wwPDB EM Validation Summary Report (i)

Oct 21, 2024 – 12:16 PM JST

PDB ID	:	7E5S
EMDB ID	:	EMD-30994
Title	:	SARS-CoV-2 S trimer with four-antibody cocktail complex
Authors	:	Sun, Y.; Wang, L.; Wang, N.; Feng, R.; Wang, X.
Deposited on	:	2021-02-20
Resolution	:	3.60 Å(reported)

This is a wwPDB EM Validation Summary 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 (i) 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 (i)) were used in the production of this report:

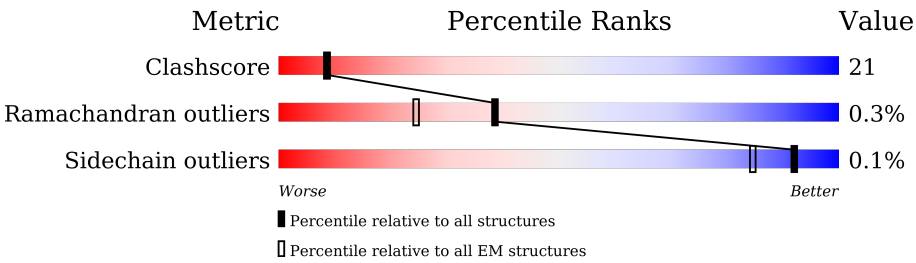
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	59% 24% 16%
1	B	1281	• 63% 20% 16%
1	C	1281	• 64% 19% 16%
2	D	210	9% 41% 9% 50%
2	H	210	• 40% 10% 50%
3	E	223	• 41% 13% 46%
3	L	223	7% 42% 12% 46%
4	I	120	70% 64% 36%

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Mol	Chain	Length	Quality of chain
4	J	120	19% 64% 36%
5	K	108	65% 75% 25%
5	T	108	19% 78% 22%
6	N	109	15% 57% 43%
6	Q	109	17% 56% 44%
6	S	109	27% 59% 41%
7	O	111	14% 57% 41%
8	P	120	6% 49% 50%
8	U	120	8% 47% 52%
8	V	120	20% 56% 43%
9	R	223	35% 18% 47%
10	F	2	100%
10	G	2	100%
10	M	2	50% 50%
10	W	2	100%
10	X	2	100%
10	Y	2	50% 50%
10	Z	2	50% 50% 50%
10	a	2	100% 100%
10	b	2	100%
10	c	2	50% 100%
10	d	2	100% 100%
10	e	2	50% 100%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 38916 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
			Total	C	N	O	S		
1	A	1072	8366	5336	1399	1593	38	0	0
1	B	1072	8334	5324	1389	1583	38	0	0
1	C	1072	8354	5334	1397	1585	38	0	0

There are 234 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	GLY	-	expression tag	UNP P0DTC2
A	1211	ARG	-	expression tag	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	TYR	-	expression tag	UNP P0DTC2
A	1216	ILE	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	GLU	-	expression tag	UNP P0DTC2
A	1219	ALA	-	expression tag	UNP P0DTC2
A	1220	PRO	-	expression tag	UNP P0DTC2
A	1221	ARG	-	expression tag	UNP P0DTC2
A	1222	ASP	-	expression tag	UNP P0DTC2
A	1223	GLY	-	expression tag	UNP P0DTC2
A	1224	GLN	-	expression tag	UNP P0DTC2
A	1225	ALA	-	expression tag	UNP P0DTC2
A	1226	TYR	-	expression tag	UNP P0DTC2
A	1227	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1228	ARG	-	expression tag	UNP P0DTC2
A	1229	LYS	-	expression tag	UNP P0DTC2
A	1230	ASP	-	expression tag	UNP P0DTC2
A	1231	GLY	-	expression tag	UNP P0DTC2
A	1232	GLU	-	expression tag	UNP P0DTC2
A	1233	TRP	-	expression tag	UNP P0DTC2
A	1234	VAL	-	expression tag	UNP P0DTC2
A	1235	LEU	-	expression tag	UNP P0DTC2
A	1236	LEU	-	expression tag	UNP P0DTC2
A	1237	SER	-	expression tag	UNP P0DTC2
A	1238	THR	-	expression tag	UNP P0DTC2
A	1239	PHE	-	expression tag	UNP P0DTC2
A	1240	LEU	-	expression tag	UNP P0DTC2
A	1241	GLY	-	expression tag	UNP P0DTC2
A	1242	ARG	-	expression tag	UNP P0DTC2
A	1243	SER	-	expression tag	UNP P0DTC2
A	1244	LEU	-	expression tag	UNP P0DTC2
A	1245	GLU	-	expression tag	UNP P0DTC2
A	1246	VAL	-	expression tag	UNP P0DTC2
A	1247	LEU	-	expression tag	UNP P0DTC2
A	1248	PHE	-	expression tag	UNP P0DTC2
A	1249	GLN	-	expression tag	UNP P0DTC2
A	1250	GLY	-	expression tag	UNP P0DTC2
A	1251	PRO	-	expression tag	UNP P0DTC2
A	1252	GLY	-	expression tag	UNP P0DTC2
A	1253	TRP	-	expression tag	UNP P0DTC2
A	1254	SER	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
A	1256	PRO	-	expression tag	UNP P0DTC2
A	1257	GLN	-	expression tag	UNP P0DTC2
A	1258	PHE	-	expression tag	UNP P0DTC2
A	1259	GLU	-	expression tag	UNP P0DTC2
A	1260	LYS	-	expression tag	UNP P0DTC2
A	1261	GLY	-	expression tag	UNP P0DTC2
A	1262	GLY	-	expression tag	UNP P0DTC2
A	1263	GLY	-	expression tag	UNP P0DTC2
A	1264	SER	-	expression tag	UNP P0DTC2
A	1265	GLY	-	expression tag	UNP P0DTC2
A	1266	GLY	-	expression tag	UNP P0DTC2
A	1267	GLY	-	expression tag	UNP P0DTC2
A	1268	SER	-	expression tag	UNP P0DTC2
A	1269	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1270	GLY	-	expression tag	UNP P0DTC2
A	1271	SER	-	expression tag	UNP P0DTC2
A	1272	SER	-	expression tag	UNP P0DTC2
A	1273	ALA	-	expression tag	UNP P0DTC2
A	1274	TRP	-	expression tag	UNP P0DTC2
A	1275	SER	-	expression tag	UNP P0DTC2
A	1276	HIS	-	expression tag	UNP P0DTC2
A	1277	PRO	-	expression tag	UNP P0DTC2
A	1278	GLN	-	expression tag	UNP P0DTC2
A	1279	PHE	-	expression tag	UNP P0DTC2
A	1280	GLU	-	expression tag	UNP P0DTC2
A	1281	LYS	-	expression tag	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	GLY	-	expression tag	UNP P0DTC2
B	1211	ARG	-	expression tag	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	TYR	-	expression tag	UNP P0DTC2
B	1216	ILE	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	GLU	-	expression tag	UNP P0DTC2
B	1219	ALA	-	expression tag	UNP P0DTC2
B	1220	PRO	-	expression tag	UNP P0DTC2
B	1221	ARG	-	expression tag	UNP P0DTC2
B	1222	ASP	-	expression tag	UNP P0DTC2
B	1223	GLY	-	expression tag	UNP P0DTC2
B	1224	GLN	-	expression tag	UNP P0DTC2
B	1225	ALA	-	expression tag	UNP P0DTC2
B	1226	TYR	-	expression tag	UNP P0DTC2
B	1227	VAL	-	expression tag	UNP P0DTC2
B	1228	ARG	-	expression tag	UNP P0DTC2
B	1229	LYS	-	expression tag	UNP P0DTC2
B	1230	ASP	-	expression tag	UNP P0DTC2
B	1231	GLY	-	expression tag	UNP P0DTC2
B	1232	GLU	-	expression tag	UNP P0DTC2
B	1233	TRP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1234	VAL	-	expression tag	UNP P0DTC2
B	1235	LEU	-	expression tag	UNP P0DTC2
B	1236	LEU	-	expression tag	UNP P0DTC2
B	1237	SER	-	expression tag	UNP P0DTC2
B	1238	THR	-	expression tag	UNP P0DTC2
B	1239	PHE	-	expression tag	UNP P0DTC2
B	1240	LEU	-	expression tag	UNP P0DTC2
B	1241	GLY	-	expression tag	UNP P0DTC2
B	1242	ARG	-	expression tag	UNP P0DTC2
B	1243	SER	-	expression tag	UNP P0DTC2
B	1244	LEU	-	expression tag	UNP P0DTC2
B	1245	GLU	-	expression tag	UNP P0DTC2
B	1246	VAL	-	expression tag	UNP P0DTC2
B	1247	LEU	-	expression tag	UNP P0DTC2
B	1248	PHE	-	expression tag	UNP P0DTC2
B	1249	GLN	-	expression tag	UNP P0DTC2
B	1250	GLY	-	expression tag	UNP P0DTC2
B	1251	PRO	-	expression tag	UNP P0DTC2
B	1252	GLY	-	expression tag	UNP P0DTC2
B	1253	TRP	-	expression tag	UNP P0DTC2
B	1254	SER	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	PRO	-	expression tag	UNP P0DTC2
B	1257	GLN	-	expression tag	UNP P0DTC2
B	1258	PHE	-	expression tag	UNP P0DTC2
B	1259	GLU	-	expression tag	UNP P0DTC2
B	1260	LYS	-	expression tag	UNP P0DTC2
B	1261	GLY	-	expression tag	UNP P0DTC2
B	1262	GLY	-	expression tag	UNP P0DTC2
B	1263	GLY	-	expression tag	UNP P0DTC2
B	1264	SER	-	expression tag	UNP P0DTC2
B	1265	GLY	-	expression tag	UNP P0DTC2
B	1266	GLY	-	expression tag	UNP P0DTC2
B	1267	GLY	-	expression tag	UNP P0DTC2
B	1268	SER	-	expression tag	UNP P0DTC2
B	1269	GLY	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	SER	-	expression tag	UNP P0DTC2
B	1273	ALA	-	expression tag	UNP P0DTC2
B	1274	TRP	-	expression tag	UNP P0DTC2
B	1275	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1276	HIS	-	expression tag	UNP P0DTC2
B	1277	PRO	-	expression tag	UNP P0DTC2
B	1278	GLN	-	expression tag	UNP P0DTC2
B	1279	PHE	-	expression tag	UNP P0DTC2
B	1280	GLU	-	expression tag	UNP P0DTC2
B	1281	LYS	-	expression tag	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	GLY	-	expression tag	UNP P0DTC2
C	1211	ARG	-	expression tag	UNP P0DTC2
C	1212	GLY	-	expression tag	UNP P0DTC2
C	1213	SER	-	expression tag	UNP P0DTC2
C	1214	GLY	-	expression tag	UNP P0DTC2
C	1215	TYR	-	expression tag	UNP P0DTC2
C	1216	ILE	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	GLU	-	expression tag	UNP P0DTC2
C	1219	ALA	-	expression tag	UNP P0DTC2
C	1220	PRO	-	expression tag	UNP P0DTC2
C	1221	ARG	-	expression tag	UNP P0DTC2
C	1222	ASP	-	expression tag	UNP P0DTC2
C	1223	GLY	-	expression tag	UNP P0DTC2
C	1224	GLN	-	expression tag	UNP P0DTC2
C	1225	ALA	-	expression tag	UNP P0DTC2
C	1226	TYR	-	expression tag	UNP P0DTC2
C	1227	VAL	-	expression tag	UNP P0DTC2
C	1228	ARG	-	expression tag	UNP P0DTC2
C	1229	LYS	-	expression tag	UNP P0DTC2
C	1230	ASP	-	expression tag	UNP P0DTC2
C	1231	GLY	-	expression tag	UNP P0DTC2
C	1232	GLU	-	expression tag	UNP P0DTC2
C	1233	TRP	-	expression tag	UNP P0DTC2
C	1234	VAL	-	expression tag	UNP P0DTC2
C	1235	LEU	-	expression tag	UNP P0DTC2
C	1236	LEU	-	expression tag	UNP P0DTC2
C	1237	SER	-	expression tag	UNP P0DTC2
C	1238	THR	-	expression tag	UNP P0DTC2
C	1239	PHE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1240	LEU	-	expression tag	UNP P0DTC2
C	1241	GLY	-	expression tag	UNP P0DTC2
C	1242	ARG	-	expression tag	UNP P0DTC2
C	1243	SER	-	expression tag	UNP P0DTC2
C	1244	LEU	-	expression tag	UNP P0DTC2
C	1245	GLU	-	expression tag	UNP P0DTC2
C	1246	VAL	-	expression tag	UNP P0DTC2
C	1247	LEU	-	expression tag	UNP P0DTC2
C	1248	PHE	-	expression tag	UNP P0DTC2
C	1249	GLN	-	expression tag	UNP P0DTC2
C	1250	GLY	-	expression tag	UNP P0DTC2
C	1251	PRO	-	expression tag	UNP P0DTC2
C	1252	GLY	-	expression tag	UNP P0DTC2
C	1253	TRP	-	expression tag	UNP P0DTC2
C	1254	SER	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
C	1256	PRO	-	expression tag	UNP P0DTC2
C	1257	GLN	-	expression tag	UNP P0DTC2
C	1258	PHE	-	expression tag	UNP P0DTC2
C	1259	GLU	-	expression tag	UNP P0DTC2
C	1260	LYS	-	expression tag	UNP P0DTC2
C	1261	GLY	-	expression tag	UNP P0DTC2
C	1262	GLY	-	expression tag	UNP P0DTC2
C	1263	GLY	-	expression tag	UNP P0DTC2
C	1264	SER	-	expression tag	UNP P0DTC2
C	1265	GLY	-	expression tag	UNP P0DTC2
C	1266	GLY	-	expression tag	UNP P0DTC2
C	1267	GLY	-	expression tag	UNP P0DTC2
C	1268	SER	-	expression tag	UNP P0DTC2
C	1269	GLY	-	expression tag	UNP P0DTC2
C	1270	GLY	-	expression tag	UNP P0DTC2
C	1271	SER	-	expression tag	UNP P0DTC2
C	1272	SER	-	expression tag	UNP P0DTC2
C	1273	ALA	-	expression tag	UNP P0DTC2
C	1274	TRP	-	expression tag	UNP P0DTC2
C	1275	SER	-	expression tag	UNP P0DTC2
C	1276	HIS	-	expression tag	UNP P0DTC2
C	1277	PRO	-	expression tag	UNP P0DTC2
C	1278	GLN	-	expression tag	UNP P0DTC2
C	1279	PHE	-	expression tag	UNP P0DTC2
C	1280	GLU	-	expression tag	UNP P0DTC2
C	1281	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called H014 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	105	704	447	116	140	1	0	0
2	H	105	704	447	116	140	1	0	0

- Molecule 3 is a protein called H014 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	120	903	575	144	182	2	0	0
3	L	120	903	575	144	182	2	0	0

- Molecule 4 is a protein called P17 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	I	120	912	571	162	175	4	0	0
4	J	120	912	571	162	175	4	0	0

- Molecule 5 is a protein called P17 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	108	817	511	137	167	2	0	0
5	T	108	817	511	137	167	2	0	0

- Molecule 6 is a protein called FC05 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	N	109	788	491	132	163	2	0	0
6	Q	109	788	491	132	163	2	0	0
6	S	109	788	491	132	163	2	0	0

- Molecule 7 is a protein called HB27 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	O	110	806	506	138	160	2	0	0

- Molecule 8 is a protein called FC05 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	P	120	927	585	148	187	7	0	0
			Total	C	N	O	S		
8	U	120	927	585	148	187	7	0	0
			Total	C	N	O	S		
8	V	120	931	587	149	188	7	0	0

- Molecule 9 is a protein called HB27 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	R	119	899	566	157	172	4	0	0

- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	F	2	28	16	2	10	0	0
			Total	C	N	O		
10	G	2	28	16	2	10	0	0
			Total	C	N	O		
10	M	2	28	16	2	10	0	0
			Total	C	N	O		
10	W	2	28	16	2	10	0	0
			Total	C	N	O		
10	X	2	28	16	2	10	0	0
			Total	C	N	O		
10	Y	2	28	16	2	10	0	0
			Total	C	N	O		
10	Z	2	28	16	2	10	0	0
			Total	C	N	O		
10	a	2	28	16	2	10	0	0

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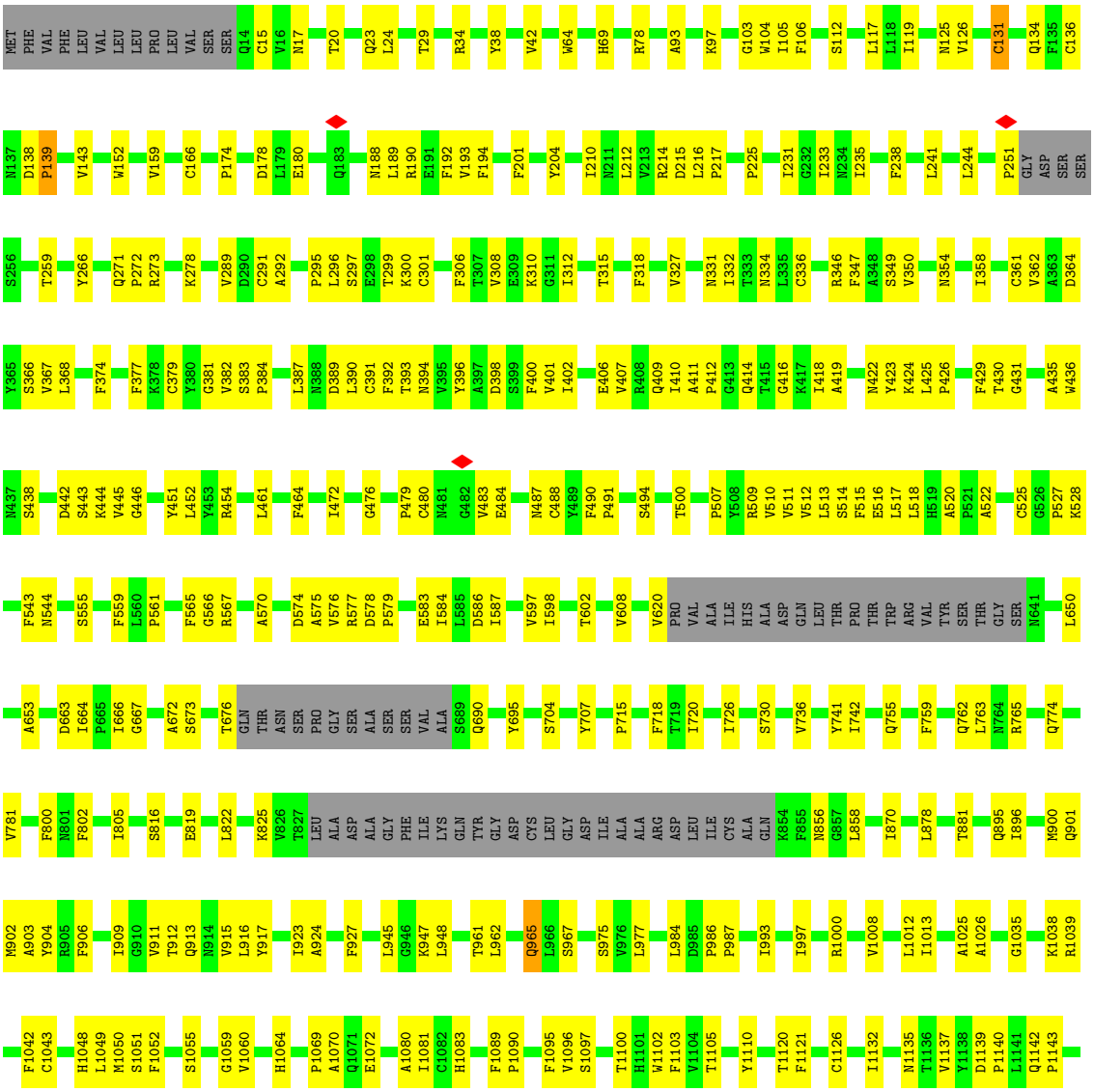
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	b	2	28	16	2	10	0	0
			Total	C	N	O		
10	c	2	28	16	2	10	0	0
			Total	C	N	O		
10	d	2	28	16	2	10	0	0
			Total	C	N	O		
10	e	2	28	16	2	10	0	0

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: 59% 24% 16%



S1147 PHE LYS GLU GLU LEU ASP LYS TYR PHE LYS ASN HIS THR SER PRO ASP VAL ASP LEU GLY ASP ILE SER GLY ILE ASN ALA SER VAL VAL ASN LEU ASN GLU VAL ALA LYS ASN LEU GLU SER LEU ILE ASP LEU GLN GLU LEU GLY LYS TYR

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

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

- Molecule 1: Spike glycoprotein

Chain B: 63% 20% 16%

MET PHE VAL PHE LEU VAL LEU LEU PRO LEU VAL SER SER Q14 C15 L18 T19 T20 R21 T22 Q23 L24 V42 F43 H49 S50 T51 W64 F65 H66 A67 T76 K77 R78 F79 D80 A93 R102 G103 W104 I105 F106 S112 Q115 L118 I119 V120 N121 N125

V126 C131 Q134 F135 C136 P139 V143 K147 W152 R158 V159 C166 Q173 P174 D178 L179 Q183 F186 L189 R190 V193 D198 G199 Y200 Y204 S205 T208 P209 I210 N211 L212 D215 L223 L226 V227 D228 L229 P230 I231 G232

I233 N234 I235 L242 A243 L244 P251 GLY ASP SER SER S256 G257 W258 T259 A264 Y265 Y266 L270 L296 T299 L303 K304 V308 E309 K310 T315 T323 E324 S325 I326 V327 R328 F329 P330 N331 I332 T333 N334 L335 C336 T345 A348 S349 V350 W353

I358 V362 A363 S375 G379 Y380 L387 N388 D389 V395 F400 V401 I402 R403 V407 P412 G416 K417 I418 A419 D420 Y421 N422 D427 C432 W436 N437 S438 L441 V445 G446 G447 N448 Y451 L452 Y453 R454 L455 F456 R457 K458 S459 N460 I468

S469 T470 E471 I472 Y473 Q474 A475 G476 S477 T478 P479 C480 N481 E484 N487 C488 Y489 F490 P491 L492 Q493 S494 Y495 G496 F497 N501 Y505 R509 L517 L518 H519 A520 P521 A522 T523 V524 C525 G526 P527 K528 K529 S530 T531 N532 L533 N542 F543 N544 G545 L546 T547 S555

F559 F562 Q563 Q564 R567 D568 I569 T573 V576 R577 D578 P579 I584 L585 D586 I587 T599 P600 G601 T602 V608 A609 V610 L611 Y612 V620 PRO VAL ALA ILE HIS ALA ASP GLN LEU THR PRO THR TRP ARG VAL TYR SER THR GLY SER N641 I666 I670

C671 A672 T676 GLN THR ASN SER PRO GLY SER ALA SER SER VAL ALA S689 L699 S704 Y707 S708 S711 P715 T716 N717 F718 T719 I720 T723 I726 C749 L752 L753 F759 K790 F797 F800 N801 F802 S803 Q804 I805 S816 E819

L822 K825 V826 T827 LEU ALA ASP ALA GLY PHE ILE LYS GLN TYR GLY ASP CYS LEU GLY ASP ILE ALA ALA ARG ASP LEU ILE CYS ALA GLN K854 F855 N856 G857 L858 L864 L878 W886 L894 Q895 F898 M902 A903 Y904 L916 I923 A924 F927 L945

L948 T961 L962 V963 K964 Q965 S968 L977 I980 R983 A989 E990 V991 Q992 I993 L1001 Q1002 S1003 L1012 I1013 E1031 S1037 C1043 G1044 H1048 F1052 P1053 Q1054 G1059 V1060 V1061 H1064 V1065 T1066 A1070 Q1071 E1072 K1073 A1078 P1079 A1080

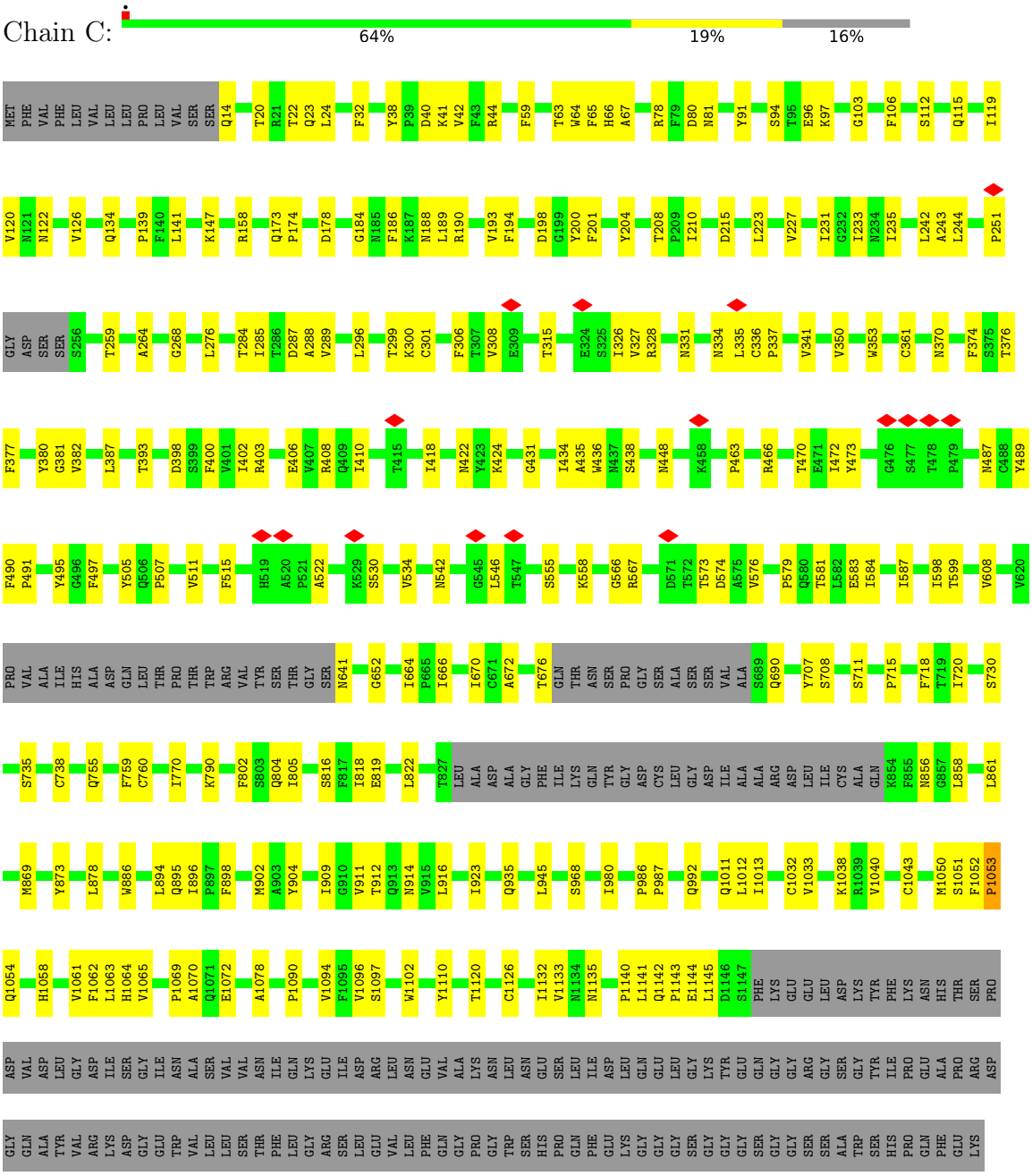
H1083 D1084 G1085 P1090 V1096 S1097 W1102 Y1110 T1120 C1126 I1132 V1133 N1134 N1135 T1136 V1137 P1140 L1141 Q1142 P1143 E1144 L1145 D1146 S1147 PHE LYS GLU GLU LEU ASP LYS TYR PHE LYS ASN HIS THR SER PRO ASP VAL ASP LEU ASP ASP ILE SER GLY ILE ASN ALA SER

VAL VAL ASN ILE GLN LYS GLU ILE ASP ARG LEU ASN GLU VAL ALA LYS ASN LEU ASN SER LEU ILE ASP LEU GLU ILE ASP LEU GLN GLU LEU LEU LYS TYR GLU GLN GLY GLY ARG GLY SER GLY TYR ILE PRO GLU ALA PRO ARG ASP GLY GLN ALA TYR VAL ARG LYS ASP GLY GLU TRP VAL LEU

LEU SER THR PHE LEU GLY ARG SER LEU GLU VAL LEU PHE GLN GLY PRO GLY TRP SER HIS PRO GLN PHE GLU LYS GLY GLY GLY SER GLY GLY SER GLY GLY SER SER ALA TRP SER HIS PRO GLN PHE GLU LYS

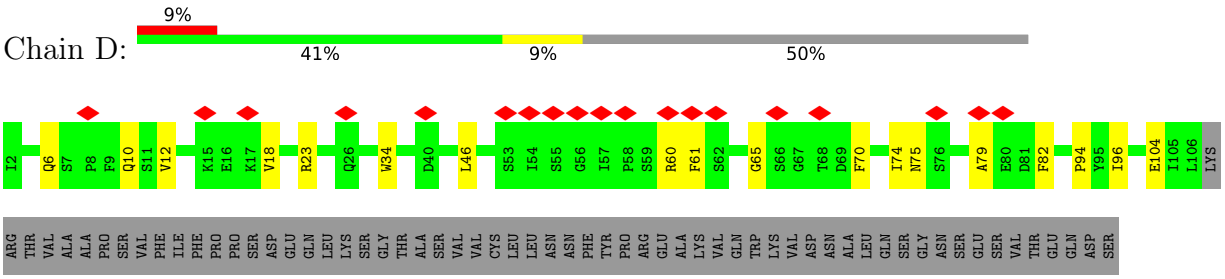
- Molecule 1: Spike glycoprotein

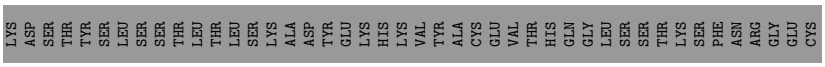
Chain C:



- Molecule 2: H014 light chain

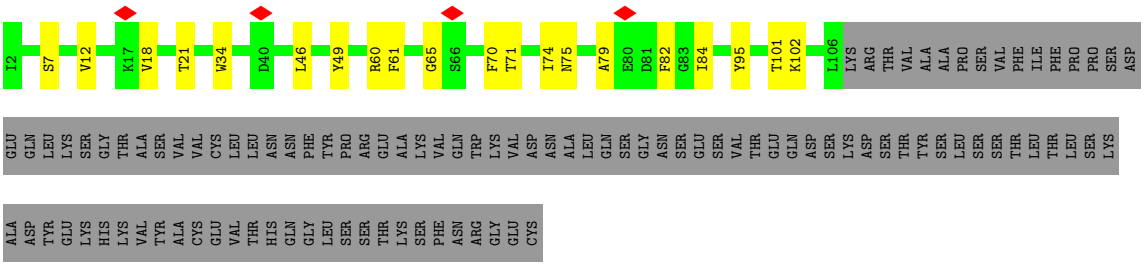
Chain D:





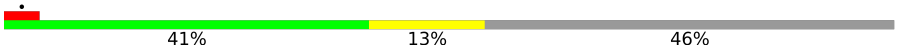
- Molecule 2: H014 light chain

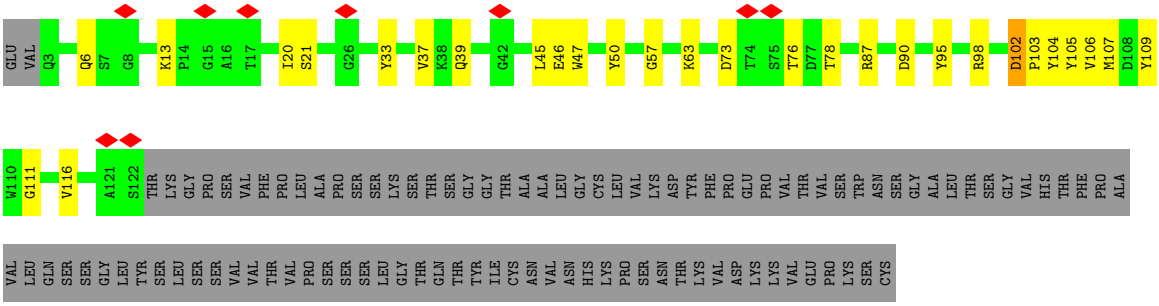
Chain H:



- Molecule 3: H014 heavy chain

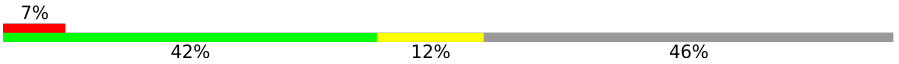
Chain E:

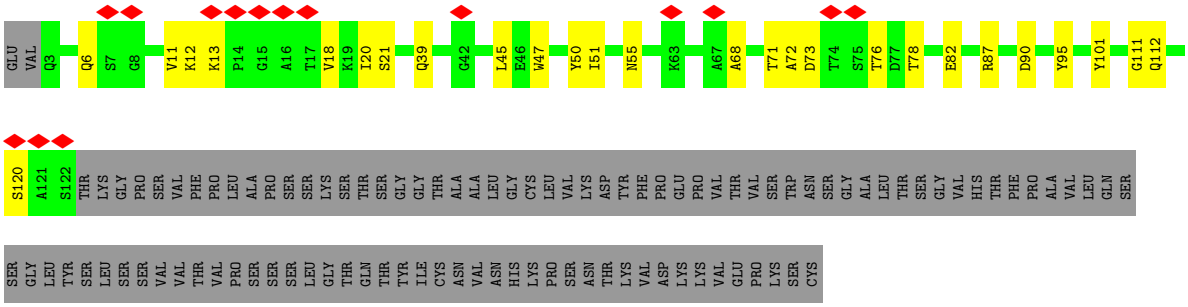




- Molecule 3: H014 heavy chain

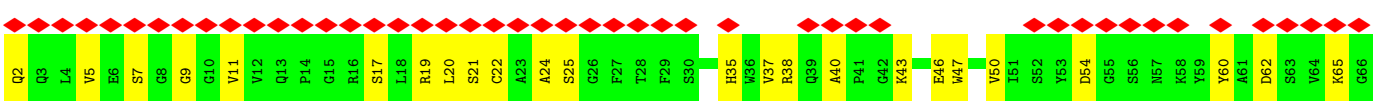
Chain L:

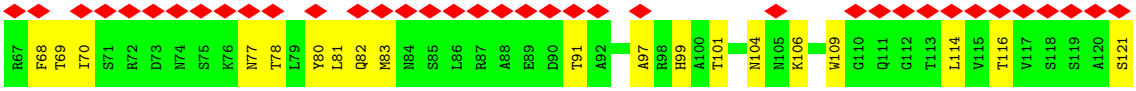




- Molecule 4: P17 heavy chain

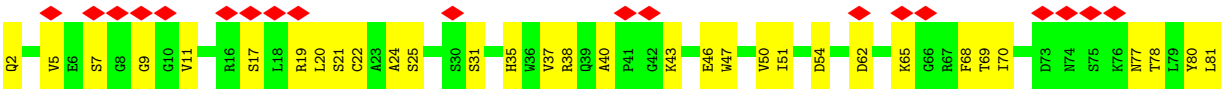
Chain I:

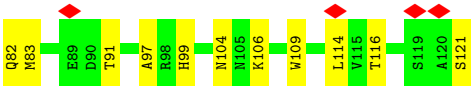




• Molecule 4: P17 heavy chain

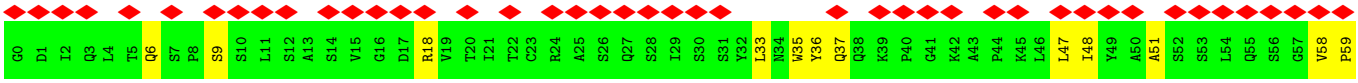
Chain J:

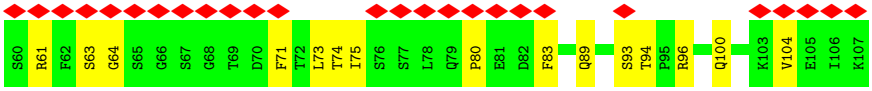




• Molecule 5: P17 light chain

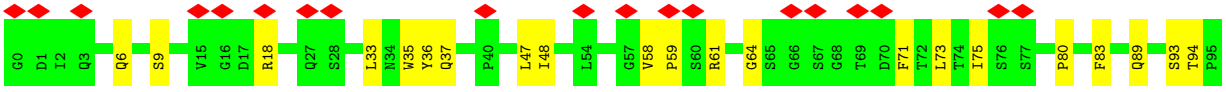
Chain K:

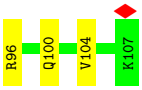




• Molecule 5: P17 light chain

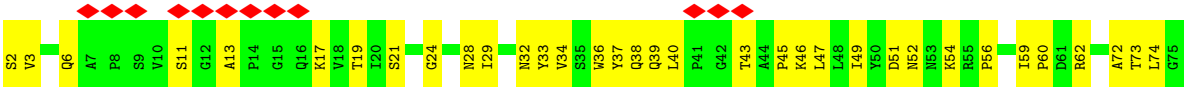
Chain T:

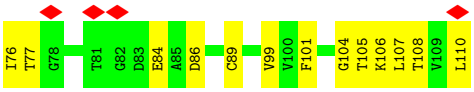




• Molecule 6: FC05 light chain

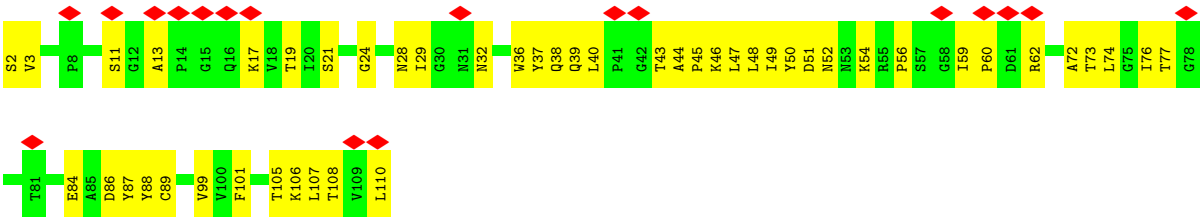
Chain N:





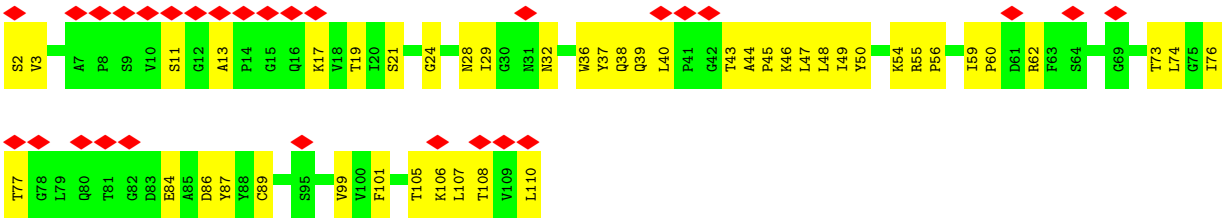
• Molecule 6: FC05 light chain

Chain Q: 17% 56% 44%



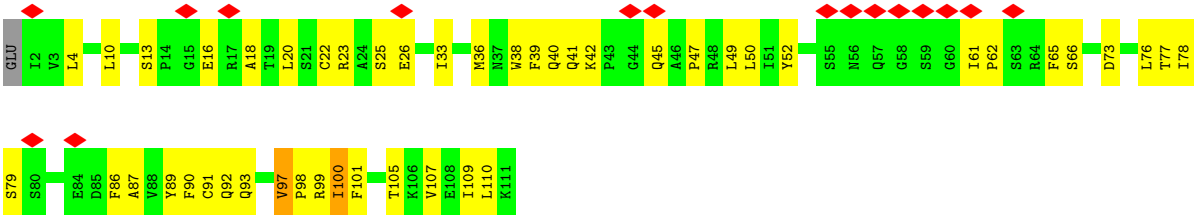
- Molecule 6: FC05 light chain

Chain S: 27% 59% 41%



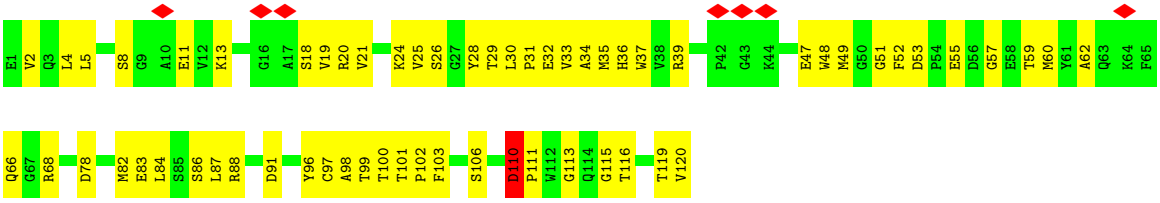
- Molecule 7: HB27 light chain

Chain O: 14% 57% 41%



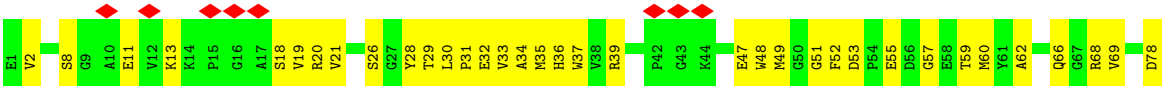
- Molecule 8: FC05 heavy chain

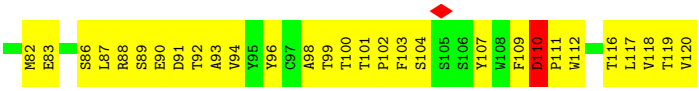
Chain P: 6% 49% 50%



- Molecule 8: FC05 heavy chain

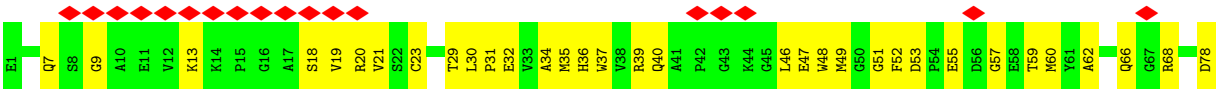
Chain U: 8% 47% 52%

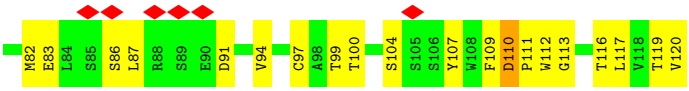




• Molecule 8: FC05 heavy chain

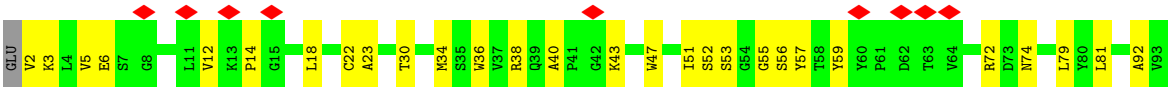
Chain V:

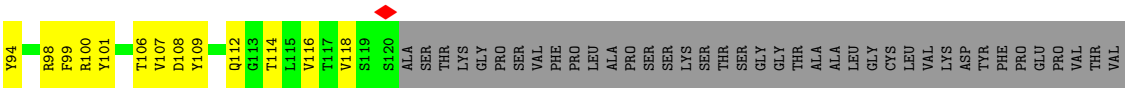




• Molecule 9: HB27 heavy chain

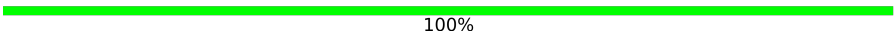
Chain R:





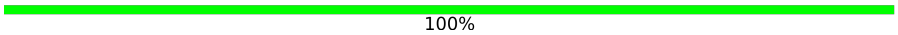
• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:



• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

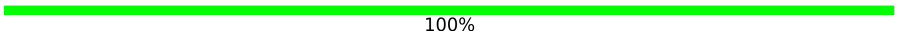
Chain G:



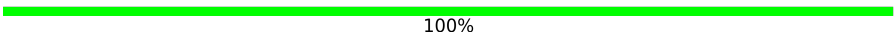
• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W: 

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X: 

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:

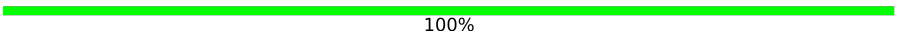
• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:

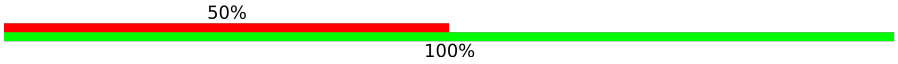
• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b: 

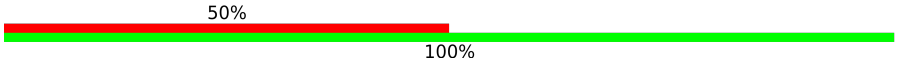
• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c: 

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e: 

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	133167	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 ($e^-/Å^2$)	60	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	0.033	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	416.0, 416.0, 416.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	A	0.63	0/8560	0.63	1/11652 (0.0%)
1	B	0.63	0/8529	0.63	0/11615
1	C	0.63	0/8549	0.62	0/11639
2	D	0.46	0/722	0.58	0/992
2	H	0.45	0/722	0.59	0/992
3	E	0.62	0/927	0.68	0/1266
3	L	0.60	0/927	0.64	0/1266
4	I	0.38	0/931	0.61	0/1262
4	J	0.40	0/931	0.61	0/1262
5	K	0.56	0/834	0.62	0/1131
5	T	0.57	0/834	0.62	0/1131
6	N	0.32	0/804	0.53	0/1095
6	Q	0.32	0/804	0.52	0/1095
6	S	0.30	0/804	0.51	0/1095
7	O	0.53	0/823	0.66	0/1118
8	P	0.44	0/951	0.63	1/1294 (0.1%)
8	U	0.44	0/951	0.61	1/1294 (0.1%)
8	V	0.47	0/955	0.61	0/1299
9	R	0.59	0/919	0.65	0/1246
All	All	0.58	0/39477	0.62	3/53744 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	131	CYS	N-CA-CB	8.19	125.33	110.60
8	P	110	ASP	CB-CA-C	7.46	125.32	110.40
8	U	110	ASP	CB-CA-C	5.94	122.27	110.40

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	8366	0	8159	426	0
1	B	8334	0	8110	343	0
1	C	8354	0	8142	280	0
2	D	704	0	565	10	0
2	H	704	0	565	19	0
3	E	903	0	825	47	0
3	L	903	0	825	30	0
4	I	912	0	874	33	0
4	J	912	0	874	30	0
5	K	817	0	800	33	0
5	T	817	0	800	22	0
6	N	788	0	766	47	0
6	Q	788	0	766	56	0
6	S	788	0	766	56	0
7	O	806	0	758	51	0
8	P	927	0	872	56	0
8	U	927	0	872	75	0
8	V	931	0	878	75	0
9	R	899	0	865	43	0
10	F	28	0	25	0	0
10	G	28	0	25	0	0
10	M	28	0	25	6	0
10	W	28	0	25	0	0
10	X	28	0	25	0	0
10	Y	28	0	25	0	0
10	Z	28	0	25	4	0
10	a	28	0	25	0	0
10	b	28	0	25	0	0
10	c	28	0	25	0	0
10	d	28	0	25	0	0
10	e	28	0	25	0	0
All	All	38916	0	37382	1585	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 21.

The worst 5 of 1585 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)
3:L:47:TRP:CZ2	3:L:50:TYR:HD2	1.22	1.56
3:L:47:TRP:HZ2	3:L:50:TYR:CD2	1.27	1.53
1:B:1044:GLY:HA3	1:B:1064:HIS:CE1	1.43	1.50
9:R:94:TYR:CE2	9:R:116:VAL:HG21	1.46	1.46
1:A:565:PHE:CD1	1:A:576:VAL:HG12	1.50	1.46

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	1062/1281 (83%)	1034 (97%)	27 (2%)	1 (0%)	48	79
1	B	1062/1281 (83%)	1025 (96%)	35 (3%)	2 (0%)	44	73
1	C	1062/1281 (83%)	1031 (97%)	29 (3%)	2 (0%)	44	73
2	D	103/210 (49%)	86 (84%)	17 (16%)	0	100	100
2	H	103/210 (49%)	89 (86%)	14 (14%)	0	100	100
3	E	118/223 (53%)	111 (94%)	6 (5%)	1 (1%)	16	51
3	L	118/223 (53%)	113 (96%)	5 (4%)	0	100	100
4	I	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
4	J	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
5	K	106/108 (98%)	103 (97%)	3 (3%)	0	100	100
5	T	106/108 (98%)	103 (97%)	3 (3%)	0	100	100
6	N	107/109 (98%)	100 (94%)	7 (6%)	0	100	100
6	Q	107/109 (98%)	100 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	S	107/109 (98%)	100 (94%)	7 (6%)	0	100	100
7	O	108/111 (97%)	97 (90%)	7 (6%)	4 (4%)	2	22
8	P	118/120 (98%)	109 (92%)	8 (7%)	1 (1%)	16	51
8	U	118/120 (98%)	109 (92%)	7 (6%)	2 (2%)	7	37
8	V	118/120 (98%)	109 (92%)	7 (6%)	2 (2%)	7	37
9	R	117/223 (52%)	109 (93%)	8 (7%)	0	100	100
All	All	4976/6186 (80%)	4738 (95%)	223 (4%)	15 (0%)	38	67

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	O	100	ILE
8	P	110	ASP
8	U	110	ASP
8	V	110	ASP
1	B	334	ASN

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	933/1106 (84%)	930 (100%)	3 (0%)	91	96
1	B	925/1106 (84%)	925 (100%)	0	100	100
1	C	929/1106 (84%)	927 (100%)	2 (0%)	92	96
2	D	60/189 (32%)	60 (100%)	0	100	100
2	H	60/189 (32%)	60 (100%)	0	100	100
3	E	92/190 (48%)	91 (99%)	1 (1%)	70	83
3	L	92/190 (48%)	92 (100%)	0	100	100
4	I	95/98 (97%)	95 (100%)	0	100	100
4	J	95/98 (97%)	95 (100%)	0	100	100
5	K	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	T	93/93 (100%)	93 (100%)	0	100	100
6	N	88/88 (100%)	88 (100%)	0	100	100
6	Q	88/88 (100%)	88 (100%)	0	100	100
6	S	88/88 (100%)	88 (100%)	0	100	100
7	O	85/95 (90%)	85 (100%)	0	100	100
8	P	100/101 (99%)	100 (100%)	0	100	100
8	U	100/101 (99%)	100 (100%)	0	100	100
8	V	101/101 (100%)	101 (100%)	0	100	100
9	R	92/184 (50%)	92 (100%)	0	100	100
All	All	4209/5304 (79%)	4203 (100%)	6 (0%)	92	97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	495	TYR
1	C	759	PHE
3	E	33	TYR
1	A	759	PHE
1	A	318	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	487	ASN
2	H	91	ASN
8	U	40	GLN
1	C	675	GLN
2	D	91	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

24 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	$\#\|Z\| > 2$
10	NAG	F	1	1,10	14,14,15	0.27	0	17,19,21	0.70	0
10	NAG	F	2	10	14,14,15	0.28	0	17,19,21	0.73	0
10	NAG	G	1	1,10	14,14,15	0.26	0	17,19,21	0.72	0
10	NAG	G	2	10	14,14,15	0.28	0	17,19,21	0.69	0
10	NAG	M	1	1,10	14,14,15	0.27	0	17,19,21	0.67	0
10	NAG	M	2	10	14,14,15	0.26	0	17,19,21	0.70	0
10	NAG	W	1	1,10	14,14,15	0.28	0	17,19,21	0.71	0
10	NAG	W	2	10	14,14,15	0.28	0	17,19,21	0.71	0
10	NAG	X	1	1,10	14,14,15	0.30	0	17,19,21	0.85	0
10	NAG	X	2	10	14,14,15	0.27	0	17,19,21	0.67	0
10	NAG	Y	1	1,10	14,14,15	2.15	1 (7%)	17,19,21	2.41	4 (23%)
10	NAG	Y	2	10	14,14,15	0.26	0	17,19,21	0.70	0
10	NAG	Z	1	1,10	14,14,15	0.28	0	17,19,21	0.61	0
10	NAG	Z	2	10	14,14,15	0.27	0	17,19,21	0.69	0
10	NAG	a	1	1,10	14,14,15	0.27	0	17,19,21	0.67	0
10	NAG	a	2	10	14,14,15	0.28	0	17,19,21	0.69	0
10	NAG	b	1	1,10	14,14,15	0.27	0	17,19,21	0.72	0
10	NAG	b	2	10	14,14,15	0.28	0	17,19,21	0.69	0
10	NAG	c	1	1,10	14,14,15	0.28	0	17,19,21	0.69	0
10	NAG	c	2	10	14,14,15	0.27	0	17,19,21	0.70	0
10	NAG	d	1	1,10	14,14,15	0.27	0	17,19,21	0.69	0
10	NAG	d	2	10	14,14,15	0.26	0	17,19,21	0.69	0
10	NAG	e	1	1,10	14,14,15	0.28	0	17,19,21	0.62	0
10	NAG	e	2	10	14,14,15	0.28	0	17,19,21	0.71	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
10	NAG	F	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	F	2	10	-	2/6/23/26	0/1/1/1
10	NAG	G	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	G	2	10	-	0/6/23/26	0/1/1/1
10	NAG	M	1	1,10	-	3/6/23/26	0/1/1/1
10	NAG	M	2	10	-	0/6/23/26	0/1/1/1
10	NAG	W	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	W	2	10	-	2/6/23/26	0/1/1/1
10	NAG	X	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	X	2	10	-	0/6/23/26	0/1/1/1
10	NAG	Y	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	Y	2	10	-	0/6/23/26	0/1/1/1
10	NAG	Z	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	Z	2	10	-	2/6/23/26	0/1/1/1
10	NAG	a	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	a	2	10	-	0/6/23/26	0/1/1/1
10	NAG	b	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	b	2	10	-	2/6/23/26	0/1/1/1
10	NAG	c	1	1,10	-	3/6/23/26	0/1/1/1
10	NAG	c	2	10	-	0/6/23/26	0/1/1/1
10	NAG	d	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	d	2	10	-	0/6/23/26	0/1/1/1
10	NAG	e	1	1,10	-	0/6/23/26	0/1/1/1
10	NAG	e	2	10	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	Y	1	NAG	C1-C2	7.99	1.64	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	Y	1	NAG	O5-C1-C2	-7.78	99.00	111.29
10	Y	1	NAG	C1-O5-C5	4.87	118.78	112.19
10	Y	1	NAG	C4-C3-C2	-2.25	107.72	111.02
10	Y	1	NAG	C1-C2-N2	2.19	114.24	110.49

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	F	2	NAG	O7-C7-N2-C2
10	Z	2	NAG	C8-C7-N2-C2
10	Z	2	NAG	O7-C7-N2-C2
10	c	1	NAG	C8-C7-N2-C2
10	c	1	NAG	O7-C7-N2-C2

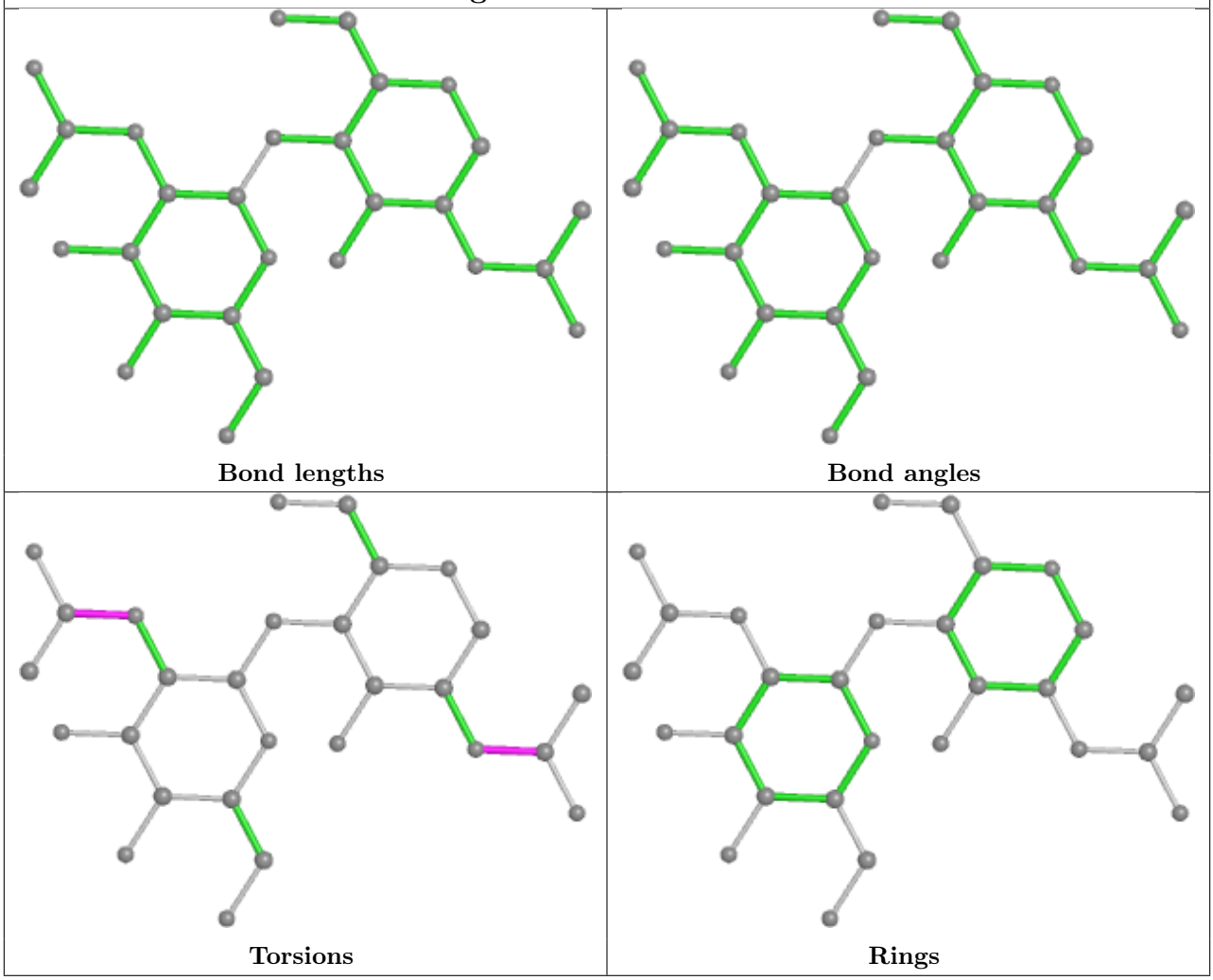
There are no ring outliers.

2 monomers are involved in 10 short contacts:

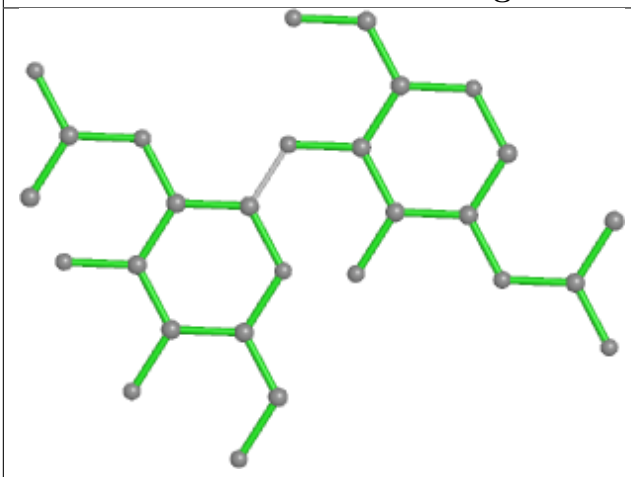
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	Z	1	NAG	4	0
10	M	1	NAG	6	0

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

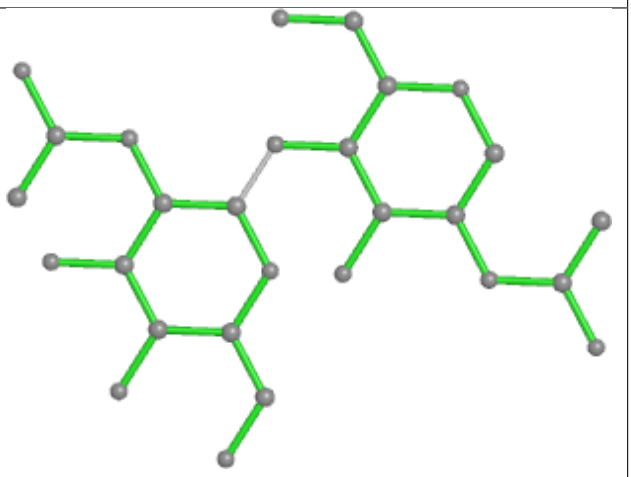
Oligosaccharide Chain F



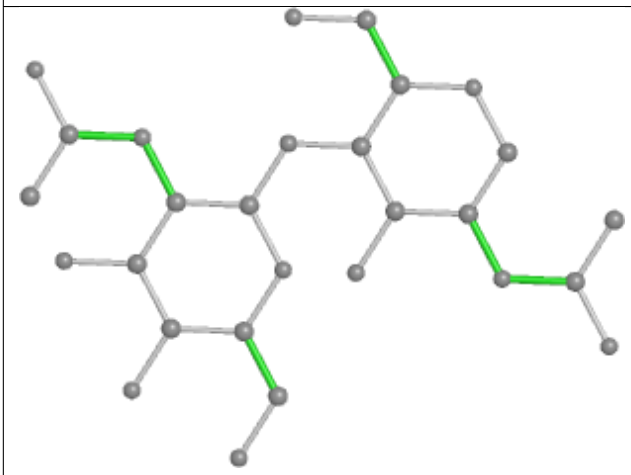
Oligosaccharide Chain G



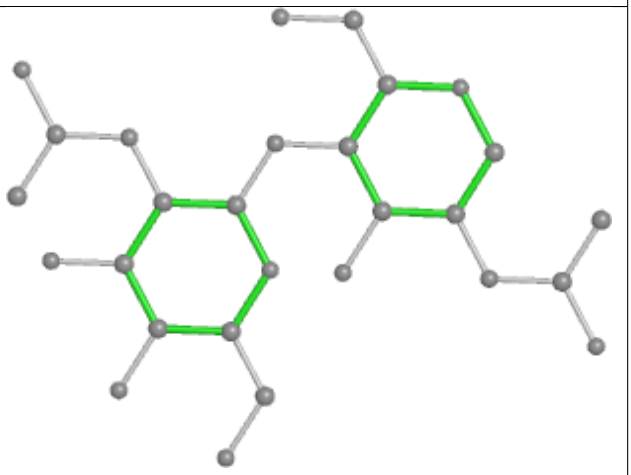
Bond lengths



Bond angles

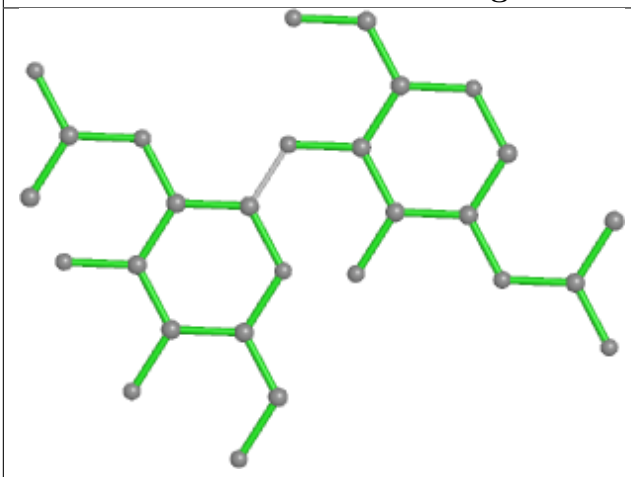


Torsions

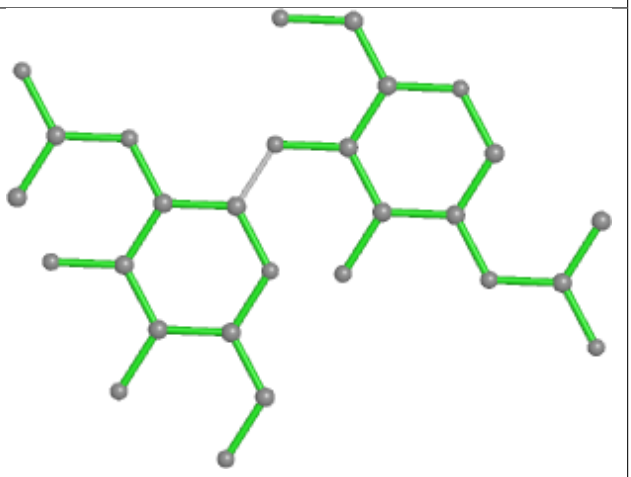


Rings

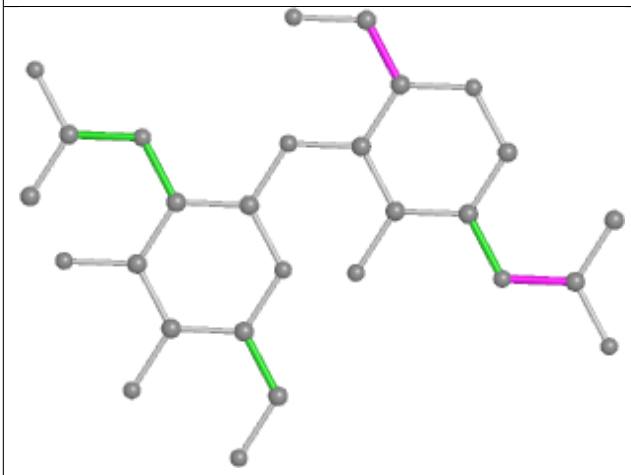
Oligosaccharide Chain M



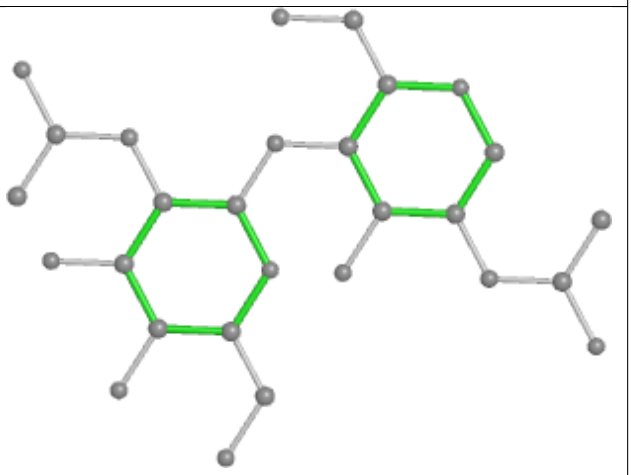
Bond lengths



Bond angles

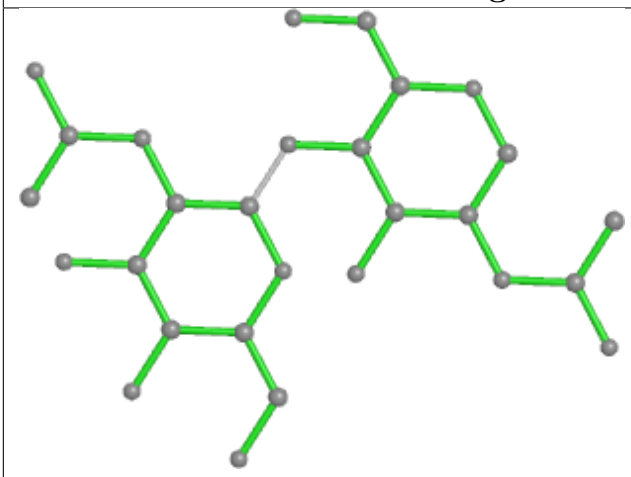


Torsions

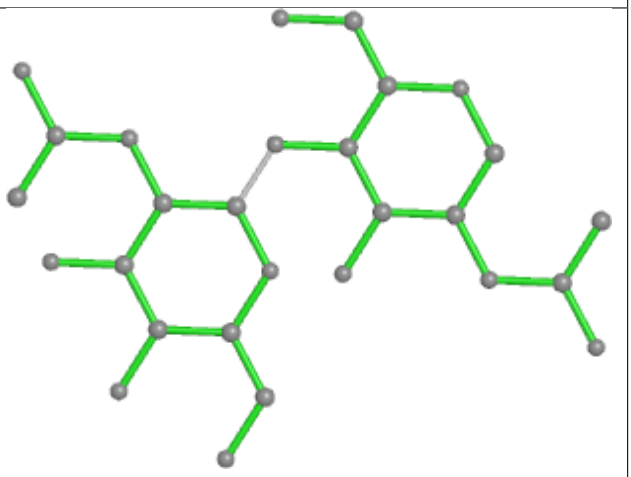


Rings

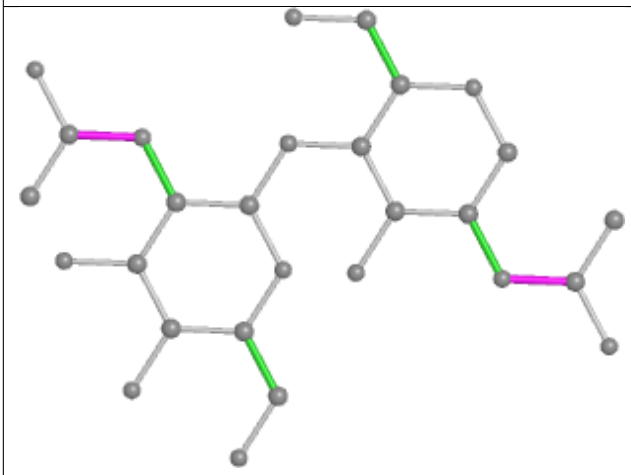
Oligosaccharide Chain W



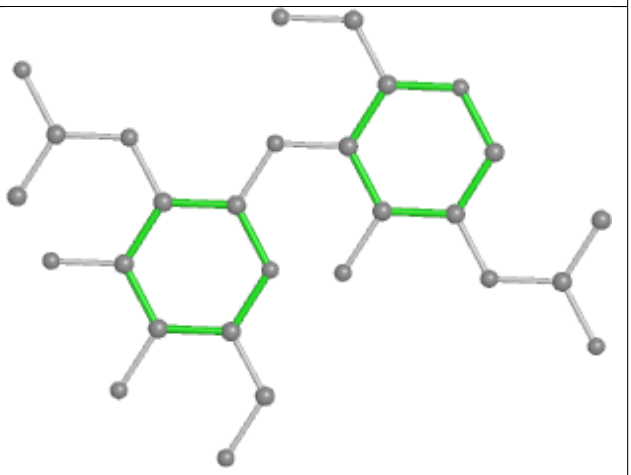
Bond lengths



Bond angles

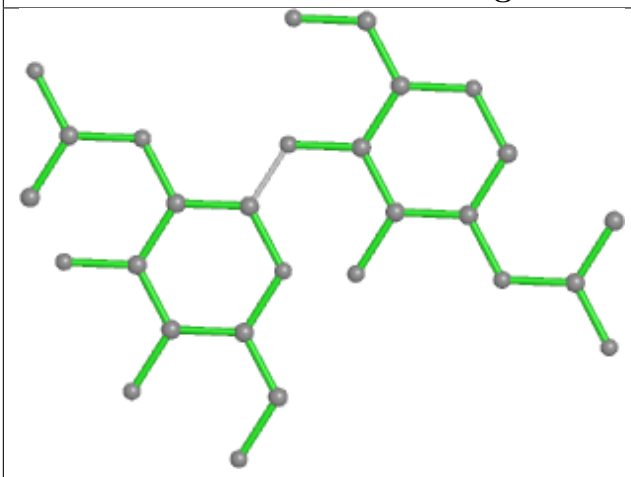


Torsions

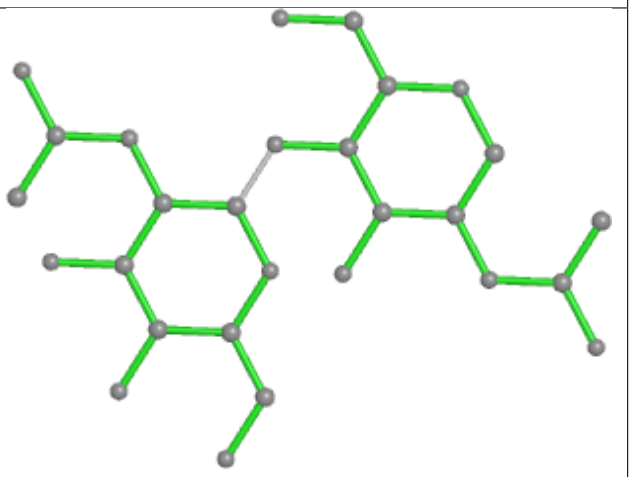


Rings

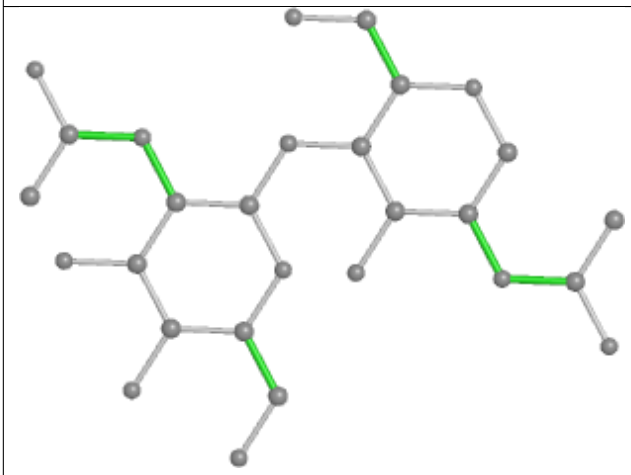
Oligosaccharide Chain X



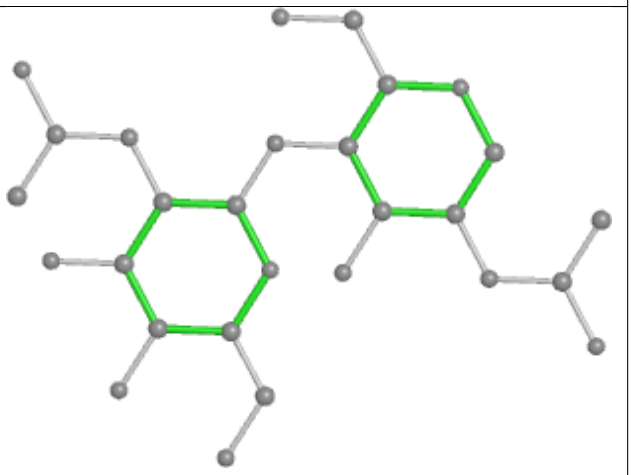
Bond lengths



Bond angles

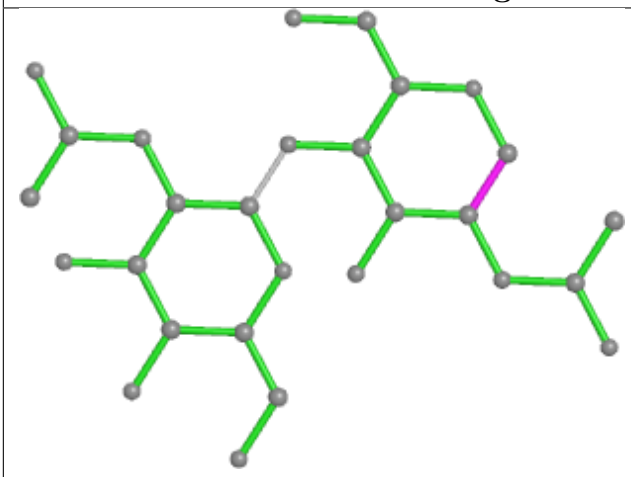


Torsions

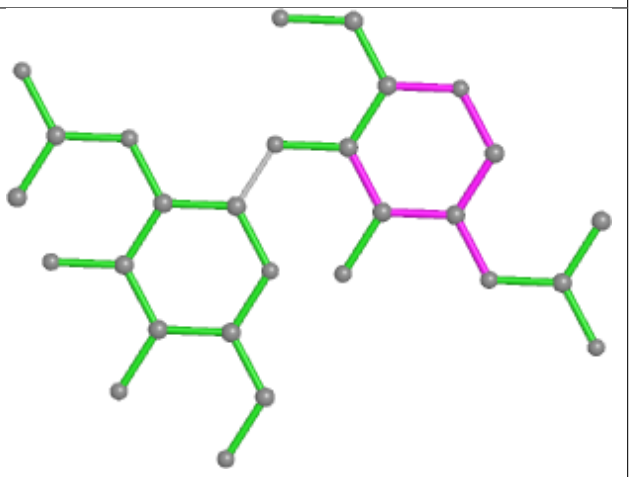


Rings

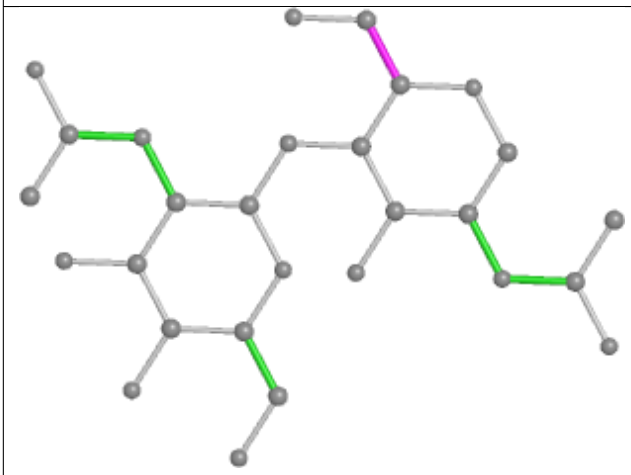
Oligosaccharide Chain Y



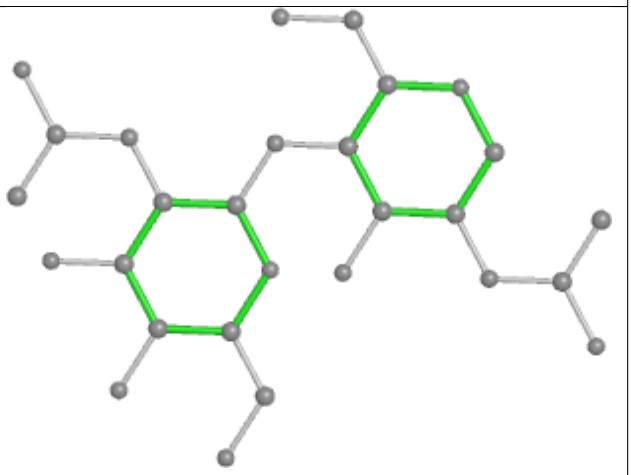
Bond lengths



Bond angles

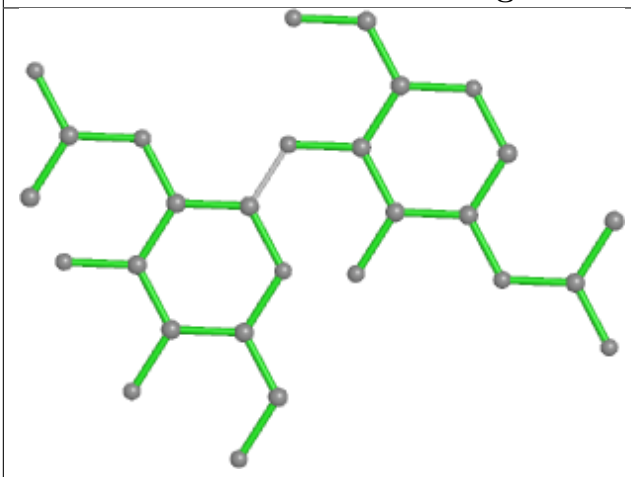


Torsions

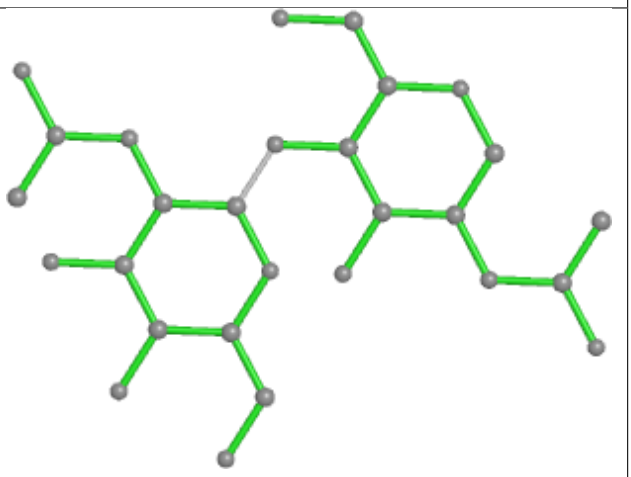


Rings

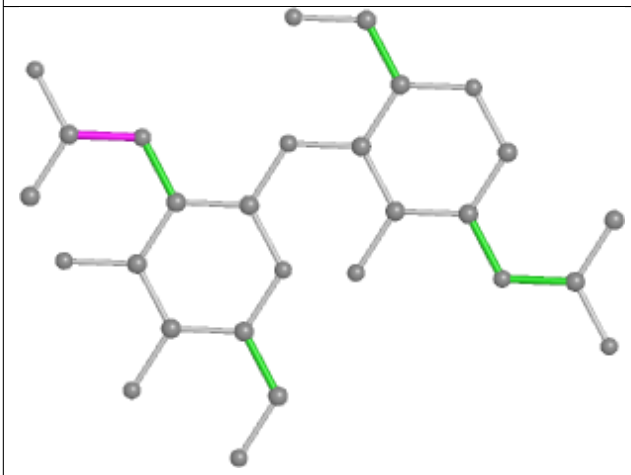
Oligosaccharide Chain Z



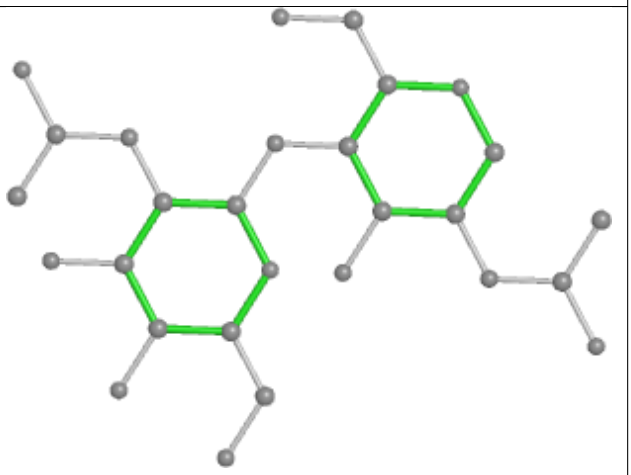
Bond lengths



Bond angles

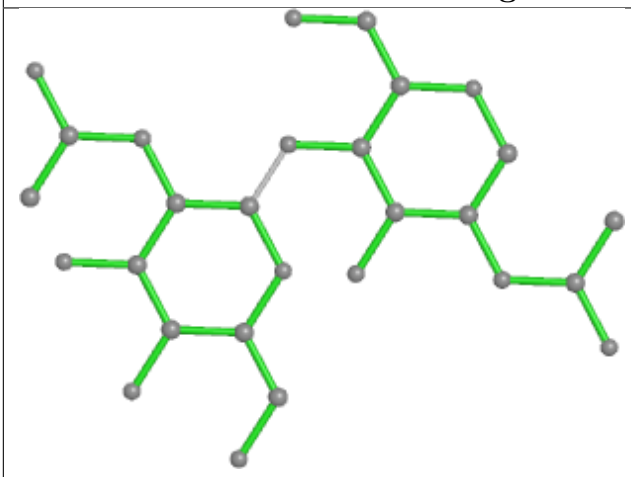


Torsions

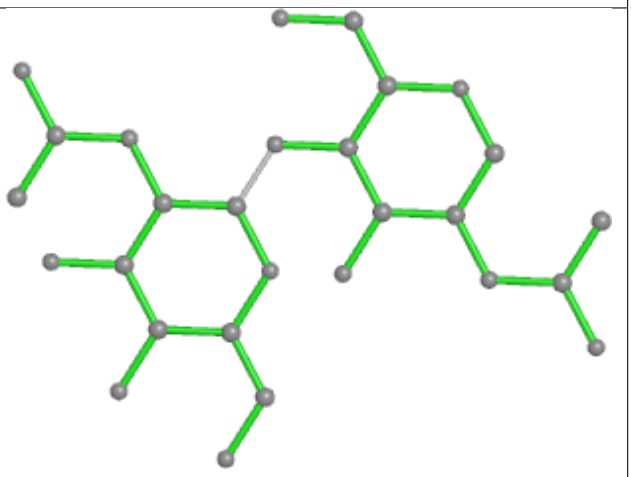


Rings

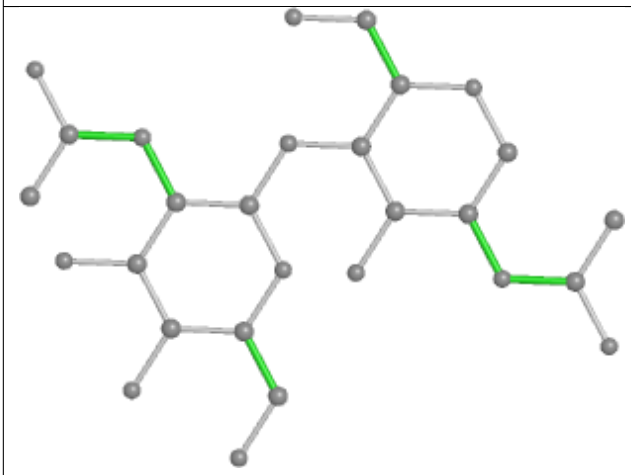
Oligosaccharide Chain a



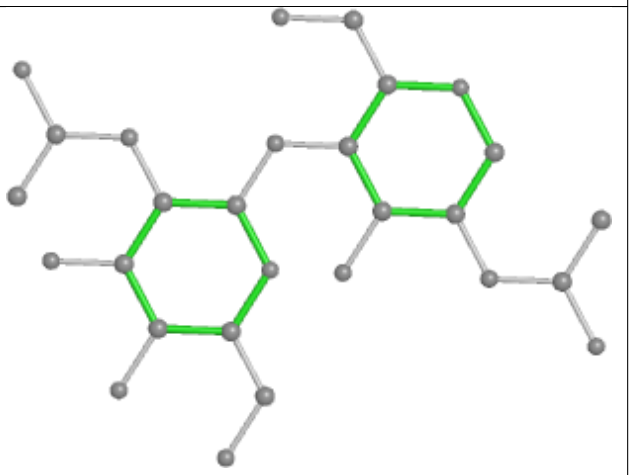
Bond lengths



Bond angles

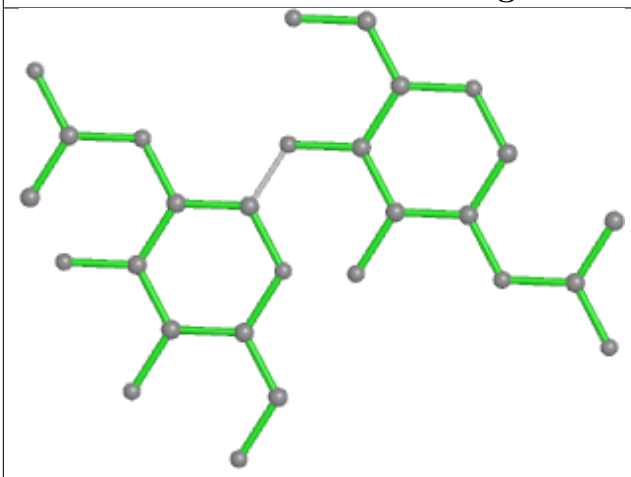


Torsions

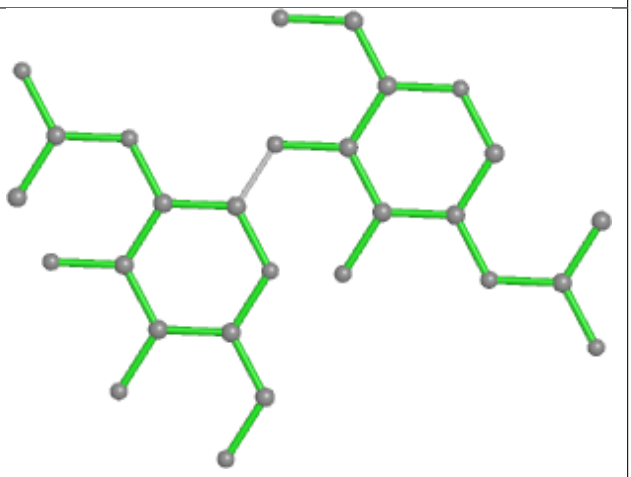


Rings

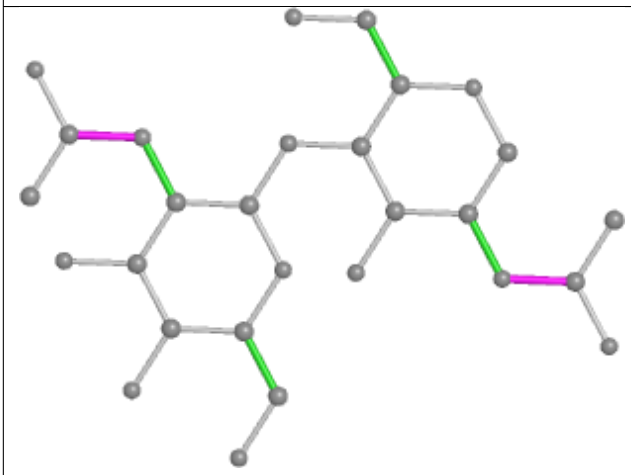
Oligosaccharide Chain b



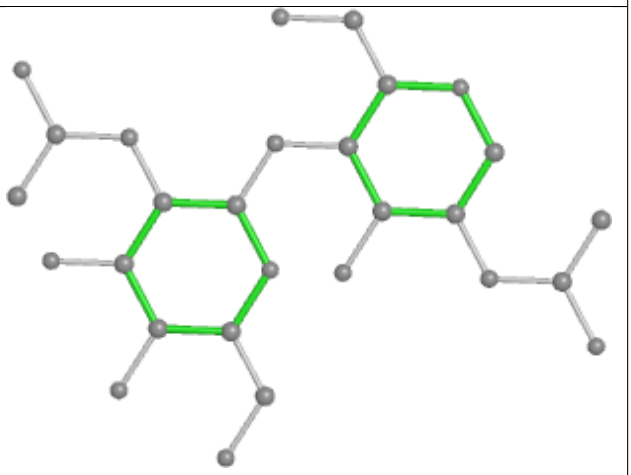
Bond lengths



Bond angles

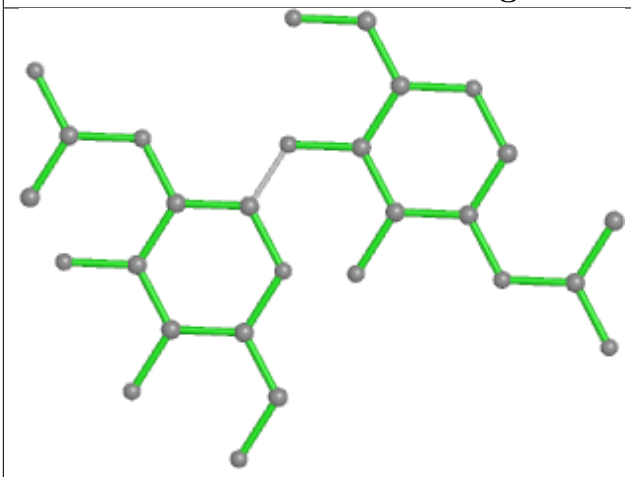


Torsions

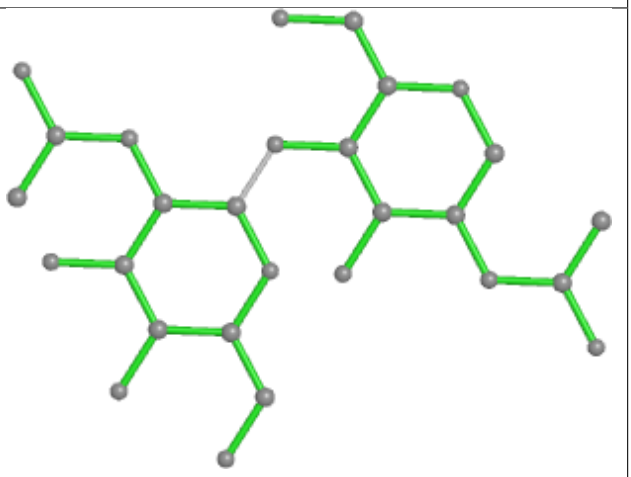


Rings

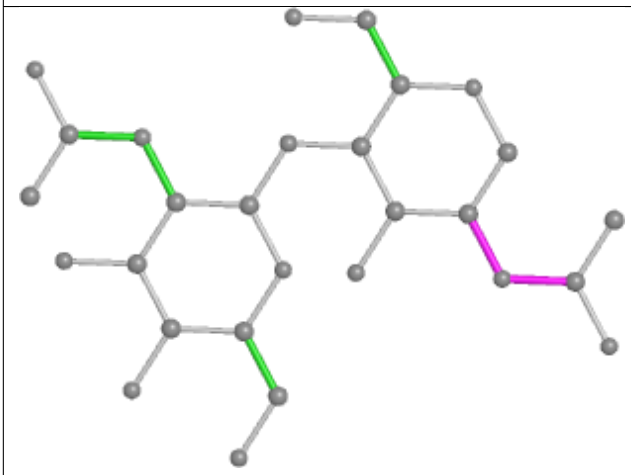
Oligosaccharide Chain c



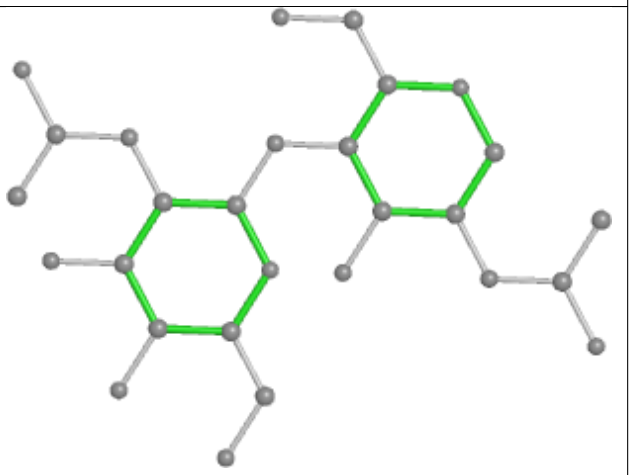
Bond lengths



Bond angles

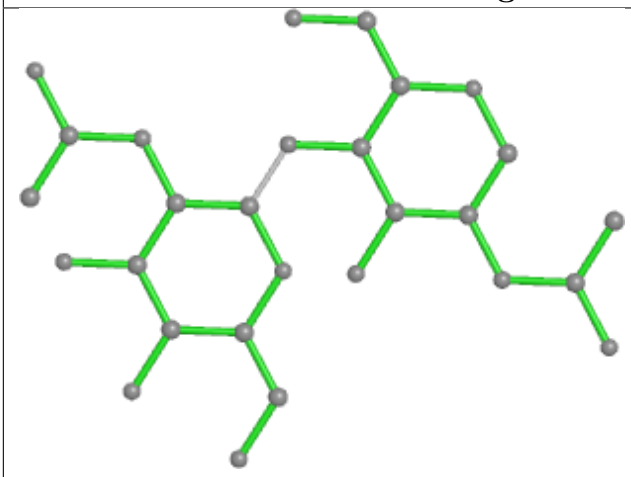


Torsions

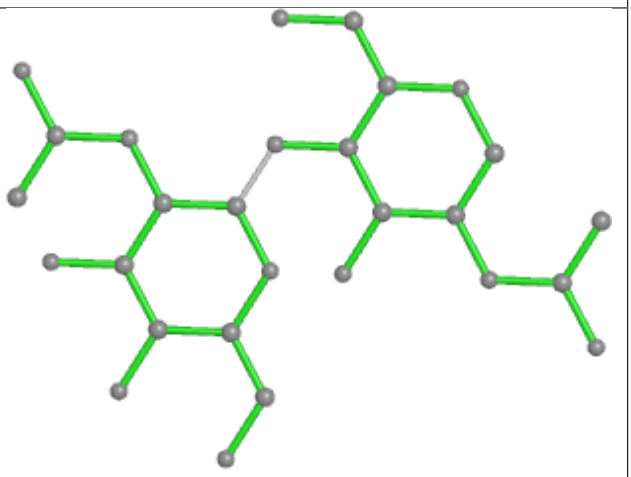


Rings

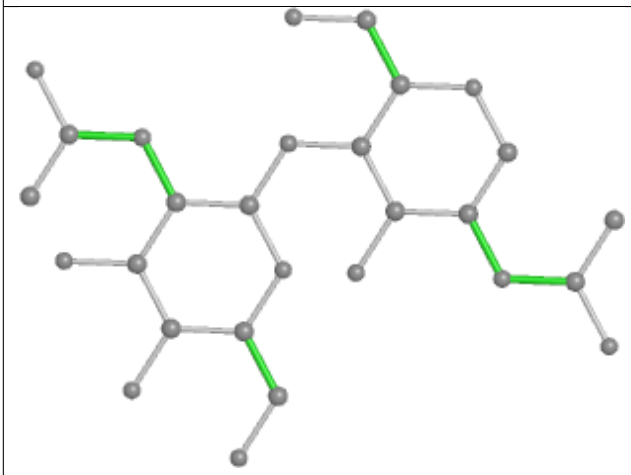
Oligosaccharide Chain d



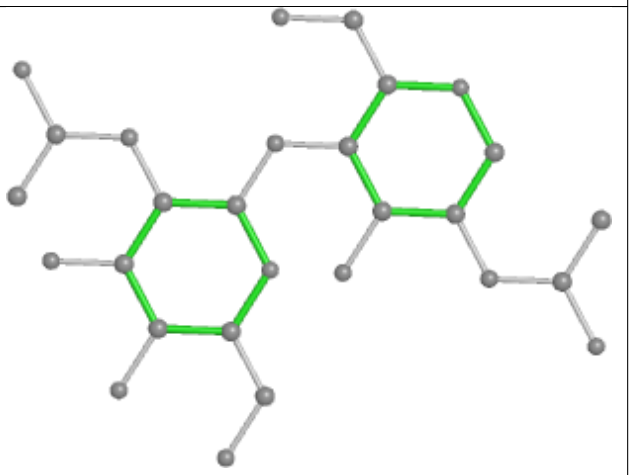
Bond lengths



Bond angles

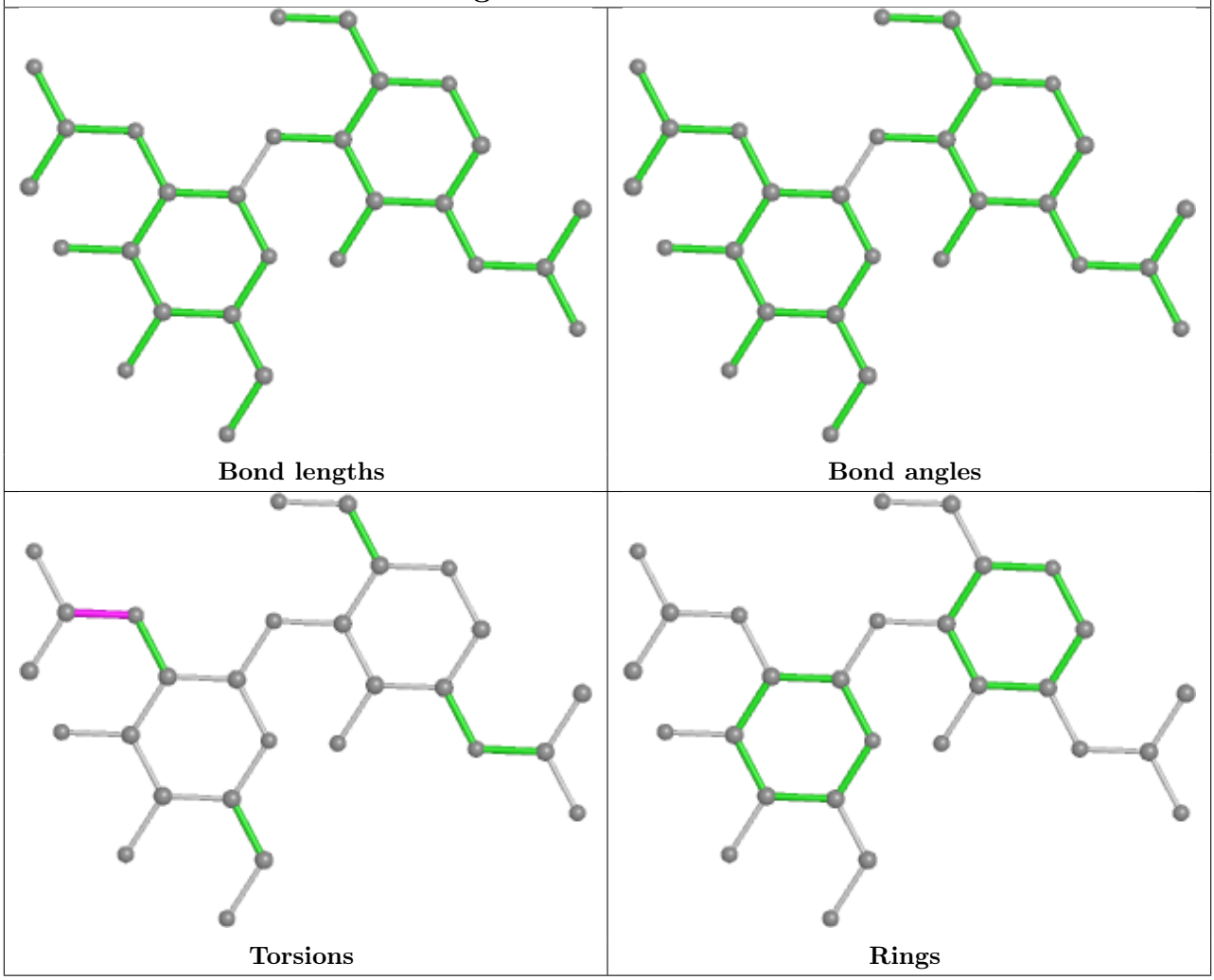


Torsions



Rings

Oligosaccharide Chain e



5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

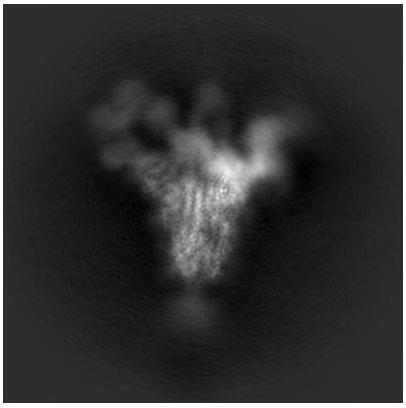
6 Map visualisation (i)

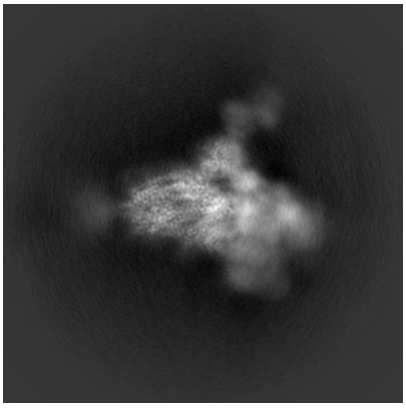
This section contains visualisations of the EMDB entry EMD-30994. These allow visual inspection of the internal detail of the map and identification of artifacts.

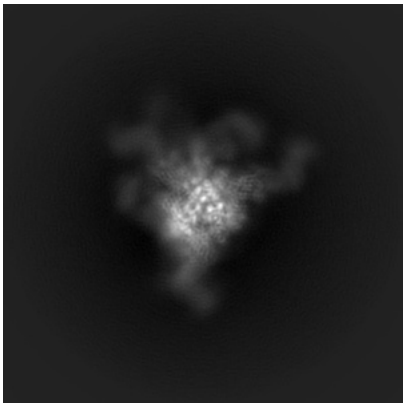
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map


X

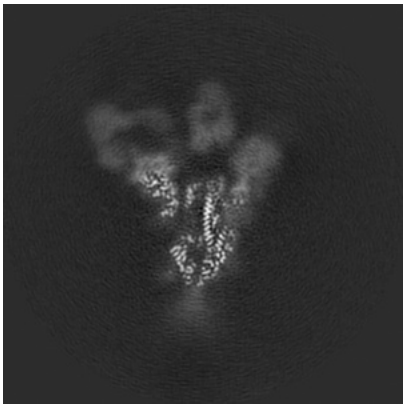

Y

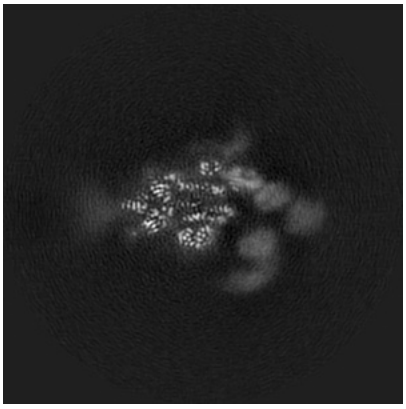

Z

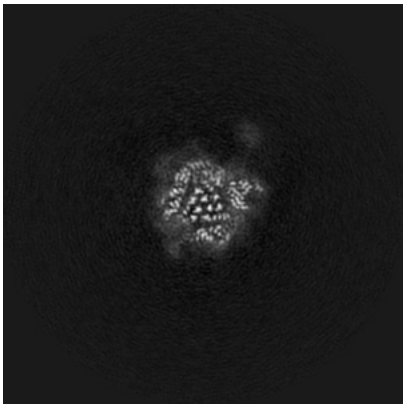
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map


X Index: 200

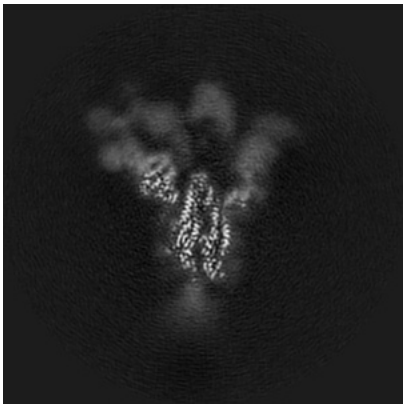

Y Index: 200

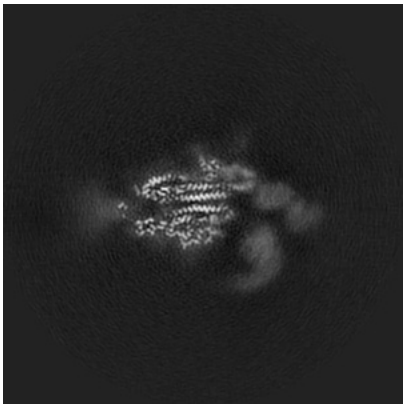

Z Index: 200

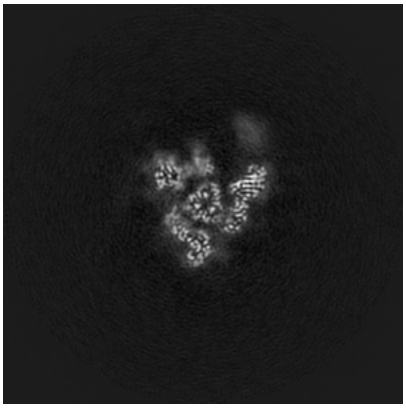
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 191

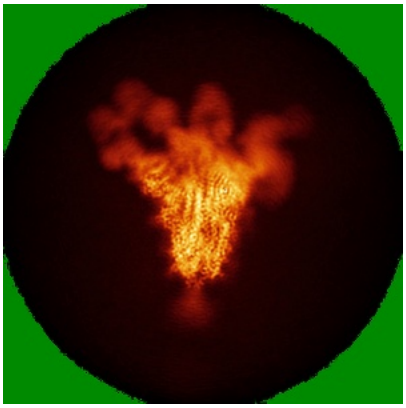

Y Index: 195

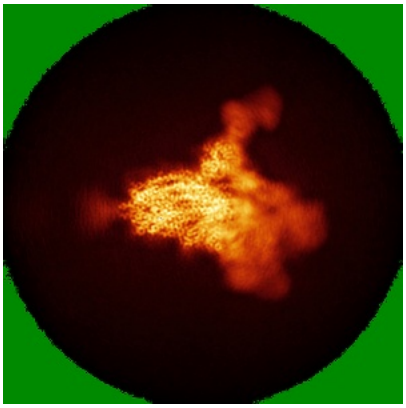

Z Index: 213

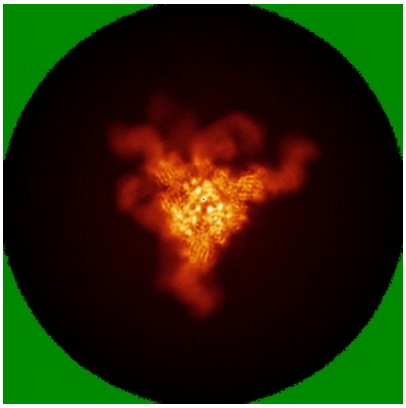
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map


X


Y


Z

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

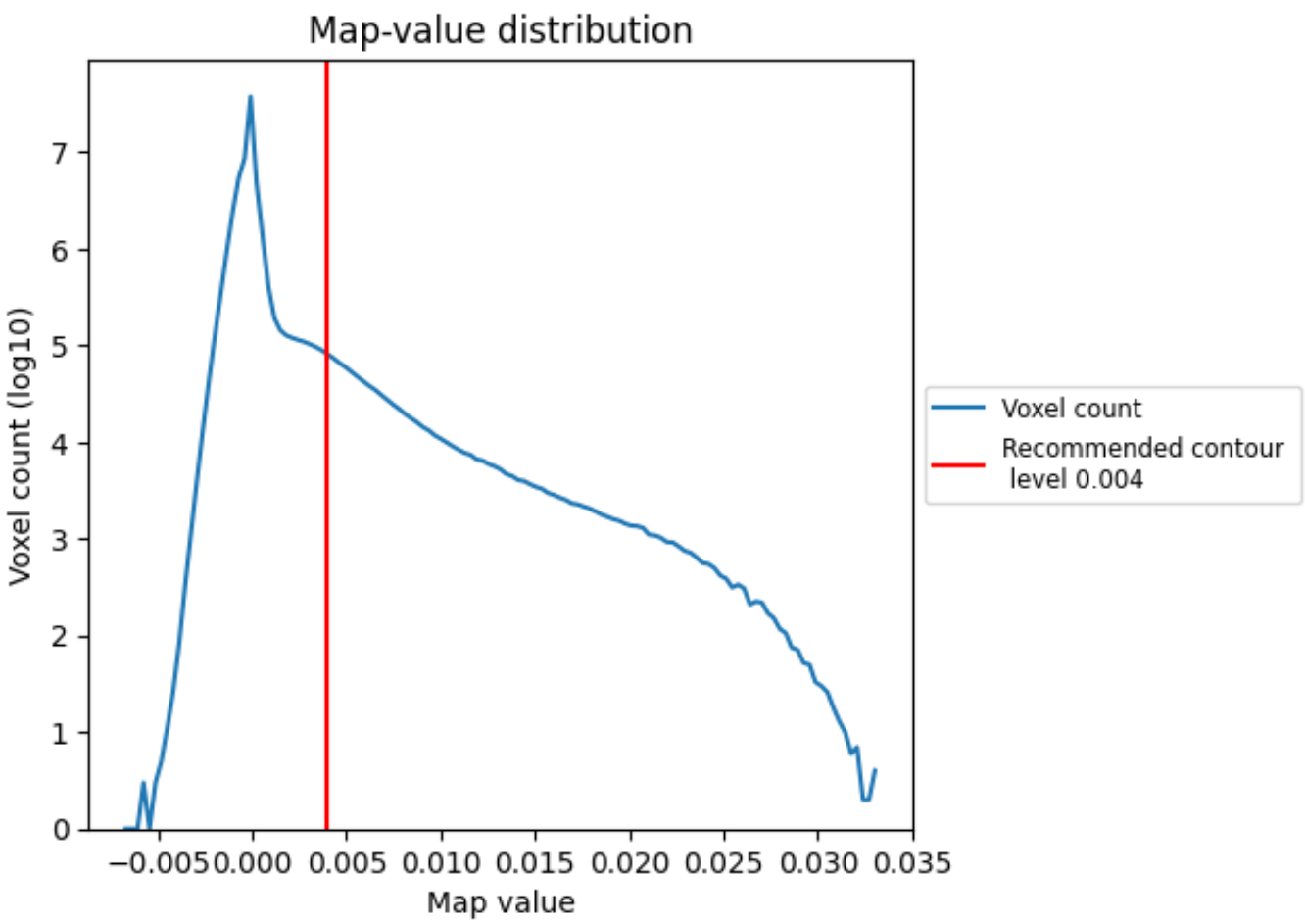
6.6 Mask visualisation (i)

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

7 Map analysis (i)

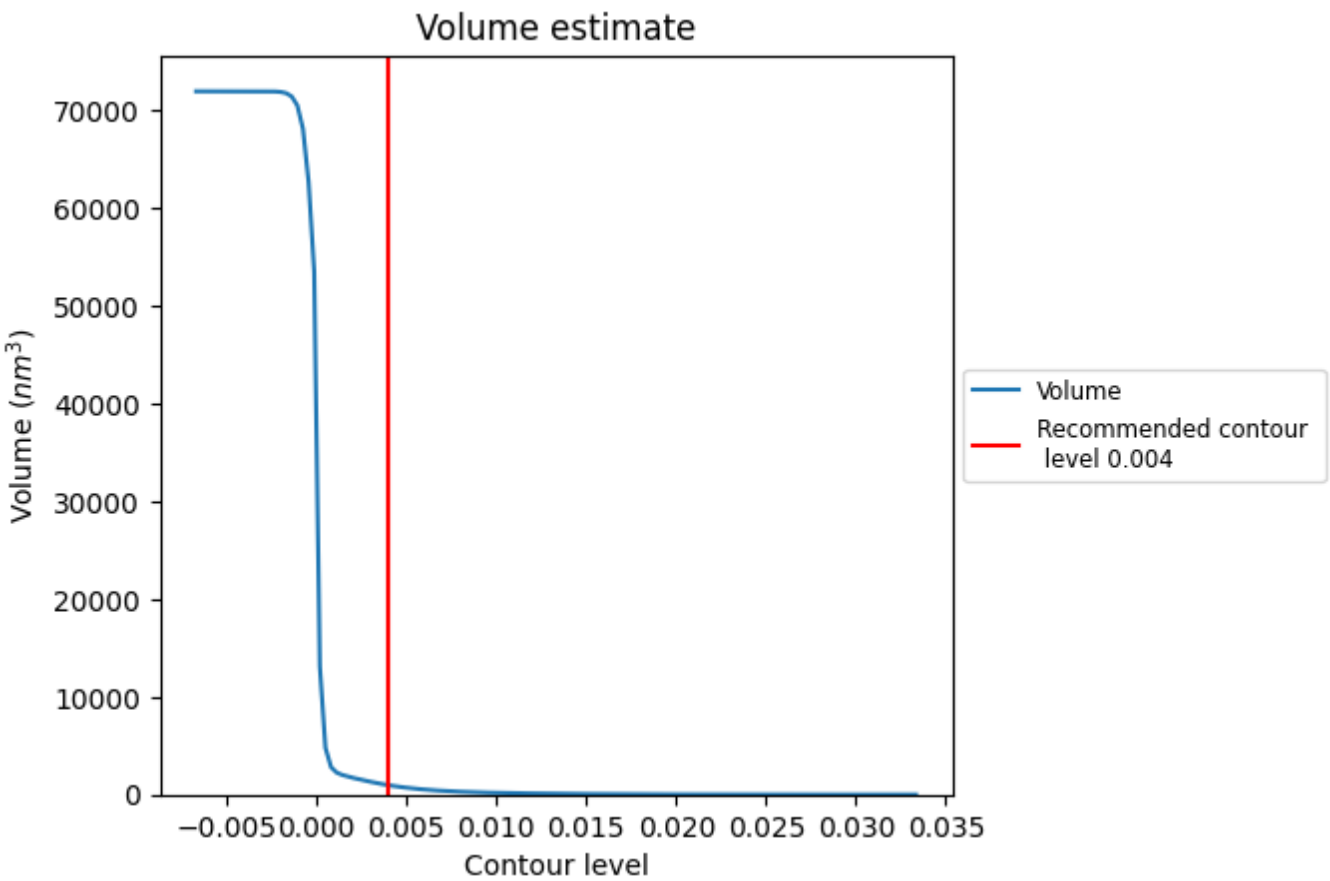
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

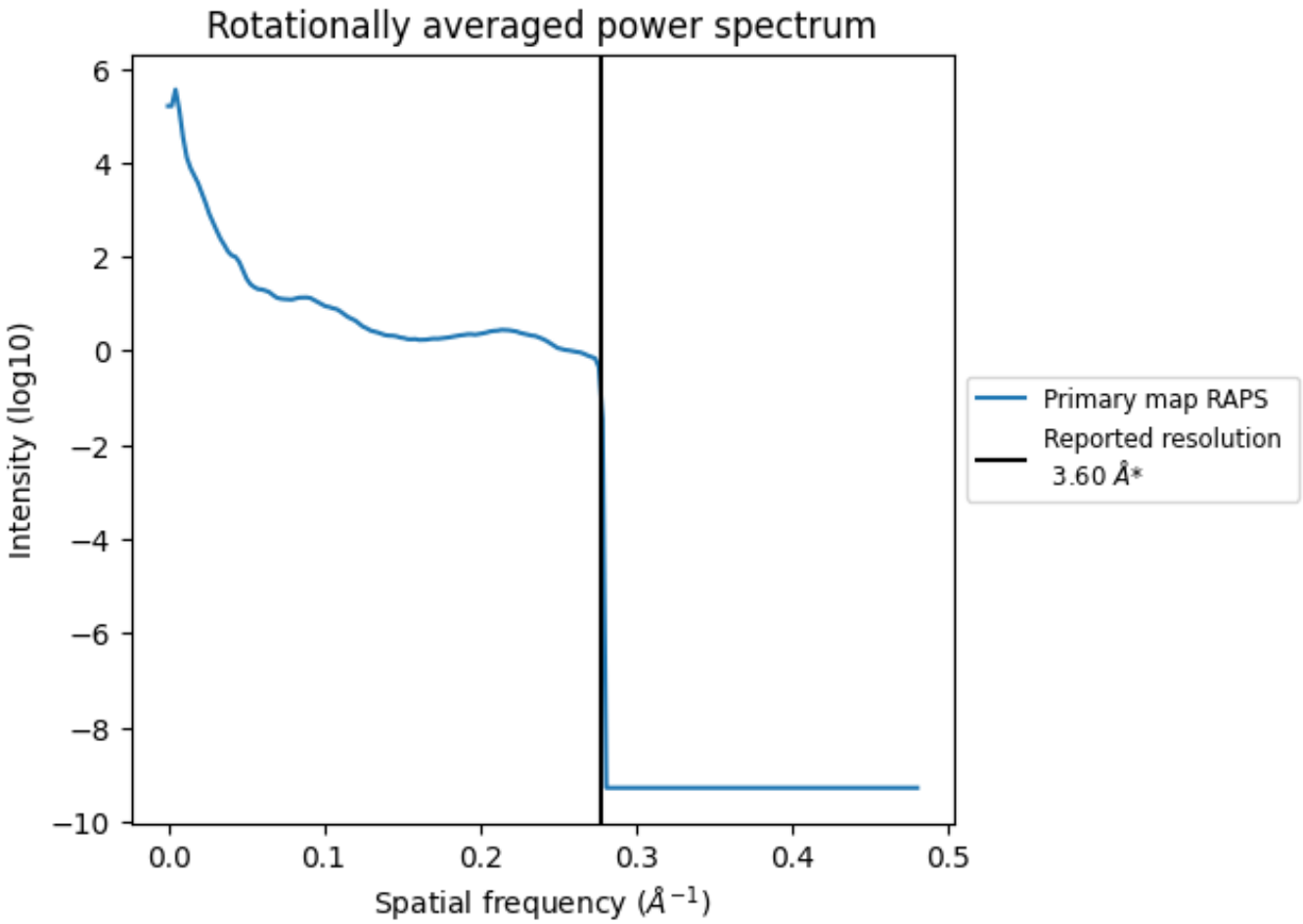
7.2 Volume estimate (i)



The volume at the recommended contour level is 960 nm^3; this corresponds to an approximate mass of 867 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 0.278 Å^{-1}

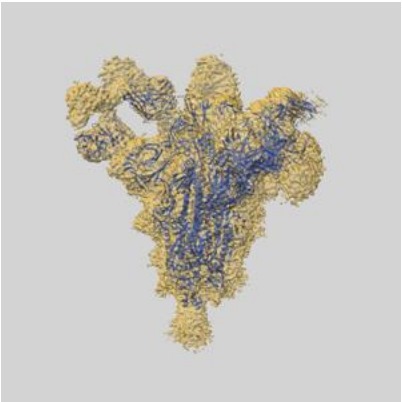
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

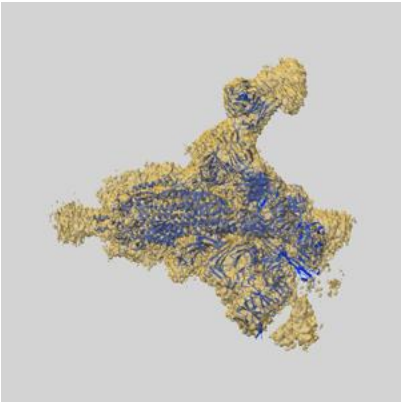
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-30994 and PDB model 7E5S. Per-residue inclusion information can be found in section 3 on page 13.

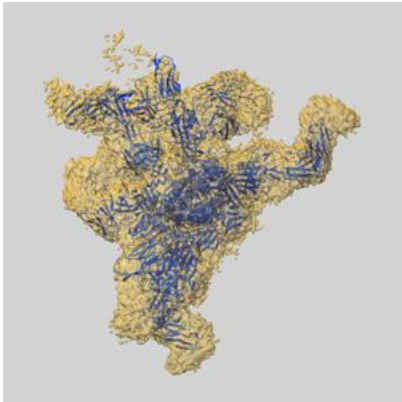
9.1 Map-model overlay (i)



X



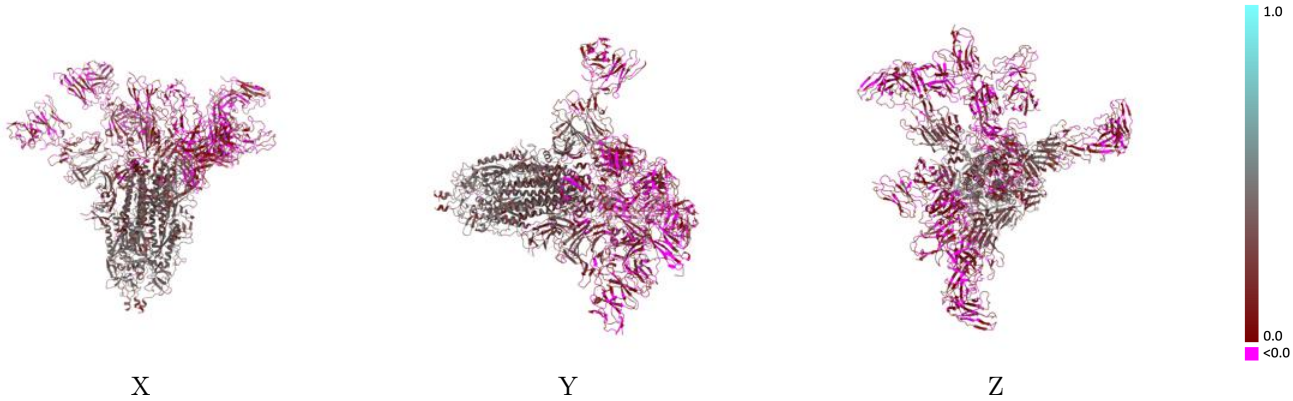
Y



Z

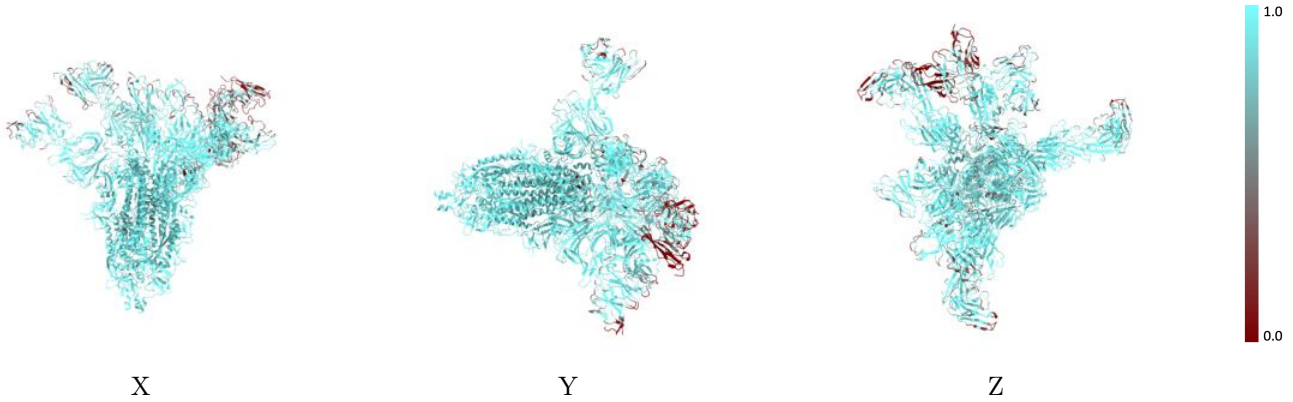
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



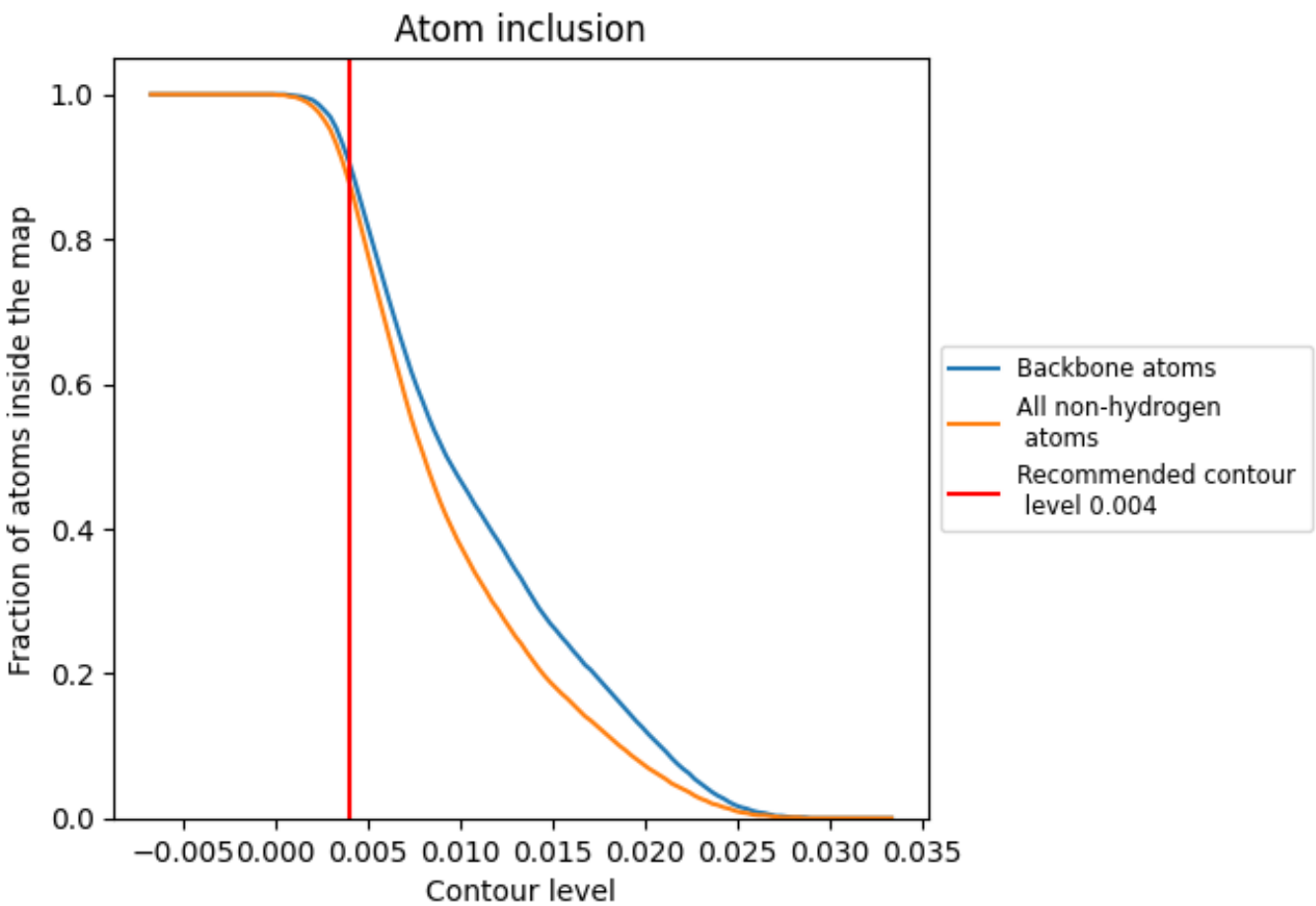
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.004).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8790	0.1870
A	0.9690	0.2720
B	0.9310	0.2550
C	0.9540	0.2340
D	0.7670	0.0700
E	0.9030	0.0870
F	0.8930	0.1940
G	0.9640	0.2160
H	0.8970	0.0740
I	0.3040	0.0220
J	0.7390	0.0180
K	0.3620	0.0540
L	0.8330	0.0830
M	0.8570	0.2840
N	0.8080	0.0620
O	0.7990	0.0620
P	0.8900	0.0760
Q	0.7770	0.0710
R	0.8280	0.0830
S	0.6760	0.0580
T	0.7890	0.0930
U	0.8690	0.0710
V	0.7780	0.0830
W	0.9290	0.2570
X	0.8570	0.1200
Y	0.6430	0.2420
Z	0.5000	0.0290
a	0.1070	-0.1710
b	0.7140	0.1410
c	0.3570	0.0200
d	0.1070	-0.0270
e	0.5360	0.0490