Full wwPDB EM Validation Report (i)

Nov 6, 2022 – 08:58 AM EST

PDB ID	:	6CM3
EMDB ID	:	EMD-7516
Title	:	BG505 SOSIP in complex with sCD4, 17b, 8ANC195
Authors	:	Wang, H.; Bjorkman, P.J.
Deposited on	:	2018-03-02
Resolution	:	3.54 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 (i)) were used in the production of this report:

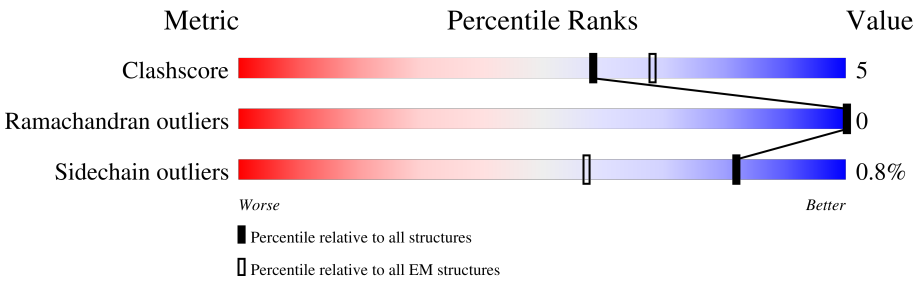
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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 3.54 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	153	73% • • 23%
1	B	153	73% • • 23%
1	C	153	73% • • 23%
2	D	481	66% 11% 23%
2	E	481	66% 11% 23%
2	F	481	67% 10% 23%
3	G	192	42% 8% 49%
3	H	192	42% 8% 49%

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Mol	Chain	Length	Quality of chain
3	I	192	42% 9% 49%
4	J	214	13% 40% 10% 50%
4	L	214	12% 40% 10% 50%
4	N	214	13% 40% 10% 50%
5	K	229	7% 45% 10% 45%
5	M	229	6% 45% 10% 45%
5	O	229	7% 46% 9% 45%
6	P	244	44% 10% 46%
6	R	244	44% 10% 46%
6	T	244	44% 9% 46%
7	Q	215	44% 6% 50%
7	S	215	45% 5% 50%
7	U	215	45% 5% 50%
8	V	2	100%
8	W	2	100%
8	X	2	100%
8	b	2	100%
8	f	2	100%
8	j	2	100%
9	Y	10	30% 70%
9	c	10	20% 80%
9	g	10	30% 70%
10	Z	5	20% 80%
10	d	5	20% 80%
10	h	5	20% 80%

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Mol	Chain	Length	Quality of chain
11	a	5	20% 80%
11	e	5	20% 80%
11	i	5	20% 80%

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 25455 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 Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	118	897	575	154	163	5	0	0
1	B	118	897	575	154	163	5	0	0
1	C	118	897	575	154	163	5	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	559	PRO	ILE	conflict	UNP Q2N0S7
A	605	CYS	THR	conflict	UNP Q2N0S7
B	559	PRO	ILE	conflict	UNP Q2N0S7
B	605	CYS	THR	conflict	UNP Q2N0S7
C	559	PRO	ILE	conflict	UNP Q2N0S7
C	605	CYS	THR	conflict	UNP Q2N0S7

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	372	2814	1779	488	523	24	0	0
2	E	372	2814	1779	488	523	24	0	0
2	F	372	2814	1779	488	523	24	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	332	ASN	THR	conflict	UNP Q2N0S5
D	501	CYS	ALA	conflict	UNP Q2N0S5
D	509	ARG	GLU	conflict	UNP Q2N0S5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	510	ARG	LYS	conflict	UNP Q2N0S5
D	512	ARG	-	expression tag	UNP Q2N0S5
D	513	ARG	-	expression tag	UNP Q2N0S5
E	332	ASN	THR	conflict	UNP Q2N0S5
E	501	CYS	ALA	conflict	UNP Q2N0S5
E	509	ARG	GLU	conflict	UNP Q2N0S5
E	510	ARG	LYS	conflict	UNP Q2N0S5
E	512	ARG	-	expression tag	UNP Q2N0S5
E	513	ARG	-	expression tag	UNP Q2N0S5
F	332	ASN	THR	conflict	UNP Q2N0S5
F	501	CYS	ALA	conflict	UNP Q2N0S5
F	509	ARG	GLU	conflict	UNP Q2N0S5
F	510	ARG	LYS	conflict	UNP Q2N0S5
F	512	ARG	-	expression tag	UNP Q2N0S5
F	513	ARG	-	expression tag	UNP Q2N0S5

- Molecule 3 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	97	775	487	136	150	2	0	0
			Total	C	N	O	S		
3	H	97	775	487	136	150	2	0	0
			Total	C	N	O	S		
3	I	97	775	487	136	150	2	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	183	ILE	-	expression tag	UNP P01730
G	184	ASP	-	expression tag	UNP P01730
G	185	GLY	-	expression tag	UNP P01730
G	186	ARG	-	expression tag	UNP P01730
G	187	HIS	-	expression tag	UNP P01730
G	188	HIS	-	expression tag	UNP P01730
G	189	HIS	-	expression tag	UNP P01730
G	190	HIS	-	expression tag	UNP P01730
G	191	HIS	-	expression tag	UNP P01730
G	192	HIS	-	expression tag	UNP P01730
H	183	ILE	-	expression tag	UNP P01730
H	184	ASP	-	expression tag	UNP P01730
H	185	GLY	-	expression tag	UNP P01730

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Chain	Residue	Modelled	Actual	Comment	Reference
H	186	ARG	-	expression tag	UNP P01730
H	187	HIS	-	expression tag	UNP P01730
H	188	HIS	-	expression tag	UNP P01730
H	189	HIS	-	expression tag	UNP P01730
H	190	HIS	-	expression tag	UNP P01730
H	191	HIS	-	expression tag	UNP P01730
H	192	HIS	-	expression tag	UNP P01730
I	183	ILE	-	expression tag	UNP P01730
I	184	ASP	-	expression tag	UNP P01730
I	185	GLY	-	expression tag	UNP P01730
I	186	ARG	-	expression tag	UNP P01730
I	187	HIS	-	expression tag	UNP P01730
I	188	HIS	-	expression tag	UNP P01730
I	189	HIS	-	expression tag	UNP P01730
I	190	HIS	-	expression tag	UNP P01730
I	191	HIS	-	expression tag	UNP P01730
I	192	HIS	-	expression tag	UNP P01730

- Molecule 4 is a protein called 17b Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	107	819	512	141	163	3	0	0
			Total	C	N	O	S		
4	L	107	819	512	141	163	3	0	0
			Total	C	N	O	S		
4	N	107	819	512	141	163	3	0	0

- Molecule 5 is a protein called 17b Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	127	985	621	168	193	3	0	0
			Total	C	N	O	S		
5	M	127	985	621	168	193	3	0	0
			Total	C	N	O	S		
5	O	127	985	621	168	193	3	0	0

- Molecule 6 is a protein called 8ANC195 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	P	131	1007	639	173	192	3	0	0
6	R	131	1007	639	173	192	3	0	0
6	T	131	1007	639	173	192	3	0	0

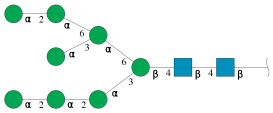
- Molecule 7 is a protein called 8ANC195 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	Q	107	810	509	140	158	3	0	0
7	S	107	810	509	140	158	3	0	0
7	U	107	810	509	140	158	3	0	0

- Molecule 8 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

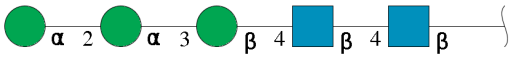
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	V	2	28	16	2	10	0	0
8	W	2	28	16	2	10	0	0
8	X	2	28	16	2	10	0	0
8	b	2	28	16	2	10	0	0
8	f	2	28	16	2	10	0	0
8	j	2	28	16	2	10	0	0

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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.



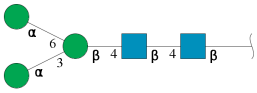
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	Y	10	116	64	2	50	0	0
9	c	10	116	64	2	50	0	0
9	g	10	116	64	2	50	0	0

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



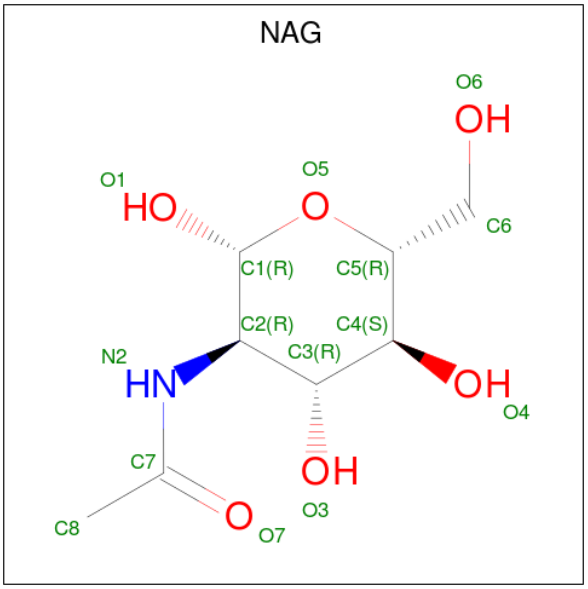
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	Z	5	61	34	2	25	0	0
10	d	5	61	34	2	25	0	0
10	h	5	61	34	2	25	0	0

- Molecule 11 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		
11	a	5	61	34	2	25	0	0
11	e	5	61	34	2	25	0	0
11	i	5	61	34	2	25	0	0

- Molecule 12 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	
12	D	1	84	48	6	30	0
			Total	C	N	O	
12	D	1	84	48	6	30	0
			Total	C	N	O	
12	D	1	84	48	6	30	0
			Total	C	N	O	
12	D	1	84	48	6	30	0
			Total	C	N	O	
12	D	1	84	48	6	30	0
			Total	C	N	O	
12	D	1	84	48	6	30	0
			Total	C	N	O	
12	E	1	84	48	6	30	0
			Total	C	N	O	
12	E	1	84	48	6	30	0
			Total	C	N	O	
12	E	1	84	48	6	30	0
			Total	C	N	O	
12	E	1	84	48	6	30	0
			Total	C	N	O	
12	E	1	84	48	6	30	0
			Total	C	N	O	
12	E	1	84	48	6	30	0

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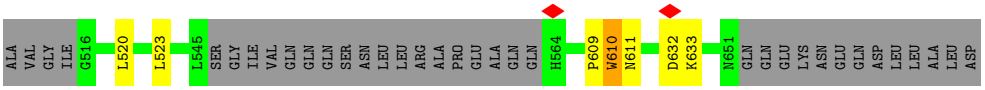
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
12	F	1	84	48	6	30	0
12	F	1	84	48	6	30	0
12	F	1	84	48	6	30	0
12	F	1	84	48	6	30	0
12	F	1	84	48	6	30	0
12	F	1	84	48	6	30	0

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.

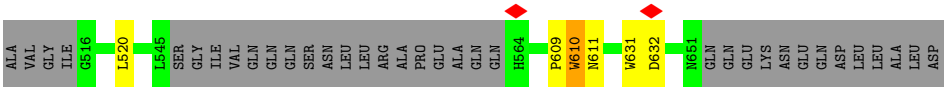
• Molecule 1: Envelope glycoprotein gp160

Chain A:



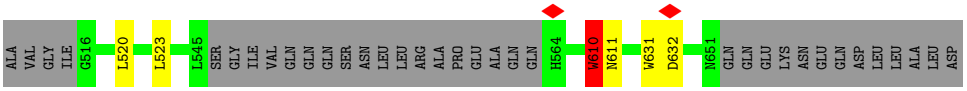
• Molecule 1: Envelope glycoprotein gp160

Chain B:



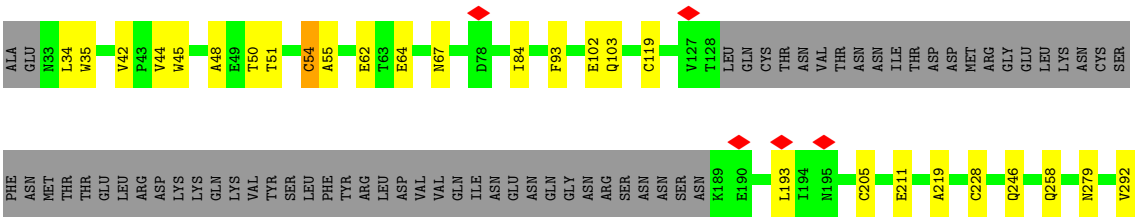
• Molecule 1: Envelope glycoprotein gp160

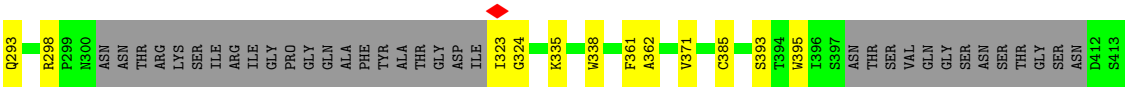
Chain C:



• Molecule 2: Envelope glycoprotein gp160

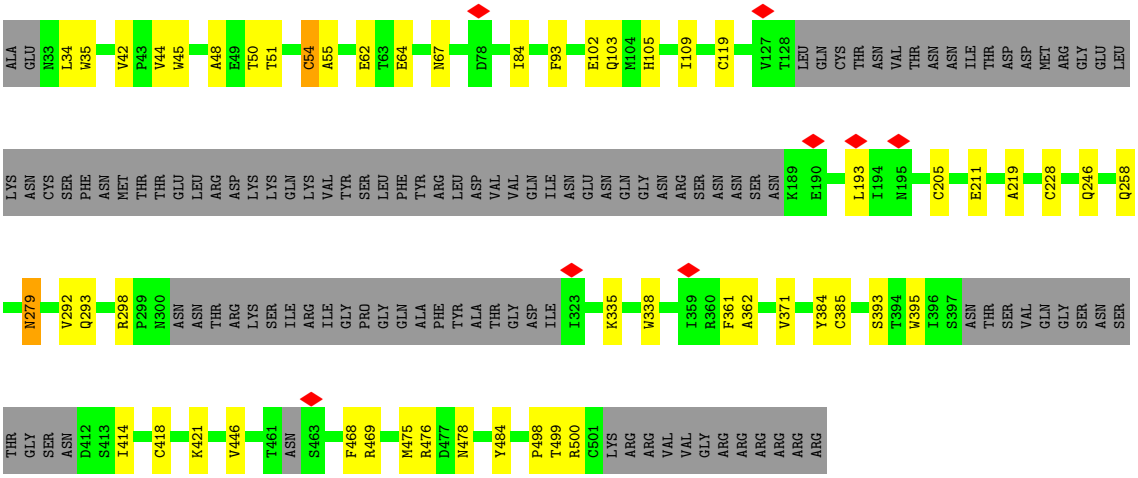
Chain D:





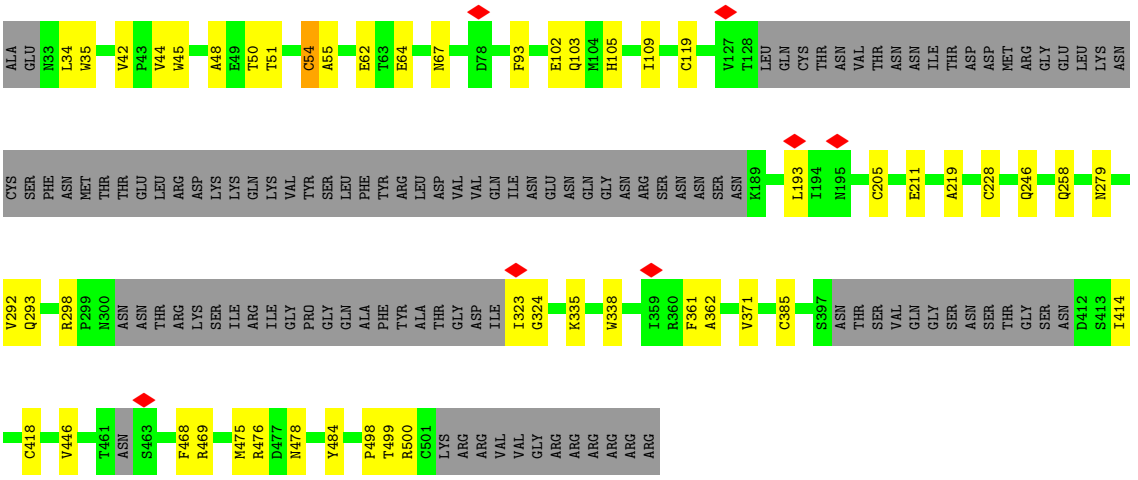
- Molecule 2: Envelope glycoprotein gp160

Chain E:



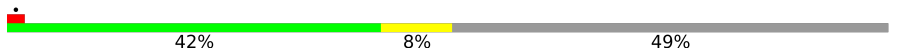
- Molecule 2: Envelope glycoprotein gp160

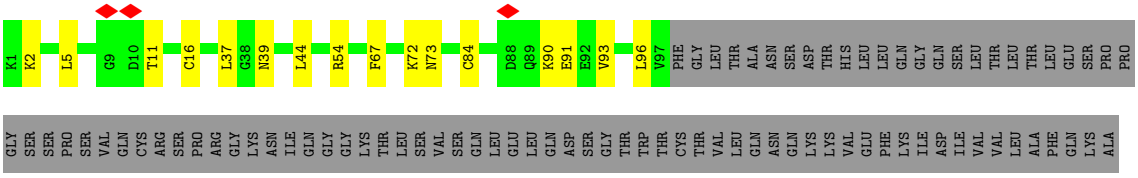
Chain F:



- Molecule 3: T-cell surface glycoprotein CD4

Chain G:





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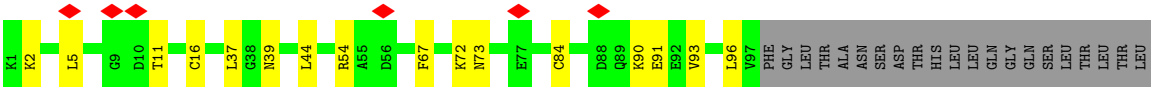
- Molecule 3: T-cell surface glycoprotein CD4

Chain H:

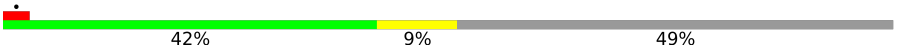


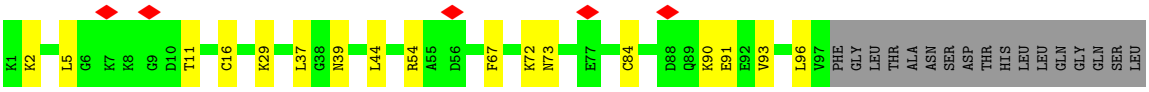
GLU SER PRO PRO GLY SER SER PRO SER VAL GLN CYS ARG SER PRO ARG GLY LYS ASN ILE GLN GLY GLY LYS THR LEU SER VAL SER GLN LEU GLU LEU GLN ASP SER GLY THR TRP THR CYS THR VAL LEU GLN ASN GLN LYS LYS VAL GLU PHE LYS ILE ASP ILE VAL VAL LEU ALA

PHE GLN LYS ALA ILE ASP GLY ARG HIS HIS HIS HIS HIS

- Molecule 3: T-cell surface glycoprotein CD4

Chain I:



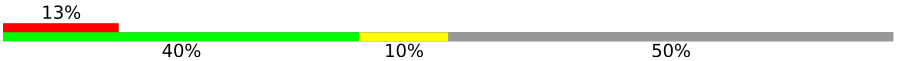


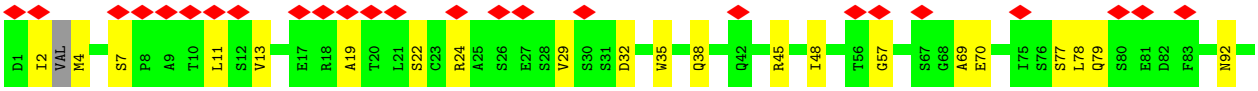
THR LEU THR LEU GLU SER PRO PRO GLY SER SER PRO SER VAL GLN CYS ARG SER PRO ARG GLY LYS ASN ILE GLN GLY GLY LYS THR LEU SER VAL SER GLN LEU GLU LEU GLN ASP SER GLY THR TRP THR CYS THR VAL LEU GLN ASN GLN LYS LYS VAL GLU PHE LYS ILE ASP ILE

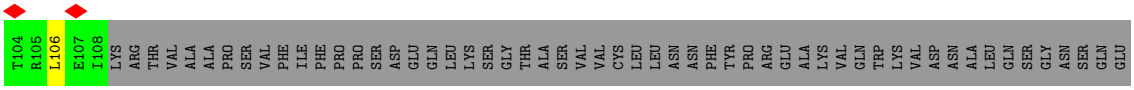
VAL VAL LEU ALA PHE GLN LYS ALA ILE ASP GLY ARG HIS HIS HIS HIS HIS

- Molecule 4: 17b Fab light chain

Chain J:



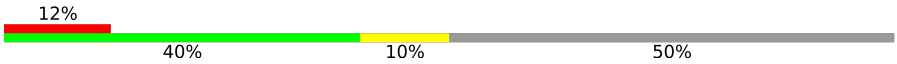


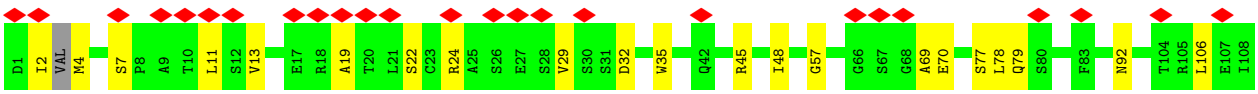


SER VAL THR GLU GLN ASP SER LYS ASP SER THR TYR SER LEU SER SER THR LEU THR LEU SER LYS ALA ASP TYR GLU LYS HIS LYS VAL TYR ALA CYS GLU VAL THR HIS GLN GLY LEU SER SER PRO VAL THR LYS SER PHE ASN ARG GLY

- Molecule 4: 17b Fab light chain

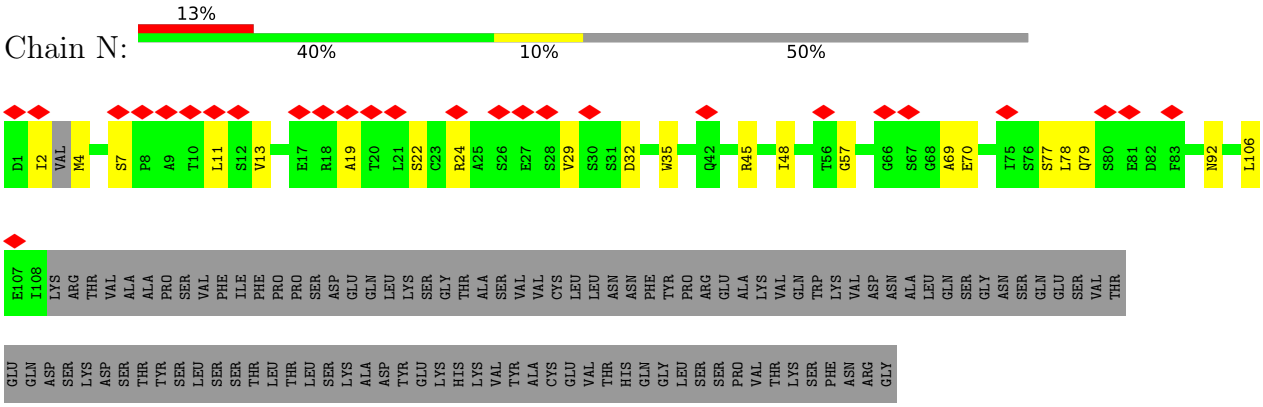
Chain L:



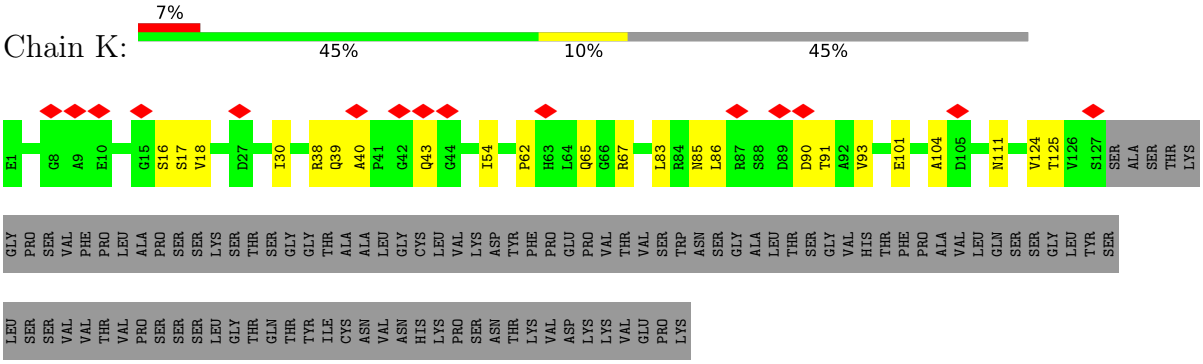


LYS ARG THR VAL ALA ALA PRO SER VAL PHE ILE PHE PRO PRO SER ASP GLU GLN LEU LYS SER GLY THR ALA SER VAL VAL CYS LEU LEU ASN ASN PHE TYR PRO ARG GLU ALA LYS VAL GLN TRP LYS VAL ASP ASN ALA LEU GLN SER GLY ASN SER GLN GLU SER VAL THR GLU GLN

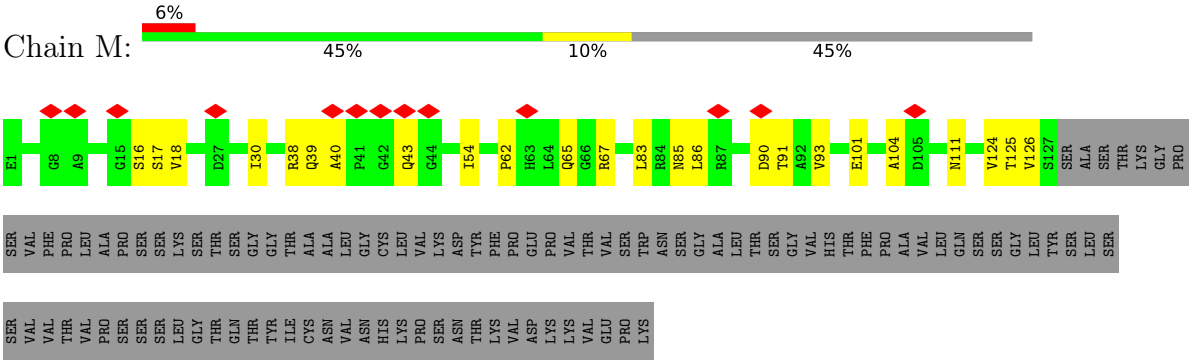
- Molecule 4: 17b Fab light chain



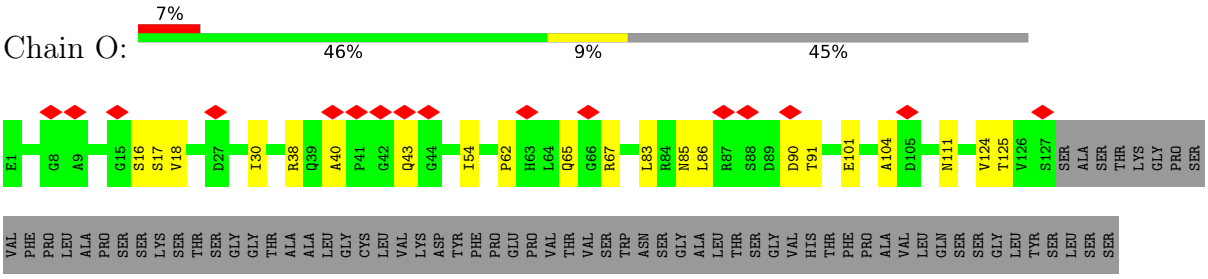
- Molecule 5: 17b Fab heavy chain



- Molecule 5: 17b Fab heavy chain

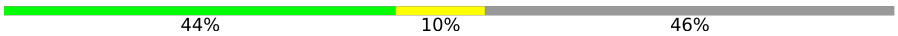


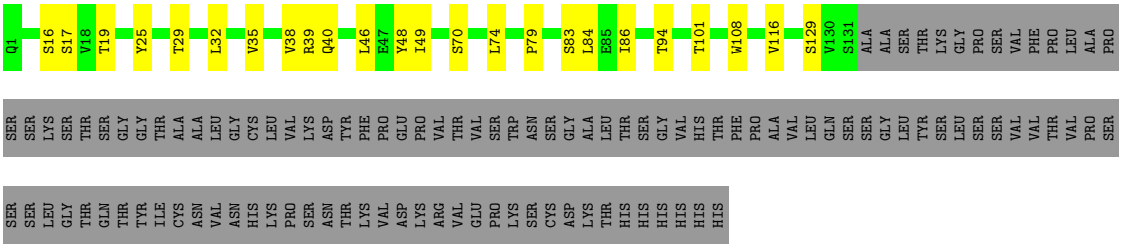
- Molecule 5: 17b Fab heavy chain



• Molecule 6: 8ANC195 Fab heavy chain

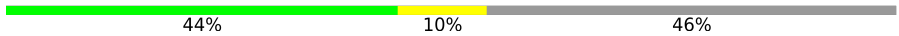
Chain P:

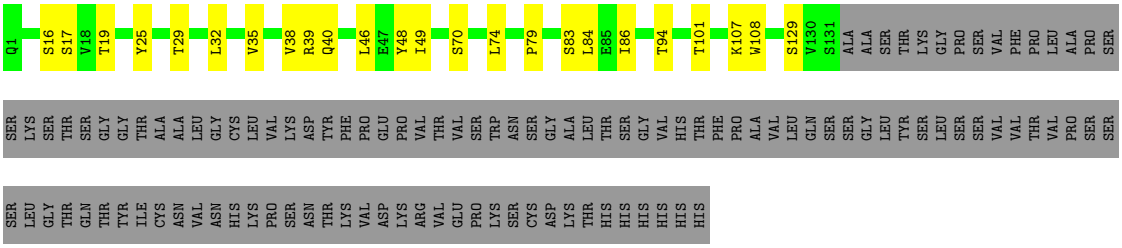




• Molecule 6: 8ANC195 Fab heavy chain

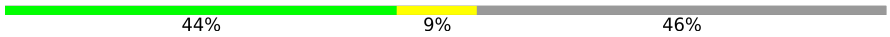
Chain R:

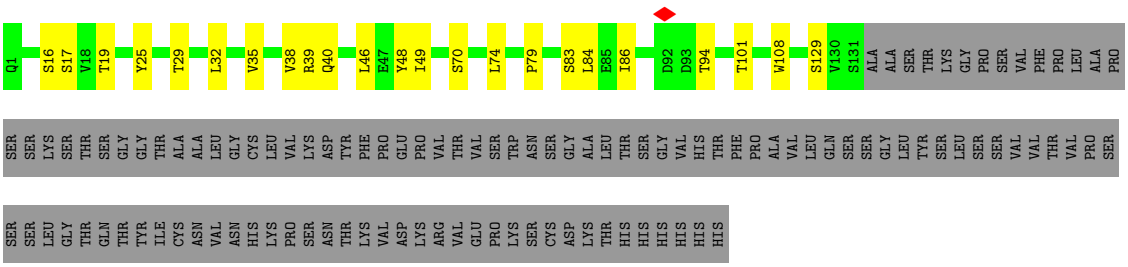




• Molecule 6: 8ANC195 Fab heavy chain

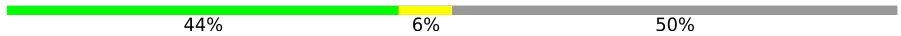
Chain T:

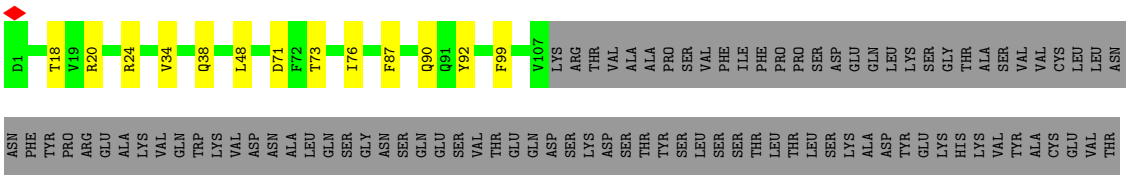




• Molecule 7: 8ANC195 Fab light chain

Chain Q:





HIS GLN GLY LEU SER SER PRO VAL THR LYS SER PHE ASN ARG GLY GLU CYS

• Molecule 7: 8ANC195 Fab light chain

Chain S: 45% 5% 50%

D1 T18 V19 R20 R24 V34 Q38 L48 D71 F72 T73 I76 F87 Q90 V107 LYS ARG THR VAL ALA ALA PRO SER VAL PHE ILE PHE PRO PRO SER ASP GLU GLN LEU LYS SER GLY THR ALA SER VAL VAL CYS LEU LEU ASN ASN PHE TYR PRO

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

SER SER PRO VAL THR LYS SER PHE ASN ARG GLY GLU CYS

• Molecule 7: 8ANC195 Fab light chain

Chain U: 45% 5% 50%

D1 T18 V19 R20 R24 V34 Q38 L48 D71 F72 T73 I76 F87 Q90 V107 LYS ARG THR VAL ALA ALA PRO SER VAL PHE ILE PHE PRO PRO SER ASP GLU GLN LEU LYS SER GLY THR ALA SER VAL VAL CYS LEU LEU ASN ASN PHE TYR PRO

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

SER SER PRO VAL THR LYS SER PHE ASN ARG GLY GLU CYS

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V: 100%

NAG1 NAG2

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W: 100%

NAG1 NAG2

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X: 100%

NAG1 NAG2

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b: 100%

NAG1 NAG2

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f: 100%

NAG1 NAG2

• Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j: 100%

NAG1 NAG2

• Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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 Y: 30% 70%

NAG1 NAG2 BMA3 MAN4 MAN5 MAN6 MAN7 MAN8 MAN9 MAN10

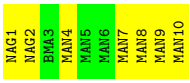
• Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c: 20% 80%

NAG1 NAG2 BMA3 MAN4 MAN5 MAN6 MAN7 MAN8 MAN9 MAN10

• Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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

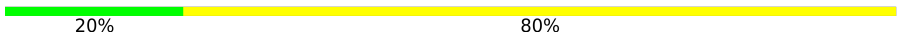
Chain g: 30% 70%



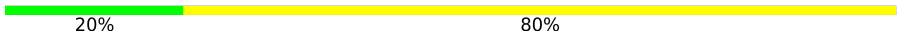
• Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:

• Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d: 

• Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h: 

• Molecule 11: 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

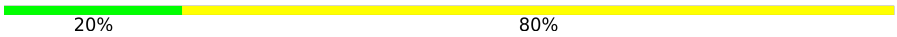
Chain a:

• Molecule 11: 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 e:

• Molecule 11: 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 i:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	143099	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 ($e^-/Å^2$)	87.5	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	0.270	Depositor
Minimum map value	-0.149	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0386	Depositor
Map size (Å)	392.99997, 392.99997, 392.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	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: MAN, NAG, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.51	0/915	0.57	0/1247
1	B	0.51	1/915 (0.1%)	0.57	0/1247
1	C	0.51	1/915 (0.1%)	0.57	0/1247
2	D	0.53	1/2878 (0.0%)	0.64	1/3929 (0.0%)
2	E	0.53	1/2878 (0.0%)	0.64	1/3929 (0.0%)
2	F	0.52	1/2878 (0.0%)	0.64	1/3929 (0.0%)
3	G	0.39	0/785	0.56	0/1053
3	H	0.39	0/785	0.56	0/1053
3	I	0.39	0/785	0.56	0/1053
4	J	0.33	0/838	0.59	1/1139 (0.1%)
4	L	0.33	0/838	0.59	1/1139 (0.1%)
4	N	0.33	0/838	0.59	1/1139 (0.1%)
5	K	0.33	0/1006	0.51	0/1365
5	M	0.33	0/1006	0.51	0/1365
5	O	0.33	0/1006	0.51	0/1365
6	P	0.49	0/1034	0.60	1/1408 (0.1%)
6	R	0.49	0/1034	0.60	1/1408 (0.1%)
6	T	0.49	0/1034	0.60	1/1408 (0.1%)
7	Q	0.43	0/828	0.58	0/1125
7	S	0.42	0/828	0.58	0/1125
7	U	0.42	0/828	0.58	0/1125
All	All	0.46	5/24852 (0.0%)	0.59	9/33798 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	45	TRP	CB-CG	-5.15	1.41	1.50
2	F	45	TRP	CB-CG	-5.14	1.41	1.50
2	D	45	TRP	CB-CG	-5.13	1.41	1.50
1	C	631	TRP	CB-CG	-5.01	1.41	1.50
1	B	631	TRP	CB-CG	-5.00	1.41	1.50

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	L	13	VAL	C-N-CA	5.86	136.36	121.70
4	N	13	VAL	C-N-CA	5.85	136.33	121.70
4	J	13	VAL	C-N-CA	5.84	136.31	121.70
6	P	74	LEU	CA-CB-CG	5.37	127.65	115.30
6	R	74	LEU	CA-CB-CG	5.35	127.61	115.30
6	T	74	LEU	CA-CB-CG	5.33	127.56	115.30
2	F	54	CYS	C-N-CA	5.25	134.83	121.70
2	D	54	CYS	C-N-CA	5.25	134.82	121.70
2	E	54	CYS	C-N-CA	5.25	134.81	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	610	TRP	Peptide
1	B	610	TRP	Peptide
1	C	610	TRP	Peptide

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	897	0	859	6	0
1	B	897	0	859	4	0
1	C	897	0	859	4	0
2	D	2814	0	2679	27	0
2	E	2814	0	2679	28	0
2	F	2814	0	2679	25	0
3	G	775	0	795	8	0
3	H	775	0	795	8	0
3	I	775	0	795	9	0
4	J	819	0	782	12	0
4	L	819	0	782	11	0
4	N	819	0	782	11	0
5	K	985	0	952	14	0
5	M	985	0	952	14	0
5	O	985	0	952	12	0
6	P	1007	0	979	15	0
6	R	1007	0	979	14	0
6	T	1007	0	979	13	0
7	Q	810	0	783	8	0
7	S	810	0	783	6	0
7	U	810	0	783	6	0
8	V	28	0	25	0	0
8	W	28	0	25	0	0
8	X	28	0	25	0	0
8	b	28	0	25	0	0
8	f	28	0	25	0	0
8	j	28	0	25	0	0
9	Y	116	0	97	0	0
9	c	116	0	97	0	0
9	g	116	0	97	0	0
10	Z	61	0	51	0	0
10	d	61	0	51	0	0
10	h	61	0	51	0	0
11	a	61	0	52	0	0
11	e	61	0	52	0	0
11	i	61	0	52	0	0
12	D	84	0	78	0	0
12	E	84	0	78	0	0
12	F	84	0	78	0	0
All	All	25455	0	24471	239	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 (239) 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:A:632:ASP:OD2	6:R:108:TRP:NE1	2.12	0.82
5:K:17:SER:HA	5:K:83:LEU:O	1.81	0.81
5:M:17:SER:HA	5:M:83:LEU:O	1.81	0.81
5:O:17:SER:HA	5:O:83:LEU:O	1.81	0.80
1:B:632:ASP:OD2	6:P:108:TRP:NE1	2.17	0.78
4:L:22:SER:OG	4:L:70:GLU:OE2	2.04	0.75
4:N:22:SER:OG	4:N:70:GLU:OE2	2.04	0.74
4:J:22:SER:OG	4:J:70:GLU:OE2	2.05	0.74
2:F:64:GLU:OE2	2:F:211:GLU:N	2.22	0.72
2:D:64:GLU:OE2	2:D:211:GLU:N	2.22	0.72
2:E:64:GLU:OE2	2:E:211:GLU:N	2.22	0.72
2:E:102:GLU:OE2	2:E:476:ARG:NH1	2.25	0.69
7:S:18:THR:HA	7:S:76:ILE:O	1.94	0.67
7:U:18:THR:HA	7:U:76:ILE:O	1.94	0.67
7:Q:18:THR:HA	7:Q:76:ILE:O	1.94	0.67
6:P:17:SER:HA	6:P:86:ILE:O	1.95	0.66
5:O:91:THR:HA	5:O:124:VAL:O	1.97	0.65
6:T:17:SER:HA	6:T:86:ILE:O	1.95	0.65
2:D:102:GLU:OE2	2:D:476:ARG:NH1	2.25	0.65
3:I:16:CYS:HB2	3:I:67:PHE:HB2	1.78	0.65
6:R:17:SER:HA	6:R:86:ILE:O	1.95	0.64
5:M:91:THR:HA	5:M:124:VAL:O	1.97	0.64
3:G:16:CYS:HB2	3:G:67:PHE:HB2	1.78	0.64
3:H:11:THR:HG22	3:H:72:LYS:HG2	1.80	0.64
3:H:16:CYS:HB2	3:H:67:PHE:HB2	1.78	0.64
5:K:91:THR:HA	5:K:124:VAL:O	1.97	0.64
3:G:11:THR:HG22	3:G:72:LYS:HG2	1.80	0.63
3:I:2:LYS:HB2	3:I:93:VAL:HG12	1.81	0.63
3:I:11:THR:HG22	3:I:72:LYS:HG2	1.80	0.63
2:E:35:TRP:H	2:E:499:THR:HG22	1.64	0.63
2:F:35:TRP:H	2:F:499:THR:HG22	1.64	0.63
2:D:35:TRP:H	2:D:499:THR:HG22	1.64	0.62
1:C:632:ASP:OD2	6:T:108:TRP:NE1	2.32	0.62
2:F:102:GLU:OE2	2:F:476:ARG:NH1	2.25	0.61
3:H:2:LYS:HB2	3:H:93:VAL:HG12	1.80	0.61
3:G:2:LYS:HB2	3:G:93:VAL:HG12	1.80	0.61
2:D:475:MET:SD	2:D:478:ASN:ND2	2.74	0.61
2:E:475:MET:SD	2:E:478:ASN:ND2	2.74	0.60
2:F:475:MET:SD	2:F:478:ASN:ND2	2.74	0.60
2:E:54:CYS:HB2	2:E:55:ALA:HB2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:219:ALA:O	2:E:246:GLN:NE2	2.37	0.58
2:F:219:ALA:O	2:F:246:GLN:NE2	2.37	0.58
2:D:219:ALA:O	2:D:246:GLN:NE2	2.37	0.58
6:P:40:GLN:HB2	6:P:46:LEU:HD23	1.86	0.58
2:D:54:CYS:HB2	2:D:55:ALA:HB2	1.86	0.57
2:F:54:CYS:HB2	2:F:55:ALA:HB2	1.86	0.57
6:R:40:GLN:HB2	6:R:46:LEU:HD23	1.86	0.56
2:E:51:THR:HA	2:E:103:GLN:HE22	1.70	0.56
6:T:40:GLN:HB2	6:T:46:LEU:HD23	1.86	0.56
2:F:51:THR:HA	2:F:103:GLN:HE22	1.70	0.56
4:N:77:SER:OG	4:N:79:GLN:NE2	2.39	0.56
2:D:51:THR:HA	2:D:103:GLN:HE22	1.70	0.55
4:J:77:SER:OG	4:J:79:GLN:NE2	2.39	0.55
4:L:77:SER:OG	4:L:79:GLN:NE2	2.39	0.55
3:G:84:CYS:O	3:G:90:LYS:HA	2.08	0.54
3:H:84:CYS:O	3:H:90:LYS:HA	2.08	0.54
3:I:84:CYS:O	3:I:90:LYS:HA	2.08	0.54
1:A:520:LEU:HD11	2:E:246:GLN:HB2	1.90	0.53
6:R:70:SER:OG	6:R:83:SER:OG	2.27	0.53
6:T:70:SER:OG	6:T:83:SER:OG	2.27	0.52
2:E:362:ALA:HB3	2:E:469:ARG:HG2	1.92	0.52
5:K:67:ARG:NH2	5:K:85:ASN:O	2.43	0.52
5:O:67:ARG:NH2	5:O:85:ASN:O	2.43	0.52
5:M:67:ARG:NH2	5:M:85:ASN:O	2.43	0.52
5:M:62:PRO:HA	5:M:65:GLN:HE21	1.75	0.52
5:O:62:PRO:HA	5:O:65:GLN:HE21	1.75	0.51
7:S:24:ARG:NH1	7:S:71:ASP:OD1	2.44	0.51
2:D:362:ALA:HB3	2:D:469:ARG:HG2	1.92	0.51
6:P:70:SER:OG	6:P:83:SER:OG	2.27	0.51
6:R:25:TYR:HE1	6:R:79:PRO:HG3	1.76	0.51
7:Q:24:ARG:NH1	7:Q:71:ASP:OD1	2.44	0.51
5:O:16:SER:HB3	5:O:86:LEU:HD12	1.93	0.51
6:T:35:VAL:HG22	6:T:101:THR:HG22	1.93	0.51
2:F:362:ALA:HB3	2:F:469:ARG:HG2	1.92	0.50
7:U:24:ARG:NH1	7:U:71:ASP:OD1	2.44	0.50
6:P:25:TYR:HE1	6:P:79:PRO:HG3	1.76	0.50
5:K:62:PRO:HA	5:K:65:GLN:HE21	1.75	0.50
6:R:35:VAL:HG22	6:R:101:THR:HG22	1.93	0.50
2:D:62:GLU:OE1	2:D:67:ASN:ND2	2.45	0.50
6:T:25:TYR:HE1	6:T:79:PRO:HG3	1.76	0.50
4:J:38:GLN:HE22	5:K:39:GLN:HE22	1.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:16:SER:HB3	5:K:86:LEU:HD12	1.93	0.49
5:O:91:THR:HG23	5:O:125:THR:HA	1.95	0.49
6:P:35:VAL:HG22	6:P:101:THR:HG22	1.93	0.49
2:F:62:GLU:OE1	2:F:67:ASN:ND2	2.45	0.49
4:J:2:ILE:O	4:J:4:MET:N	2.46	0.49
4:J:29:VAL:HG13	4:J:92:ASN:HB2	1.95	0.49
5:M:16:SER:HB3	5:M:86:LEU:HD12	1.93	0.49
2:E:62:GLU:OE1	2:E:67:ASN:ND2	2.45	0.49
4:L:29:VAL:HG13	4:L:92:ASN:HB2	1.95	0.49
5:M:91:THR:HG23	5:M:125:THR:HA	1.95	0.49
4:L:2:ILE:O	4:L:4:MET:N	2.46	0.49
6:P:94:THR:HG23	6:P:129:SER:HA	1.95	0.49
6:R:94:THR:HG23	6:R:129:SER:HA	1.95	0.49
4:N:29:VAL:HG13	4:N:92:ASN:HB2	1.95	0.48
2:D:499:THR:OG1	2:D:500:ARG:N	2.46	0.48
4:N:2:ILE:O	4:N:4:MET:N	2.46	0.48
3:H:5:LEU:HG	3:H:96:LEU:HB2	1.95	0.48
5:K:91:THR:HG23	5:K:125:THR:HA	1.95	0.48
4:L:7:SER:HB2	4:L:22:SER:HB3	1.96	0.48
6:P:25:TYR:CE1	6:P:79:PRO:HG3	2.48	0.48
6:T:94:THR:HG23	6:T:129:SER:HA	1.95	0.48
3:I:5:LEU:HG	3:I:96:LEU:HB2	1.95	0.48
6:R:25:TYR:CE1	6:R:79:PRO:HG3	2.48	0.48
6:T:38:VAL:HG23	6:T:48:TYR:HA	1.96	0.48
4:J:19:ALA:HB2	4:J:78:LEU:HD12	1.96	0.48
5:O:30:ILE:HD12	5:O:54:ILE:HD12	1.96	0.48
6:P:38:VAL:HG23	6:P:48:TYR:HA	1.96	0.48
2:F:499:THR:OG1	2:F:500:ARG:N	2.46	0.48
3:G:5:LEU:HG	3:G:96:LEU:HB2	1.95	0.48
5:M:30:ILE:HD12	5:M:54:ILE:HD12	1.96	0.48
1:B:520:LEU:HD11	2:D:246:GLN:HB2	1.95	0.47
4:L:19:ALA:HB2	4:L:78:LEU:HD12	1.96	0.47
6:T:25:TYR:CE1	6:T:79:PRO:HG3	2.48	0.47
2:E:499:THR:OG1	2:E:500:ARG:N	2.46	0.47
4:N:19:ALA:HB2	4:N:78:LEU:HD12	1.96	0.47
4:J:7:SER:HB2	4:J:22:SER:HB3	1.96	0.47
3:H:84:CYS:HB2	3:H:91:GLU:HB2	1.97	0.47
4:J:45:ARG:NH2	4:J:57:GLY:O	2.48	0.47
4:N:45:ARG:NH2	4:N:57:GLY:O	2.48	0.47
6:P:39:ARG:HB3	6:P:49:ILE:HD11	1.97	0.47
6:R:39:ARG:HB3	6:R:49:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:7:SER:HB2	4:N:22:SER:HB3	1.96	0.47
4:L:45:ARG:NH2	4:L:57:GLY:O	2.48	0.46
2:E:335:LYS:HD3	2:E:414:ILE:HD11	1.98	0.46
3:G:84:CYS:HB2	3:G:91:GLU:HB2	1.97	0.46
6:T:39:ARG:HB3	6:T:49:ILE:HD11	1.97	0.46
2:D:258:GLN:NE2	2:D:371:VAL:O	2.49	0.46
2:D:292:VAL:HG11	2:D:338:TRP:HE3	1.80	0.46
5:O:18:VAL:HG12	5:O:83:LEU:HB2	1.98	0.46
6:R:38:VAL:HG23	6:R:48:TYR:HA	1.96	0.46
2:E:258:GLN:NE2	2:E:371:VAL:O	2.49	0.46
7:S:38:GLN:HB2	7:S:48:LEU:HD11	1.98	0.46
2:D:335:LYS:HD3	2:D:414:ILE:HD11	1.97	0.46
7:U:38:GLN:HB2	7:U:48:LEU:HD11	1.98	0.46
5:K:30:ILE:HD12	5:K:54:ILE:HD12	1.96	0.46
2:E:292:VAL:HG11	2:E:338:TRP:HE3	1.80	0.46
4:N:11:LEU:HB3	4:N:106:LEU:HG	1.98	0.46
1:A:609:PRO:HA	2:E:35:TRP:HB3	1.98	0.45
2:F:119:CYS:N	2:F:205:CYS:SG	2.89	0.45
5:M:18:VAL:HG12	5:M:83:LEU:HB2	1.98	0.45
5:M:91:THR:HG1	5:M:126:VAL:H	1.64	0.45
2:F:258:GLN:NE2	2:F:371:VAL:O	2.49	0.45
2:F:292:VAL:HG11	2:F:338:TRP:HE3	1.80	0.45
4:L:11:LEU:HB3	4:L:106:LEU:HG	1.97	0.45
2:D:119:CYS:N	2:D:205:CYS:SG	2.89	0.45
3:I:84:CYS:HB2	3:I:91:GLU:HB2	1.97	0.45
7:Q:38:GLN:HB2	7:Q:48:LEU:HD11	1.98	0.45
2:E:119:CYS:N	2:E:205:CYS:SG	2.89	0.45
4:J:11:LEU:HB3	4:J:106:LEU:HG	1.98	0.45
7:Q:76:ILE:HD11	7:Q:87:PHE:HE2	1.82	0.45
5:O:40:ALA:HB3	5:O:43:GLN:HB2	1.99	0.45
2:E:385:CYS:HA	2:E:418:CYS:HA	1.99	0.45
5:K:18:VAL:HG12	5:K:83:LEU:HB2	1.98	0.45
4:J:29:VAL:HG12	4:J:32:ASP:H	1.81	0.44
4:N:29:VAL:HG12	4:N:32:ASP:H	1.81	0.44
7:S:76:ILE:HD11	7:S:87:PHE:HE2	1.82	0.44
2:F:335:LYS:HD3	2:F:414:ILE:HD11	1.97	0.44
5:O:54:ILE:HG21	5:O:104:ALA:HB1	1.99	0.44
5:K:54:ILE:HG21	5:K:104:ALA:HB1	1.99	0.44
6:P:19:THR:HA	6:P:84:LEU:O	2.18	0.44
5:M:54:ILE:HG21	5:M:104:ALA:HB1	1.99	0.44
2:D:323:ILE:HA	2:D:324:GLY:HA2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:393:SER:OG	2:E:395:TRP:NE1	2.47	0.44
4:L:29:VAL:HG12	4:L:32:ASP:H	1.81	0.44
6:P:46:LEU:HB2	7:Q:99:PHE:CD2	2.51	0.44
1:C:520:LEU:HD11	2:F:246:GLN:HB2	2.00	0.44
2:F:34:LEU:HD12	2:F:498:PRO:HB3	2.00	0.43
5:K:38:ARG:HH22	5:K:90:ASP:HA	1.83	0.43
7:U:76:ILE:HD11	7:U:87:PHE:HE2	1.82	0.43
5:M:40:ALA:HB3	5:M:43:GLN:HB2	1.99	0.43
2:E:48:ALA:HB1	2:E:50:THR:HG23	2.00	0.43
5:K:40:ALA:HB3	5:K:43:GLN:HB2	1.99	0.43
6:R:19:THR:HA	6:R:84:LEU:O	2.18	0.43
2:D:393:SER:OG	2:D:395:TRP:NE1	2.47	0.43
2:F:385:CYS:HA	2:F:418:CYS:HA	1.99	0.43
5:M:38:ARG:HH22	5:M:90:ASP:HA	1.83	0.43
2:F:323:ILE:HA	2:F:324:GLY:HA2	1.82	0.43
5:K:39:GLN:N	5:K:93:VAL:O	2.50	0.43
5:O:38:ARG:HH22	5:O:90:ASP:HA	1.83	0.43
2:E:279:ASN:O	3:I:29:LYS:NZ	2.42	0.43
3:G:37:LEU:HD22	3:G:44:LEU:HD11	2.01	0.43
7:Q:34:VAL:HA	7:Q:90:GLN:O	2.18	0.43
2:D:385:CYS:HA	2:D:418:CYS:HA	1.99	0.43
3:H:54:ARG:NH1	3:H:73:ASN:O	2.52	0.43
3:I:37:LEU:HD22	3:I:44:LEU:HD11	2.01	0.43
6:P:16:SER:OG	6:P:17:SER:N	2.51	0.43
2:D:48:ALA:HB1	2:D:50:THR:HG23	2.00	0.43
2:E:34:LEU:HD12	2:E:498:PRO:HB3	2.00	0.43
2:F:48:ALA:HB1	2:F:50:THR:HG23	2.00	0.43
3:G:54:ARG:NH1	3:G:73:ASN:O	2.52	0.43
3:H:37:LEU:HD22	3:H:44:LEU:HD11	2.01	0.43
3:I:54:ARG:NH1	3:I:73:ASN:O	2.52	0.43
7:U:34:VAL:HA	7:U:90:GLN:O	2.18	0.43
6:T:16:SER:OG	6:T:17:SER:N	2.51	0.42
7:S:34:VAL:HA	7:S:90:GLN:O	2.19	0.42
1:B:520:LEU:HB3	2:D:84:ILE:HD13	2.01	0.42
6:T:19:THR:HA	6:T:84:LEU:O	2.18	0.42
2:D:34:LEU:HD12	2:D:498:PRO:HB3	2.00	0.42
2:E:42:VAL:HG12	2:E:44:VAL:HG23	2.02	0.42
2:F:42:VAL:HG12	2:F:44:VAL:HG23	2.02	0.42
5:M:39:GLN:N	5:M:93:VAL:O	2.50	0.42
1:C:610:TRP:CZ3	2:F:498:PRO:HG3	2.54	0.42
2:E:293:GLN:HE21	2:E:446:VAL:HG13	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:361:PHE:HE1	2:E:468:PHE:HD2	1.68	0.42
2:D:293:GLN:HE21	2:D:446:VAL:HG13	1.84	0.41
4:L:35:TRP:HD1	4:L:48:ILE:HB	1.85	0.41
2:D:361:PHE:HE1	2:D:468:PHE:HD2	1.68	0.41
2:F:361:PHE:HE1	2:F:468:PHE:HD2	1.68	0.41
6:R:16:SER:OG	6:R:17:SER:N	2.51	0.41
2:E:93:PHE:CE2	2:E:228:CYS:HB2	2.56	0.41
5:M:101:GLU:OE1	5:M:111:ASN:N	2.53	0.41
2:F:293:GLN:HE21	2:F:446:VAL:HG13	1.84	0.41
5:K:101:GLU:OE1	5:K:111:ASN:N	2.53	0.41
4:N:35:TRP:HD1	4:N:48:ILE:HB	1.85	0.41
6:P:116:VAL:HG12	7:Q:92:TYR:HB2	2.02	0.41
2:E:105:HIS:O	2:E:109:ILE:HG12	2.21	0.41
4:L:24:ARG:HH21	4:L:69:ALA:HB3	1.86	0.41
4:N:24:ARG:HH21	4:N:69:ALA:HB3	1.85	0.41
2:D:93:PHE:CE2	2:D:228:CYS:HB2	2.56	0.41
4:J:35:TRP:HD1	4:J:48:ILE:HB	1.85	0.41
1:A:633:LYS:HE2	6:R:107:LYS:O	2.21	0.41
1:C:523:LEU:HD13	1:C:523:LEU:HA	1.82	0.41
5:O:101:GLU:OE1	5:O:111:ASN:N	2.53	0.41
7:Q:20:ARG:HG3	7:Q:73:THR:HG23	2.03	0.41
1:B:609:PRO:HA	2:D:35:TRP:HB3	2.03	0.40
7:U:20:ARG:HG3	7:U:73:THR:HG23	2.03	0.40
2:D:42:VAL:HG12	2:D:44:VAL:HG23	2.02	0.40
2:E:384:TYR:HD2	2:E:421:LYS:HD2	1.86	0.40
4:J:24:ARG:HH21	4:J:69:ALA:HB3	1.86	0.40
6:R:29:THR:HG23	6:R:32:LEU:H	1.86	0.40
6:T:29:THR:HG23	6:T:32:LEU:H	1.86	0.40
1:A:520:LEU:HB3	2:E:84:ILE:HD13	2.03	0.40
2:D:422:GLN:HE22	2:D:437:PRO:HA	1.87	0.40
2:F:105:HIS:O	2:F:109:ILE:HG12	2.21	0.40
7:S:20:ARG:HG3	7:S:73:THR:HG23	2.03	0.40
1:A:523:LEU:HD13	1:A:523:LEU:HA	1.82	0.40
2:F:93:PHE:CE2	2:F:228:CYS:HB2	2.56	0.40
6:P:29:THR:HG23	6:P:32:LEU:H	1.86	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	114/153 (74%)	109 (96%)	5 (4%)	0	100	100
1	B	114/153 (74%)	109 (96%)	5 (4%)	0	100	100
1	C	114/153 (74%)	109 (96%)	5 (4%)	0	100	100
2	D	362/481 (75%)	324 (90%)	38 (10%)	0	100	100
2	E	362/481 (75%)	323 (89%)	39 (11%)	0	100	100
2	F	362/481 (75%)	323 (89%)	39 (11%)	0	100	100
3	G	95/192 (50%)	84 (88%)	11 (12%)	0	100	100
3	H	95/192 (50%)	84 (88%)	11 (12%)	0	100	100
3	I	95/192 (50%)	84 (88%)	11 (12%)	0	100	100
4	J	103/214 (48%)	94 (91%)	9 (9%)	0	100	100
4	L	103/214 (48%)	94 (91%)	9 (9%)	0	100	100
4	N	103/214 (48%)	94 (91%)	9 (9%)	0	100	100
5	K	125/229 (55%)	115 (92%)	10 (8%)	0	100	100
5	M	125/229 (55%)	114 (91%)	11 (9%)	0	100	100
5	O	125/229 (55%)	114 (91%)	11 (9%)	0	100	100
6	P	129/244 (53%)	118 (92%)	11 (8%)	0	100	100
6	R	129/244 (53%)	118 (92%)	11 (8%)	0	100	100
6	T	129/244 (53%)	118 (92%)	11 (8%)	0	100	100
7	Q	105/215 (49%)	97 (92%)	8 (8%)	0	100	100
7	S	105/215 (49%)	96 (91%)	9 (9%)	0	100	100
7	U	105/215 (49%)	97 (92%)	8 (8%)	0	100	100
All	All	3099/5184 (60%)	2818 (91%)	281 (9%)	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	90/129 (70%)	88 (98%)	2 (2%)	52	78
1	B	90/129 (70%)	88 (98%)	2 (2%)	52	78
1	C	90/129 (70%)	88 (98%)	2 (2%)	52	78
2	D	306/428 (72%)	302 (99%)	4 (1%)	69	87
2	E	306/428 (72%)	302 (99%)	4 (1%)	69	87
2	F	306/428 (72%)	302 (99%)	4 (1%)	69	87
3	G	89/173 (51%)	88 (99%)	1 (1%)	73	88
3	H	89/173 (51%)	88 (99%)	1 (1%)	73	88
3	I	89/173 (51%)	88 (99%)	1 (1%)	73	88
4	J	88/184 (48%)	88 (100%)	0	100	100
4	L	88/184 (48%)	88 (100%)	0	100	100
4	N	88/184 (48%)	88 (100%)	0	100	100
5	K	105/193 (54%)	105 (100%)	0	100	100
5	M	105/193 (54%)	105 (100%)	0	100	100
5	O	105/193 (54%)	105 (100%)	0	100	100
6	P	112/210 (53%)	112 (100%)	0	100	100
6	R	112/210 (53%)	112 (100%)	0	100	100
6	T	112/210 (53%)	112 (100%)	0	100	100
7	Q	85/182 (47%)	85 (100%)	0	100	100
7	S	85/182 (47%)	85 (100%)	0	100	100
7	U	85/182 (47%)	85 (100%)	0	100	100
All	All	2625/4497 (58%)	2604 (99%)	21 (1%)	82	92

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	610	TRP

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Mol	Chain	Res	Type
1	A	611	ASN
1	B	610	TRP
1	B	611	ASN
1	C	610	TRP
1	C	611	ASN
2	D	193	LEU
2	D	279	ASN
2	D	298	ARG
2	D	484	TYR
2	E	193	LEU
2	E	279	ASN
2	E	298	ARG
2	E	484	TYR
2	F	193	LEU
2	F	279	ASN
2	F	298	ARG
2	F	484	TYR
3	G	39	ASN
3	H	39	ASN
3	I	39	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	611	ASN
1	B	611	ASN
1	C	611	ASN
2	D	66	HIS
2	D	103	GLN
2	D	280	ASN
2	E	66	HIS
2	E	103	GLN
2	E	279	ASN
2	E	280	ASN
2	F	103	GLN
2	F	279	ASN
2	F	280	ASN
3	G	39	ASN
3	H	39	ASN
3	I	39	ASN
4	J	38	GLN
4	J	79	GLN

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Mol	Chain	Res	Type
5	K	39	GLN
5	K	65	GLN
4	L	79	GLN
5	M	65	GLN
4	N	79	GLN
5	O	65	GLN

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)

72 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	$\#\|Z\| > 2$
8	NAG	V	1	8,1	14,14,15	0.45	0	17,19,21	1.50	4 (23%)
8	NAG	V	2	8	14,14,15	0.23	0	17,19,21	1.53	3 (17%)
8	NAG	W	1	8,1	14,14,15	0.45	0	17,19,21	1.44	3 (17%)
8	NAG	W	2	8	14,14,15	0.23	0	17,19,21	1.53	3 (17%)
8	NAG	X	1	8,1	14,14,15	0.45	0	17,19,21	1.40	2 (11%)
8	NAG	X	2	8	14,14,15	0.24	0	17,19,21	1.56	3 (17%)
9	NAG	Y	1	2,9	14,14,15	0.56	0	17,19,21	1.10	1 (5%)
9	MAN	Y	10	9	11,11,12	0.22	0	15,15,17	0.93	1 (6%)
9	NAG	Y	2	9	14,14,15	0.40	0	17,19,21	1.02	2 (11%)
9	BMA	Y	3	9	11,11,12	0.24	0	15,15,17	0.96	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
9	MAN	Y	4	9	11,11,12	0.20	0	15,15,17	1.07	1 (6%)
9	MAN	Y	5	9	11,11,12	0.25	0	15,15,17	0.90	0
9	MAN	Y	6	9	11,11,12	0.21	0	15,15,17	0.87	0
9	MAN	Y	7	9	11,11,12	0.32	0	15,15,17	1.14	2 (13%)
9	MAN	Y	8	9	11,11,12	0.21	0	15,15,17	1.07	1 (6%)
9	MAN	Y	9	9	11,11,12	0.28	0	15,15,17	0.98	1 (6%)
10	NAG	Z	1	2,10	14,14,15	0.50	0	17,19,21	1.40	3 (17%)
10	NAG	Z	2	10	14,14,15	0.37	0	17,19,21	1.17	2 (11%)
10	BMA	Z	3	10	11,11,12	0.20	0	15,15,17	1.14	2 (13%)
10	MAN	Z	4	10	11,11,12	0.20	0	15,15,17	1.01	0
10	MAN	Z	5	2,10	11,11,12	0.49	0	15,15,17	1.52	4 (26%)
11	NAG	a	1	2,11	14,14,15	0.54	0	17,19,21	1.45	3 (17%)
11	NAG	a	2	11	14,14,15	0.32	0	17,19,21	0.87	1 (5%)
11	BMA	a	3	11	11,11,12	0.16	0	15,15,17	1.25	1 (6%)
11	MAN	a	4	11	11,11,12	0.23	0	15,15,17	0.77	0
11	MAN	a	5	11	11,11,12	0.27	0	15,15,17	0.90	1 (6%)
8	NAG	b	1	2,8	14,14,15	0.47	0	17,19,21	1.24	3 (17%)
8	NAG	b	2	8	14,14,15	0.47	0	17,19,21	1.55	3 (17%)
9	NAG	c	1	2,9	14,14,15	0.52	0	17,19,21	1.10	1 (5%)
9	MAN	c	10	9	11,11,12	0.23	0	15,15,17	0.91	1 (6%)
9	NAG	c	2	9	14,14,15	0.43	0	17,19,21	0.99	1 (5%)
9	BMA	c	3	9	11,11,12	0.25	0	15,15,17	0.94	0
9	MAN	c	4	9	11,11,12	0.17	0	15,15,17	1.09	1 (6%)
9	MAN	c	5	9	11,11,12	0.26	0	15,15,17	0.88	0
9	MAN	c	6	9	11,11,12	0.22	0	15,15,17	0.98	1 (6%)
9	MAN	c	7	9	11,11,12	0.33	0	15,15,17	1.13	1 (6%)
9	MAN	c	8	9	11,11,12	0.21	0	15,15,17	1.07	1 (6%)
9	MAN	c	9	9	11,11,12	0.28	0	15,15,17	0.94	1 (6%)
10	NAG	d	1	2,10	14,14,15	0.50	0	17,19,21	1.43	3 (17%)
10	NAG	d	2	10	14,14,15	0.36	0	17,19,21	1.15	2 (11%)
10	BMA	d	3	10	11,11,12	0.19	0	15,15,17	1.13	1 (6%)
10	MAN	d	4	10	11,11,12	0.21	0	15,15,17	1.05	0
10	MAN	d	5	2,10	11,11,12	0.48	0	15,15,17	1.49	3 (20%)
11	NAG	e	1	2,11	14,14,15	0.53	0	17,19,21	1.47	3 (17%)
11	NAG	e	2	11	14,14,15	0.32	0	17,19,21	0.86	1 (5%)
11	BMA	e	3	11	11,11,12	0.18	0	15,15,17	1.32	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
11	MAN	e	4	11	11,11,12	0.23	0	15,15,17	0.78	0
11	MAN	e	5	11	11,11,12	0.27	0	15,15,17	0.90	1 (6%)
8	NAG	f	1	2,8	14,14,15	0.45	0	17,19,21	1.22	2 (11%)
8	NAG	f	2	8	14,14,15	0.49	0	17,19,21	1.57	4 (23%)
9	NAG	g	1	2,9	14,14,15	0.55	0	17,19,21	1.12	1 (5%)
9	MAN	g	10	9	11,11,12	0.21	0	15,15,17	0.93	1 (6%)
9	NAG	g	2	9	14,14,15	0.42	0	17,19,21	0.97	1 (5%)
9	BMA	g	3	9	11,11,12	0.23	0	15,15,17	0.93	0
9	MAN	g	4	9	11,11,12	0.20	0	15,15,17	1.04	1 (6%)
9	MAN	g	5	9	11,11,12	0.25	0	15,15,17	0.90	0
9	MAN	g	6	9	11,11,12	0.22	0	15,15,17	0.89	0
9	MAN	g	7	9	11,11,12	0.33	0	15,15,17	1.12	1 (6%)
9	MAN	g	8	9	11,11,12	0.20	0	15,15,17	1.08	1 (6%)
9	MAN	g	9	9	11,11,12	0.29	0	15,15,17	0.98	1 (6%)
10	NAG	h	1	2,10	14,14,15	0.50	0	17,19,21	1.36	3 (17%)
10	NAG	h	2	10	14,14,15	0.37	0	17,19,21	1.15	2 (11%)
10	BMA	h	3	10	11,11,12	0.18	0	15,15,17	1.12	1 (6%)
10	MAN	h	4	10	11,11,12	0.21	0	15,15,17	1.04	0
10	MAN	h	5	2,10	11,11,12	0.47	0	15,15,17	1.48	4 (26%)
11	NAG	i	1	2,11	14,14,15	0.53	0	17,19,21	1.45	3 (17%)
11	NAG	i	2	11	14,14,15	0.33	0	17,19,21	0.86	1 (5%)
11	BMA	i	3	11	11,11,12	0.16	0	15,15,17	1.30	2 (13%)
11	MAN	i	4	11	11,11,12	0.23	0	15,15,17	0.79	0
11	MAN	i	5	11	11,11,12	0.27	0	15,15,17	0.91	1 (6%)
8	NAG	j	1	2,8	14,14,15	0.45	0	17,19,21	1.27	3 (17%)
8	NAG	j	2	8	14,14,15	0.48	0	17,19,21	1.56	4 (23%)

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	NAG	V	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	V	2	8	-	1/6/23/26	0/1/1/1
8	NAG	W	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	W	2	8	-	1/6/23/26	0/1/1/1
8	NAG	X	1	8,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	X	2	8	-	1/6/23/26	0/1/1/1
9	NAG	Y	1	2,9	-	0/6/23/26	0/1/1/1
9	MAN	Y	10	9	-	2/2/19/22	0/1/1/1
9	NAG	Y	2	9	-	0/6/23/26	0/1/1/1
9	BMA	Y	3	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	4	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	5	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	6	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	7	9	-	0/2/19/22	0/1/1/1
9	MAN	Y	8	9	-	1/2/19/22	0/1/1/1
9	MAN	Y	9	9	-	0/2/19/22	0/1/1/1
10	NAG	Z	1	2,10	-	0/6/23/26	0/1/1/1
10	NAG	Z	2	10	-	2/6/23/26	0/1/1/1
10	BMA	Z	3	10	-	0/2/19/22	0/1/1/1
10	MAN	Z	4	10	-	1/2/19/22	0/1/1/1
10	MAN	Z	5	2,10	-	1/2/19/22	0/1/1/1
11	NAG	a	1	2,11	-	2/6/23/26	0/1/1/1
11	NAG	a	2	11	-	0/6/23/26	0/1/1/1
11	BMA	a	3	11	-	2/2/19/22	0/1/1/1
11	MAN	a	4	11	-	1/2/19/22	0/1/1/1
11	MAN	a	5	11	-	0/2/19/22	0/1/1/1
8	NAG	b	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	b	2	8	-	1/6/23/26	0/1/1/1
9	NAG	c	1	2,9	-	0/6/23/26	0/1/1/1
9	MAN	c	10	9	-	2/2/19/22	0/1/1/1
9	NAG	c	2	9	-	0/6/23/26	0/1/1/1
9	BMA	c	3	9	-	0/2/19/22	0/1/1/1
9	MAN	c	4	9	-	0/2/19/22	0/1/1/1
9	MAN	c	5	9	-	1/2/19/22	0/1/1/1
9	MAN	c	6	9	-	2/2/19/22	0/1/1/1
9	MAN	c	7	9	-	0/2/19/22	0/1/1/1
9	MAN	c	8	9	-	2/2/19/22	0/1/1/1
9	MAN	c	9	9	-	0/2/19/22	0/1/1/1
10	NAG	d	1	2,10	-	0/6/23/26	0/1/1/1
10	NAG	d	2	10	-	2/6/23/26	0/1/1/1
10	BMA	d	3	10	-	0/2/19/22	0/1/1/1
10	MAN	d	4	10	-	1/2/19/22	0/1/1/1
10	MAN	d	5	2,10	-	1/2/19/22	0/1/1/1
11	NAG	e	1	2,11	-	2/6/23/26	0/1/1/1
11	NAG	e	2	11	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	BMA	e	3	11	-	2/2/19/22	0/1/1/1
11	MAN	e	4	11	-	1/2/19/22	0/1/1/1
11	MAN	e	5	11	-	0/2/19/22	0/1/1/1
8	NAG	f	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	f	2	8	-	1/6/23/26	0/1/1/1
9	NAG	g	1	2,9	-	0/6/23/26	0/1/1/1
9	MAN	g	10	9	-	2/2/19/22	0/1/1/1
9	NAG	g	2	9	-	0/6/23/26	0/1/1/1
9	BMA	g	3	9	-	0/2/19/22	0/1/1/1
9	MAN	g	4	9	-	0/2/19/22	0/1/1/1
9	MAN	g	5	9	-	0/2/19/22	0/1/1/1
9	MAN	g	6	9	-	0/2/19/22	0/1/1/1
9	MAN	g	7	9	-	0/2/19/22	0/1/1/1
9	MAN	g	8	9	-	1/2/19/22	0/1/1/1
9	MAN	g	9	9	-	0/2/19/22	0/1/1/1
10	NAG	h	1	2,10	-	0/6/23/26	0/1/1/1
10	NAG	h	2	10	-	2/6/23/26	0/1/1/1
10	BMA	h	3	10	-	0/2/19/22	0/1/1/1
10	MAN	h	4	10	-	1/2/19/22	0/1/1/1
10	MAN	h	5	2,10	-	1/2/19/22	0/1/1/1
11	NAG	i	1	2,11	-	2/6/23/26	0/1/1/1
11	NAG	i	2	11	-	0/6/23/26	0/1/1/1
11	BMA	i	3	11	-	2/2/19/22	0/1/1/1
11	MAN	i	4	11	-	1/2/19/22	0/1/1/1
11	MAN	i	5	11	-	0/2/19/22	0/1/1/1
8	NAG	j	1	2,8	-	0/6/23/26	0/1/1/1
8	NAG	j	2	8	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	f	2	NAG	C2-N2-C7	4.35	129.10	122.90
8	j	2	NAG	C2-N2-C7	4.32	129.05	122.90
8	b	2	NAG	C2-N2-C7	4.27	128.98	122.90
8	V	2	NAG	C2-N2-C7	3.82	128.34	122.90
8	X	2	NAG	C2-N2-C7	3.79	128.30	122.90
8	W	2	NAG	C2-N2-C7	3.75	128.25	122.90
10	d	1	NAG	C2-N2-C7	-3.27	118.24	122.90
10	Z	1	NAG	C2-N2-C7	-3.22	118.32	122.90
10	h	1	NAG	C2-N2-C7	-3.18	118.37	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	e	3	BMA	O5-C5-C6	3.17	112.18	107.20
11	e	1	NAG	C2-N2-C7	-3.10	118.48	122.90
11	a	3	BMA	O5-C5-C6	3.08	112.04	107.20
11	i	3	BMA	O5-C5-C6	3.04	111.97	107.20
11	a	1	NAG	C2-N2-C7	-2.94	118.72	122.90
11	i	1	NAG	C2-N2-C7	-2.91	118.76	122.90
9	c	4	MAN	O5-C1-C2	-2.85	106.38	110.77
8	X	1	NAG	C1-O5-C5	2.85	116.05	112.19
10	Z	1	NAG	C1-O5-C5	2.84	116.04	112.19
10	d	1	NAG	C1-O5-C5	2.81	116.00	112.19
10	Z	2	NAG	C2-N2-C7	-2.81	118.90	122.90
10	Z	5	MAN	O4-C4-C3	-2.81	103.86	110.35
11	a	1	NAG	C1-O5-C5	2.80	115.99	112.19
11	i	1	NAG	C1-O5-C5	2.78	115.96	112.19
8	W	1	NAG	C1-O5-C5	2.78	115.96	112.19
10	h	5	MAN	O4-C4-C3	-2.76	103.98	110.35
8	V	1	NAG	O4-C4-C5	-2.73	102.51	109.30
10	d	5	MAN	O4-C4-C3	-2.73	104.04	110.35
10	h	2	NAG	C2-N2-C7	-2.72	119.03	122.90
10	Z	1	NAG	O5-C1-C2	-2.72	106.99	111.29
10	Z	5	MAN	C1-C2-C3	-2.70	106.34	109.67
10	d	2	NAG	C2-N2-C7	-2.70	119.06	122.90
9	c	8	MAN	O5-C1-C2	-2.69	106.61	110.77
9	g	8	MAN	O5-C1-C2	-2.69	106.62	110.77
9	Y	4	MAN	O5-C1-C2	-2.69	106.63	110.77
10	d	5	MAN	C1-C2-C3	-2.65	106.41	109.67
11	e	1	NAG	C1-O5-C5	2.64	115.76	112.19
10	d	3	BMA	O3-C3-C2	-2.63	104.96	109.99
10	h	1	NAG	C1-O5-C5	2.62	115.74	112.19
10	d	1	NAG	O5-C1-C2	-2.61	107.17	111.29
8	V	1	NAG	C1-C2-N2	-2.60	106.05	110.49
9	g	4	MAN	O5-C1-C2	-2.59	106.77	110.77
11	i	2	NAG	C1-O5-C5	2.59	115.70	112.19
10	h	5	MAN	C1-C2-C3	-2.59	106.48	109.67
9	Y	8	MAN	O5-C1-C2	-2.59	106.78	110.77
8	V	1	NAG	C1-O5-C5	2.58	115.69	112.19
10	Z	3	BMA	O3-C3-C2	-2.58	105.06	109.99
11	e	2	NAG	C1-O5-C5	2.57	115.67	112.19
10	Z	5	MAN	O4-C4-C5	-2.55	102.97	109.30
10	h	3	BMA	O3-C3-C2	-2.55	105.12	109.99
11	a	2	NAG	C1-O5-C5	2.52	115.61	112.19
10	Z	2	NAG	O5-C1-C2	-2.50	107.35	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	d	2	NAG	O5-C1-C2	-2.48	107.37	111.29
9	g	7	MAN	O5-C1-C2	-2.48	106.95	110.77
10	h	1	NAG	O5-C1-C2	-2.47	107.39	111.29
9	Y	7	MAN	O5-C1-C2	-2.47	106.96	110.77
9	c	7	MAN	O5-C1-C2	-2.46	106.97	110.77
10	h	5	MAN	O4-C4-C5	-2.44	103.23	109.30
10	h	2	NAG	O5-C1-C2	-2.42	107.46	111.29
8	X	1	NAG	C2-N2-C7	-2.41	119.47	122.90
8	f	1	NAG	C3-C4-C5	-2.41	105.94	110.24
10	d	5	MAN	O4-C4-C5	-2.41	103.31	109.30
8	j	1	NAG	C3-C4-C5	-2.41	105.95	110.24
8	j	2	NAG	C1-O5-C5	2.40	115.44	112.19
8	b	1	NAG	C3-C4-C5	-2.39	105.98	110.24
9	g	1	NAG	C1-O5-C5	-2.38	108.97	112.19
9	g	10	MAN	O5-C1-C2	-2.37	107.12	110.77
9	g	9	MAN	O5-C5-C6	2.35	110.89	107.20
8	f	2	NAG	C1-O5-C5	2.34	115.37	112.19
9	c	1	NAG	C1-O5-C5	-2.34	109.02	112.19
8	V	2	NAG	O5-C1-C2	-2.34	107.60	111.29
9	Y	10	MAN	O5-C1-C2	-2.32	107.18	110.77
9	Y	9	MAN	O5-C5-C6	2.30	110.81	107.20
8	b	2	NAG	O7-C7-N2	2.29	126.17	121.95
8	b	2	NAG	C1-O5-C5	2.29	115.29	112.19
9	c	10	MAN	O5-C1-C2	-2.28	107.26	110.77
8	X	2	NAG	C1-O5-C5	2.25	115.24	112.19
8	j	2	NAG	O7-C7-N2	2.25	126.09	121.95
8	f	2	NAG	O7-C7-N2	2.24	126.08	121.95
11	i	1	NAG	O5-C1-C2	-2.23	107.77	111.29
8	W	2	NAG	O5-C1-C2	-2.22	107.78	111.29
8	W	1	NAG	C2-N2-C7	-2.21	119.75	122.90
9	Y	1	NAG	C1-O5-C5	-2.19	109.23	112.19
8	f	1	NAG	O4-C4-C3	-2.18	105.32	110.35
8	j	1	NAG	O4-C4-C3	-2.17	105.33	110.35
11	e	1	NAG	O5-C1-C2	-2.17	107.87	111.29
11	i	3	BMA	O3-C3-C2	-2.16	105.85	109.99
8	X	2	NAG	O5-C1-C2	-2.16	107.87	111.29
9	Y	2	NAG	O4-C4-C3	-2.15	105.39	110.35
11	e	3	BMA	O3-C3-C2	-2.14	105.89	109.99
8	j	1	NAG	C4-C3-C2	2.14	114.16	111.02
8	V	1	NAG	C2-N2-C7	-2.14	119.86	122.90
8	W	2	NAG	C1-O5-C5	2.14	115.08	112.19
8	b	1	NAG	O4-C4-C3	-2.13	105.43	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	a	5	MAN	O5-C1-C2	-2.13	107.49	110.77
11	e	5	MAN	O5-C1-C2	-2.13	107.49	110.77
8	W	1	NAG	O4-C4-C5	-2.12	104.02	109.30
9	c	6	MAN	O5-C1-C2	-2.12	107.49	110.77
11	i	5	MAN	O5-C1-C2	-2.11	107.51	110.77
9	Y	7	MAN	C1-C2-C3	-2.11	107.08	109.67
9	c	2	NAG	O4-C4-C3	-2.09	105.52	110.35
11	a	1	NAG	O5-C1-C2	-2.08	108.00	111.29
11	e	3	BMA	C6-C5-C4	-2.07	108.15	113.00
8	b	1	NAG	C4-C3-C2	2.07	114.06	111.02
9	c	9	MAN	O5-C1-C2	-2.07	107.57	110.77
10	Z	5	MAN	O5-C1-C2	-2.05	107.61	110.77
9	Y	2	NAG	C1-O5-C5	2.04	114.96	112.19
10	Z	3	BMA	O5-C1-C2	-2.04	107.63	110.77
8	f	2	NAG	O5-C1-C2	-2.03	108.09	111.29
8	j	2	NAG	O5-C1-C2	-2.02	108.10	111.29
10	h	5	MAN	O5-C1-C2	-2.01	107.66	110.77
9	g	2	NAG	O4-C4-C3	-2.01	105.69	110.35
8	V	2	NAG	C1-O5-C5	2.01	114.91	112.19

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	d	2	NAG	O5-C5-C6-O6
10	h	2	NAG	O5-C5-C6-O6
11	a	1	NAG	C4-C5-C6-O6
11	e	1	NAG	C4-C5-C6-O6
11	i	1	NAG	C4-C5-C6-O6
10	d	2	NAG	C4-C5-C6-O6
10	h	2	NAG	C4-C5-C6-O6
10	Z	2	NAG	O5-C5-C6-O6
11	a	1	NAG	O5-C5-C6-O6
11	e	1	NAG	O5-C5-C6-O6
11	i	1	NAG	O5-C5-C6-O6
10	Z	2	NAG	C4-C5-C6-O6
9	c	8	MAN	O5-C5-C6-O6
9	c	6	MAN	O5-C5-C6-O6
9	Y	10	MAN	O5-C5-C6-O6
9	Y	8	MAN	O5-C5-C6-O6
9	g	8	MAN	O5-C5-C6-O6
10	Z	5	MAN	O5-C5-C6-O6

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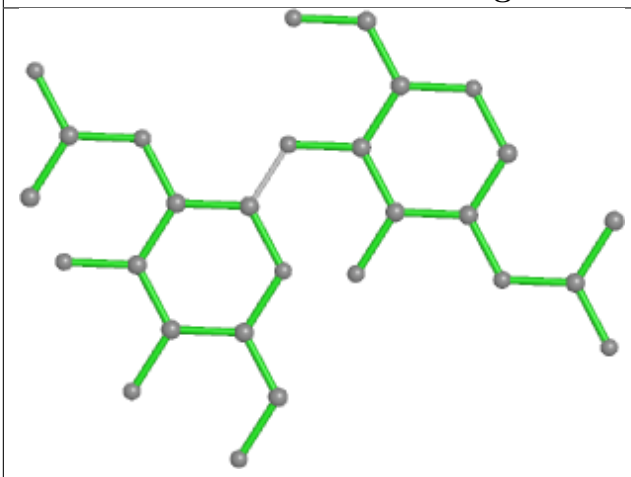
Mol	Chain	Res	Type	Atoms
10	d	5	MAN	O5-C5-C6-O6
10	h	5	MAN	O5-C5-C6-O6
10	Z	4	MAN	C4-C5-C6-O6
11	a	4	MAN	O5-C5-C6-O6
11	e	4	MAN	O5-C5-C6-O6
11	i	4	MAN	O5-C5-C6-O6
10	d	4	MAN	C4-C5-C6-O6
11	i	3	BMA	O5-C5-C6-O6
10	h	4	MAN	C4-C5-C6-O6
11	e	3	BMA	O5-C5-C6-O6
11	i	3	BMA	C4-C5-C6-O6
9	c	10	MAN	O5-C5-C6-O6
11	e	3	BMA	C4-C5-C6-O6
9	g	10	MAN	O5-C5-C6-O6
9	Y	10	MAN	C4-C5-C6-O6
11	a	3	BMA	C4-C5-C6-O6
11	a	3	BMA	O5-C5-C6-O6
9	c	8	MAN	C4-C5-C6-O6
9	c	6	MAN	C4-C5-C6-O6
9	c	5	MAN	O5-C5-C6-O6
9	c	10	MAN	C4-C5-C6-O6
8	V	2	NAG	C3-C2-N2-C7
8	W	2	NAG	C3-C2-N2-C7
8	X	2	NAG	C3-C2-N2-C7
8	b	2	NAG	C3-C2-N2-C7
8	f	2	NAG	C3-C2-N2-C7
8	j	2	NAG	C3-C2-N2-C7
9	g	10	MAN	C4-C5-C6-O6

There are no ring outliers.

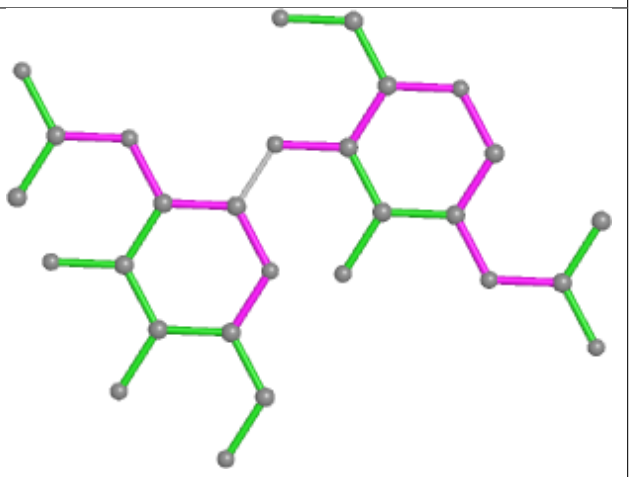
No monomer is involved in short contacts.

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

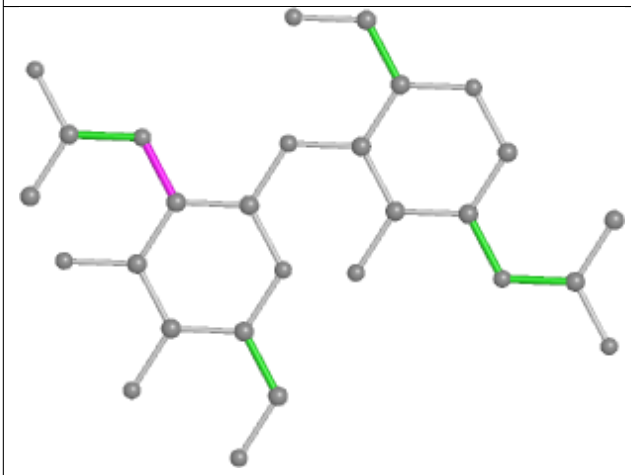
Oligosaccharide Chain V



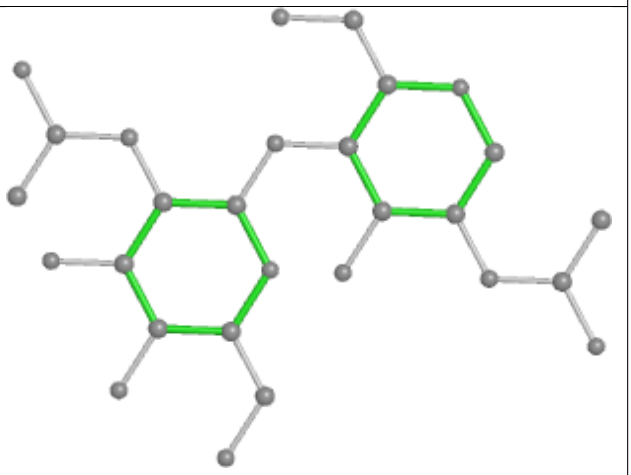
Bond lengths



Bond angles

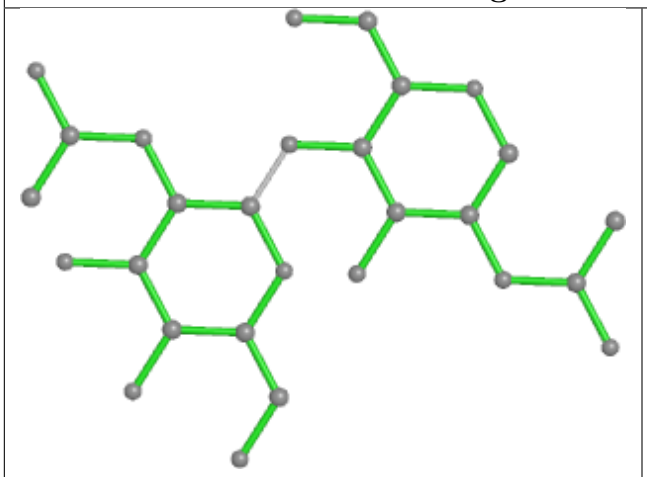


Torsions

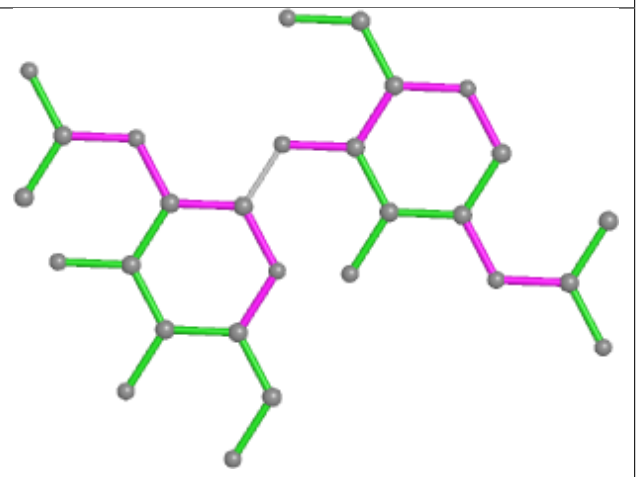


Rings

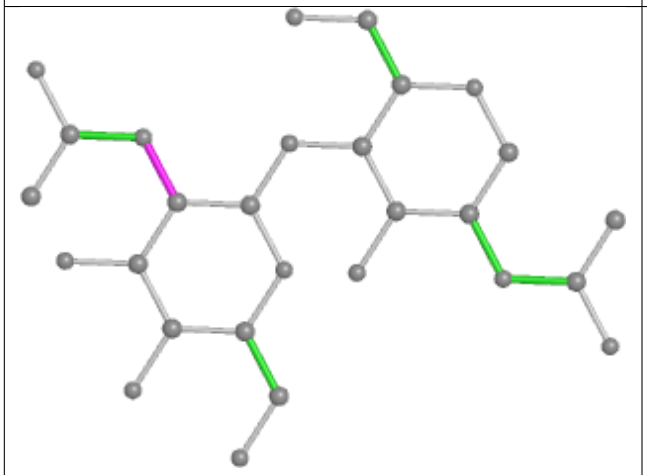
Oligosaccharide Chain W



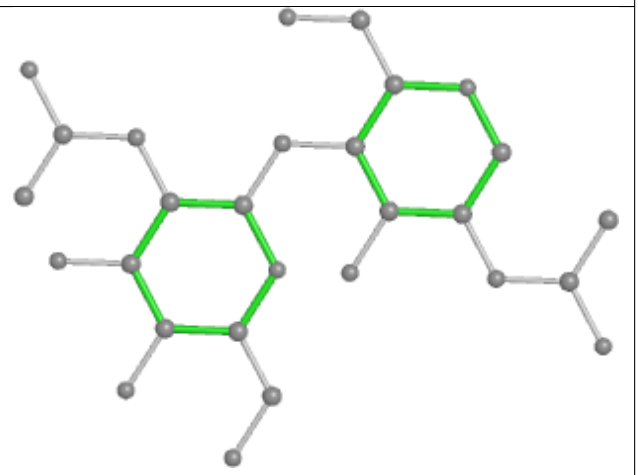
Bond lengths



Bond angles

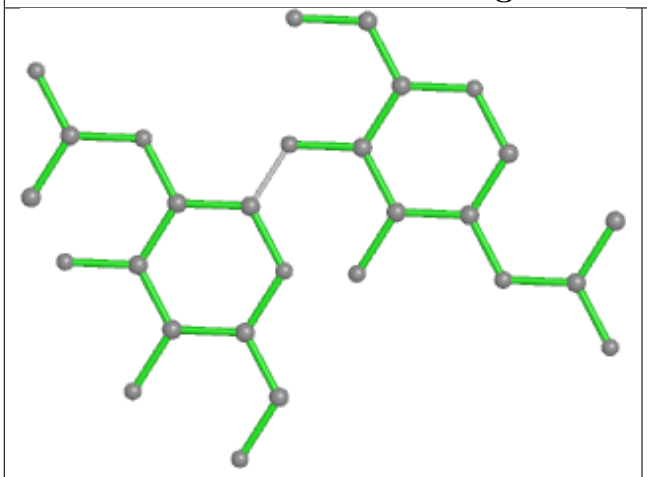


Torsions

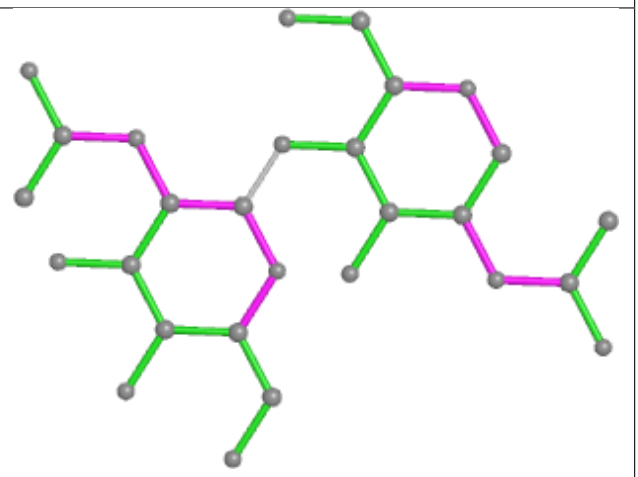


Rings

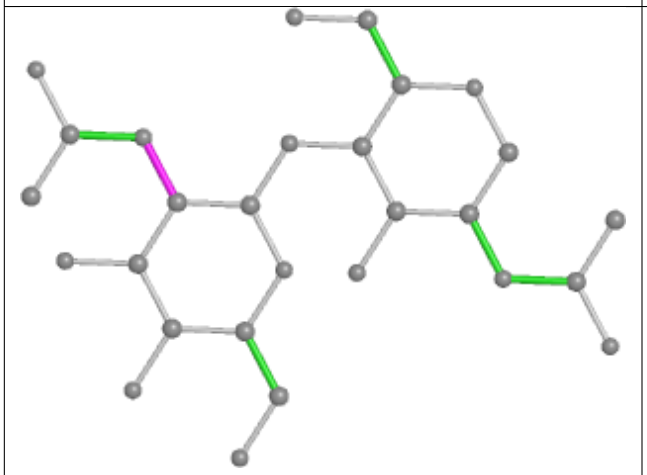
Oligosaccharide Chain X



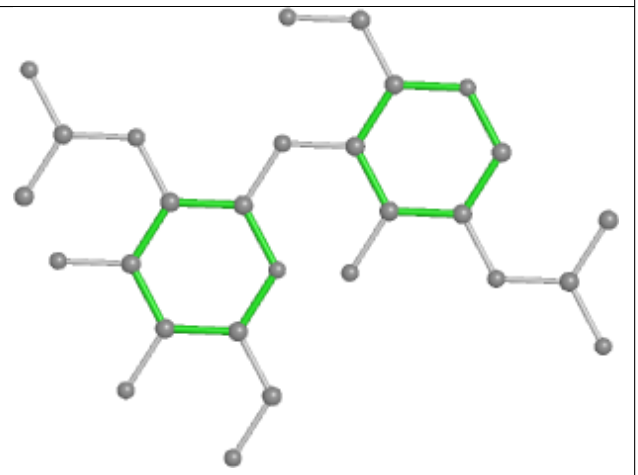
Bond lengths



Bond angles

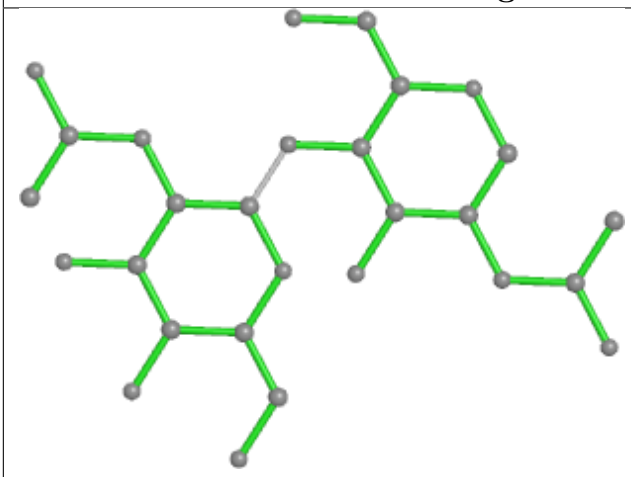


Torsions

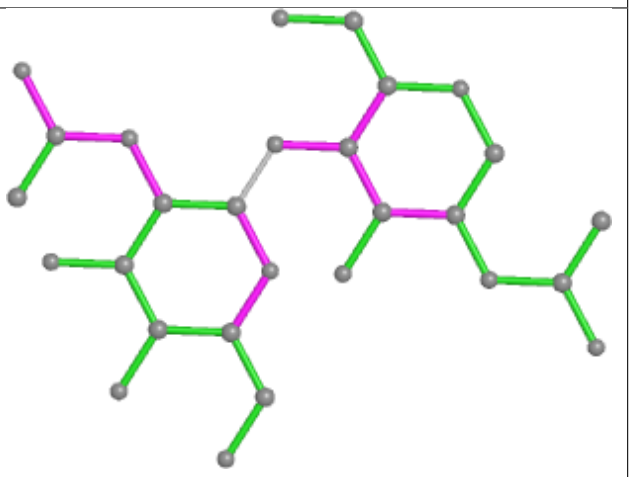


Rings

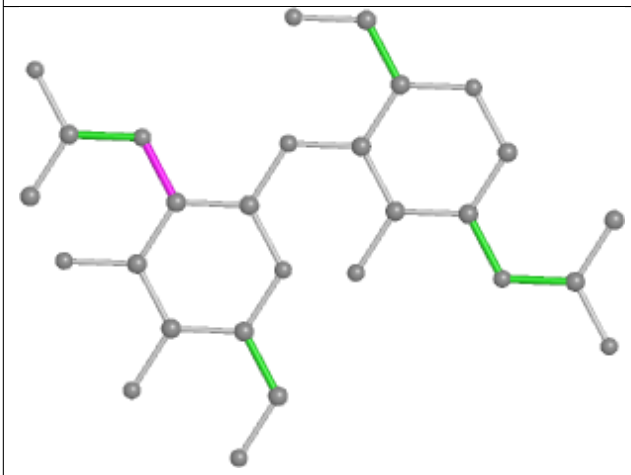
Oligosaccharide Chain b



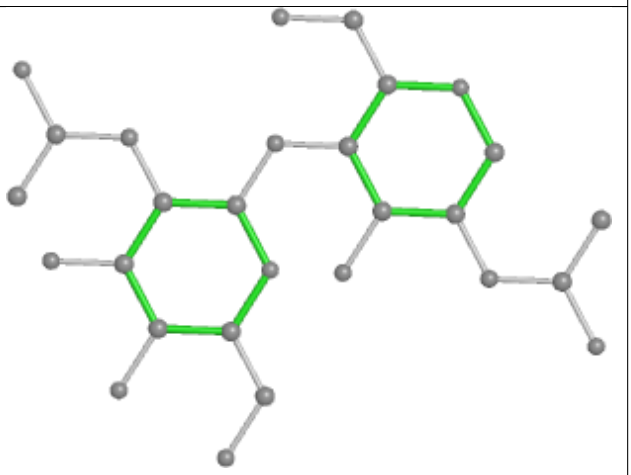
Bond lengths



Bond angles

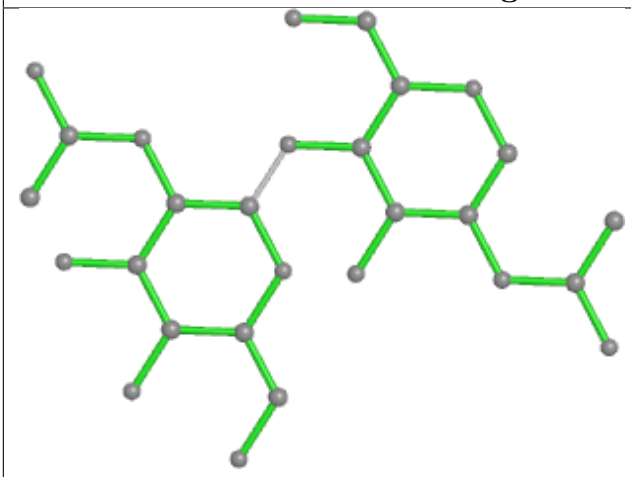


Torsions

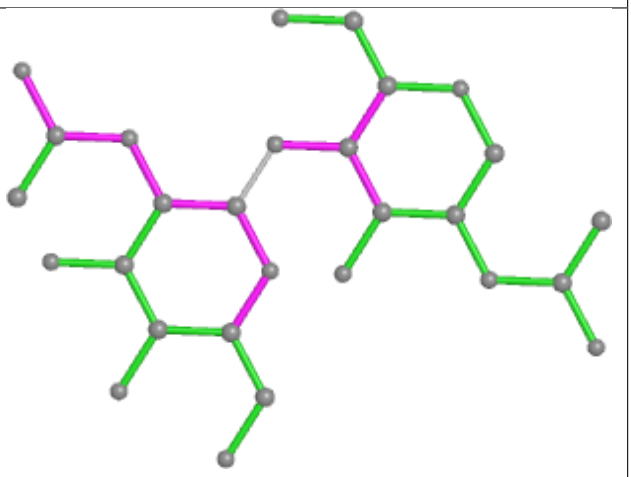


Rings

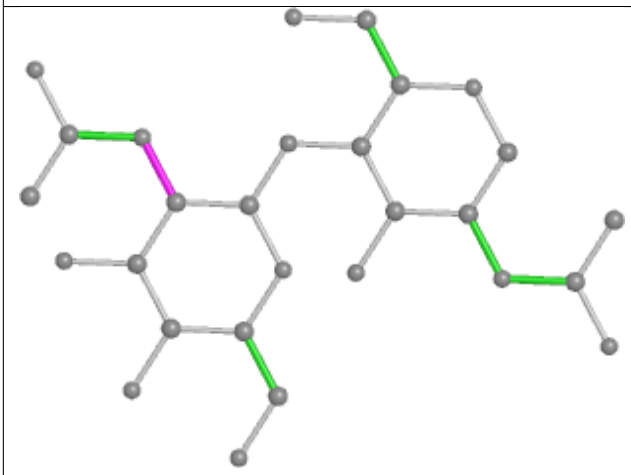
Oligosaccharide Chain f



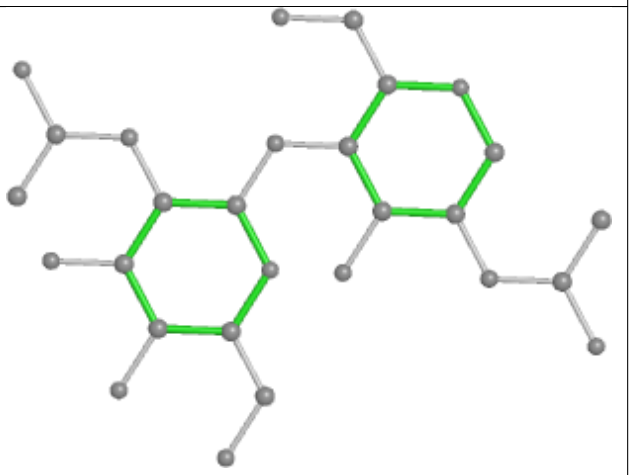
Bond lengths



Bond angles

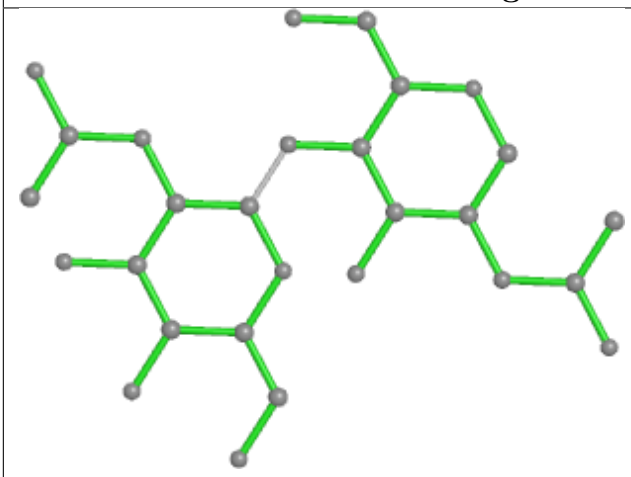


Torsions

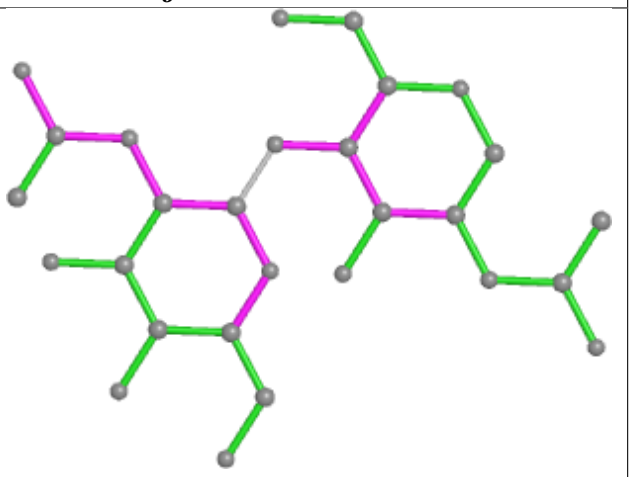


Rings

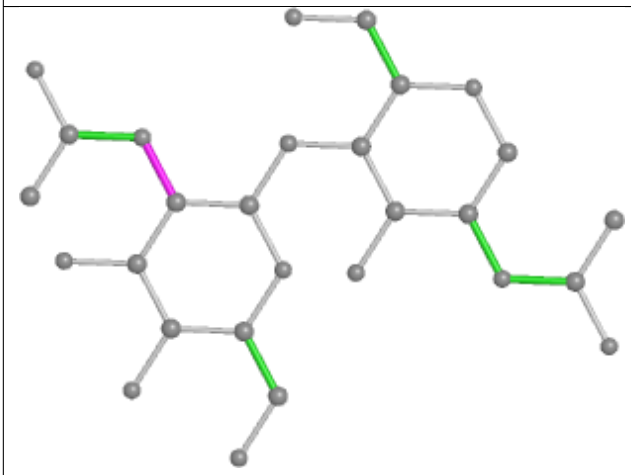
Oligosaccharide Chain j



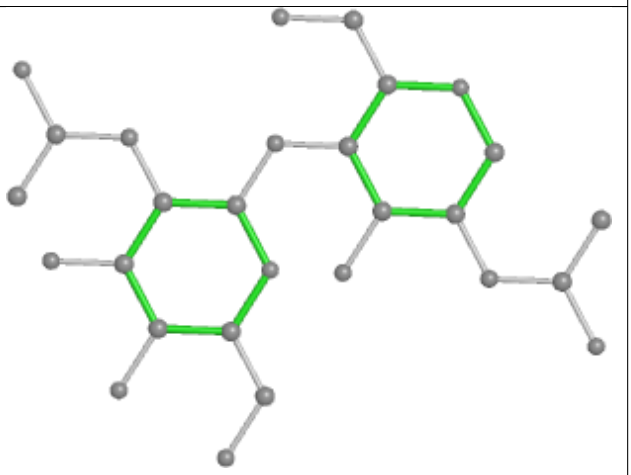
Bond lengths



Bond angles

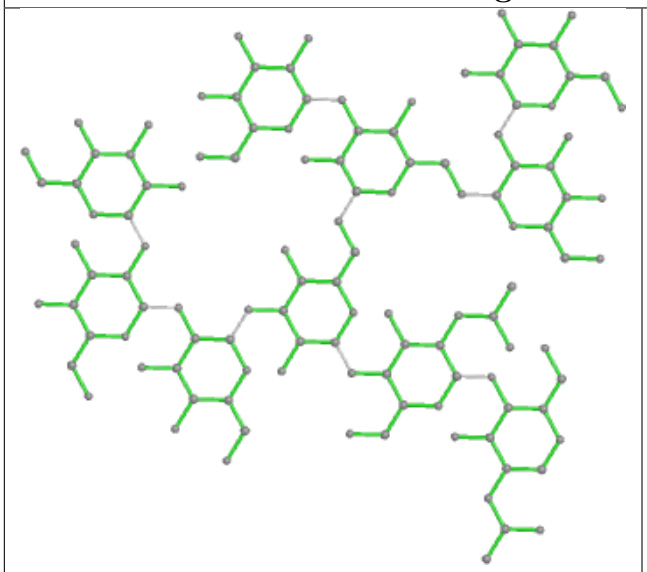


Torsions

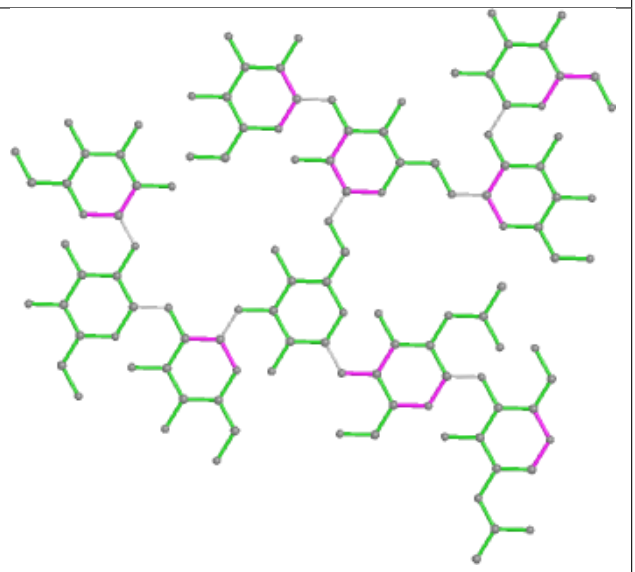


Rings

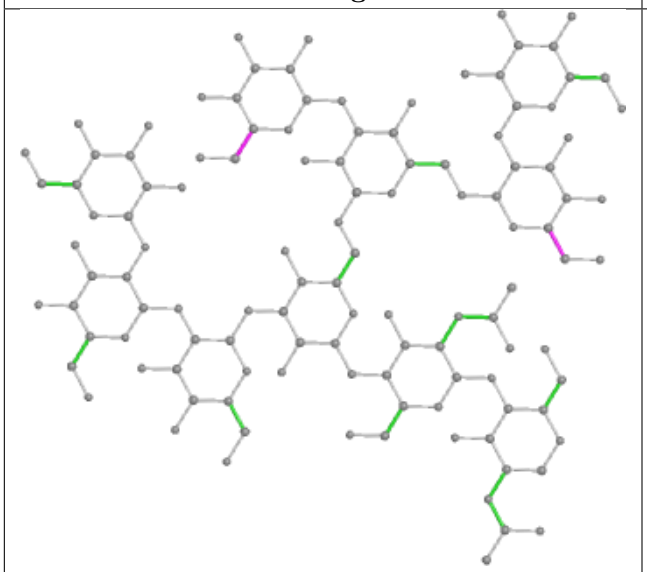
Oligosaccharide Chain Y



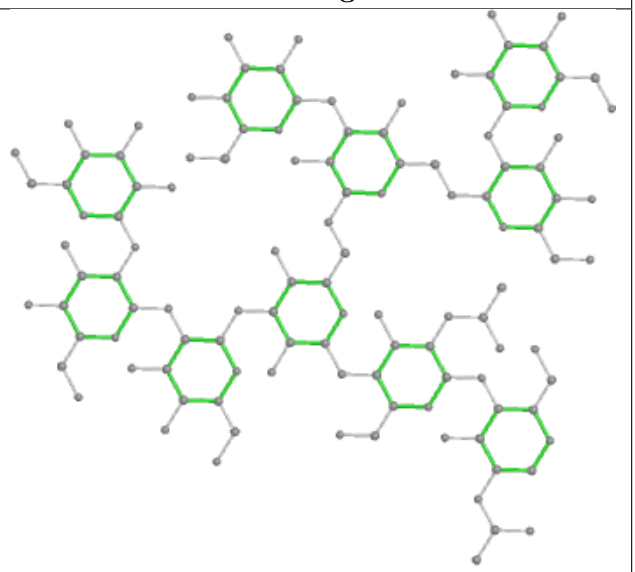
Bond lengths



Bond angles

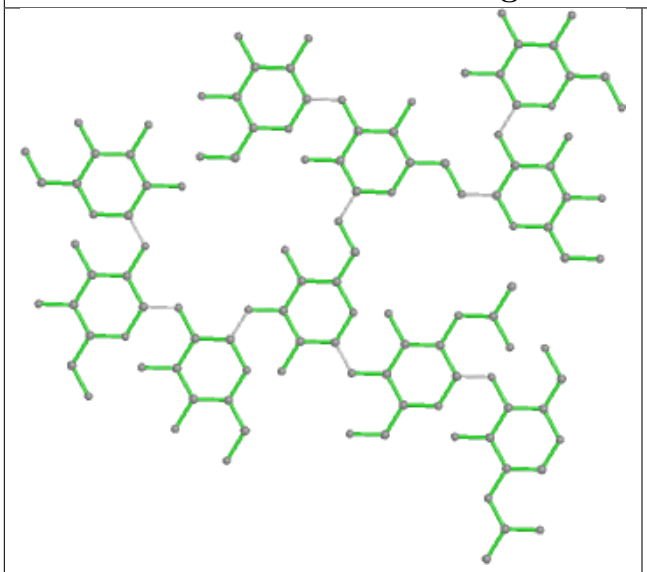


Torsions

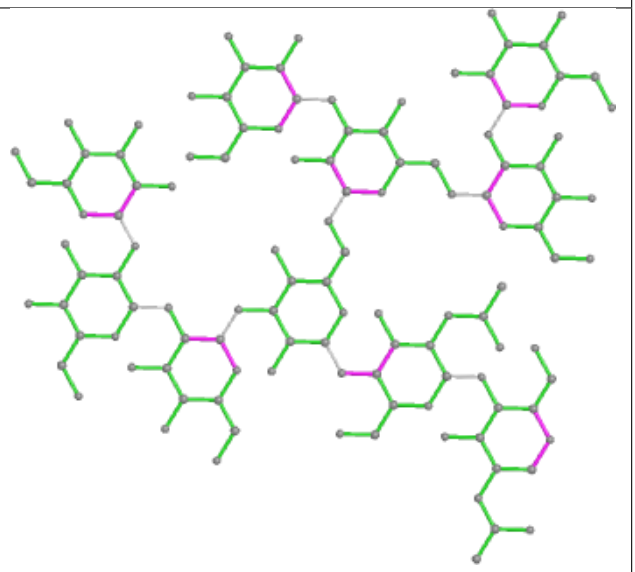


Rings

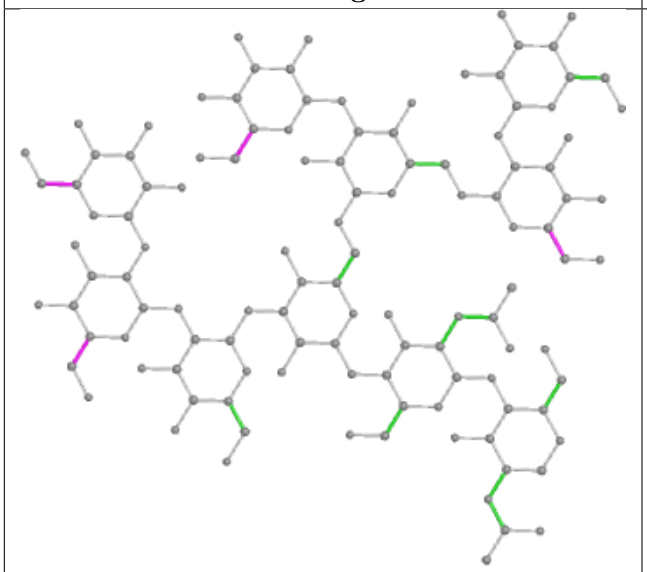
Oligosaccharide Chain c



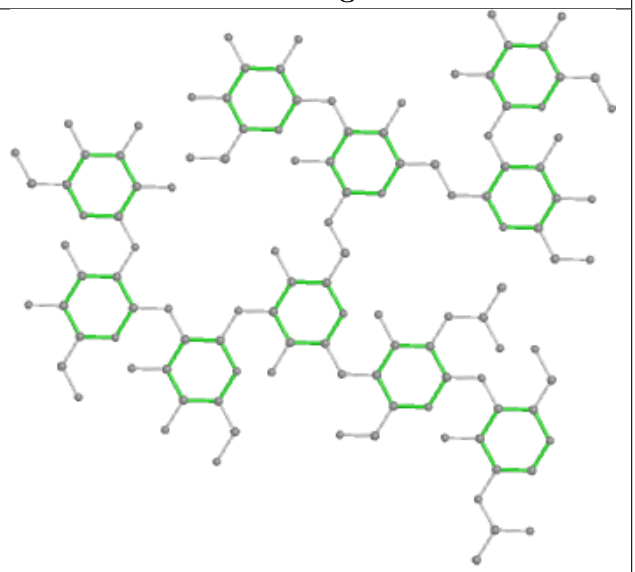
Bond lengths



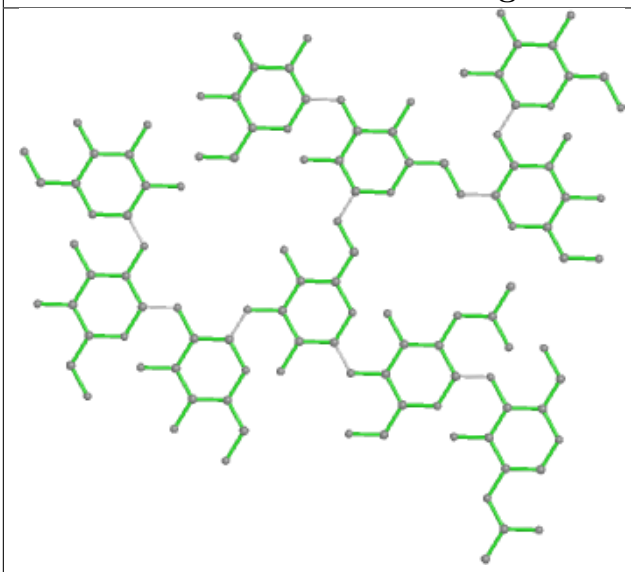
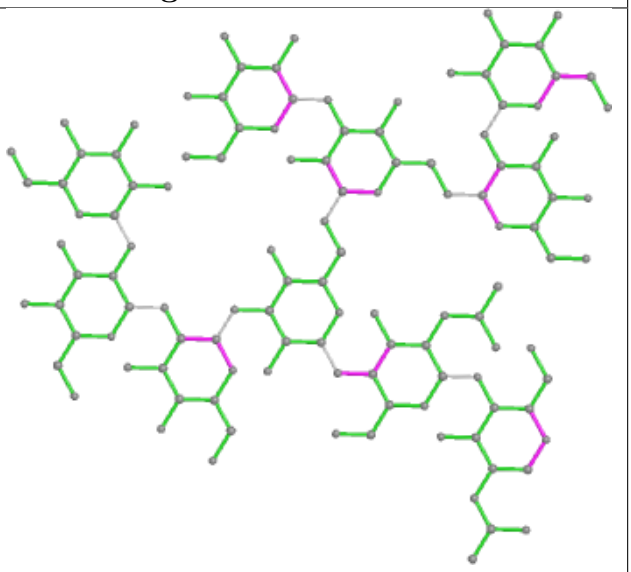
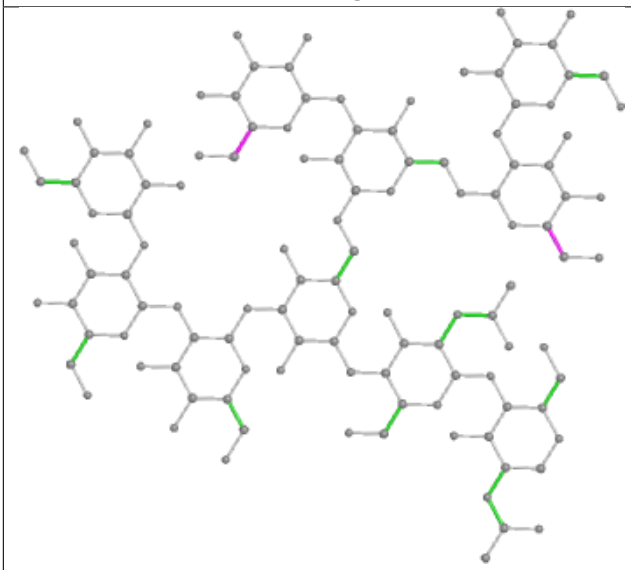
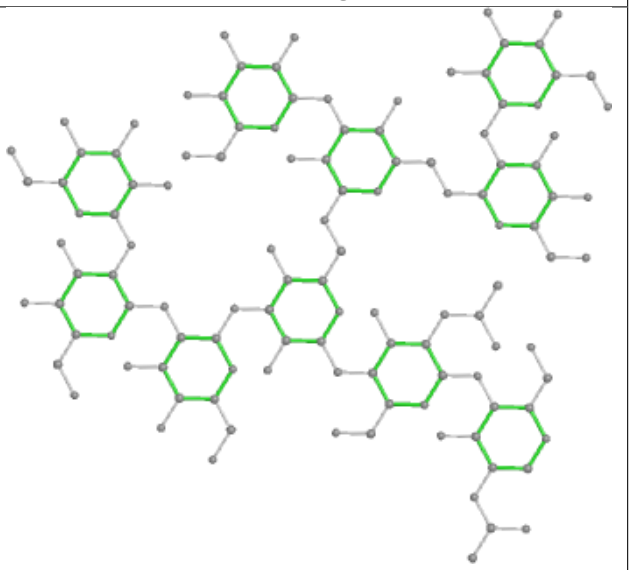
Bond angles



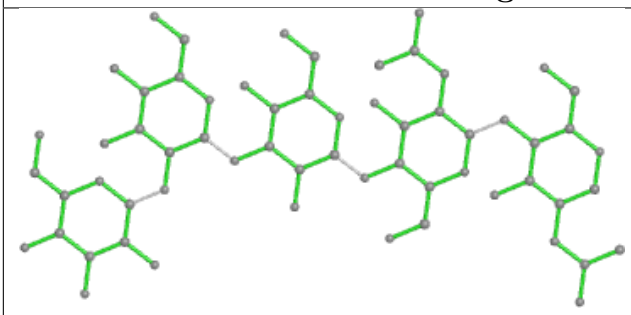
Torsions



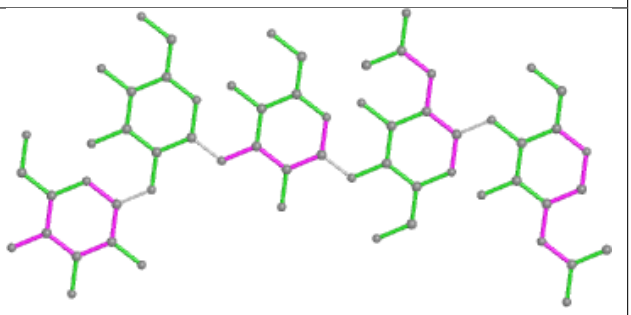
Rings

Oligosaccharide Chain g	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

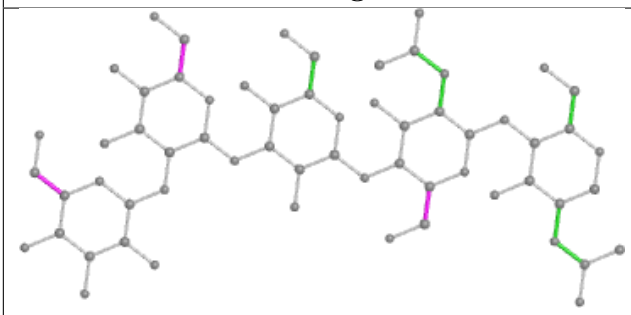
Oligosaccharide Chain Z



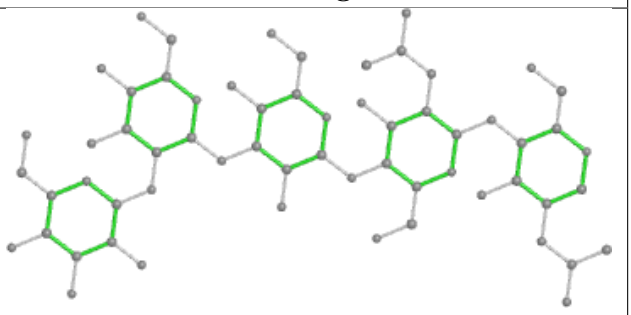
Bond lengths



Bond angles

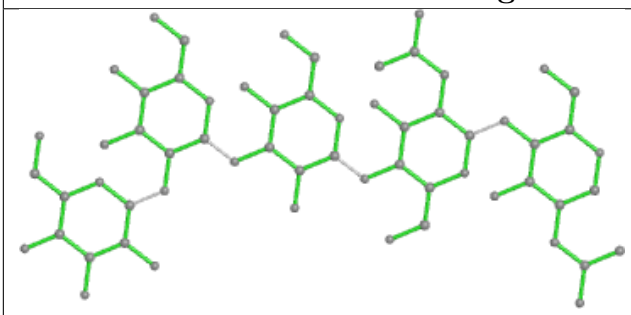


Torsions

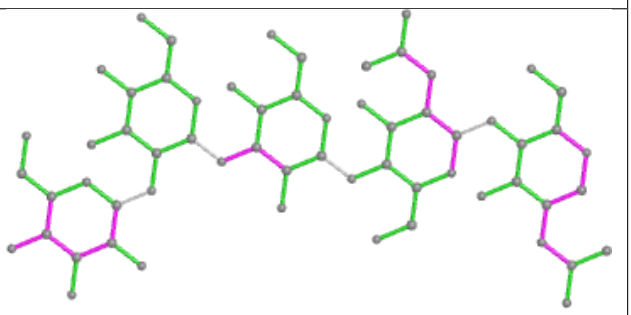


Rings

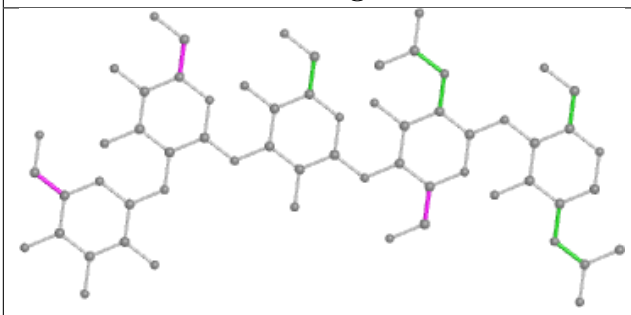
Oligosaccharide Chain d



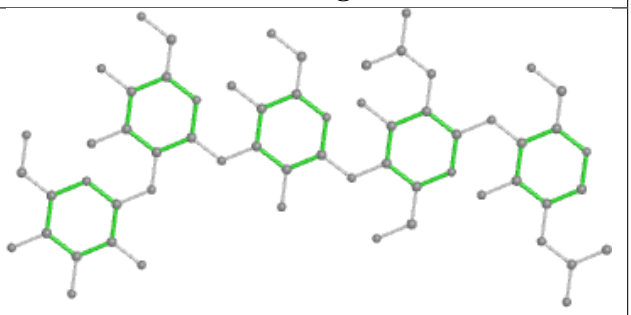
Bond lengths



Bond angles

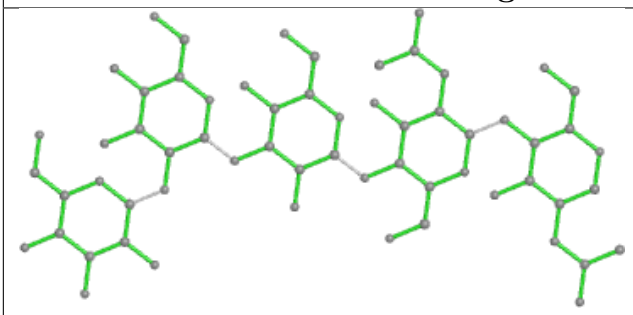


Torsions

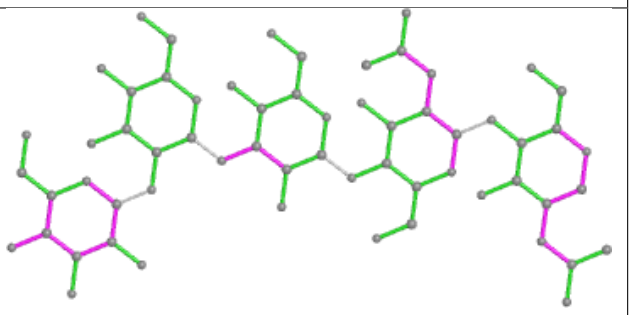


Rings

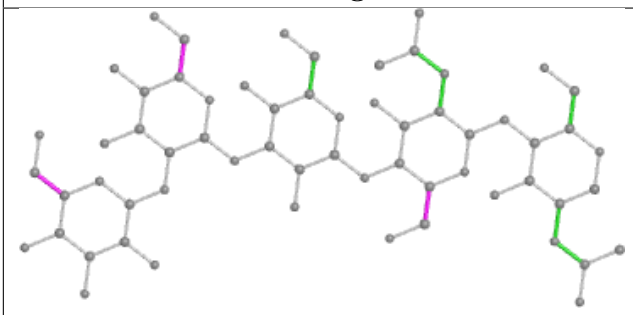
Oligosaccharide Chain h



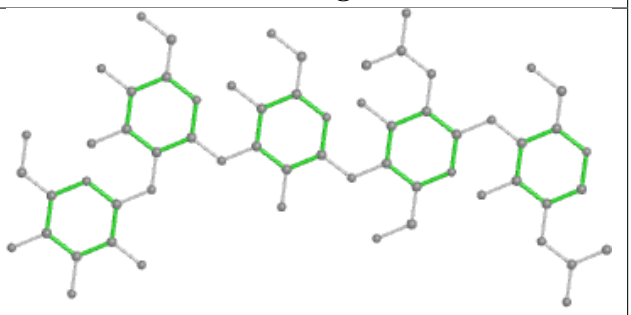
Bond lengths



Bond angles

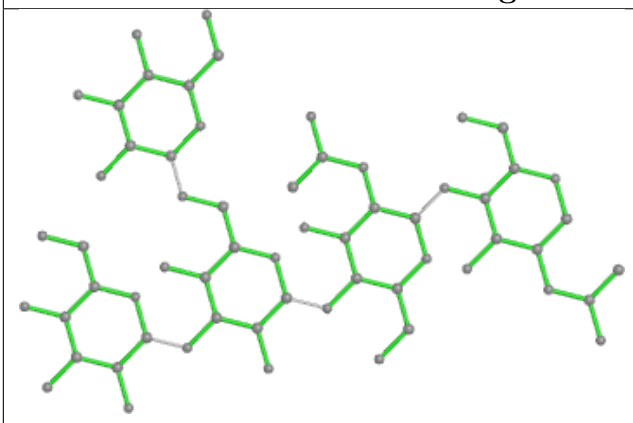


Torsions

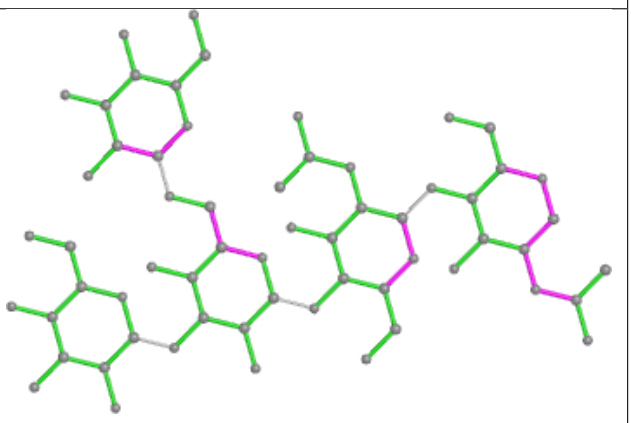


Rings

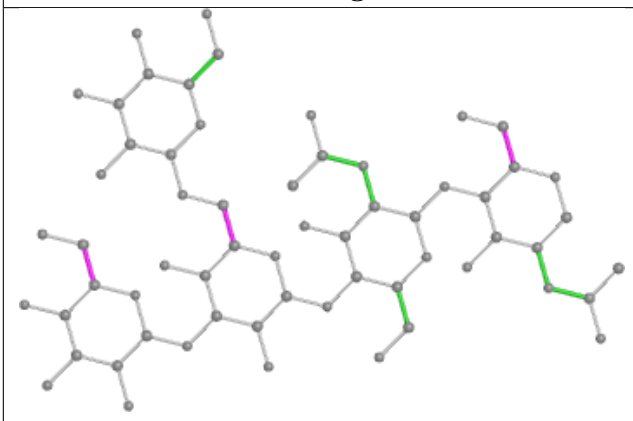
Oligosaccharide Chain a



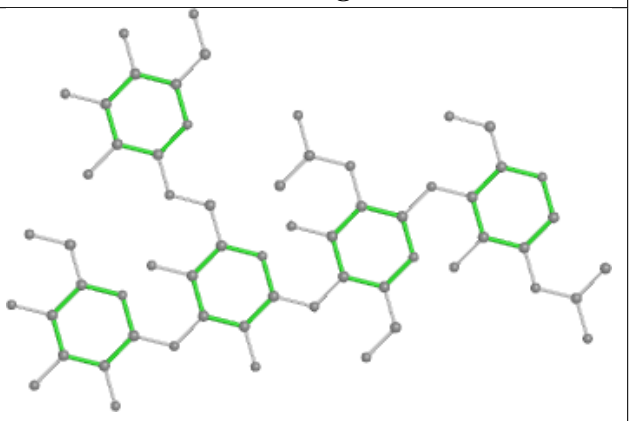
Bond lengths



Bond angles

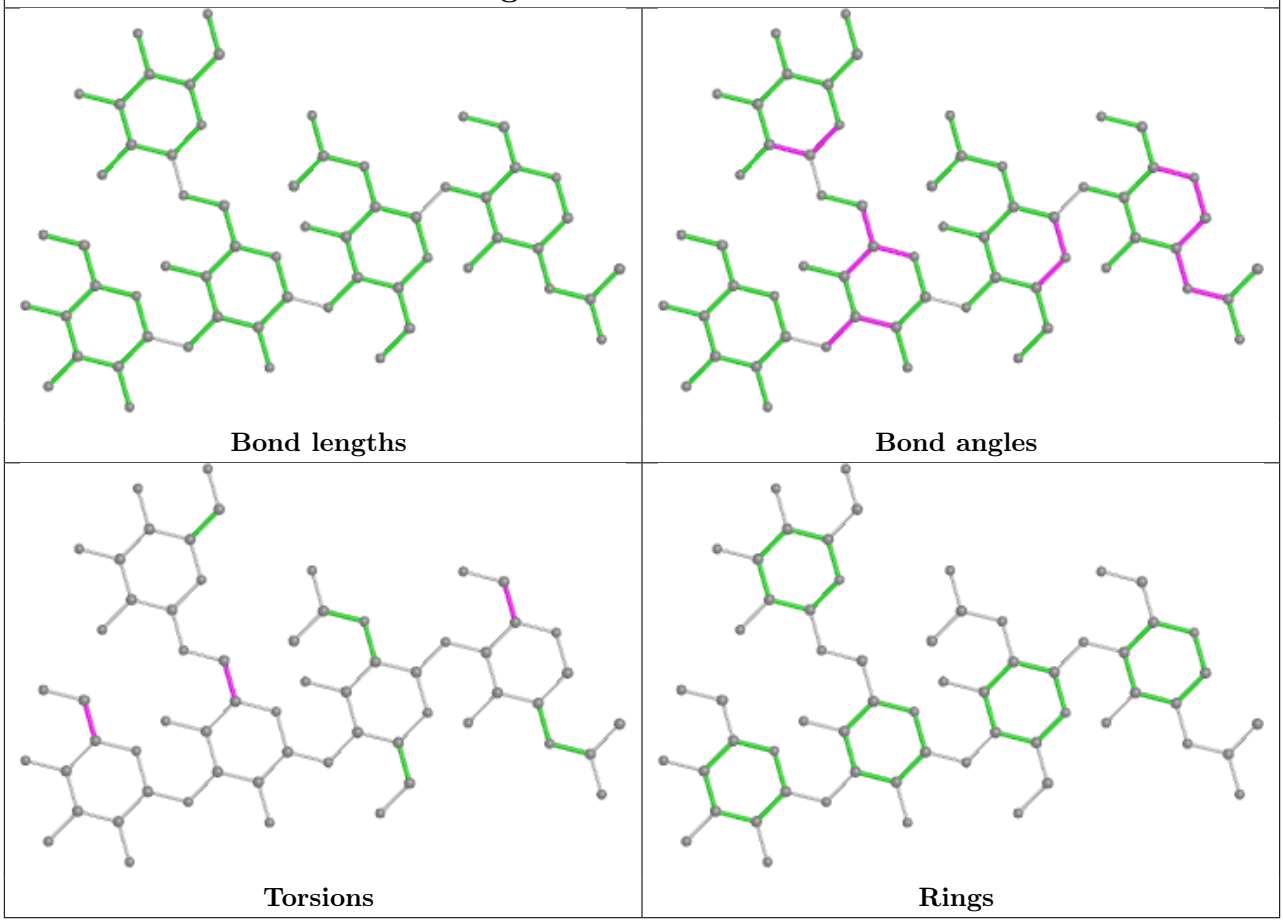


Torsions

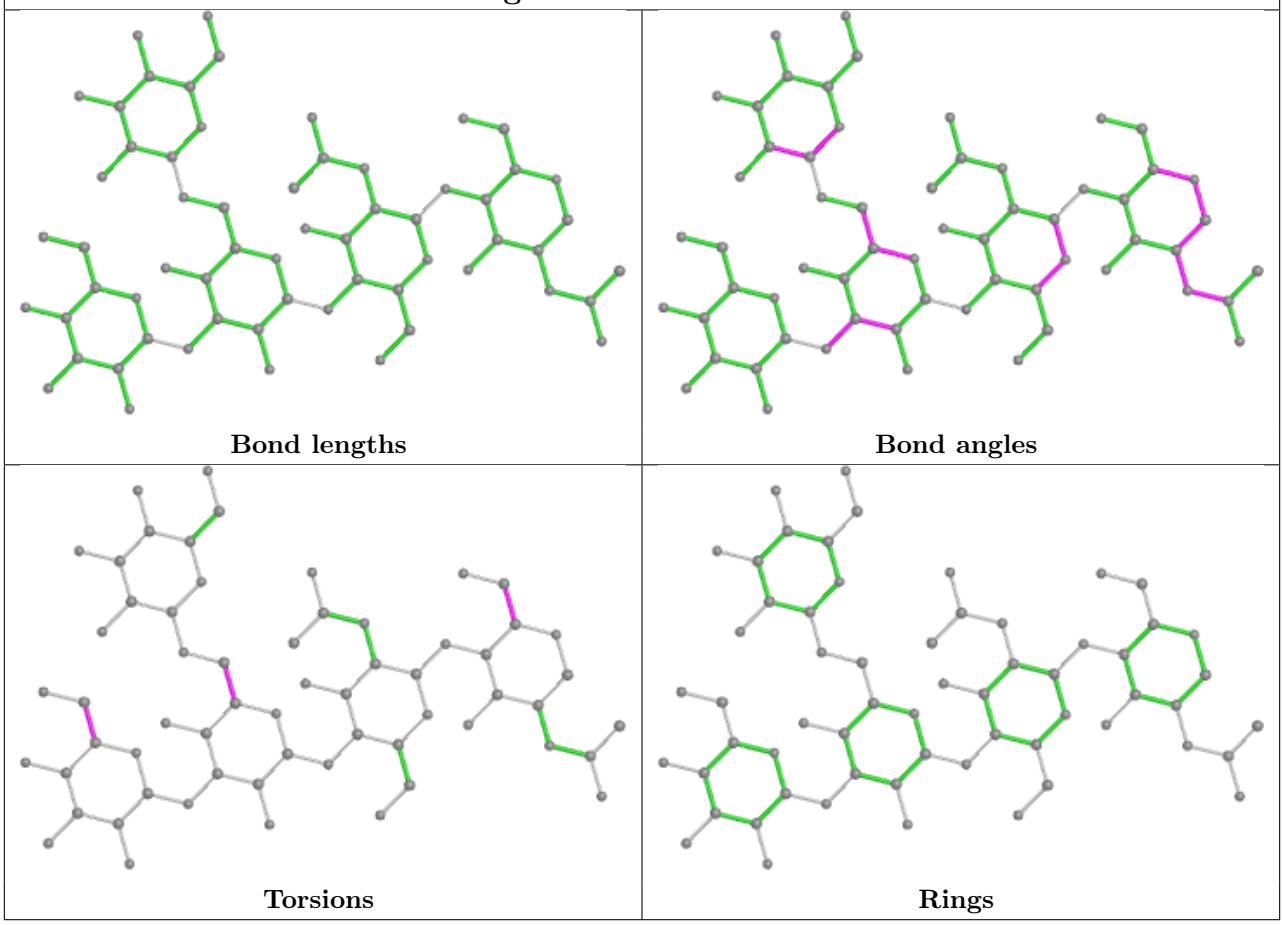


Rings

Oligosaccharide Chain e



Oligosaccharide Chain i



5.6 Ligand geometry (i)

18 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
12	NAG	E	627	2	14,14,15	0.35	0	17,19,21	0.78	0
12	NAG	E	624	2	14,14,15	0.34	0	17,19,21	0.93	1 (5%)
12	NAG	D	627	2	14,14,15	0.37	0	17,19,21	0.78	0
12	NAG	F	627	2	14,14,15	0.38	0	17,19,21	0.78	0
12	NAG	D	621	2	14,14,15	0.29	0	17,19,21	0.85	0
12	NAG	F	622	2	14,14,15	0.33	0	17,19,21	1.13	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
12	NAG	E	621	2	14,14,15	0.28	0	17,19,21	0.81	0
12	NAG	D	623	2	14,14,15	0.40	0	17,19,21	0.75	0
12	NAG	F	623	2	14,14,15	0.41	0	17,19,21	0.73	0
12	NAG	F	624	2	14,14,15	0.34	0	17,19,21	0.95	1 (5%)
12	NAG	E	623	2	14,14,15	0.41	0	17,19,21	0.75	0
12	NAG	E	622	2	14,14,15	0.33	0	17,19,21	1.10	2 (11%)
12	NAG	D	622	2	14,14,15	0.32	0	17,19,21	1.14	2 (11%)
12	NAG	F	621	2	14,14,15	0.30	0	17,19,21	0.84	0
12	NAG	F	628	2	14,14,15	0.34	0	17,19,21	1.23	1 (5%)
12	NAG	E	628	2	14,14,15	0.34	0	17,19,21	1.26	1 (5%)
12	NAG	D	624	2	14,14,15	0.34	0	17,19,21	0.92	0
12	NAG	D	628	2	14,14,15	0.34	0	17,19,21	1.23	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	E	627	2	-	0/6/23/26	0/1/1/1
12	NAG	E	624	2	-	2/6/23/26	0/1/1/1
12	NAG	D	627	2	-	0/6/23/26	0/1/1/1
12	NAG	F	627	2	-	0/6/23/26	0/1/1/1
12	NAG	D	621	2	-	2/6/23/26	0/1/1/1
12	NAG	F	622	2	-	0/6/23/26	0/1/1/1
12	NAG	E	621	2	-	2/6/23/26	0/1/1/1
12	NAG	D	623	2	-	2/6/23/26	0/1/1/1
12	NAG	F	623	2	-	2/6/23/26	0/1/1/1
12	NAG	F	624	2	-	2/6/23/26	0/1/1/1
12	NAG	E	623	2	-	2/6/23/26	0/1/1/1
12	NAG	E	622	2	-	0/6/23/26	0/1/1/1
12	NAG	D	622	2	-	0/6/23/26	0/1/1/1
12	NAG	F	621	2	-	2/6/23/26	0/1/1/1
12	NAG	F	628	2	-	3/6/23/26	0/1/1/1
12	NAG	E	628	2	-	3/6/23/26	0/1/1/1
12	NAG	D	624	2	-	2/6/23/26	0/1/1/1
12	NAG	D	628	2	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	E	628	NAG	C1-O5-C5	3.48	116.91	112.19
12	D	628	NAG	C1-O5-C5	3.35	116.74	112.19
12	F	628	NAG	C1-O5-C5	3.35	116.73	112.19
12	D	622	NAG	C1-O5-C5	2.92	116.14	112.19
12	E	622	NAG	C1-O5-C5	2.88	116.09	112.19
12	F	622	NAG	C1-O5-C5	2.82	116.01	112.19
12	F	622	NAG	O5-C1-C2	-2.23	107.77	111.29
12	D	622	NAG	O5-C1-C2	-2.17	107.86	111.29
12	E	622	NAG	O5-C1-C2	-2.09	107.99	111.29
12	F	624	NAG	C2-N2-C7	2.05	125.81	122.90
12	E	624	NAG	C2-N2-C7	2.02	125.77	122.90

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	D	628	NAG	C8-C7-N2-C2
12	D	628	NAG	O7-C7-N2-C2
12	E	628	NAG	C8-C7-N2-C2
12	E	628	NAG	O7-C7-N2-C2
12	F	628	NAG	C8-C7-N2-C2
12	F	628	NAG	O7-C7-N2-C2
12	F	628	NAG	O5-C5-C6-O6
12	E	628	NAG	O5-C5-C6-O6
12	D	628	NAG	O5-C5-C6-O6
12	E	621	NAG	O5-C5-C6-O6
12	F	621	NAG	O5-C5-C6-O6
12	F	623	NAG	O5-C5-C6-O6
12	E	621	NAG	C4-C5-C6-O6
12	F	624	NAG	O5-C5-C6-O6
12	F	621	NAG	C4-C5-C6-O6
12	E	623	NAG	O5-C5-C6-O6
12	D	623	NAG	O5-C5-C6-O6
12	F	624	NAG	C4-C5-C6-O6
12	E	624	NAG	O5-C5-C6-O6
12	D	621	NAG	O5-C5-C6-O6
12	E	624	NAG	C4-C5-C6-O6
12	D	621	NAG	C4-C5-C6-O6
12	D	624	NAG	C4-C5-C6-O6
12	D	624	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
12	F	623	NAG	C4-C5-C6-O6
12	E	623	NAG	C4-C5-C6-O6
12	D	623	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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.

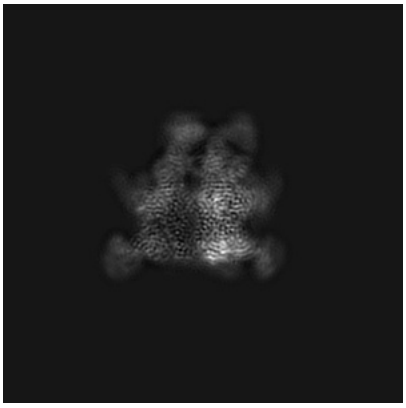
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-7516. These allow visual inspection of the internal detail of the map and identification of artifacts.

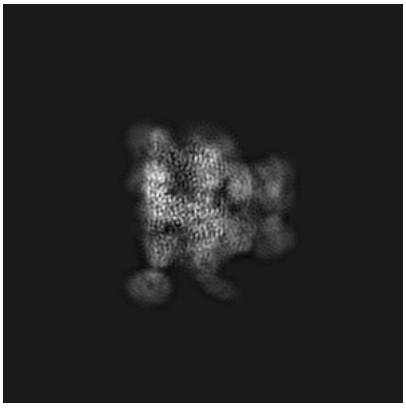
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

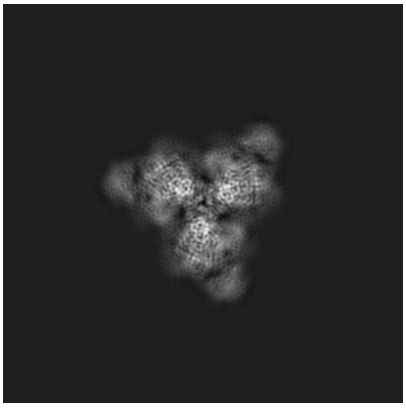
6.1.1 Primary map



X



Y

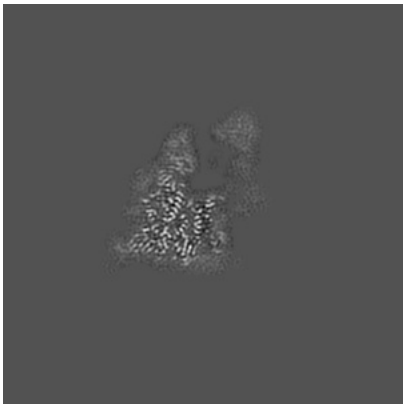


Z

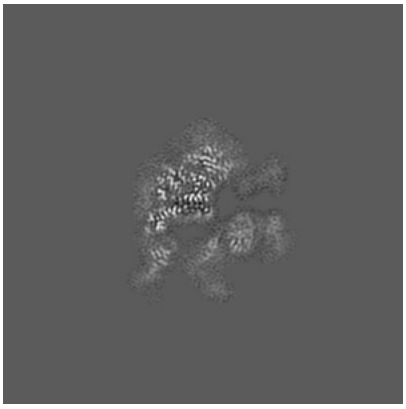
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

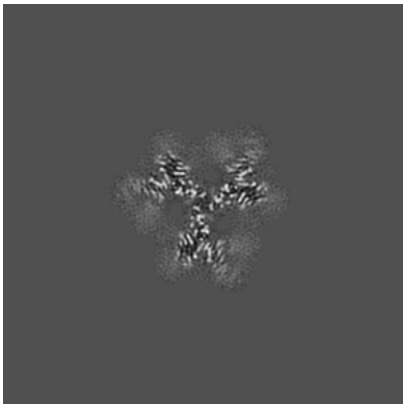
6.2.1 Primary map



X Index: 150



Y Index: 150

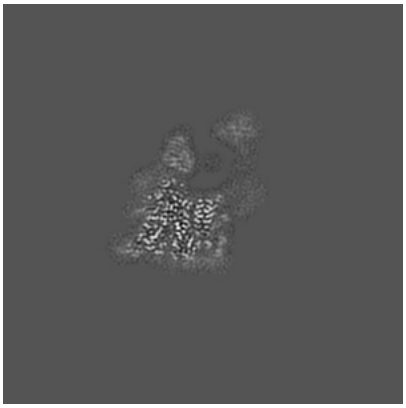


Z Index: 150

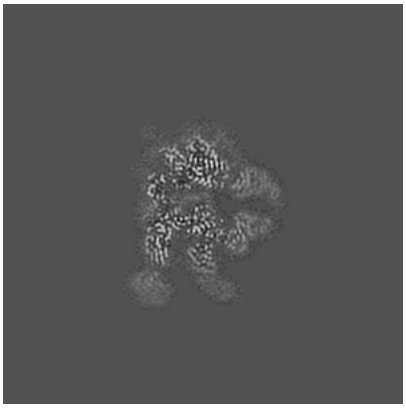
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 148



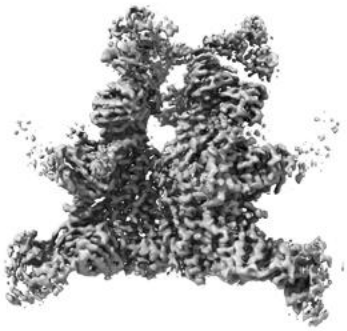
Y Index: 160

Z Index: 119

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 0.0386. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

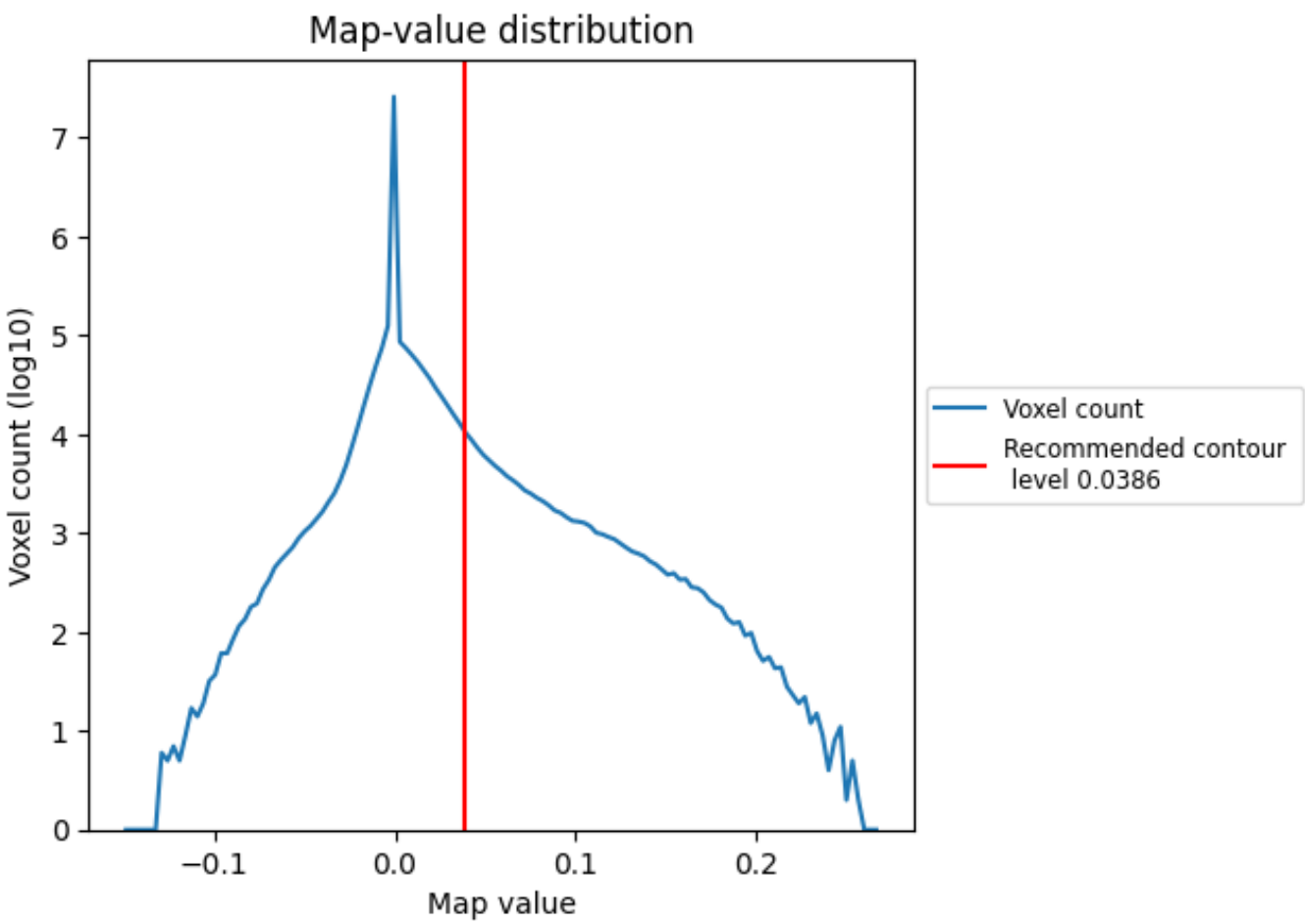
6.5 Mask visualisation (i)

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

7 Map analysis (i)

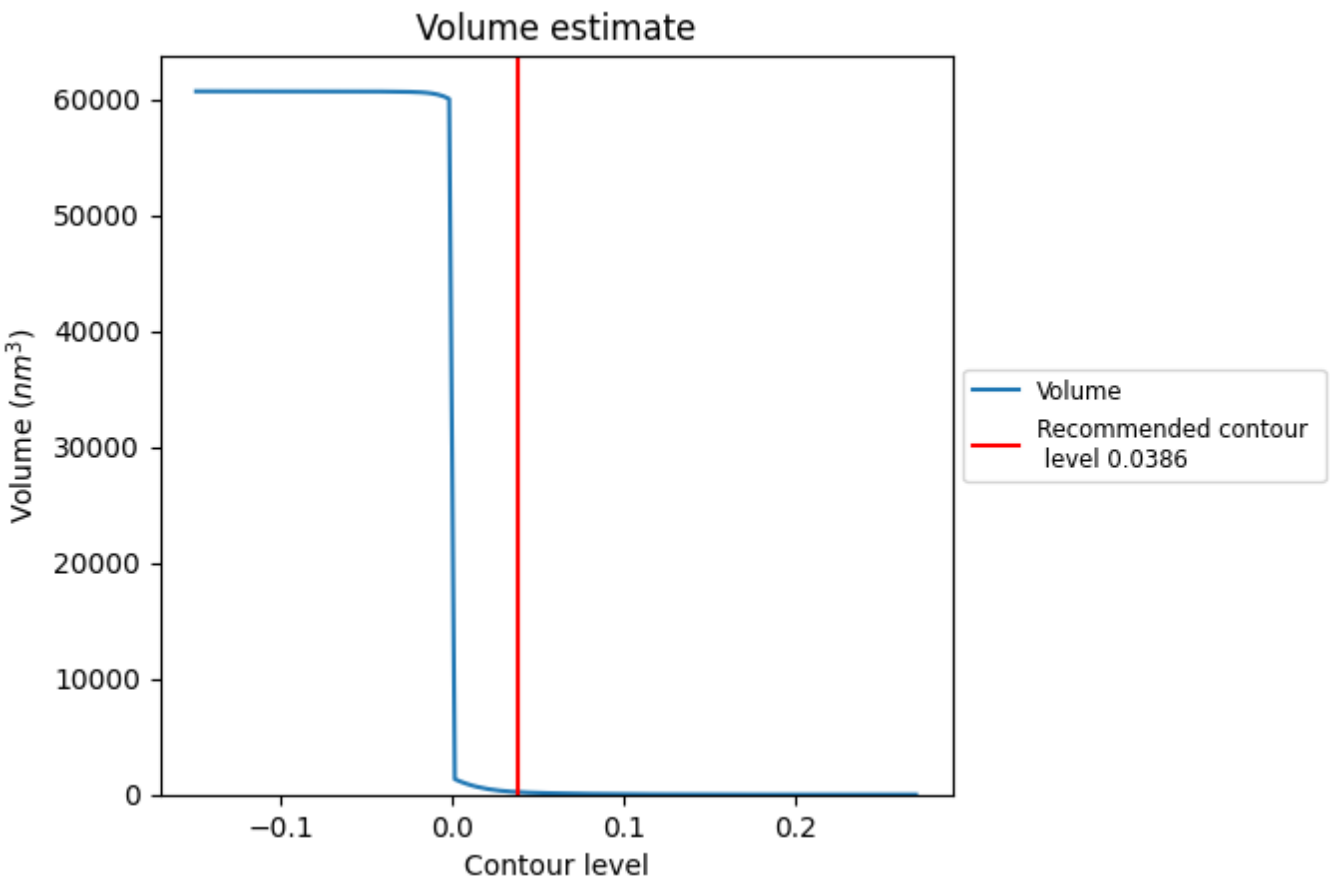
This section contains the results of statistical analysis of the map.

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.

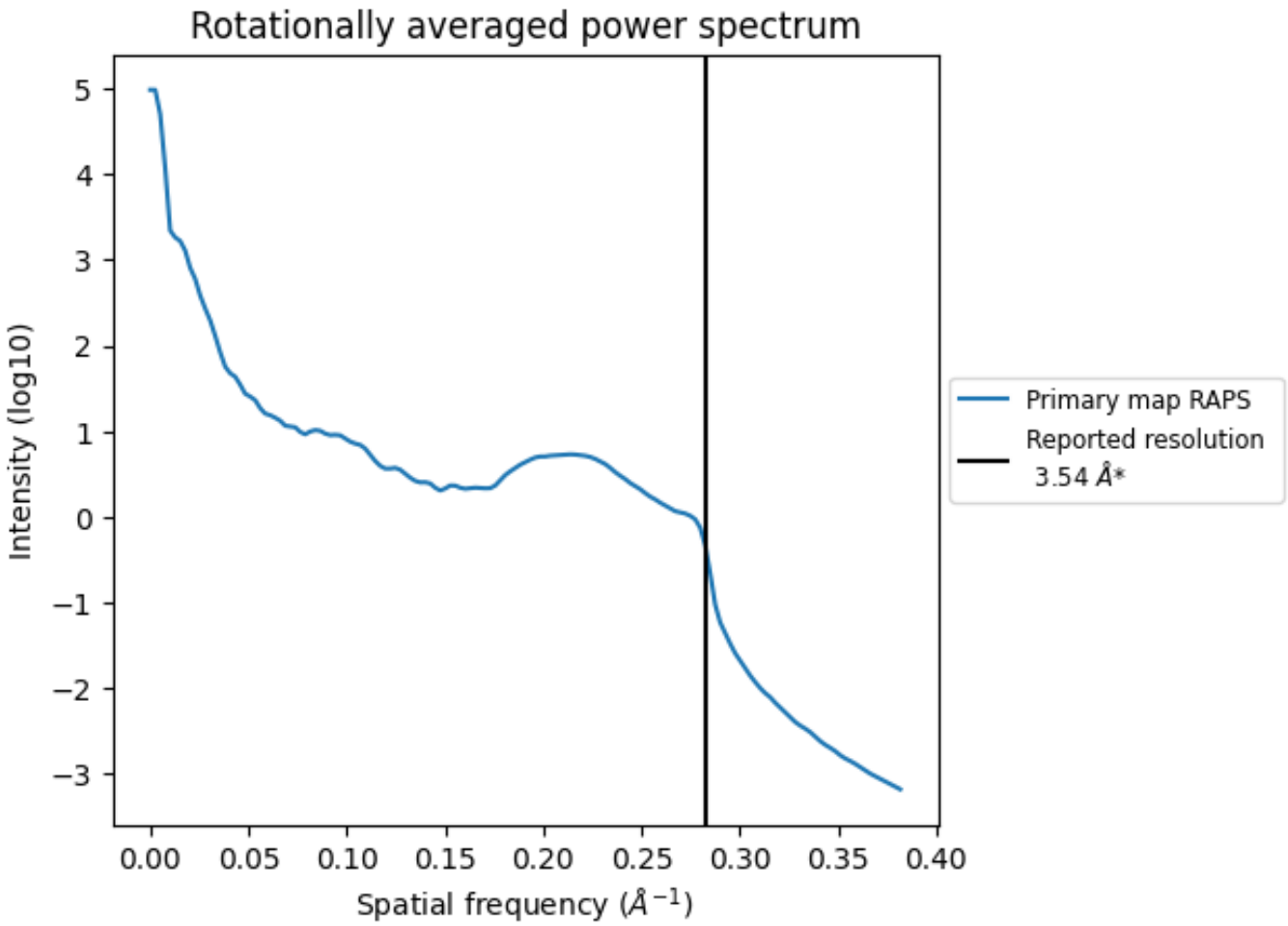
7.2 Volume estimate (i)



The volume at the recommended contour level is 210 nm^3; this corresponds to an approximate mass of 190 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)

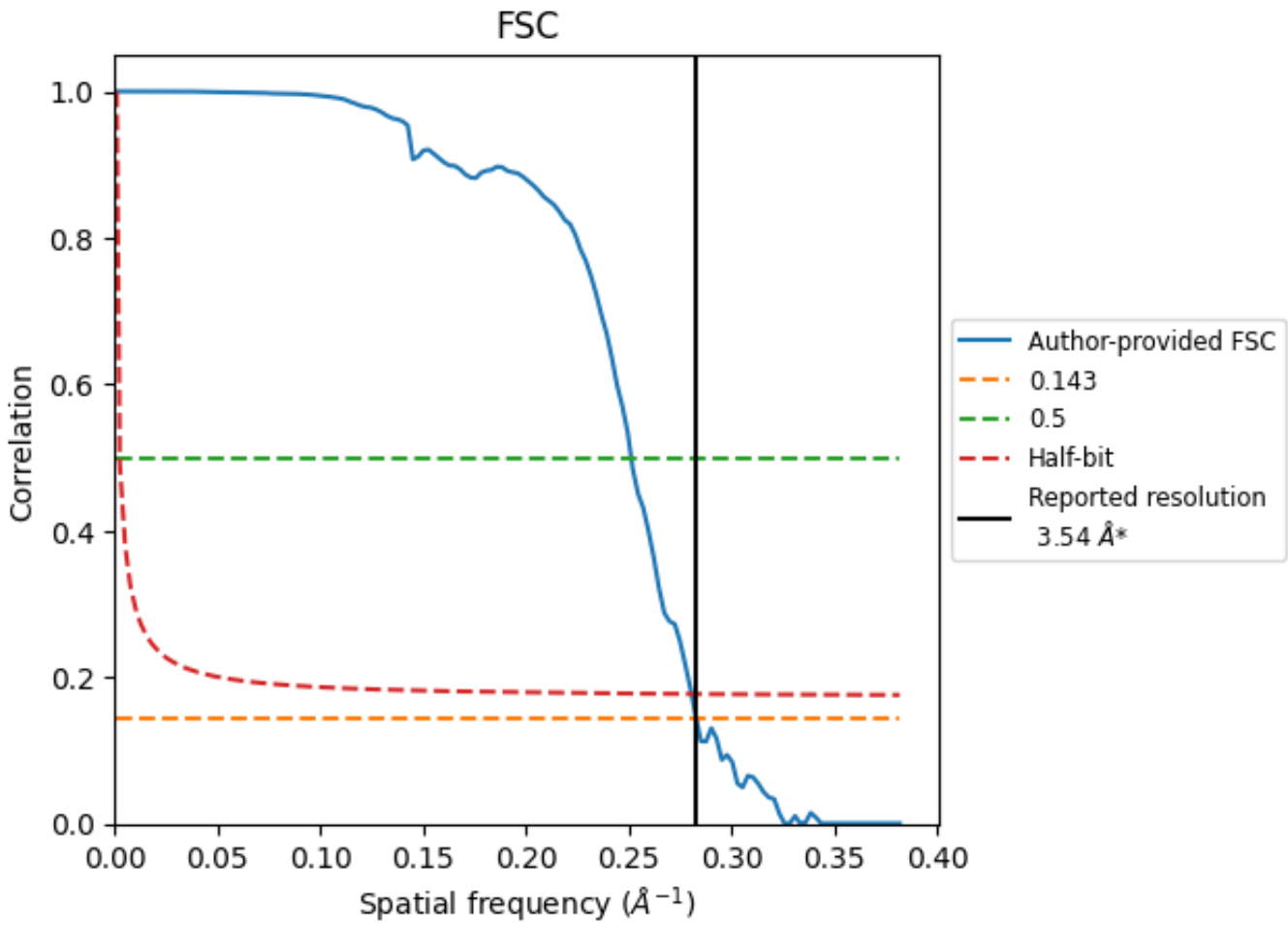


*Reported resolution corresponds to spatial frequency of 0.282 Å^{-1}

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 0.282 Å^{-1}

8.2 Resolution estimates (i)

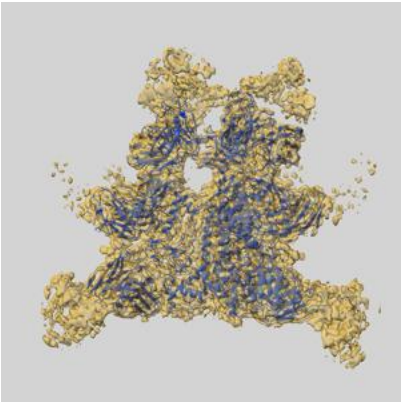
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	3.98	3.57
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

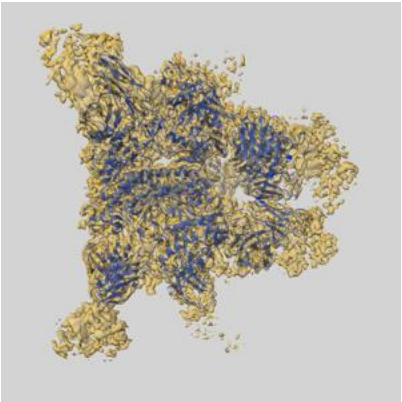
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-7516 and PDB model 6CM3. Per-residue inclusion information can be found in section 3 on page 12.

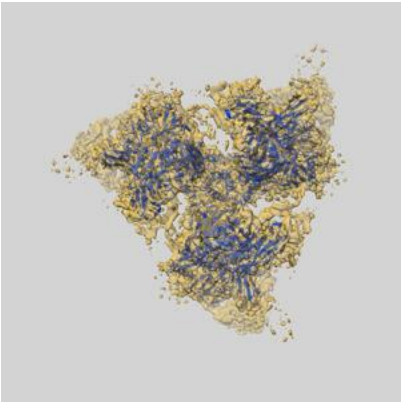
9.1 Map-model overlay (i)



X



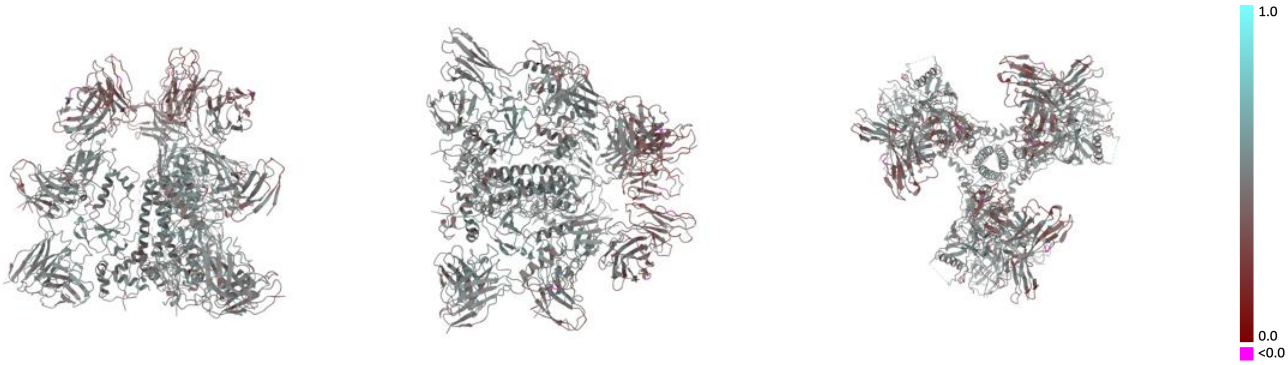
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0386 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.

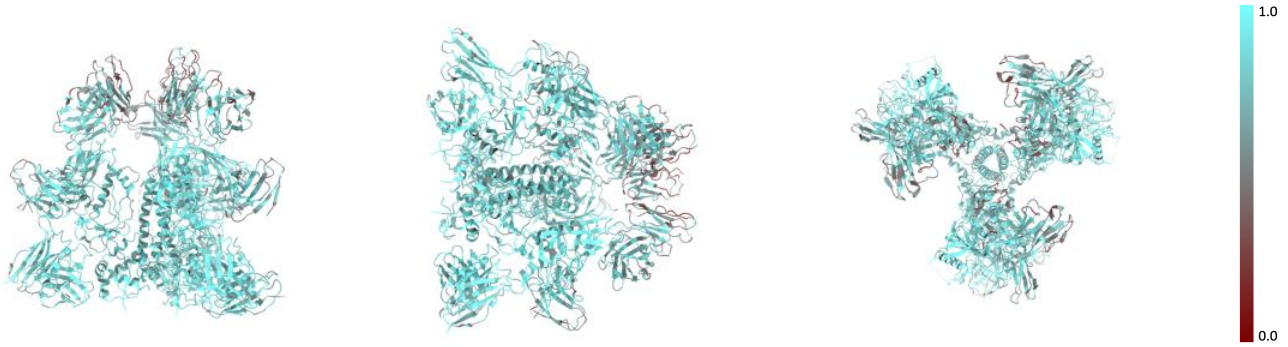
9.2 Q-score mapped to coordinate model (i)



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.

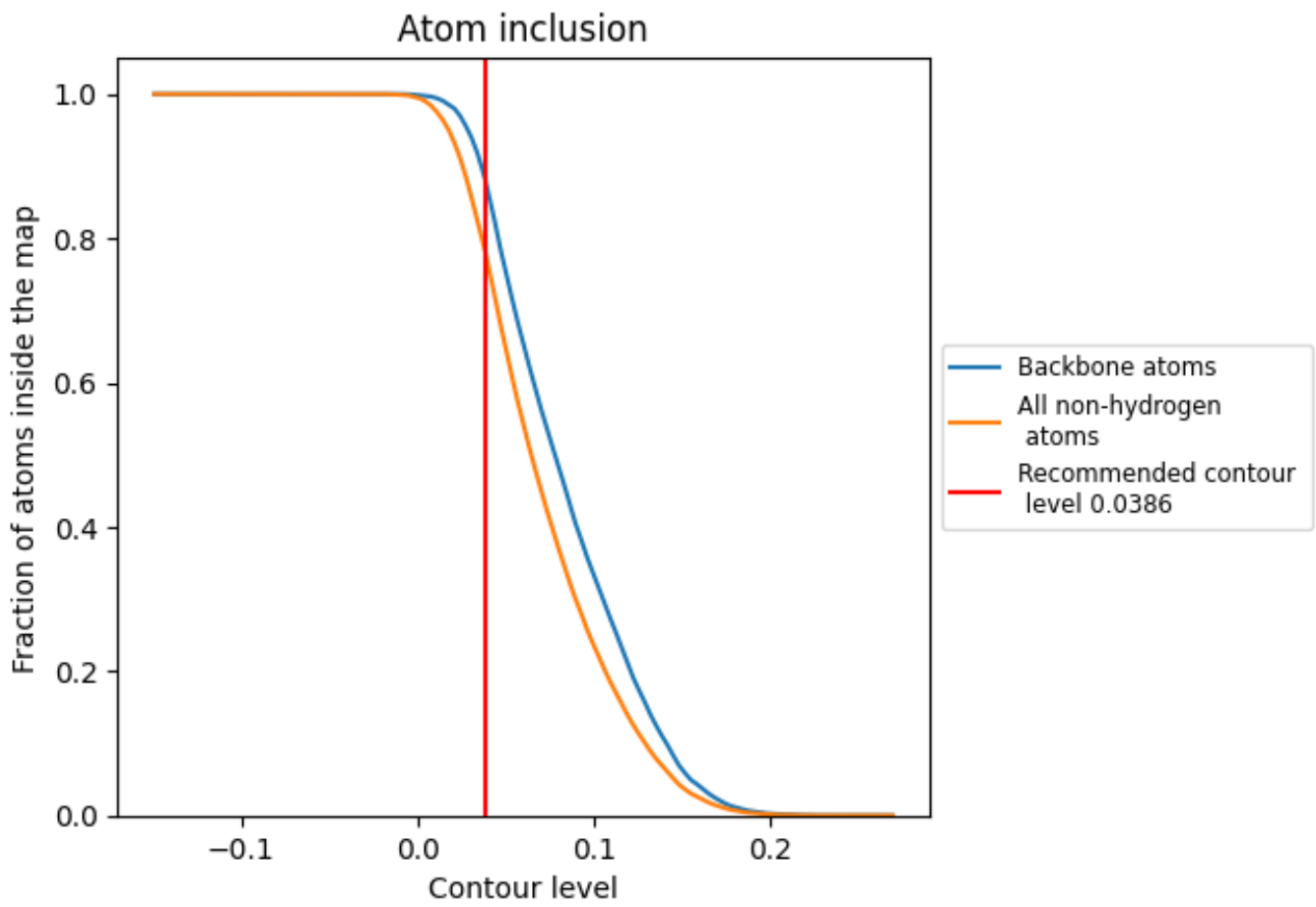
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0386).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 78% 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 (0.0386) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7822	0.4650
A	0.8464	0.4960
B	0.8544	0.5010
C	0.8419	0.4980
D	0.8366	0.4920
E	0.8355	0.4940
F	0.8383	0.4930
G	0.7102	0.4450
H	0.7037	0.4470
I	0.6997	0.4450
J	0.5972	0.3600
K	0.6846	0.4140
L	0.6035	0.3650
M	0.6815	0.4120
N	0.5947	0.3620
O	0.6774	0.4090
P	0.8423	0.4990
Q	0.8142	0.4710
R	0.8413	0.4910
S	0.8104	0.4740
T	0.8362	0.5000
U	0.8104	0.4740
V	0.7500	0.4620
W	0.7857	0.4690
X	0.7857	0.4510
Y	0.8362	0.4750
Z	0.8361	0.5080
a	0.7541	0.4640
b	0.8214	0.4640
c	0.8276	0.4690
d	0.8197	0.5170
e	0.7541	0.4520
f	0.8571	0.4720
g	0.8448	0.4710
h	0.8361	0.5180

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Chain	Atom inclusion	Q-score
i	0.7541	0.4530
j	0.8571	0.4820