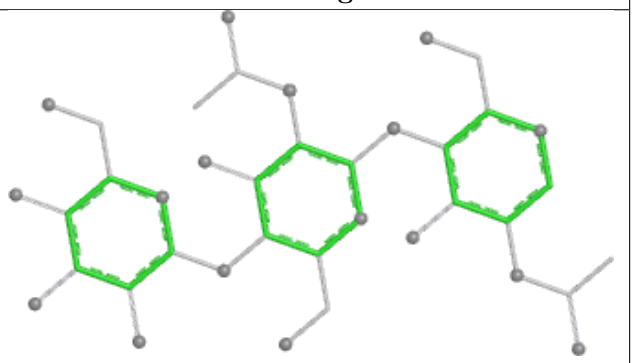
Bond lengths



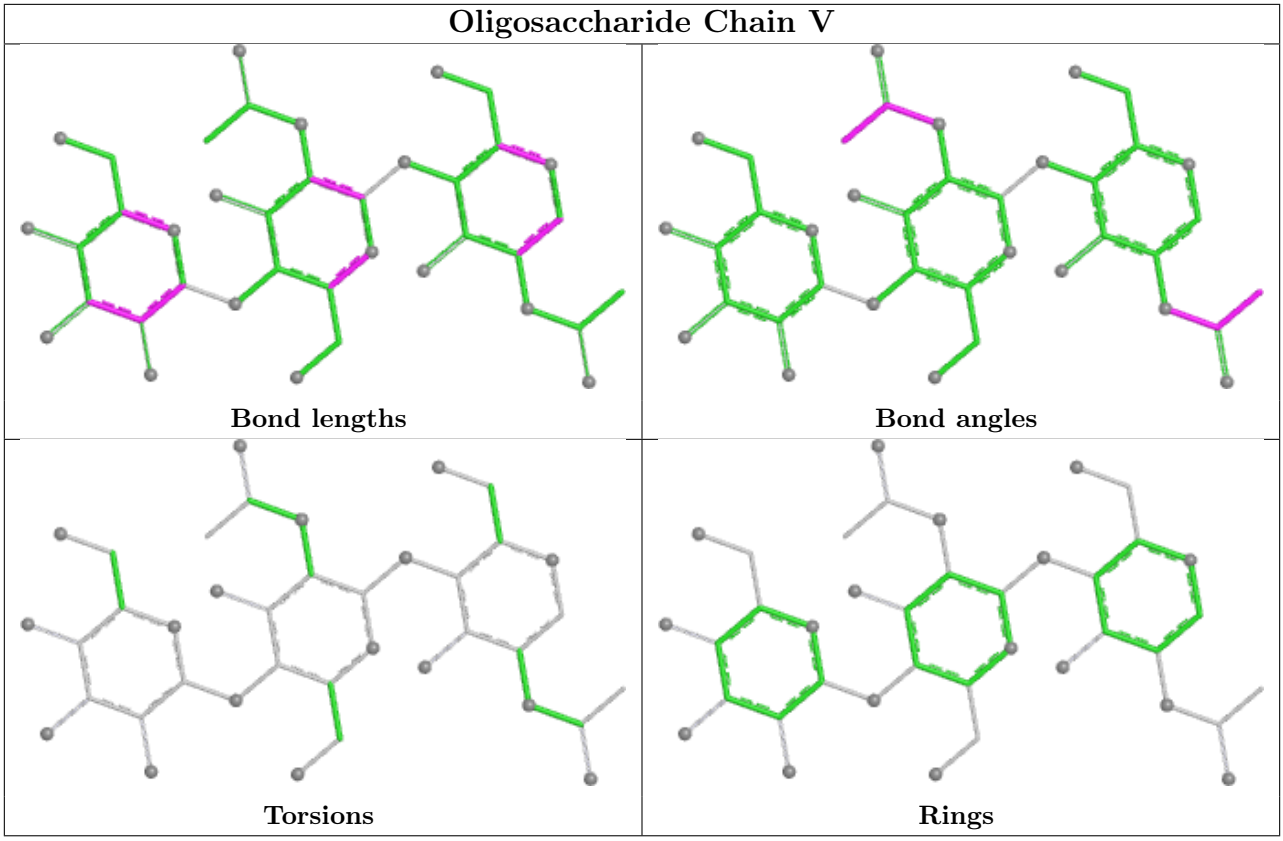
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

33 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	NAG	B	1304	1	14,14,15	1.59	2 (14%)	17,19,21	0.95	1 (5%)
6	NAG	A	1305	1	14,14,15	1.64	2 (14%)	17,19,21	0.85	0
6	NAG	E	1305	1	14,14,15	1.64	2 (14%)	17,19,21	0.85	0
6	NAG	B	1308	1	14,14,15	1.64	2 (14%)	17,19,21	0.91	1 (5%)
6	NAG	E	1301	1	14,14,15	1.66	2 (14%)	17,19,21	0.91	1 (5%)
6	NAG	B	1301	1	14,14,15	1.66	2 (14%)	17,19,21	0.91	1 (5%)
6	NAG	B	1303	1	14,14,15	1.74	2 (14%)	17,19,21	1.08	1 (5%)
6	NAG	B	1305	1	14,14,15	1.64	2 (14%)	17,19,21	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	NAG	A	1310	1	14,14,15	1.63	2 (14%)	17,19,21	0.94	0
6	NAG	A	1302	1	14,14,15	1.57	2 (14%)	17,19,21	0.98	1 (5%)
6	NAG	A	1311	1	14,14,15	1.78	3 (21%)	17,19,21	0.96	1 (5%)
6	NAG	A	1309	1	14,14,15	1.61	2 (14%)	17,19,21	0.99	1 (5%)
6	NAG	B	1311	1	14,14,15	1.78	3 (21%)	17,19,21	0.97	1 (5%)
6	NAG	E	1309	1	14,14,15	1.61	2 (14%)	17,19,21	0.99	1 (5%)
6	NAG	A	1307	1	14,14,15	1.60	2 (14%)	17,19,21	1.04	1 (5%)
6	NAG	A	1306	1	14,14,15	1.57	2 (14%)	17,19,21	1.01	1 (5%)
6	NAG	E	1304	1	14,14,15	1.57	2 (14%)	17,19,21	0.94	1 (5%)
6	NAG	E	1310	1	14,14,15	1.61	2 (14%)	17,19,21	0.94	0
6	NAG	E	1307	1	14,14,15	1.61	2 (14%)	17,19,21	1.05	1 (5%)
6	NAG	E	1308	1	14,14,15	1.65	2 (14%)	17,19,21	0.91	1 (5%)
6	NAG	B	1306	1	14,14,15	1.58	2 (14%)	17,19,21	1.01	1 (5%)
6	NAG	A	1301	1	14,14,15	1.65	2 (14%)	17,19,21	0.91	1 (5%)
6	NAG	A	1308	1	14,14,15	1.65	2 (14%)	17,19,21	0.92	1 (5%)
6	NAG	E	1306	1	14,14,15	1.56	2 (14%)	17,19,21	1.01	1 (5%)
6	NAG	A	1303	1	14,14,15	1.74	2 (14%)	17,19,21	1.08	1 (5%)
6	NAG	E	1303	1	14,14,15	1.74	2 (14%)	17,19,21	1.08	1 (5%)
6	NAG	B	1302	1	14,14,15	1.57	2 (14%)	17,19,21	0.98	1 (5%)
6	NAG	B	1309	1	14,14,15	1.61	2 (14%)	17,19,21	1.00	1 (5%)
6	NAG	E	1302	1	14,14,15	1.57	2 (14%)	17,19,21	0.98	1 (5%)
6	NAG	E	1311	1	14,14,15	1.78	3 (21%)	17,19,21	0.96	0
6	NAG	A	1304	1	14,14,15	1.57	2 (14%)	17,19,21	0.95	1 (5%)
6	NAG	B	1307	1	14,14,15	1.61	2 (14%)	17,19,21	1.04	1 (5%)
6	NAG	B	1310	1	14,14,15	1.62	2 (14%)	17,19,21	0.94	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1305	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1301	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1310	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1302	1	-	1/6/23/26	0/1/1/1
6	NAG	A	1311	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1311	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1309	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1310	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1307	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1308	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1308	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1302	1	-	1/6/23/26	0/1/1/1
6	NAG	B	1309	1	-	0/6/23/26	0/1/1/1
6	NAG	E	1302	1	-	1/6/23/26	0/1/1/1
6	NAG	E	1311	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1307	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1310	1	-	0/6/23/26	0/1/1/1

All (69) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	1311	NAG	C1-C2	5.23	1.59	1.52
6	A	1311	NAG	C1-C2	5.20	1.59	1.52
6	B	1311	NAG	C1-C2	5.18	1.59	1.52
6	A	1303	NAG	C1-C2	4.92	1.59	1.52
6	B	1303	NAG	C1-C2	4.91	1.59	1.52
6	E	1303	NAG	C1-C2	4.90	1.59	1.52
6	B	1301	NAG	C1-C2	4.82	1.58	1.52
6	E	1301	NAG	C1-C2	4.81	1.58	1.52
6	A	1301	NAG	C1-C2	4.78	1.58	1.52
6	A	1310	NAG	C1-C2	4.73	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	1310	NAG	C1-C2	4.68	1.58	1.52
6	E	1310	NAG	C1-C2	4.66	1.58	1.52
6	E	1308	NAG	C1-C2	4.63	1.58	1.52
6	A	1308	NAG	C1-C2	4.63	1.58	1.52
6	B	1305	NAG	C1-C2	4.62	1.58	1.52
6	E	1305	NAG	C1-C2	4.62	1.58	1.52
6	A	1305	NAG	C1-C2	4.61	1.58	1.52
6	B	1308	NAG	C1-C2	4.58	1.58	1.52
6	B	1307	NAG	C1-C2	4.50	1.58	1.52
6	A	1309	NAG	C1-C2	4.49	1.58	1.52
6	E	1307	NAG	C1-C2	4.48	1.58	1.52
6	B	1309	NAG	C1-C2	4.47	1.58	1.52
6	E	1309	NAG	C1-C2	4.47	1.58	1.52
6	A	1307	NAG	C1-C2	4.43	1.58	1.52
6	B	1304	NAG	C1-C2	4.34	1.58	1.52
6	E	1302	NAG	C1-C2	4.30	1.58	1.52
6	B	1302	NAG	C1-C2	4.29	1.58	1.52
6	A	1302	NAG	C1-C2	4.29	1.58	1.52
6	A	1304	NAG	C1-C2	4.27	1.58	1.52
6	E	1304	NAG	C1-C2	4.25	1.58	1.52
6	B	1306	NAG	C1-C2	4.10	1.57	1.52
6	A	1306	NAG	C1-C2	4.09	1.57	1.52
6	E	1306	NAG	C1-C2	4.07	1.57	1.52
6	B	1303	NAG	O5-C5	2.68	1.48	1.43
6	E	1303	NAG	O5-C5	2.64	1.48	1.43
6	A	1303	NAG	O5-C5	2.63	1.48	1.43
6	A	1304	NAG	O5-C5	2.58	1.48	1.43
6	B	1304	NAG	O5-C5	2.57	1.48	1.43
6	A	1305	NAG	O5-C5	2.57	1.48	1.43
6	E	1305	NAG	O5-C5	2.56	1.48	1.43
6	E	1304	NAG	O5-C5	2.55	1.48	1.43
6	B	1305	NAG	O5-C5	2.55	1.48	1.43
6	E	1308	NAG	O5-C5	2.54	1.48	1.43
6	B	1308	NAG	O5-C5	2.51	1.48	1.43
6	A	1308	NAG	O5-C5	2.50	1.48	1.43
6	A	1307	NAG	O5-C5	2.49	1.48	1.43
6	B	1307	NAG	O5-C5	2.47	1.48	1.43
6	B	1309	NAG	O5-C5	2.47	1.48	1.43
6	E	1309	NAG	O5-C5	2.47	1.48	1.43
6	A	1309	NAG	O5-C5	2.46	1.48	1.43
6	E	1307	NAG	O5-C5	2.46	1.48	1.43
6	E	1306	NAG	O5-C5	2.44	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	1306	NAG	O5-C5	2.43	1.48	1.43
6	A	1306	NAG	O5-C5	2.43	1.48	1.43
6	A	1301	NAG	O5-C5	2.42	1.48	1.43
6	B	1301	NAG	O5-C5	2.41	1.48	1.43
6	E	1301	NAG	O5-C5	2.41	1.48	1.43
6	B	1302	NAG	O5-C5	2.38	1.48	1.43
6	E	1302	NAG	O5-C5	2.36	1.48	1.43
6	A	1302	NAG	O5-C5	2.35	1.48	1.43
6	E	1310	NAG	O5-C5	2.33	1.48	1.43
6	B	1310	NAG	O5-C5	2.33	1.48	1.43
6	A	1310	NAG	O5-C5	2.31	1.47	1.43
6	A	1311	NAG	O5-C5	2.26	1.47	1.43
6	B	1311	NAG	O5-C5	2.25	1.47	1.43
6	E	1311	NAG	O5-C5	2.24	1.47	1.43
6	A	1311	NAG	C3-C2	2.15	1.57	1.52
6	E	1311	NAG	C3-C2	2.14	1.57	1.52
6	B	1311	NAG	C3-C2	2.14	1.57	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	E	1307	NAG	C8-C7-N2	2.71	120.61	116.12
6	A	1307	NAG	C8-C7-N2	2.69	120.57	116.12
6	B	1307	NAG	C8-C7-N2	2.68	120.57	116.12
6	B	1303	NAG	C8-C7-N2	2.60	120.44	116.12
6	A	1303	NAG	C8-C7-N2	2.60	120.43	116.12
6	E	1303	NAG	C8-C7-N2	2.60	120.43	116.12
6	B	1309	NAG	C8-C7-N2	2.50	120.27	116.12
6	A	1309	NAG	C8-C7-N2	2.49	120.25	116.12
6	E	1309	NAG	C8-C7-N2	2.49	120.25	116.12
6	E	1306	NAG	C8-C7-N2	2.34	120.00	116.12
6	A	1306	NAG	C8-C7-N2	2.33	119.98	116.12
6	B	1306	NAG	C8-C7-N2	2.33	119.98	116.12
6	A	1302	NAG	C8-C7-N2	2.20	119.77	116.12
6	B	1302	NAG	C8-C7-N2	2.20	119.77	116.12
6	E	1302	NAG	C8-C7-N2	2.19	119.74	116.12
6	A	1308	NAG	C8-C7-N2	2.17	119.72	116.12
6	B	1301	NAG	C8-C7-N2	2.17	119.71	116.12
6	E	1308	NAG	C8-C7-N2	2.16	119.71	116.12
6	B	1308	NAG	C8-C7-N2	2.16	119.70	116.12
6	A	1301	NAG	C8-C7-N2	2.16	119.70	116.12
6	E	1301	NAG	C8-C7-N2	2.16	119.69	116.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	1304	NAG	C8-C7-N2	2.12	119.64	116.12
6	E	1304	NAG	C8-C7-N2	2.12	119.63	116.12
6	A	1304	NAG	C8-C7-N2	2.11	119.61	116.12
6	B	1311	NAG	C8-C7-N2	2.01	119.44	116.12
6	A	1311	NAG	C8-C7-N2	2.01	119.44	116.12

There are no chirality outliers.

All (3) torsion outliers are listed below:

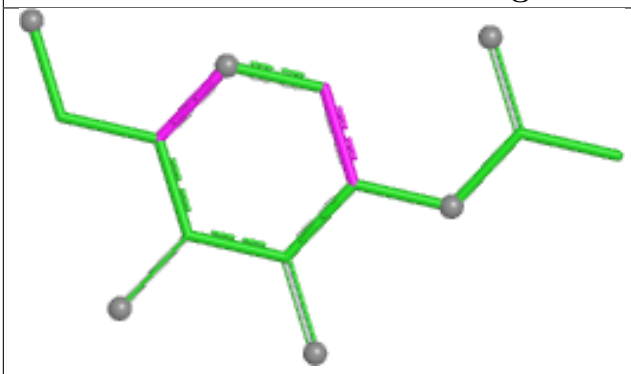
Mol	Chain	Res	Type	Atoms
6	E	1302	NAG	C4-C5-C6-O6
6	B	1302	NAG	C4-C5-C6-O6
6	A	1302	NAG	C4-C5-C6-O6

There are no ring outliers.

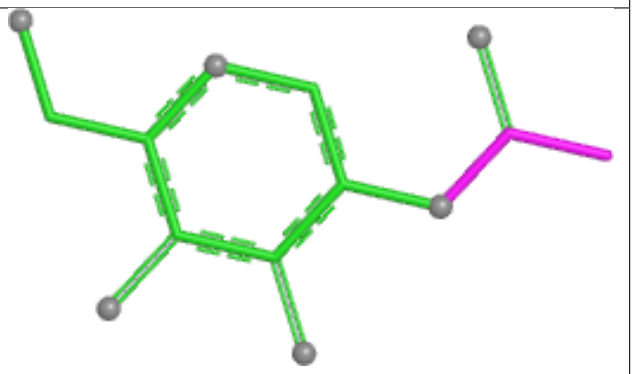
No monomer is involved in short contacts.

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

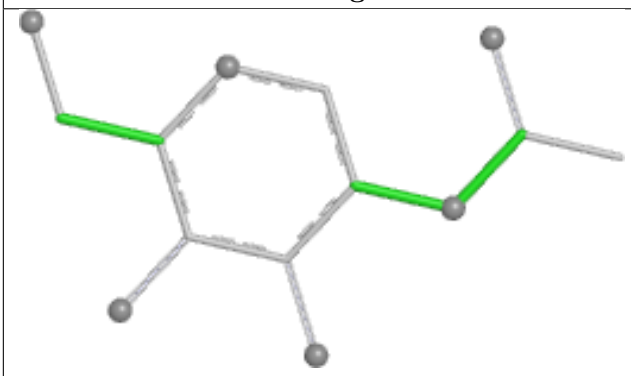
Ligand NAG B 1304



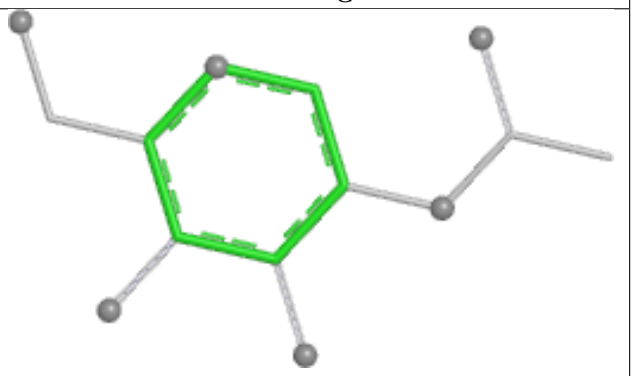
Bond lengths



Bond angles

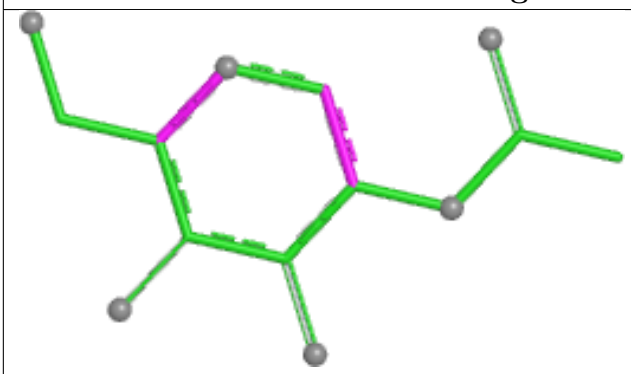


Torsions

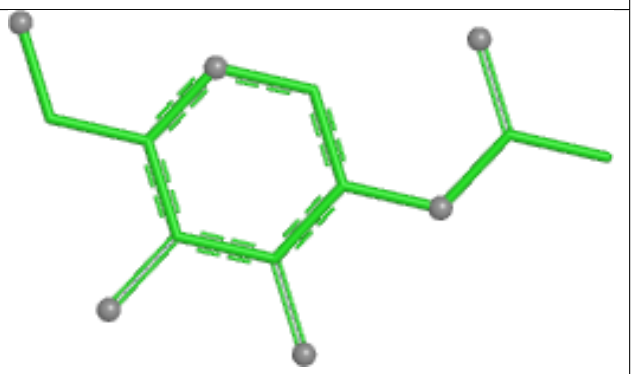


Rings

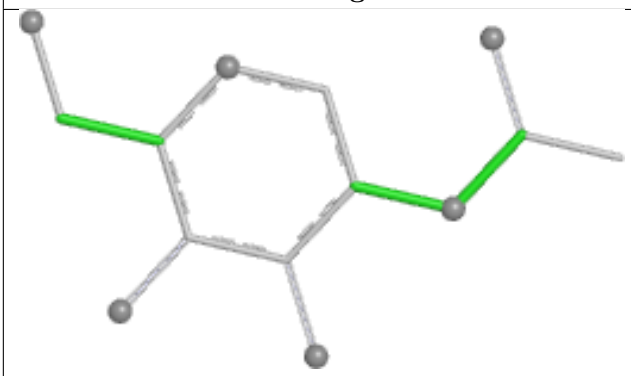
Ligand NAG A 1305



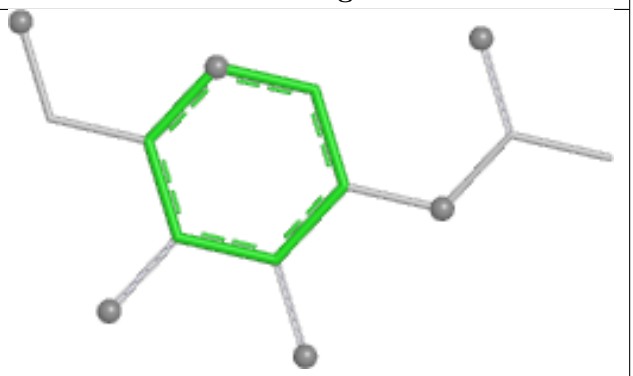
Bond lengths



Bond angles

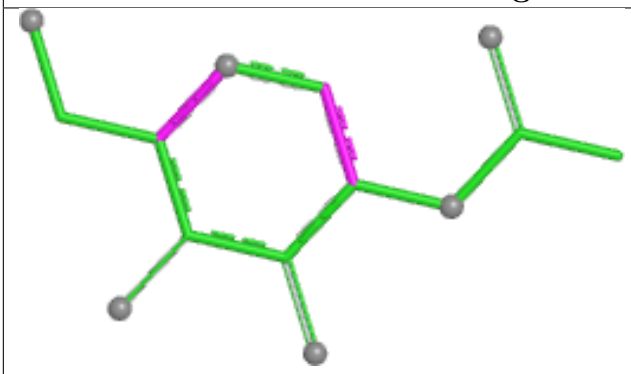


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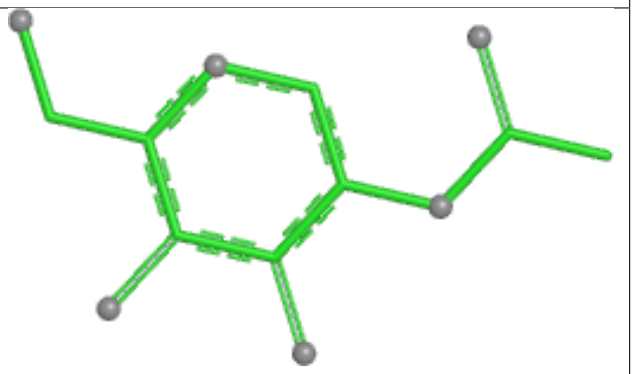


Rings

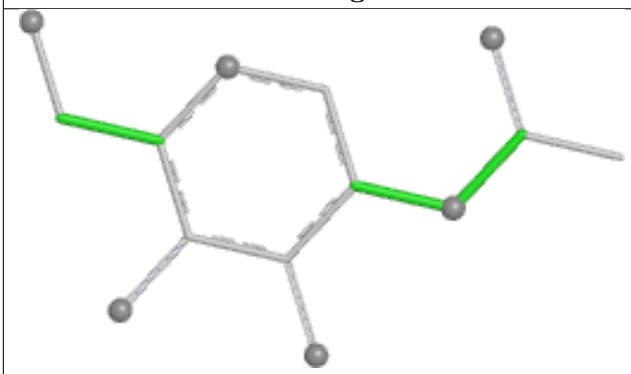
Ligand NAG E 1305



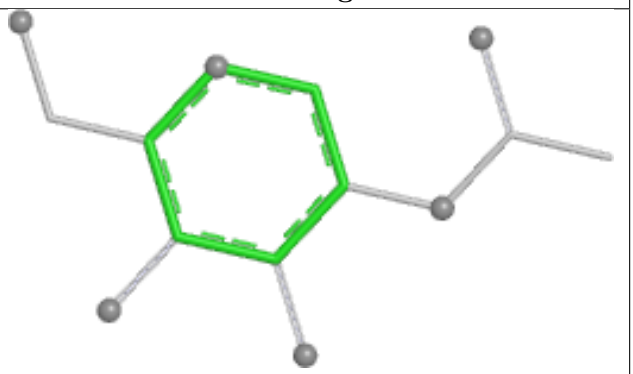
Bond lengths



Bond angles

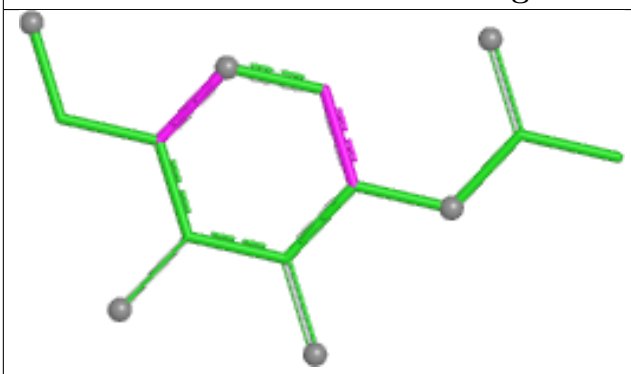


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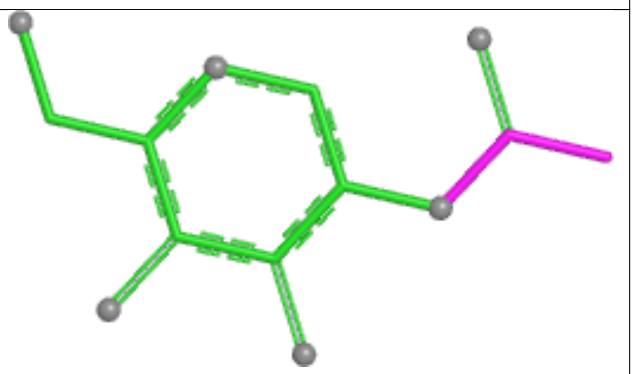


Rings

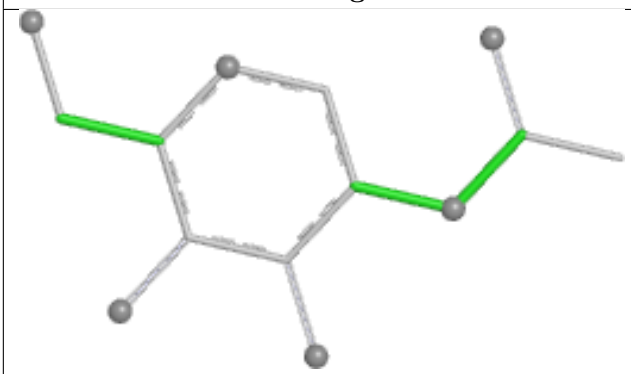
Ligand NAG B 1308



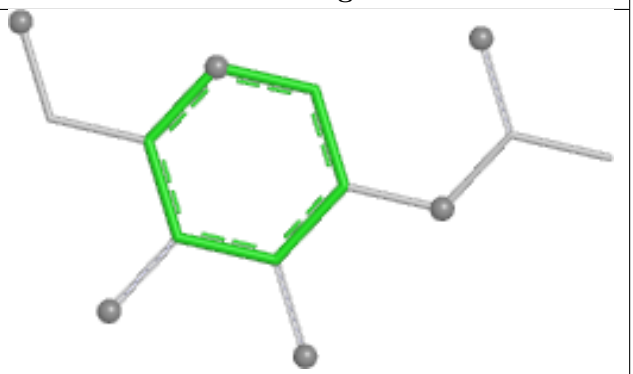
Bond lengths



Bond angles

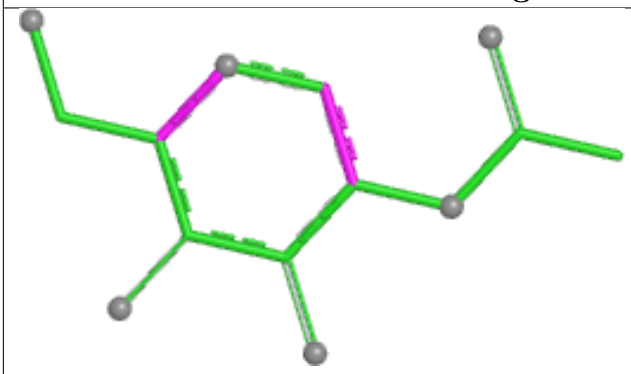


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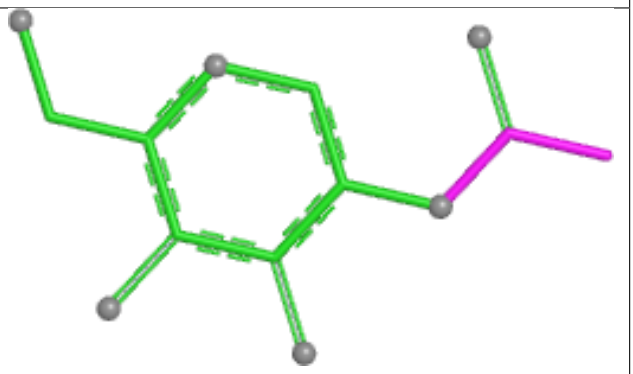


Rings

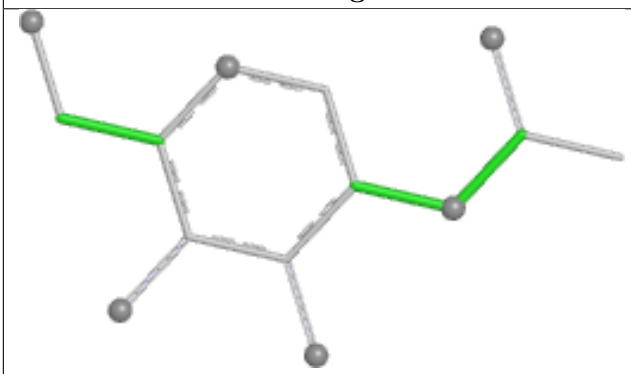
Ligand NAG E 1301



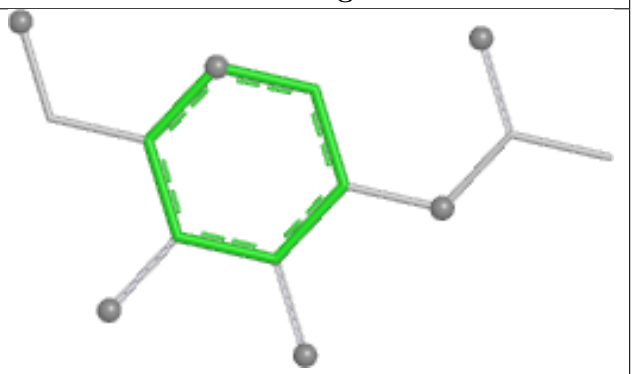
Bond lengths



Bond angles

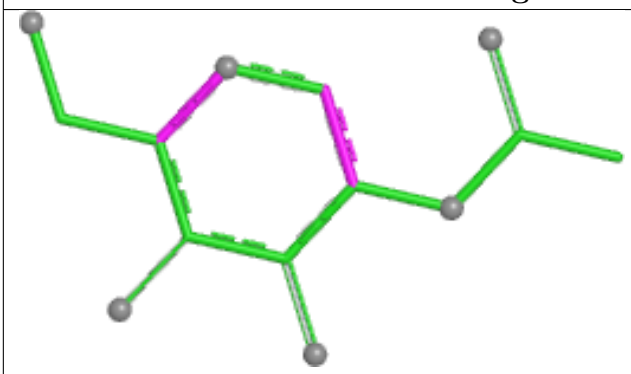


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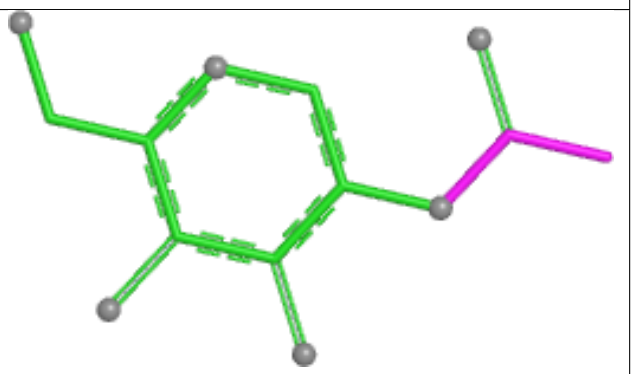


Rings

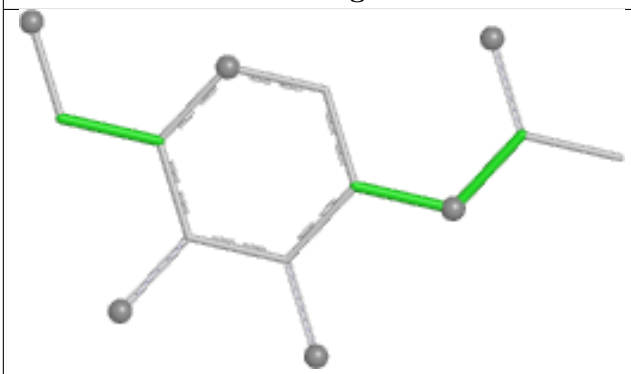
Ligand NAG B 1301



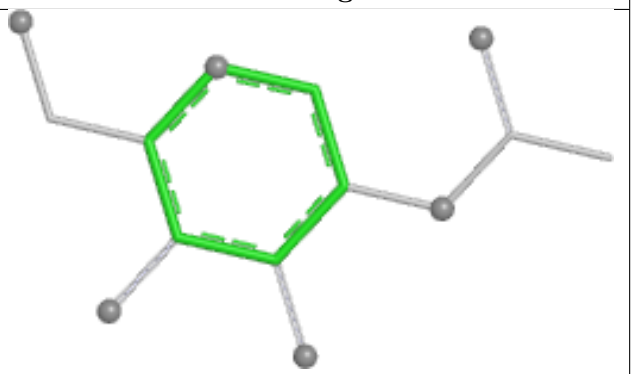
Bond lengths



Bond angles

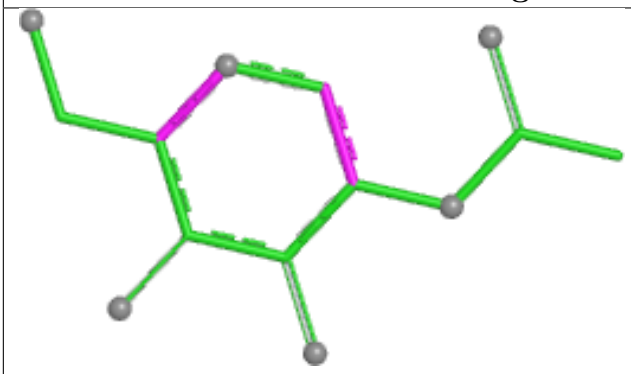


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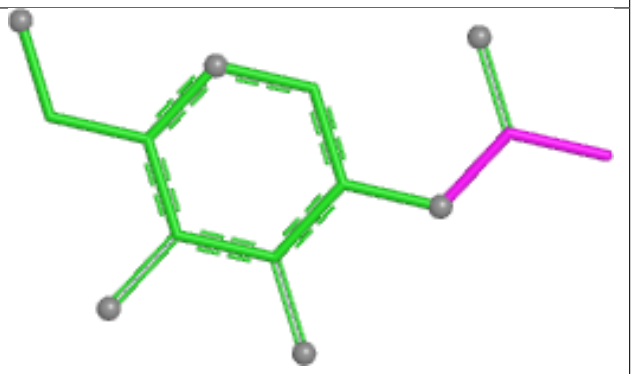


Rings

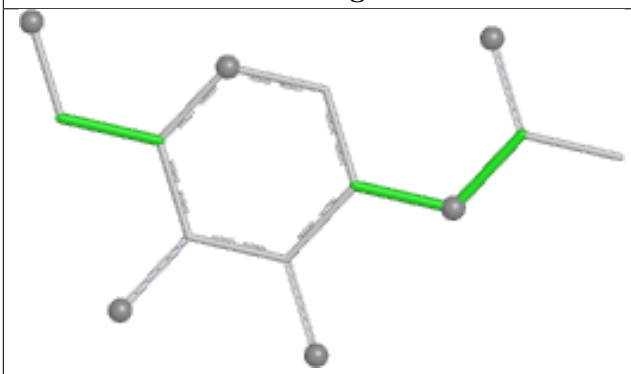
Ligand NAG B 1303



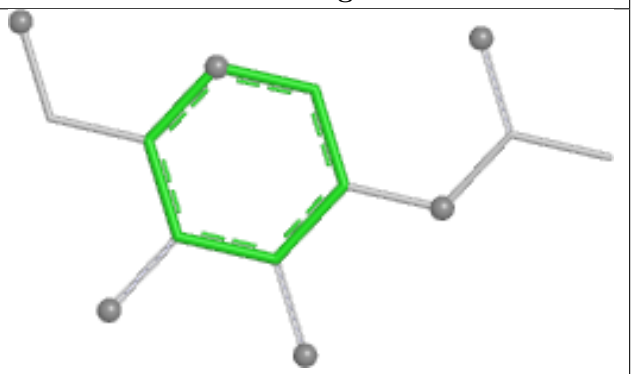
Bond lengths



Bond angles

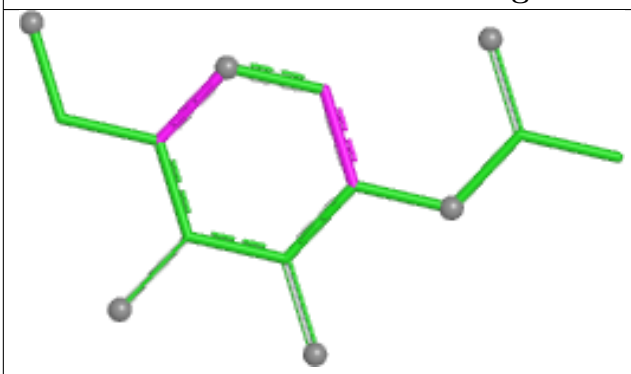


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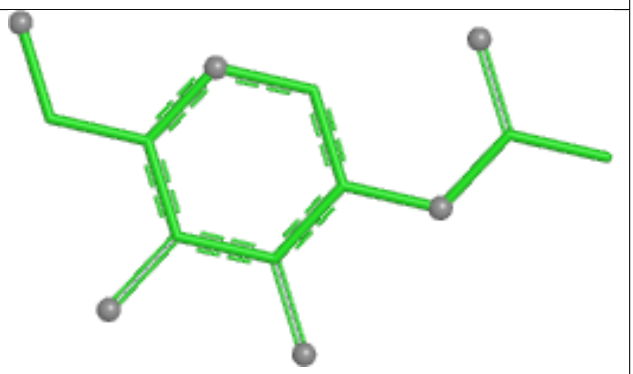


Rings

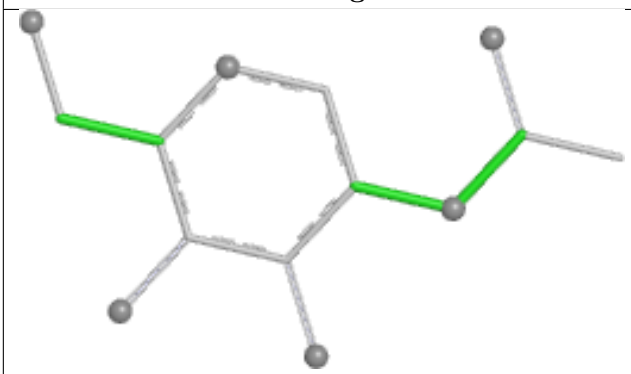
Ligand NAG B 1305



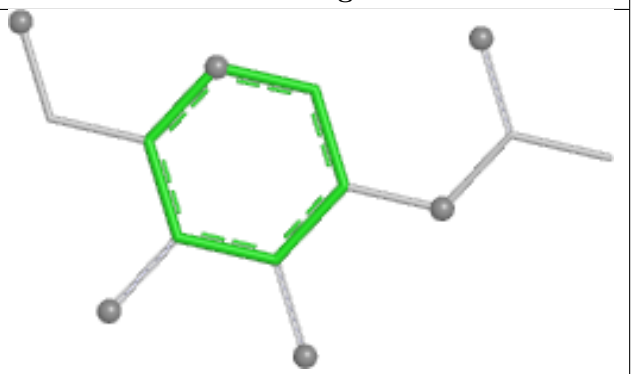
Bond lengths



Bond angles

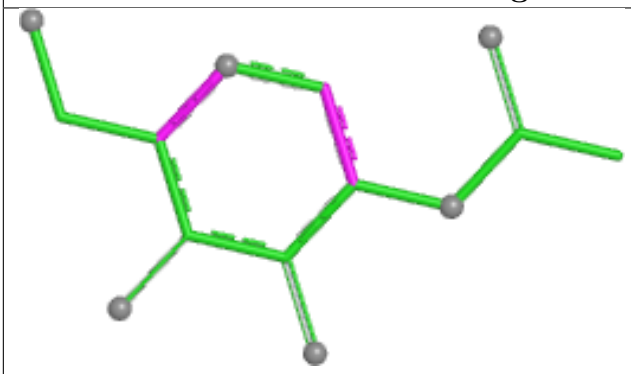


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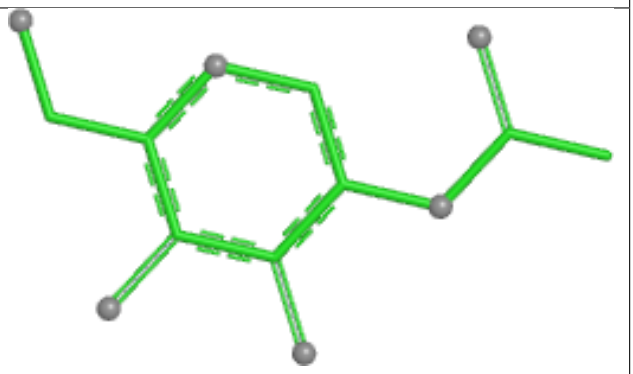


Rings

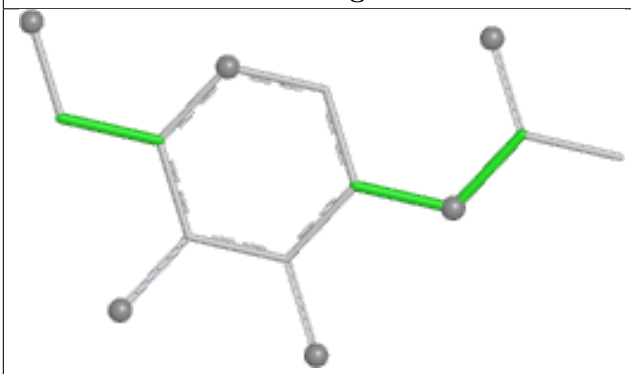
Ligand NAG A 1310



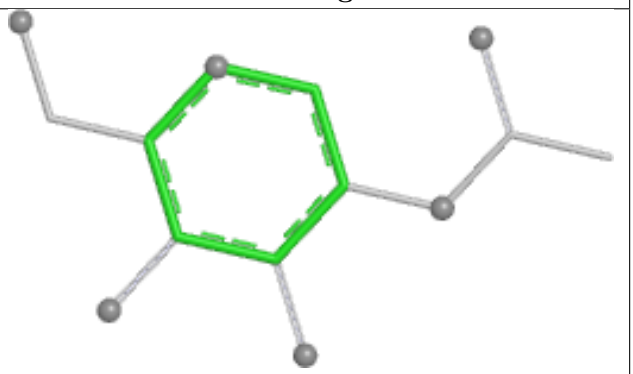
Bond lengths



Bond angles

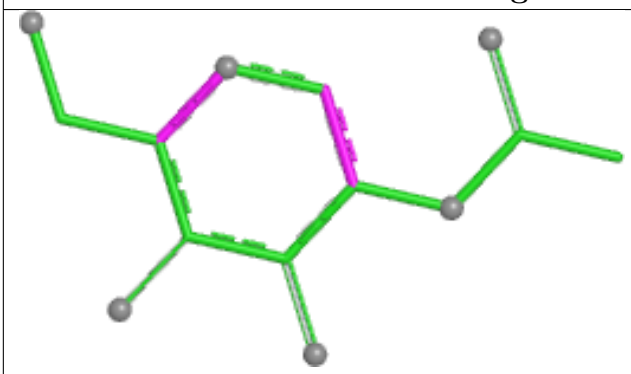


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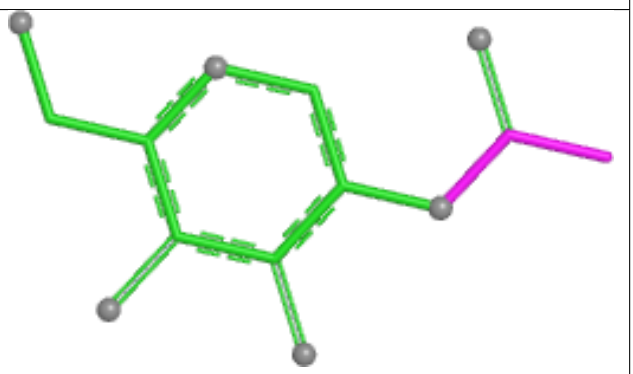


Rings

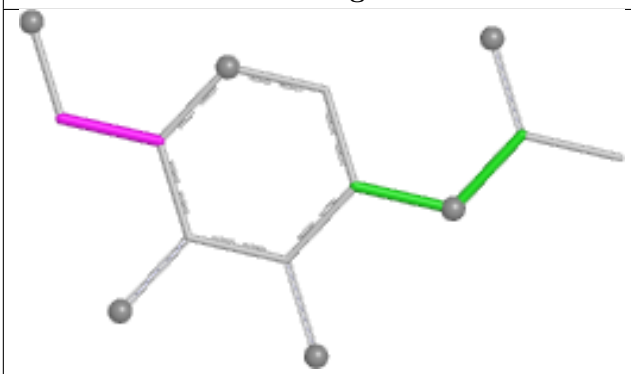
Ligand NAG A 1302



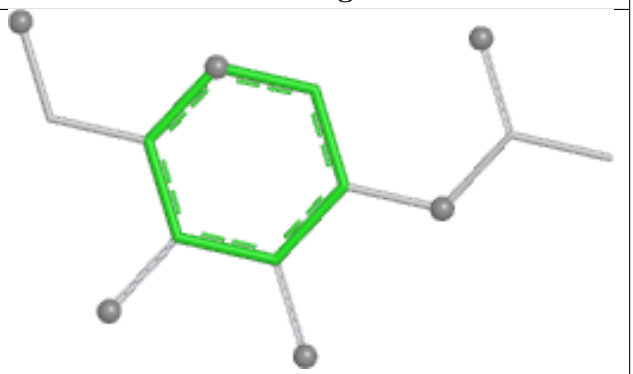
Bond lengths



Bond angles

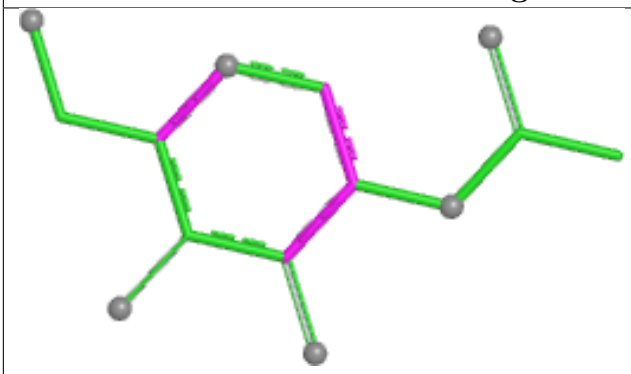


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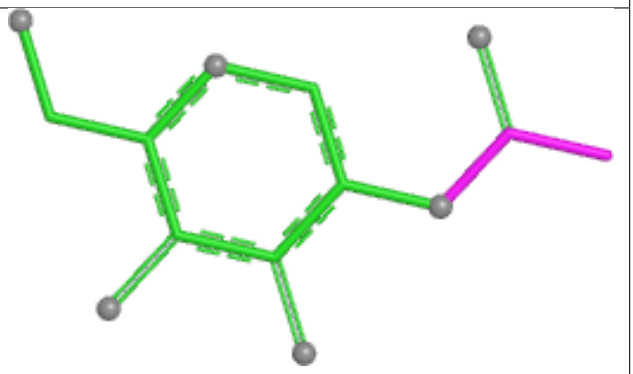


Rings

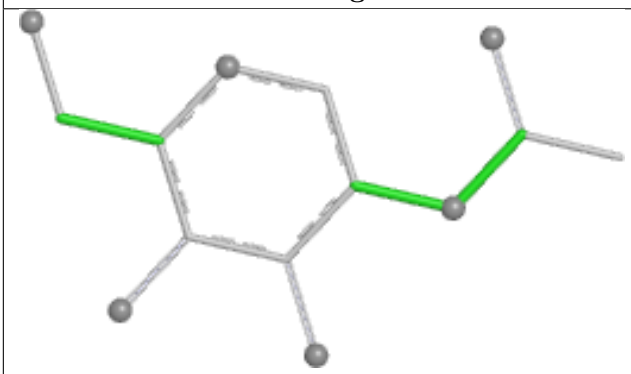
Ligand NAG A 1311



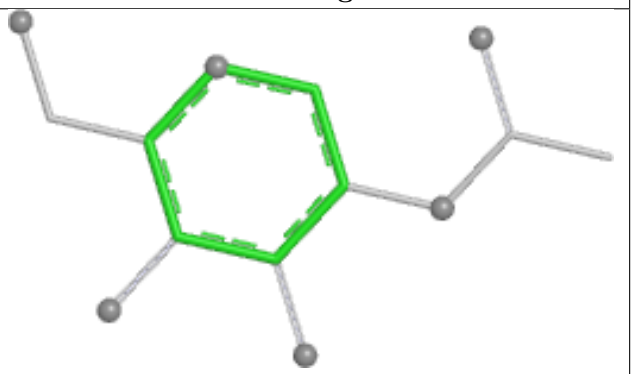
Bond lengths



Bond angles

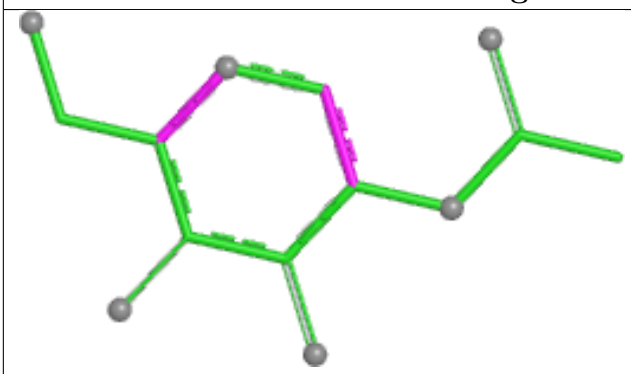


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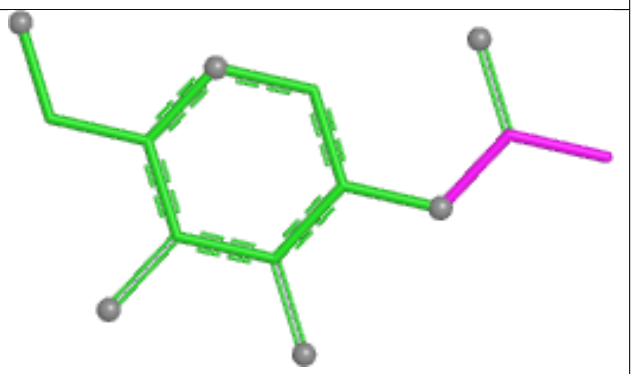


Rings

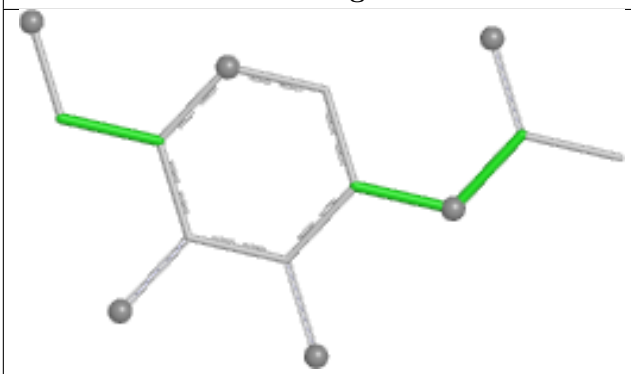
Ligand NAG A 1309



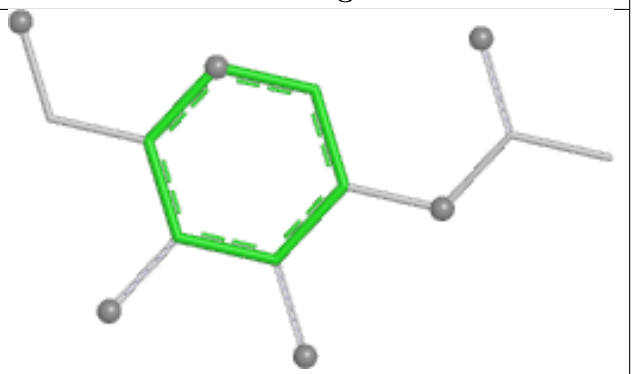
Bond lengths



Bond angles

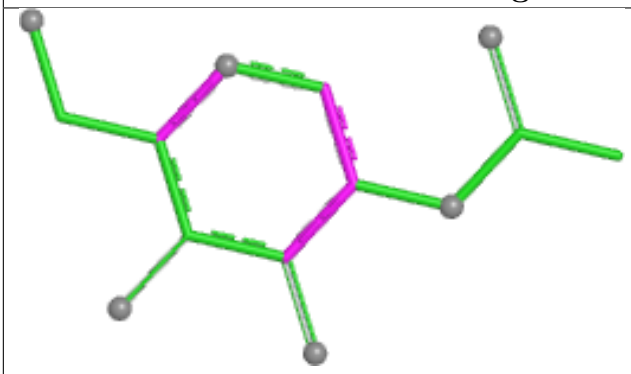


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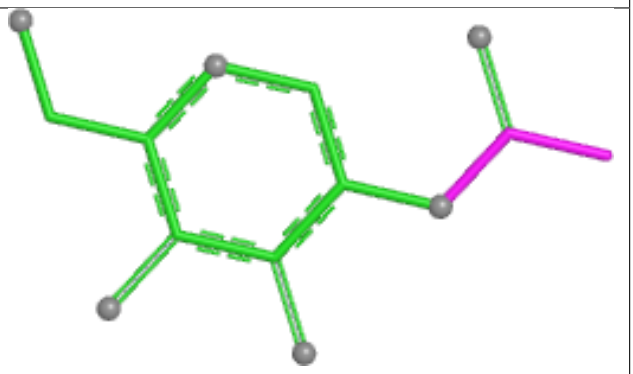


Rings

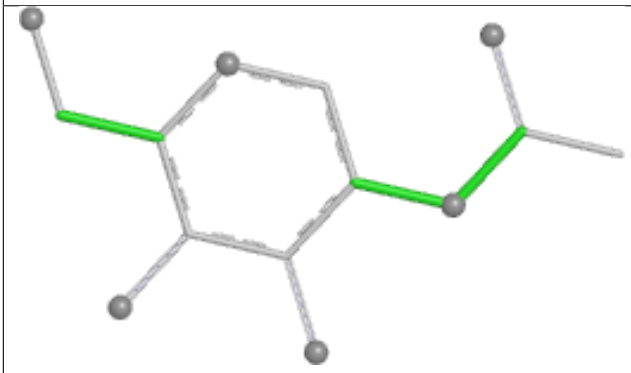
Ligand NAG B 1311



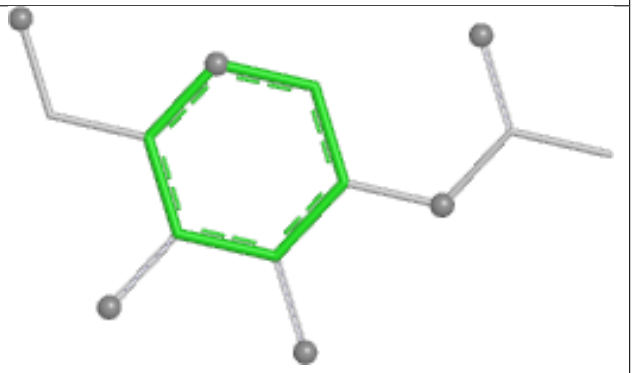
Bond lengths



Bond angles

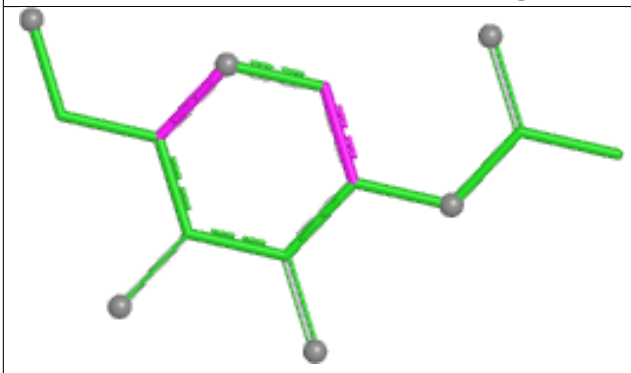


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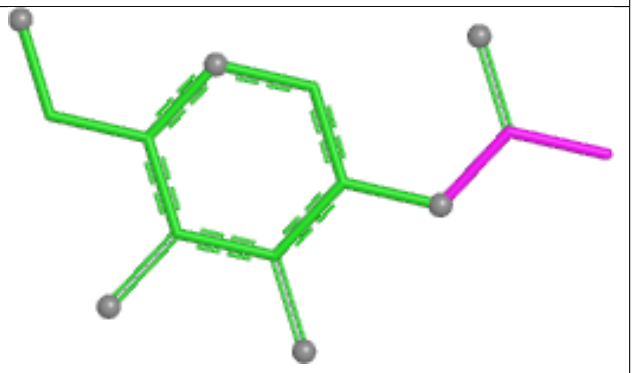


Rings

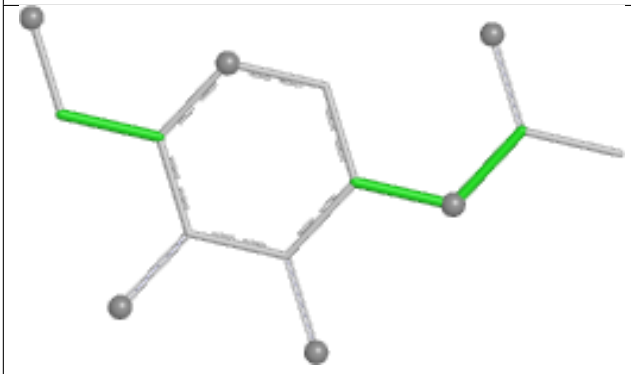
Ligand NAG E 1309



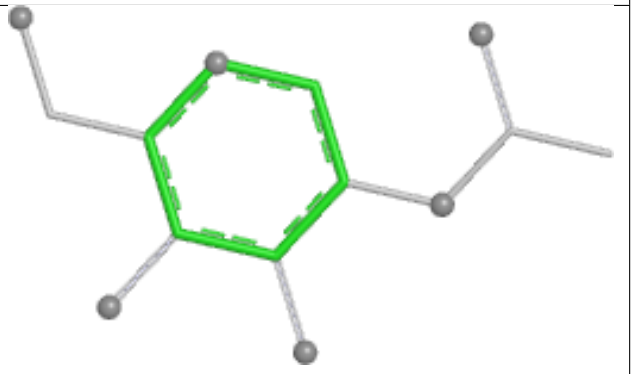
Bond lengths



Bond angles

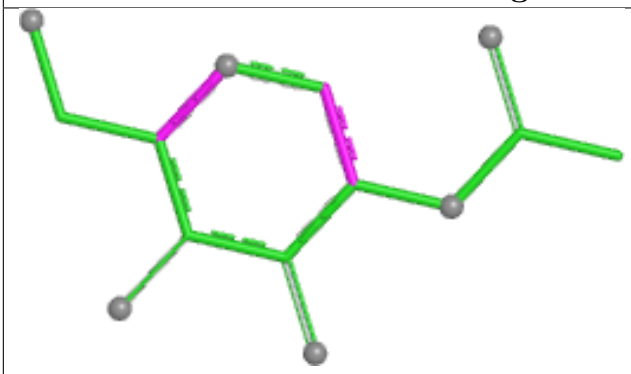


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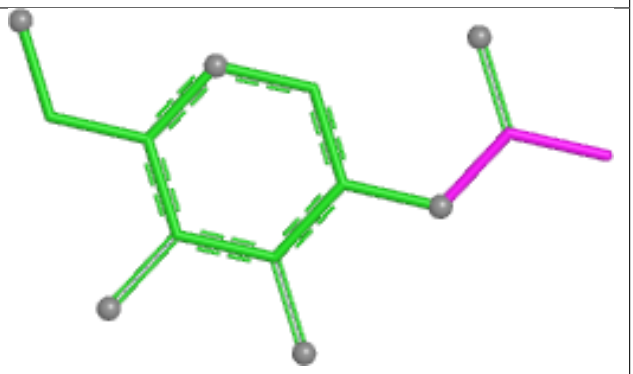


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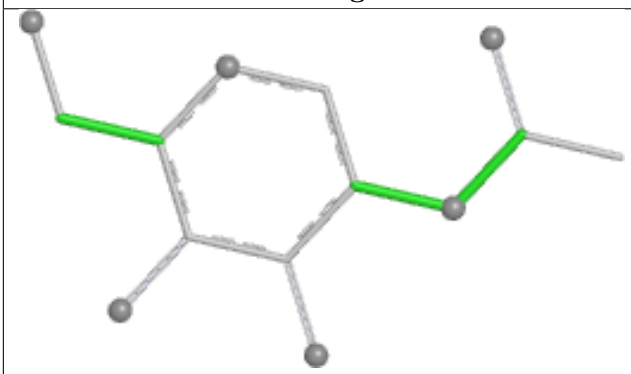
Ligand NAG A 1307



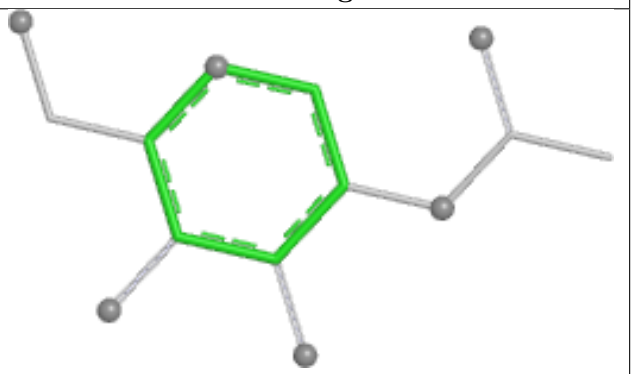
Bond lengths



Bond angles

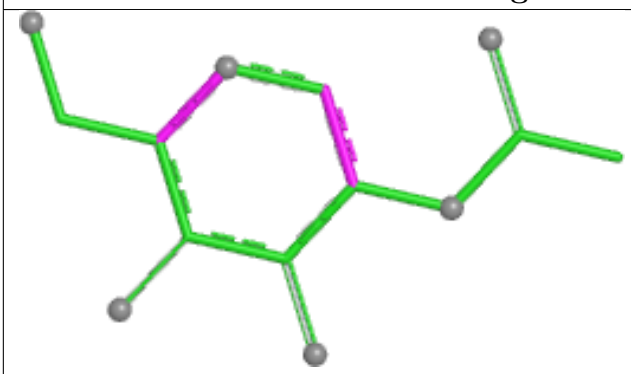


Torsions

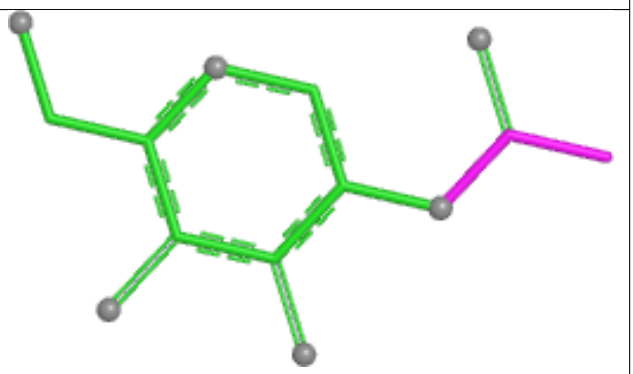


Rings

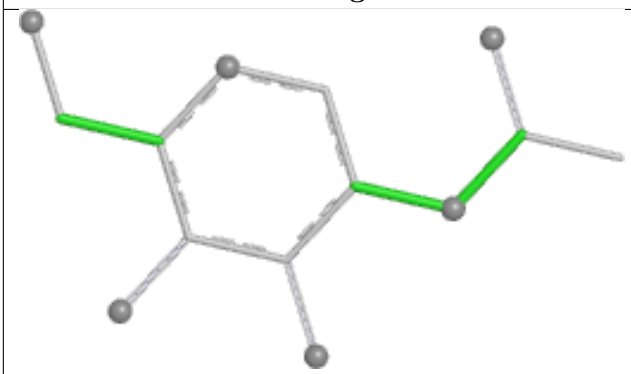
Ligand NAG A 1306



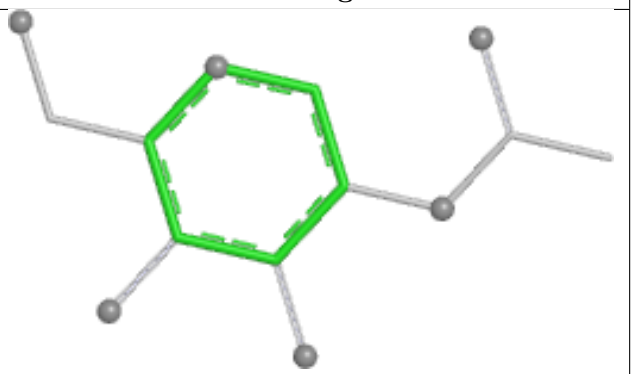
Bond lengths



Bond angles

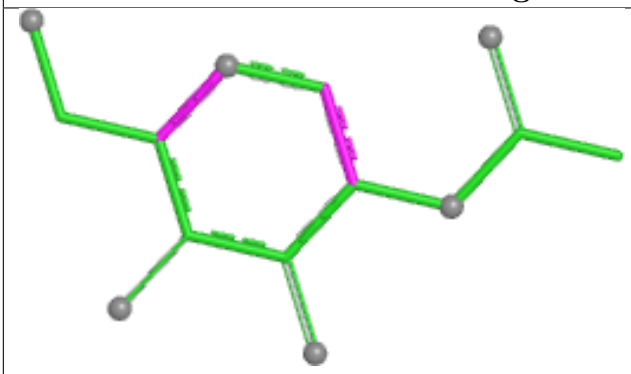


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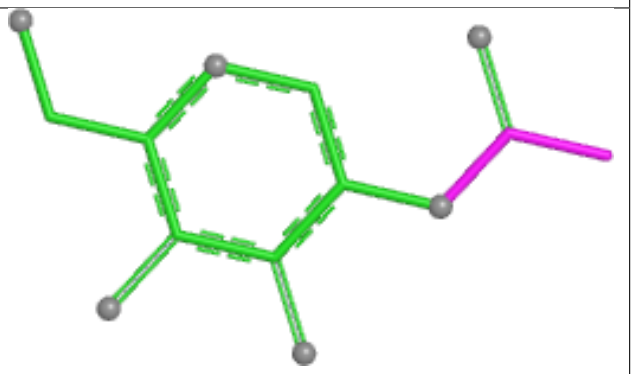


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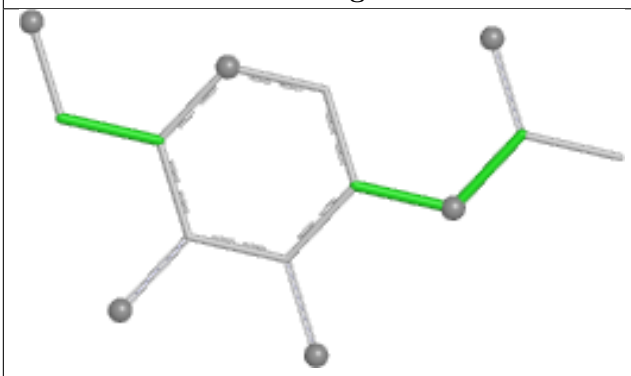
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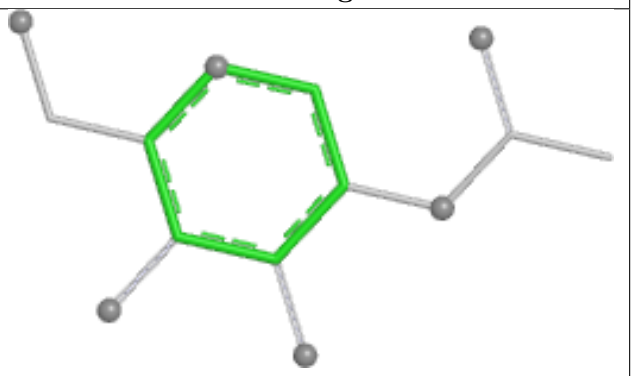
Bond lengths



Bond angles

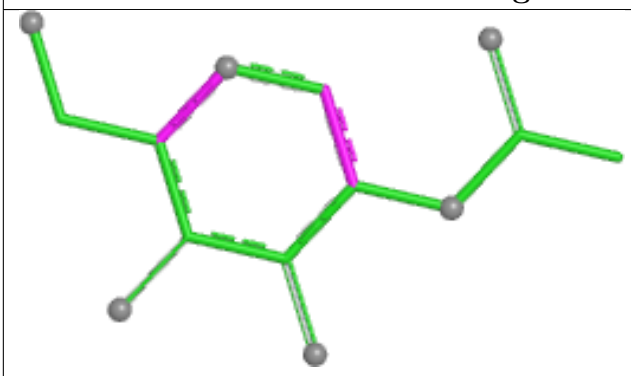


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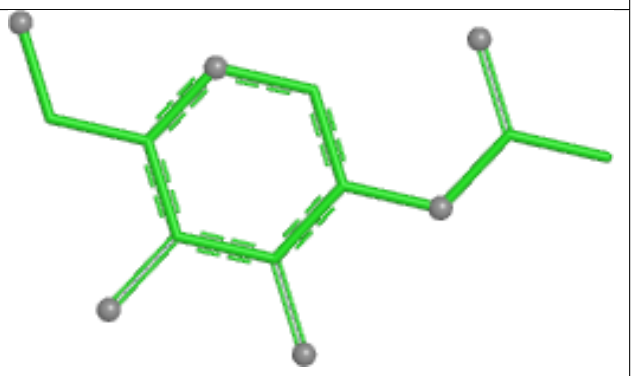


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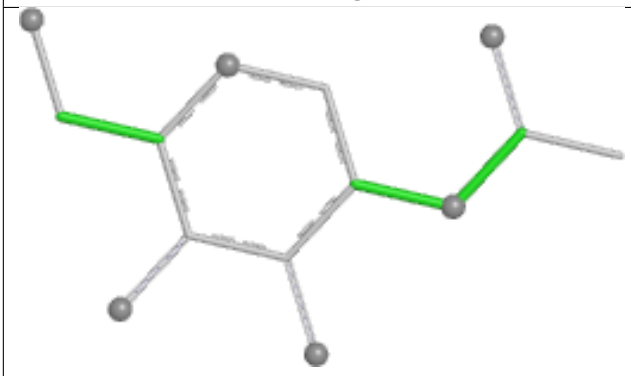
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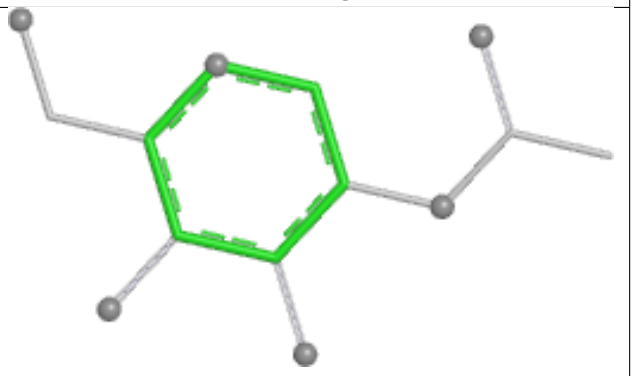
Bond lengths



Bond angles

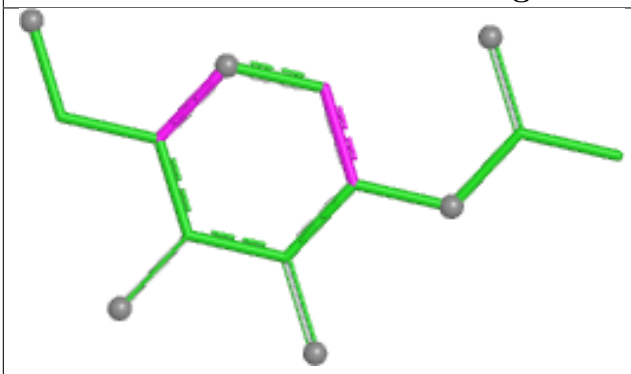


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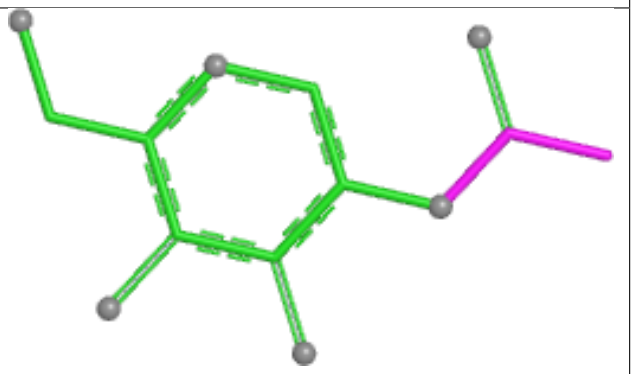


Rings

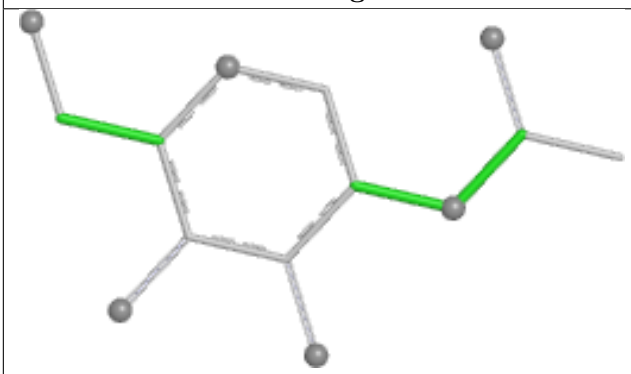
Ligand NAG E 1307



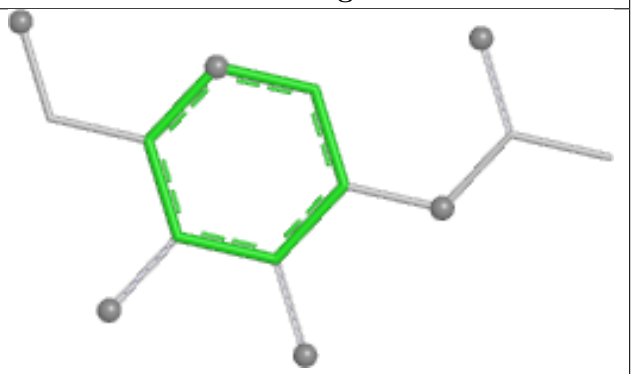
Bond lengths



Bond angles

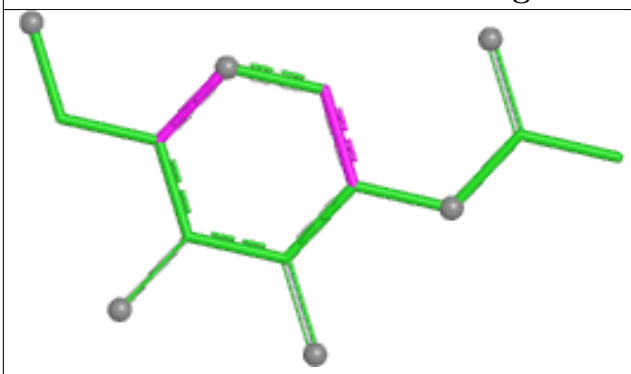


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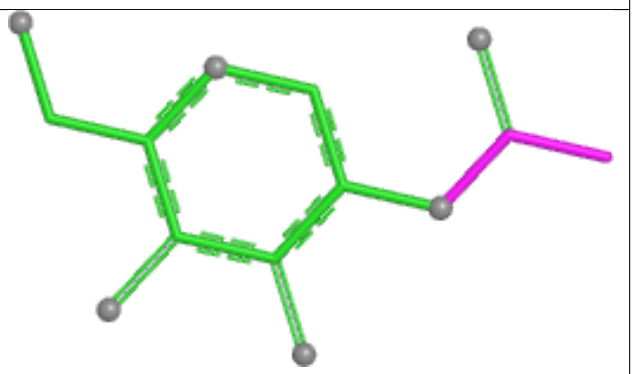


Rings

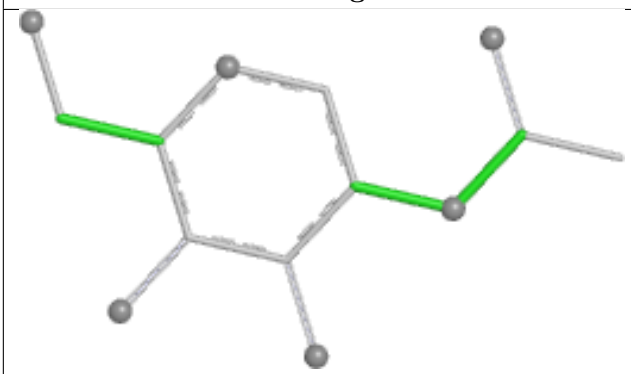
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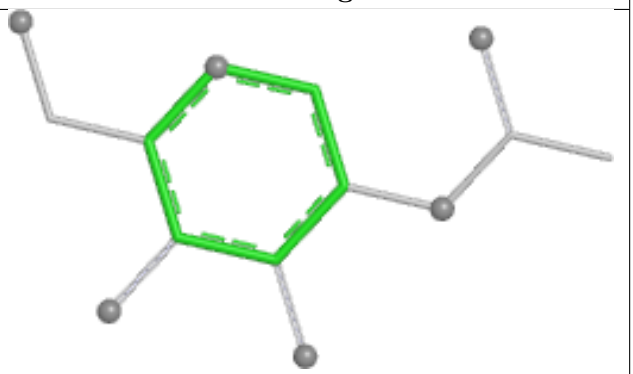
Bond lengths



Bond angles

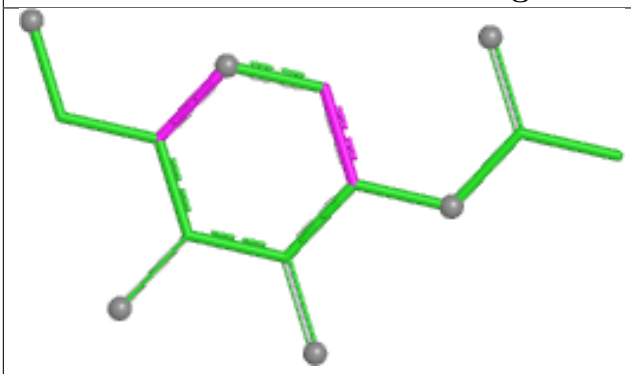


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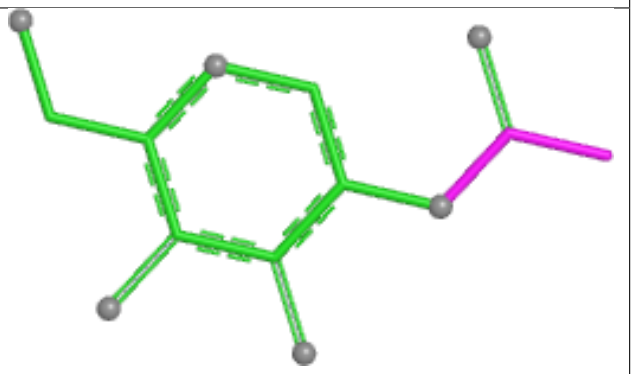


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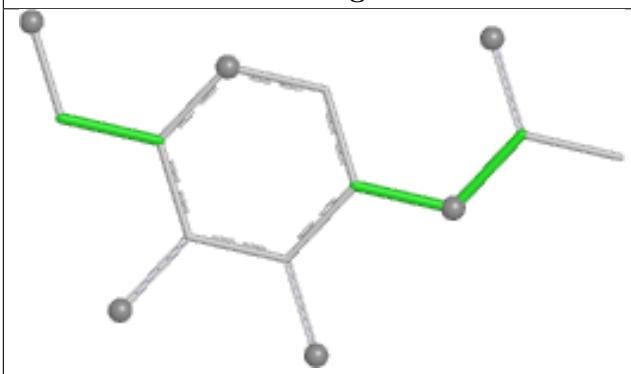
Ligand NAG B 1306



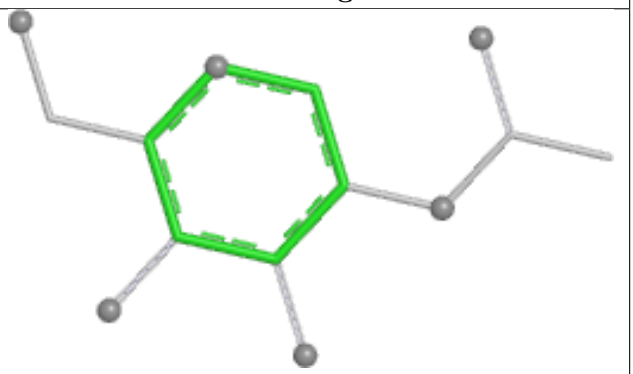
Bond lengths



Bond angles

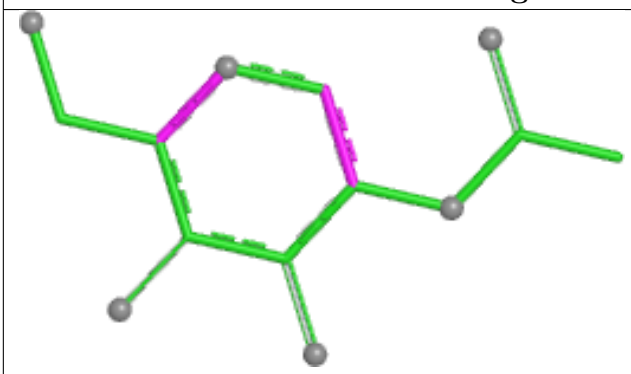


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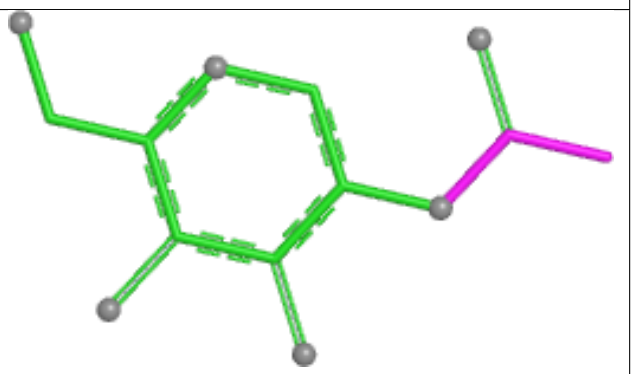


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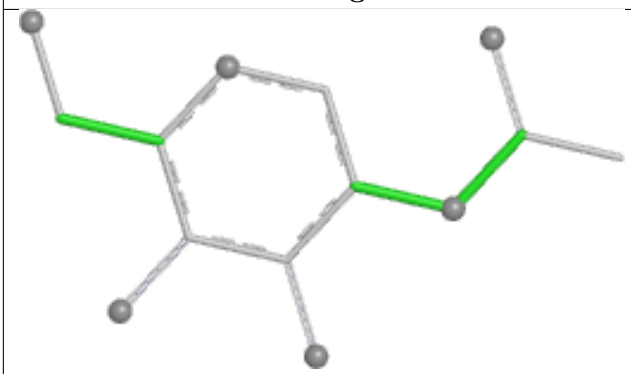
Ligand NAG A 1301



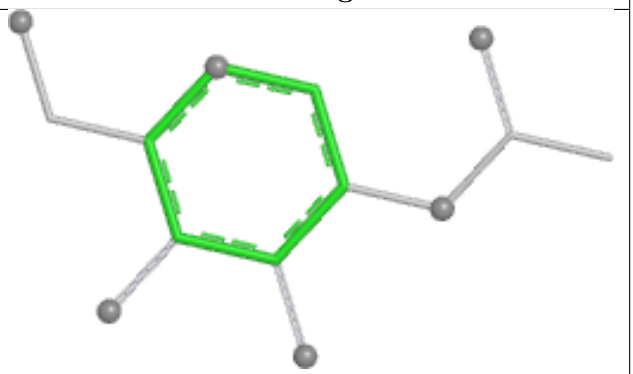
Bond lengths



Bond angles

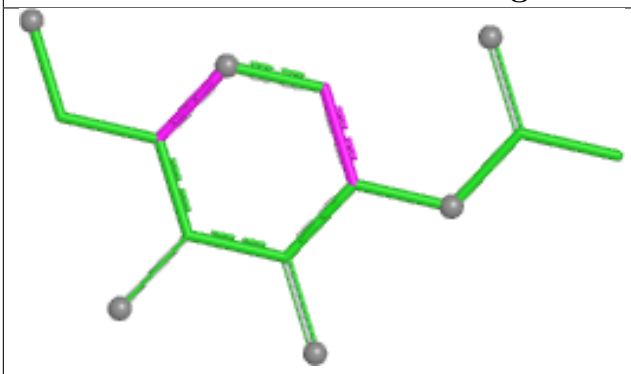


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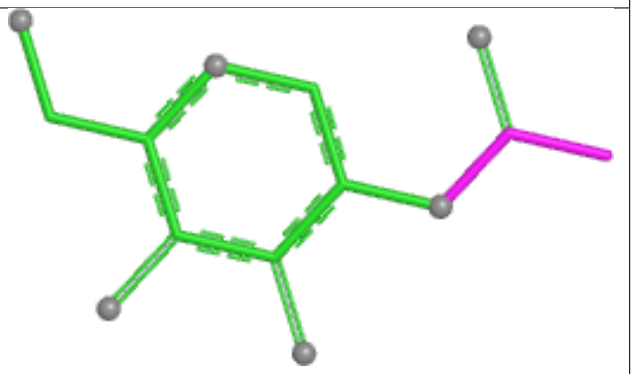


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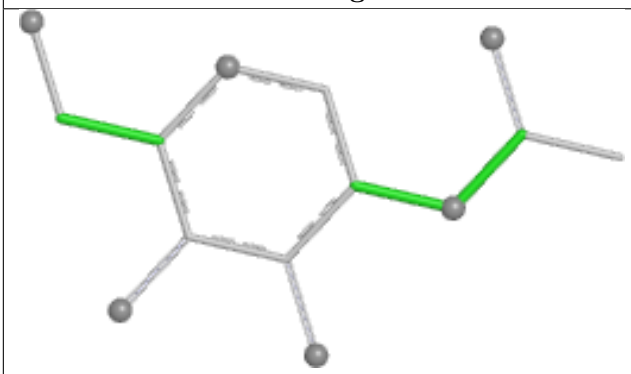
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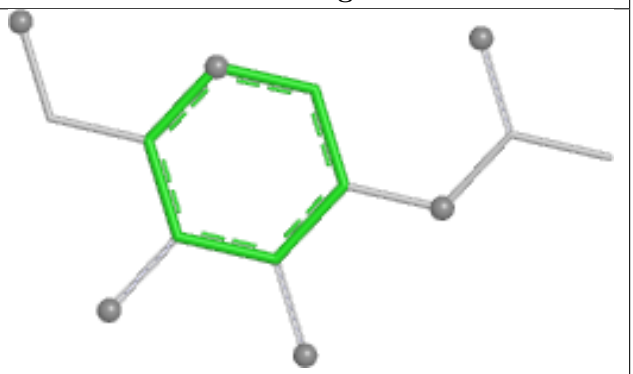
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Bond angles

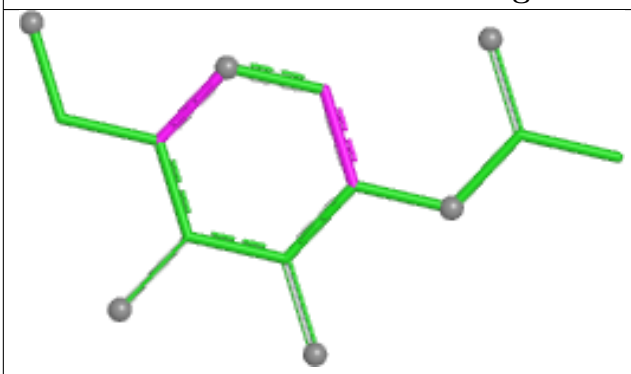


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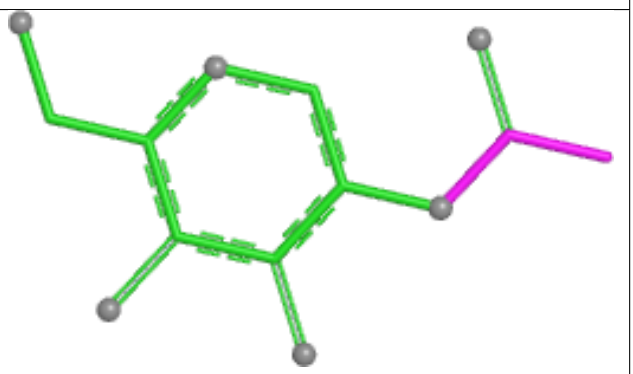


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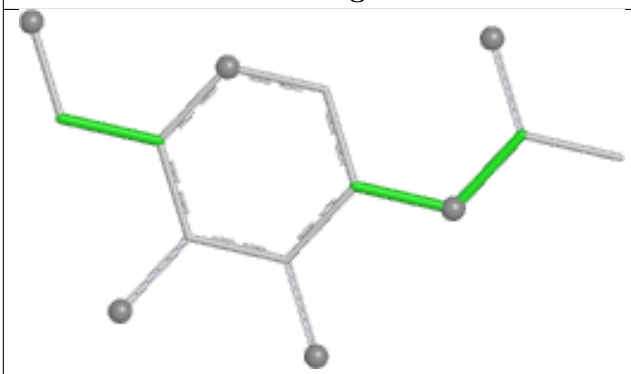
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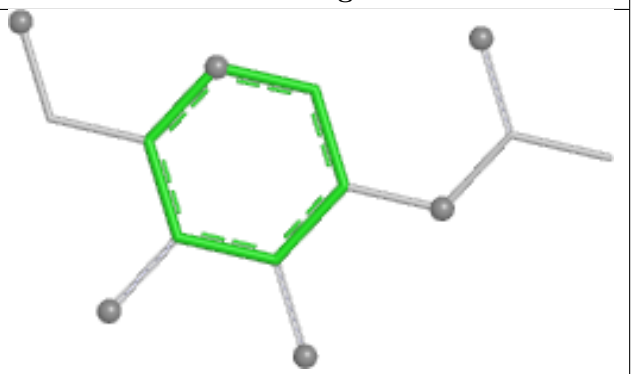
Bond lengths



Bond angles

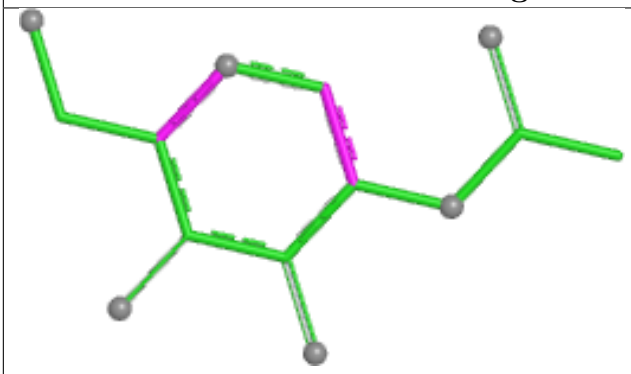


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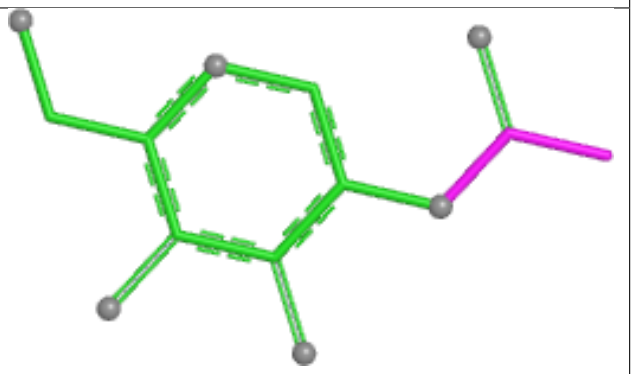


Rings

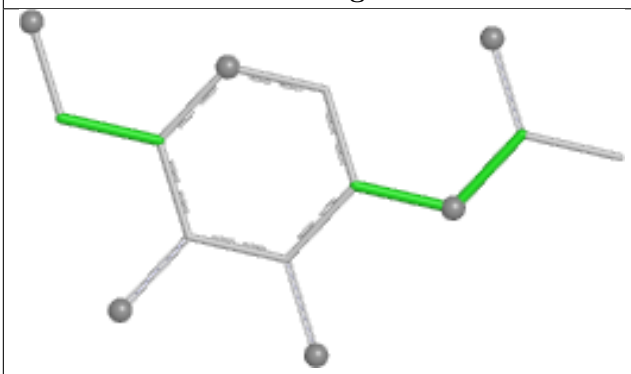
Ligand NAG A 1303



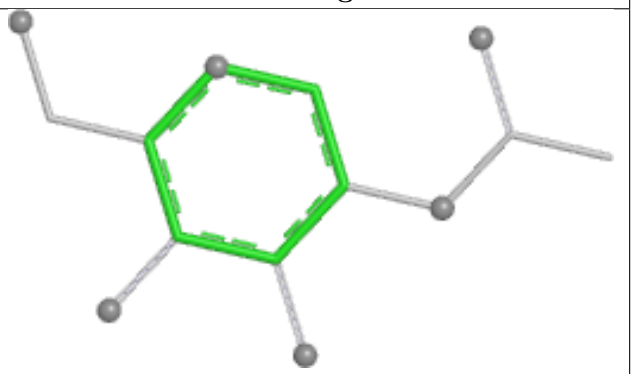
Bond lengths



Bond angles

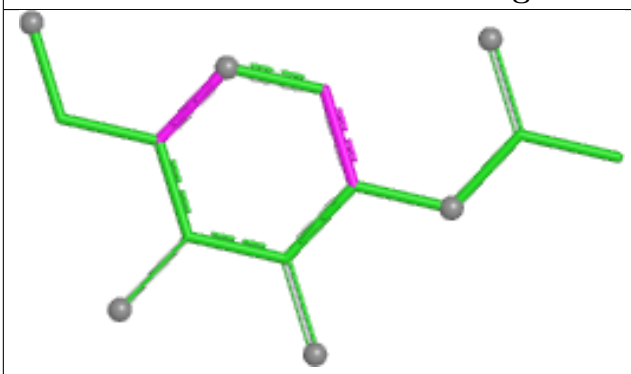


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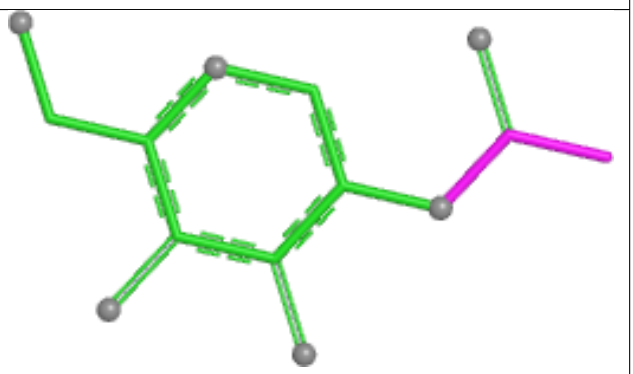


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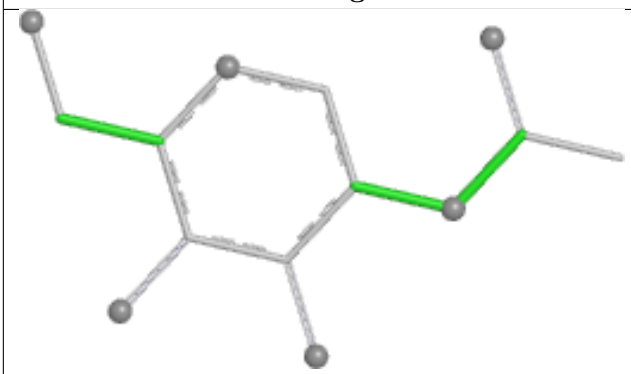
Ligand NAG E 1303



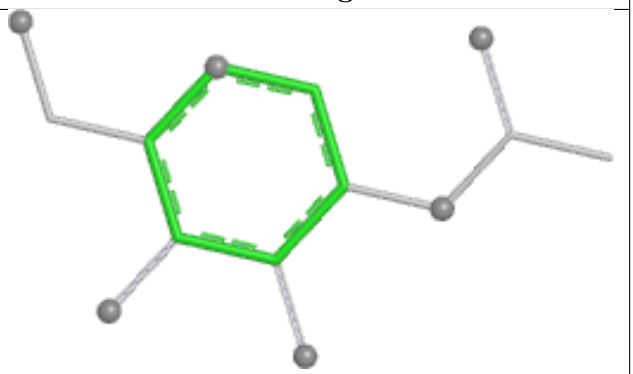
Bond lengths



Bond angles

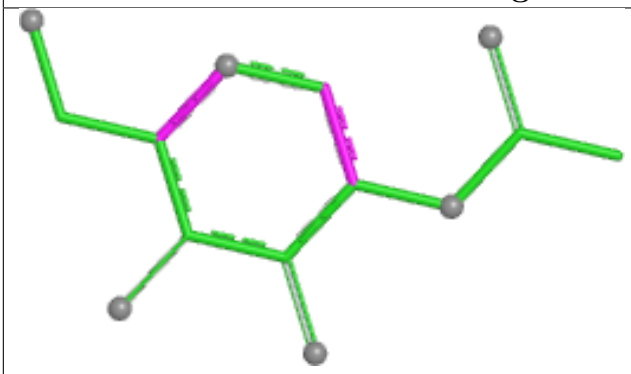


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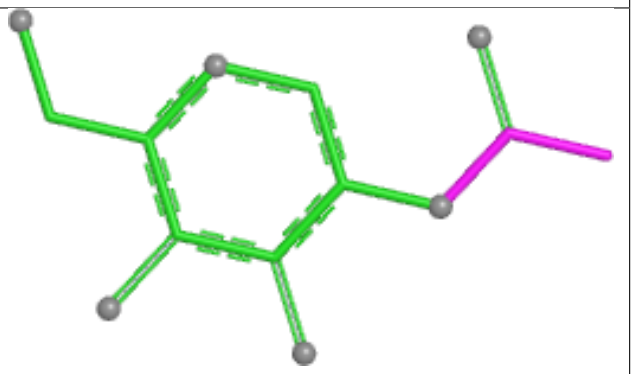


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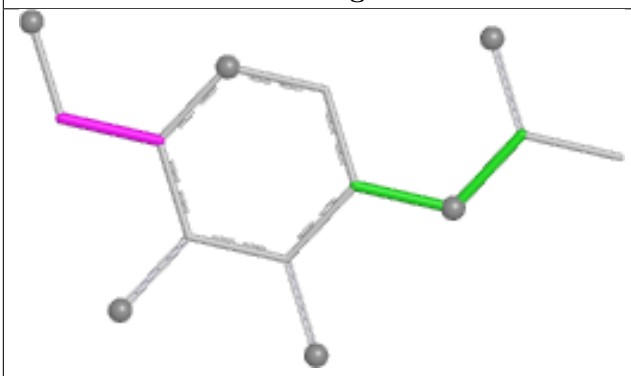
Ligand NAG B 1302



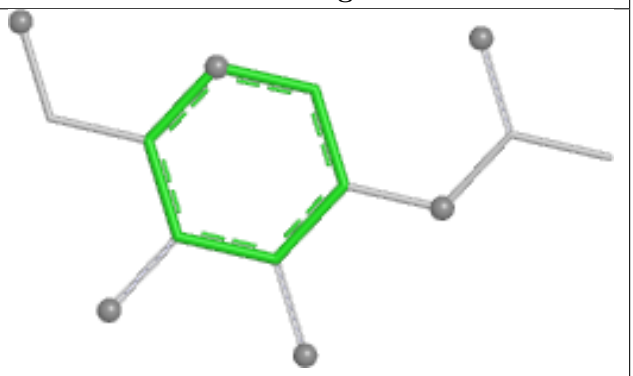
Bond lengths



Bond angles

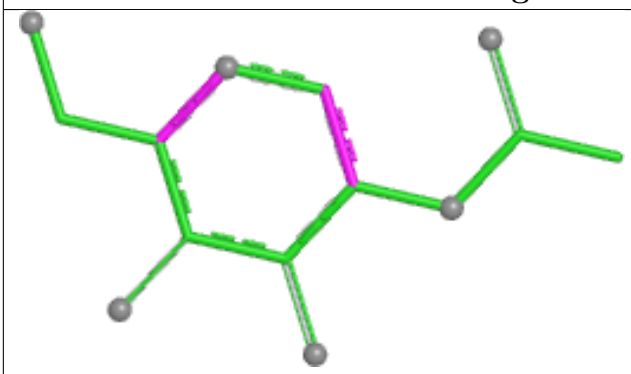


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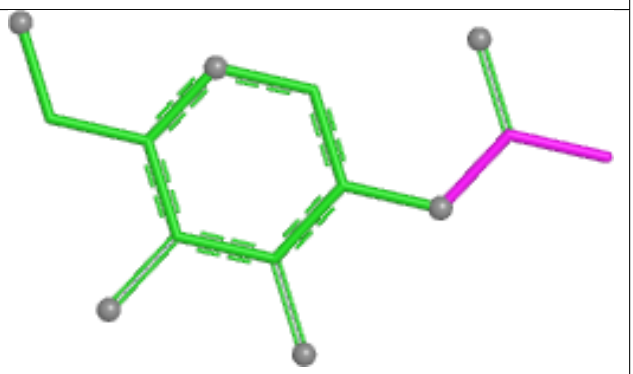


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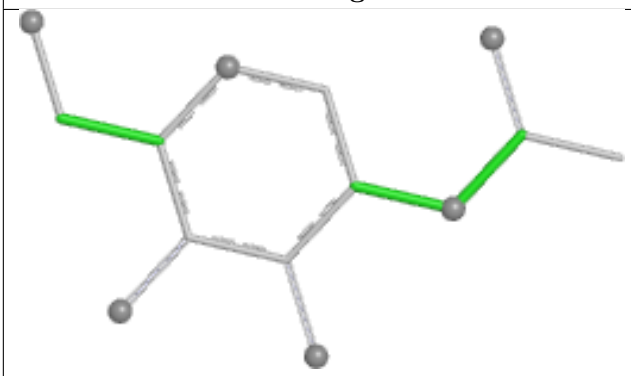
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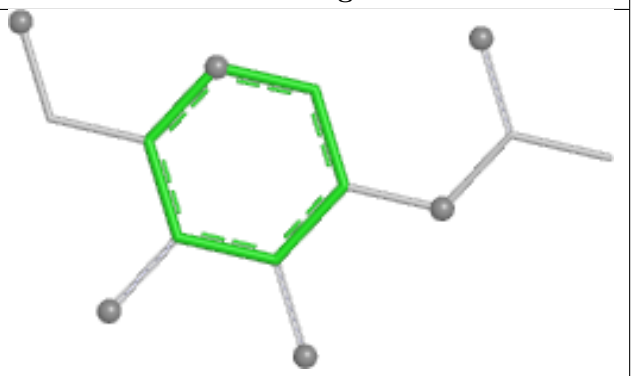
Bond lengths



Bond angles

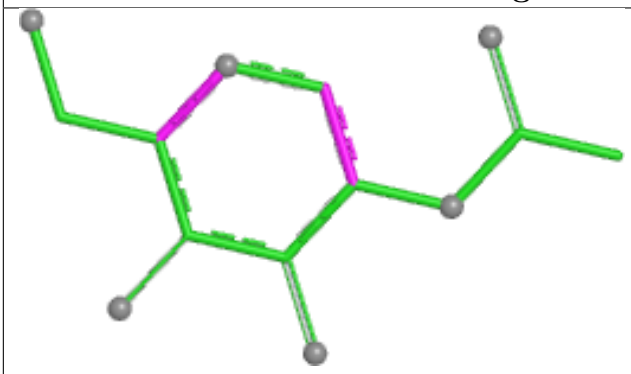


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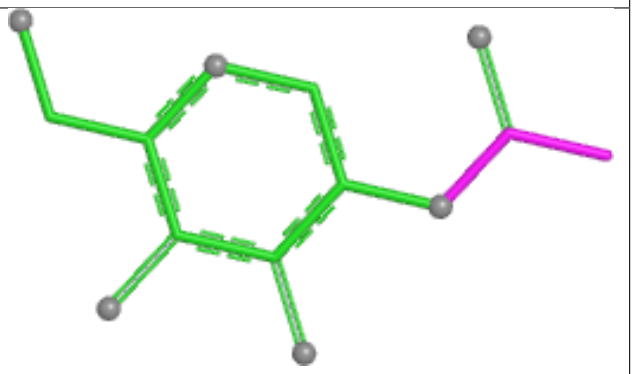


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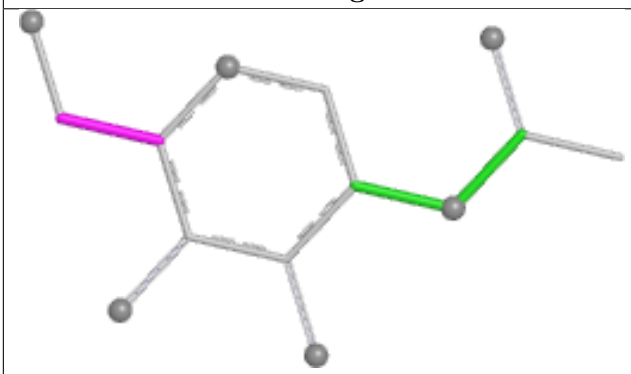
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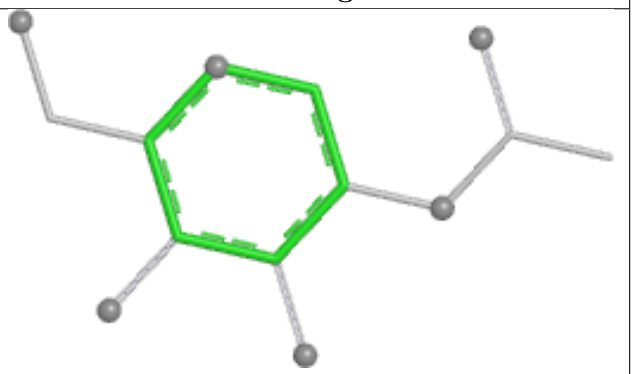
Bond lengths



Bond angles

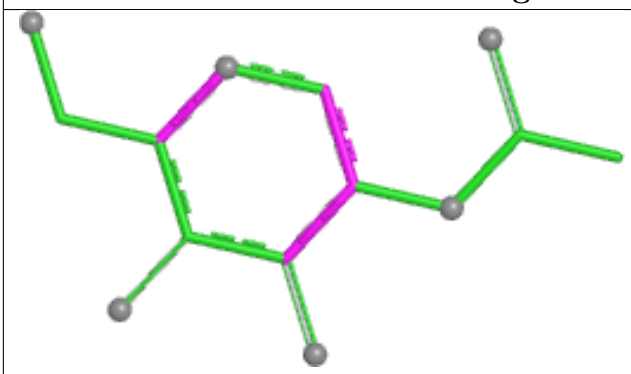


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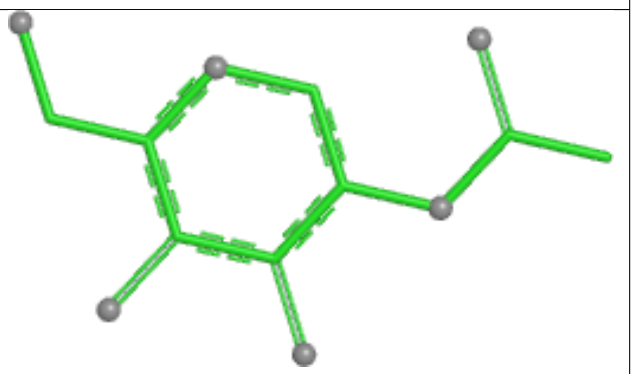


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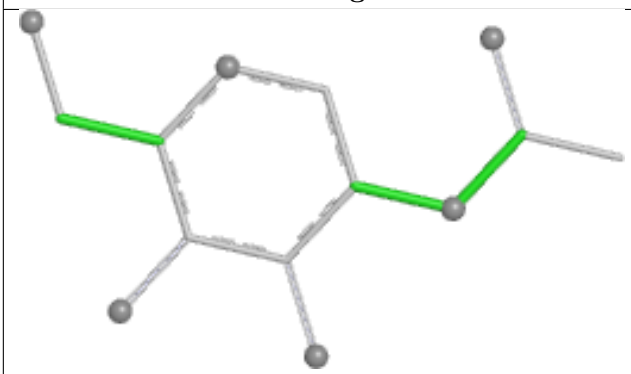
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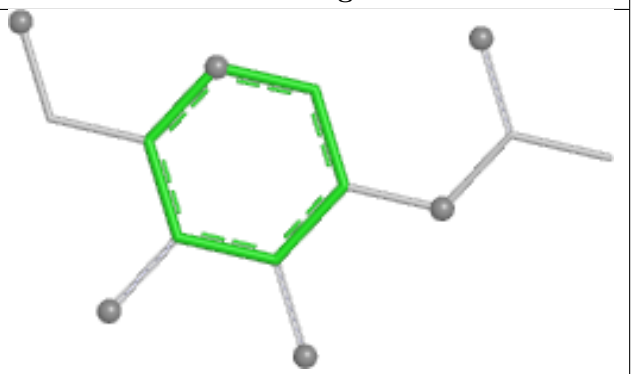
Bond lengths



Bond angles

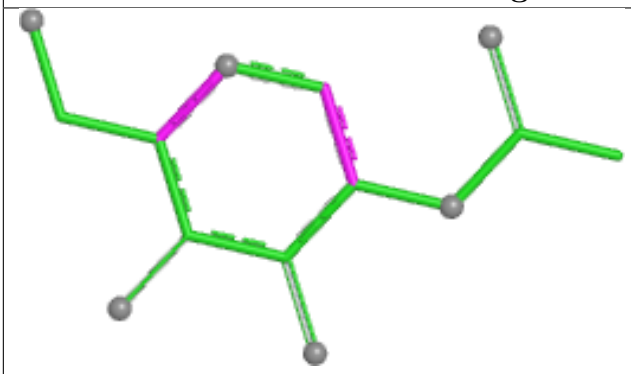


Torsions

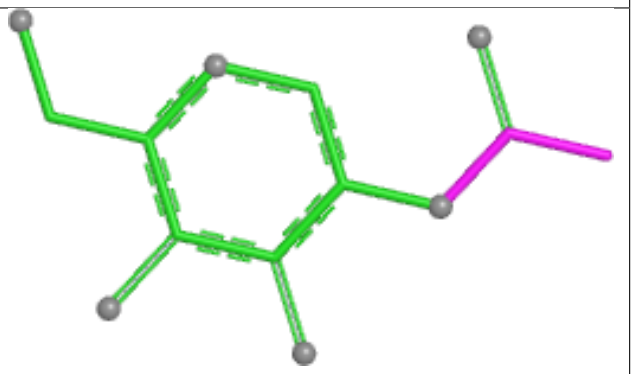


Rings

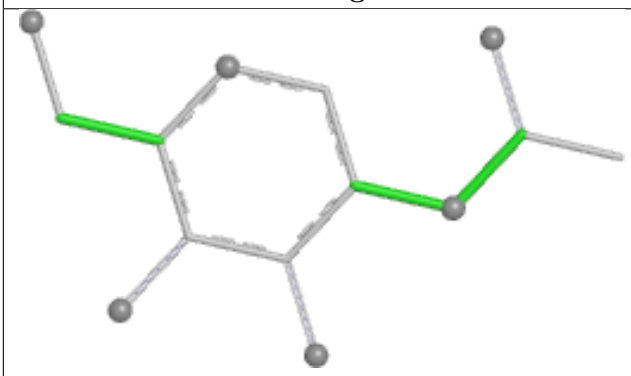
Ligand NAG A 1304



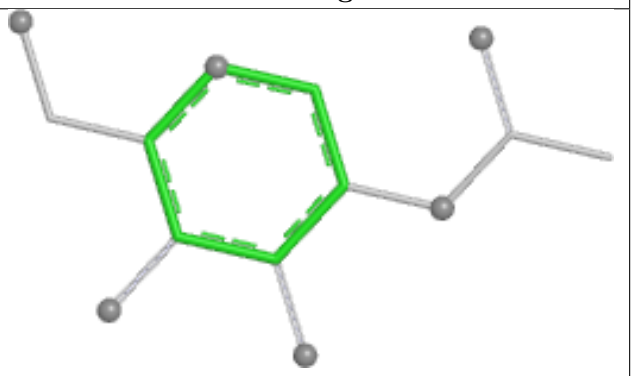
Bond lengths



Bond angles

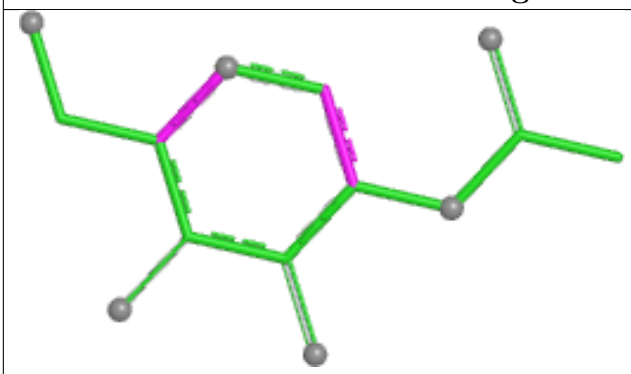


Torsions

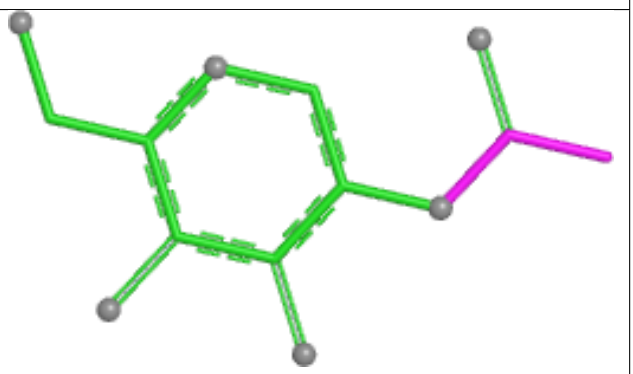


Rings

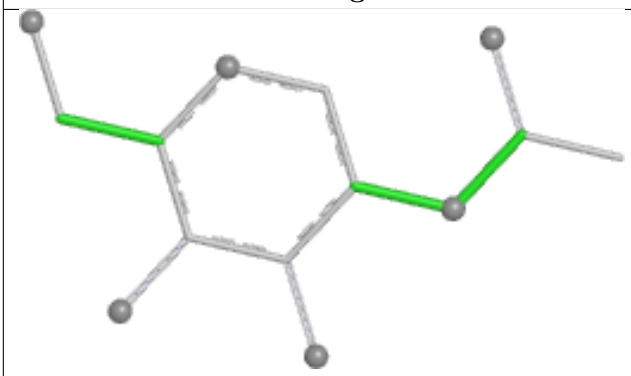
Ligand NAG B 1307



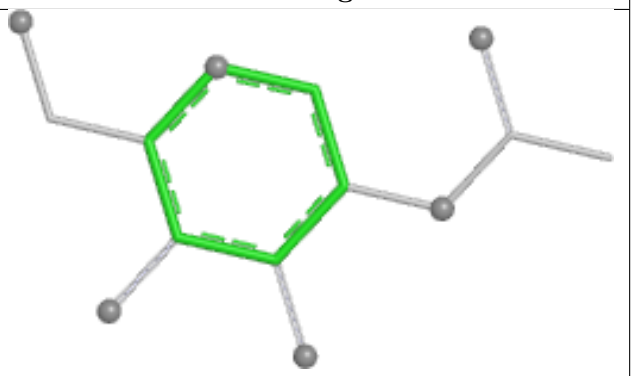
Bond lengths



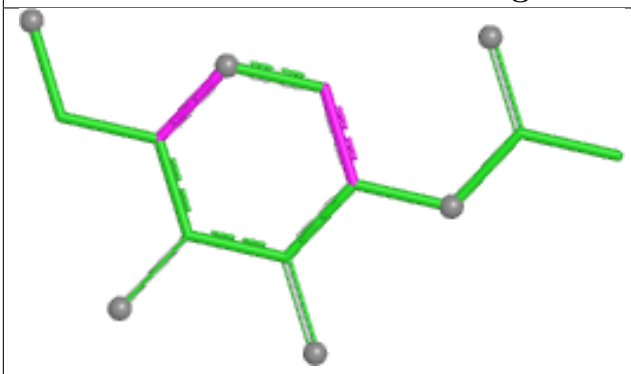
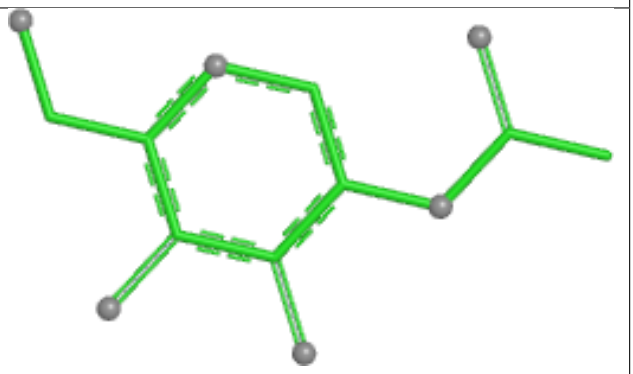
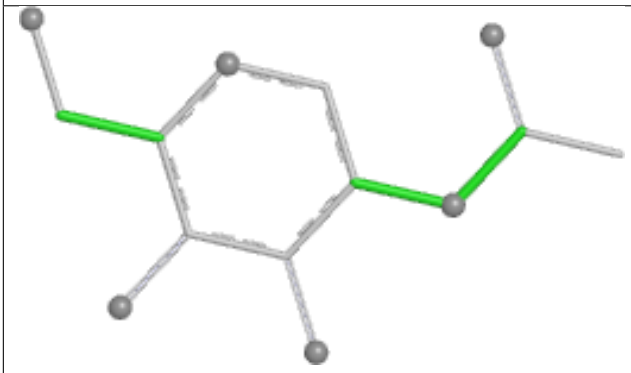
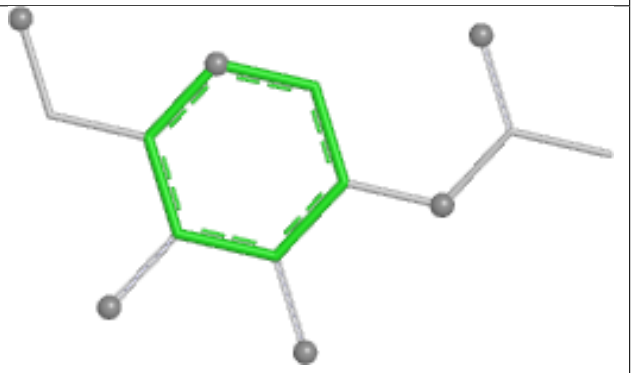
Bond angles



Torsions



Rings

Ligand NAG B 1310	
	
Bond lengths	Bond angles
	
Torsions	Rings

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.

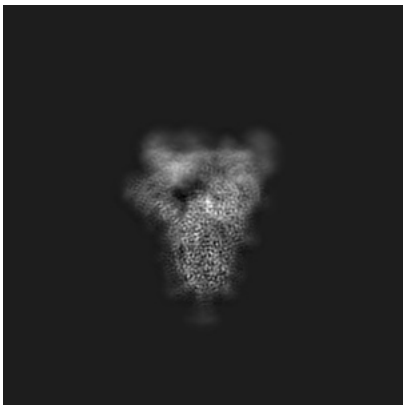
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-22506. These allow visual inspection of the internal detail of the map and identification of artifacts.

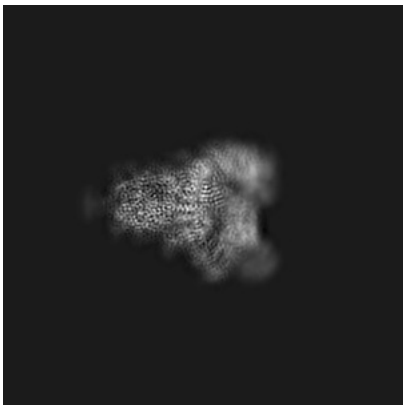
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

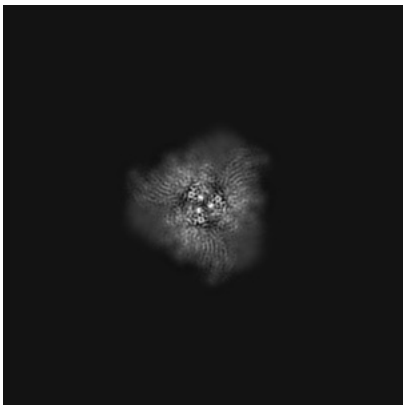
6.1.1 Primary map



X

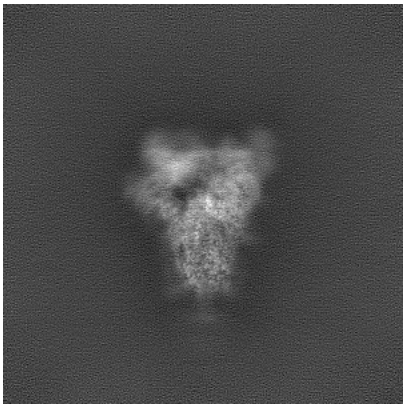


Y

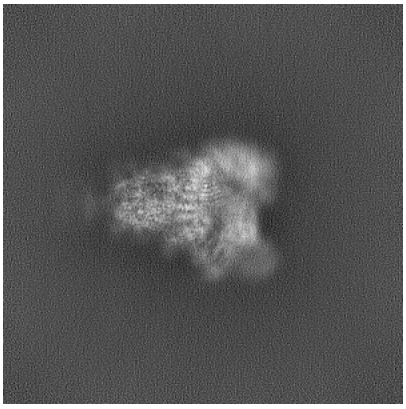


Z

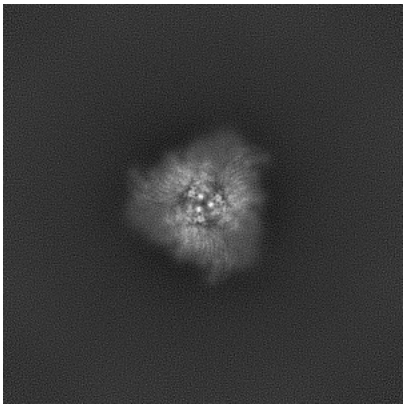
6.1.2 Raw map



X



Y

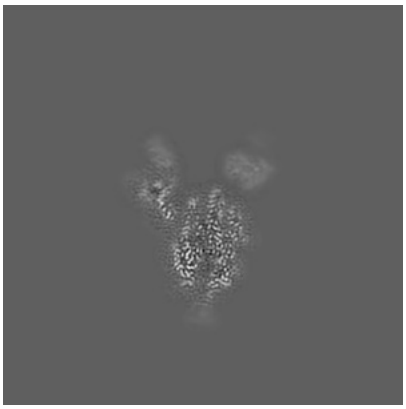


Z

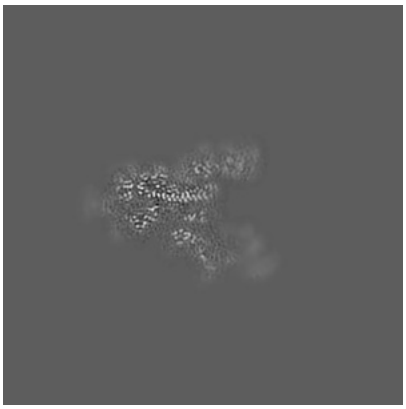
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

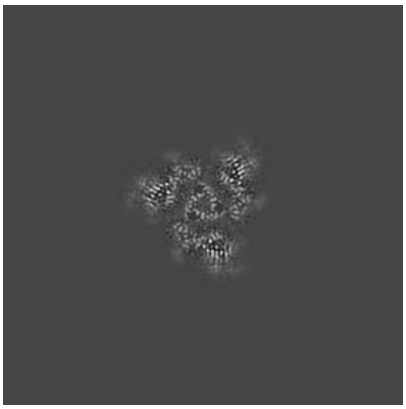
6.2.1 Primary map



X Index: 200

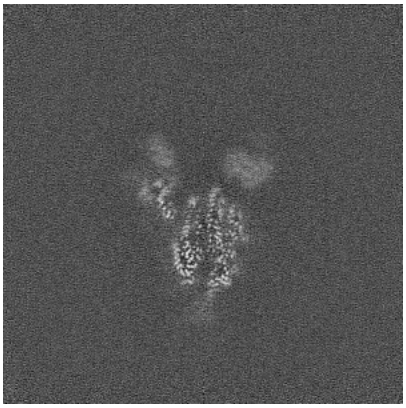


Y Index: 200

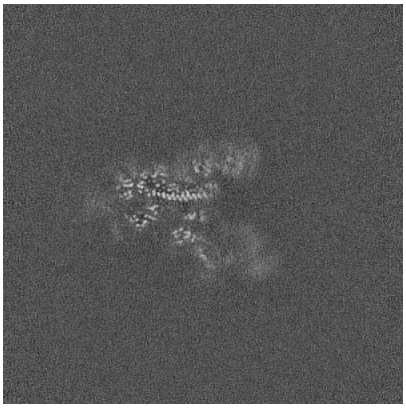


Z Index: 200

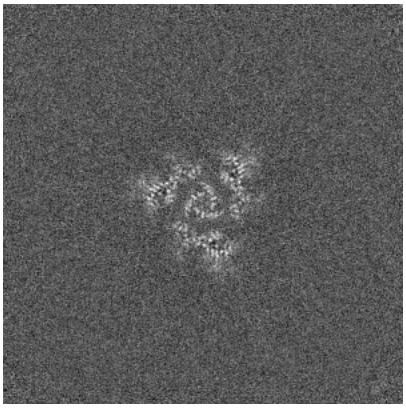
6.2.2 Raw map



X Index: 200



Y Index: 200

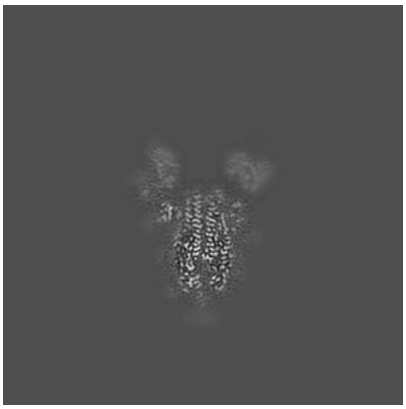


Z Index: 200

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: 195

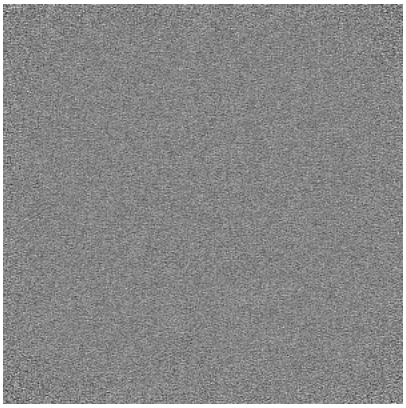


Y Index: 208

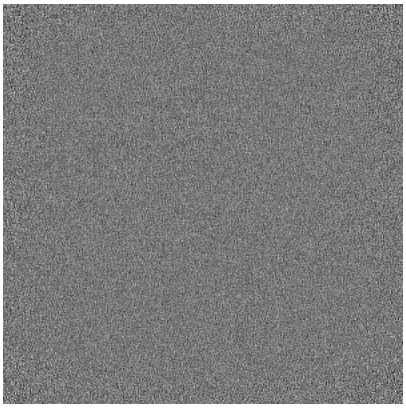


Z Index: 198

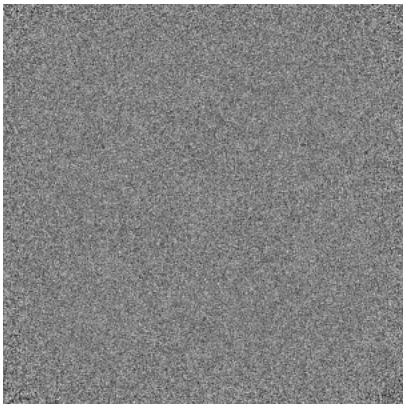
6.3.2 Raw map



X Index: 0



Y Index: 0

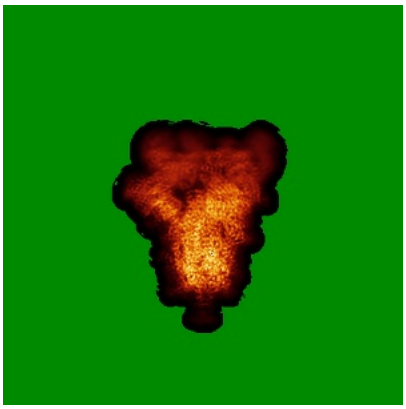


Z Index: 0

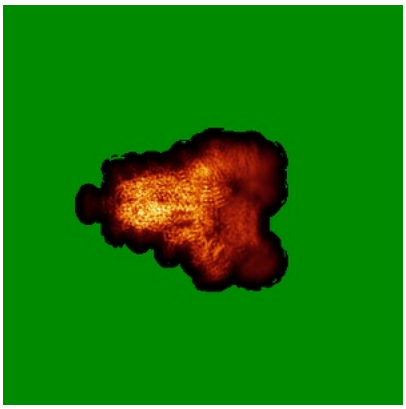
The images above show the largest variance slices of the map in three orthogonal directions.

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

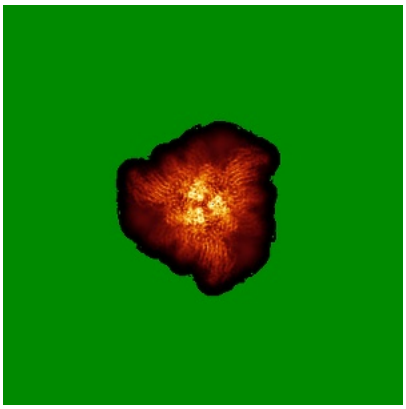
6.4.1 Primary map



X

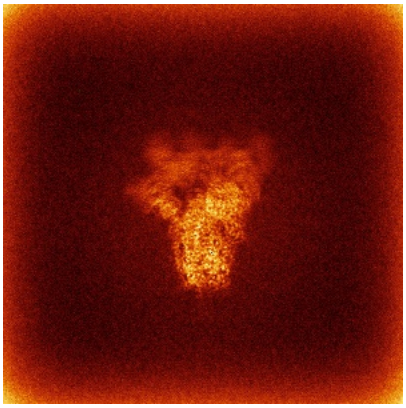


Y

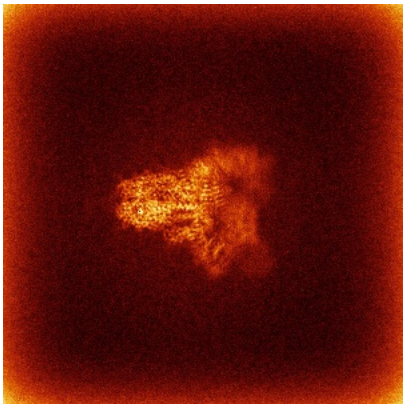


Z

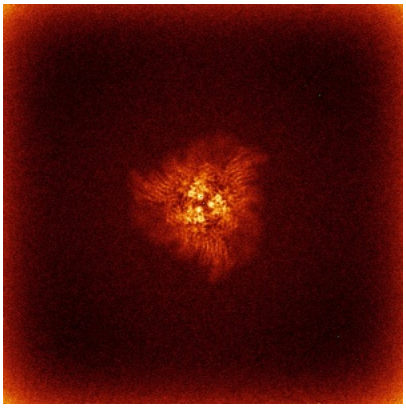
6.4.2 Raw map



X



Y

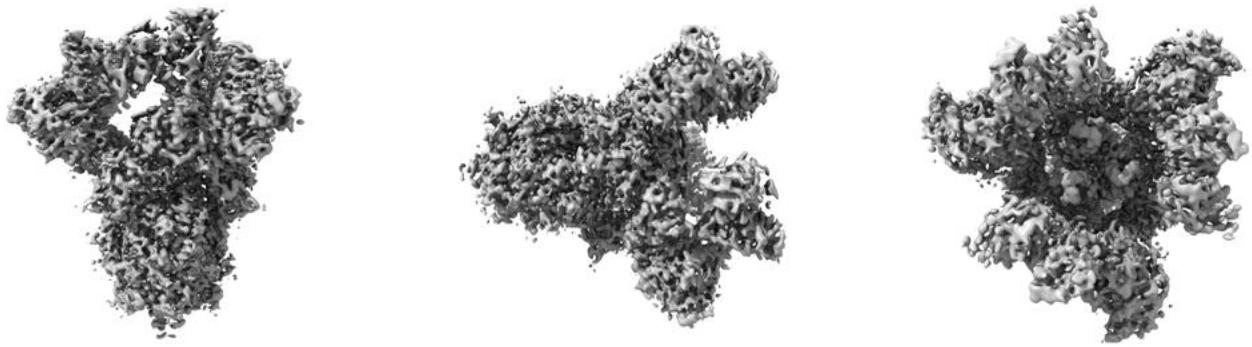


Z

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

6.5 Orthogonal surface views (i)

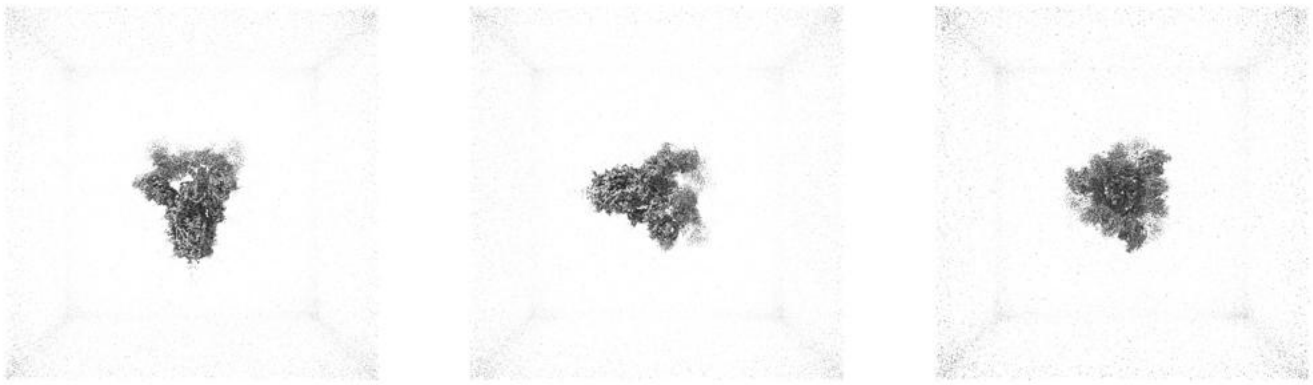
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

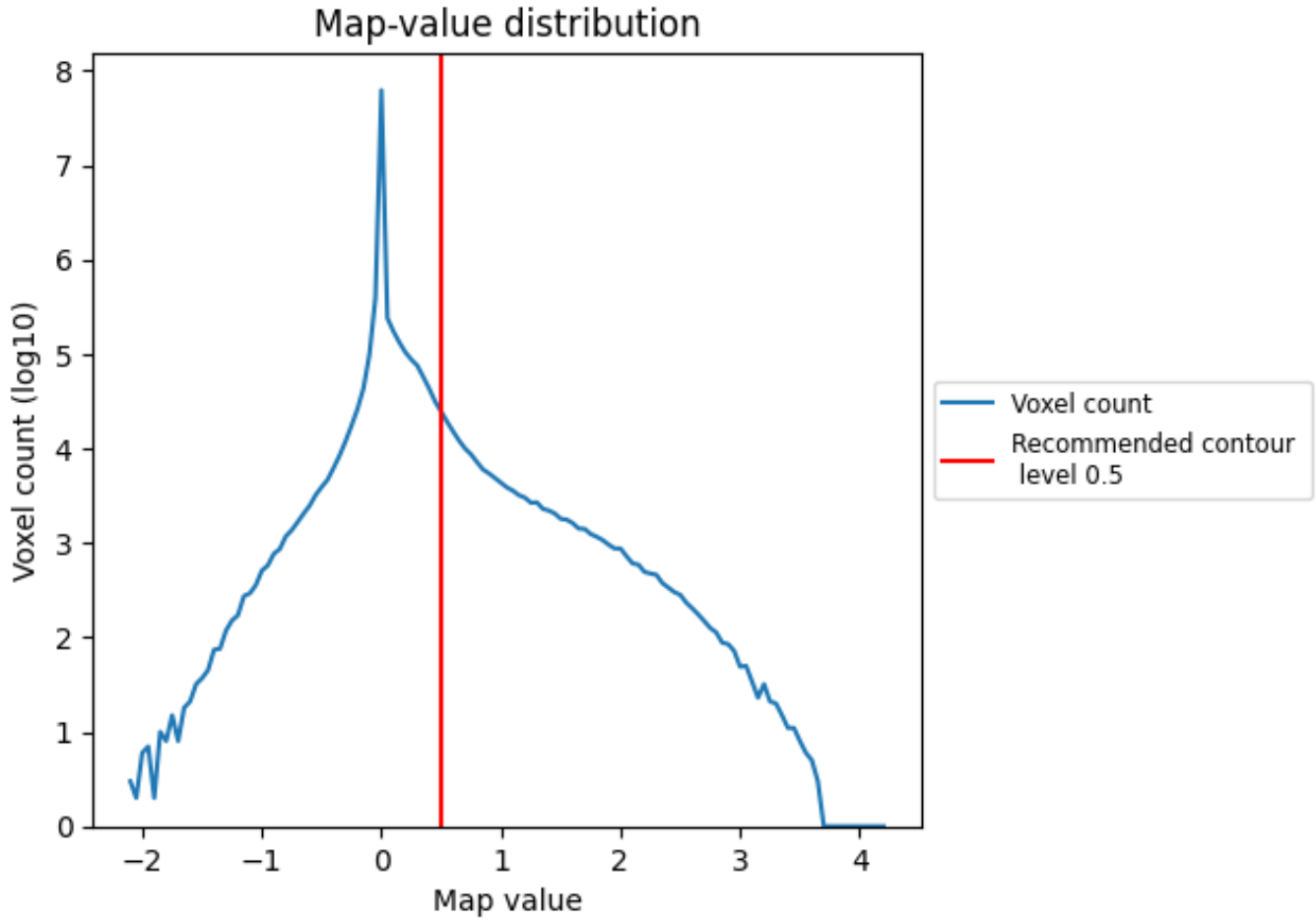
6.6 Mask visualisation (i)

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

7 Map analysis

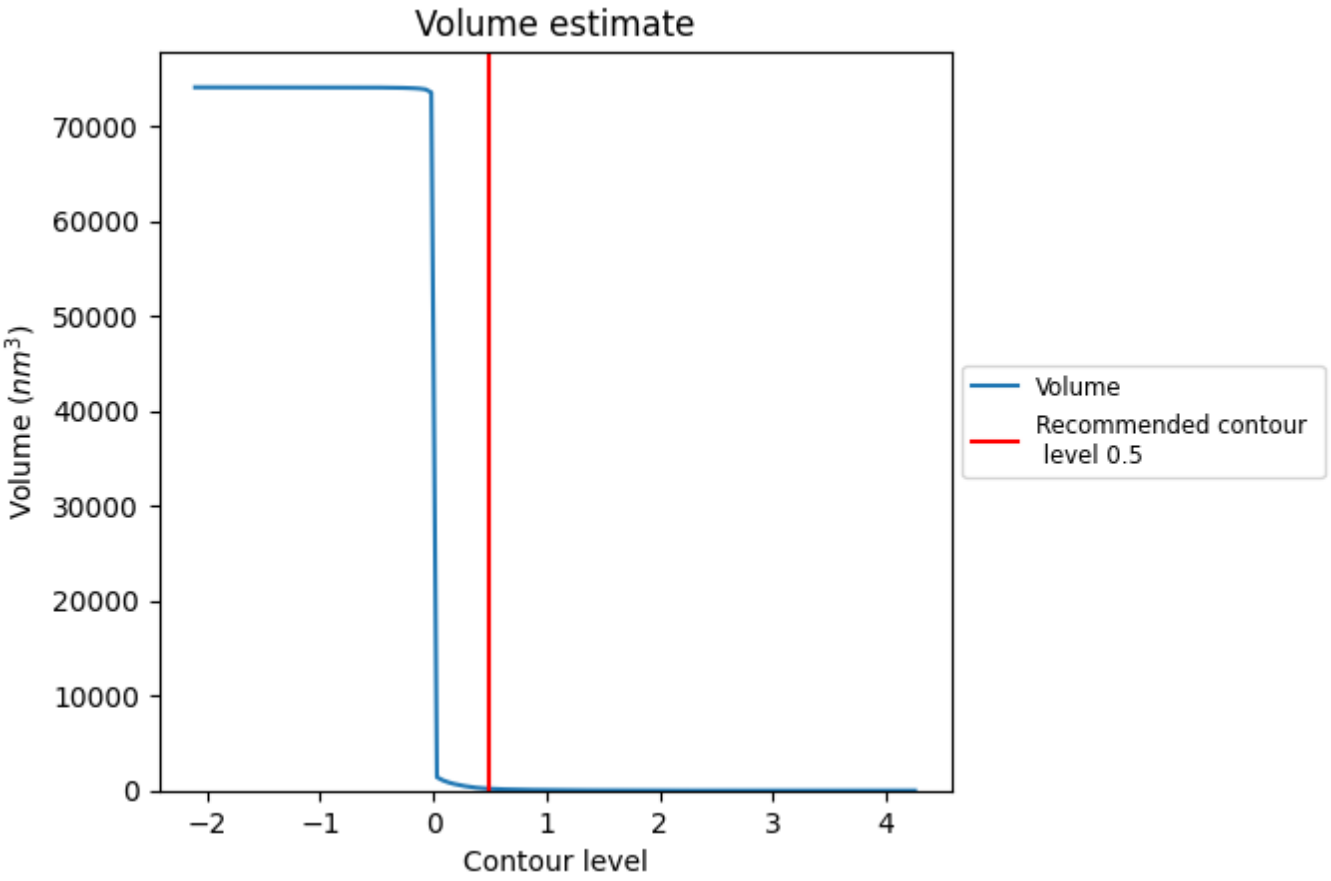
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

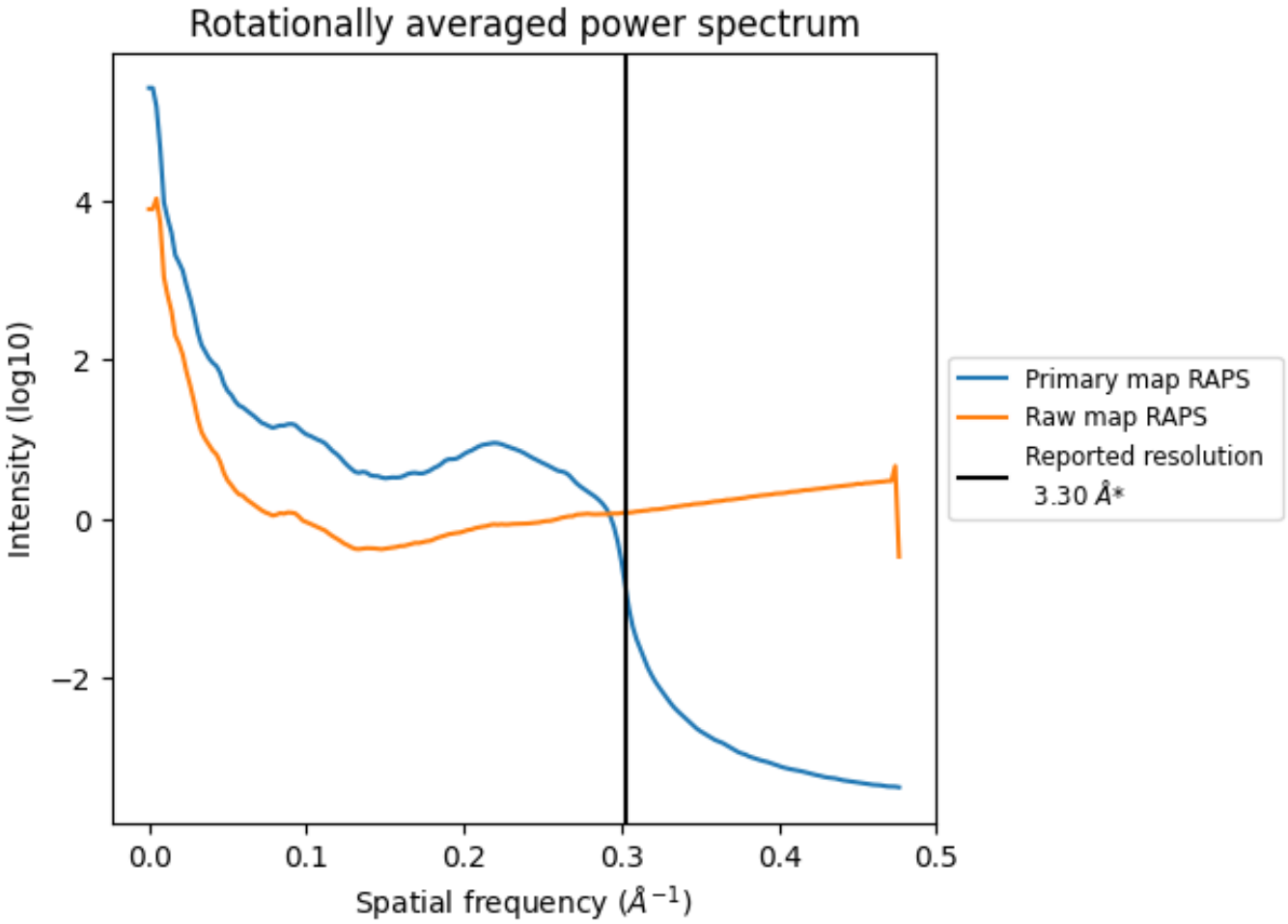
7.2 Volume estimate



The volume at the recommended contour level is 190 nm^3; this corresponds to an approximate mass of 172 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)

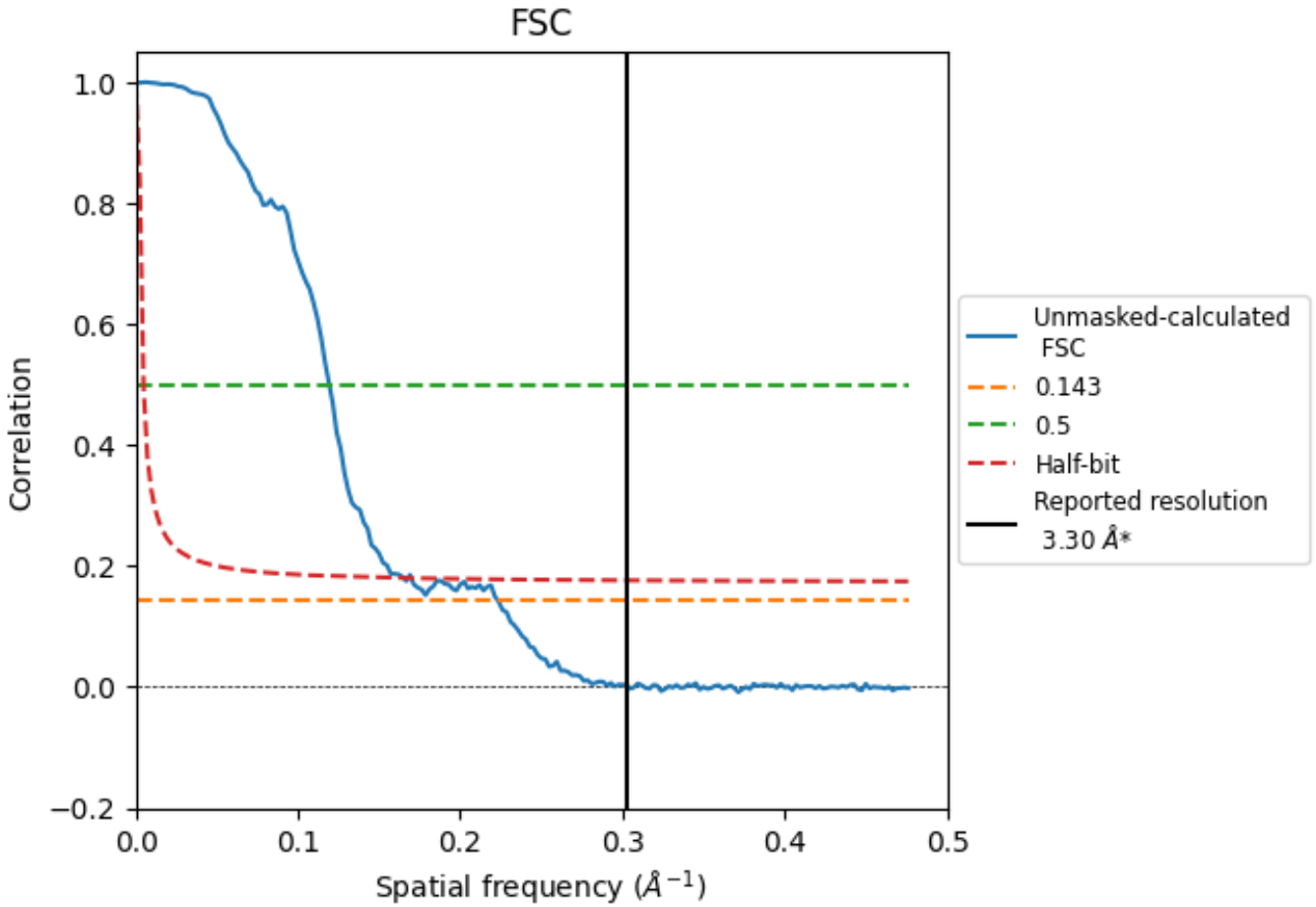


*Reported resolution corresponds to spatial frequency of 0.303 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

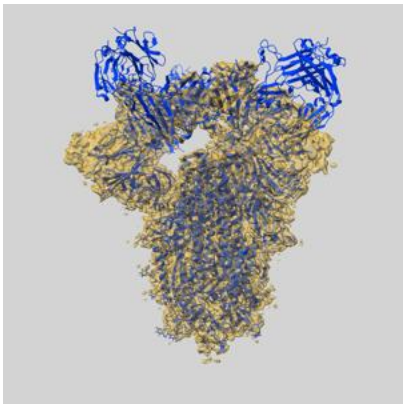
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	8.39	6.06

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.48 differs from the reported value 3.3 by more than 10 %

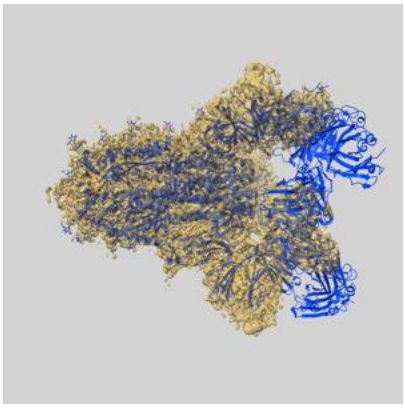
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-22506 and PDB model 7JVC. Per-residue inclusion information can be found in section 3 on page 15.

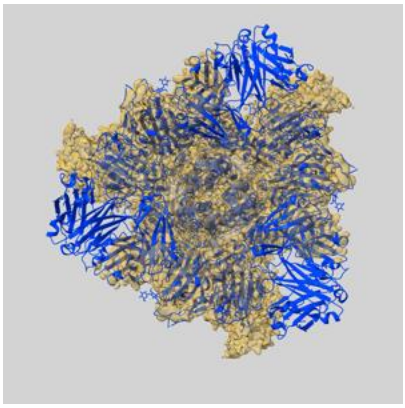
9.1 Map-model overlay



X



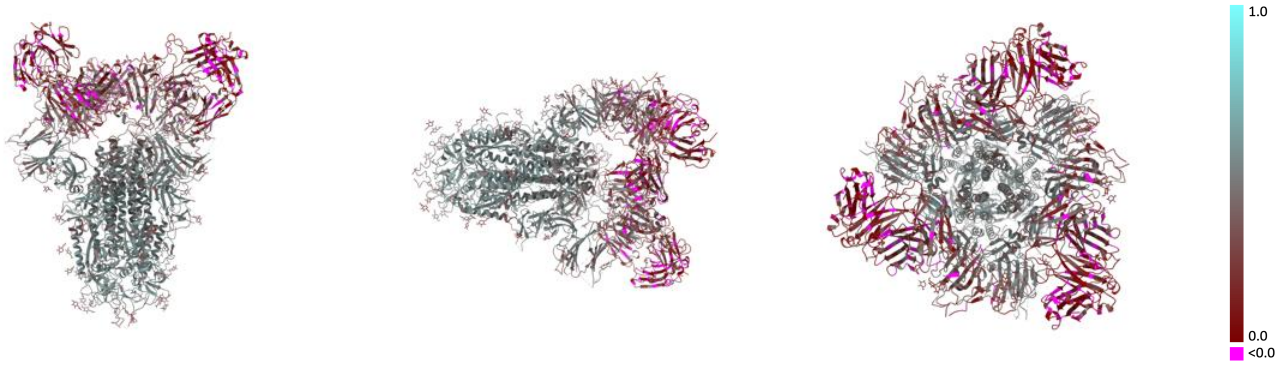
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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)



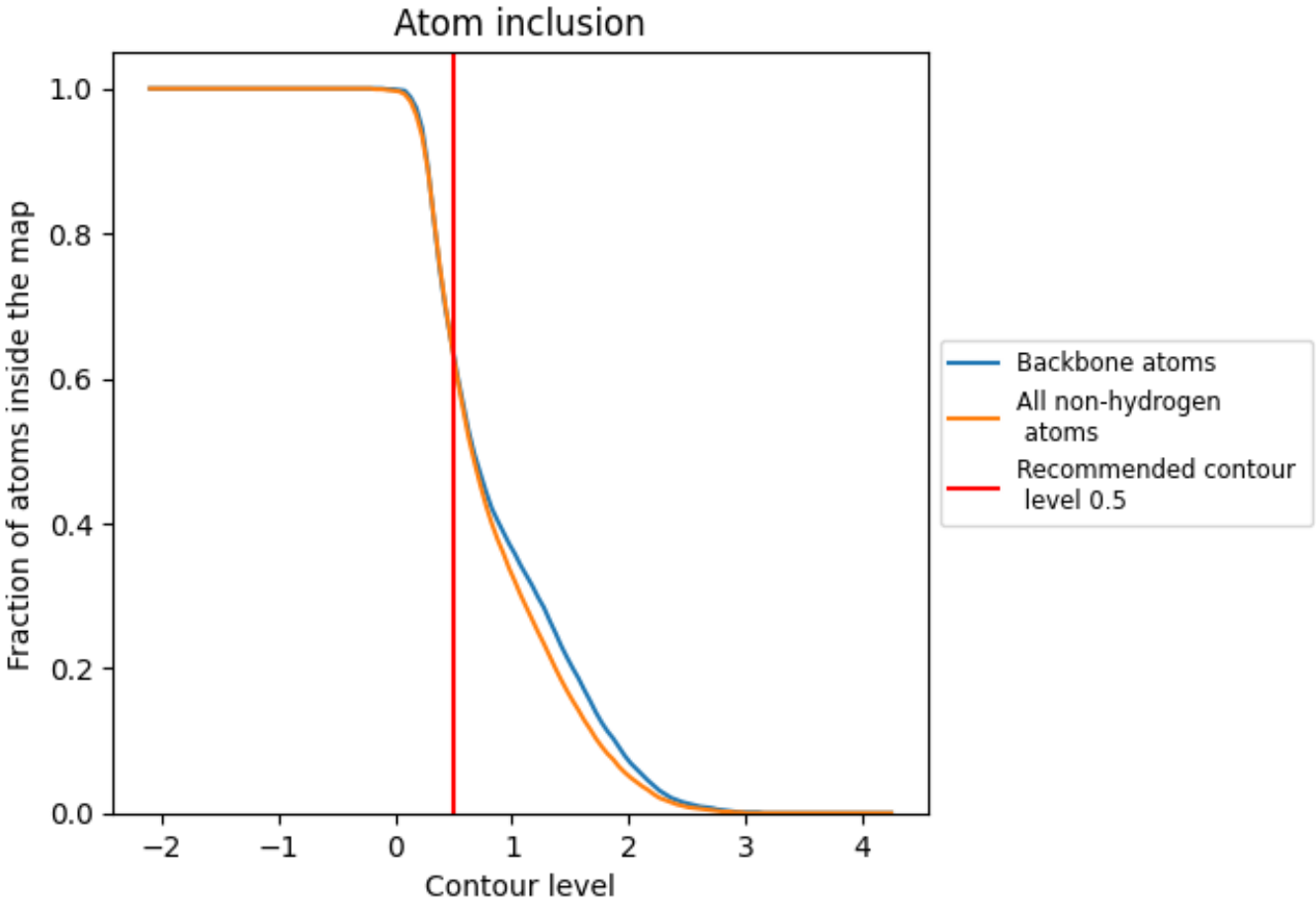
X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)

This section was not generated.

9.4 Atom inclusion (i)



At the recommended contour level, 63% of all backbone atoms, 63% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6300	0.3910
A	0.7800	0.4590
B	0.7780	0.4600
C	0.1640	0.1440
D	0.1150	0.1850
E	0.7790	0.4600
F	0.1700	0.1400
G	0.1130	0.1870
H	0.1670	0.1420
I	0.6430	0.3800
J	0.5710	0.3010
K	0.0000	0.1640
L	0.1190	0.1840
M	0.6430	0.4390
N	0.3930	0.2700
O	0.6430	0.4090
P	0.5710	0.2930
Q	0.0000	0.1320
R	0.6070	0.4200
S	0.4290	0.2930
T	0.6430	0.4000
U	0.5710	0.2960
V	0.0000	0.1390
W	0.6430	0.4200
X	0.4290	0.2830

