Full wwPDB EM Validation Report (i)

Nov 12, 2022 – 03:48 PM EST

PDB ID	:	6PV8
EMDB ID	:	EMD-20488
Title	:	Human alpha3beta4 nicotinic acetylcholine receptor in complex with AT-1001
Authors	:	Gharpure, A.; Teng, J.; Zhuang, Y.; Noviello, C.M.; Walsh, R.M.; Cabuco, R.; Howard, R.J.; Zaveri, N.T.; Lindahl, E.; Hibbs, R.E.
Deposited on	:	2019-07-19
Resolution	:	3.87 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 (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 (1)) were used in the production of this report:

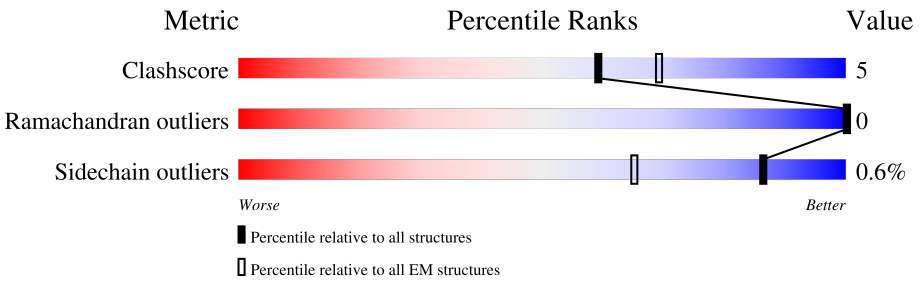
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.87 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	525	65% 9% 26%
1	D	525	64% 9% 26%
2	B	538	5% 63% 9% 28%
2	C	538	6% 61% 10% 28%
2	E	538	64% 8% 28%
3	F	219	50% 47%
3	H	219	52% 47%
4	G	213	42% 7% 51%

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Mol	Chain	Length	Quality of chain
4	I	213	46% 51%
5	J	2	50% 100%
5	P	2	100%
6	K	5	20% 40% 60%
6	M	5	40% 60% 40%
6	O	5	60% 80% 20%
6	Q	5	20% 40% 60%
6	S	5	40% 80% 20%
7	L	3	67% 100%
7	N	3	67% 67% 33%
7	R	3	33% 100%

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 20051 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 Fusion protein of Neuronal acetylcholine receptor subunit alpha-3 and Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	387	3167	2096	489	562	20	0	0
1	D	387	3167	2096	489	562	20	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	328A	TRP	MET	conflict	UNP A0A3W4NZ06
A	331R	ILE	HIS	conflict	UNP A0A3W4NZ06
A	331V	LEU	-	linker	UNP A0A3W4NZ06
D	328A	TRP	MET	conflict	UNP A0A3W4NZ06
D	331R	ILE	HIS	conflict	UNP A0A3W4NZ06
D	331V	LEU	-	linker	UNP A0A3W4NZ06

- Molecule 2 is a protein called Fusion protein of Neuronal acetylcholine receptor subunit beta-4 and Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	388	3149	2055	512	561	21	0	0
2	C	385	3126	2041	506	558	21	0	0
2	E	388	3149	2055	512	561	21	0	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	328S	TRP	MET	conflict	UNP A0A3W4NZ06
B	332J	ILE	HIS	conflict	UNP A0A3W4NZ06
B	332N	LEU	-	linker	UNP A0A3W4NZ06

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Chain	Residue	Modelled	Actual	Comment	Reference
B	478	SER	-	expression tag	UNP P30926
B	479	ALA	-	expression tag	UNP P30926
B	480	TRP	-	expression tag	UNP P30926
B	481	SER	-	expression tag	UNP P30926
B	482	HIS	-	expression tag	UNP P30926
B	483	PRO	-	expression tag	UNP P30926
B	484	GLN	-	expression tag	UNP P30926
B	485	PHE	-	expression tag	UNP P30926
B	486	GLU	-	expression tag	UNP P30926
B	487	LYS	-	expression tag	UNP P30926
C	328S	TRP	MET	conflict	UNP A0A3W4NZ06
C	332J	ILE	HIS	conflict	UNP A0A3W4NZ06
C	332N	LEU	-	linker	UNP A0A3W4NZ06
C	478	SER	-	expression tag	UNP P30926
C	479	ALA	-	expression tag	UNP P30926
C	480	TRP	-	expression tag	UNP P30926
C	481	SER	-	expression tag	UNP P30926
C	482	HIS	-	expression tag	UNP P30926
C	483	PRO	-	expression tag	UNP P30926
C	484	GLN	-	expression tag	UNP P30926
C	485	PHE	-	expression tag	UNP P30926
C	486	GLU	-	expression tag	UNP P30926
C	487	LYS	-	expression tag	UNP P30926
E	328S	TRP	MET	conflict	UNP A0A3W4NZ06
E	332J	ILE	HIS	conflict	UNP A0A3W4NZ06
E	332N	LEU	-	linker	UNP A0A3W4NZ06
E	478	SER	-	expression tag	UNP P30926
E	479	ALA	-	expression tag	UNP P30926
E	480	TRP	-	expression tag	UNP P30926
E	481	SER	-	expression tag	UNP P30926
E	482	HIS	-	expression tag	UNP P30926
E	483	PRO	-	expression tag	UNP P30926
E	484	GLN	-	expression tag	UNP P30926
E	485	PHE	-	expression tag	UNP P30926
E	486	GLU	-	expression tag	UNP P30926
E	487	LYS	-	expression tag	UNP P30926

- Molecule 3 is a protein called IgG2b Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	F	117	911	580	147	179	5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	117	911	580	147	179	5	0	0

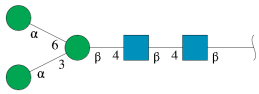
- Molecule 4 is a protein called Kappa Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	G	105	792	494	131	160	7	0	0
4	I	105	792	494	131	160	7	0	0

- Molecule 5 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		
5	J	2	28	16	2	10	0	0
5	P	2	28	16	2	10	0	0

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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
			Total	C	N	O		
6	K	5	61	34	2	25	0	0
6	M	5	61	34	2	25	0	0
6	O	5	61	34	2	25	0	0
6	Q	5	61	34	2	25	0	0

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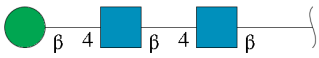
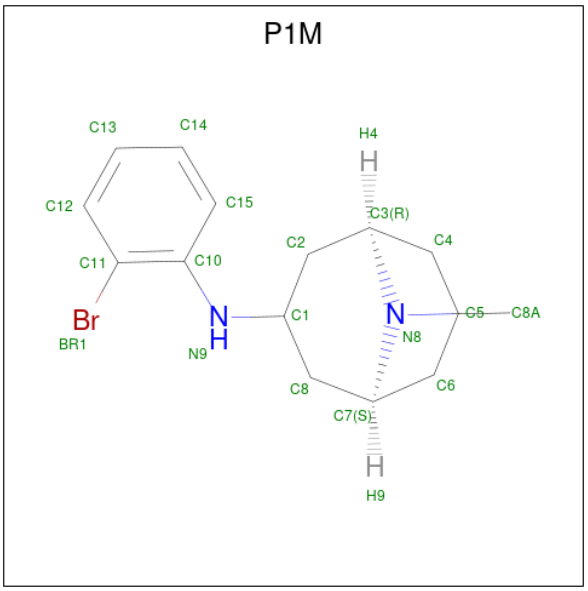
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	S	5	61	34	2	25	0	0

- Molecule 7 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
			Total	C	N	O		
7	L	3	39	22	2	15	0	0
7	N	3	39	22	2	15	0	0
7	R	3	39	22	2	15	0	0

- Molecule 8 is (3-endo)-N-(2-bromophenyl)-9-methyl-9-azabicyclo[3.3.1]nonan-3-amine (three-letter code: P1M) (formula: $C_{15}H_{21}BrN_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	Br	C	N	
8	A	1	18	1	15	2	0

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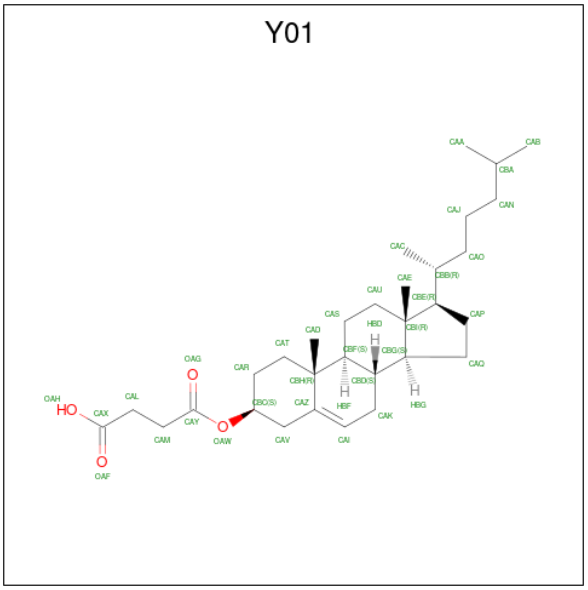
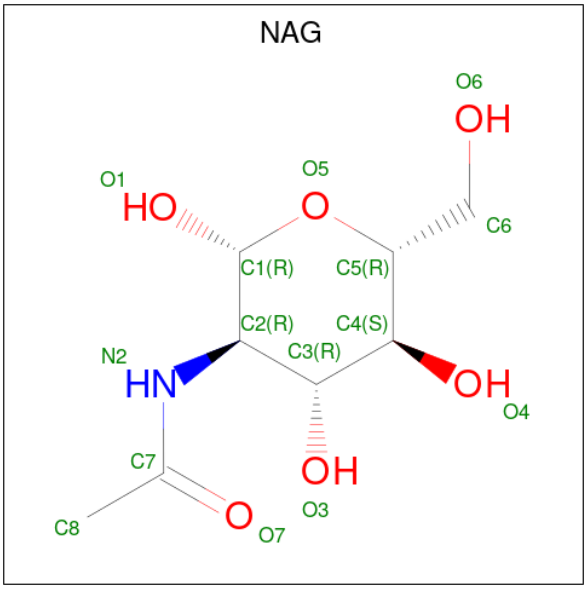
Mol	Chain	Residues	Atoms				AltConf
			Total	Br	C	N	
8	D	1	18	1	15	2	0

- Molecule 9 is CHOLESTEROL HEMISUCCINATE (three-letter code: Y01) (formula: $C_{31}H_{50}O_4$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O		
9	A	1	56	54	2		0
			Total	C	O		
9	A	1	56	54	2		0
			Total	C	O		
9	B	1	56	54	2		0
			Total	C	O		
9	B	1	56	54	2		0
			Total	C	O		
9	C	1	56	54	2		0
			Total	C	O		
9	C	1	56	54	2		0
			Total	C	O		
9	D	1	56	54	2		0
			Total	C	O		
9	D	1	56	54	2		0
			Total	C	O		
9	E	1	56	54	2		0
			Total	C	O		
9	E	1	56	54	2		0

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
10	B	1	28	16	2	10	0
			Total	C	N	O	
10	B	1	28	16	2	10	0
			Total	C	N	O	
10	C	1	28	16	2	10	0
			Total	C	N	O	
10	C	1	28	16	2	10	0
			Total	C	N	O	
10	E	1	28	16	2	10	0
			Total	C	N	O	
10	E	1	28	16	2	10	0

- Molecule 11 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
			Total	Na	
11	B	1	1	1	0

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
12	A	2	2	2	0

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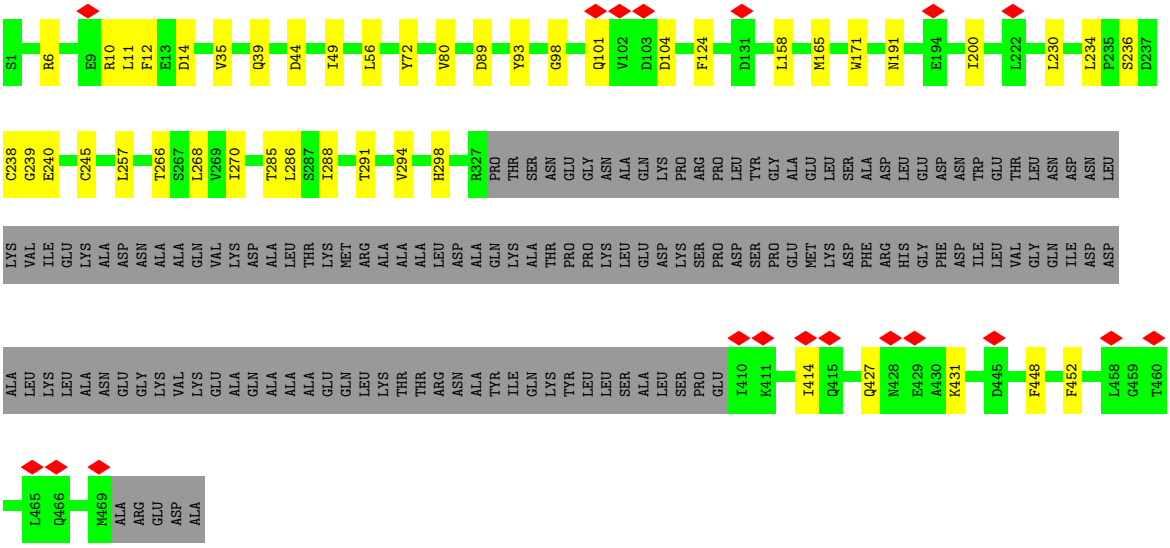
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
12	B	3	3	3	0
			Total	O	
12	D	2	2	2	0
			Total	O	
12	E	1	1	1	0

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.

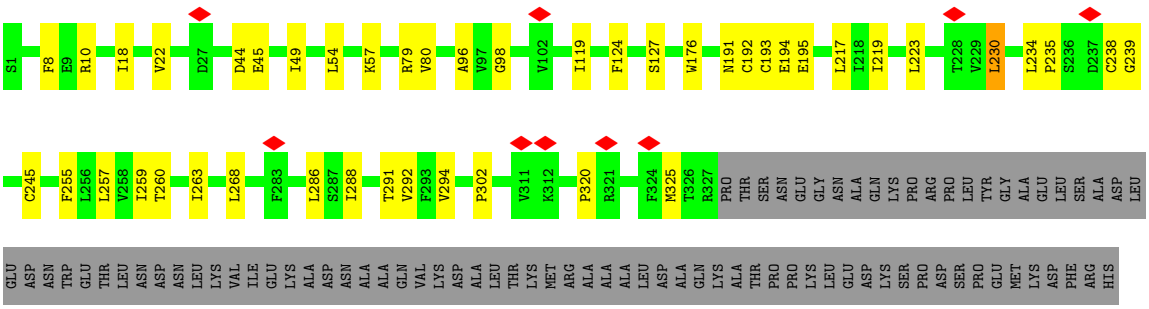
• Molecule 1: Fusion protein of Neuronal acetylcholine receptor subunit alpha-3 and Soluble cytochrome b562

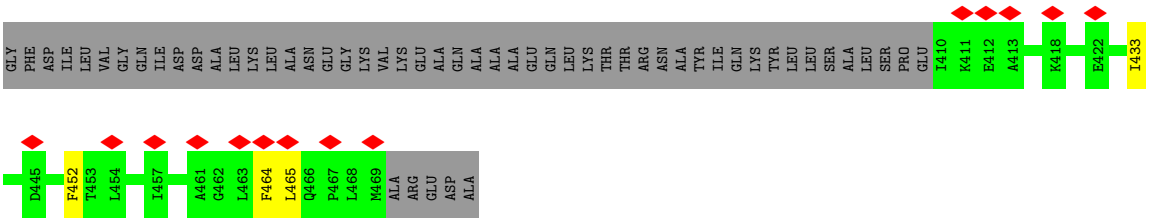
Chain A:



• Molecule 1: Fusion protein of Neuronal acetylcholine receptor subunit alpha-3 and Soluble cytochrome b562

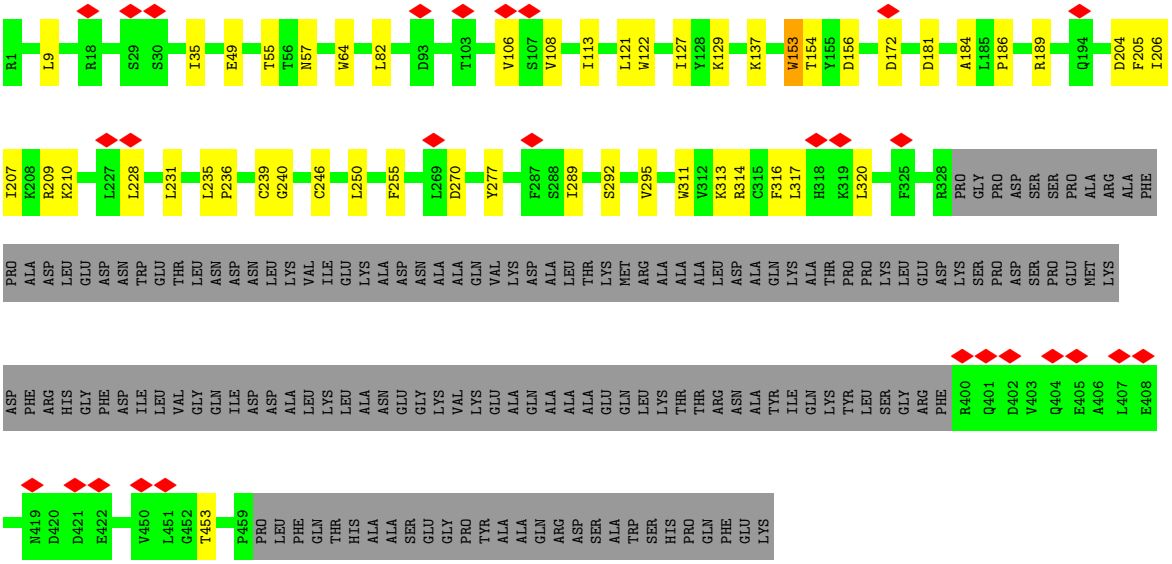
Chain D:





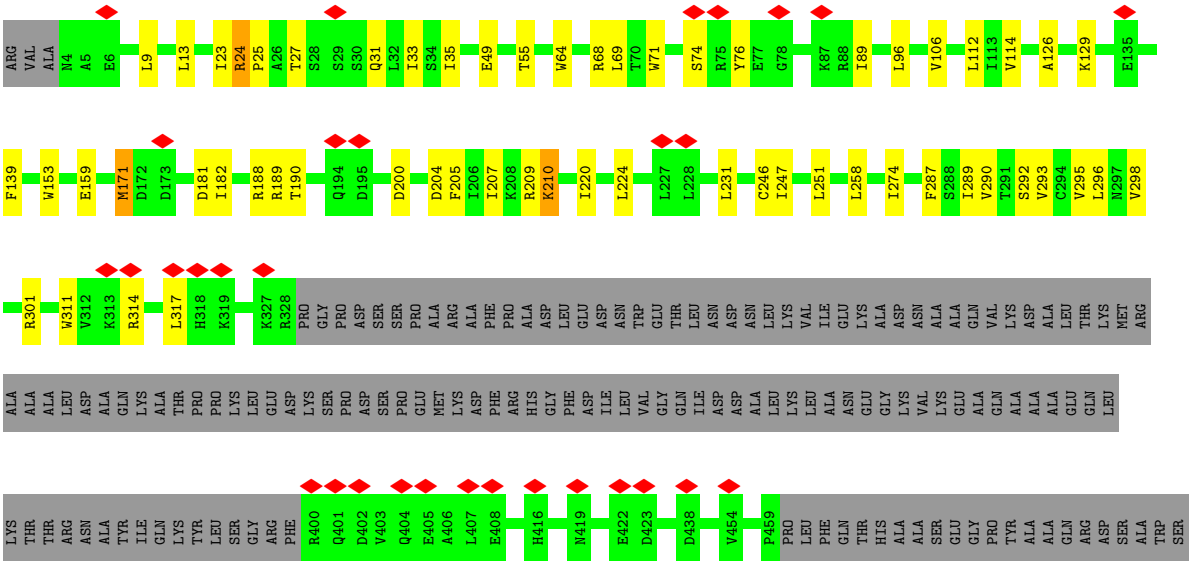
• Molecule 2: Fusion protein of Neuronal acetylcholine receptor subunit beta-4 and Soluble cytochrome b562

Chain B:



• Molecule 2: Fusion protein of Neuronal acetylcholine receptor subunit beta-4 and Soluble cytochrome b562

Chain C:



HIS PRO GLN PHE GLU LYS

• Molecule 2: Fusion protein of Neuronal acetylcholine receptor subunit beta-4 and Soluble cytochrome b562

Chain E:

R1 V2 A3 N4 Q38 T55 T56 N57 V58 W59 V79 P85 I89 T103 V106 S107 V108 L112 L123 I127 Y128 K129 W153 T154 D172 A184 R188 R189 D204 F205 I206 L227 L228 L231 L235 P236 S237 E241 K242 C246

I247 L251 F255 K276 F287 S288 I289 V290 L296 N297 V298 R301 R314 C315 F316 L317 H318 K319 L320 F323 K327 R328 PRO GLY PRO ASP SER SER PRO ALA ARG ALA PHE PRO ALA ASP LEU GLU ASP ASN TRP GLU THR LEU ASN ASP ASN LEU LYS VAL ILE

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

LEU ALA ASN GLU GLY LYS VAL LYS GLU ALA GLN ALA ALA ALA GLU GLN LEU LYS THR THR ARG ASN ALA TYR ILE GLN LYS TYR LEU SER GLY ARG PHE R400 Q401 D402 V403 Q404 E405 A406 L407 E408 G409 Q415 Q424 E428 D438 F447 L451 P459 PRO LEU PHE

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

• Molecule 3: IgG2b Fab heavy chain

Chain F:

GLN V21 Q25 S26 G27 L30 V31 R32 S36 R57 A61 L64 E65 W66 S94 A103 D108 D109 C115 D127 V137 SER SER ALA LYS THR THR PRO PRO SER VAL TYR PRO LEU ALA PRO GLY CYS GLY ASP THR THR GLY SER SER VAL THR LEU

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

HIS PRO ALA SER SER THR THR VAL ASP LYS LYS LEU GLU PRO

• Molecule 3: IgG2b Fab heavy chain

Chain H:

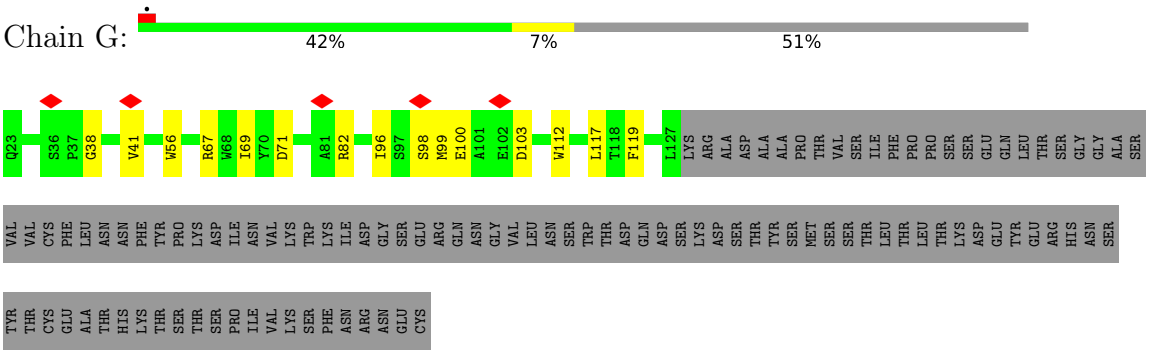
GLN V21 G27 L30 V31 R57 H60 W66 I67 M100 L105 D108 V137 SER SER ALA LYS THR THR PRO PRO SER VAL TYR PRO LEU ALA PRO GLY CYS GLY ASP THR THR GLY SER SER VAL THR LEU GLY CYS LEU VAL LYS GLY TYR PHE PRO GLU SER

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

LEU GLU PRO

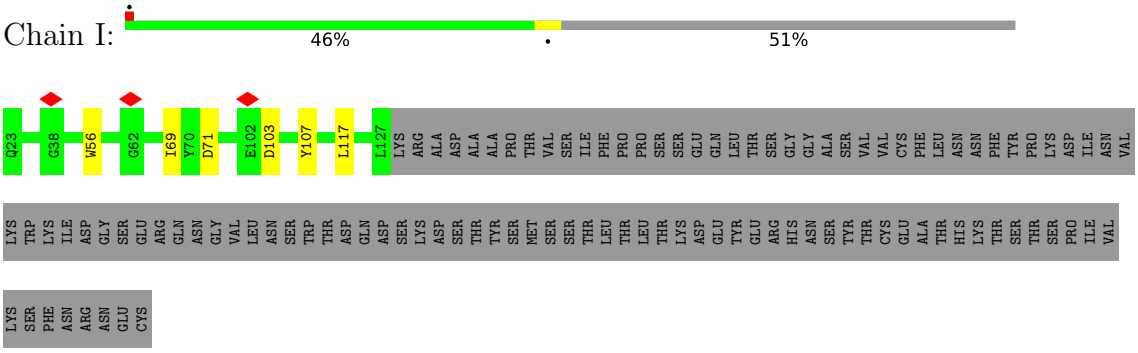
• Molecule 4: Kappa Fab light chain

Chain G:



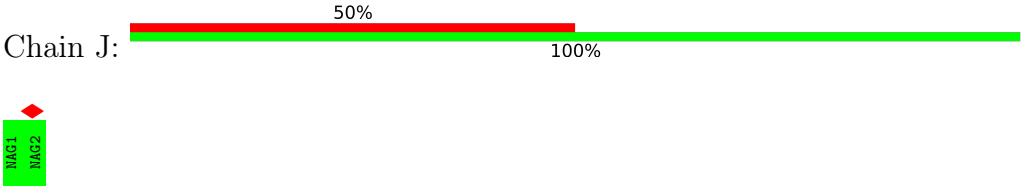
• Molecule 4: Kappa Fab light chain

Chain I:



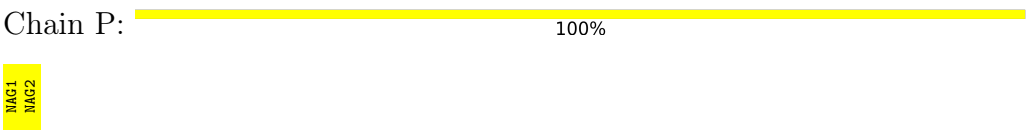
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:



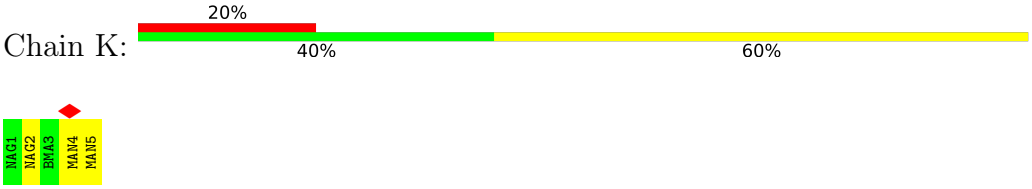
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:



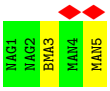
• Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:



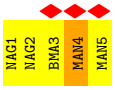
• Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:



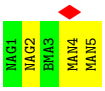
• Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:



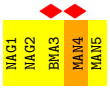
• Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:



• Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:



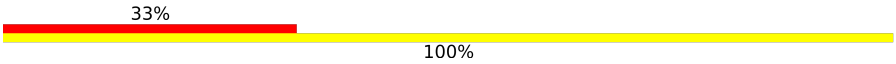
• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:

• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:

• Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R: 

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	93080	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 ($e^-/Å^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	59523	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.095	Depositor
Minimum map value	-0.061	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	251.99998, 251.99998, 251.99998	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	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: NA, NAG, MAN, Y01, BMA, P1M

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	0.39	1/3252 (0.0%)	0.56	2/4431 (0.0%)
1	D	0.32	0/3252	0.55	1/4431 (0.0%)
2	B	0.30	0/3228	0.57	1/4402 (0.0%)
2	C	0.35	0/3205	0.60	2/4371 (0.0%)
2	E	0.30	0/3228	0.58	1/4402 (0.0%)
3	F	0.29	0/936	0.54	1/1273 (0.1%)
3	H	0.29	0/936	0.54	0/1273
4	G	0.29	0/811	0.56	0/1099
4	I	0.29	0/811	0.54	0/1099
All	All	0.33	1/19659 (0.0%)	0.57	8/26781 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	234	LEU	C-N	12.92	1.58	1.34

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	234	LEU	O-C-N	-6.34	109.06	121.10
2	E	231	LEU	CA-CB-CG	5.58	128.14	115.30
2	C	96	LEU	CA-CB-CG	5.53	128.02	115.30
1	A	230	LEU	CA-CB-CG	5.49	127.92	115.30
1	D	230	LEU	CA-CB-CG	5.44	127.81	115.30
2	C	231	LEU	CA-CB-CG	5.35	127.61	115.30
3	F	64	LEU	CA-CB-CG	5.32	127.52	115.30
2	B	231	LEU	CA-CB-CG	5.01	126.81	115.30

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	3167	0	3214	33	0
1	D	3167	0	3214	37	0
2	B	3149	0	3203	35	0
2	C	3126	0	3173	47	0
2	E	3149	0	3203	26	0
3	F	911	0	865	7	0
3	H	911	0	865	2	0
4	G	792	0	757	10	0
4	I	792	0	757	4	0
5	J	28	0	25	0	0
5	P	28	0	25	0	0
6	K	61	0	52	0	0
6	M	61	0	52	0	0
6	O	61	0	52	1	0
6	Q	61	0	52	0	0
6	S	61	0	52	1	0
7	L	39	0	34	0	0
7	N	39	0	34	2	0
7	R	39	0	34	0	0
8	A	18	0	0	2	0
8	D	18	0	0	0	0
9	A	56	0	90	4	0
9	B	56	0	90	2	0
9	C	56	0	90	4	0
9	D	56	0	90	4	0
9	E	56	0	90	5	0
10	B	28	0	26	0	0
10	C	28	0	26	3	0
10	E	28	0	26	0	0
11	B	1	0	0	0	0
12	A	2	0	0	0	0
12	B	3	0	0	0	0
12	D	2	0	0	0	0
12	E	1	0	0	0	0
All	All	20051	0	20191	194	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 5.

All (194) 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:D:234:LEU:HD12	1:D:235:PRO:HD2	1.16	1.14
1:D:234:LEU:CD1	1:D:235:PRO:HD2	2.01	0.90
2:E:188:ARG:NH1	2:E:204:ASP:OD2	2.11	0.83
1:D:57:LYS:HG3	1:D:119:ILE:CD1	2.13	0.79
1:D:234:LEU:HD12	1:D:235:PRO:CD	2.08	0.76
1:D:239:GLY:O	2:E:241:GLU:OE2	2.06	0.74
2:C:181:ASP:OD2	2:C:210:LYS:HE2	1.88	0.73
2:C:23:ILE:O	2:C:23:ILE:HD12	1.87	0.73
2:C:159:GLU:OE2	1:D:79:ARG:NH1	2.24	0.71
2:C:9:LEU:HD21	2:C:13:LEU:HD12	1.73	0.70
2:B:121:LEU:HD23	2:B:122:TRP:N	2.06	0.69
1:A:236:SER:OG	1:A:298:HIS:CD2	2.47	0.67
4:G:100:GLU:HB3	4:G:103:ASP:HB2	1.77	0.67
2:C:23:ILE:HD11	2:C:68:ARG:NH2	2.11	0.66
2:C:9:LEU:C	2:C:9:LEU:HD23	2.16	0.65
10:C:702:NAG:O7	10:C:702:NAG:O3	2.11	0.64
2:C:24:ARG:HD2	2:C:24:ARG:O	1.98	0.63
2:B:57:ASN:HB3	2:B:127:ILE:HG22	1.80	0.63
2:C:13:LEU:HD11	2:C:71:TRP:CE3	2.34	0.63
1:D:22:VAL:O	2:E:4:ASN:ND2	2.32	0.63
2:B:121:LEU:HD23	2:B:121:LEU:C	2.20	0.62
2:E:247:ILE:O	2:E:251:LEU:HD13	2.00	0.61
2:C:181:ASP:CG	2:C:210:LYS:HE2	2.21	0.61
4:G:82:ARG:HD2	4:G:98:SER:HB3	1.82	0.61
4:G:38:GLY:H	4:G:99:MET:HB3	1.65	0.61
2:C:55:THR:HG22	2:C:129:LYS:HG2	1.83	0.60
2:C:89:ILE:HD11	2:C:112:LEU:HD11	1.83	0.59
2:B:137:LYS:NZ	2:B:270:ASP:OD2	2.36	0.58
1:D:57:LYS:HG3	1:D:119:ILE:HD12	1.85	0.58
2:C:190:THR:HB	2:C:200:ASP:HB3	1.86	0.57
2:C:205:PHE:HB3	2:C:207:ILE:HD11	1.86	0.57
2:E:242:LYS:HD3	2:E:296:LEU:HD12	1.86	0.57
1:D:10:ARG:NH2	4:G:71:ASP:OD1	2.37	0.57
3:F:25:GLN:NE2	3:F:115:CYS:SG	2.76	0.56
2:B:55:THR:HG22	2:B:129:LYS:HG2	1.88	0.56
2:B:246:CYS:HB3	2:B:289:ILE:HG12	1.88	0.56
2:B:316:PHE:CD1	2:B:320:LEU:HD12	2.41	0.56
2:E:235:LEU:HD12	2:E:236:PRO:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:GLU:OE2	2:B:209:ARG:NH2	2.39	0.56
3:F:127:ASP:OD1	4:G:67:ARG:NH1	2.39	0.55
2:C:247:ILE:O	2:C:251:LEU:HD13	2.06	0.55
1:D:217:LEU:HD21	1:D:259:ILE:HD12	1.88	0.55
4:G:56:TRP:HB2	4:G:69:ILE:HB	1.88	0.54
1:D:45:GLU:OE2	1:D:176:TRP:HZ2	1.89	0.54
1:D:96:ALA:HB2	1:D:127:SER:HB3	1.89	0.54
1:D:191:ASN:HD22	2:E:172:ASP:HB3	1.72	0.54
2:C:220:ILE:O	2:C:224:LEU:HB2	2.07	0.53
2:C:49:GLU:OE2	2:C:209:ARG:NH2	2.41	0.53
2:C:246:CYS:HB3	2:C:289:ILE:HG12	1.91	0.53
2:E:298:VAL:HG12	2:E:301:ARG:HE	1.74	0.53
2:B:313:LYS:HA	2:B:317:LEU:HD12	1.91	0.53
9:D:710:Y01:HAC3	9:E:711:Y01:HAB1	1.91	0.53
1:D:44:ASP:HB2	1:D:49:ILE:HG22	1.90	0.53
2:C:9:LEU:HD23	2:C:9:LEU:O	2.09	0.53
3:H:67:ILE:HD13	3:H:100:MET:HE1	1.91	0.53
1:A:245:CYS:HB3	1:A:288:ILE:HG22	1.91	0.52
1:A:10:ARG:NH2	4:I:71:ASP:OD1	2.42	0.52
2:E:237:SER:HA	2:E:242:LYS:HD2	1.91	0.52
1:A:240:GLU:HA	1:A:240:GLU:OE1	2.10	0.52
2:B:205:PHE:HB3	2:B:207:ILE:HD11	1.92	0.52
1:D:219:ILE:O	1:D:223:LEU:HB2	2.09	0.52
1:A:291:THR:HA	1:A:294:VAL:HG12	1.92	0.51
2:C:9:LEU:HB2	2:C:76:TYR:CD1	2.45	0.51
8:A:701:P1M:BR1	2:B:113:ILE:HD12	2.66	0.51
2:B:316:PHE:HD1	2:B:320:LEU:HD12	1.76	0.50
2:B:235:LEU:HD12	2:B:236:PRO:HD2	1.92	0.50
1:A:286:LEU:HD22	1:A:452:PHE:HZ	1.75	0.50
1:D:18:ILE:HG21	2:E:85:PRO:HG3	1.93	0.50
2:B:181:ASP:OD1	2:B:210:LYS:NZ	2.37	0.50
1:D:291:THR:HA	1:D:294:VAL:HG12	1.93	0.50
2:E:153:TRP:CD1	2:E:154:THR:HG23	2.47	0.49
1:A:427:GLN:HG2	1:A:431:LYS:HE3	1.93	0.49
1:A:35:VAL:HG13	1:A:165:MET:HG3	1.93	0.49
1:A:288:ILE:HA	1:A:291:THR:HG22	1.94	0.49
4:I:103:ASP:OD1	4:I:107:TYR:OH	2.31	0.49
1:A:6:ARG:HH21	1:A:72:TYR:HD1	1.60	0.49
2:C:9:LEU:CD2	2:C:13:LEU:HD12	2.43	0.49
1:D:8:PHE:HE1	1:D:80:VAL:HG12	1.78	0.49
2:E:316:PHE:HE2	9:E:712:Y01:HAV2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:ASN:HD22	2:B:172:ASP:HB3	1.78	0.49
2:C:293:VAL:HG21	1:D:230:LEU:HD21	1.93	0.48
1:A:101:GLN:HG2	2:B:108:VAL:HG13	1.95	0.48
2:C:296:LEU:HD23	1:D:235:PRO:CG	2.42	0.48
2:C:298:VAL:HG12	2:C:301:ARG:HE	1.79	0.48
1:A:44:ASP:HB2	1:A:49:ILE:HG22	1.95	0.48
9:D:710:Y01:HAP1	9:D:710:Y01:HAO1	1.68	0.48
2:C:9:LEU:HD21	2:C:13:LEU:CD1	2.43	0.47
2:C:35:ILE:HG22	2:C:64:TRP:HB3	1.95	0.47
2:B:35:ILE:HG22	2:B:64:TRP:HB3	1.96	0.47
2:E:59:TRP:HB3	2:E:123:LEU:HD21	1.95	0.47
2:E:184:ALA:HB3	2:E:206:ILE:HD11	1.96	0.47
4:G:41:VAL:HB	4:G:96:ILE:HB	1.97	0.47
2:B:184:ALA:HB3	2:B:206:ILE:HD11	1.95	0.47
2:E:57:ASN:HB3	2:E:127:ILE:HG22	1.97	0.47
2:C:258:LEU:HD11	1:D:255:PHE:HE1	1.80	0.47
1:D:257:LEU:HD22	2:E:255:PHE:HZ	1.80	0.47
1:D:288:ILE:HA	1:D:291:THR:HG22	1.95	0.47
2:E:89:ILE:HD11	2:E:112:LEU:HD11	1.97	0.47
2:C:287:PHE:HA	2:C:290:VAL:HG12	1.96	0.46
2:C:13:LEU:HD11	2:C:71:TRP:CD2	2.50	0.46
3:F:57:ARG:HH12	3:F:109:ASP:HA	1.79	0.46
1:D:54:LEU:HD12	1:D:124:PHE:HD2	1.80	0.46
2:B:250:LEU:HD11	2:C:224:LEU:HD21	1.98	0.46
2:C:23:ILE:CD1	2:C:68:ARG:NH2	2.79	0.46
2:E:246:CYS:HB3	2:E:289:ILE:HG12	1.97	0.46
7:N:1:NAG:H62	7:N:2:NAG:C7	2.45	0.46
1:A:257:LEU:HD22	2:B:255:PHE:HZ	1.81	0.46
9:A:710:Y01:HAO2	9:A:710:Y01:HAP1	1.51	0.46
1:D:320:PRO:HB3	1:D:325:MET:HB2	1.99	0.45
1:A:104:ASP:OD1	1:A:104:ASP:N	2.48	0.45
9:B:712:Y01:HAE2	9:B:712:Y01:HBB	1.74	0.45
2:C:311:TRP:HA	2:C:314:ARG:HG2	1.97	0.45
2:B:106:VAL:HG12	2:B:108:VAL:H	1.81	0.45
8:A:701:P1M:C12	2:B:121:LEU:HD22	2.47	0.45
9:A:710:Y01:HAE2	9:A:710:Y01:HBB	1.75	0.45
2:C:106:VAL:HG13	2:C:126:ALA:HB2	1.98	0.45
2:B:9:LEU:HD22	2:B:82:LEU:HG	1.99	0.45
2:B:153:TRP:HD1	2:B:154:THR:HG23	1.82	0.45
2:C:74:SER:HB2	10:C:702:NAG:HN2	1.82	0.45
2:C:25:PRO:HG2	2:C:33:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ASP:OD1	1:A:89:ASP:N	2.50	0.44
2:C:13:LEU:CD1	2:C:71:TRP:CE3	2.99	0.44
2:E:320:LEU:HA	2:E:323:PHE:HB3	1.98	0.44
9:E:712:Y01:HAC3	9:E:712:Y01:HAJ1	1.80	0.44
3:F:25:GLN:HE22	3:F:115:CYS:H	1.65	0.44
2:B:277:TYR:HE1	2:B:453:THR:HG22	1.82	0.44
2:C:27:THR:N	2:C:31:GLN:OE1	2.51	0.44
2:B:239:CYS:SG	2:B:240:GLY:N	2.90	0.44
10:C:702:NAG:HO3	10:C:702:NAG:C7	2.24	0.44
1:A:12:PHE:HZ	1:A:80:VAL:HG11	1.83	0.44
2:B:153:TRP:CD1	2:B:154:THR:HG23	2.52	0.44
2:B:311:TRP:HA	2:B:314:ARG:HG2	1.99	0.44
1:D:292:VAL:HG23	2:E:235:LEU:HD13	1.98	0.44
1:D:302:PRO:HB3	1:D:433:ILE:HG21	2.00	0.44
2:E:227:LEU:HD21	9:E:711:Y01:HAB2	1.99	0.44
1:D:98:GLY:H	2:E:127:ILE:HD11	1.82	0.43
1:A:11:LEU:HD23	1:A:12:PHE:CE2	2.52	0.43
2:E:2:VAL:HG23	4:G:112:TRP:HZ2	1.82	0.43
2:B:121:LEU:C	2:B:121:LEU:CD2	2.86	0.43
1:D:464:PHE:HD2	1:D:465:LEU:HD12	1.83	0.43
4:I:56:TRP:HB2	4:I:69:ILE:HB	2.00	0.43
9:C:711:Y01:HAO1	9:C:711:Y01:HAP1	1.72	0.43
1:A:414:ILE:HG23	2:E:406:ALA:HB2	2.00	0.43
2:C:139:PHE:HD2	2:C:274:ILE:HD12	1.83	0.43
1:D:192:CYS:SG	1:D:193:CYS:N	2.92	0.43
2:E:55:THR:HG22	2:E:129:LYS:HG2	2.01	0.43
1:A:98:GLY:H	2:B:127:ILE:HD11	1.83	0.43
2:B:292:SER:HA	2:B:295:VAL:HG12	2.01	0.42
9:A:709:Y01:HAO1	9:A:709:Y01:HAP1	1.65	0.42
1:D:238:CYS:SG	1:D:239:GLY:N	2.92	0.42
1:D:260:THR:HA	1:D:263:ILE:HG12	2.01	0.42
1:A:14:ASP:OD1	1:A:14:ASP:N	2.52	0.42
1:A:270:ILE:H	1:A:270:ILE:HG13	1.74	0.42
2:B:186:PRO:HG2	2:B:204:ASP:HB2	2.01	0.42
7:N:1:NAG:O7	7:N:1:NAG:H3	2.19	0.42
1:A:238:CYS:SG	1:A:239:GLY:N	2.92	0.42
2:B:156:ASP:N	2:B:156:ASP:OD1	2.52	0.42
3:F:64:LEU:HG	4:G:119:PHE:HD2	1.85	0.42
2:C:296:LEU:HD23	1:D:235:PRO:HG3	2.01	0.41
1:A:39:GLN:HB3	1:A:171:TRP:HB3	2.03	0.41
9:D:709:Y01:HAD2	9:D:709:Y01:HAS2	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:LEU:HD21	1:A:124:PHE:HE2	1.86	0.41
9:B:711:Y01:HAE2	9:B:711:Y01:HBB	1.84	0.41
2:C:171:MET:SD	2:C:182:ILE:HD12	2.60	0.41
2:E:287:PHE:HA	2:E:290:VAL:HG12	2.03	0.41
1:D:245:CYS:HB3	1:D:288:ILE:HG22	2.02	0.41
1:A:93:TYR:N	1:A:93:TYR:HD1	2.19	0.41
2:C:9:LEU:C	2:C:9:LEU:CD2	2.86	0.41
1:A:285:THR:HG23	2:B:228:LEU:HD11	2.02	0.41
1:A:448:PHE:HZ	9:A:709:Y01:HAI	1.85	0.41
2:C:23:ILE:HD12	2:C:23:ILE:C	2.39	0.41
9:E:712:Y01:HAE2	9:E:712:Y01:HBB	1.77	0.41
2:C:69:LEU:HD23	2:C:114:VAL:HG21	2.03	0.41
1:A:158:LEU:HB3	1:A:200:ILE:HD11	2.03	0.41
1:A:266:THR:HG22	1:A:268:LEU:H	1.86	0.41
2:C:188:ARG:NH2	2:C:204:ASP:OD2	2.54	0.41
9:C:712:Y01:HBB	9:C:712:Y01:HAE2	1.78	0.41
3:F:66:TRP:CD1	4:G:117:LEU:HD23	2.56	0.41
6:S:3:BMA:H3	6:S:4:MAN:H2	1.75	0.41
1:A:93:TYR:N	1:A:93:TYR:CD1	2.89	0.41
1:A:268:LEU:HD12	1:A:268:LEU:HA	1.96	0.41
2:C:292:SER:HA	2:C:295:VAL:HG12	2.02	0.41
1:D:286:LEU:HD22	1:D:452:PHE:HZ	1.86	0.41
2:C:296:LEU:HD22	1:D:234:LEU:HD11	2.02	0.40
2:C:69:LEU:N	2:C:69:LEU:HD12	2.37	0.40
9:C:712:Y01:HAC3	9:C:712:Y01:HAJ1	1.80	0.40
1:D:194:GLU:HG3	1:D:195:GLU:HG3	2.03	0.40
3:H:66:TRP:CD1	4:I:117:LEU:HD23	2.56	0.40
1:A:288:ILE:HD11	2:B:228:LEU:HD22	2.03	0.40
9:C:711:Y01:HBB	9:C:711:Y01:HAE2	1.76	0.40
9:D:710:Y01:HAE2	9:D:710:Y01:HBB	1.78	0.40
3:F:25:GLN:NE2	3:F:115:CYS:H	2.20	0.40
2:C:247:ILE:HD13	2:C:247:ILE:HA	1.97	0.40
6:O:3:BMA:H3	6:O:4:MAN:H2	1.84	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	383/525 (73%)	366 (96%)	17 (4%)	0	100	100
1	D	383/525 (73%)	366 (96%)	17 (4%)	0	100	100
2	B	384/538 (71%)	361 (94%)	23 (6%)	0	100	100
2	C	381/538 (71%)	363 (95%)	18 (5%)	0	100	100
2	E	384/538 (71%)	368 (96%)	16 (4%)	0	100	100
3	F	115/219 (52%)	109 (95%)	6 (5%)	0	100	100
3	H	115/219 (52%)	112 (97%)	3 (3%)	0	100	100
4	G	103/213 (48%)	94 (91%)	9 (9%)	0	100	100
4	I	103/213 (48%)	96 (93%)	7 (7%)	0	100	100
All	All	2351/3528 (67%)	2235 (95%)	116 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	359/470 (76%)	359 (100%)	0	100	100
1	D	359/470 (76%)	358 (100%)	1 (0%)	92	95
2	B	362/482 (75%)	360 (99%)	2 (1%)	86	91
2	C	360/482 (75%)	354 (98%)	6 (2%)	60	78
2	E	362/482 (75%)	358 (99%)	4 (1%)	73	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	98/188 (52%)	98 (100%)	0	100	100
3	H	98/188 (52%)	97 (99%)	1 (1%)	76	86
4	G	88/187 (47%)	88 (100%)	0	100	100
4	I	88/187 (47%)	88 (100%)	0	100	100
All	All	2174/3136 (69%)	2160 (99%)	14 (1%)	86	91

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	153	TRP
2	B	189	ARG
2	C	24	ARG
2	C	153	TRP
2	C	171	MET
2	C	189	ARG
2	C	210	LYS
2	C	317	LEU
1	D	268	LEU
2	E	38	GLN
2	E	79	VAL
2	E	153	TRP
2	E	189	ARG
3	H	57	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	191	ASN
1	A	298	HIS
2	B	144	GLN
1	D	16	ASN
1	D	191	ASN
1	D	317	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)

38 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	$\#\|Z\| > 2$
5	NAG	J	1	1,5	14,14,15	0.37	0	17,19,21	0.58	0
5	NAG	J	2	5	14,14,15	0.26	0	17,19,21	0.43	0
6	NAG	K	1	1,6	14,14,15	0.20	0	17,19,21	0.55	0
6	NAG	K	2	6	14,14,15	0.28	0	17,19,21	0.71	1 (5%)
6	BMA	K	3	6	11,11,12	0.85	0	15,15,17	0.92	0
6	MAN	K	4	6	11,11,12	0.76	0	15,15,17	1.19	2 (13%)
6	MAN	K	5	6	11,11,12	0.82	0	15,15,17	1.08	2 (13%)
7	NAG	L	1	7,2	14,14,15	0.52	0	17,19,21	1.09	2 (11%)
7	NAG	L	2	7	14,14,15	0.34	0	17,19,21	1.00	1 (5%)
7	BMA	L	3	7	11,11,12	0.78	0	15,15,17	0.90	1 (6%)
6	NAG	M	1	6,2	14,14,15	0.22	0	17,19,21	0.70	0
6	NAG	M	2	6	14,14,15	0.28	0	17,19,21	0.54	0
6	BMA	M	3	6	11,11,12	0.87	0	15,15,17	1.21	1 (6%)
6	MAN	M	4	6	11,11,12	0.25	0	15,15,17	0.62	0
6	MAN	M	5	6	11,11,12	0.83	1 (9%)	15,15,17	1.25	2 (13%)
7	NAG	N	1	7,2	14,14,15	0.39	0	17,19,21	1.24	1 (5%)
7	NAG	N	2	7	14,14,15	0.31	0	17,19,21	0.68	0
7	BMA	N	3	7	11,11,12	0.84	0	15,15,17	0.96	1 (6%)
6	NAG	O	1	6,2	14,14,15	0.39	0	17,19,21	0.61	1 (5%)
6	NAG	O	2	6	14,14,15	0.38	0	17,19,21	1.06	1 (5%)
6	BMA	O	3	6	11,11,12	0.72	0	15,15,17	0.95	0
6	MAN	O	4	6	11,11,12	0.89	1 (9%)	15,15,17	1.10	2 (13%)
6	MAN	O	5	6	11,11,12	0.82	0	15,15,17	1.31	2 (13%)
5	NAG	P	1	1,5	14,14,15	0.32	0	17,19,21	0.63	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	NAG	P	2	5	14,14,15	0.76	1 (7%)	17,19,21	2.23	3 (17%)
6	NAG	Q	1	1,6	14,14,15	0.20	0	17,19,21	0.58	0
6	NAG	Q	2	6	14,14,15	0.28	0	17,19,21	0.78	1 (5%)
6	BMA	Q	3	6	11,11,12	0.91	0	15,15,17	0.86	0
6	MAN	Q	4	6	11,11,12	0.86	0	15,15,17	1.05	2 (13%)
6	MAN	Q	5	6	11,11,12	0.88	0	15,15,17	1.09	2 (13%)
7	NAG	R	1	7,2	14,14,15	0.54	0	17,19,21	1.10	1 (5%)
7	NAG	R	2	7	14,14,15	0.32	0	17,19,21	0.99	1 (5%)
7	BMA	R	3	7	11,11,12	0.93	1 (9%)	15,15,17	1.30	1 (6%)
6	NAG	S	1	6,2	14,14,15	0.34	0	17,19,21	0.64	1 (5%)
6	NAG	S	2	6	14,14,15	0.36	0	17,19,21	1.17	2 (11%)
6	BMA	S	3	6	11,11,12	0.94	0	15,15,17	1.01	0
6	MAN	S	4	6	11,11,12	1.13	2 (18%)	15,15,17	1.10	2 (13%)
6	MAN	S	5	6	11,11,12	0.79	0	15,15,17	1.13	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	J	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	J	2	5	-	2/6/23/26	0/1/1/1
6	NAG	K	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	K	2	6	-	0/6/23/26	0/1/1/1
6	BMA	K	3	6	-	0/2/19/22	0/1/1/1
6	MAN	K	4	6	-	0/2/19/22	0/1/1/1
6	MAN	K	5	6	-	0/2/19/22	0/1/1/1
7	NAG	L	1	7,2	-	3/6/23/26	0/1/1/1
7	NAG	L	2	7	-	3/6/23/26	0/1/1/1
7	BMA	L	3	7	-	1/2/19/22	0/1/1/1
6	NAG	M	1	6,2	-	2/6/23/26	0/1/1/1
6	NAG	M	2	6	-	2/6/23/26	0/1/1/1
6	BMA	M	3	6	-	2/2/19/22	0/1/1/1
6	MAN	M	4	6	-	0/2/19/22	0/1/1/1
6	MAN	M	5	6	-	2/2/19/22	0/1/1/1
7	NAG	N	1	7,2	-	1/6/23/26	0/1/1/1
7	NAG	N	2	7	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BMA	N	3	7	-	1/2/19/22	0/1/1/1
6	NAG	O	1	6,2	-	1/6/23/26	0/1/1/1
6	NAG	O	2	6	-	3/6/23/26	0/1/1/1
6	BMA	O	3	6	-	0/2/19/22	0/1/1/1
6	MAN	O	4	6	-	2/2/19/22	0/1/1/1
6	MAN	O	5	6	-	0/2/19/22	0/1/1/1
5	NAG	P	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	P	2	5	-	5/6/23/26	0/1/1/1
6	NAG	Q	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	0/6/23/26	0/1/1/1
6	BMA	Q	3	6	-	0/2/19/22	0/1/1/1
6	MAN	Q	4	6	-	0/2/19/22	0/1/1/1
6	MAN	Q	5	6	-	1/2/19/22	0/1/1/1
7	NAG	R	1	7,2	-	3/6/23/26	0/1/1/1
7	NAG	R	2	7	-	1/6/23/26	0/1/1/1
7	BMA	R	3	7	-	1/2/19/22	0/1/1/1
6	NAG	S	1	6,2	-	2/6/23/26	0/1/1/1
6	NAG	S	2	6	-	3/6/23/26	0/1/1/1
6	BMA	S	3	6	-	0/2/19/22	0/1/1/1
6	MAN	S	4	6	-	0/2/19/22	0/1/1/1
6	MAN	S	5	6	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	S	4	MAN	C1-C2	2.64	1.58	1.52
7	R	3	BMA	C1-C2	2.24	1.57	1.52
6	M	5	MAN	C1-C2	2.21	1.57	1.52
5	P	2	NAG	C1-C2	2.18	1.55	1.52
6	O	4	MAN	C1-C2	2.04	1.56	1.52
6	S	4	MAN	C2-C3	2.01	1.55	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	P	2	NAG	C2-N2-C7	7.79	134.00	122.90
6	O	5	MAN	C1-O5-C5	3.82	117.36	112.19
7	N	1	NAG	C3-C4-C5	3.69	116.83	110.24
5	P	2	NAG	C1-C2-N2	3.61	116.65	110.49
7	R	3	BMA	C1-O5-C5	3.39	116.79	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	K	4	MAN	C1-O5-C5	3.31	116.68	112.19
6	S	5	MAN	C1-O5-C5	3.15	116.46	112.19
7	R	1	NAG	C2-N2-C7	3.13	127.36	122.90
6	O	2	NAG	C2-N2-C7	3.12	127.34	122.90
7	L	2	NAG	C2-N2-C7	3.10	127.31	122.90
7	L	1	NAG	C2-N2-C7	3.08	127.29	122.90
7	R	2	NAG	C2-N2-C7	3.08	127.29	122.90
6	M	5	MAN	C1-O5-C5	3.07	116.36	112.19
6	S	2	NAG	C2-N2-C7	3.05	127.25	122.90
6	S	2	NAG	C1-O5-C5	2.82	116.02	112.19
6	M	3	BMA	C1-O5-C5	2.79	115.97	112.19
6	Q	5	MAN	C1-O5-C5	2.79	115.97	112.19
6	O	5	MAN	O2-C2-C3	-2.78	104.57	110.14
6	K	5	MAN	C1-O5-C5	2.71	115.86	112.19
6	Q	4	MAN	C1-O5-C5	2.68	115.82	112.19
6	Q	2	NAG	C1-O5-C5	2.47	115.54	112.19
6	O	4	MAN	O2-C2-C3	-2.41	105.32	110.14
6	S	5	MAN	O2-C2-C3	-2.40	105.33	110.14
6	K	5	MAN	O2-C2-C3	-2.40	105.33	110.14
6	O	4	MAN	C1-O5-C5	2.37	115.41	112.19
6	S	4	MAN	C1-O5-C5	2.25	115.25	112.19
6	Q	4	MAN	O2-C2-C3	-2.23	105.67	110.14
7	N	3	BMA	C1-O5-C5	2.21	115.19	112.19
7	L	1	NAG	C1-O5-C5	2.21	115.19	112.19
6	Q	5	MAN	O2-C2-C3	-2.21	105.71	110.14
5	P	1	NAG	C1-O5-C5	2.17	115.13	112.19
6	M	5	MAN	O2-C2-C3	-2.15	105.83	110.14
6	K	2	NAG	C1-O5-C5	2.14	115.09	112.19
5	P	2	NAG	C8-C7-N2	2.12	119.69	116.10
6	S	4	MAN	O2-C2-C3	-2.11	105.91	110.14
7	L	3	BMA	C1-O5-C5	2.08	115.01	112.19
6	S	1	NAG	C1-O5-C5	2.07	114.99	112.19
6	K	4	MAN	O2-C2-C3	-2.00	106.12	110.14
6	O	1	NAG	C1-O5-C5	2.00	114.90	112.19

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	P	1	NAG	O5-C5-C6-O6
6	Q	1	NAG	O5-C5-C6-O6
6	M	3	BMA	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
6	S	1	NAG	O5-C5-C6-O6
7	L	1	NAG	O5-C5-C6-O6
6	O	2	NAG	O5-C5-C6-O6
5	P	1	NAG	C4-C5-C6-O6
6	S	2	NAG	O5-C5-C6-O6
6	M	2	NAG	O5-C5-C6-O6
6	M	3	BMA	O5-C5-C6-O6
6	Q	1	NAG	C4-C5-C6-O6
6	M	1	NAG	O5-C5-C6-O6
7	L	2	NAG	O5-C5-C6-O6
6	O	2	NAG	C4-C5-C6-O6
6	M	1	NAG	C4-C5-C6-O6
6	M	2	NAG	C4-C5-C6-O6
7	L	2	NAG	C4-C5-C6-O6
5	P	2	NAG	C4-C5-C6-O6
6	S	1	NAG	C4-C5-C6-O6
7	L	1	NAG	C4-C5-C6-O6
5	P	2	NAG	C8-C7-N2-C2
5	P	2	NAG	O7-C7-N2-C2
7	N	2	NAG	C8-C7-N2-C2
5	J	2	NAG	O5-C5-C6-O6
6	S	2	NAG	C4-C5-C6-O6
7	N	2	NAG	C1-C2-N2-C7
7	R	1	NAG	O5-C5-C6-O6
6	K	1	NAG	O5-C5-C6-O6
6	K	1	NAG	C4-C5-C6-O6
6	O	4	MAN	C4-C5-C6-O6
6	M	5	MAN	C4-C5-C6-O6
7	N	2	NAG	O7-C7-N2-C2
7	R	3	BMA	O5-C5-C6-O6
5	P	2	NAG	O5-C5-C6-O6
6	O	4	MAN	O5-C5-C6-O6
6	M	5	MAN	O5-C5-C6-O6
7	L	3	BMA	O5-C5-C6-O6
7	N	3	BMA	O5-C5-C6-O6
6	Q	5	MAN	O5-C5-C6-O6
5	J	1	NAG	O5-C5-C6-O6
6	O	1	NAG	C4-C5-C6-O6
7	R	1	NAG	C4-C5-C6-O6
6	O	2	NAG	C3-C2-N2-C7
6	S	2	NAG	C3-C2-N2-C7
7	N	1	NAG	C3-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
5	J	2	NAG	C4-C5-C6-O6
5	P	2	NAG	C3-C2-N2-C7
7	L	1	NAG	C3-C2-N2-C7
7	L	2	NAG	C3-C2-N2-C7
7	R	1	NAG	C3-C2-N2-C7
7	R	2	NAG	C3-C2-N2-C7

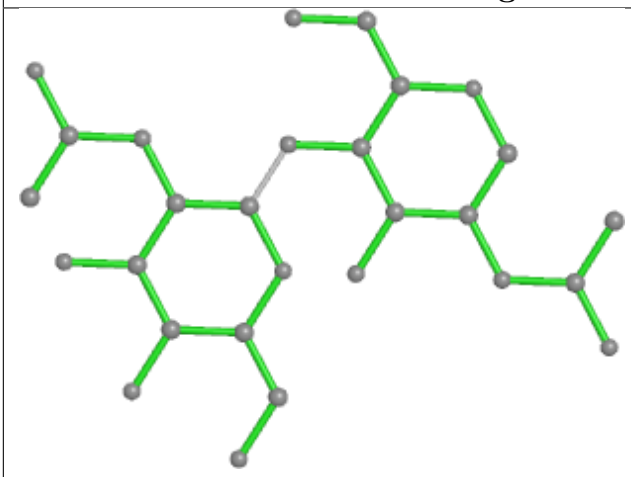
There are no ring outliers.

6 monomers are involved in 4 short contacts:

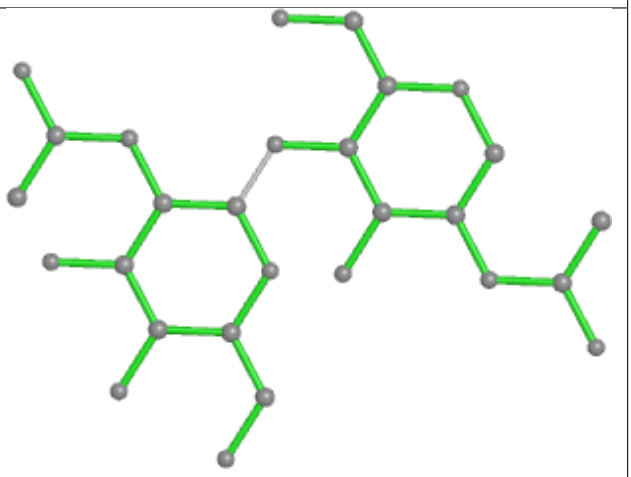
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	N	1	NAG	2	0
6	S	3	BMA	1	0
7	N	2	NAG	1	0
6	O	3	BMA	1	0
6	O	4	MAN	1	0
6	S	4	MAN	1	0

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

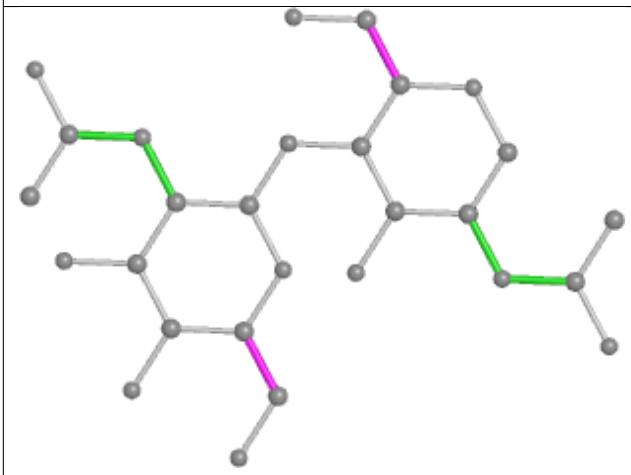
Oligosaccharide Chain J



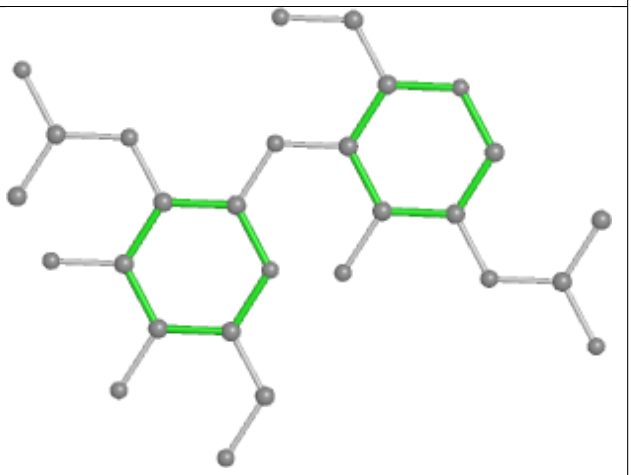
Bond lengths



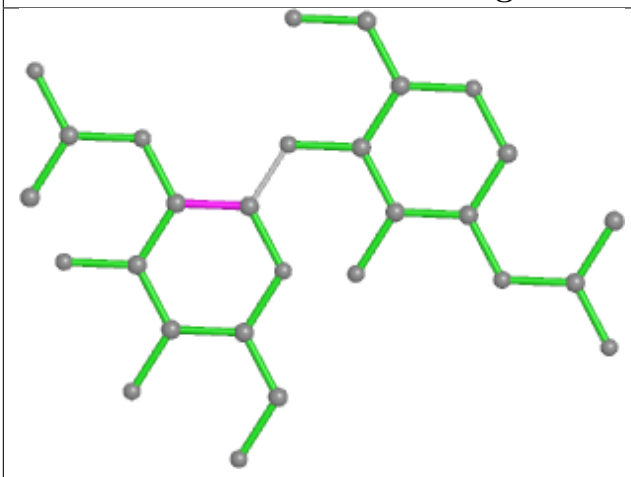
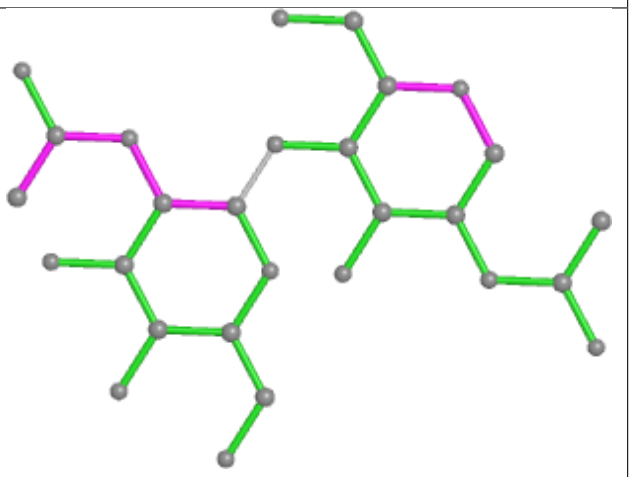
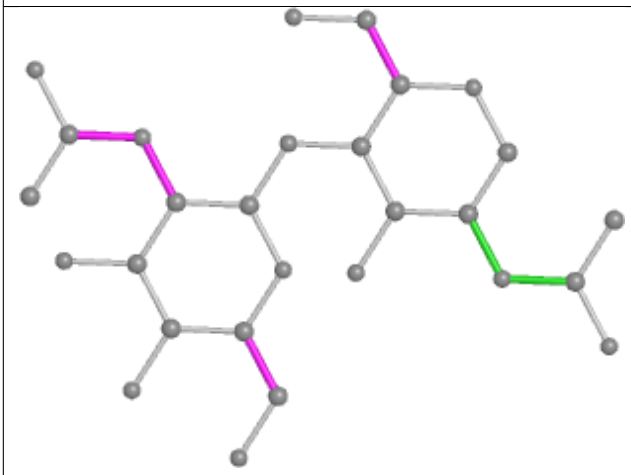
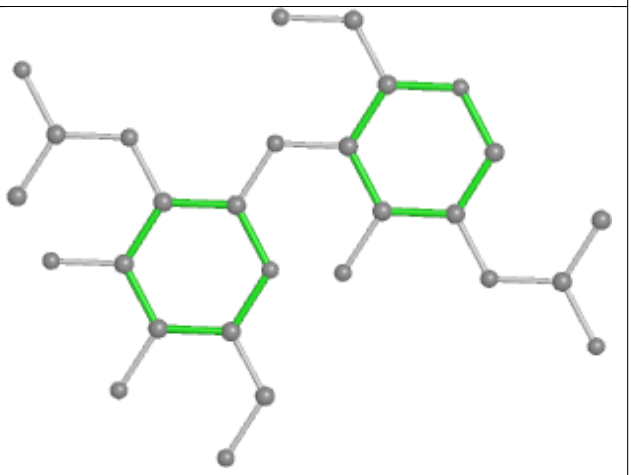
Bond angles



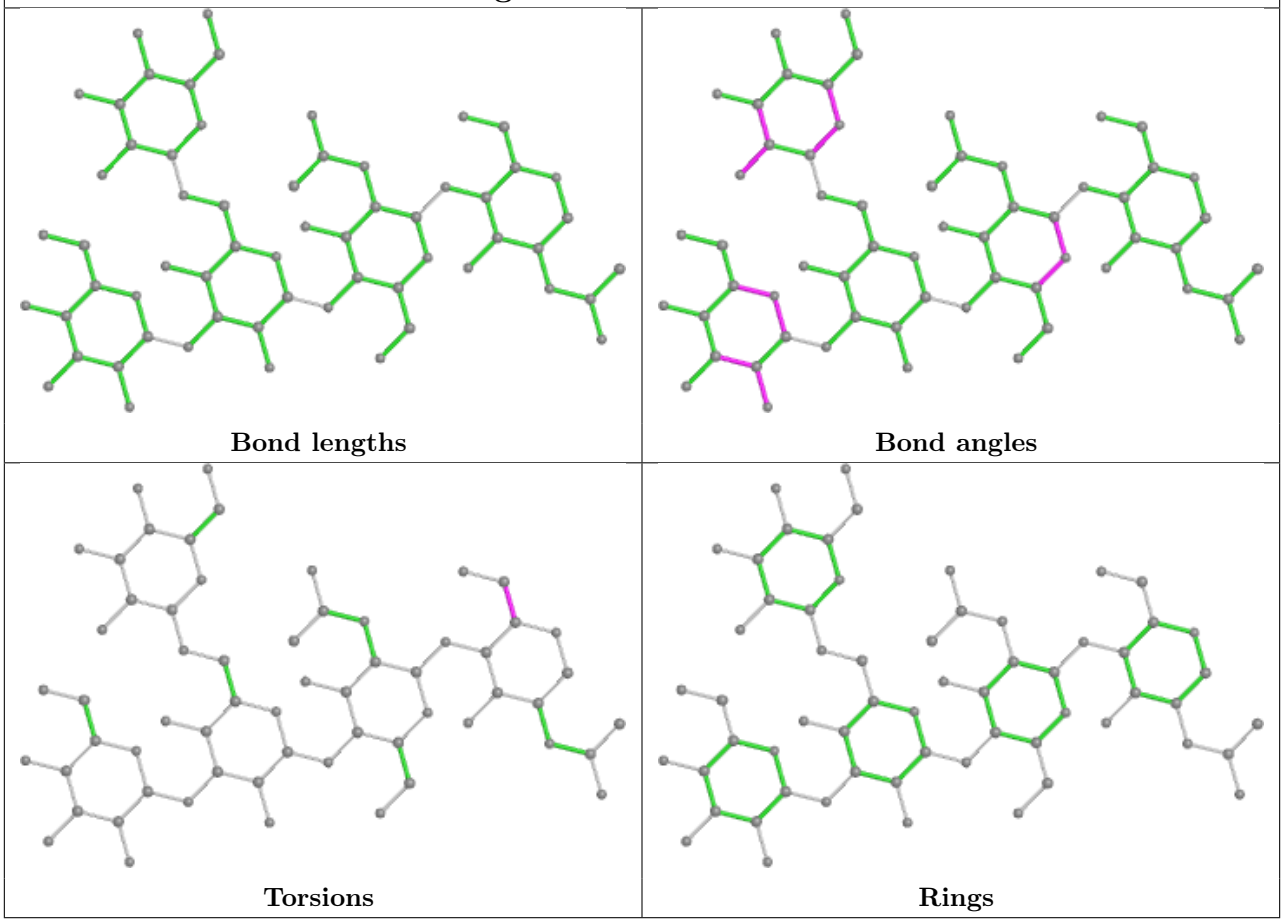
Torsions

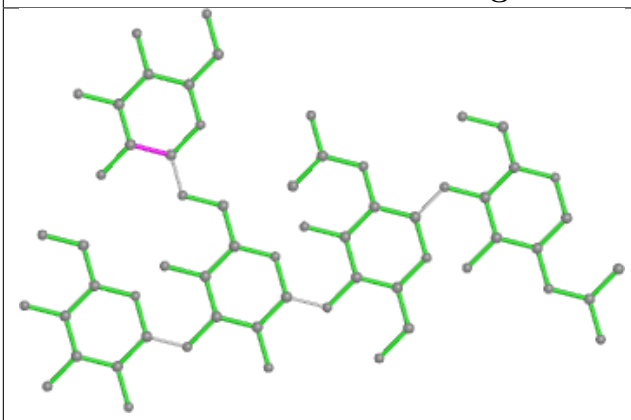
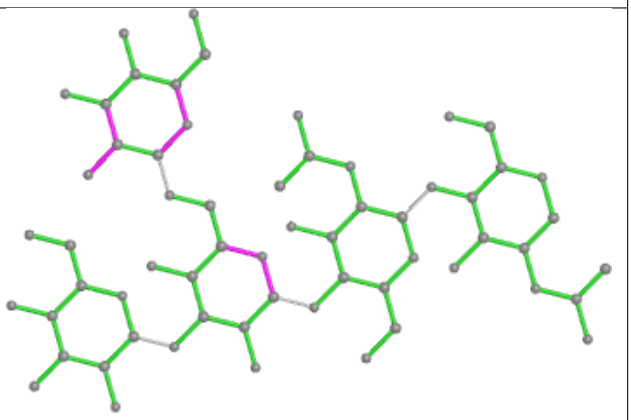
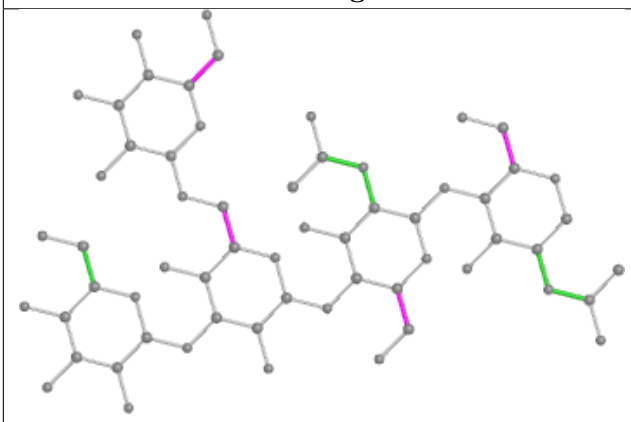
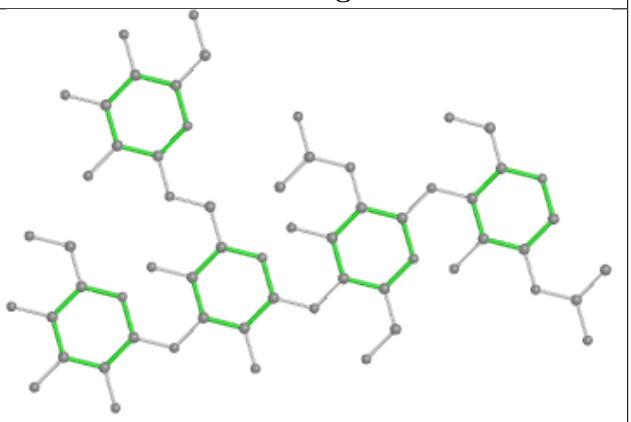


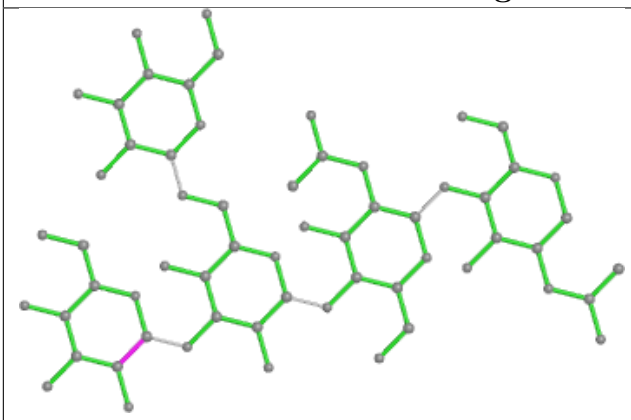
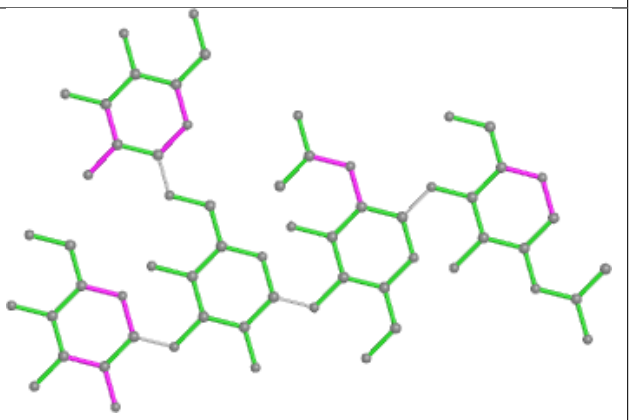
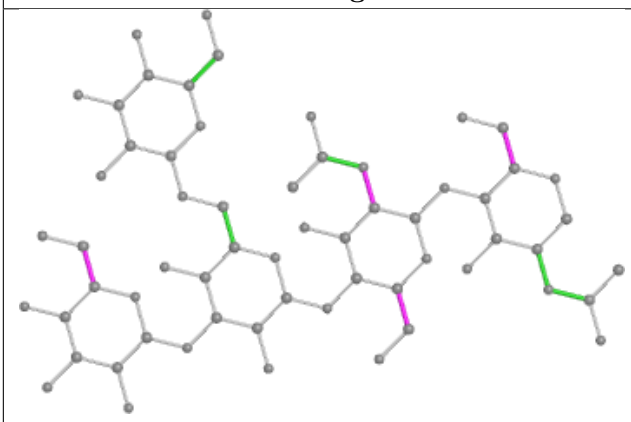
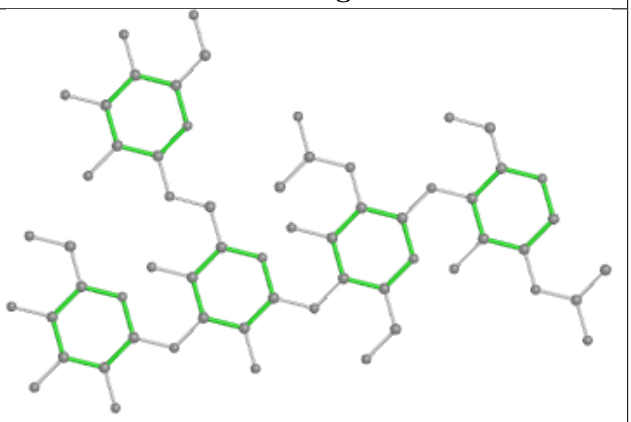
Rings

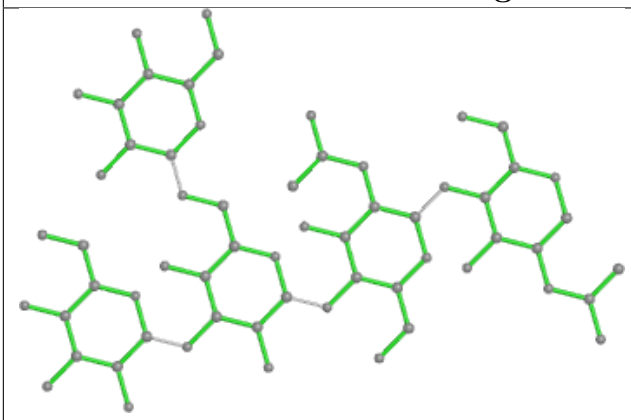
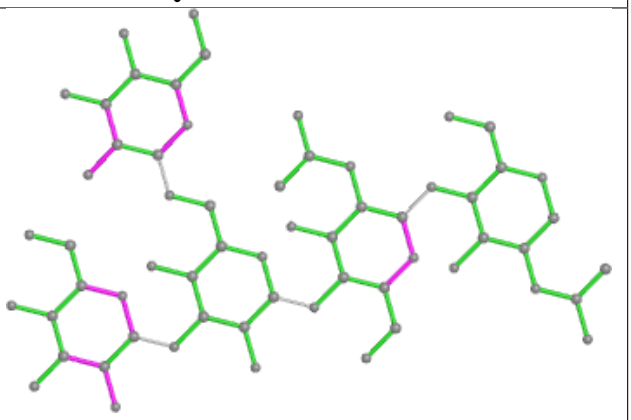
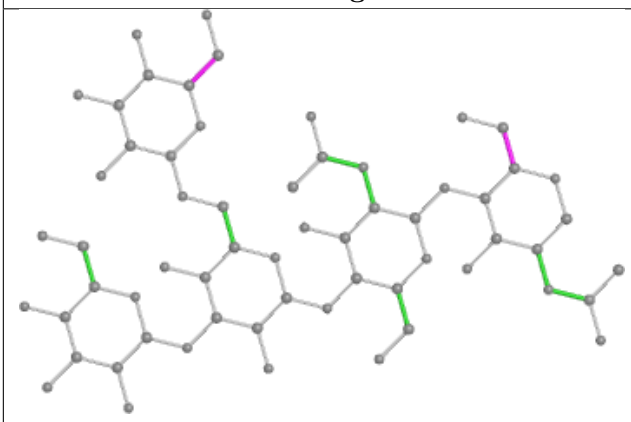
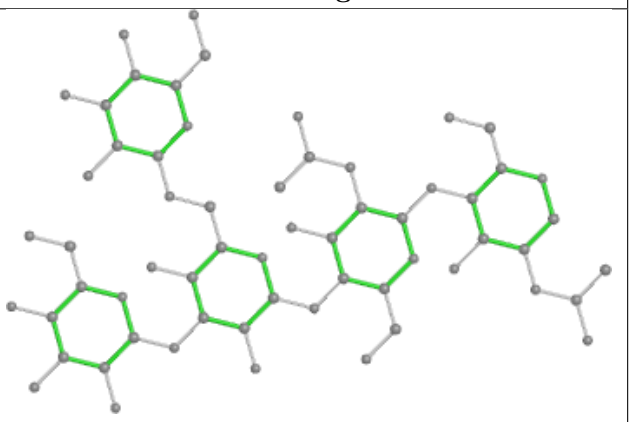
Oligosaccharide Chain P	
 Bond lengths	 Bond angles
 Torsions	 Rings

Oligosaccharide Chain K

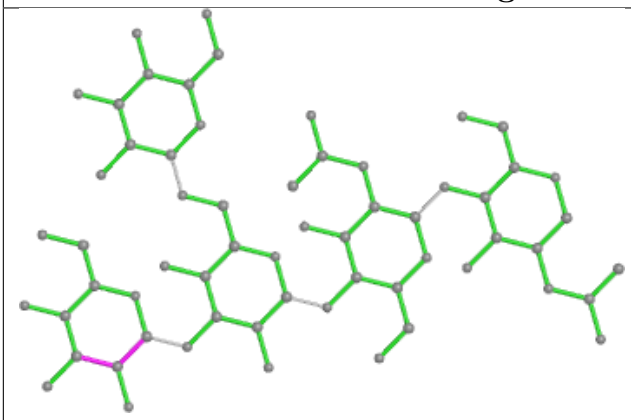


Oligosaccharide Chain M	
 Bond lengths	 Bond angles
 Torsions	 Rings

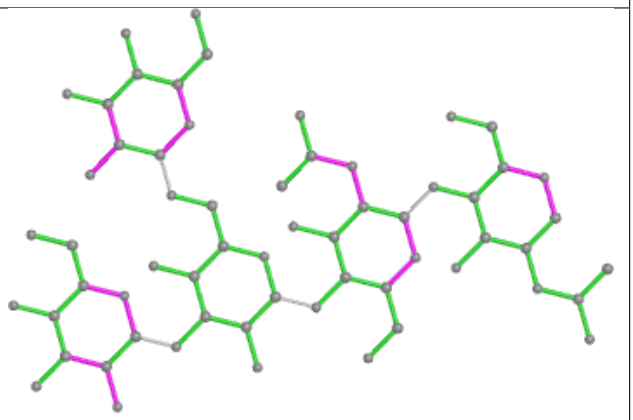
Oligosaccharide Chain O	
 Bond lengths	 Bond angles
 Torsions	 Rings

Oligosaccharide Chain Q	
 Bond lengths	 Bond angles
 Torsions	 Rings

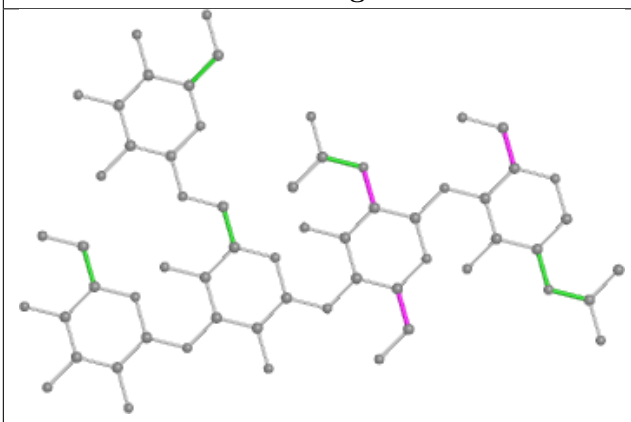
Oligosaccharide Chain S



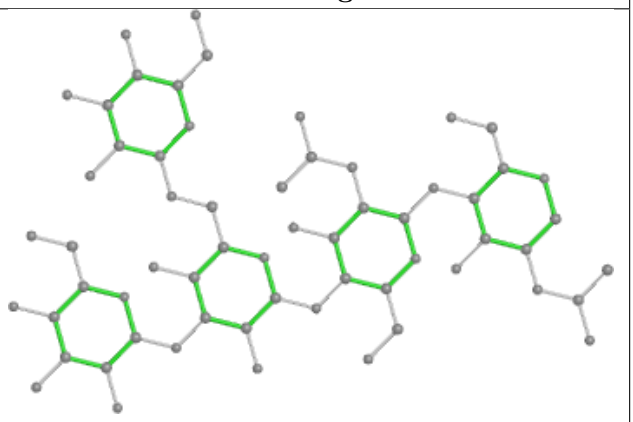
Bond lengths



Bond angles

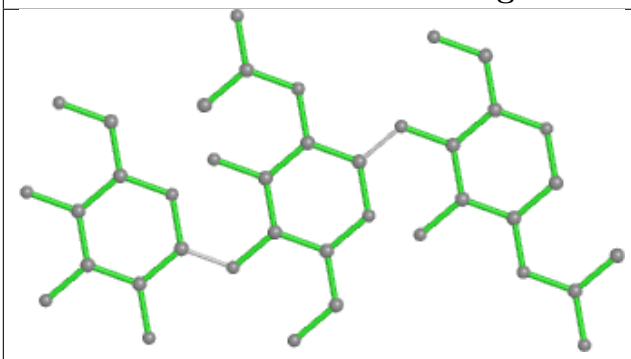


Torsions

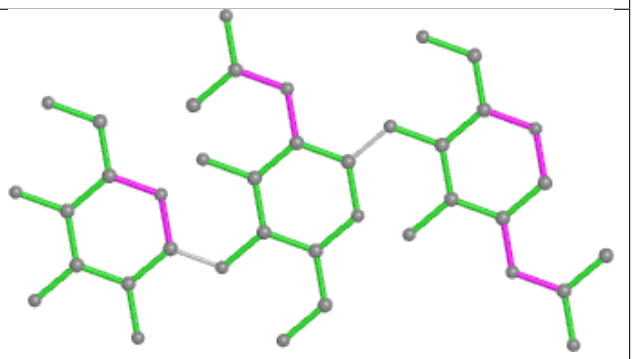


Rings

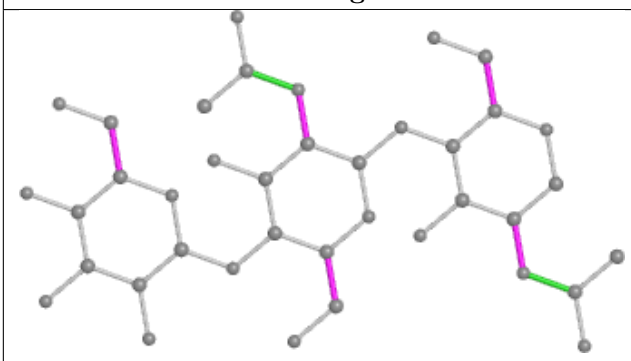
Oligosaccharide Chain L



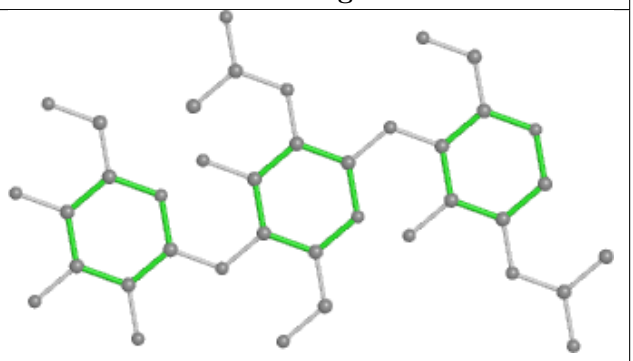
Bond lengths



Bond angles

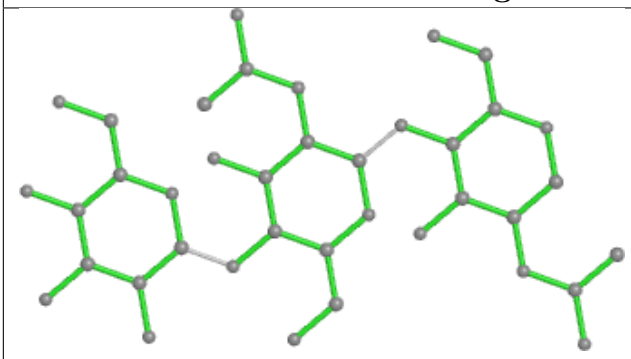


Torsions

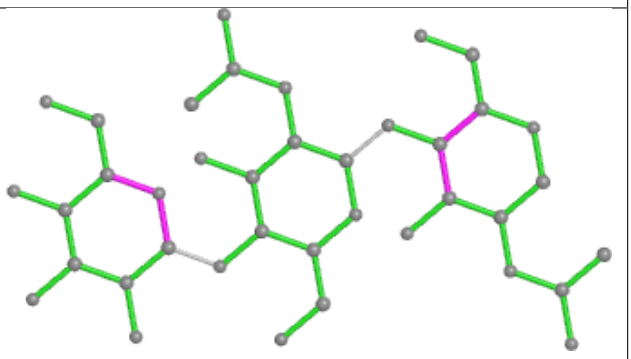


Rings

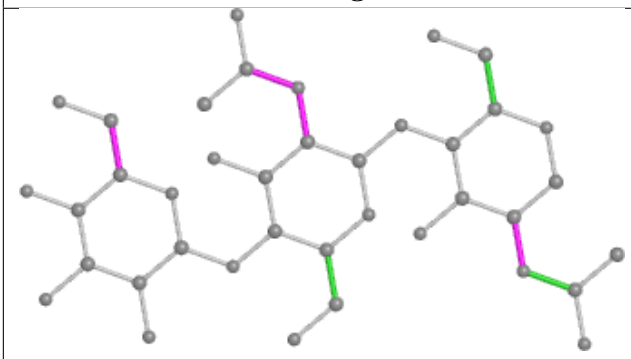
Oligosaccharide Chain N



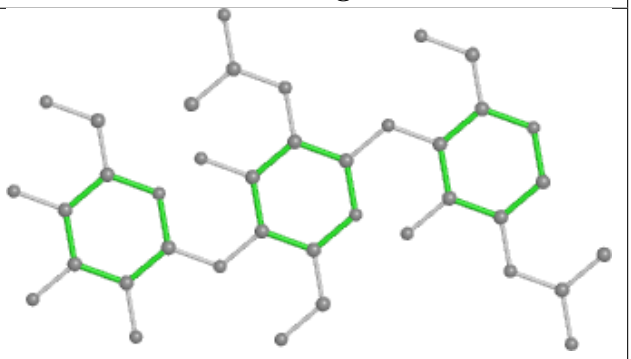
Bond lengths



Bond angles

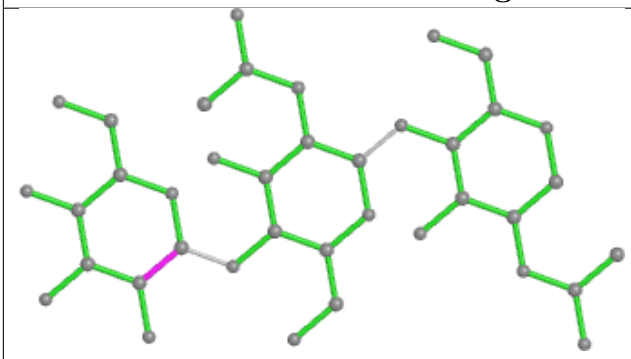


Torsions

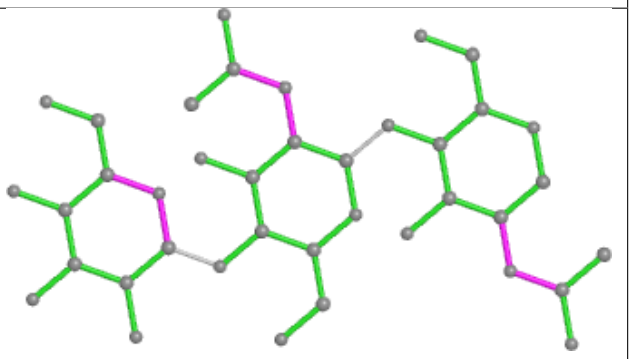


Rings

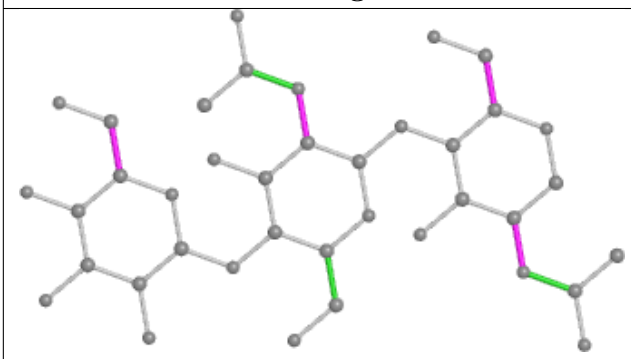
Oligosaccharide Chain R



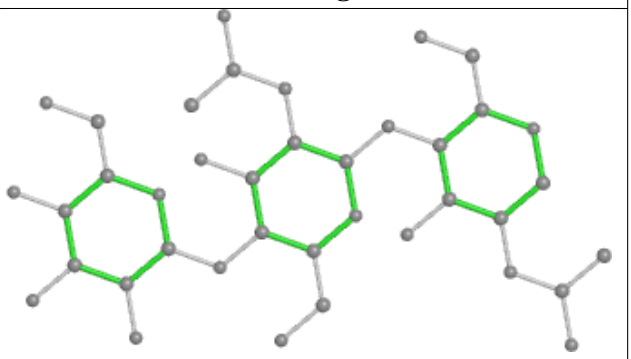
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 1 is monoatomic - leaving 18 for Mogul analysis.

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	$\#\|Z\| > 2$
8	P1M	D	701	-	20,20,20	1.74	3 (15%)	27,28,28	1.87	5 (18%)
9	Y01	D	709	-	31,31,38	0.64	0	48,48,57	1.37	6 (12%)
9	Y01	B	711	-	31,31,38	0.66	0	48,48,57	1.22	5 (10%)
8	P1M	A	701	-	20,20,20	1.69	3 (15%)	27,28,28	1.81	4 (14%)
9	Y01	A	710	-	31,31,38	0.68	0	48,48,57	1.39	7 (14%)
10	NAG	C	701	2	14,14,15	0.48	0	17,19,21	0.53	0
9	Y01	C	712	-	31,31,38	0.67	0	48,48,57	1.28	6 (12%)
10	NAG	E	702	2	14,14,15	0.33	0	17,19,21	0.57	0
9	Y01	C	711	-	31,31,38	0.62	0	48,48,57	1.42	7 (14%)
9	Y01	E	711	-	31,31,38	0.66	0	48,48,57	1.27	4 (8%)
10	NAG	B	702	2	14,14,15	0.33	0	17,19,21	0.56	0
10	NAG	B	701	2	14,14,15	0.48	0	17,19,21	0.54	0
10	NAG	E	701	2	14,14,15	0.56	0	17,19,21	0.98	1 (5%)
9	Y01	A	709	-	31,31,38	0.61	0	48,48,57	1.45	8 (16%)
10	NAG	C	702	2	14,14,15	0.27	0	17,19,21	0.65	0
9	Y01	E	712	-	31,31,38	0.66	1 (3%)	48,48,57	1.43	6 (12%)
9	Y01	D	710	-	31,31,38	0.64	0	48,48,57	1.36	6 (12%)
9	Y01	B	712	-	31,31,38	0.68	1 (3%)	48,48,57	1.24	5 (10%)

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
8	P1M	D	701	-	-	3/4/26/26	0/4/3/3
9	Y01	D	709	-	-	6/10/68/77	0/4/4/4
9	Y01	B	711	-	-	6/10/68/77	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	P1M	A	701	-	-	0/4/26/26	0/4/3/3
9	Y01	A	710	-	-	7/10/68/77	0/4/4/4
10	NAG	C	701	2	-	2/6/23/26	0/1/1/1
9	Y01	C	712	-	-	6/10/68/77	0/4/4/4
10	NAG	E	702	2	-	2/6/23/26	0/1/1/1
9	Y01	C	711	-	-	6/10/68/77	0/4/4/4
9	Y01	E	711	-	-	4/10/68/77	0/4/4/4
10	NAG	B	702	2	-	2/6/23/26	0/1/1/1
10	NAG	B	701	2	-	2/6/23/26	0/1/1/1
10	NAG	E	701	2	-	2/6/23/26	0/1/1/1
9	Y01	A	709	-	-	4/10/68/77	0/4/4/4
10	NAG	C	702	2	-	4/6/23/26	0/1/1/1
9	Y01	E	712	-	-	6/10/68/77	0/4/4/4
9	Y01	D	710	-	-	4/10/68/77	0/4/4/4
9	Y01	B	712	-	-	4/10/68/77	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	701	P1M	C3-N8	5.22	1.53	1.47
8	A	701	P1M	C3-N8	5.17	1.53	1.47
8	D	701	P1M	C7-N8	4.17	1.52	1.47
8	A	701	P1M	C7-N8	3.71	1.51	1.47
9	B	712	Y01	CBH-CBF	-2.09	1.52	1.56
9	E	712	Y01	CBH-CBF	-2.01	1.52	1.56
8	D	701	P1M	C13-C12	-2.00	1.34	1.38
8	A	701	P1M	C10-C11	-2.00	1.36	1.39

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	701	P1M	BR1-C11-C10	-5.64	114.80	119.83
8	D	701	P1M	C2-C1-N9	4.65	117.69	110.60
9	C	711	Y01	CBI-CBE-CBB	-4.42	112.56	119.49
8	D	701	P1M	BR1-C11-C10	-4.34	115.96	119.83
8	D	701	P1M	C8A-N8-C3	4.14	116.51	113.16
8	A	701	P1M	C8A-N8-C3	4.11	116.48	113.16
9	A	710	Y01	CBI-CBE-CBB	-4.09	113.08	119.49
9	D	710	Y01	CBI-CBE-CBB	-3.81	113.52	119.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	D	701	P1M	C8-C1-C2	-3.80	107.78	111.13
9	E	712	Y01	CBI-CBE-CBB	-3.48	114.03	119.49
9	C	712	Y01	CBI-CBE-CBB	-3.42	114.12	119.49
9	E	712	Y01	CBI-CBG-CBD	-3.39	109.36	114.38
9	A	709	Y01	CBI-CBE-CBB	-3.38	114.19	119.49
9	A	709	Y01	CAK-CBD-CBG	-3.24	106.20	110.91
9	A	709	Y01	CBC-CAV-CAZ	-3.23	106.55	112.03
9	D	709	Y01	CBI-CBE-CBB	-3.19	114.49	119.49
9	C	711	Y01	CBI-CBG-CBD	-3.13	109.75	114.38
9	C	712	Y01	CAC-CBB-CBE	-3.09	108.19	112.92
9	E	712	Y01	CBC-CAV-CAZ	-3.08	106.79	112.03
9	B	712	Y01	CBI-CBE-CBB	-3.03	114.74	119.49
10	E	701	NAG	C2-N2-C7	3.02	127.20	122.90
8	A	701	P1M	BR1-C11-C12	3.01	123.67	117.81
9	A	710	Y01	CBI-CBG-CBD	-3.00	109.94	114.38
9	D	709	Y01	CBH-CBF-CBD	-2.99	108.25	112.73
8	A	701	P1M	C8-C1-N9	-2.95	106.10	110.60
9	D	710	Y01	CAC-CBB-CBE	-2.84	108.57	112.92
9	D	709	Y01	CBI-CBG-CBD	-2.80	110.23	114.38
9	E	711	Y01	CAC-CBB-CAO	-2.76	106.04	110.36
9	A	709	Y01	CAR-CBC-CAV	-2.73	106.56	110.31
9	B	711	Y01	CBC-CAV-CAZ	-2.69	107.46	112.03
9	A	709	Y01	CAV-CAZ-CAI	-2.64	116.80	120.61
9	D	710	Y01	CAK-CBD-CBG	-2.61	107.13	110.91
9	B	712	Y01	CAV-CAZ-CAI	-2.53	116.96	120.61
9	A	710	Y01	CBF-CBD-CBG	-2.53	105.71	109.09
9	C	711	Y01	CBC-CAV-CAZ	-2.52	107.76	112.03
9	C	711	Y01	CAC-CBB-CBE	-2.50	109.10	112.92
9	D	710	Y01	CBF-CBH-CAZ	2.47	113.53	109.65
9	E	711	Y01	CAR-CBC-CAV	-2.44	106.95	110.31
9	E	711	Y01	CBC-CAV-CAZ	-2.42	107.92	112.03
9	A	710	Y01	CAV-CAZ-CAI	-2.41	117.13	120.61
9	E	712	Y01	CAC-CBB-CBE	-2.41	109.24	112.92
9	B	711	Y01	CAR-CBC-CAV	-2.40	107.02	110.31
9	D	709	Y01	CAD-CBH-CBF	-2.39	108.83	111.68
9	A	709	Y01	CAC-CBB-CAO	-2.36	106.67	110.36
9	E	711	Y01	CAP-CBE-CBB	-2.32	108.55	112.15
9	B	712	Y01	CAC-CBB-CAO	-2.32	106.72	110.36
9	C	711	Y01	CBF-CBD-CBG	-2.29	106.02	109.09
8	D	701	P1M	BR1-C11-C12	2.24	122.17	117.81
9	A	709	Y01	CBF-CBH-CAZ	2.24	113.16	109.65
9	E	712	Y01	CAV-CAZ-CAI	-2.23	117.39	120.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	B	712	Y01	CBI-CBG-CBD	-2.22	111.10	114.38
9	B	711	Y01	CBI-CBG-CBD	-2.21	111.11	114.38
9	E	712	Y01	CAR-CBC-CAV	-2.17	107.33	110.31
9	C	711	Y01	CBF-CBH-CAZ	2.15	113.02	109.65
9	A	710	Y01	CAC-CBB-CBE	-2.15	109.63	112.92
9	C	712	Y01	CAD-CBH-CBF	-2.14	109.12	111.68
9	C	712	Y01	CBI-CBG-CBD	-2.11	111.26	114.38
9	B	712	Y01	CAD-CBH-CBF	-2.11	109.17	111.68
9	B	711	Y01	CAV-CAZ-CAI	-2.11	117.57	120.61
9	D	709	Y01	CAV-CAZ-CAI	-2.10	117.58	120.61
9	C	712	Y01	CAV-CAZ-CAI	-2.09	117.59	120.61
9	D	710	Y01	CBI-CBG-CBD	-2.09	111.29	114.38
9	A	710	Y01	CAP-CAQ-CBG	-2.07	101.03	105.13
9	B	711	Y01	CBI-CBE-CBB	-2.06	116.27	119.49
9	A	710	Y01	CAV-CAZ-CBH	2.04	119.14	116.42
9	D	710	Y01	CAV-CAZ-CAI	-2.04	117.67	120.61
9	D	709	Y01	CAC-CBB-CBE	-2.03	109.81	112.92
9	C	712	Y01	CAV-CAZ-CBH	2.02	119.10	116.42
9	A	709	Y01	CAC-CBB-CBE	-2.01	109.84	112.92
9	C	711	Y01	CAJ-CAO-CBB	-2.01	109.26	115.03

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	D	701	P1M	C2-C1-N9-C10
8	D	701	P1M	C11-C10-N9-C1
8	D	701	P1M	C15-C10-N9-C1
9	C	711	Y01	CAC-CBB-CBE-CBI
9	C	712	Y01	CAC-CBB-CBE-CBI
9	D	710	Y01	CAC-CBB-CBE-CBI
10	C	702	NAG	O7-C7-N2-C2
9	A	710	Y01	CAJ-CAO-CBB-CAC
9	A	709	Y01	CAC-CBB-CBE-CAP
9	C	711	Y01	CAC-CBB-CBE-CAP
9	A	709	Y01	CAC-CBB-CBE-CBI
9	A	710	Y01	CAC-CBB-CBE-CBI
9	D	709	Y01	CAC-CBB-CBE-CBI
9	E	712	Y01	CAC-CBB-CBE-CBI
9	A	710	Y01	CAO-CBB-CBE-CBI
10	C	702	NAG	C8-C7-N2-C2
9	A	710	Y01	CAC-CBB-CBE-CAP

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Mol	Chain	Res	Type	Atoms
9	C	712	Y01	CAC-CBB-CBE-CAP
9	D	709	Y01	CAC-CBB-CBE-CAP
9	D	710	Y01	CAC-CBB-CBE-CAP
9	E	712	Y01	CAC-CBB-CBE-CAP
9	B	712	Y01	CAC-CBB-CBE-CBI
9	A	710	Y01	CAO-CBB-CBE-CAP
9	A	709	Y01	CAO-CBB-CBE-CBI
9	C	711	Y01	CAO-CBB-CBE-CBI
9	C	712	Y01	CAO-CBB-CBE-CBI
9	D	709	Y01	CAO-CBB-CBE-CBI
9	D	710	Y01	CAO-CBB-CBE-CBI
9	E	712	Y01	CAO-CBB-CBE-CBI
9	C	711	Y01	CAO-CBB-CBE-CAP
9	C	712	Y01	CAO-CBB-CBE-CAP
9	D	710	Y01	CAO-CBB-CBE-CAP
9	E	712	Y01	CAO-CBB-CBE-CAP
9	B	712	Y01	CAO-CBB-CBE-CBI
10	B	702	NAG	O5-C5-C6-O6
10	C	701	NAG	O5-C5-C6-O6
10	E	702	NAG	O5-C5-C6-O6
10	E	702	NAG	C4-C5-C6-O6
10	C	701	NAG	C4-C5-C6-O6
9	B	712	Y01	CAC-CBB-CBE-CAP
10	B	701	NAG	C4-C5-C6-O6
9	A	709	Y01	CAO-CBB-CBE-CAP
9	B	711	Y01	CAJ-CAO-CBB-CBE
9	C	711	Y01	CAJ-CAO-CBB-CBE
10	B	702	NAG	C4-C5-C6-O6
9	A	710	Y01	CAJ-CAO-CBB-CBE
9	C	711	Y01	CAJ-CAO-CBB-CAC
9	D	709	Y01	CAO-CBB-CBE-CAP
10	C	702	NAG	C1-C2-N2-C7
10	B	701	NAG	O5-C5-C6-O6
9	B	711	Y01	CAJ-CAO-CBB-CAC
9	D	709	Y01	CAJ-CAO-CBB-CAC
9	D	709	Y01	CAJ-CAO-CBB-CBE
10	E	701	NAG	O5-C5-C6-O6
9	E	711	Y01	CAO-CAJ-CAN-CBA
9	E	711	Y01	CAN-CAJ-CAO-CBB
9	E	712	Y01	CAN-CAJ-CAO-CBB
9	B	712	Y01	CAO-CBB-CBE-CAP
9	B	711	Y01	CAN-CAJ-CAO-CBB

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Mol	Chain	Res	Type	Atoms
9	A	710	Y01	CAN-CAJ-CAO-CBB
10	C	702	NAG	C3-C2-N2-C7
9	E	712	Y01	CAO-CAJ-CAN-CBA
9	B	711	Y01	CAO-CBB-CBE-CBI
9	E	711	Y01	CAJ-CAN-CBA-CAA
9	E	711	Y01	CAJ-CAN-CBA-CAB
9	B	711	Y01	CAC-CBB-CBE-CBI
9	C	712	Y01	CAJ-CAO-CBB-CAC
9	B	711	Y01	CAO-CBB-CBE-CAP
9	C	712	Y01	CAN-CAJ-CAO-CBB
10	E	701	NAG	C3-C2-N2-C7

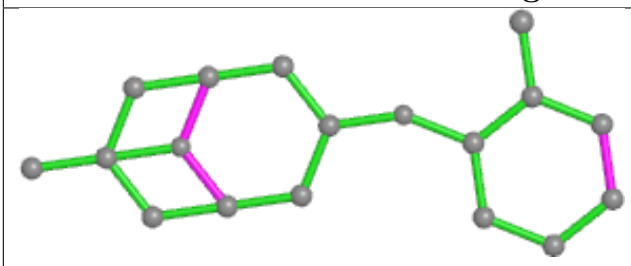
There are no ring outliers.

12 monomers are involved in 23 short contacts:

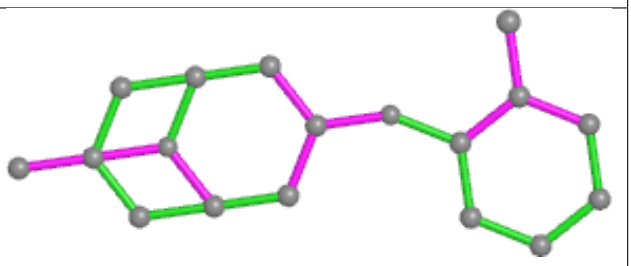
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	709	Y01	1	0
9	B	711	Y01	1	0
8	A	701	P1M	2	0
9	A	710	Y01	2	0
9	C	712	Y01	2	0
9	C	711	Y01	2	0
9	E	711	Y01	2	0
9	A	709	Y01	2	0
10	C	702	NAG	3	0
9	E	712	Y01	3	0
9	D	710	Y01	3	0
9	B	712	Y01	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

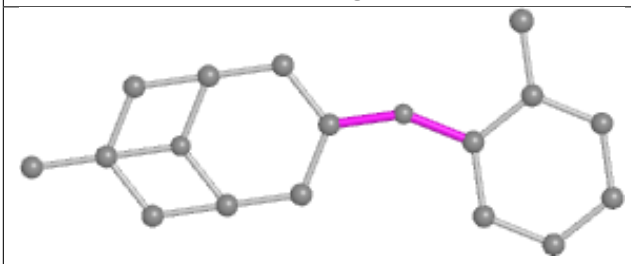
Ligand P1M D 701



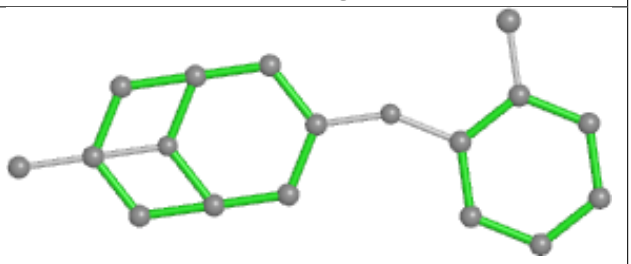
Bond lengths



Bond angles

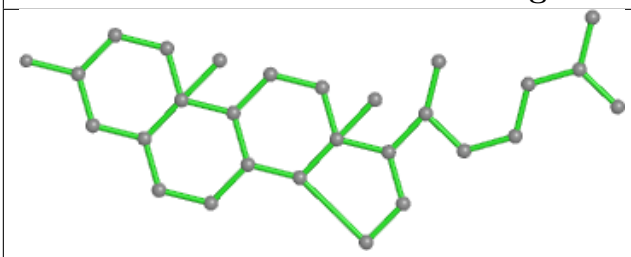


Torsions

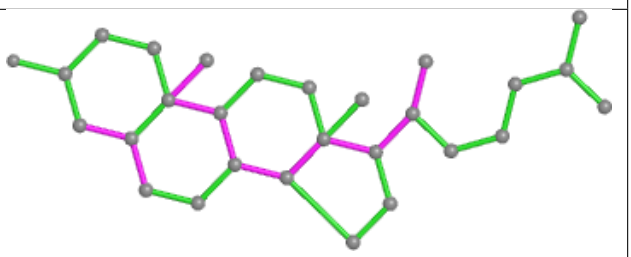


Rings

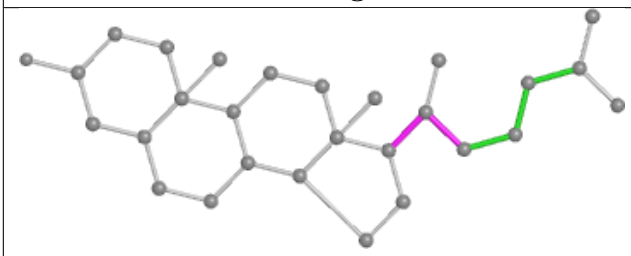
Ligand Y01 D 709



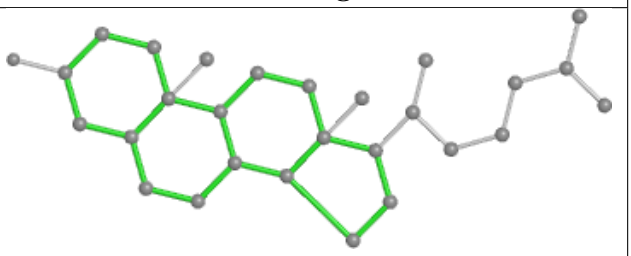
Bond lengths



Bond angles

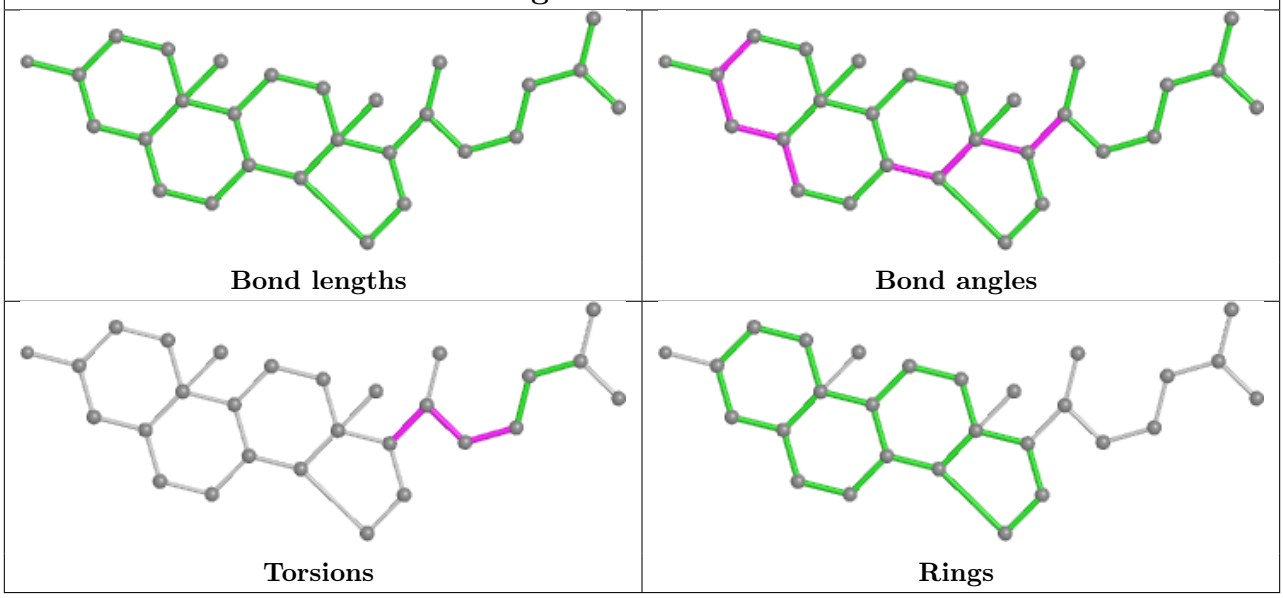


Torsions

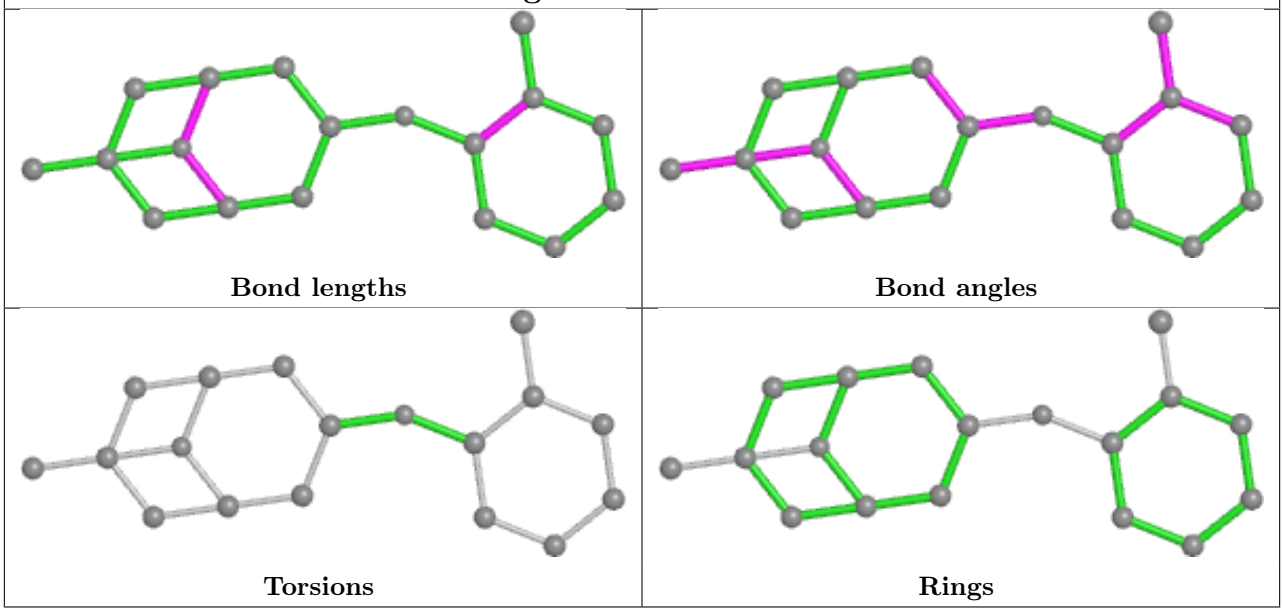


Rings

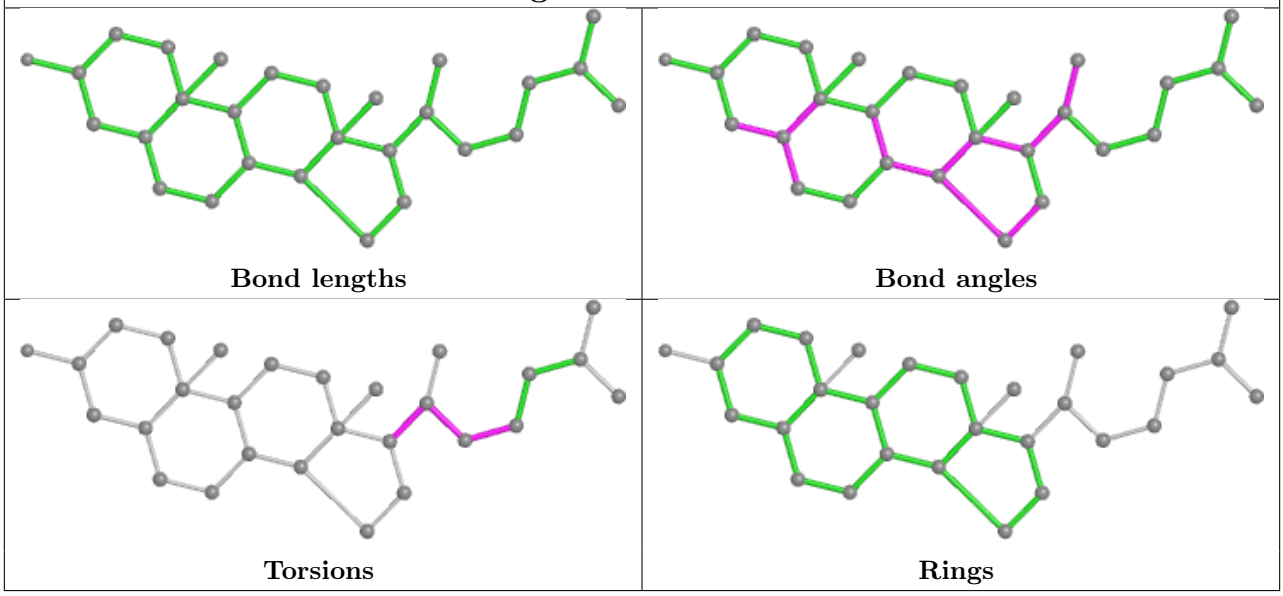
Ligand Y01 B 711



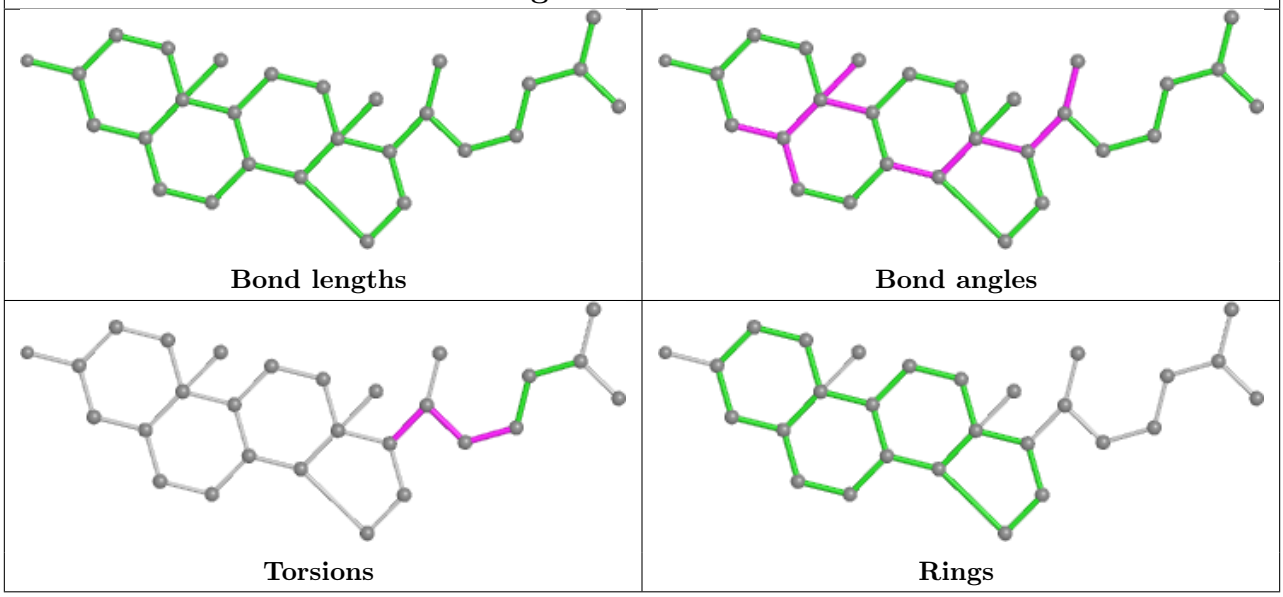
Ligand P1M A 701



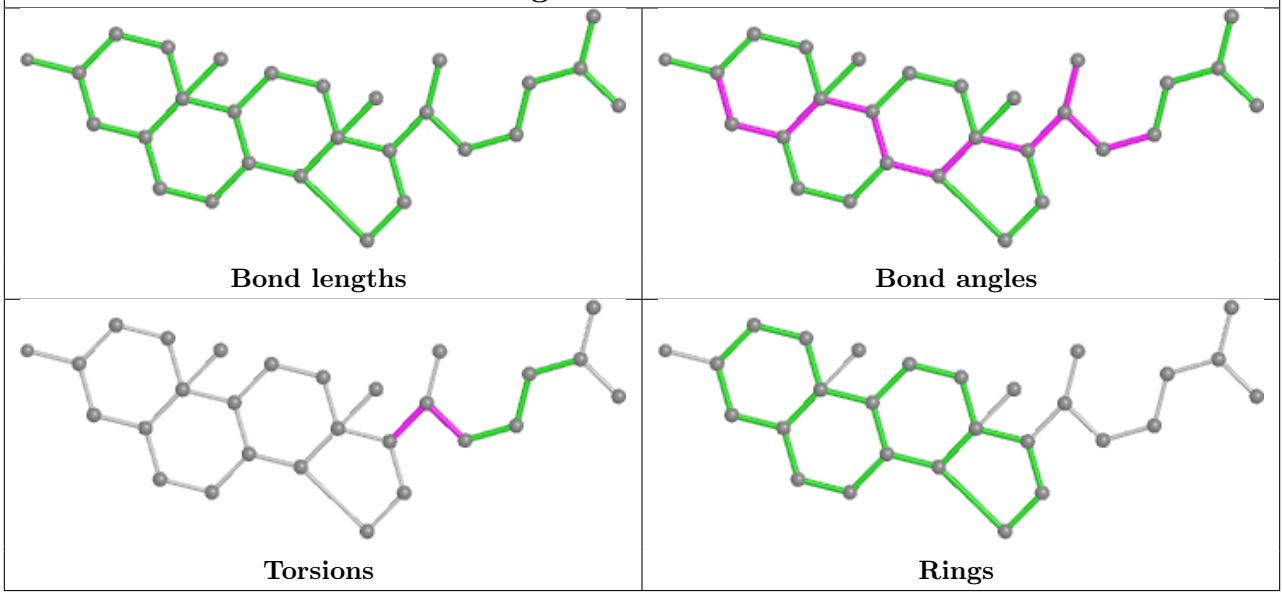
Ligand Y01 A 710



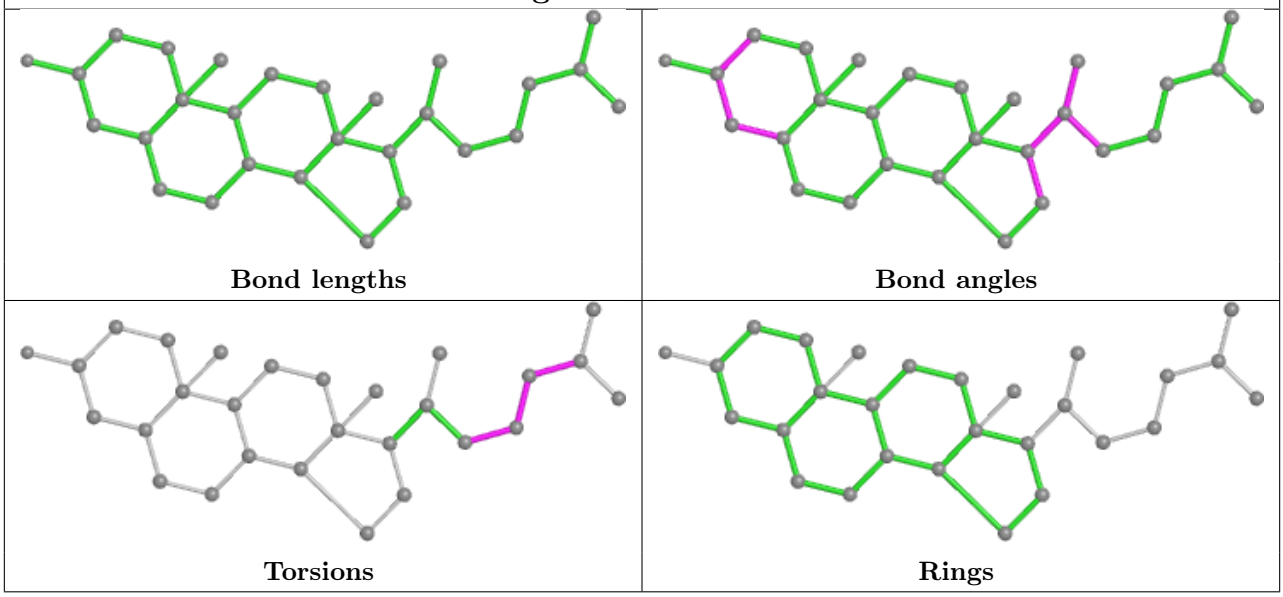
Ligand Y01 C 712



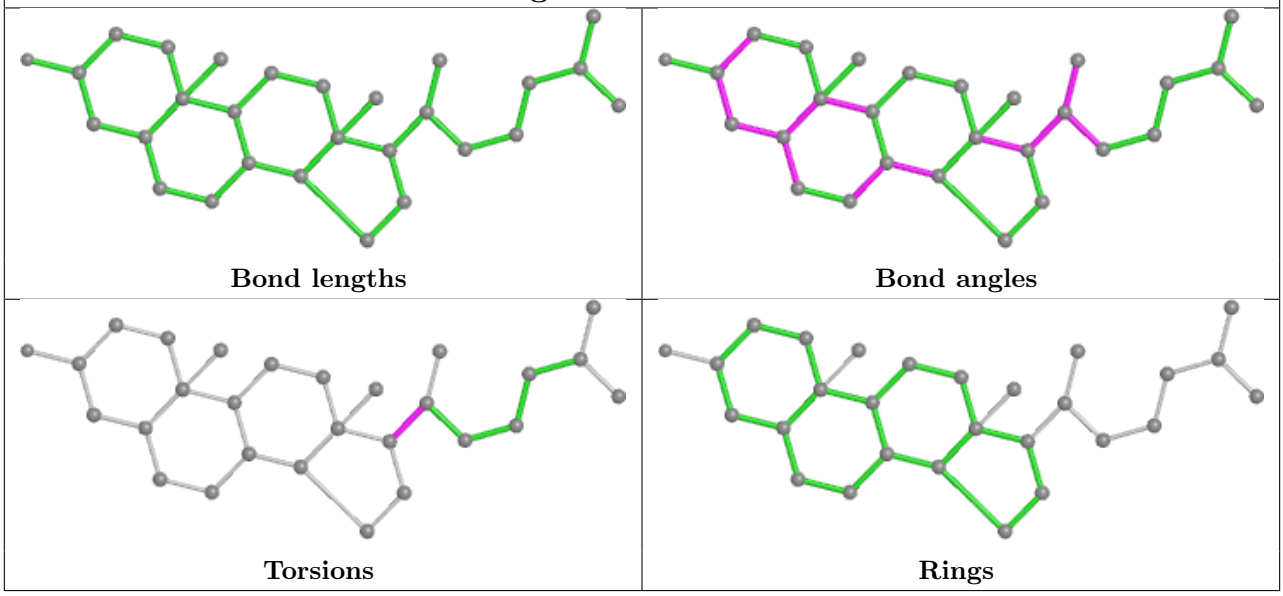
Ligand Y01 C 711



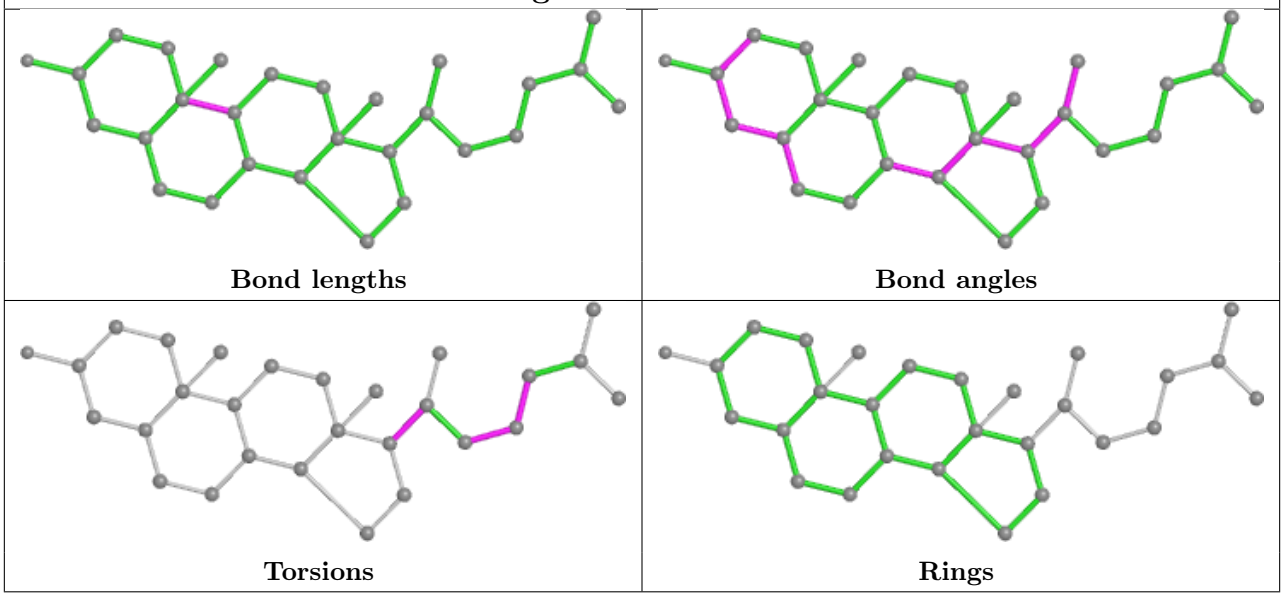
Ligand Y01 E 711

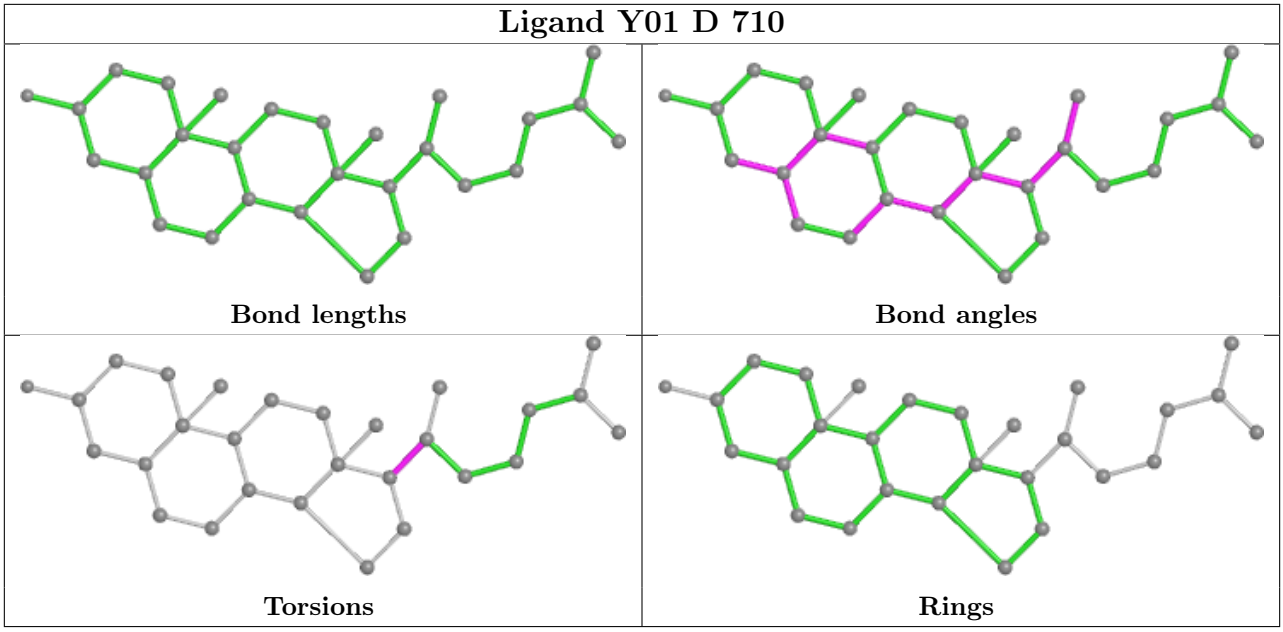


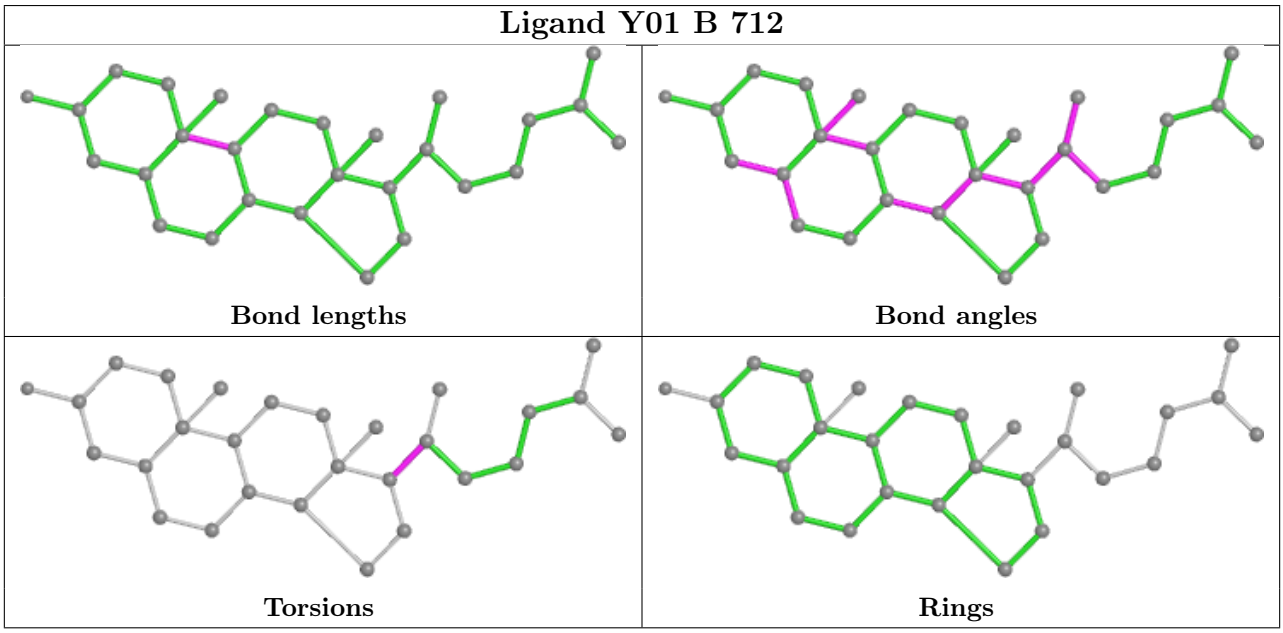
Ligand Y01 A 709



Ligand Y01 E 712







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.

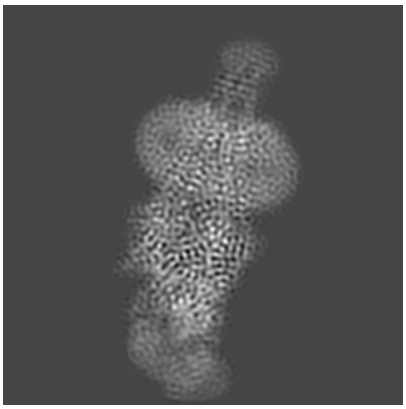
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-20488. These allow visual inspection of the internal detail of the map and identification of artifacts.

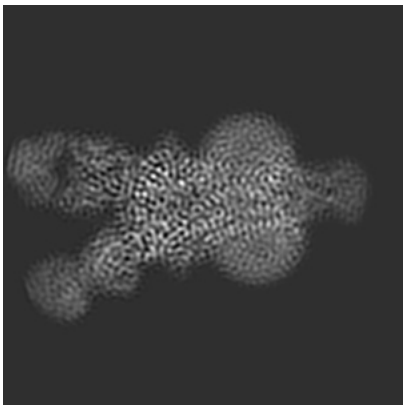
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

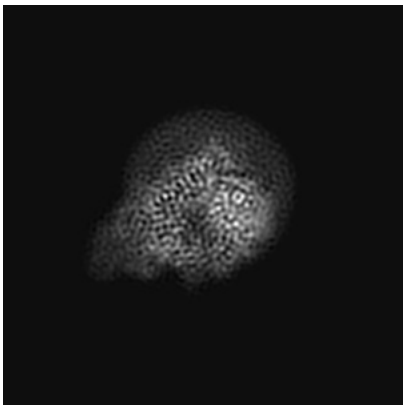
6.1.1 Primary map



X

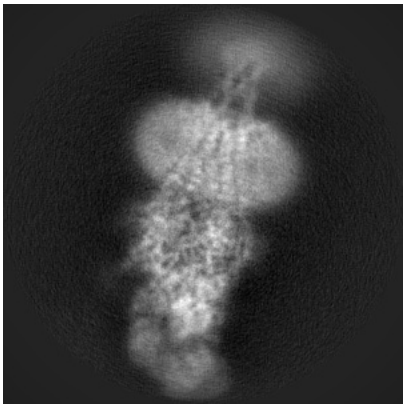


Y

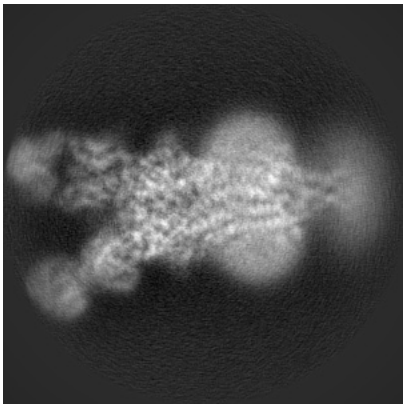


Z

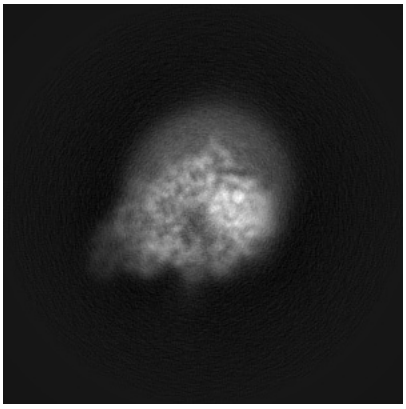
6.1.2 Raw map



X



Y

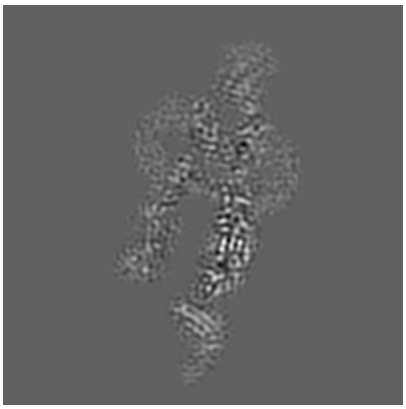


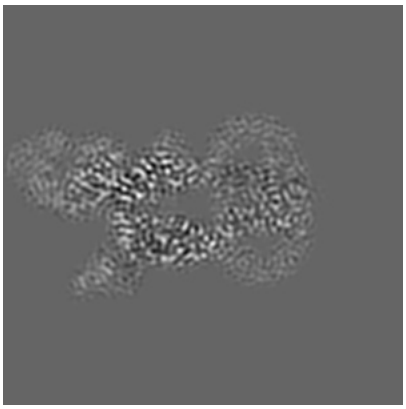
Z

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

6.2 Central slices (i)

6.2.1 Primary map

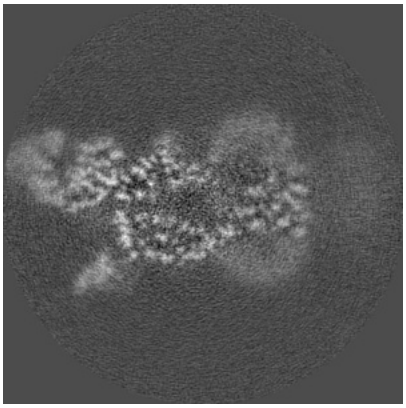

X Index: 150

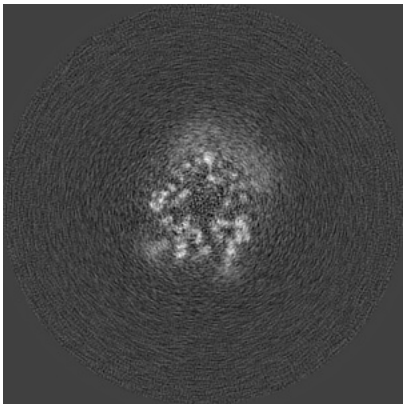

Y Index: 150

Z Index: 150

6.2.2 Raw map

X Index: 150

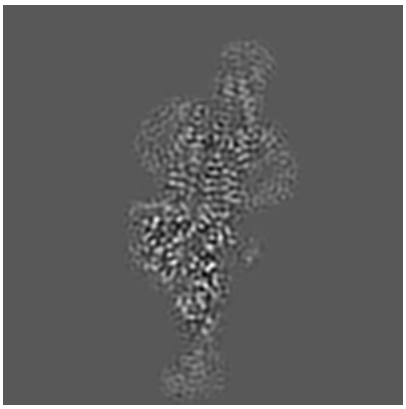

Y Index: 150

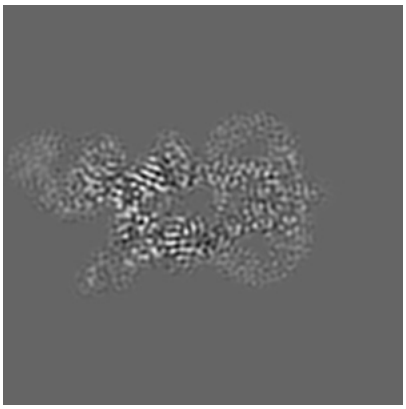

Z Index: 150

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

6.3 Largest variance slices (i)

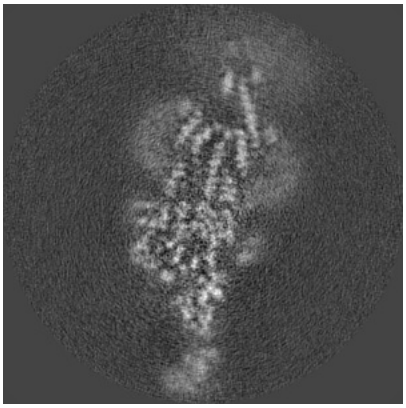
6.3.1 Primary map

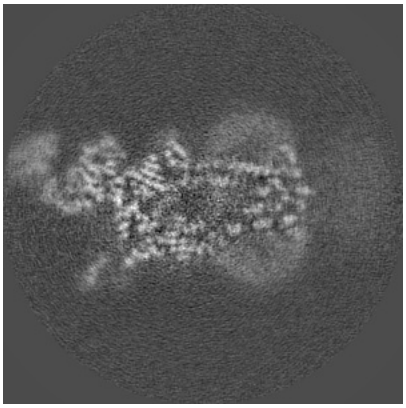

X Index: 169

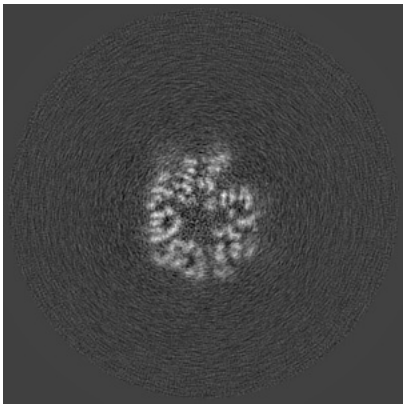

Y Index: 154

Z Index: 112

6.3.2 Raw map


X Index: 167

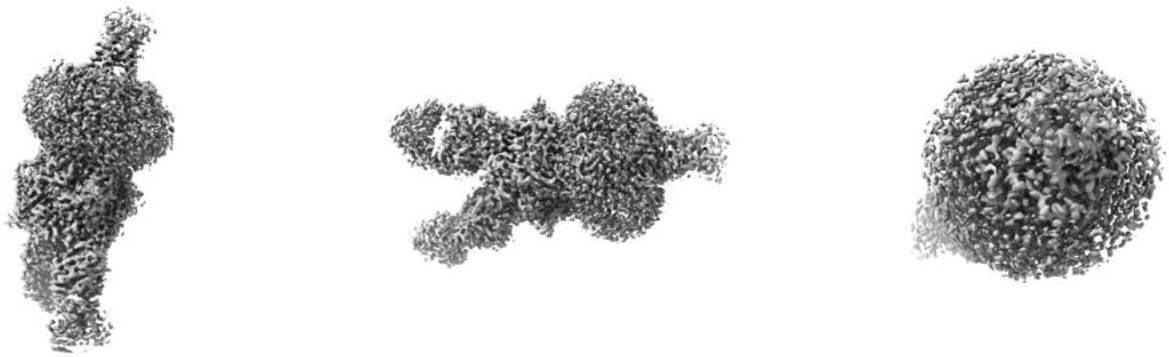

Y Index: 154


Z Index: 112

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

6.4 Orthogonal surface views (i)

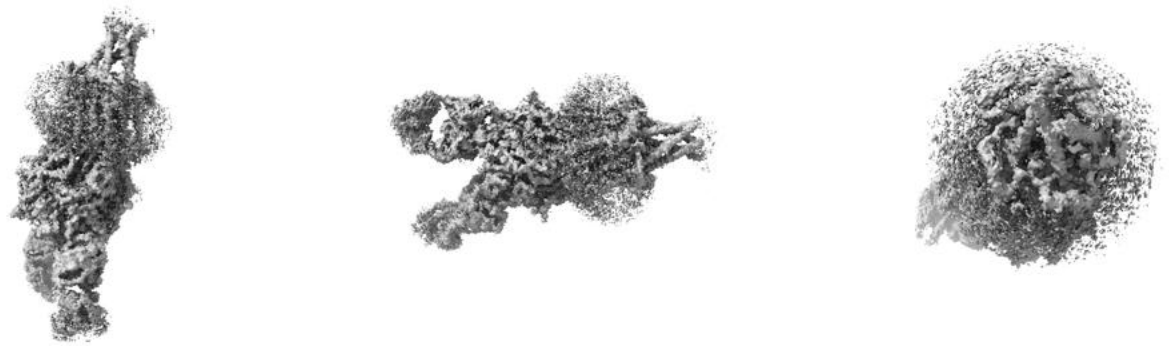
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

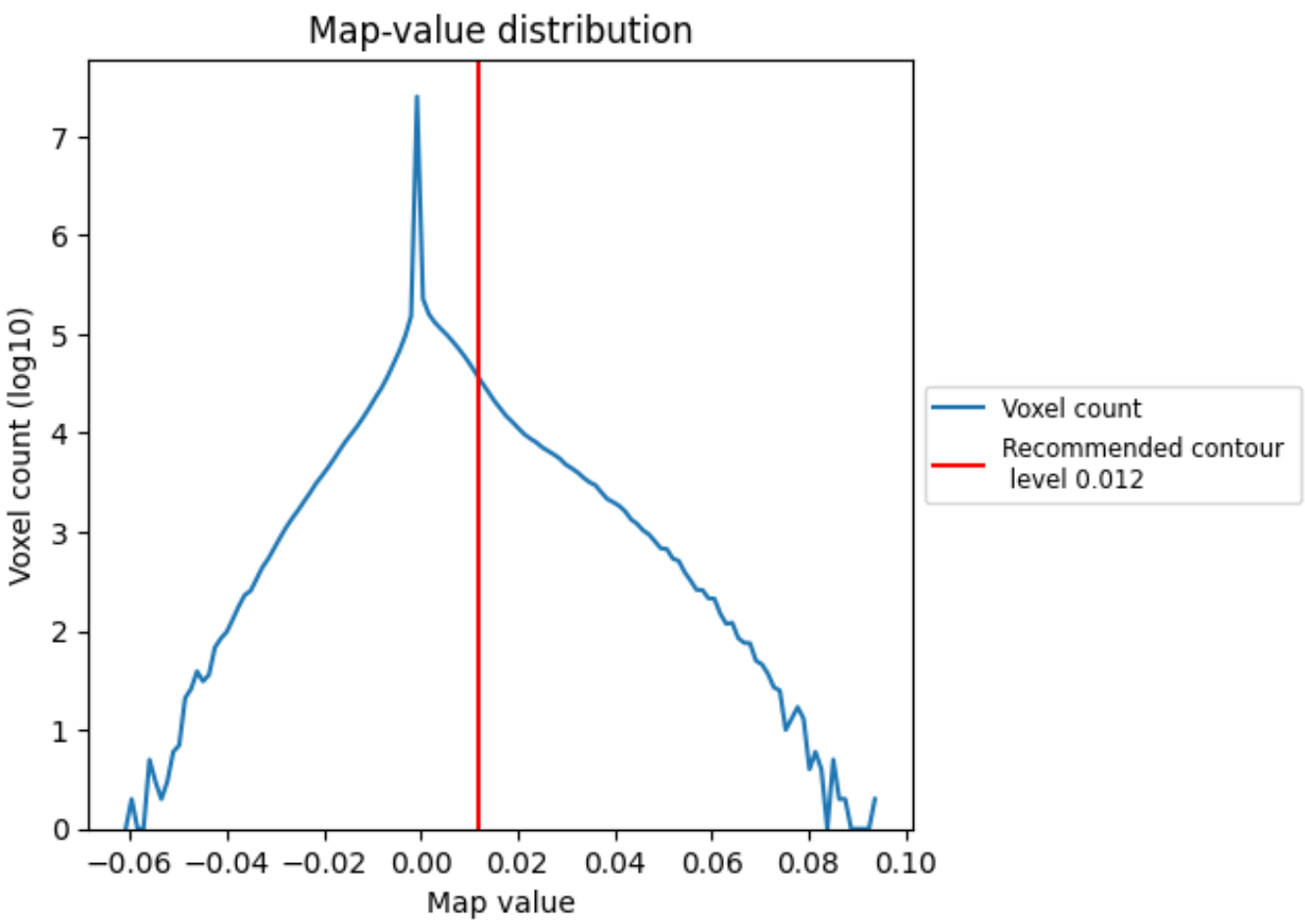
6.5 Mask visualisation (i)

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

7 Map analysis (i)

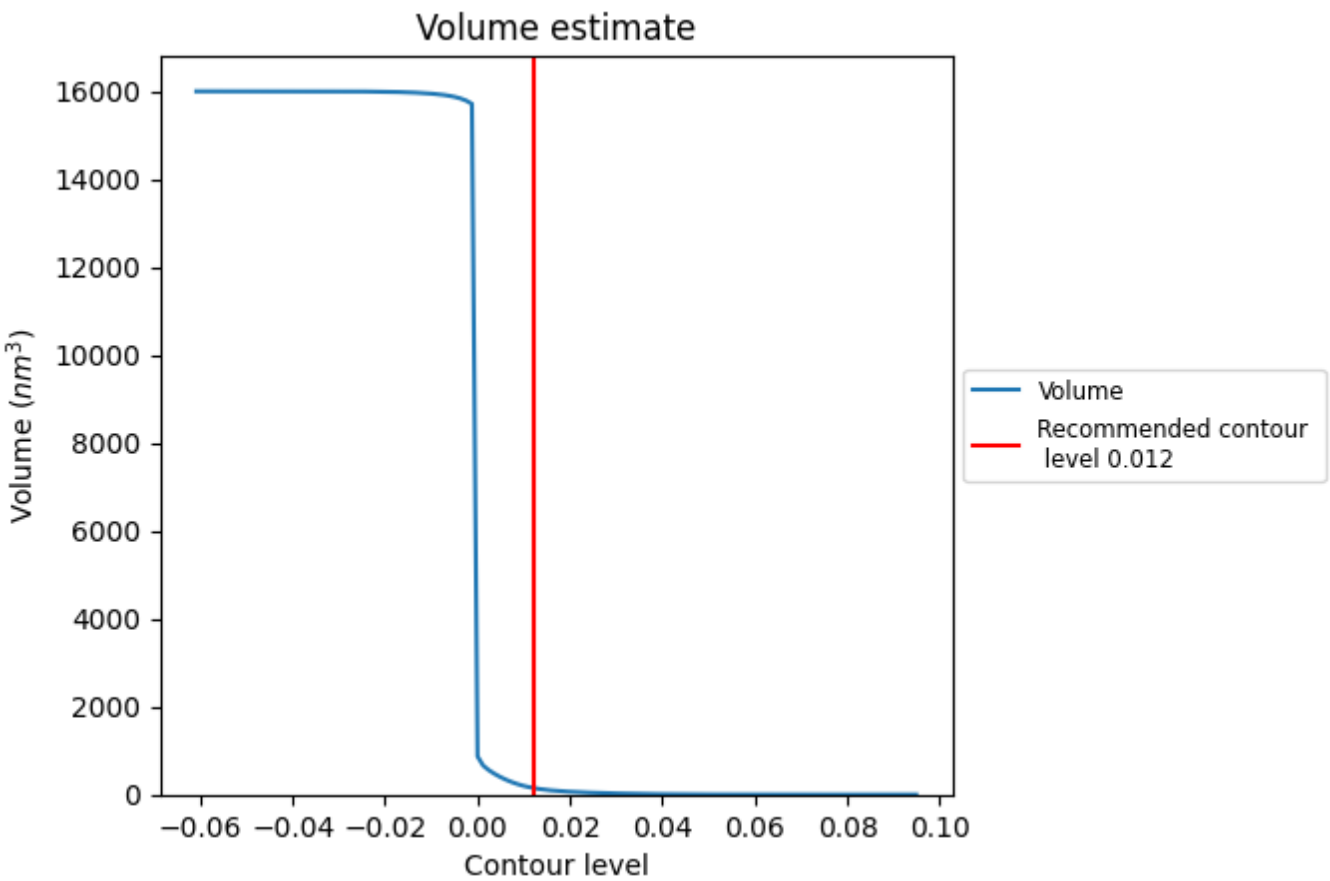
This section contains the results of statistical analysis of the map.

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.

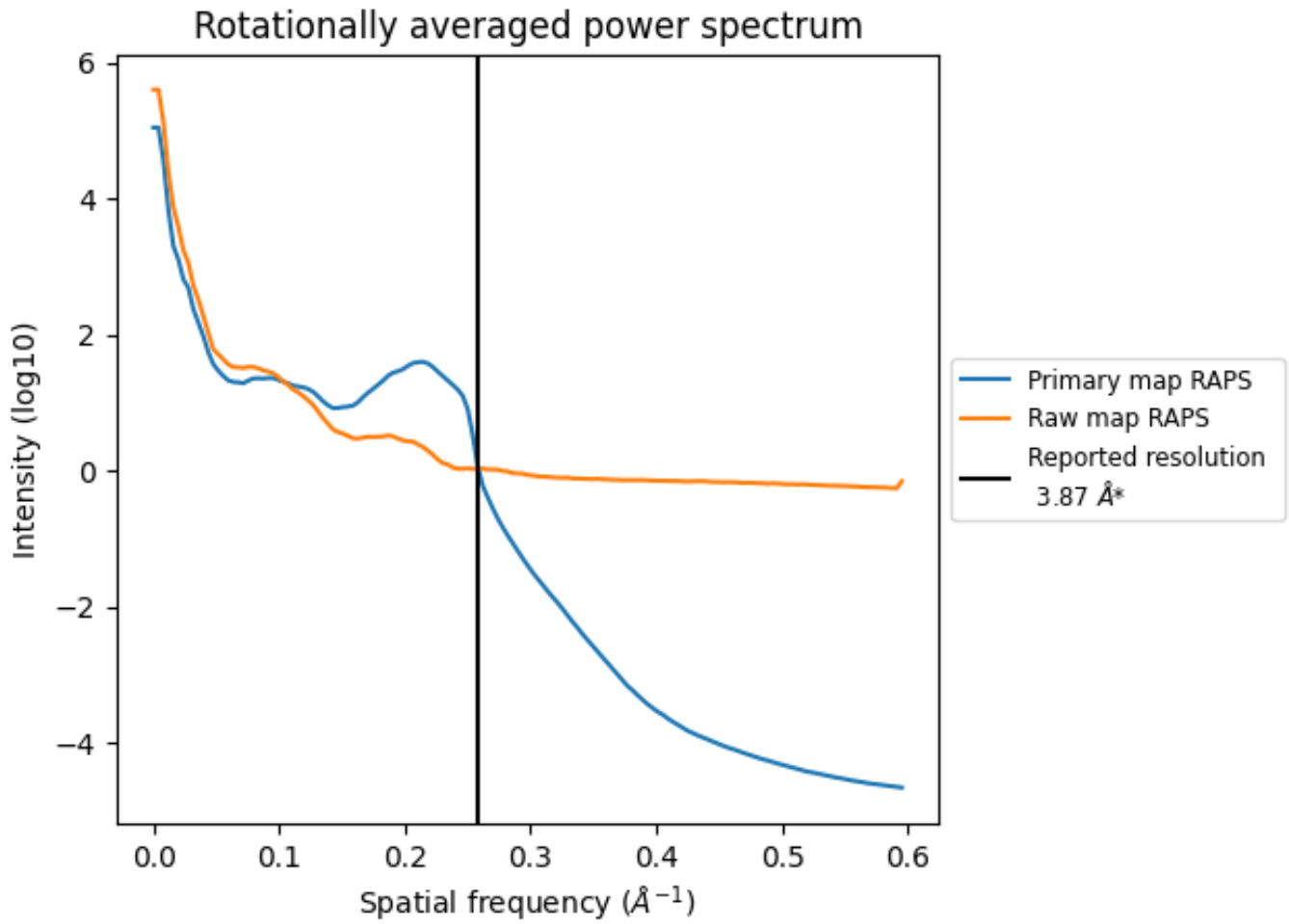
7.2 Volume estimate (i)



The volume at the recommended contour level is 151 nm^3; this corresponds to an approximate mass of 137 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)

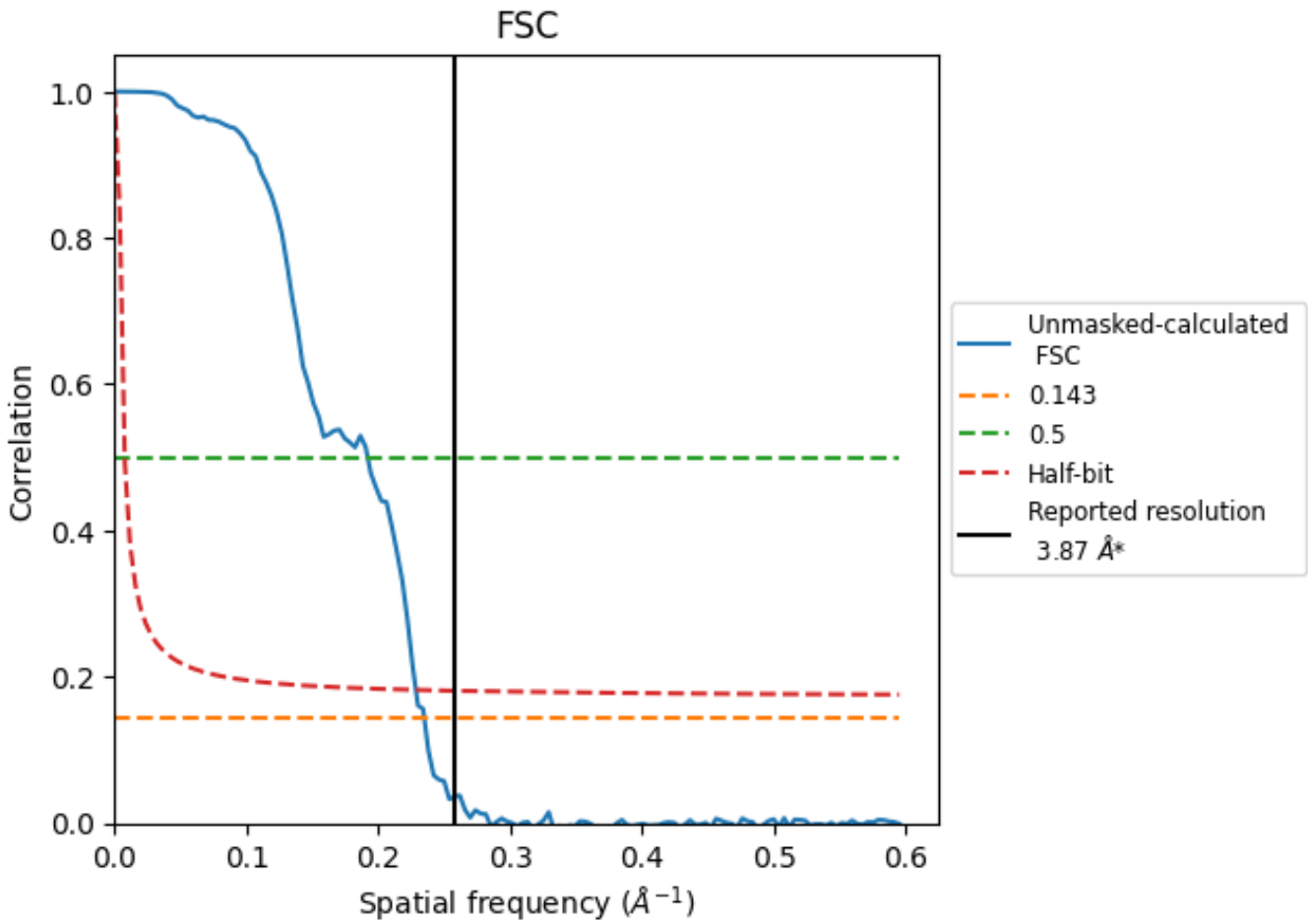


*Reported resolution corresponds to spatial frequency of 0.258 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.258 Å^{-1}

8.2 Resolution estimates (i)

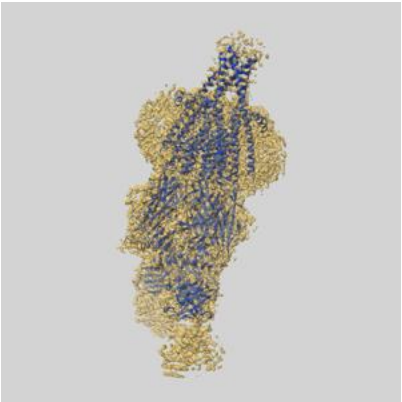
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.87	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.26	5.21	4.37

*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 4.26 differs from the reported value 3.87 by more than 10 %

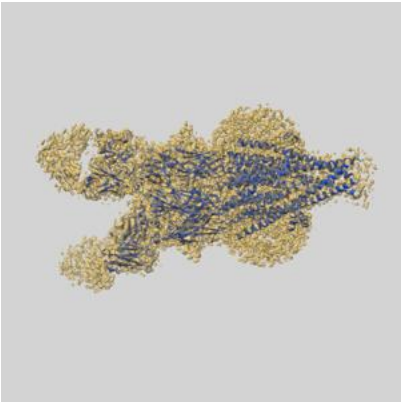
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-20488 and PDB model 6PV8. Per-residue inclusion information can be found in section 3 on page 11.

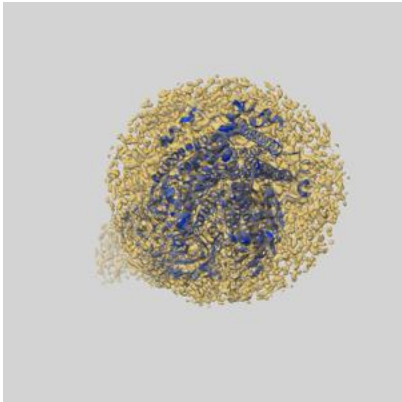
9.1 Map-model overlay (i)



X



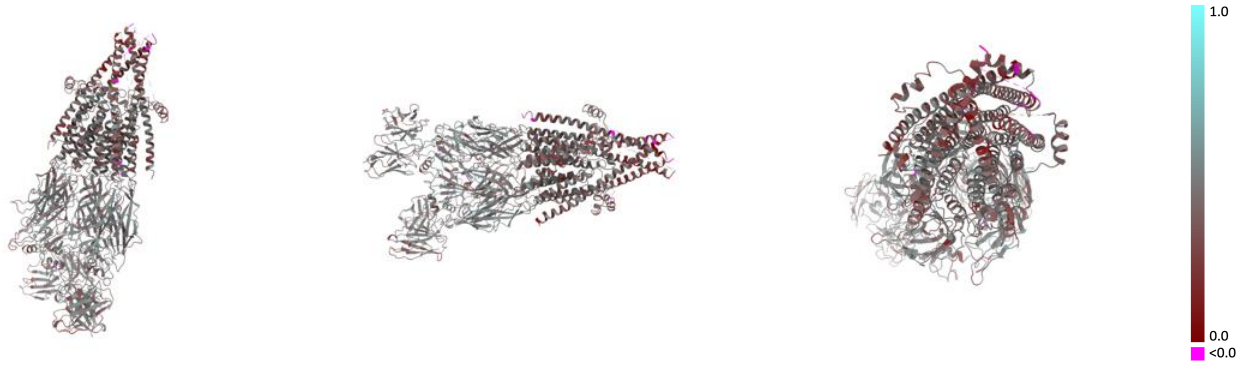
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.012 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.

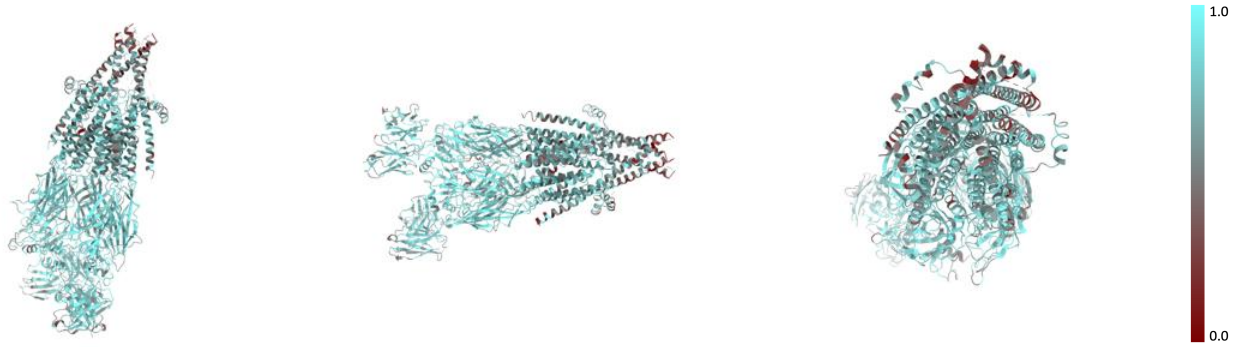
9.2 Q-score mapped to coordinate model (i)



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.

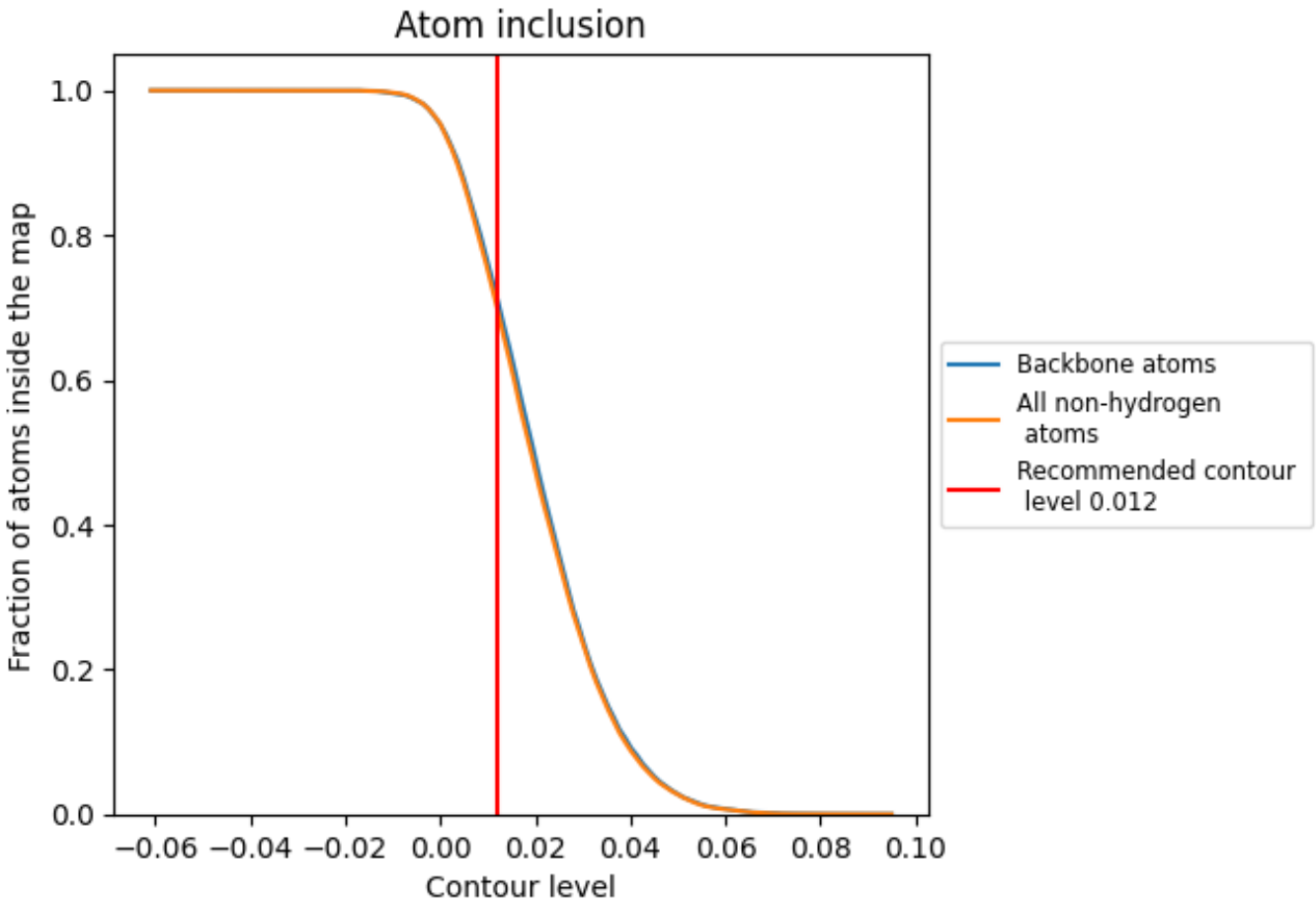
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.012).

9.4 Atom inclusion (i)



At the recommended contour level, 71% of all backbone atoms, 70% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6996	0.4160
A	0.7208	0.4280
B	0.6878	0.4070
C	0.6831	0.4050
D	0.7193	0.4250
E	0.7183	0.4230
F	0.7045	0.4030
G	0.7237	0.4180
H	0.7225	0.4240
I	0.7391	0.4330
J	0.4643	0.3930
K	0.6721	0.4100
L	0.3077	0.2470
M	0.5082	0.3160
N	0.3077	0.2170
O	0.4262	0.3020
P	0.6071	0.3630
Q	0.7049	0.4210
R	0.4615	0.2820
S	0.5082	0.3510