Full wwPDB X-ray Structure Validation Report (i)

Nov 2, 2026 – 06:11 AM EST

PDB ID	:	9Z1F / pdb_00009z1f
Title	:	Crystal structure of NJ receptor binding domain in complex with human ACE2
Authors	:	Feng, Z.; Wilson, I.A.
Deposited on	:	2025-11-04
Resolution	:	2.50 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
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:

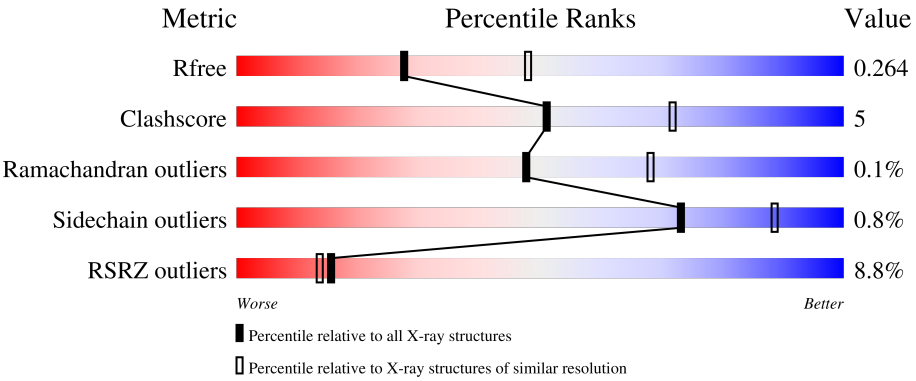
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	203	32% 71% 23% 5%
1	N	203	7% 83% 11% 5%
2	B	597	5% 88% 12%
2	E	597	5% 85% 15%
3	M	6	100%

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Mol	Chain	Length	Quality of chain
4	C	7	86% 14%
5	D	2	100%
5	F	2	100%
5	G	2	50% 50%
5	H	2	50% 50%
5	I	2	100%
5	J	2	50% 50%
5	K	2	50% 50%
6	L	3	33% 67%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 13349 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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.

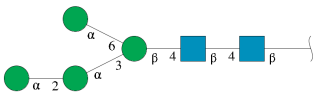
- Molecule 1 is a protein called NJ spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	N	192	Total	C	N	O	S	0	0	0
			1527	974	264	281	8			
1	A	192	Total	C	N	O	S	0	0	0
			1527	974	264	281	8			

- Molecule 2 is a protein called Angiotensin-converting enzyme 2.

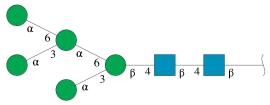
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	597	Total	C	N	O	S	0	0	0
			4870	3115	806	920	29			
2	E	596	Total	C	N	O	S	0	0	0
			4862	3111	805	917	29			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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				ZeroOcc	AltConf	Trace
3	M	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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.



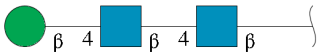
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	C	7	Total C N O 83 46 2 35	0	0	0

- 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	ZeroOcc	AltConf	Trace
5	D	2	Total C N O 28 16 2 10	0	0	0
5	F	2	Total C N O 28 16 2 10	0	0	0
5	H	2	Total C N O 28 16 2 10	0	0	0
5	G	2	Total C N O 28 16 2 10	0	0	0
5	I	2	Total C N O 28 16 2 10	0	0	0
5	J	2	Total C N O 28 16 2 10	0	0	0
5	K	2	Total C N O 28 16 2 10	0	0	0

- Molecule 6 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.

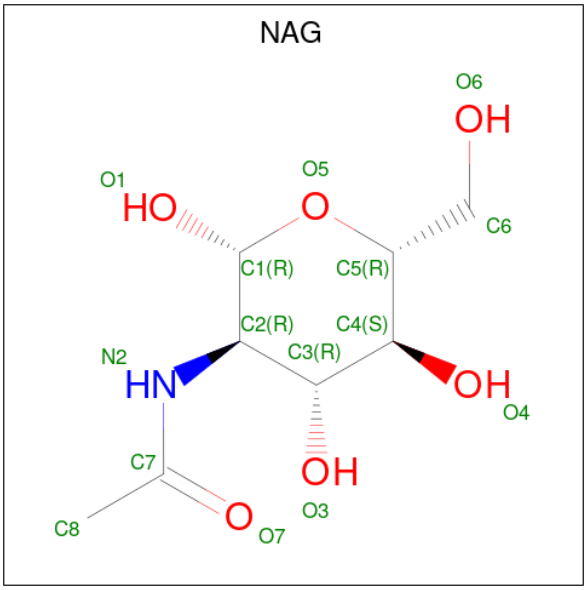


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	L	3	Total C N O 39 22 2 15	0	0	0

- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

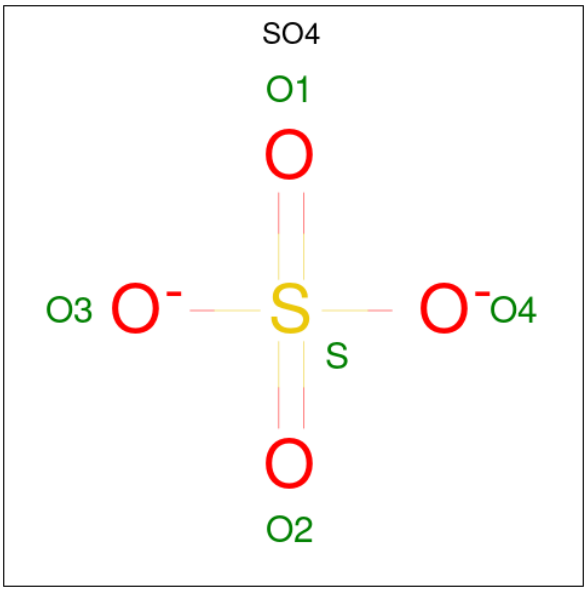
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Zn 1 1	0	0
7	E	1	Total Zn 1 1	0	0

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 9 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	E	1	Total O S 5 4 1	0	0
9	E	1	Total O S 5 4 1	0	0
9	E	1	Total O S 5 4 1	0	0
9	E	1	Total O S 5 4 1	0	0
9	E	1	Total O S 5 4 1	0	0
9	E	1	Total O S 5 4 1	0	0

- Molecule 10 is water.

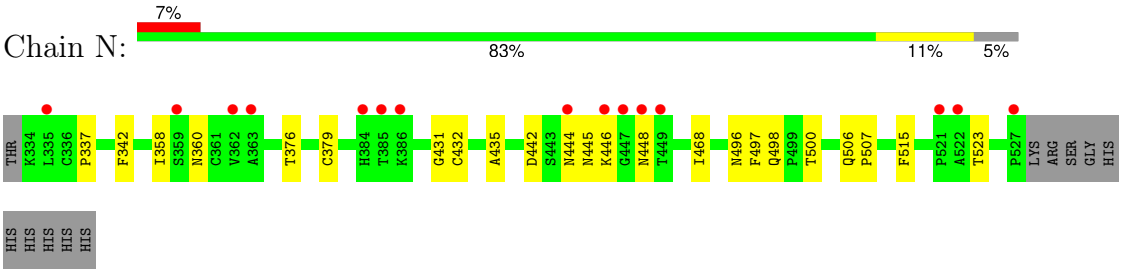
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	N	17	Total O 17 17	0	0
10	A	2	Total O 2 2	0	0
10	B	8	Total O 8 8	0	0
10	E	58	Total O 58 58	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

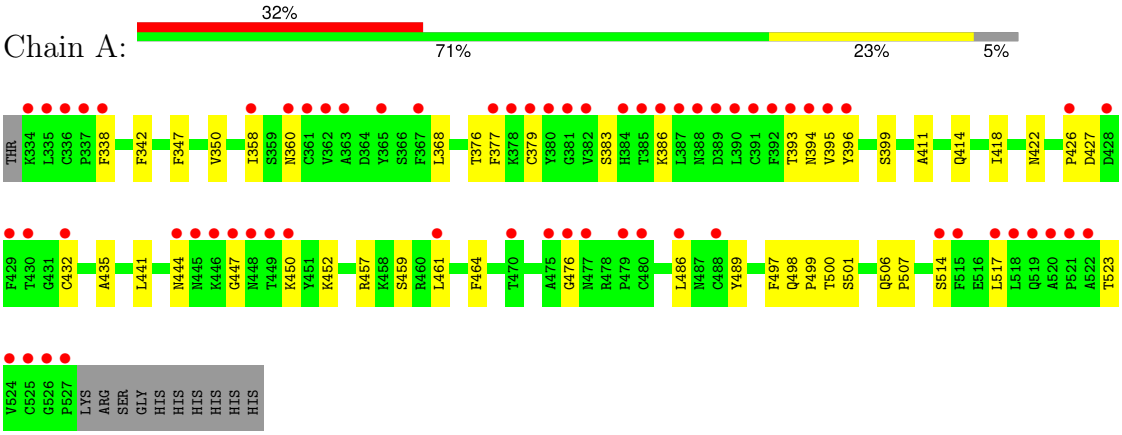
• Molecule 1: NJ spike protein S1

Chain N:



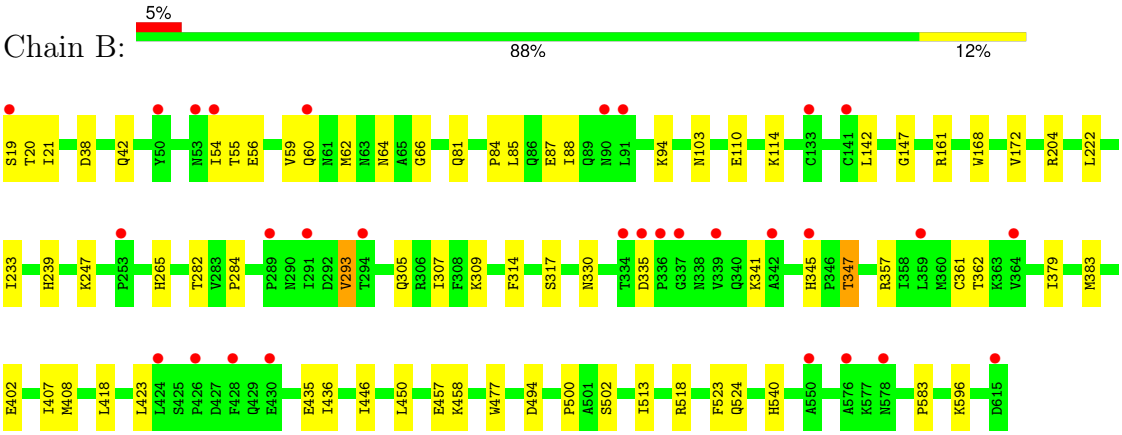
• Molecule 1: NJ spike protein S1

Chain A:



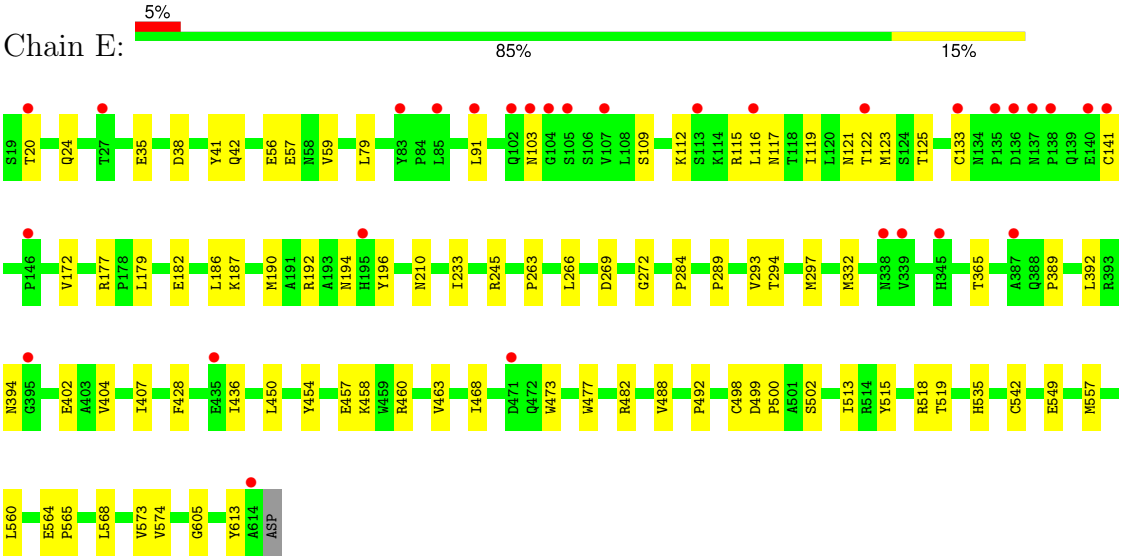
• Molecule 2: Angiotensin-converting enzyme 2

Chain B:



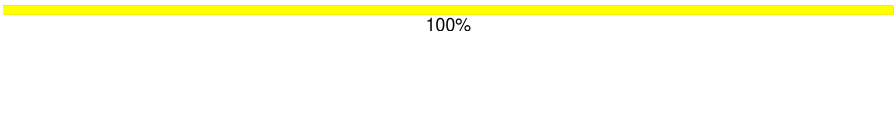
• Molecule 2: Angiotensin-converting enzyme 2

Chain E:



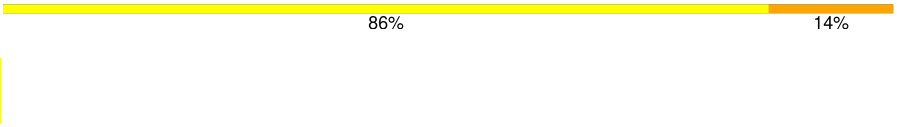
• Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:



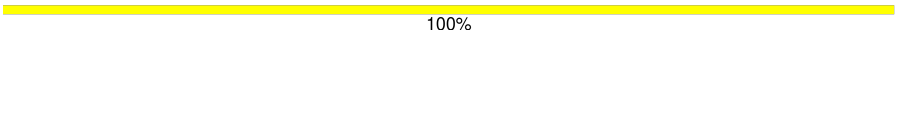
• Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:



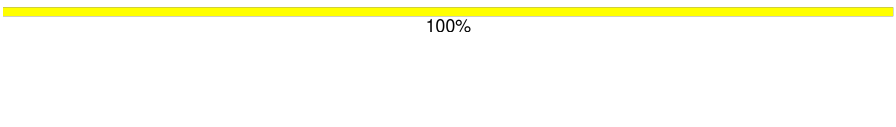
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:



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

Chain F:



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

Chain H:





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

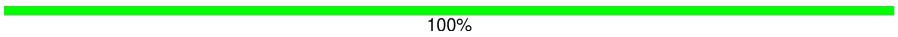
Chain G:





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

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

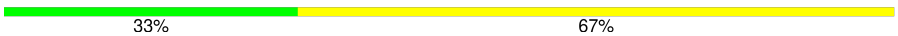
Chain K:





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

Chain L:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	81.57Å 123.02Å 110.36Å 90.00° 91.05° 90.00°	Depositor
Resolution (Å)	36.73 – 2.50 36.73 – 2.50	Depositor EDS
% Data completeness (in resolution range)	82.2 (36.73-2.50) 82.1 (36.73-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.219 , 0.264 0.219 , 0.264	Depositor DCC
R_{free} test set	1992 reflections (2.65%)	wwPDB-VP
Wilson B-factor (Å^2)	37.2	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 34.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.024 for h,-k,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	13349	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SO4, BMA, NAG, MAN

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	0.10	0/1568	0.31	0/2128
1	N	0.09	0/1568	0.28	0/2128
2	B	0.09	0/5007	0.26	0/6803
2	E	0.11	0/4999	0.27	0/6792
All	All	0.10	0/13142	0.27	0/17851

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1527	0	1469	30	0
1	N	1527	0	1469	12	0
2	B	4870	0	4638	43	0
2	E	4862	0	4634	56	0
3	M	72	0	61	0	0
4	C	83	0	70	1	0
5	D	28	0	25	1	0
5	F	28	0	25	1	0
5	G	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	28	0	25	0	0
5	I	28	0	25	0	0
5	J	28	0	25	0	0
5	K	28	0	25	0	0
6	L	39	0	34	0	0
7	B	1	0	0	0	0
7	E	1	0	0	0	0
8	B	28	0	26	0	0
8	E	28	0	26	0	0
9	E	30	0	0	0	0
10	A	2	0	0	0	0
10	B	8	0	0	2	0
10	E	58	0	0	3	0
10	N	17	0	0	0	0
All	All	13349	0	12602	135	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 (135) 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)
2:B:293:VAL:HG11	2:B:423:LEU:HB3	1.70	0.72
2:E:560:LEU:HD13	2:E:564:GLU:HG3	1.71	0.70
2:B:88:ILE:O	2:B:94:LYS:NZ	2.26	0.69
2:E:245:ARG:NH2	2:E:605:GLY:O	2.24	0.68
2:B:345:HIS:HD2	2:B:347:THR:HG23	1.61	0.66
1:A:500:THR:HG1	2:E:41:TYR:HH	1.43	0.66
2:E:57:GLU:N	2:E:57:GLU:OE2	2.31	0.62
1:N:442:ASP:HA	1:N:448:ASN:HB2	1.80	0.62
2:E:192:ARG:NH2	10:E:803:HOH:O	2.32	0.61
2:B:330:ASN:HB3	2:B:357:ARG:HH21	1.65	0.60
2:E:389:PRO:HG2	2:E:392:LEU:HD12	1.83	0.59
2:E:177:ARG:HB2	2:E:498:CYS:HB2	1.83	0.59
2:E:121:ASN:O	2:E:122:THR:HG22	2.03	0.58
1:N:498:GLN:NE2	2:B:42:GLN:OE1	2.36	0.58
1:A:500:THR:OG1	2:E:41:TYR:OH	2.16	0.58
2:E:515:TYR:HA	2:E:518:ARG:HG2	1.85	0.57
1:A:393:THR:O	1:A:523:THR:OG1	2.20	0.56
1:N:342:PHE:HB2	4:C:1:NAG:H82	1.87	0.56
2:E:116:LEU:HD22	2:E:186:LEU:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:294:THR:HG23	2:E:365:THR:HA	1.88	0.56
2:E:402:GLU:HB3	2:E:518:ARG:HD3	1.88	0.55
2:B:345:HIS:CD2	2:B:347:THR:HG23	2.40	0.55
1:A:486:LEU:HD21	2:E:79:LEU:HD22	1.90	0.53
2:E:115:ARG:C	2:E:117:ASN:H	2.15	0.53
2:E:190:MET:O	2:E:194:ASN:ND2	2.31	0.53
1:A:342:PHE:HB2	5:D:1:NAG:H82	1.91	0.53
1:A:393:THR:HG23	1:A:517:LEU:HA	1.91	0.53
2:E:482:ARG:HH11	2:E:488:VAL:HG23	1.75	0.52
1:A:358:ILE:HB	1:A:395:VAL:HB	1.92	0.52
1:A:506:GLN:HG3	1:A:507:PRO:HD2	1.92	0.52
2:B:110:GLU:HG3	2:B:114:LYS:HD2	1.92	0.52
2:E:122:THR:HA	2:E:125:THR:HB	1.91	0.52
2:E:233:ILE:HD13	2:E:450:LEU:HD13	1.92	0.51
2:B:407:ILE:HG13	2:B:408:MET:HE2	1.90	0.51
1:A:396:TYR:HB2	1:A:514:SER:HB2	1.93	0.51
2:E:269:ASP:OD1	2:E:272:GLY:N	2.40	0.51
1:N:376:THR:HB	1:N:435:ALA:HB3	1.93	0.50
2:E:573:VAL:HG13	2:E:574:VAL:HG13	1.93	0.50
2:E:20:THR:O	2:E:24:GLN:HG3	2.12	0.49
2:E:549:GLU:H	2:E:549:GLU:CD	2.20	0.49
2:B:239:HIS:CE1	2:B:596:LYS:HG2	2.47	0.49
1:A:457:ARG:HH12	1:A:461:LEU:HD12	1.78	0.49
2:B:54:ILE:HG22	2:B:341:LYS:O	2.13	0.48
2:B:477:TRP:CE3	2:B:500:PRO:HG3	2.48	0.48
2:B:59:VAL:O	2:B:60:GLN:HB2	2.12	0.48
1:A:444:ASN:O	1:A:499:PRO:HD3	2.14	0.48
2:B:379:ILE:O	2:B:383:MET:HG2	2.13	0.48
1:A:383:SER:HB3	1:A:386:LYS:HG2	1.96	0.48
2:E:518:ARG:HG3	2:E:519:THR:N	2.29	0.48
1:A:393:THR:OG1	1:A:394:ASN:N	2.46	0.47
2:B:21:ILE:HD12	2:B:87:GLU:HG3	1.95	0.47
2:B:307:ILE:HB	10:B:801:HOH:O	2.15	0.47
2:B:457:GLU:HG2	2:B:513:ILE:HB	1.97	0.47
2:E:121:ASN:C	2:E:123:MET:H	2.23	0.46
2:E:454:TYR:O	2:E:458:LYS:HB2	2.16	0.46
2:B:81:GLN:NE2	2:B:103:ASN:OD1	2.48	0.46
2:E:457:GLU:HG2	2:E:513:ILE:HB	1.98	0.46
2:E:565:PRO:HG2	2:E:568:LEU:HB3	1.97	0.46
1:A:418:ILE:HA	1:A:422:ASN:HD22	1.80	0.46
2:B:142:LEU:HB3	2:B:147:GLY:HA3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:446:ILE:HD13	2:B:523:PHE:HZ	1.81	0.46
2:B:204:ARG:HG2	2:B:222:LEU:HD23	1.97	0.46
1:A:447:GLY:HA3	1:A:497:PHE:O	2.16	0.46
2:B:284:PRO:HG2	2:B:436:ILE:HG22	1.98	0.46
1:A:457:ARG:HD3	1:A:459:SER:O	2.16	0.46
1:A:476:GLY:HA2	2:E:24:GLN:NE2	2.31	0.45
2:B:435:GLU:HG3	2:B:540:HIS:NE2	2.31	0.45
2:B:247:LYS:HB2	2:B:282:THR:HG22	1.98	0.45
1:A:379:CYS:HA	1:A:432:CYS:HA	1.99	0.45
2:E:116:LEU:HD11	2:E:187:LYS:HG2	1.97	0.45
2:E:263:PRO:HG2	2:E:266:LEU:HD12	1.97	0.45
2:E:119:ILE:HG22	2:E:179:LEU:HD22	1.97	0.45
1:A:450:LYS:O	1:A:452:LYS:NZ	2.46	0.45
2:E:133:CYS:HA	2:E:141:CYS:HA	1.99	0.45
2:B:19:SER:OG	2:B:20:THR:N	2.50	0.45
2:E:460:ARG:HA	2:E:463:VAL:HB	1.99	0.45
2:B:335:ASP:HB3	2:B:361:CYS:HB3	1.98	0.45
2:E:557:MET:HB3	2:E:557:MET:HE3	1.87	0.44
1:A:368:LEU:HB3	1:A:377:PHE:CZ	2.51	0.44
2:E:109:SER:HB3	2:E:112:LYS:HB2	1.99	0.44
2:E:57:GLU:H	2:E:57:GLU:CD	2.26	0.44
2:B:362:THR:HG21	10:B:801:HOH:O	2.18	0.44
2:E:56:GLU:O	2:E:59:VAL:HG12	2.17	0.44
1:A:350:VAL:HG22	1:A:422:ASN:HB3	2.00	0.44
1:A:498:GLN:NE2	2:E:42:GLN:OE1	2.41	0.44
2:B:85:LEU:HD22	2:B:94:LYS:HG2	1.99	0.44
1:N:506:GLN:HG3	1:N:507:PRO:HD2	1.99	0.43
2:B:233:ILE:HD13	2:B:450:LEU:HD13	2.00	0.43
1:A:347:PHE:CE2	1:A:399:SER:HB2	2.53	0.43
2:B:21:ILE:HD13	2:B:84:PRO:HD2	2.00	0.43
2:E:38:ASP:O	2:E:42:GLN:HG2	2.18	0.43
1:A:376:THR:HB	1:A:435:ALA:HB3	2.01	0.43
2:B:402:GLU:HB3	2:B:518:ARG:HD2	2.00	0.43
2:E:289:PRO:HB2	2:E:428:PHE:HE1	1.83	0.43
2:B:62:MET:O	2:B:66:GLY:N	2.45	0.43
1:N:497:PHE:CD2	1:N:507:PRO:HB3	2.54	0.43
2:E:192:ARG:HA	2:E:196:TYR:O	2.19	0.42
1:N:444:ASN:O	1:N:446:LYS:N	2.52	0.42
1:N:379:CYS:HA	1:N:432:CYS:HA	2.00	0.42
1:A:411:ALA:HB3	1:A:414:GLN:HG3	2.02	0.42
1:A:360:ASN:HA	1:A:523:THR:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:499:ASP:O	2:E:502:SER:OG	2.32	0.42
1:N:431:GLY:HA2	1:N:515:PHE:CD2	2.54	0.42
2:B:524:GLN:HG2	2:B:583:PRO:HG2	2.00	0.42
2:E:182:GLU:HG2	2:E:186:LEU:HD23	2.02	0.42
2:E:468:ILE:HG22	2:E:473:TRP:HD1	1.84	0.42
2:E:535:HIS:CD2	2:E:542:CYS:HB2	2.55	0.42
2:B:55:THR:O	2:B:59:VAL:HG12	2.19	0.42
2:E:177:ARG:HH22	2:E:473:TRP:HB2	1.84	0.42
2:B:38:ASP:O	2:B:42:GLN:HG2	2.20	0.42
1:A:427:ASP:OD1	1:A:427:ASP:N	2.51	0.41
1:N:360:ASN:H	1:N:523:THR:HB	1.85	0.41
2:E:103:ASN:ND2	10:E:805:HOH:O	2.48	0.41
2:B:60:GLN:O	2:B:64:ASN:ND2	2.53	0.41
2:B:494:ASP:OD1	2:B:494:ASP:N	2.45	0.41
2:E:293:VAL:O	2:E:297:MET:HG3	2.21	0.41
2:E:332:MET:HE2	2:E:332:MET:HB3	1.74	0.41
2:E:492:PRO:HG3	2:E:613:TYR:CD1	2.56	0.41
1:N:337:PRO:HD2	1:N:358:ILE:HG23	2.02	0.41
1:N:446:LYS:HE3	1:N:496:ASN:HD21	1.86	0.41
2:B:314:PHE:O	2:B:317:SER:OG	2.35	0.41
2:B:458:LYS:HE2	2:B:458:LYS:HB2	1.94	0.41
2:E:91:LEU:H	2:E:91:LEU:HD23	1.85	0.41
2:B:168:TRP:CD1	2:B:502:SER:HB2	2.56	0.41
2:E:35:GLU:OE1	10:E:801:HOH:O	2.22	0.41
2:E:477:TRP:CD2	2:E:500:PRO:HG3	2.55	0.41
1:A:426:PRO:HD3	1:A:464:PHE:CE1	2.56	0.41
1:A:338:PHE:CE1	1:A:358:ILE:HG13	2.56	0.40
2:E:284:PRO:HG2	2:E:436:ILE:HG22	2.02	0.40
2:E:404:VAL:HA	2:E:407:ILE:HD12	2.02	0.40
1:A:441:LEU:HD13	5:F:2:NAG:H83	2.03	0.40
2:B:56:GLU:OE1	2:B:59:VAL:HG13	2.21	0.40
2:B:161:ARG:NE	2:B:265:HIS:O	2.51	0.40
2:B:305:GLN:O	2:B:309:LYS:HG2	2.21	0.40
2:B:62:MET:HE3	2:B:62:MET:HB3	1.78	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 X-ray entries followed by that with respect to entries of similar resolution.

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	190/203 (94%)	175 (92%)	15 (8%)	0	100 100
1	N	190/203 (94%)	183 (96%)	6 (3%)	1 (0%)	24 43
2	B	595/597 (100%)	586 (98%)	9 (2%)	0	100 100
2	E	594/597 (100%)	582 (98%)	12 (2%)	0	100 100
All	All	1569/1600 (98%)	1526 (97%)	42 (3%)	1 (0%)	48 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	445	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	170/180 (94%)	168 (99%)	2 (1%)	63 83
1	N	170/180 (94%)	168 (99%)	2 (1%)	63 83
2	B	527/527 (100%)	523 (99%)	4 (1%)	73 88
2	E	526/527 (100%)	523 (99%)	3 (1%)	78 91
All	All	1393/1414 (98%)	1382 (99%)	11 (1%)	73 88

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	468	ILE
1	N	500	THR
1	A	489	TYR
1	A	501	SER
2	B	172	VAL
2	B	293	VAL
2	B	347	THR
2	B	418	LEU
2	E	172	VAL
2	E	210	ASN
2	E	394	ASN

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

Mol	Chain	Res	Type
1	A	474	GLN
1	A	487	ASN
2	B	86	GLN
2	B	117	ASN
2	B	239	HIS
2	B	345	HIS
2	B	417	HIS
2	B	508	ASN
2	B	599	ASN
2	E	24	GLN
2	E	60	GLN
2	E	117	ASN
2	E	221	GLN
2	E	531	GLN
2	E	540	HIS

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)

30 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	C	1	1,4	14,14,15	0.72	0	17,19,21	1.04	1 (5%)
4	NAG	C	2	4	14,14,15	0.73	0	17,19,21	0.85	1 (5%)
4	BMA	C	3	4	11,11,12	0.83	0	15,15,17	2.85	6 (40%)
4	MAN	C	4	4	11,11,12	0.81	1 (9%)	15,15,17	1.04	1 (6%)
4	MAN	C	5	4	11,11,12	0.77	0	15,15,17	0.95	1 (6%)
4	MAN	C	6	4	11,11,12	0.71	0	15,15,17	1.09	1 (6%)
4	MAN	C	7	4	11,11,12	0.69	0	15,15,17	1.30	1 (6%)
5	NAG	D	1	1,5	14,14,15	0.71	0	17,19,21	0.91	0
5	NAG	D	2	5	14,14,15	0.78	0	17,19,21	2.31	2 (11%)
5	NAG	F	1	1,5	14,14,15	0.85	0	17,19,21	1.28	1 (5%)
5	NAG	F	2	5	14,14,15	0.72	0	17,19,21	0.79	0
5	NAG	G	1	2,5	14,14,15	0.70	0	17,19,21	1.01	1 (5%)
5	NAG	G	2	5	14,14,15	0.72	0	17,19,21	0.92	0
5	NAG	H	1	2,5	14,14,15	0.70	0	17,19,21	0.81	0
5	NAG	H	2	5	14,14,15	0.70	0	17,19,21	0.89	1 (5%)
5	NAG	I	1	2,5	14,14,15	0.72	0	17,19,21	0.80	0
5	NAG	I	2	5	14,14,15	0.74	0	17,19,21	0.86	0
5	NAG	J	1	2,5	14,14,15	0.72	0	17,19,21	0.93	1 (5%)
5	NAG	J	2	5	14,14,15	0.72	0	17,19,21	0.80	0
5	NAG	K	1	2,5	14,14,15	0.70	0	17,19,21	0.96	0
5	NAG	K	2	5	14,14,15	0.70	0	17,19,21	0.90	1 (5%)
6	NAG	L	1	6,2	14,14,15	0.74	0	17,19,21	0.97	0
6	NAG	L	2	6	14,14,15	0.68	0	17,19,21	1.27	2 (11%)
6	BMA	L	3	6	11,11,12	0.88	0	15,15,17	2.58	6 (40%)
3	NAG	M	1	1,3	14,14,15	0.72	0	17,19,21	0.89	1 (5%)
3	NAG	M	2	3	14,14,15	0.75	0	17,19,21	1.00	2 (11%)
3	BMA	M	3	3	11,11,12	0.87	0	15,15,17	2.24	6 (40%)
3	MAN	M	4	3	11,11,12	0.64	0	15,15,17	1.36	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	MAN	M	5	3	11,11,12	0.79	1 (9%)	15,15,17	0.90	1 (6%)
3	MAN	M	6	3	11,11,12	0.66	0	15,15,17	1.35	1 (6%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	5	MAN	O5-C1	-2.01	1.40	1.43
4	C	4	MAN	O5-C1	-2.00	1.40	1.43

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	3	BMA	C1-O5-C5	8.64	123.77	112.19
5	D	2	NAG	C2-N2-C7	8.19	133.88	122.90
6	L	3	BMA	C1-O5-C5	7.25	121.91	112.19
3	M	3	BMA	C1-O5-C5	5.59	119.67	112.19
3	M	6	MAN	C1-O5-C5	4.36	118.02	112.19
3	M	4	MAN	C1-O5-C5	4.35	118.01	112.19
6	L	3	BMA	C3-C4-C5	3.83	117.17	110.23
4	C	7	MAN	C1-O5-C5	3.66	117.10	112.19
4	C	3	BMA	C3-C4-C5	3.58	116.73	110.23
6	L	2	NAG	C2-N2-C7	3.39	127.44	122.90
3	M	3	BMA	C3-C4-C5	3.37	116.34	110.23
6	L	3	BMA	C2-C3-C4	3.34	116.73	110.86
5	F	1	NAG	O5-C1-C2	-3.07	106.55	111.29
4	C	3	BMA	O5-C5-C4	2.79	117.61	110.83
4	C	6	MAN	C1-O5-C5	2.78	115.92	112.19
3	M	3	BMA	C2-C3-C4	2.67	115.56	110.86
5	D	2	NAG	C8-C7-N2	2.67	120.54	116.12
3	M	3	BMA	O4-C4-C3	-2.64	104.15	110.38
4	C	3	BMA	O4-C4-C3	-2.57	104.31	110.38
6	L	2	NAG	O5-C1-C2	-2.54	107.36	111.29
4	C	3	BMA	C2-C3-C4	2.53	115.31	110.86
4	C	1	NAG	C1-O5-C5	2.50	115.54	112.19
3	M	1	NAG	C1-O5-C5	2.39	115.38	112.19
4	C	5	MAN	C1-O5-C5	2.35	115.34	112.19
3	M	2	NAG	O5-C1-C2	-2.35	107.65	111.29
3	M	3	BMA	O5-C5-C4	2.31	116.45	110.83
3	M	2	NAG	O4-C4-C3	-2.29	104.99	110.38
6	L	3	BMA	O5-C5-C4	2.24	116.28	110.83
4	C	4	MAN	C1-O5-C5	2.23	115.18	112.19
6	L	3	BMA	O4-C4-C3	-2.15	105.31	110.38
3	M	3	BMA	O3-C3-C2	-2.11	105.74	110.05
5	G	1	NAG	C1-O5-C5	2.11	115.01	112.19
6	L	3	BMA	O3-C3-C2	-2.11	105.75	110.05
5	J	1	NAG	C1-O5-C5	2.10	114.99	112.19
3	M	5	MAN	C1-O5-C5	2.09	114.98	112.19
4	C	2	NAG	O5-C1-C2	-2.08	108.07	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	K	2	NAG	O5-C1-C2	-2.07	108.09	111.29
5	H	2	NAG	O5-C1-C2	-2.06	108.11	111.29
4	C	3	BMA	O3-C3-C4	2.02	115.14	110.38

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	5	MAN	O5-C5-C6-O6
3	M	2	NAG	O5-C5-C6-O6
4	C	5	MAN	C4-C5-C6-O6
4	C	4	MAN	O5-C5-C6-O6
3	M	6	MAN	O5-C5-C6-O6
3	M	6	MAN	C4-C5-C6-O6
3	M	2	NAG	C4-C5-C6-O6
5	D	2	NAG	C8-C7-N2-C2
5	D	2	NAG	O7-C7-N2-C2
5	H	2	NAG	C8-C7-N2-C2
5	H	2	NAG	O7-C7-N2-C2
5	G	2	NAG	C8-C7-N2-C2
5	G	2	NAG	O7-C7-N2-C2
5	K	1	NAG	C8-C7-N2-C2
5	K	1	NAG	O7-C7-N2-C2
5	K	2	NAG	C8-C7-N2-C2
5	K	2	NAG	O7-C7-N2-C2
5	D	1	NAG	O5-C5-C6-O6
5	F	2	NAG	O5-C5-C6-O6
4	C	7	MAN	O5-C5-C6-O6
4	C	6	MAN	O5-C5-C6-O6
6	L	3	BMA	C4-C5-C6-O6
6	L	2	NAG	C1-C2-N2-C7
4	C	4	MAN	C4-C5-C6-O6
6	L	2	NAG	C3-C2-N2-C7
5	D	2	NAG	C1-C2-N2-C7
5	D	1	NAG	C4-C5-C6-O6
5	D	2	NAG	C3-C2-N2-C7
3	M	3	BMA	C4-C5-C6-O6

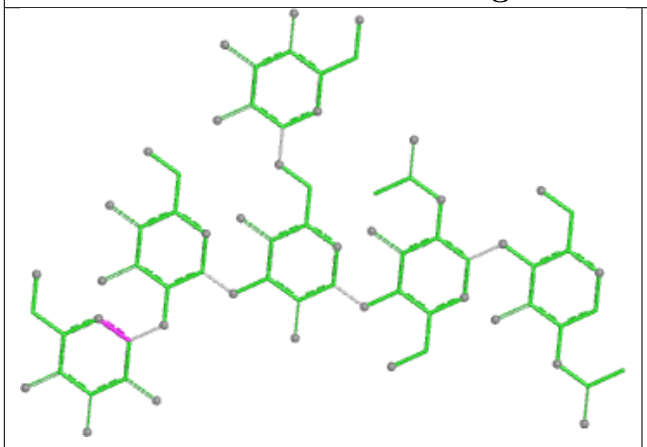
There are no ring outliers.

3 monomers are involved in 3 short contacts:

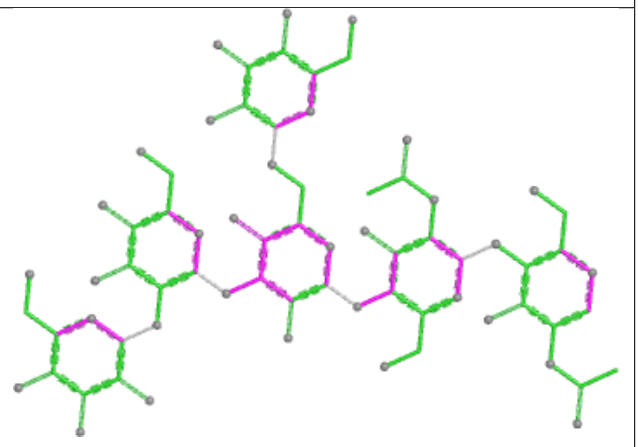
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	2	NAG	1	0
5	D	1	NAG	1	0
4	C	1	NAG	1	0

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

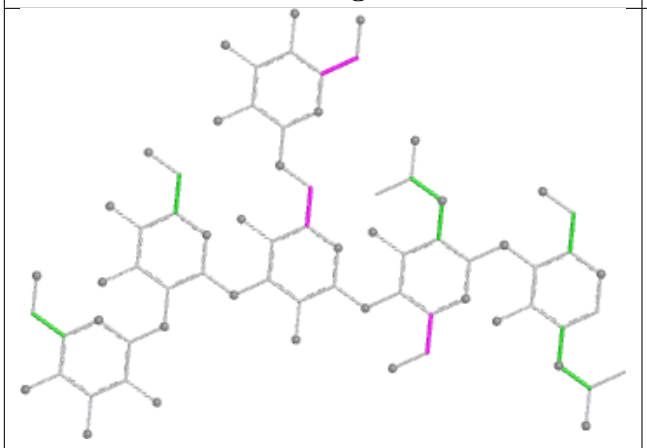
Oligosaccharide Chain M



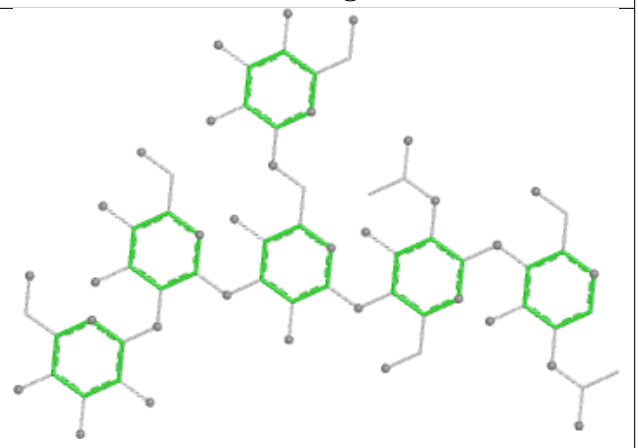
Bond lengths



Bond angles

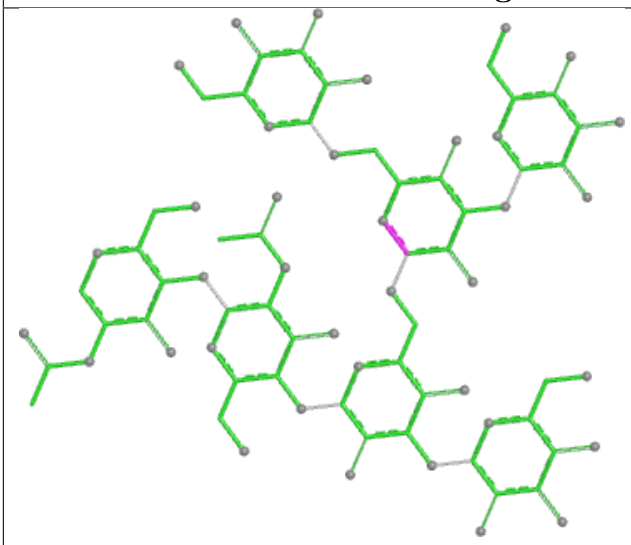


Torsions

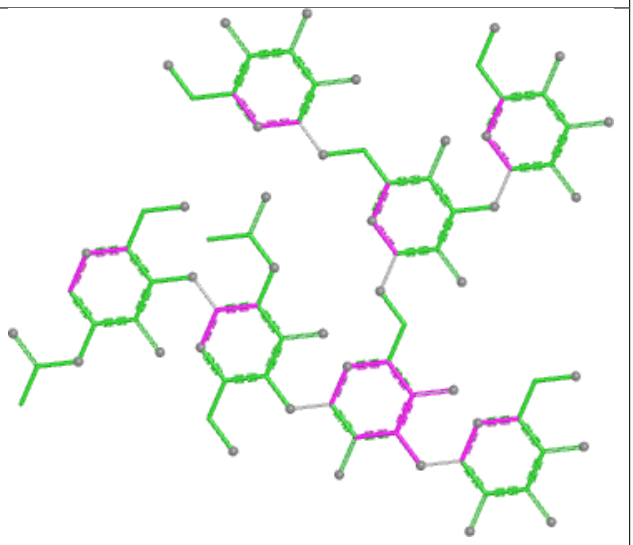


Rings

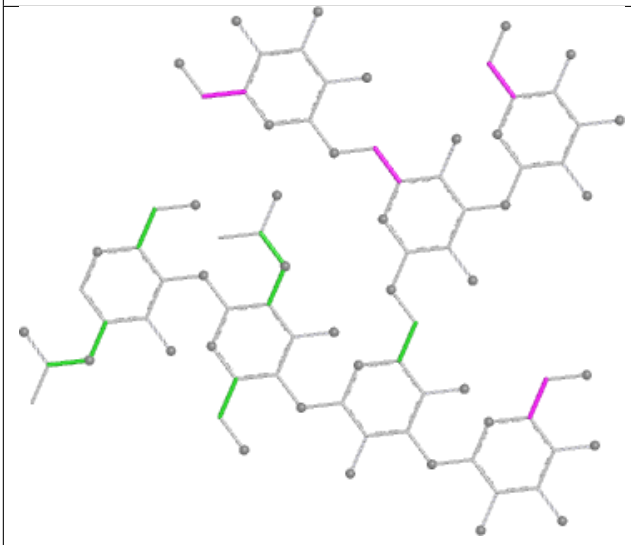
Oligosaccharide Chain C



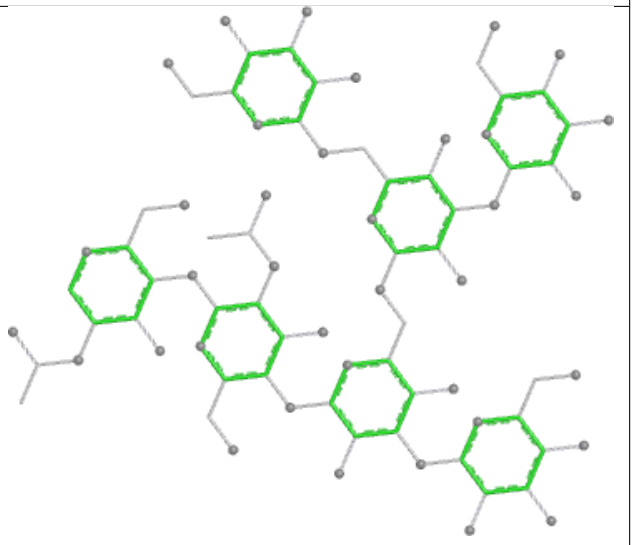
Bond lengths



Bond angles

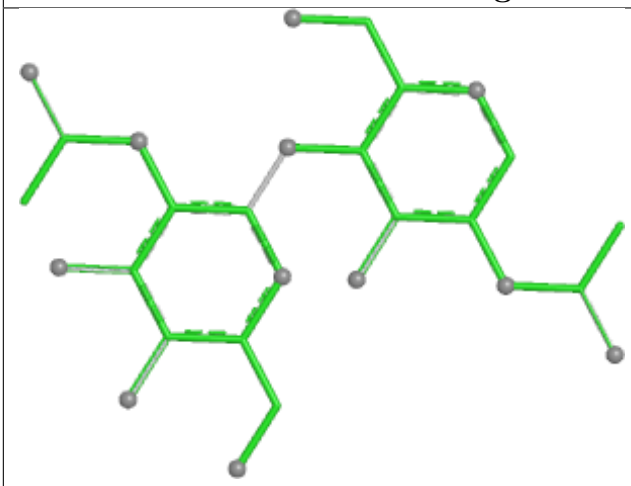


Torsions

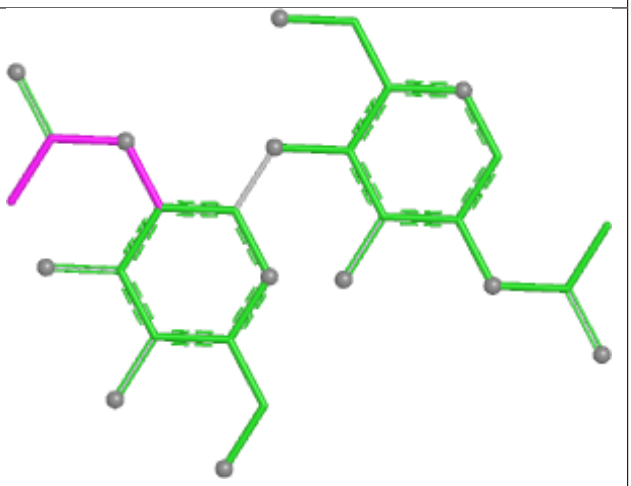


Rings

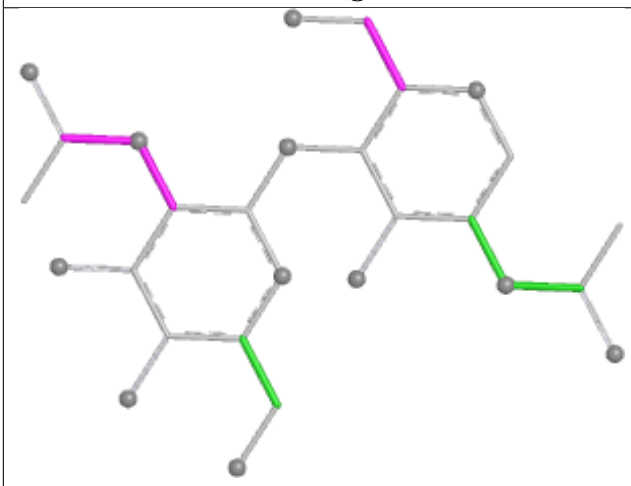
Oligosaccharide Chain D



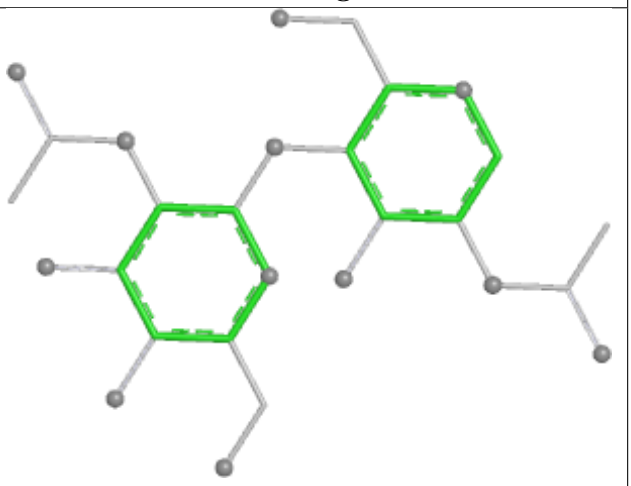
Bond lengths



Bond angles

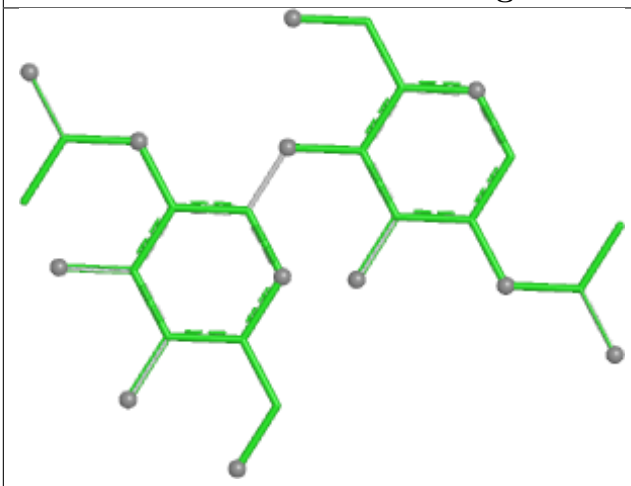


Torsions

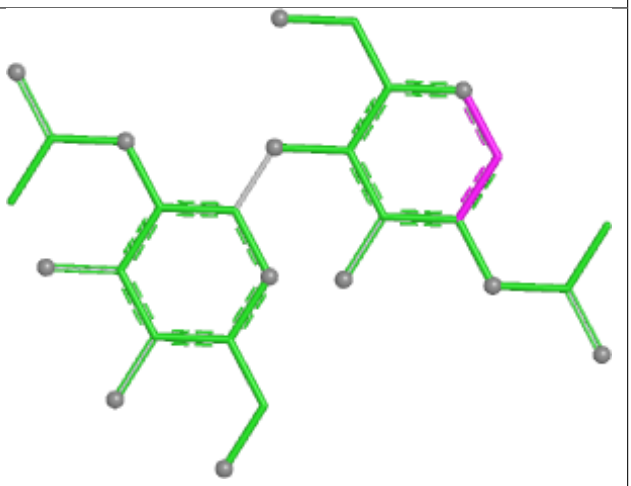


Rings

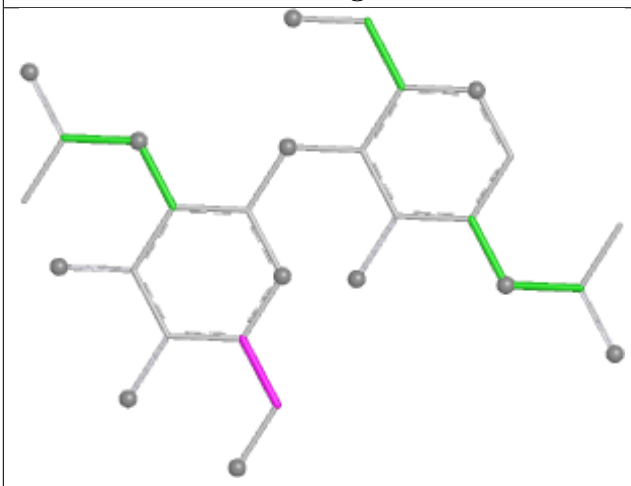
Oligosaccharide Chain F



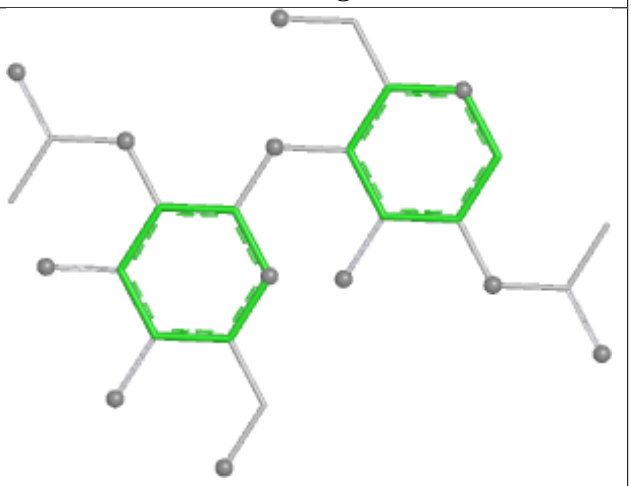
Bond lengths



Bond angles

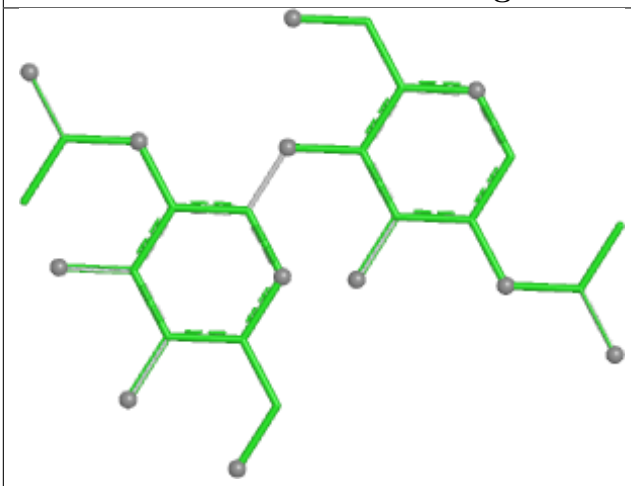


Torsions

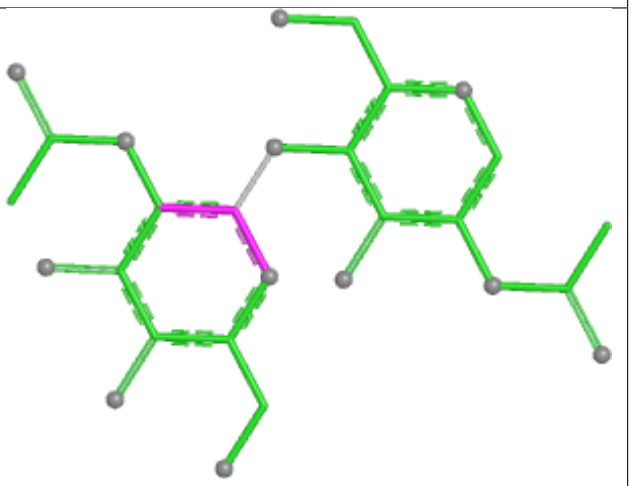


Rings

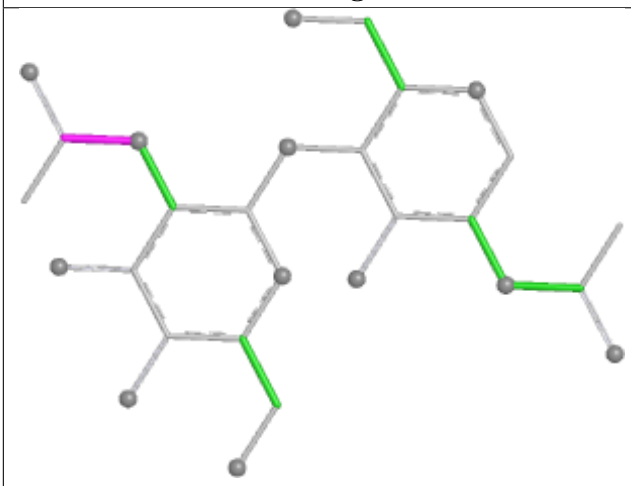
Oligosaccharide Chain H



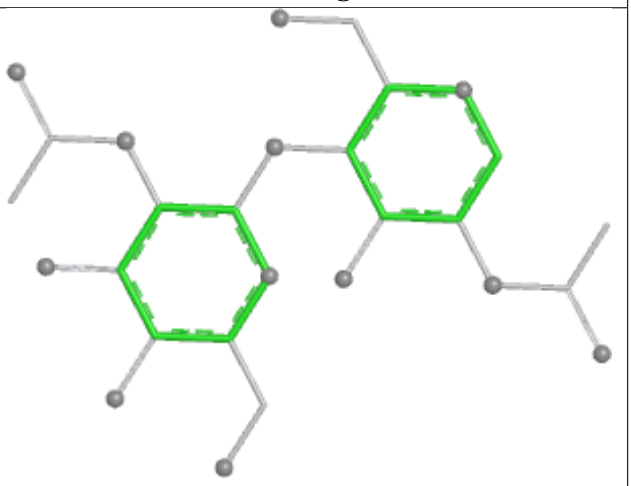
Bond lengths



Bond angles

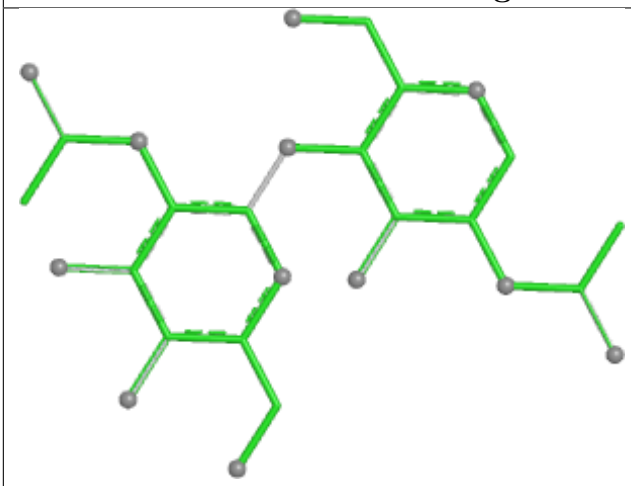


Torsions

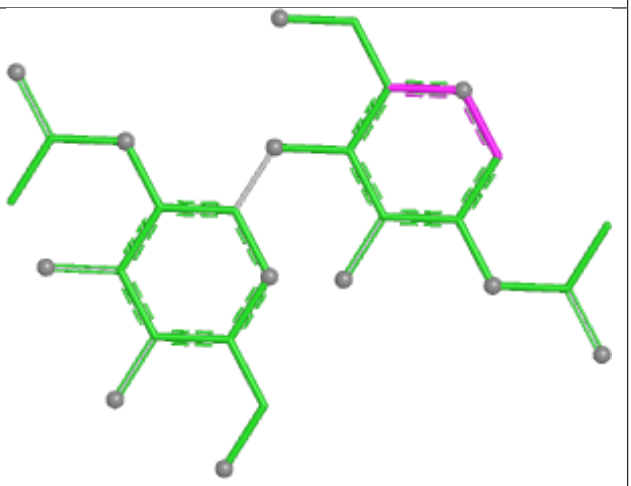


Rings

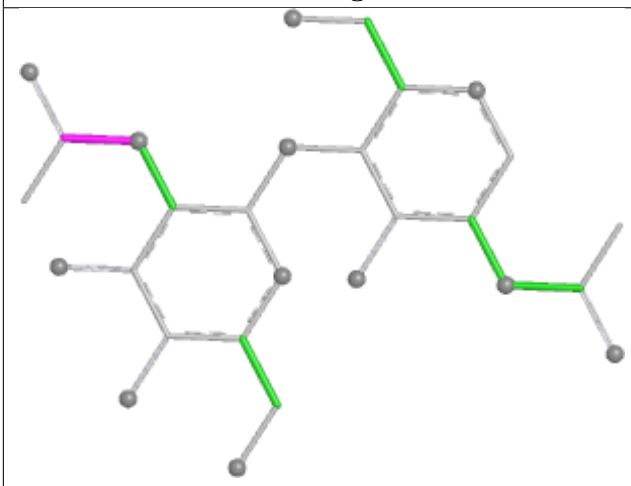
Oligosaccharide Chain G



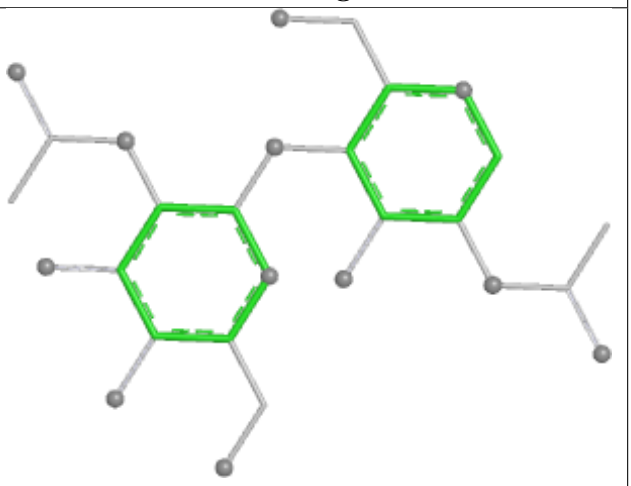
Bond lengths



Bond angles

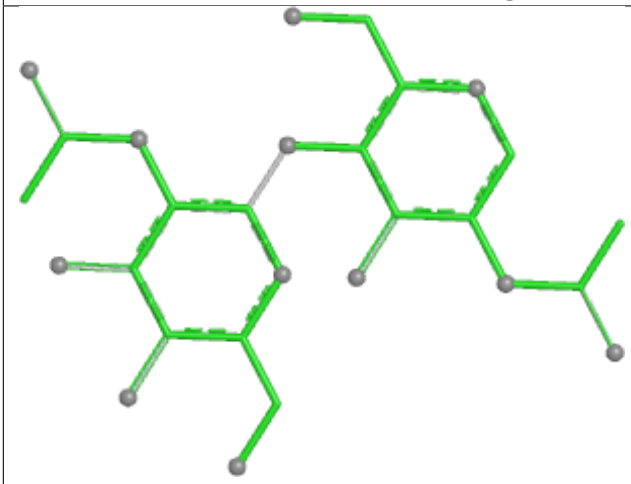


Torsions

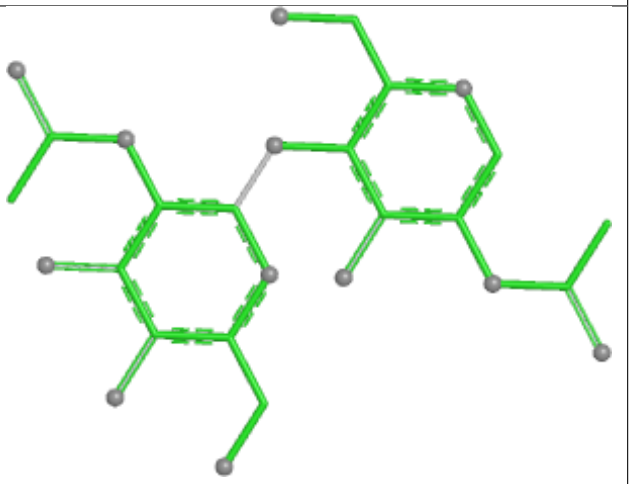


Rings

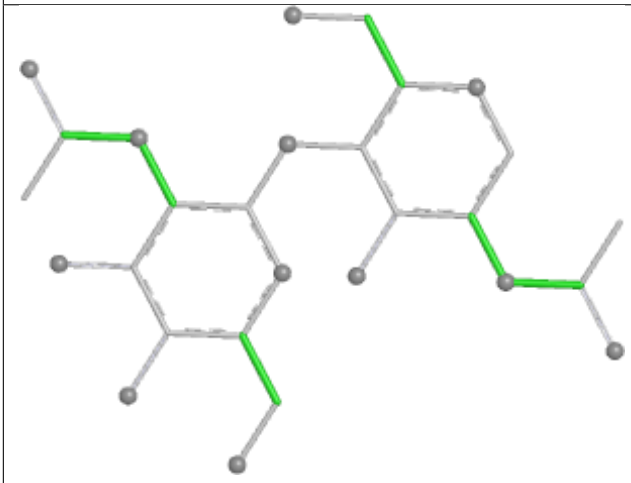
Oligosaccharide Chain I



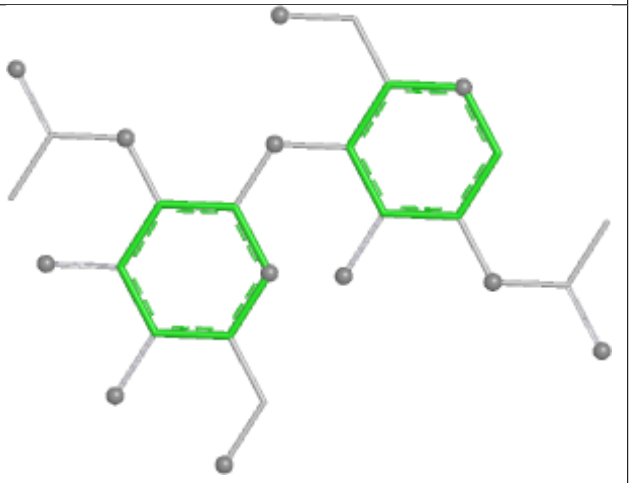
Bond lengths



Bond angles

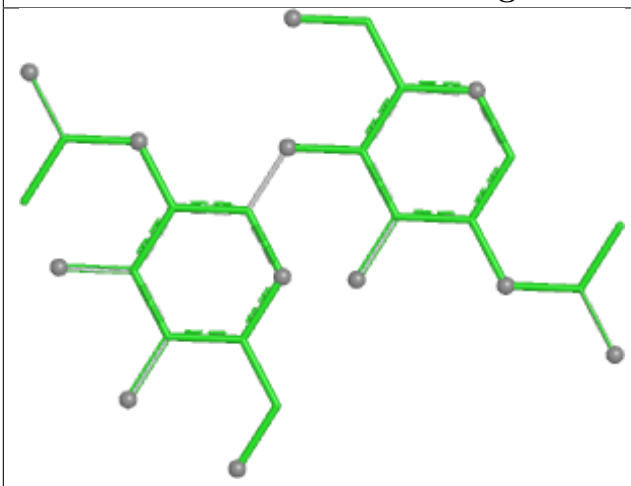


Torsions

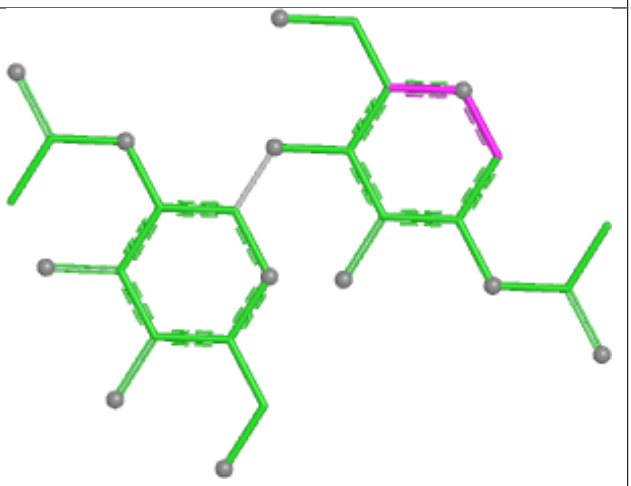


Rings

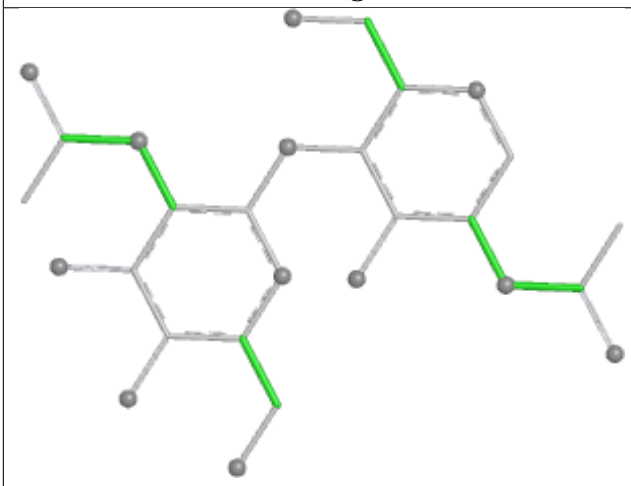
Oligosaccharide Chain J



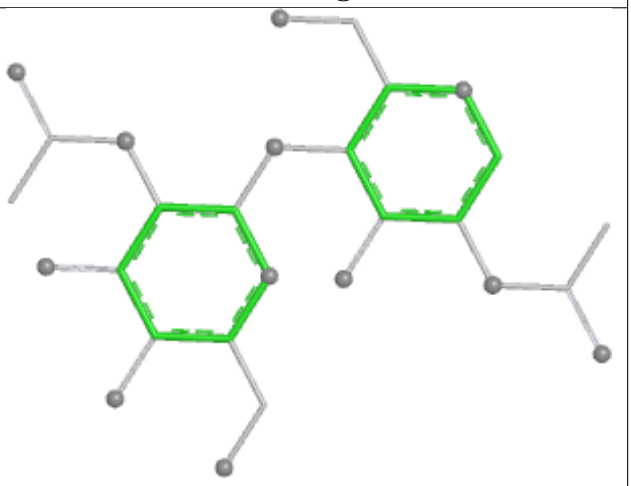
Bond lengths



Bond angles

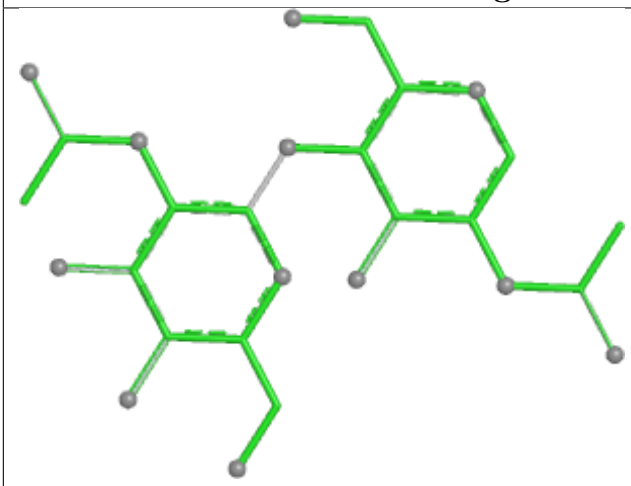


Torsions

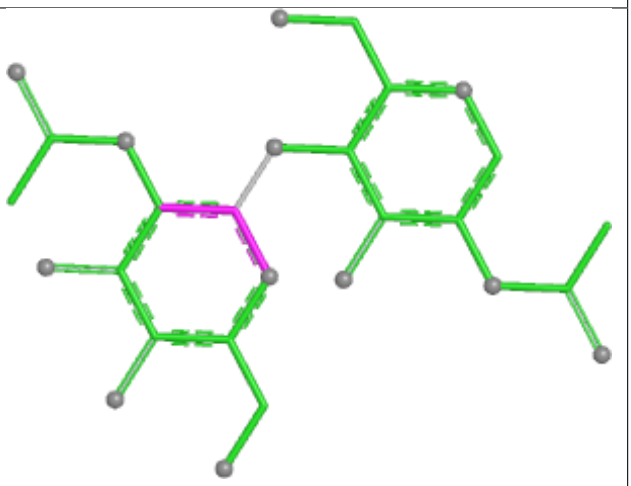


Rings

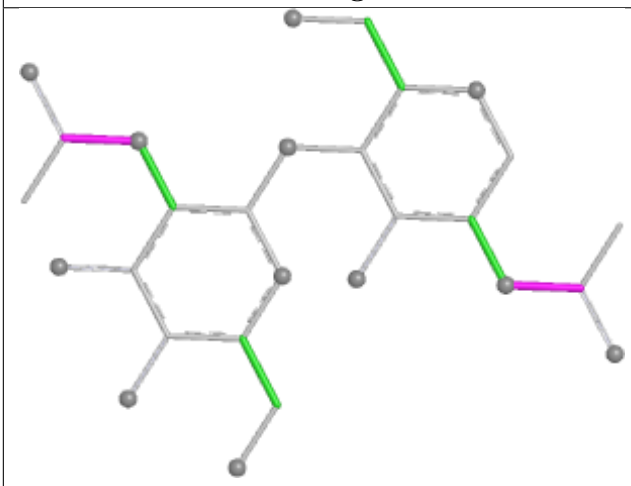
Oligosaccharide Chain K



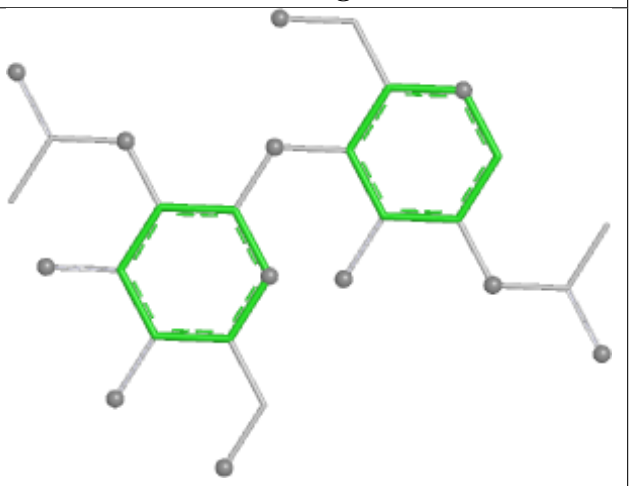
Bond lengths



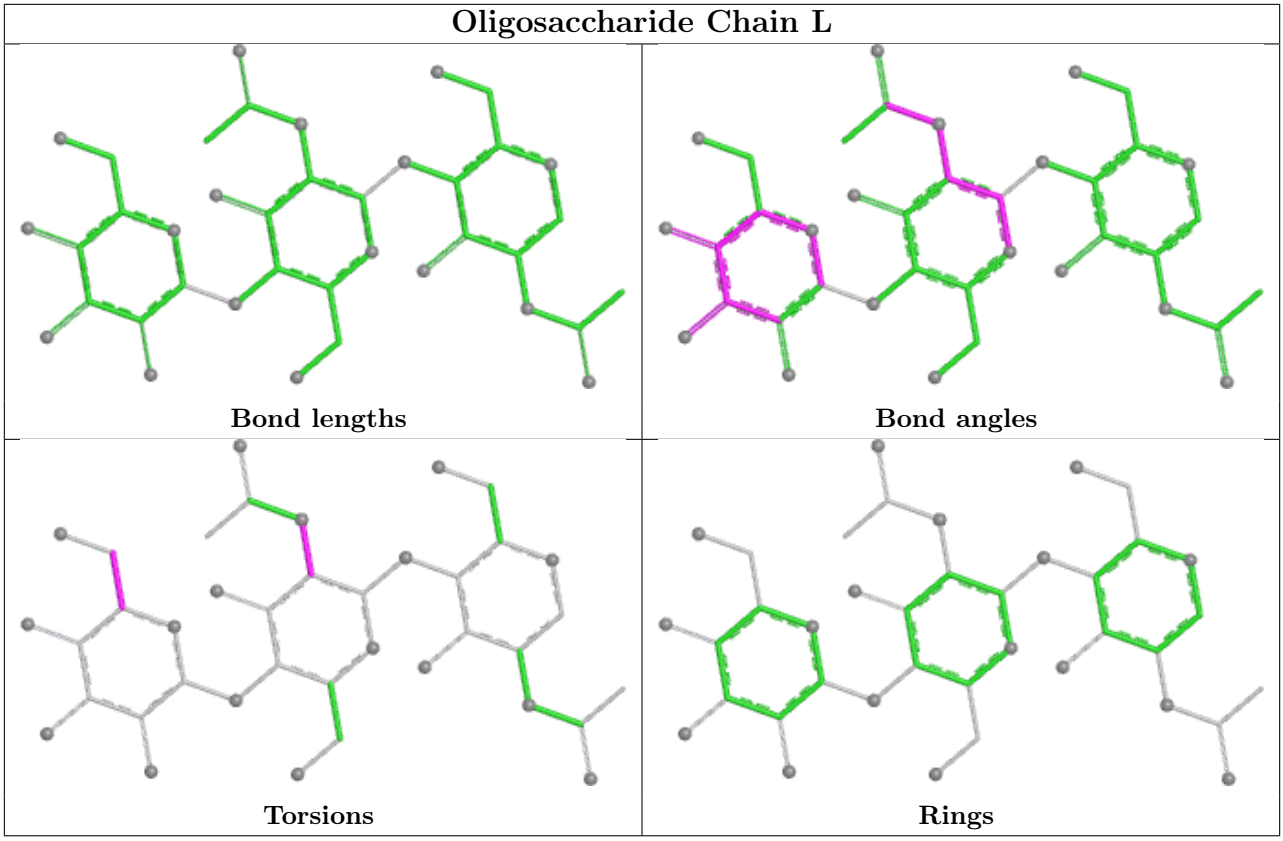
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	NAG	E	708	2	14,14,15	0.71	0	17,19,21	0.76	0
9	SO4	E	707	-	4,4,4	0.66	0	6,6,6	0.05	0
9	SO4	E	704	-	4,4,4	0.67	0	6,6,6	0.09	0
9	SO4	E	706	-	4,4,4	0.67	0	6,6,6	0.09	0
9	SO4	E	705	-	4,4,4	0.68	0	6,6,6	0.06	0
9	SO4	E	703	-	4,4,4	0.67	0	6,6,6	0.09	0
8	NAG	B	703	2	14,14,15	0.71	0	17,19,21	1.49	3 (17%)
8	NAG	B	702	2	14,14,15	0.65	0	17,19,21	1.28	3 (17%)
9	SO4	E	702	-	4,4,4	0.67	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	NAG	E	709	2	14,14,15	0.70	0	17,19,21	0.82	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	E	709	2	-	0/6/23/26	0/1/1/1
8	NAG	E	708	2	-	0/6/23/26	0/1/1/1
8	NAG	B	703	2	-	4/6/23/26	0/1/1/1
8	NAG	B	702	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	B	703	NAG	C2-N2-C7	3.95	128.19	122.90
8	B	702	NAG	C2-N2-C7	2.99	126.90	122.90
8	B	703	NAG	O5-C1-C2	-2.98	106.68	111.29
8	B	702	NAG	O5-C1-C2	-2.22	107.86	111.29
8	B	703	NAG	C1-C2-N2	2.18	113.87	110.43
8	B	702	NAG	C4-C3-C2	-2.17	107.84	111.02

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	703	NAG	O5-C5-C6-O6
8	B	702	NAG	C4-C5-C6-O6
8	B	703	NAG	C1-C2-N2-C7
8	B	703	NAG	C4-C5-C6-O6
8	B	703	NAG	C3-C2-N2-C7
8	B	702	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	192/203 (94%)	1.47	64 (33%) 1 1	32, 58, 102, 111	0
1	N	192/203 (94%)	0.42	15 (7%) 19 17	16, 36, 71, 94	0
2	B	597/597 (100%)	0.42	30 (5%) 34 30	18, 40, 70, 101	0
2	E	596/597 (99%)	0.28	30 (5%) 34 30	14, 36, 66, 102	0
All	All	1577/1600 (98%)	0.49	139 (8%) 15 14	14, 40, 80, 111	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	449	THR	5.5
1	A	390	LEU	5.1
1	A	449	THR	4.9
1	A	395	VAL	4.9
1	A	335	LEU	4.8
2	B	54	ILE	4.8
1	A	380	TYR	4.5
2	E	85	LEU	4.5
2	B	334	THR	4.3
1	A	387	LEU	4.3
2	B	339	VAL	4.1
1	A	358	ILE	4.1
1	N	447	GLY	4.1
1	A	520	ALA	3.9
2	E	136	ASP	3.8
1	A	362	VAL	3.8
1	A	432	CYS	3.8
1	A	446	LYS	3.8
2	B	60	GLN	3.7
1	A	392	PHE	3.7
2	B	336	PRO	3.6

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Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	N	521	PRO	3.6
2	E	146	PRO	3.5
2	E	122	THR	3.5
1	A	517	LEU	3.5
1	A	518	LEU	3.4
1	N	448	ASN	3.3
1	A	384	HIS	3.3
2	E	345	HIS	3.3
1	A	445	ASN	3.3
1	A	448	ASN	3.2
1	A	527	PRO	3.2
1	A	386	LYS	3.2
1	A	365	TYR	3.2
2	E	138	PRO	3.2
2	E	116	LEU	3.1
2	E	395	GLY	3.1
2	B	291	ILE	3.1
2	E	141	CYS	3.1
1	A	521	PRO	3.1
2	B	337	GLY	3.1
2	E	614	ALA	3.1
1	A	334	LYS	3.0
2	E	83	TYR	3.0
1	A	379	CYS	3.0
1	A	388	ASN	3.0
1	A	389	ASP	2.9
1	A	475	ALA	2.9
2	E	471	ASP	2.9
1	A	381	GLY	2.9
2	B	424	LEU	2.9
1	A	337	PRO	2.8
1	A	480	CYS	2.8
1	A	430	THR	2.8
1	N	444	ASN	2.7
1	A	396	TYR	2.7
1	N	384	HIS	2.7
1	A	525	CYS	2.7
1	A	486	LEU	2.7
1	A	391	CYS	2.7
1	A	461	LEU	2.7
1	A	363	ALA	2.7
1	A	385	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	336	CYS	2.6
2	B	359	LEU	2.6
2	B	430	GLU	2.6
1	A	470	THR	2.6
2	E	27	THR	2.6
1	A	476	GLY	2.6
1	A	515	PHE	2.6
1	N	335	LEU	2.6
1	A	444	ASN	2.6
2	E	133	CYS	2.6
2	B	550	ALA	2.6
1	A	361	CYS	2.5
2	E	435	GLU	2.5
1	A	514	SER	2.5
2	E	387	ALA	2.5
1	N	527	PRO	2.4
1	A	450	LYS	2.4
2	B	615	ASP	2.4
1	A	519	GLN	2.4
2	B	345	HIS	2.4
2	B	342	ALA	2.4
1	A	426	PRO	2.4
2	E	140	GLU	2.4
2	E	104	GLY	2.4
2	B	53	ASN	2.4
1	N	446	LYS	2.4
1	A	382	VAL	2.4
2	B	253	PRO	2.4
2	E	135	PRO	2.4
1	A	526	GLY	2.4
2	E	339	VAL	2.4
2	B	578	ASN	2.4
1	N	522	ALA	2.4
1	A	447	GLY	2.3
2	B	141	CYS	2.3
2	B	19	SER	2.3
1	A	367	PHE	2.3
2	B	364	VAL	2.3
1	N	363	ALA	2.3
2	E	113	SER	2.3
1	A	377	PHE	2.3
2	E	20	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	428	ASP	2.3
1	A	338	PHE	2.3
1	A	522	ALA	2.2
2	E	102	GLN	2.2
1	A	378	LYS	2.2
2	B	426	PRO	2.2
2	E	107	VAL	2.2
1	N	386	LYS	2.2
1	A	393	THR	2.2
2	B	91	LEU	2.2
1	A	429	PHE	2.2
2	E	91	LEU	2.2
2	E	105	SER	2.2
2	B	428	PHE	2.1
1	A	360	ASN	2.1
2	E	195	HIS	2.1
2	B	576	ALA	2.1
1	A	477	ASN	2.1
2	B	294	THR	2.1
2	B	50	TYR	2.1
1	N	362	VAL	2.1
1	A	524	VAL	2.1
1	A	394	ASN	2.1
2	B	90	ASN	2.1
2	E	338	ASN	2.1
2	B	335	ASP	2.1
1	A	488	CYS	2.1
2	E	103	ASN	2.0
1	N	385	THR	2.0
1	N	359	SER	2.0
2	B	289	PRO	2.0
2	B	133	CYS	2.0
2	E	137	ASN	2.0
1	A	479	PRO	2.0

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

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

6.3 Carbohydrates (i)

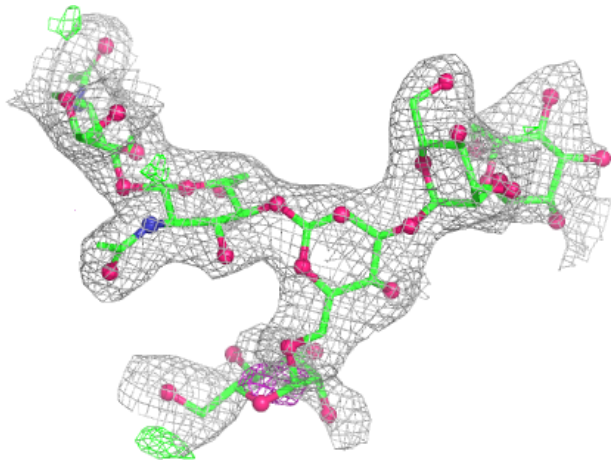
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

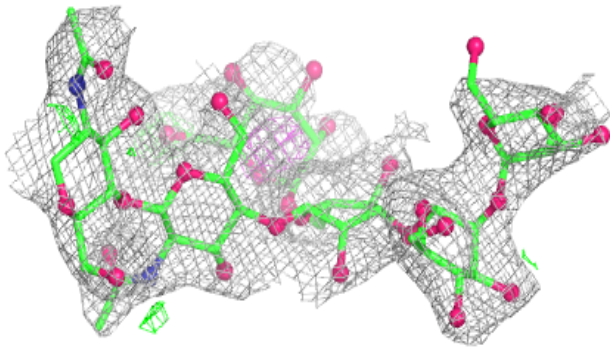
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NAG	J	2	14/15	0.19	0.22	50,59,66,77	0
3	NAG	M	2	14/15	0.54	0.17	39,43,51,62	0
3	BMA	M	3	11/12	-	-	46,52,65,68	0
3	MAN	M	4	11/12	-	-	39,49,53,63	0
3	MAN	M	5	11/12	-	-	59,69,79,97	0
3	MAN	M	6	11/12	-	-	56,81,90,91	0
4	NAG	C	1	14/15	-	-	34,52,56,63	0
4	NAG	C	2	14/15	-	-	43,67,73,77	0
4	BMA	C	3	11/12	-	-	70,77,81,90	0
4	MAN	C	4	11/12	-	-	52,55,62,63	0
4	MAN	C	5	11/12	-	-	45,61,66,68	0
4	MAN	C	6	11/12	-	-	61,67,82,84	0
4	MAN	C	7	11/12	-	-	48,65,72,74	0
5	NAG	D	1	14/15	-	-	61,68,80,86	0
5	NAG	D	2	14/15	-	-	81,92,96,96	0
5	NAG	G	2	14/15	0.55	0.18	93,109,116,119	0
5	NAG	I	2	14/15	0.56	0.17	67,74,78,80	0
5	NAG	J	1	14/15	0.64	0.16	41,51,55,60	0
5	NAG	H	1	14/15	0.66	0.16	39,57,67,67	0
5	NAG	K	2	14/15	0.71	0.14	56,79,93,100	0
5	NAG	H	2	14/15	0.76	0.15	66,78,85,95	0
3	NAG	M	1	14/15	0.77	0.12	40,48,57,58	0
5	NAG	F	2	14/15	0.78	0.14	57,76,80,86	0
6	NAG	L	2	14/15	0.82	0.12	67,79,91,100	0
5	NAG	K	1	14/15	0.83	0.12	44,55,67,68	0
5	NAG	I	1	14/15	0.85	0.12	63,68,75,78	0
6	NAG	L	1	14/15	0.87	0.10	34,53,65,74	0
5	NAG	G	1	14/15	0.88	0.11	59,80,103,104	0
5	NAG	F	1	14/15	0.89	0.09	58,81,93,95	0
6	BMA	L	3	11/12	-	-	87,98,102,105	0

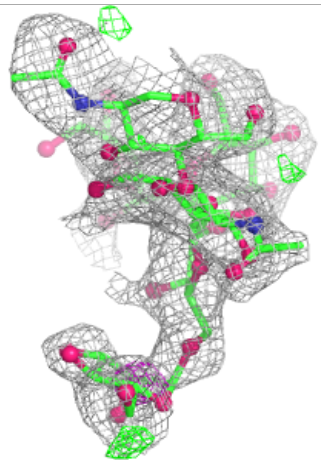
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain M:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

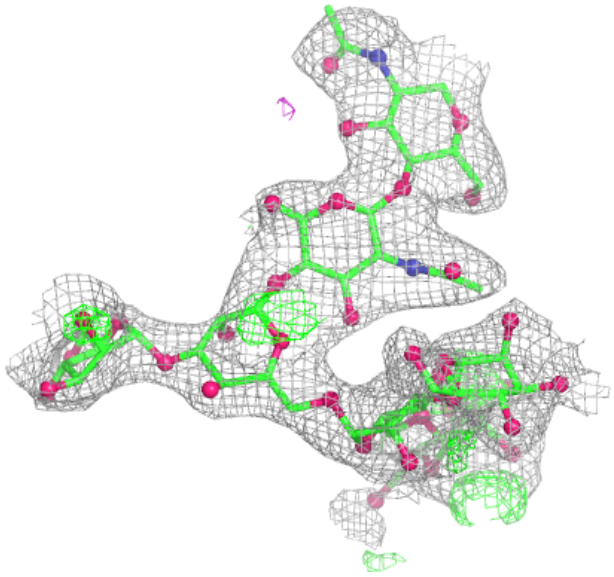


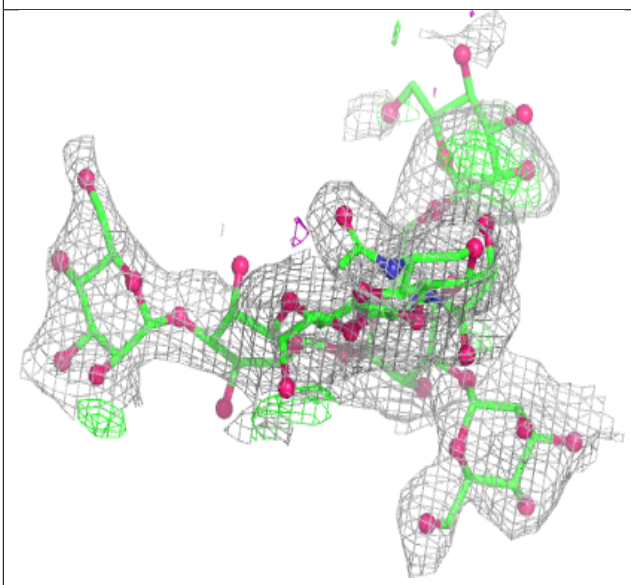


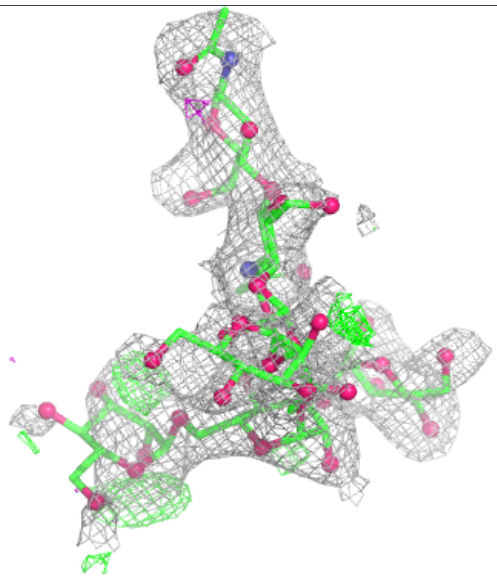


Electron density around Chain C:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

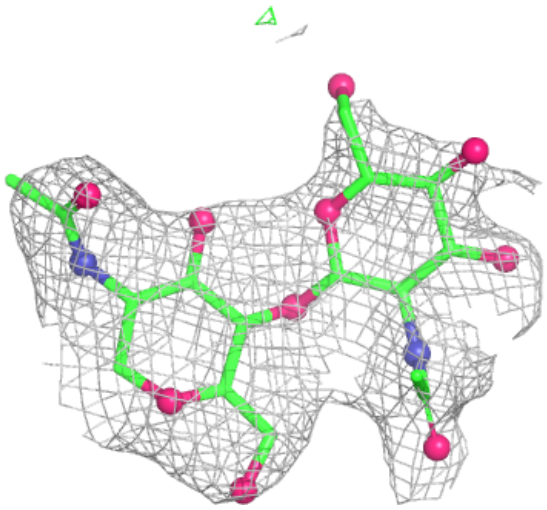


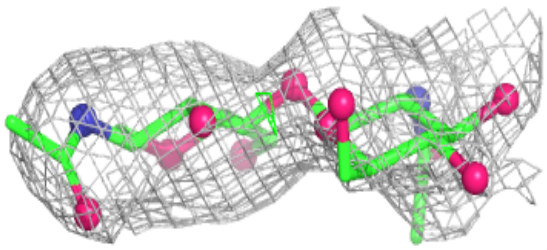


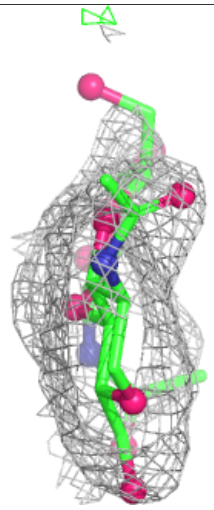


Electron density around Chain D:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

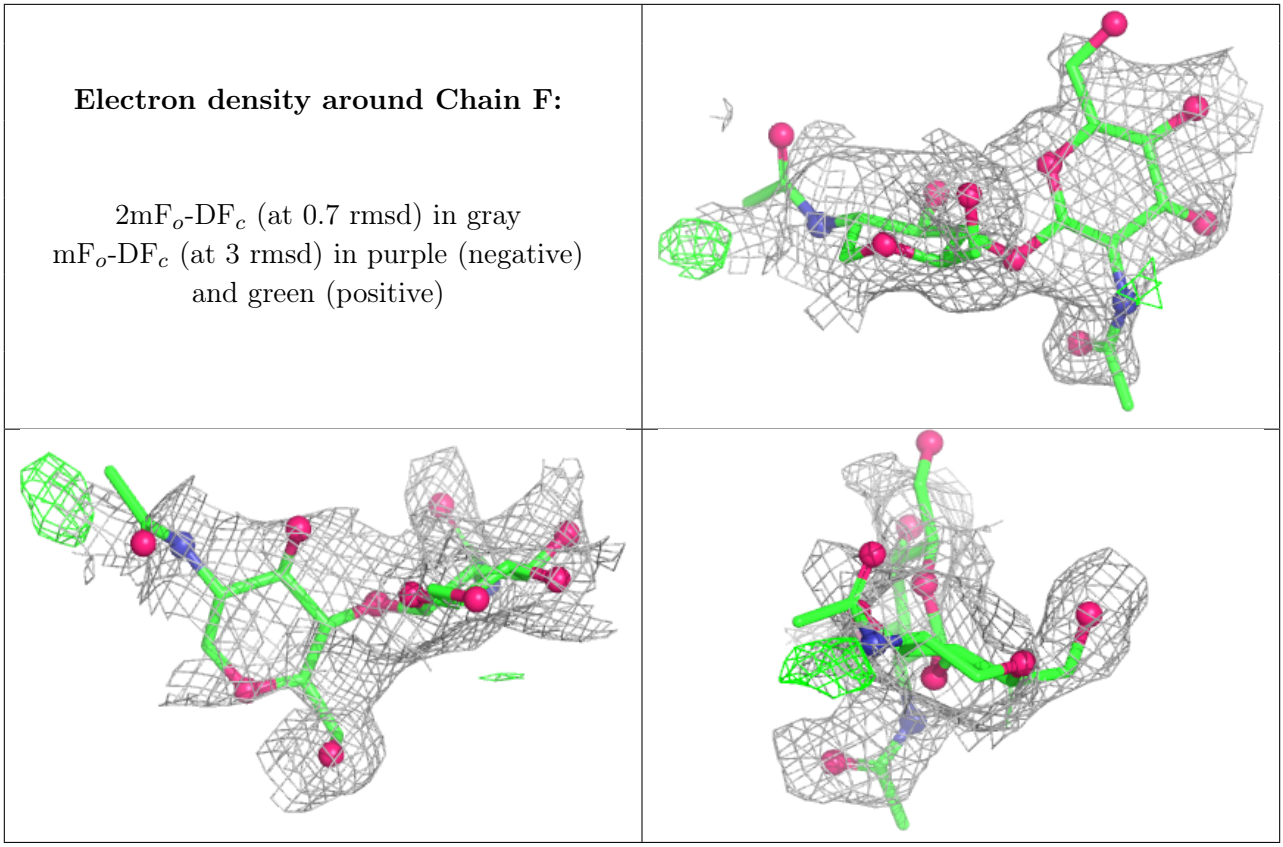






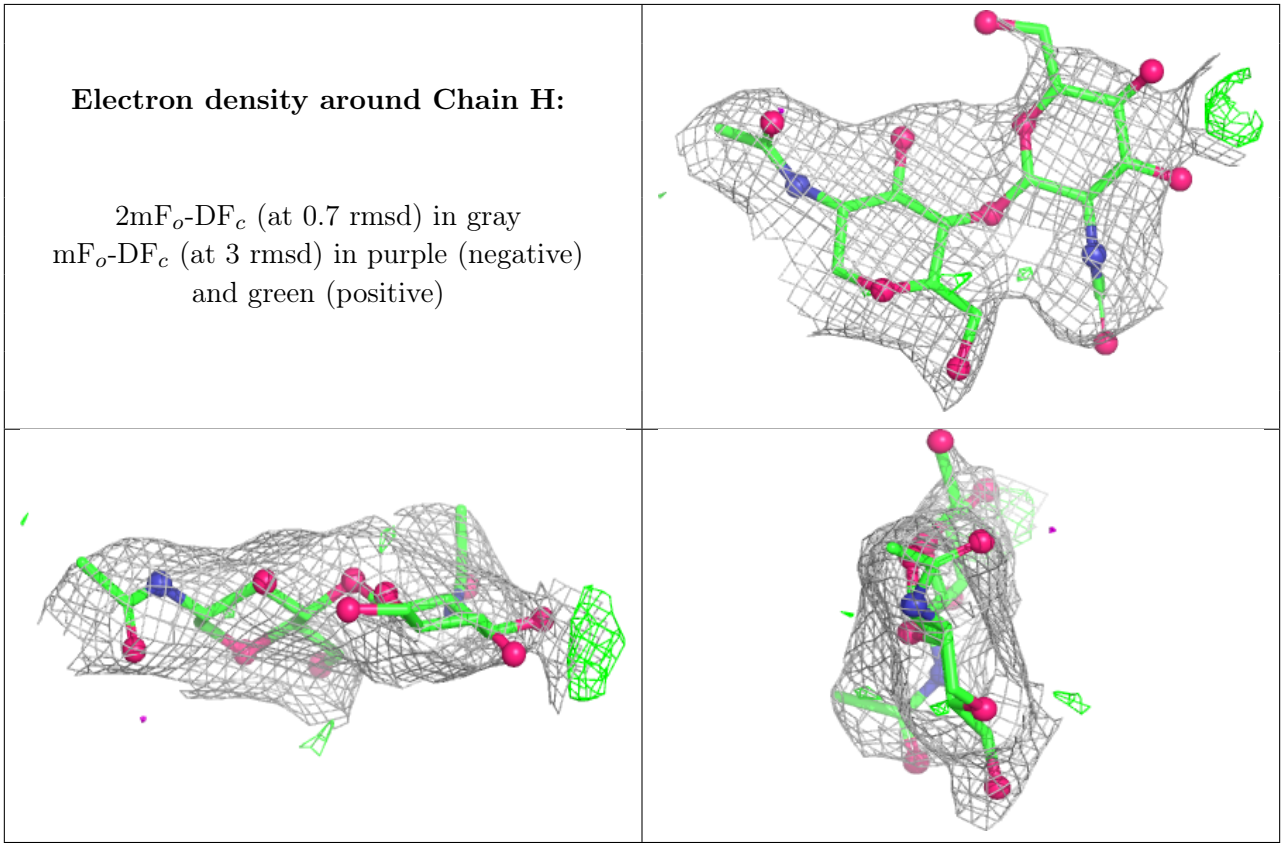
Electron density around Chain F:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



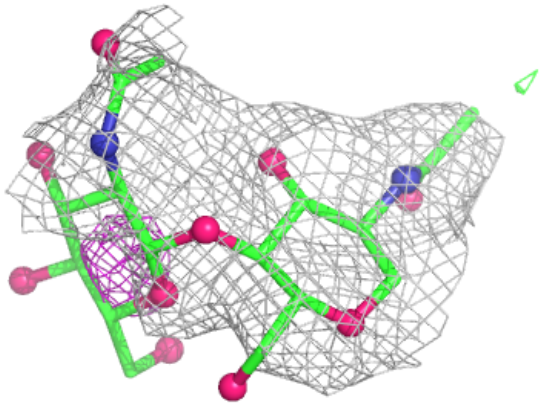
Electron density around Chain H:

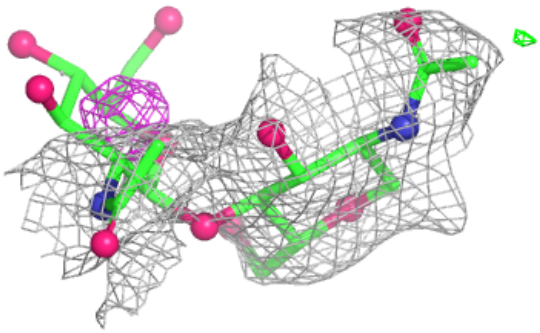
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

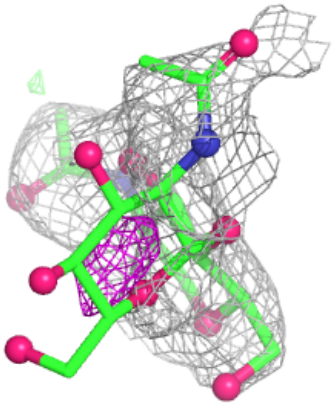


Electron density around Chain G:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

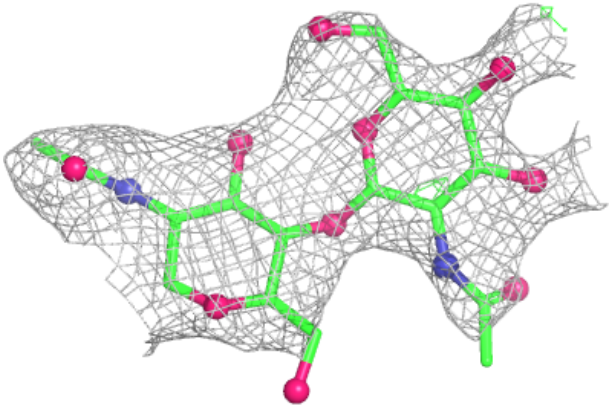


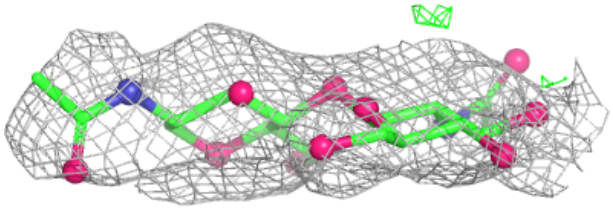


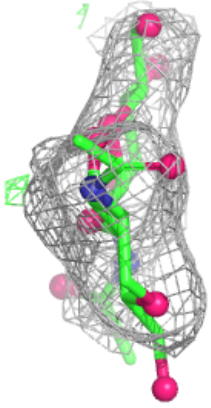


Electron density around Chain I:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

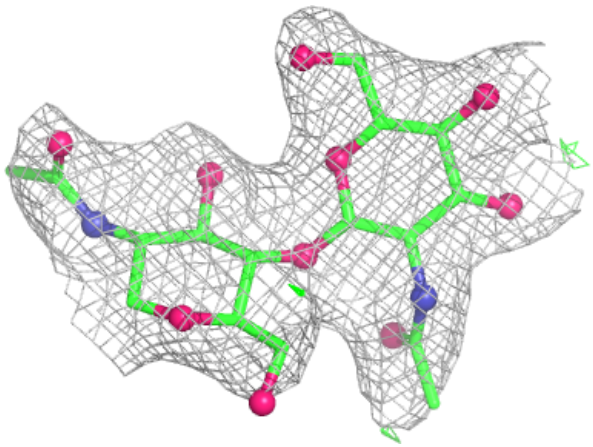


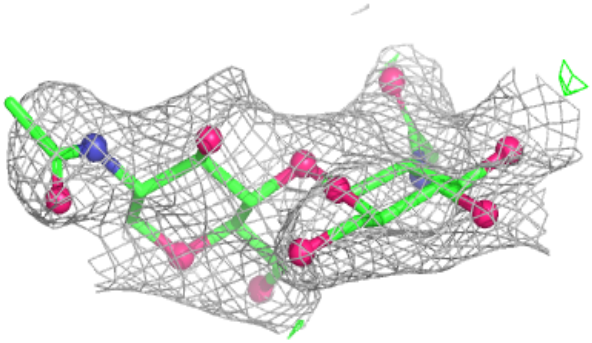


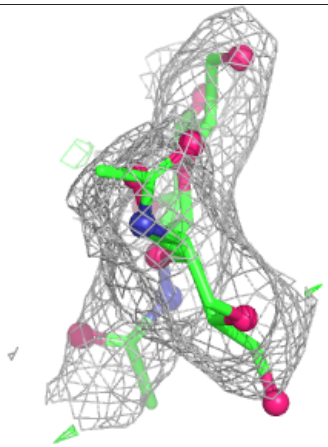


Electron density around Chain J:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

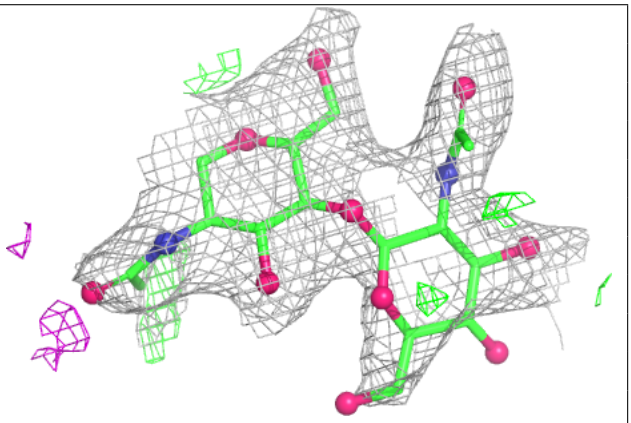


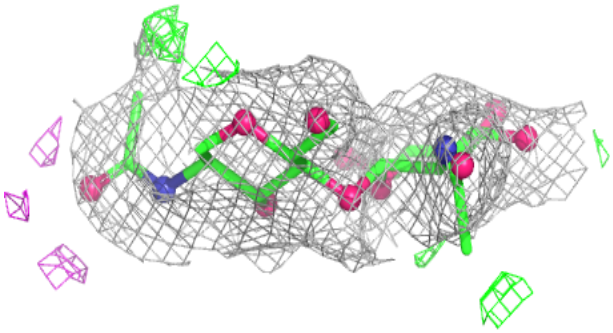


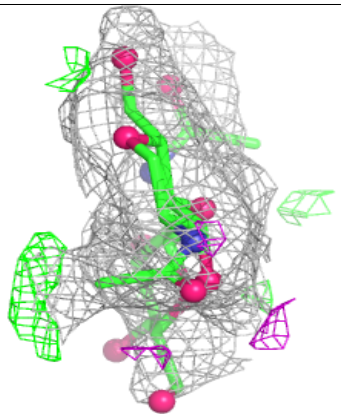


Electron density around Chain K:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

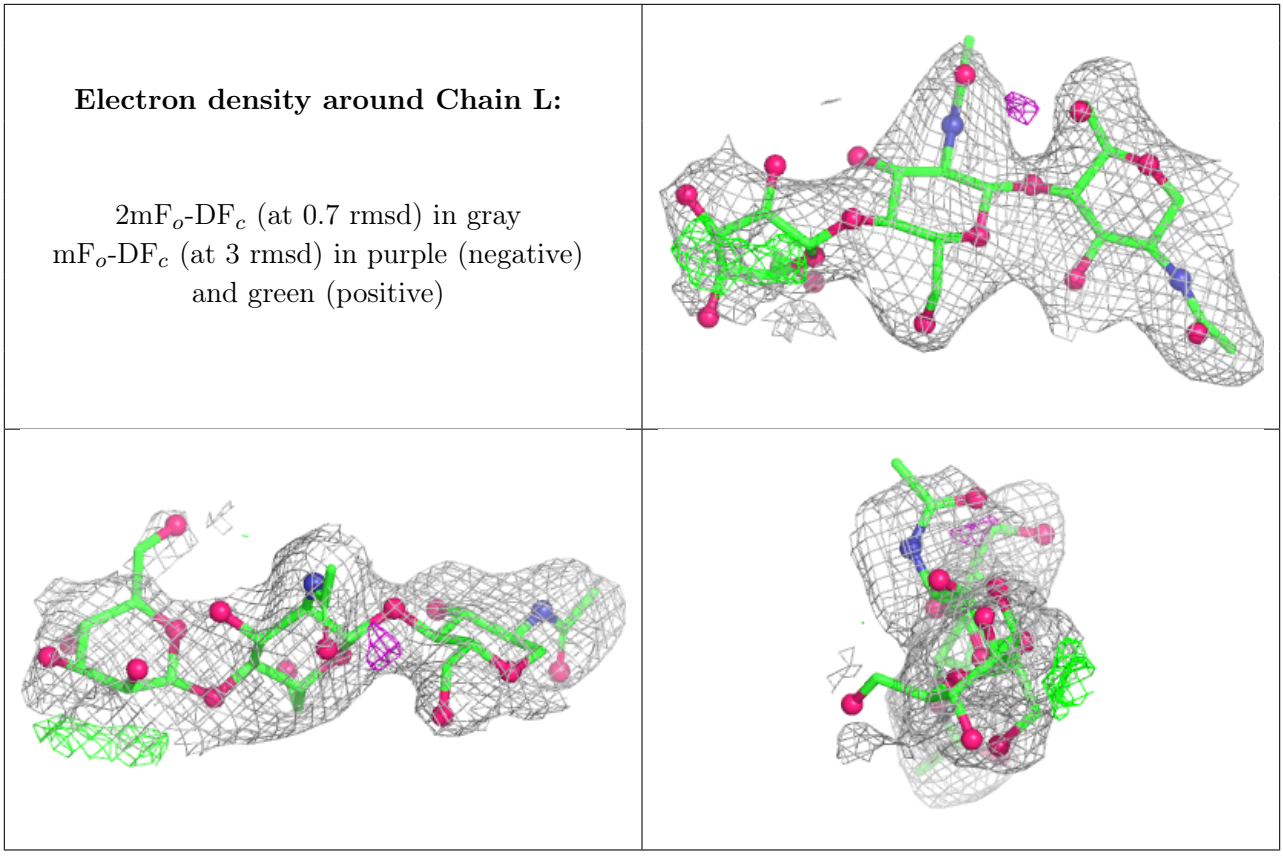






Electron density around Chain L:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	NAG	B	702	14/15	0.47	0.21	52,75,90,92	0
8	NAG	B	703	14/15	0.48	0.17	81,98,102,104	0
9	SO4	E	704	5/5	0.66	0.12	73,76,85,109	0
8	NAG	E	709	14/15	0.70	0.14	64,72,83,91	0
9	SO4	E	703	5/5	0.82	0.21	54,66,78,103	0
9	SO4	E	705	5/5	0.82	0.23	52,59,104,108	0
9	SO4	E	707	5/5	0.84	0.40	33,56,62,70	0
9	SO4	E	706	5/5	0.85	0.23	44,61,81,91	0
8	NAG	E	708	14/15	0.86	0.11	33,55,68,75	0
9	SO4	E	702	5/5	0.90	0.24	44,48,66,71	0
7	ZN	B	701	1/1	0.95	0.07	71,71,71,71	0
7	ZN	E	701	1/1	0.95	0.06	57,57,57,57	0

6.5 Other polymers (i)

There are no such residues in this entry.