



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 02:39 PM UTC

PDB ID : 4EI5 / pdb_00004ei5
Title : Crystal Structure of XV19 TCR in complex with CD1d-sulfatide C24:1
Authors : Patel, O.; Gras, S.; Rossjohn, J.
Deposited on : 2012-04-04
Resolution : 3.10 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

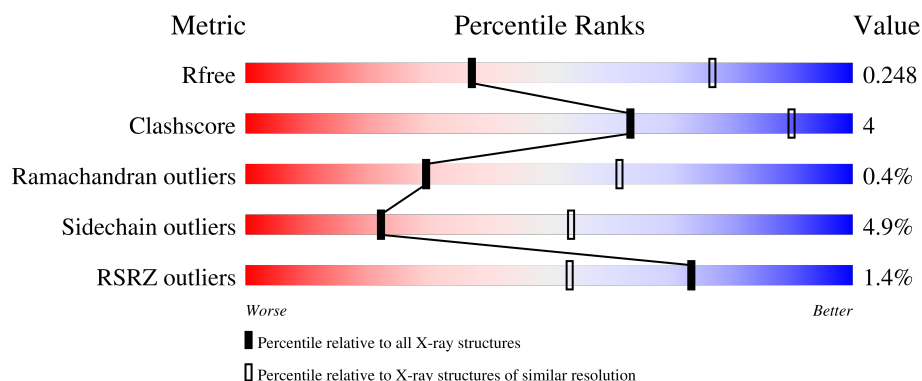
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 $\leq 5\%$. 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	302	78% 18% ..
1	E	302	3% 76% 16% 7%
2	B	99	80% 18% ..
2	F	99	78% 18% .
3	C	208	83% 12% ..

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Mol	Chain	Length	Quality of chain
3	G	208	
4	D	245	
4	H	245	
5	I	4	
6	J	2	
6	L	2	
7	K	3	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	FLC	A	408	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 13206 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 Antigen-presenting glycoprotein CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2346	1493	408	432	13			
1	E	280	Total	C	N	O	S	0	0	0
			2229	1420	387	410	12			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	HIS	ASP	SEE REMARK 999	UNP P11609
A	280	GLY	-	expression tag	UNP P11609
A	281	SER	-	expression tag	UNP P11609
A	282	LEU	-	expression tag	UNP P11609
A	283	HIS	-	expression tag	UNP P11609
A	284	HIS	-	expression tag	UNP P11609
A	285	ILE	-	expression tag	UNP P11609
A	286	LEU	-	expression tag	UNP P11609
A	287	ASP	-	expression tag	UNP P11609
A	288	ALA	-	expression tag	UNP P11609
A	289	GLN	-	expression tag	UNP P11609
A	290	LYS	-	expression tag	UNP P11609
A	291	MET	-	expression tag	UNP P11609
A	292	VAL	-	expression tag	UNP P11609
A	293	TRP	-	expression tag	UNP P11609
A	294	ASN	-	expression tag	UNP P11609
A	295	HIS	-	expression tag	UNP P11609
A	296	ARG	-	expression tag	UNP P11609
A	297	HIS	-	expression tag	UNP P11609
A	298	HIS	-	expression tag	UNP P11609
A	299	HIS	-	expression tag	UNP P11609
A	300	HIS	-	expression tag	UNP P11609
A	301	HIS	-	expression tag	UNP P11609
A	302	HIS	-	expression tag	UNP P11609
E	201	HIS	ASP	SEE REMARK 999	UNP P11609

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Chain	Residue	Modelled	Actual	Comment	Reference
E	280	GLY	-	expression tag	UNP P11609
E	281	SER	-	expression tag	UNP P11609
E	282	LEU	-	expression tag	UNP P11609
E	283	HIS	-	expression tag	UNP P11609
E	284	HIS	-	expression tag	UNP P11609
E	285	ILE	-	expression tag	UNP P11609
E	286	LEU	-	expression tag	UNP P11609
E	287	ASP	-	expression tag	UNP P11609
E	288	ALA	-	expression tag	UNP P11609
E	289	GLN	-	expression tag	UNP P11609
E	290	LYS	-	expression tag	UNP P11609
E	291	MET	-	expression tag	UNP P11609
E	292	VAL	-	expression tag	UNP P11609
E	293	TRP	-	expression tag	UNP P11609
E	294	ASN	-	expression tag	UNP P11609
E	295	HIS	-	expression tag	UNP P11609
E	296	ARG	-	expression tag	UNP P11609
E	297	HIS	-	expression tag	UNP P11609
E	298	HIS	-	expression tag	UNP P11609
E	299	HIS	-	expression tag	UNP P11609
E	300	HIS	-	expression tag	UNP P11609
E	301	HIS	-	expression tag	UNP P11609
E	302	HIS	-	expression tag	UNP P11609

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	98	Total	C	N	O	S	0	0	0
			809	517	137	148	7			
2	F	95	Total	C	N	O	S	0	0	0
			782	502	131	143	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ALA	ASP	SEE REMARK 999	UNP P01887
F	85	ALA	ASP	SEE REMARK 999	UNP P01887

- Molecule 3 is a protein called Valpha1 XV19 Type II Natural Killer T cell receptor (mouse variable domain, human constant domain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	201	Total	C	N	O	S	0	0	0
			1578	985	268	316	9			
3	G	172	Total	C	N	O	S	0	1	0
			1364	855	229	273	7			

- Molecule 4 is a protein called Vbeta16 XV19 Type II Natural Killer T cell receptor (mouse variable domain, human constant domain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	242	Total	C	N	O	S	0	0	0
			1961	1262	327	363	9			
4	H	230	Total	C	N	O	S	0	0	0
			1862	1198	309	346	9			

- Molecule 5 is an oligosaccharide called 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.



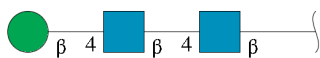
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



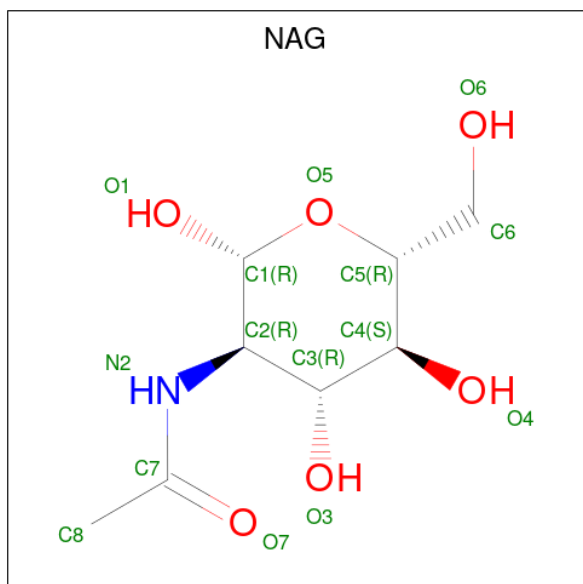
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
6	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



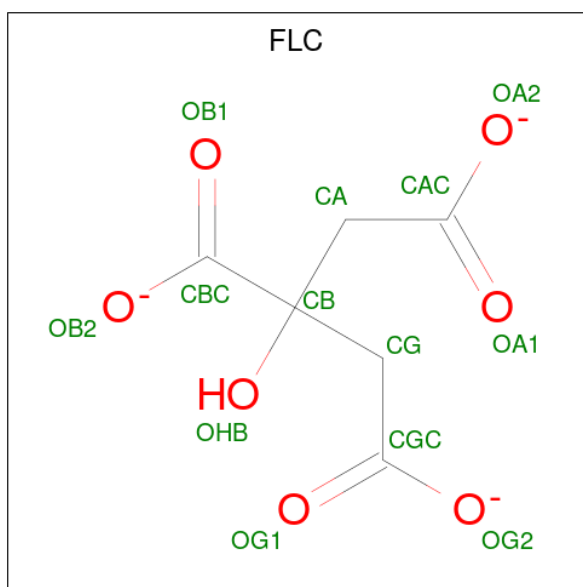
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	K	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



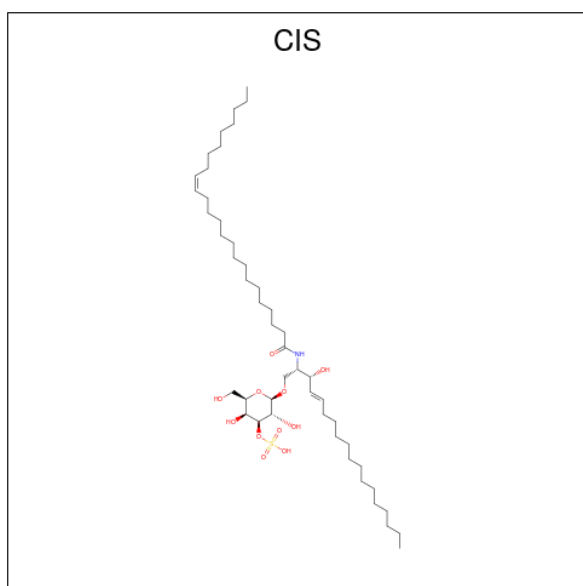
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is CITRATE ANION (CCD ID: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 10 is (15Z)-N-((1S,2R,3E)-2-HYDROXY-1-[[[(3-O-SULFO-BETA-D-GALACTO PYRANOSYL)OXY]METHYL]HEPTADEC-3-ENYL)TETRACOS-15-ENAMIDE (CCD ID: CIS) (formula: C₄₈H₉₁NO₁₁S).

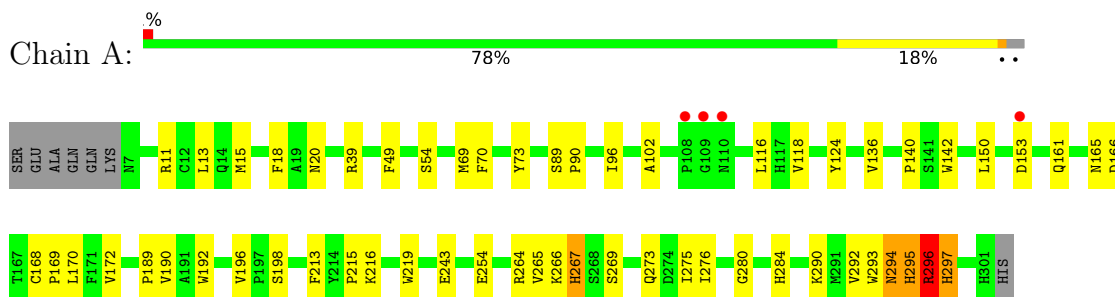


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	N	O	S	0	0
			55	42	1	11	1		
10	E	1	Total	C	N	O	S	0	0
			34	21	1	11	1		

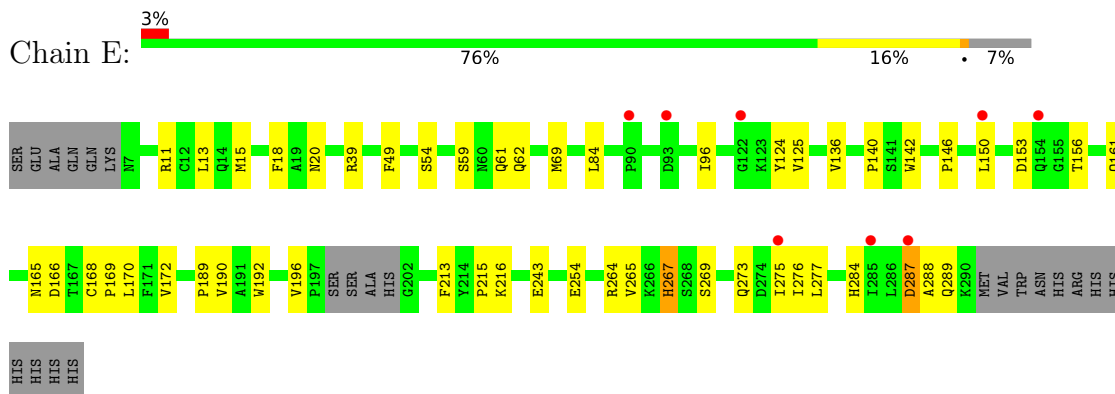
3 Residue-property plots

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.

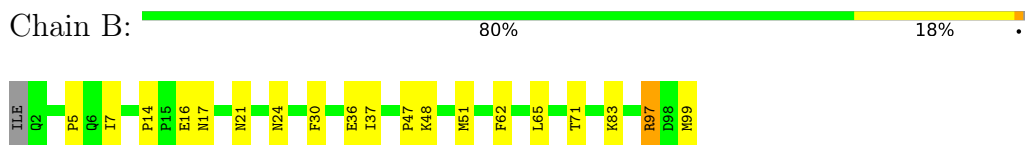
- Molecule 1: Antigen-presenting glycoprotein CD1d1



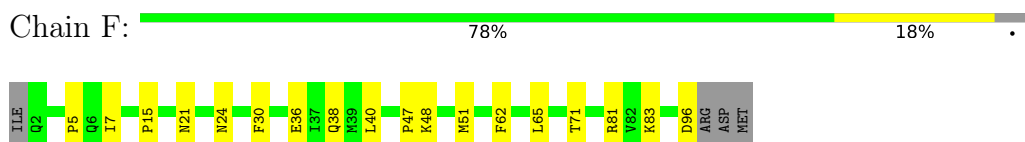
- Molecule 1: Antigen-presenting glycoprotein CD1d1



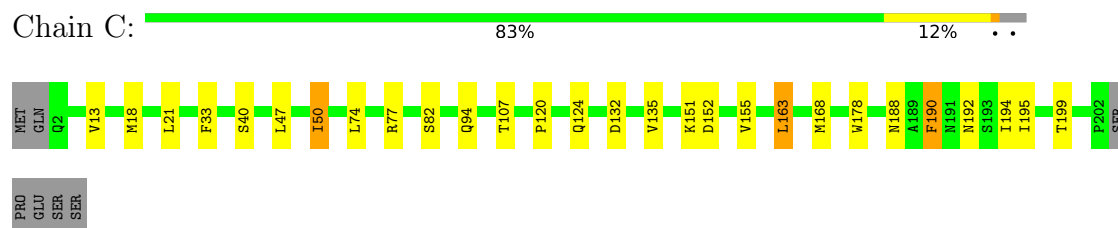
- Molecule 2: Beta-2-microglobulin



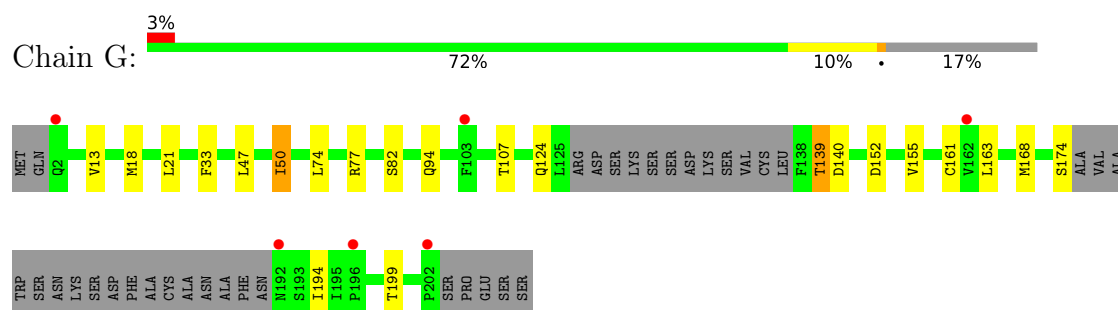
- Molecule 2: Beta-2-microglobulin



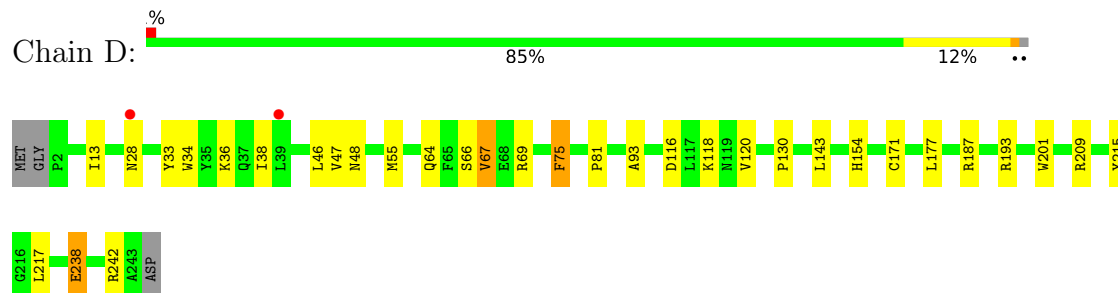
- Molecule 3: Valpha1 XV19 Type II Natural Killer T cell receptor (mouse variable domain, human constant domain)



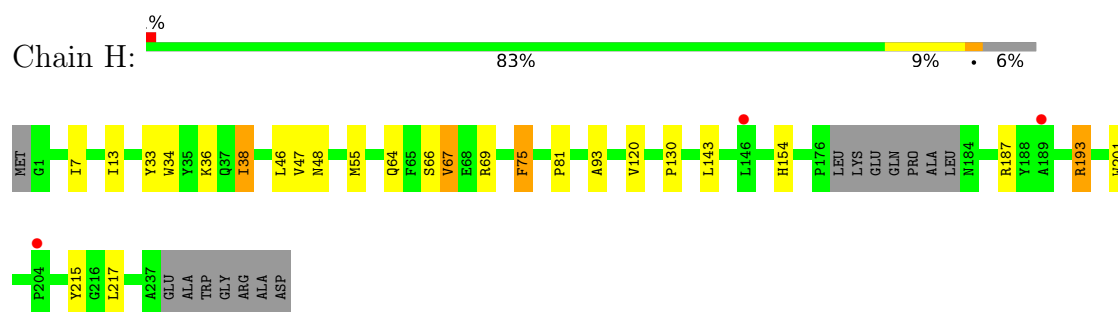
- Molecule 3: Valpha1 XV19 Type II Natural Killer T cell receptor (mouse variable domain, human constant domain)



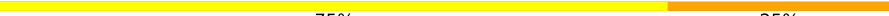
- Molecule 4: Vbeta16 XV19 Type II Natural Killer T cell receptor (mouse variable domain, human constant domain)



- Molecule 4: Vbeta16 XV19 Type II Natural Killer T cell receptor (mouse variable domain, human constant domain)

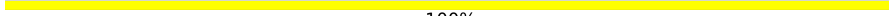


- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  75% 25%

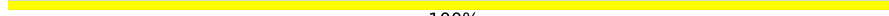
MAG1
MAG2
BMA3
MAN4

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

Chain J:  100%

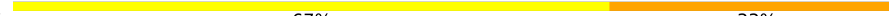
MAG1
MAG2

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

Chain L:  100%

MAG1
MAG2

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

Chain K:  67% 33%

MAG1
MAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	102.74Å 140.71Å 160.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	105.88 – 3.10 105.88 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.6 (105.88-3.10) 98.6 (105.88-3.10)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 3.13Å)	Xtriage
Refinement program	BUSTER-TNT, BUSTER 2.10.0	Depositor
R, R_{free}	0.197 , 0.227 0.213 , 0.248	Depositor DCC
R_{free} test set	2152 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	78.8	Xtriage
Anisotropy	0.412	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 106.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13206	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: BMA, FLC, CIS, 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	0.76	1/2417 (0.0%)	1.27	11/3291 (0.3%)
1	E	0.72	0/2294	1.26	13/3121 (0.4%)
2	B	0.71	0/835	1.11	2/1133 (0.2%)
2	F	0.67	0/808	1.12	3/1098 (0.3%)
3	C	0.71	0/1617	1.15	2/2189 (0.1%)
3	G	0.69	0/1400	1.14	1/1893 (0.1%)
4	D	0.69	0/2021	1.09	2/2750 (0.1%)
4	H	0.67	1/1918 (0.1%)	1.09	2/2609 (0.1%)
All	All	0.71	2/13310 (0.0%)	1.17	36/18084 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	294	ASN	C-N	5.10	1.40	1.33
4	H	7	ILE	CA-C	5.07	1.56	1.52

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	HIS	N-CA-C	9.39	124.69	109.76
1	A	295	HIS	CA-C-N	8.55	137.87	121.54
1	A	295	HIS	C-N-CA	8.55	137.87	121.54
1	E	284	HIS	CA-C-N	8.07	136.23	121.70
1	E	284	HIS	C-N-CA	8.07	136.23	121.70
2	F	71	THR	CB-CA-C	6.66	117.13	110.33
2	B	71	THR	CB-CA-C	6.44	116.90	110.33
3	G	33	PHE	N-CA-C	6.44	120.02	109.72
1	E	288	ALA	CA-C-N	6.43	133.83	121.54
1	E	288	ALA	C-N-CA	6.43	133.83	121.54
1	A	295	HIS	N-CA-C	6.35	124.33	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	33	PHE	N-CA-C	6.27	119.75	109.72
1	E	287	ASP	N-CA-C	6.24	118.80	109.25
1	A	153	ASP	CA-CB-CG	5.78	118.38	112.60
2	B	21	ASN	CA-CB-CG	5.61	118.21	112.60
1	E	153	ASP	CA-CB-CG	5.57	118.17	112.60
1	A	216	LYS	N-CA-C	5.51	121.11	113.45
1	E	166	ASP	CA-CB-CG	5.50	118.10	112.60
1	E	20	ASN	CA-CB-CG	5.49	118.09	112.60
1	E	125	VAL	N-CA-C	5.39	116.65	112.12
2	F	21	ASN	CA-CB-CG	5.33	117.93	112.60
2	F	96	ASP	CA-CB-CG	5.31	117.91	112.60
1	A	20	ASN	CA-CB-CG	5.30	117.91	112.60
1	A	165	ASN	N-CA-C	5.22	116.78	111.14
1	A	267	HIS	CA-C-N	5.20	127.50	120.38
1	A	267	HIS	C-N-CA	5.20	127.50	120.38
4	D	75	PHE	N-CA-C	-5.18	100.64	108.67
3	C	190	PHE	CA-CB-CG	5.17	118.97	113.80
4	D	238	GLU	N-CA-C	5.14	117.98	109.85
1	E	165	ASN	N-CA-C	5.12	116.94	111.36
1	E	267	HIS	CA-C-N	5.11	127.38	120.38
1	E	267	HIS	C-N-CA	5.11	127.38	120.38
1	A	166	ASP	CA-CB-CG	5.10	117.70	112.60
1	E	288	ALA	N-CA-C	5.09	115.88	108.14
4	H	75	PHE	N-CA-C	-5.04	100.86	108.67
4	H	38	ILE	N-CA-C	5.02	115.57	107.73

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	2346	0	2208	33	0
1	E	2229	0	2112	20	0
2	B	809	0	783	11	0
2	F	782	0	757	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1578	0	1471	9	0
3	G	1364	0	1272	7	0
4	D	1961	0	1872	13	0
4	H	1862	0	1773	12	0
5	I	50	0	43	1	0
6	J	28	0	25	0	0
6	L	28	0	25	0	0
7	K	39	0	34	1	0
8	A	14	0	13	0	0
8	E	14	0	13	0	0
9	A	13	0	5	5	0
10	A	55	0	75	3	0
10	E	34	0	32	1	0
All	All	13206	0	12513	102	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 4.

All (102) 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:295:HIS:CD2	9:A:408:FLC:OB1	2.32	0.81
1:A:196:VAL:HG21	2:B:99:MET:HG3	1.66	0.78
1:A:15:MET:HG2	2:B:62:PHE:HE1	1.53	0.73
3:C:163:LEU:HD23	4:D:171:CYS:HB2	1.71	0.73
4:D:48:ASN:HD22	4:D:55:MET:HB2	1.57	0.69
1:E:189:PRO:HB3	1:E:213:PHE:HB3	1.76	0.68
1:A:196:VAL:HG11	2:B:99:MET:HE3	1.75	0.67
4:H:48:ASN:HD22	4:H:55:MET:HB2	1.57	0.67
1:A:189:PRO:HB3	1:A:213:PHE:HB3	1.76	0.67
1:E:15:MET:HG2	2:F:62:PHE:HE1	1.60	0.66
1:A:293:TRP:CD1	2:B:97:ARG:HD2	2.30	0.66
4:H:64:GLN:HG2	4:H:81:PRO:HD2	1.78	0.65
9:A:408:FLC:OA1	9:A:408:FLC:CBC	2.44	0.65
1:E:161:GLN:HE21	7:K:1:NAG:HN2	1.46	0.64
3:G:139:THR:HG23	3:G:174:SER:HB3	1.78	0.64
1:A:161:GLN:HE21	5:I:1:NAG:HN2	1.45	0.63
4:D:69:ARG:HD2	4:D:75:PHE:HB2	1.82	0.62
4:H:69:ARG:HD2	4:H:75:PHE:HB2	1.82	0.61
3:C:190:PHE:HB3	3:C:195:ILE:HD11	1.82	0.61
1:E:168:CYS:HB3	1:E:169:PRO:HD3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:PHE:HB3	1:A:54:SER:HB2	1.83	0.61
1:A:168:CYS:HB3	1:A:169:PRO:HD3	1.82	0.60
4:H:33:TYR:HB2	4:H:93:ALA:HB3	1.85	0.59
4:D:33:TYR:HB2	4:D:93:ALA:HB3	1.85	0.58
1:E:49:PHE:HB3	1:E:54:SER:HB2	1.85	0.58
1:A:118:VAL:HG11	10:A:409:CIS:H102	1.86	0.57
1:A:124:TYR:CZ	1:A:136:VAL:HG11	2.39	0.57
1:E:59:SER:H	1:E:62:GLN:HE21	1.51	0.57
1:A:297:HIS:ND1	9:A:408:FLC:OB2	2.39	0.56
1:E:124:TYR:CZ	1:E:136:VAL:HG11	2.41	0.55
3:C:120:PRO:HB2	3:C:199:THR:HG22	1.89	0.54
4:D:64:GLN:HG3	4:D:81:PRO:HD2	1.89	0.54
2:F:5:PRO:HB3	2:F:30:PHE:HB3	1.91	0.52
1:E:59:SER:H	1:E:62:GLN:NE2	2.06	0.52
4:H:47:VAL:HG11	4:H:67:VAL:HG21	1.92	0.52
2:B:5:PRO:HB3	2:B:30:PHE:HB3	1.91	0.51
1:A:168:CYS:O	1:A:172:VAL:HG23	2.11	0.51
4:D:34:TRP:HB2	4:D:47:VAL:HG12	1.93	0.51
1:E:168:CYS:O	1:E:172:VAL:HG23	2.11	0.51
4:H:34:TRP:HB2	4:H:47:VAL:HG12	1.93	0.51
1:A:297:HIS:CE1	9:A:408:FLC:OB2	2.64	0.50
4:D:47:VAL:HG11	4:D:67:VAL:HG21	1.93	0.50
1:E:265:VAL:HB	1:E:275:ILE:HB	1.93	0.50
3:G:161:CYS:HB2	4:H:193:ARG:HH21	1.77	0.50
1:A:290:LYS:HB2	2:B:16:GLU:HG3	1.94	0.50
1:A:265:VAL:HB	1:A:275:ILE:HB	1.92	0.50
2:B:24:ASN:HB3	2:B:65:LEU:HD11	1.94	0.49
4:D:36:LYS:HB2	4:D:46:LEU:HD11	1.94	0.49
1:A:295:HIS:NE2	9:A:408:FLC:OB1	2.45	0.49
3:C:18:MET:HE2	3:C:77:ARG:HG2	1.94	0.49
3:C:135:VAL:HG12	3:C:178:TRP:HB3	1.94	0.48
1:E:84:LEU:HD22	1:E:146:PRO:HB3	1.93	0.48
3:G:21:LEU:HD12	3:G:74:LEU:HD23	1.95	0.48
4:H:36:LYS:HB2	4:H:46:LEU:HD11	1.94	0.48
2:B:37:ILE:HB	2:B:51:MET:HE1	1.94	0.48
3:G:18:MET:HE2	3:G:77:ARG:HG2	1.95	0.48
1:E:277:LEU:HD22	1:E:287:ASP:HB2	1.95	0.48
2:F:36:GLU:HB3	2:F:83:LYS:HB2	1.97	0.47
1:A:267:HIS:HD2	1:A:269:SER:OG	1.98	0.47
3:C:21:LEU:HD12	3:C:74:LEU:HD23	1.95	0.47
2:F:24:ASN:HB3	2:F:65:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:120:VAL:HG21	4:D:217:LEU:HD21	1.97	0.47
1:A:70:PHE:HE2	10:A:409:CIS:H261	1.80	0.46
2:B:36:GLU:HB3	2:B:83:LYS:HB2	1.97	0.46
1:E:140:PRO:HB2	1:E:142:TRP:CD1	2.51	0.46
1:A:294:ASN:C	1:A:294:ASN:HD22	2.23	0.46
1:E:267:HIS:HD2	1:E:269:SER:OG	1.99	0.45
3:G:139:THR:HG22	3:G:140:ASP:H	1.80	0.45
1:A:215:PRO:O	1:A:267:HIS:HE1	2.00	0.45
1:A:280:GLY:H	1:A:284:HIS:CD2	2.35	0.45
4:D:209:ARG:HG3	4:D:238:GLU:HB3	1.98	0.45
3:G:152:ASP:HB3	3:G:155:VAL:HG12	1.98	0.45
1:A:196:VAL:HG22	1:A:297:HIS:CE1	2.52	0.45
3:C:152:ASP:HB3	3:C:155:VAL:HG12	1.98	0.45
2:B:17:ASN:OD1	2:B:97:ARG:NH2	2.49	0.44
4:H:120:VAL:HG21	4:H:217:LEU:HD21	1.97	0.44
1:A:140:PRO:HB2	1:A:142:TRP:CD1	2.52	0.44
1:E:156:THR:HG23	10:E:407:CIS:H192	2.00	0.44
4:H:193:ARG:HH11	4:H:193:ARG:CG	2.32	0.43
3:G:21:LEU:HD22	3:G:107:THR:HG21	2.01	0.43
1:A:295:HIS:HB2	1:A:296:ARG:H	1.66	0.43
2:F:40:LEU:HD11	2:F:81:ARG:HB2	2.01	0.42
1:A:18:PHE:HB2	1:A:96:ILE:HB	2.01	0.42
1:A:39:ARG:O	1:A:39:ARG:HG3	2.18	0.42
1:E:39:ARG:O	1:E:39:ARG:HG3	2.20	0.42
4:H:130:PRO:HD2	4:H:201:TRP:CZ2	2.54	0.42
1:A:219:TRP:HB3	1:A:266:LYS:HB2	2.02	0.42
1:E:18:PHE:HB2	1:E:96:ILE:HB	2.02	0.42
1:A:73:TYR:CD1	10:A:409:CIS:H212	2.55	0.42
1:E:215:PRO:O	1:E:267:HIS:HE1	2.02	0.42
4:D:130:PRO:HD2	4:D:201:TRP:CZ2	2.55	0.41
4:D:154:HIS:HB3	4:D:215:TYR:HB2	2.03	0.41
3:C:21:LEU:HD22	3:C:107:THR:HG21	2.03	0.41
1:E:192:TRP:CD1	2:F:15:PRO:HD2	2.56	0.41
4:H:154:HIS:HB3	4:H:215:TYR:HB2	2.03	0.41
3:C:151:LYS:H	3:C:192:ASN:ND2	2.18	0.40
1:A:11:ARG:HB3	1:A:13:LEU:CD1	2.52	0.40
1:A:89:SER:HA	1:A:90:PRO:C	2.46	0.40
1:A:102:ALA:HB2	1:A:116:LEU:HG	2.03	0.40
4:D:116:ASP:HB3	4:D:118:LYS:HG3	2.02	0.40
1:A:192:TRP:CE3	2:B:14:PRO:HG3	2.56	0.40
1:E:11:ARG:HB3	1:E:13:LEU:CD1	2.52	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	293/302 (97%)	278 (95%)	14 (5%)	1 (0%)	36	67
1	E	276/302 (91%)	262 (95%)	13 (5%)	1 (0%)	30	61
2	B	96/99 (97%)	91 (95%)	4 (4%)	1 (1%)	12	41
2	F	93/99 (94%)	89 (96%)	3 (3%)	1 (1%)	11	39
3	C	199/208 (96%)	187 (94%)	10 (5%)	2 (1%)	12	41
3	G	167/208 (80%)	159 (95%)	7 (4%)	1 (1%)	21	52
4	D	240/245 (98%)	232 (97%)	8 (3%)	0	100	100
4	H	226/245 (92%)	218 (96%)	8 (4%)	0	100	100
All	All	1590/1708 (93%)	1516 (95%)	67 (4%)	7 (0%)	30	61

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	289	GLN
3	C	132	ASP
1	A	296	ARG
2	B	47	PRO
2	F	47	PRO
3	G	50	ILE
3	C	50	ILE

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	250/264 (95%)	238 (95%)	12 (5%)	23	54
1	E	238/264 (90%)	226 (95%)	12 (5%)	22	53
2	B	92/93 (99%)	89 (97%)	3 (3%)	33	63
2	F	89/93 (96%)	85 (96%)	4 (4%)	24	56
3	C	178/185 (96%)	167 (94%)	11 (6%)	16	46
3	G	155/185 (84%)	144 (93%)	11 (7%)	13	41
4	D	214/216 (99%)	204 (95%)	10 (5%)	23	55
4	H	205/216 (95%)	198 (97%)	7 (3%)	32	63
All	All	1421/1516 (94%)	1351 (95%)	70 (5%)	22	53

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	MET
1	A	150	LEU
1	A	170	LEU
1	A	190	VAL
1	A	198	SER
1	A	243	GLU
1	A	254	GLU
1	A	264	ARG
1	A	273	GLN
1	A	276	ILE
1	A	292	VAL
1	A	296	ARG
2	B	7	ILE
2	B	48	LYS
2	B	97	ARG
3	C	13	VAL
3	C	40	SER
3	C	47	LEU
3	C	50	ILE
3	C	82	SER
3	C	94	GLN
3	C	124	GLN
3	C	163	LEU
3	C	168	MET

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Mol	Chain	Res	Type
3	C	188	ASN
3	C	194	ILE
4	D	13	ILE
4	D	28	ASN
4	D	38	ILE
4	D	66	SER
4	D	67	VAL
4	D	143	LEU
4	D	177	LEU
4	D	187	ARG
4	D	193	ARG
4	D	242	ARG
1	E	61	GLN
1	E	69	MET
1	E	150	LEU
1	E	170	LEU
1	E	190	VAL
1	E	196	VAL
1	E	216	LYS
1	E	243	GLU
1	E	254	GLU
1	E	264	ARG
1	E	273	GLN
1	E	276	ILE
2	F	7	ILE
2	F	38	GLN
2	F	48	LYS
2	F	51	MET
3	G	13	VAL
3	G	47	LEU
3	G	50	ILE
3	G	82	SER
3	G	94	GLN
3	G	124	GLN
3	G	139	THR
3	G	163	LEU
3	G	168	MET
3	G	194	ILE
3	G	199	THR
4	H	13	ILE
4	H	38	ILE
4	H	66	SER

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Mol	Chain	Res	Type
4	H	67	VAL
4	H	143	LEU
4	H	187	ARG
4	H	193	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	134	GLN
1	A	161	GLN
1	A	248	GLN
1	A	267	HIS
1	A	284	HIS
1	A	294	ASN
3	C	2	GLN
3	C	5	GLN
3	C	144	GLN
3	C	192	ASN
4	D	10	HIS
4	D	17	GLN
4	D	48	ASN
4	D	154	HIS
4	D	213	GLN
4	D	225	GLN
1	E	14	GLN
1	E	62	GLN
1	E	134	GLN
1	E	161	GLN
1	E	267	HIS
2	F	24	ASN
3	G	2	GLN
3	G	5	GLN
3	G	144	GLN
4	H	10	HIS
4	H	17	GLN
4	H	48	ASN
4	H	154	HIS
4	H	167	HIS
4	H	213	GLN
4	H	225	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

11 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	NAG	I	1	1,5	14,14,15	1.87	5 (35%)	17,19,21	1.41	1 (5%)
5	NAG	I	2	5	14,14,15	1.86	4 (28%)	17,19,21	1.73	5 (29%)
5	BMA	I	3	5	11,11,12	1.81	4 (36%)	15,15,17	1.73	4 (26%)
5	MAN	I	4	5	11,11,12	1.91	3 (27%)	15,15,17	1.74	3 (20%)
6	NAG	J	1	6,1	14,14,15	1.93	3 (21%)	17,19,21	2.14	7 (41%)
6	NAG	J	2	6	14,14,15	1.94	4 (28%)	17,19,21	1.94	5 (29%)
7	NAG	K	1	1,7	14,14,15	1.90	5 (35%)	17,19,21	1.51	2 (11%)
7	NAG	K	2	7	14,14,15	1.88	4 (28%)	17,19,21	1.71	4 (23%)
7	BMA	K	3	7	11,11,12	1.81	4 (36%)	15,15,17	1.53	4 (26%)
6	NAG	L	1	6,1	14,14,15	1.91	3 (21%)	17,19,21	2.10	7 (41%)
6	NAG	L	2	6	14,14,15	1.91	4 (28%)	17,19,21	1.89	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
5	NAG	I	1	1,5	-	0/6/23/26	0/1/1/1

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

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	2	NAG	O5-C1	4.45	1.51	1.43
7	K	3	BMA	C4-C3	-4.30	1.41	1.52
6	L	2	NAG	O5-C1	4.29	1.50	1.43
7	K	1	NAG	O5-C1	4.20	1.50	1.43
6	J	1	NAG	O5-C1	4.17	1.50	1.43
6	L	1	NAG	O5-C1	4.13	1.50	1.43
5	I	3	BMA	C4-C3	-4.09	1.41	1.52
5	I	1	NAG	O5-C1	4.02	1.50	1.43
7	K	2	NAG	O5-C1	4.00	1.50	1.43
5	I	2	NAG	O5-C1	3.96	1.50	1.43
5	I	4	MAN	C4-C3	-3.93	1.42	1.52
6	L	1	NAG	C7-N2	3.64	1.46	1.34
6	J	1	NAG	C7-N2	3.61	1.46	1.34
6	J	2	NAG	C7-N2	3.51	1.45	1.34
6	L	2	NAG	C7-N2	3.45	1.45	1.34
5	I	1	NAG	C7-N2	3.36	1.45	1.34
7	K	2	NAG	C7-N2	3.30	1.45	1.34
7	K	1	NAG	C7-N2	3.29	1.45	1.34
5	I	2	NAG	C7-N2	3.11	1.44	1.34
5	I	4	MAN	C2-C3	-3.03	1.47	1.52
5	I	4	MAN	O5-C5	2.86	1.49	1.43
5	I	3	BMA	C2-C3	-2.61	1.48	1.52
7	K	3	BMA	C2-C3	-2.50	1.48	1.52
7	K	2	NAG	C1-C2	-2.49	1.49	1.52
5	I	3	BMA	O5-C1	-2.44	1.39	1.43
5	I	2	NAG	C3-C2	-2.43	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	1	NAG	C3-C2	-2.36	1.47	1.52
5	I	2	NAG	C1-C2	-2.35	1.49	1.52
6	J	2	NAG	C4-C3	-2.34	1.46	1.52
6	L	2	NAG	C4-C3	-2.33	1.46	1.52
7	K	2	NAG	C3-C2	-2.32	1.47	1.52
6	J	1	NAG	C4-C3	-2.25	1.46	1.52
7	K	3	BMA	O5-C1	-2.25	1.39	1.43
7	K	1	NAG	C3-C2	-2.23	1.47	1.52
7	K	3	BMA	O5-C5	2.19	1.47	1.43
7	K	1	NAG	C1-C2	-2.18	1.49	1.52
6	L	1	NAG	C4-C3	-2.16	1.46	1.52
5	I	3	BMA	O5-C5	2.16	1.47	1.43
6	J	2	NAG	C3-C2	-2.15	1.48	1.52
5	I	1	NAG	C1-C2	-2.10	1.49	1.52
5	I	1	NAG	C4-C3	-2.06	1.47	1.52
6	L	2	NAG	C3-C2	-2.05	1.48	1.52
7	K	1	NAG	C4-C3	-2.01	1.47	1.52

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	2	NAG	C1-O5-C5	4.71	118.50	112.19
6	L	2	NAG	C1-O5-C5	4.30	117.95	112.19
6	J	1	NAG	C4-C3-C2	4.22	117.20	111.02
6	L	1	NAG	C4-C3-C2	4.09	117.01	111.02
6	L	1	NAG	C3-C4-C5	3.96	117.41	110.23
6	J	1	NAG	C3-C4-C5	3.89	117.29	110.23
5	I	4	MAN	C1-O5-C5	3.87	117.37	112.19
5	I	2	NAG	C3-C4-C5	3.50	116.57	110.23
7	K	2	NAG	C3-C4-C5	3.50	116.57	110.23
5	I	2	NAG	C4-C3-C2	3.39	115.98	111.02
7	K	3	BMA	C2-C3-C4	3.35	116.75	110.86
5	I	3	BMA	C2-C3-C4	3.28	116.63	110.86
7	K	2	NAG	C4-C3-C2	3.21	115.73	111.02
6	L	2	NAG	C4-C3-C2	3.20	115.70	111.02
5	I	3	BMA	C1-O5-C5	2.97	116.17	112.19
6	J	1	NAG	O5-C1-C2	2.90	115.78	111.29
5	I	3	BMA	O3-C3-C4	2.88	117.16	110.38
6	J	2	NAG	C4-C3-C2	2.87	115.22	111.02
6	L	1	NAG	O5-C1-C2	2.86	115.72	111.29
5	I	4	MAN	C1-C2-C3	2.79	113.70	109.64
6	J	1	NAG	O6-C6-C5	2.60	120.20	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	1	NAG	O5-C5-C6	2.60	112.72	107.66
6	J	1	NAG	O5-C5-C6	2.59	112.70	107.66
5	I	1	NAG	C3-C4-C5	2.58	114.91	110.23
5	I	2	NAG	C1-C2-N2	-2.58	106.37	110.43
7	K	1	NAG	C8-C7-N2	2.55	120.36	116.12
5	I	4	MAN	C2-C3-C4	2.53	115.31	110.86
6	J	2	NAG	O5-C1-C2	2.52	115.20	111.29
7	K	1	NAG	C3-C4-C5	2.48	114.72	110.23
6	L	1	NAG	O6-C6-C5	2.45	119.66	111.33
6	L	2	NAG	O5-C1-C2	2.40	115.00	111.29
6	J	1	NAG	C8-C7-N2	2.39	120.08	116.12
6	L	2	NAG	C3-C4-C5	2.33	114.45	110.23
7	K	3	BMA	C1-O5-C5	2.30	115.27	112.19
6	L	1	NAG	C8-C7-N2	2.27	119.88	116.12
7	K	2	NAG	O5-C5-C6	2.23	112.01	107.66
6	J	2	NAG	C3-C4-C5	2.18	114.18	110.23
7	K	2	NAG	C1-C2-N2	-2.17	107.02	110.43
7	K	3	BMA	O4-C4-C3	-2.07	105.49	110.38
5	I	2	NAG	O5-C5-C6	2.07	111.69	107.66
5	I	2	NAG	O6-C6-C5	2.06	118.35	111.33
5	I	3	BMA	O6-C6-C5	2.04	118.28	111.33
6	J	2	NAG	C8-C7-N2	2.03	119.49	116.12
6	J	1	NAG	O5-C5-C4	2.03	115.76	110.83
7	K	3	BMA	O6-C6-C5	2.02	118.22	111.33
6	L	1	NAG	O5-C5-C4	2.01	115.71	110.83

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	J	1	NAG	C4-C5-C6-O6
6	L	1	NAG	C4-C5-C6-O6
6	L	1	NAG	O5-C5-C6-O6
7	K	3	BMA	O5-C5-C6-O6
5	I	3	BMA	O5-C5-C6-O6
6	J	1	NAG	O5-C5-C6-O6
7	K	2	NAG	C4-C5-C6-O6
5	I	2	NAG	C4-C5-C6-O6
6	J	2	NAG	C4-C5-C6-O6
6	L	2	NAG	C4-C5-C6-O6
7	K	2	NAG	O5-C5-C6-O6
5	I	2	NAG	O5-C5-C6-O6

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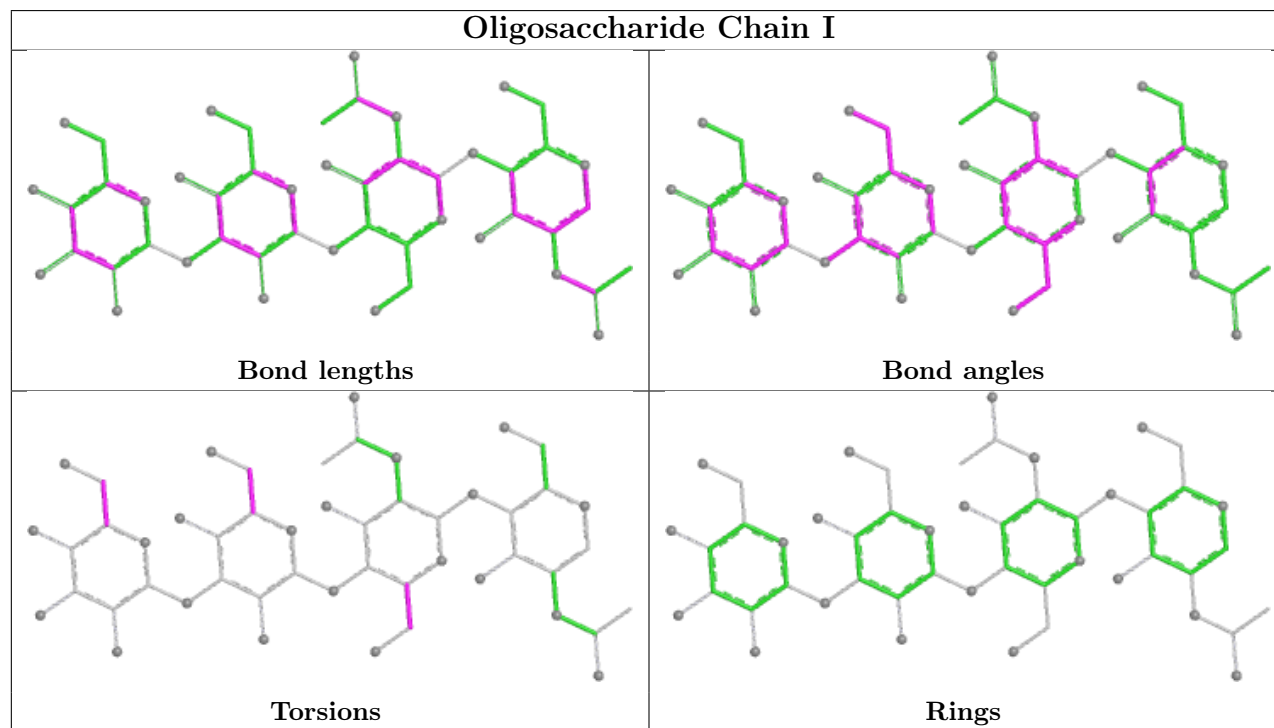
Mol	Chain	Res	Type	Atoms
6	L	2	NAG	O5-C5-C6-O6
6	J	2	NAG	O5-C5-C6-O6
5	I	4	MAN	C4-C5-C6-O6
7	K	3	BMA	C4-C5-C6-O6
5	I	3	BMA	C4-C5-C6-O6
5	I	4	MAN	O5-C5-C6-O6

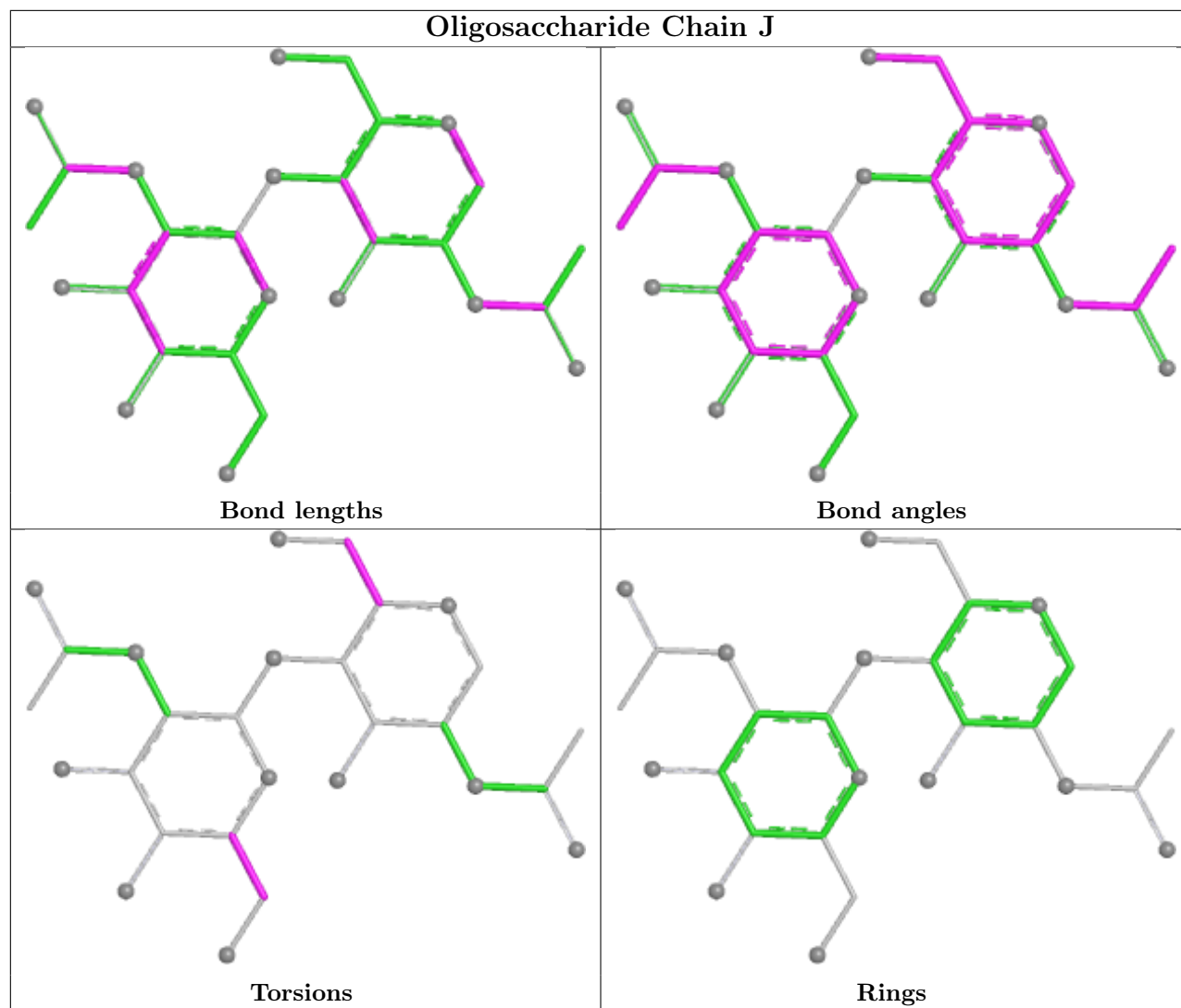
There are no ring outliers.

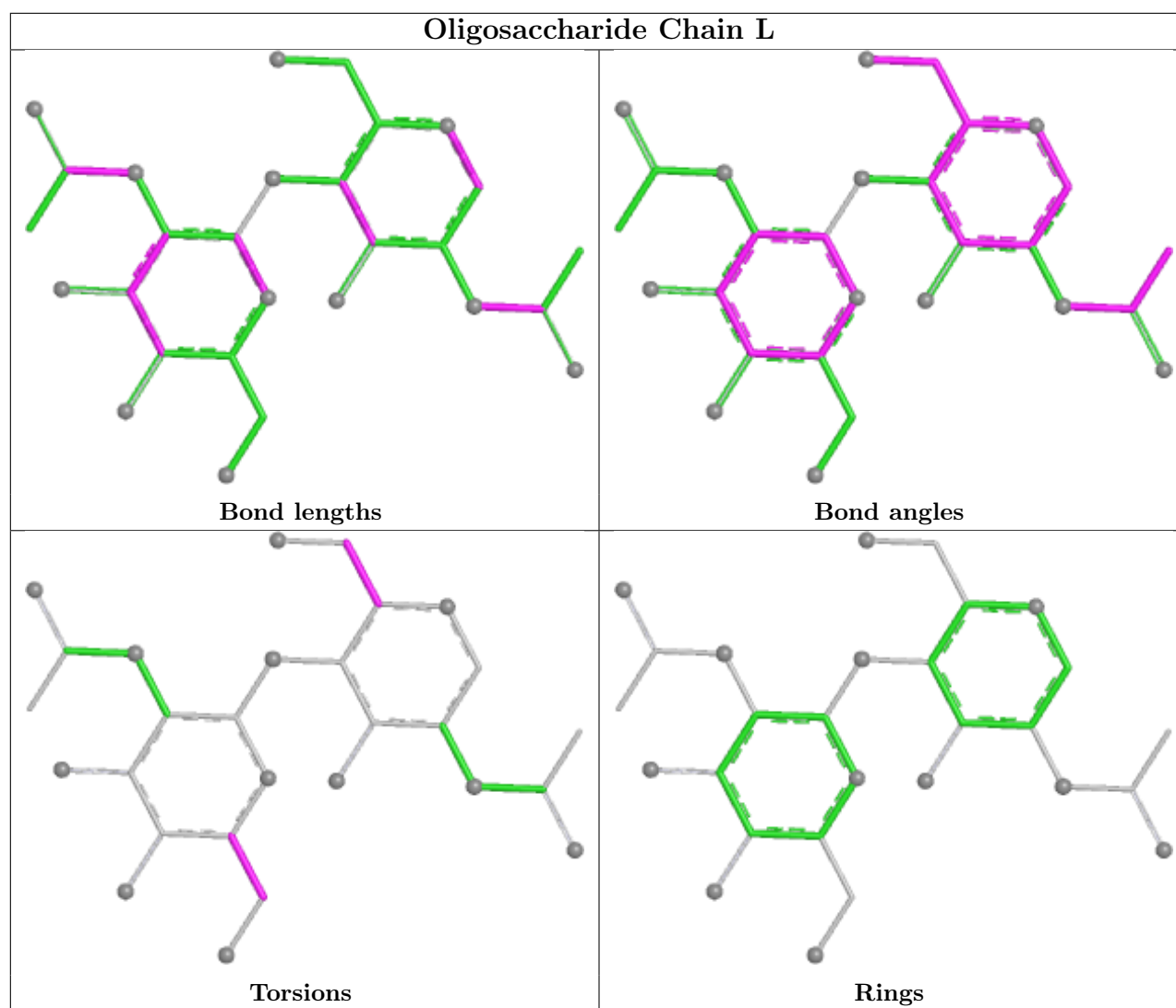
2 monomers are involved in 2 short contacts:

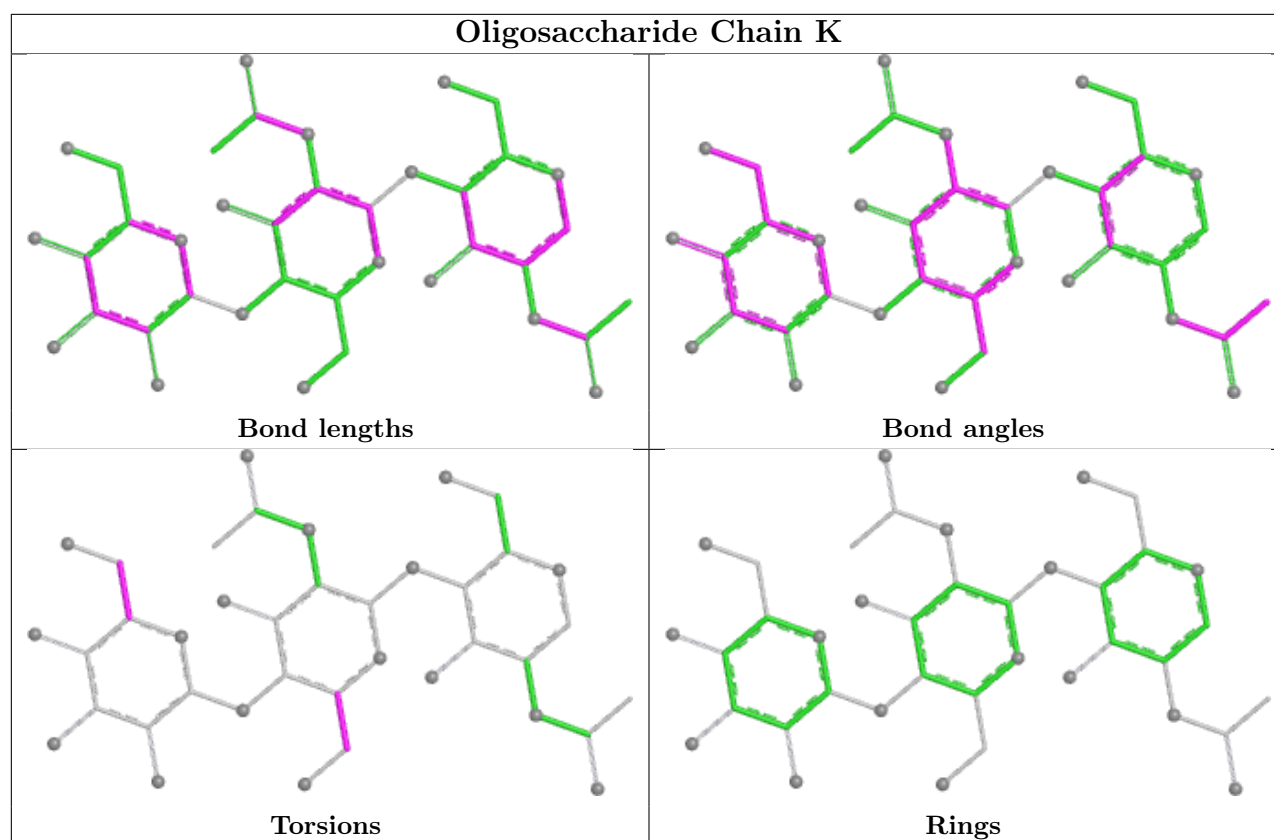
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	1	NAG	1	0
7	K	1	NAG	1	0

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









5.6 Ligand geometry [i](#)

5 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$
8	NAG	E	404	1	14,14,15	2.07	5 (35%)	17,19,21	2.29	6 (35%)
9	FLC	A	408	-	12,12,12	1.20	1 (8%)	17,17,17	1.04	1 (5%)
8	NAG	A	405	1	14,14,15	1.94	5 (35%)	17,19,21	1.80	6 (35%)
10	CIS	A	409	-	54,55,61	1.70	8 (14%)	62,66,72	1.41	10 (16%)
10	CIS	E	407	-	33,34,61	2.16	8 (24%)	41,45,72	1.77	9 (21%)

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	404	1	-	3/6/23/26	0/1/1/1
9	FLC	A	408	-	-	1/16/16/16	-
8	NAG	A	405	1	-	2/6/23/26	0/1/1/1
10	CIS	A	409	-	-	15/52/72/78	0/1/1/1
10	CIS	E	407	-	-	10/31/51/78	0/1/1/1

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	E	407	CIS	O-C43	6.77	1.51	1.40
10	A	409	CIS	O-C43	6.35	1.50	1.40
10	E	407	CIS	C18-N	5.45	1.45	1.34
10	E	407	CIS	O6-C43	5.21	1.55	1.41
10	A	409	CIS	C18-N	5.01	1.44	1.34
10	A	409	CIS	O6-C43	4.94	1.54	1.41
8	E	404	NAG	O5-C1	4.75	1.51	1.43
8	A	405	NAG	O5-C1	4.68	1.51	1.43
10	A	409	CIS	C2-C3	3.91	1.56	1.50
10	E	407	CIS	C2-C3	3.73	1.56	1.50
8	E	404	NAG	C7-N2	3.31	1.45	1.34
8	A	405	NAG	C7-N2	3.02	1.44	1.34
10	A	409	CIS	C44-C45	-3.02	1.44	1.52
10	E	407	CIS	C44-C45	-2.70	1.44	1.52
10	A	409	CIS	O4-S	-2.60	1.49	1.57
9	A	408	FLC	OB2-CBC	-2.54	1.21	1.30
10	A	409	CIS	O1-C2	-2.53	1.39	1.43
10	E	407	CIS	O4-S	-2.35	1.50	1.57
10	A	409	CIS	C3-C4	2.32	1.41	1.31
8	E	404	NAG	C3-C2	-2.31	1.47	1.52
10	E	407	CIS	C3-C4	2.31	1.41	1.31
8	A	405	NAG	C4-C3	-2.27	1.46	1.52
8	E	404	NAG	C4-C3	-2.23	1.46	1.52
8	E	404	NAG	C1-C2	-2.22	1.49	1.52
10	E	407	CIS	O1-C2	-2.14	1.39	1.43
8	A	405	NAG	C3-C2	-2.14	1.48	1.52
8	A	405	NAG	C1-C2	-2.01	1.49	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	E	404	NAG	C2-N2-C7	6.09	131.06	122.90
10	E	407	CIS	O-C43-C44	4.61	115.28	108.27
10	A	409	CIS	O-C43-C44	4.45	115.03	108.27
8	A	405	NAG	C1-C2-N2	-3.70	104.61	110.43
10	A	409	CIS	O8-S-O9	-3.29	99.53	112.24
10	E	407	CIS	O6-C47-C48	3.21	114.38	106.44
10	A	409	CIS	O10-S-O4	3.17	113.65	106.37
8	E	404	NAG	O5-C5-C6	3.15	113.78	107.66
10	E	407	CIS	C43-C44-C45	3.10	115.52	110.11
10	E	407	CIS	O10-S-O4	3.00	113.27	106.37
10	E	407	CIS	O8-S-O9	-2.99	100.70	112.24
8	A	405	NAG	O5-C5-C6	2.98	113.46	107.66
10	E	407	CIS	C46-C45-C44	2.95	114.95	110.86
10	E	407	CIS	C-O-C43	2.94	120.10	113.80
10	A	409	CIS	C46-C45-C44	2.89	114.86	110.86
10	A	409	CIS	C-O-C43	2.86	119.94	113.80
8	E	404	NAG	C1-O5-C5	2.80	115.94	112.19
10	A	409	CIS	O3-C44-C43	-2.64	103.77	110.08
8	A	405	NAG	C8-C7-N2	2.64	120.50	116.12
8	A	405	NAG	O4-C4-C5	2.55	115.60	109.32
10	A	409	CIS	C19-C18-N	2.45	120.18	115.86
10	E	407	CIS	O3-C44-C43	-2.38	104.39	110.08
8	E	404	NAG	O4-C4-C5	2.31	115.02	109.32
10	A	409	CIS	O6-C47-C48	2.31	112.15	106.44
8	E	404	NAG	C4-C3-C2	-2.30	107.64	111.02
8	E	404	NAG	O7-C7-C8	-2.29	117.97	122.05
10	E	407	CIS	C2-C1-N	2.26	113.48	109.66
10	A	409	CIS	C43-C44-C45	2.19	113.93	110.11
10	A	409	CIS	O2-C18-C19	-2.17	118.09	122.02
9	A	408	FLC	OB1-CBC-CB	-2.16	117.91	122.09
8	A	405	NAG	C1-O5-C5	2.14	115.05	112.19
8	A	405	NAG	C2-N2-C7	-2.01	120.20	122.90

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	E	404	NAG	C3-C2-N2-C7
8	E	404	NAG	O5-C5-C6-O6
8	A	405	NAG	O5-C5-C6-O6
8	A	405	NAG	C4-C5-C6-O6
8	E	404	NAG	C4-C5-C6-O6
10	E	407	CIS	O1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
10	E	407	CIS	C18-C19-C20-C21
10	E	407	CIS	C46-C47-C48-O7
10	E	407	CIS	C4-C5-C6-C7
10	A	409	CIS	C34-C35-C36-C37
10	A	409	CIS	C6-C7-C8-C9
10	A	409	CIS	C21-C22-C23-C24
10	A	409	CIS	C27-C28-C29-C30
10	A	409	CIS	C25-C26-C27-C28
10	A	409	CIS	C22-C23-C24-C25
10	A	409	CIS	C36-C37-C38-C39
10	A	409	CIS	C31-C32-C33-C34
10	A	409	CIS	C28-C29-C30-C31
10	A	409	CIS	C23-C24-C25-C26
10	A	409	CIS	C26-C27-C28-C29
10	A	409	CIS	C7-C8-C9-C10
10	E	407	CIS	C2-C3-C4-C5
10	A	409	CIS	C5-C6-C7-C8
9	A	408	FLC	CG-CB-CBC-OB1
10	E	407	CIS	C1-C2-C3-C4
10	E	407	CIS	C21-C22-C23-C24
10	E	407	CIS	N-C1-C2-O1
10	A	409	CIS	C30-C31-C32-C33
10	E	407	CIS	C46-C45-O4-S
10	E	407	CIS	C3-C4-C5-C6
10	A	409	CIS	C24-C25-C26-C27

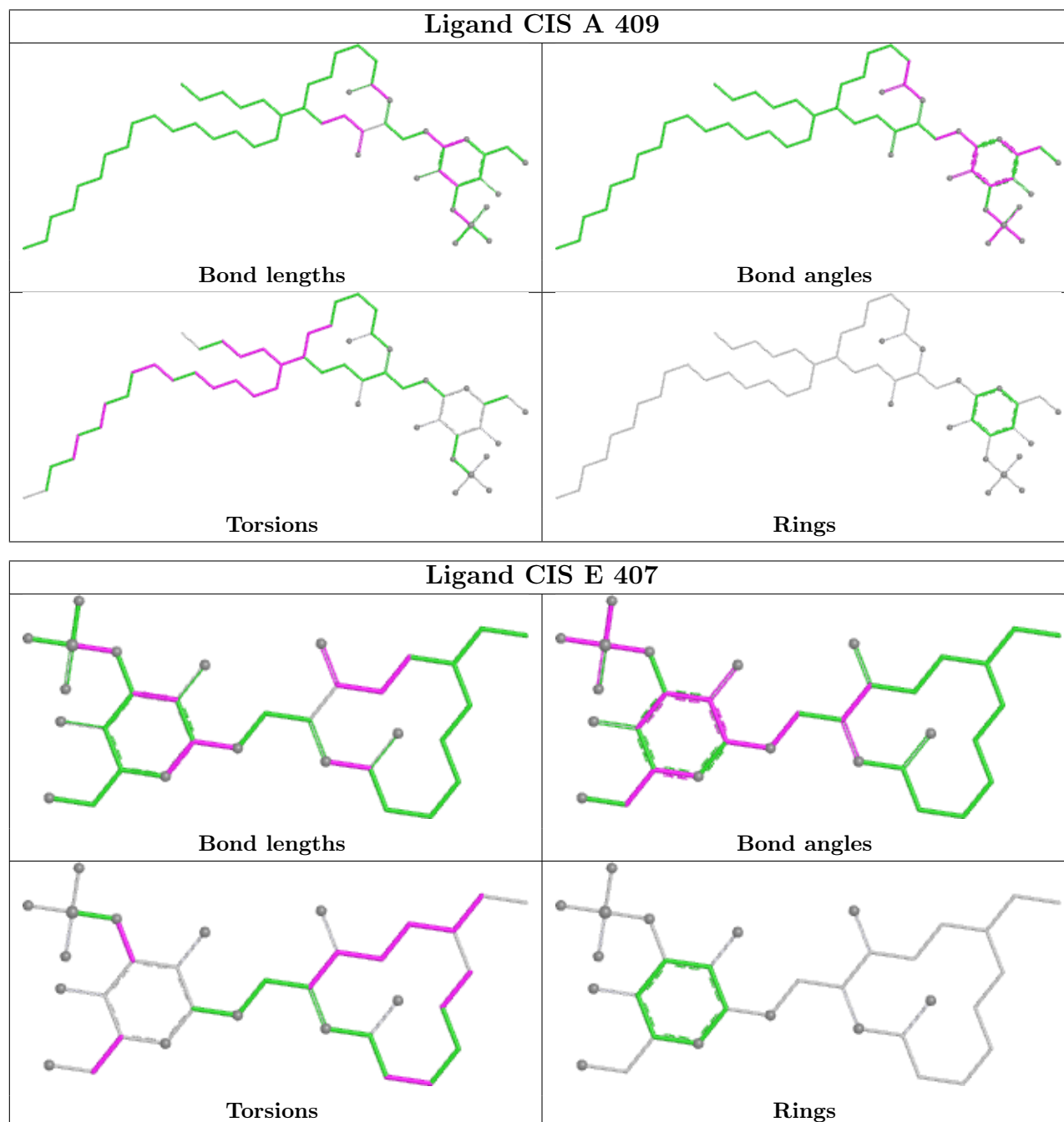
There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	408	FLC	5	0
10	A	409	CIS	3	0
10	E	407	CIS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

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, 95th 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	295/302 (97%)	-0.21	4 (1%) 73 53	50, 76, 116, 158	0
1	E	280/302 (92%)	0.04	8 (2%) 53 32	60, 109, 167, 184	0
2	B	98/99 (98%)	-0.46	0 100 100	52, 67, 92, 105	0
2	F	95/99 (95%)	-0.12	0 100 100	91, 117, 140, 153	0
3	C	201/208 (96%)	-0.22	0 100 100	48, 83, 164, 181	0
3	G	172/208 (82%)	0.07	6 (3%) 47 27	44, 77, 178, 190	1 (0%)
4	D	242/245 (98%)	-0.12	2 (0%) 82 65	49, 97, 150, 173	0
4	H	230/245 (93%)	0.11	3 (1%) 75 56	58, 126, 173, 191	0
All	All	1613/1708 (94%)	-0.09	23 (1%) 73 53	44, 96, 163, 191	1 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	109	GLY	3.8
3	G	202	PRO	3.1
1	A	153	ASP	3.1
3	G	2	GLN	3.0
1	E	150	LEU	2.8
1	E	122	GLY	2.8
1	E	285	ILE	2.7
1	E	154	GLN	2.6
4	H	146	LEU	2.6
1	E	93	ASP	2.5
3	G	162	VAL	2.5
3	G	192	ASN	2.4
1	A	108	PRO	2.4
1	E	275	ILE	2.4
1	E	90	PRO	2.4
1	E	287	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
3	G	103	PHE	2.3
3	G	196	PRO	2.3
4	D	39	LEU	2.2
4	H	189	ALA	2.2
4	H	204	PRO	2.1
1	A	110	ASN	2.1
4	D	28	ASN	2.1

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](#)

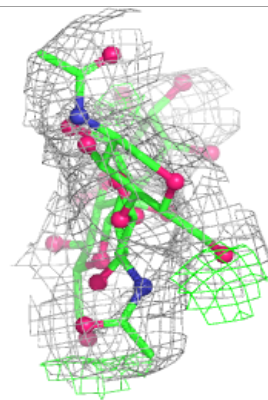
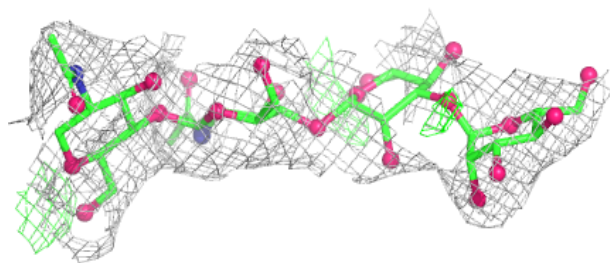
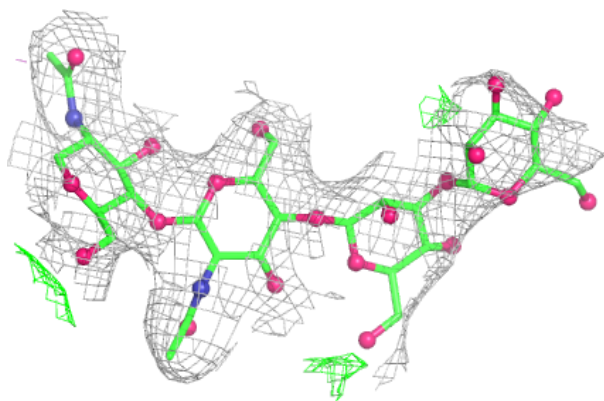
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	L	2	14/15	0.38	0.14	162,171,175,177	0
5	MAN	I	4	11/12	0.48	0.14	151,156,163,163	0
5	BMA	I	3	11/12	0.53	0.12	127,139,145,146	0
6	NAG	J	1	14/15	0.64	0.15	108,117,128,133	0
6	NAG	J	2	14/15	0.68	0.14	139,147,152,152	0
7	BMA	K	3	11/12	0.71	0.10	141,149,153,156	0
6	NAG	L	1	14/15	0.78	0.13	150,152,160,161	0
7	NAG	K	1	14/15	0.86	0.10	72,91,96,103	0
7	NAG	K	2	14/15	0.88	0.10	108,112,125,133	0
5	NAG	I	2	14/15	0.94	0.08	76,88,103,115	0
5	NAG	I	1	14/15	0.94	0.09	64,70,78,83	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.

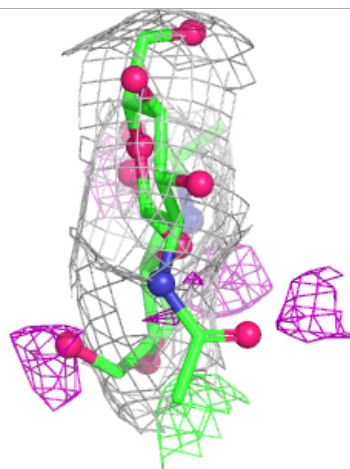
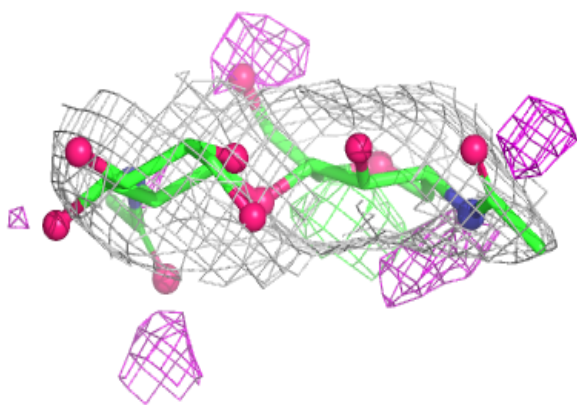
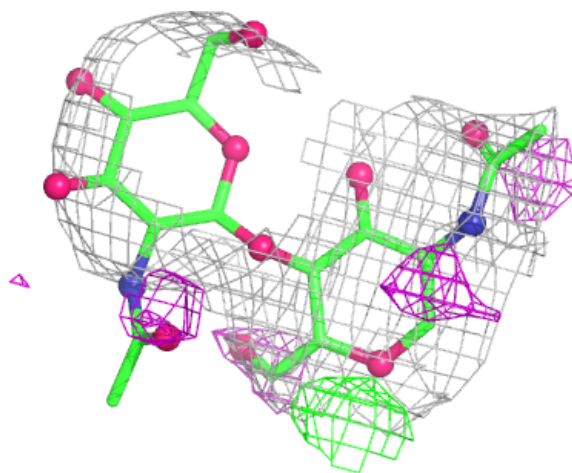
Electron density around Chain I:

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



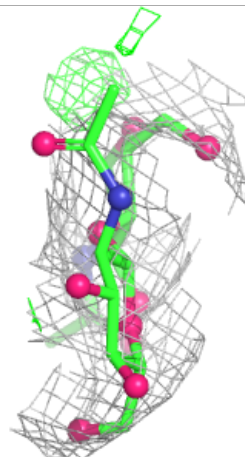
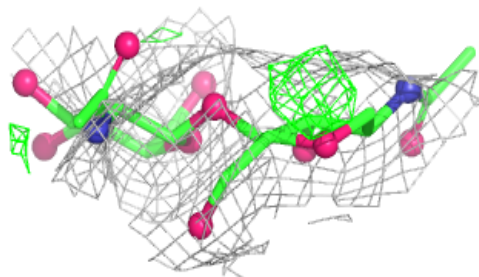
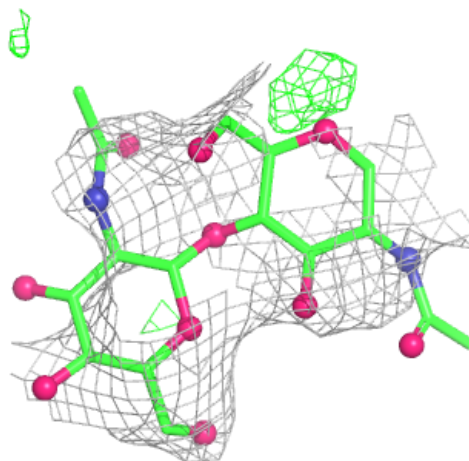
Electron density around Chain J:

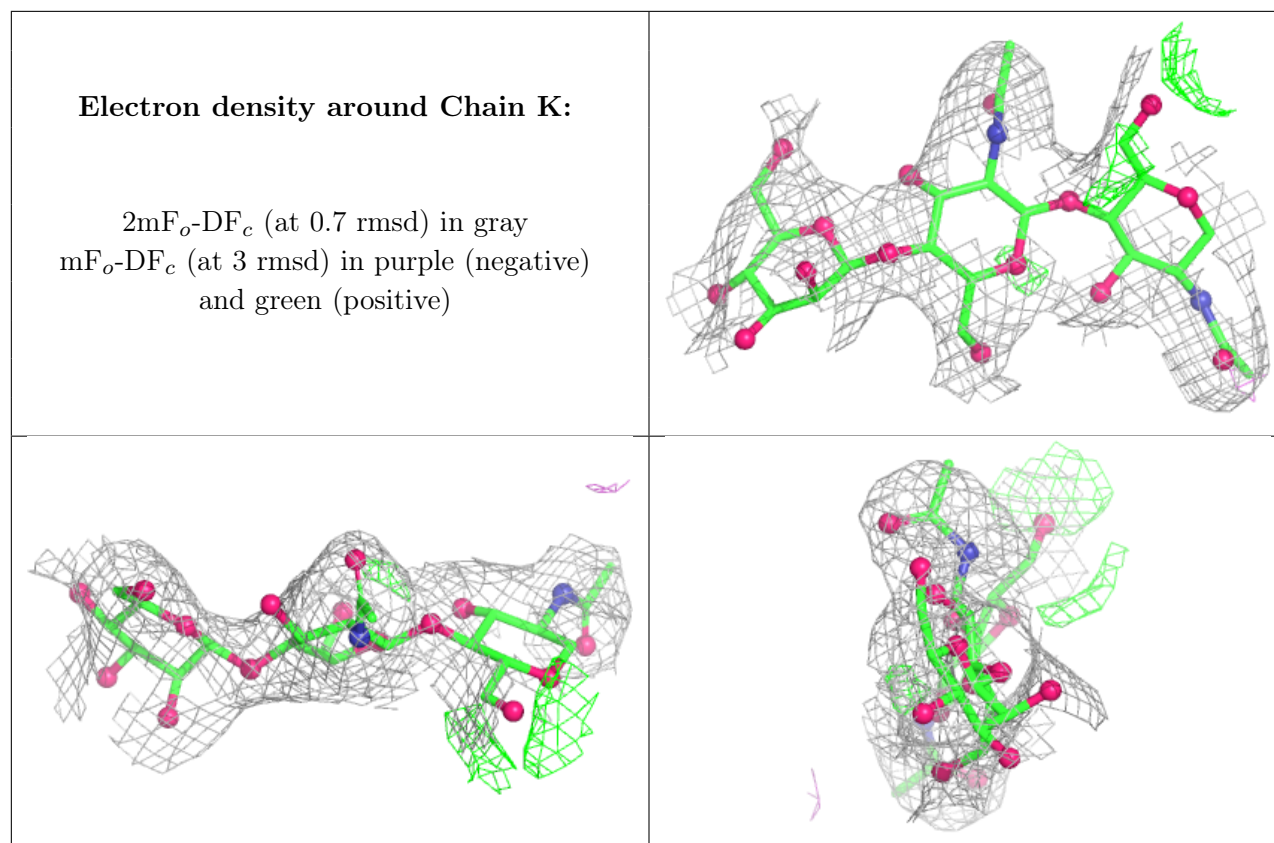
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain 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 [i](#)

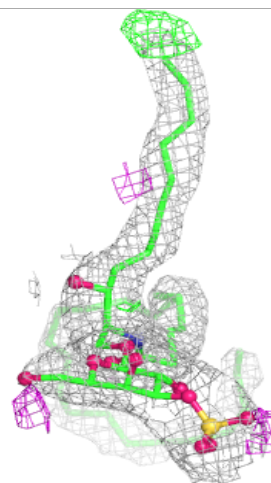
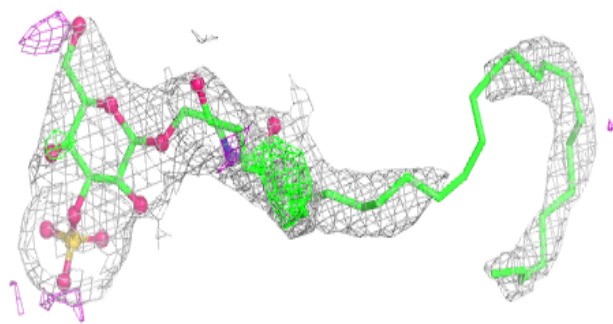
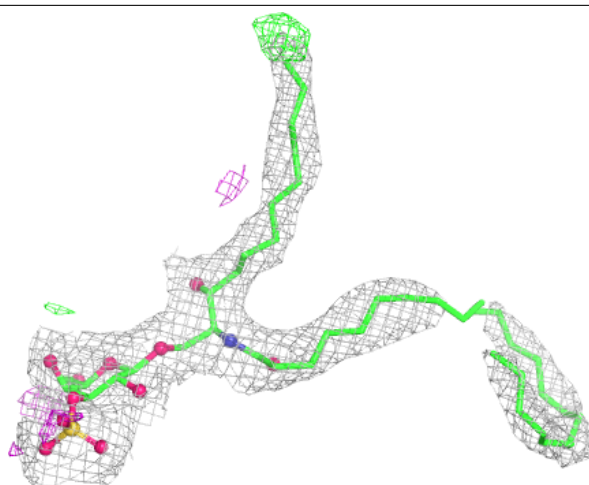
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	E	404	14/15	0.49	0.14	142,156,161,161	0
8	NAG	A	405	14/15	0.83	0.12	106,118,138,139	0
9	FLC	A	408	13/13	0.91	0.14	35,63,70,77	0
10	CIS	A	409	55/61	0.95	0.10	50,59,69,71	3
10	CIS	E	407	34/61	0.95	0.09	66,76,86,87	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

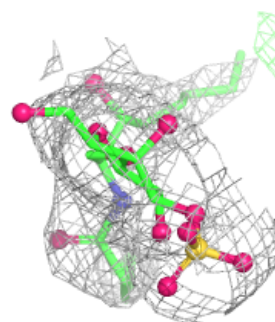
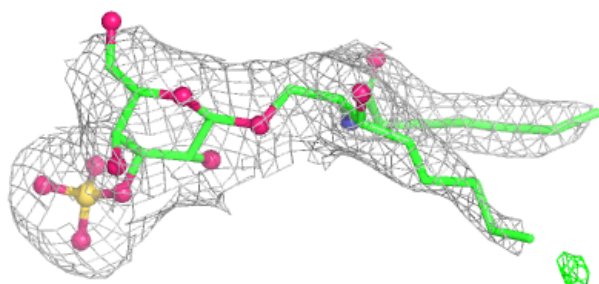
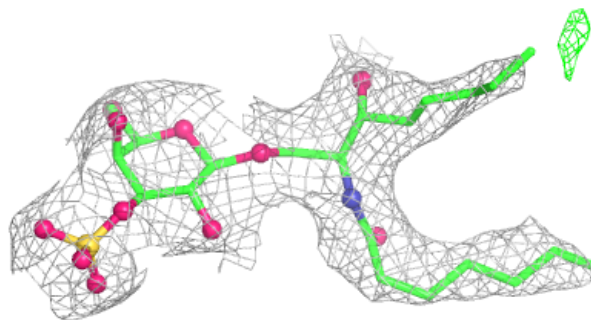
Electron density around CIS A 409:

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



Electron density around CIS E 407:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.