



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 05:55 AM EDT

PDB ID : 7UCY
Title : Integrin alaphIIBbeta3 complex with gantofiban
Authors : Lin, F.-Y.; Zhu, J.; Zhu, J.; Springer, T.A.
Deposited on : 2022-03-17
Resolution : 2.35 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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Mol	Chain	Length	Quality of chain
3	H	221	
4	F	214	
4	L	214	
5	G	5	
6	I	2	
6	K	2	
7	J	4	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 22418 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 Integrin alpha-IIb heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	454	Total	C	N	O	S	0	5	0
			3512	2232	605	667	8			
1	C	453	Total	C	N	O	S	0	6	0
			3514	2230	606	670	8			

- Molecule 2 is a protein called Isoform Beta-3C of Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	466	Total	C	N	O	S	0	5	0
			3624	2255	618	717	34			
2	D	471	Total	C	N	O	S	0	1	0
			3632	2260	621	717	34			

- Molecule 3 is a protein called 10E5 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	214	Total	C	N	O	S	0	0	0
			1631	1035	264	326	6			
3	H	216	Total	C	N	O	S	0	0	0
			1642	1041	266	329	6			

- Molecule 4 is a protein called 10E5 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	F	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			
4	L	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



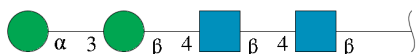
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	G	5	61	34	2	25	0	0	0

- 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
			Total	C	N	O			
6	I	2	28	16	2	10	0	0	0
6	K	2	28	16	2	10	0	0	0

- Molecule 7 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
			Total	C	N	O			
7	J	4	50	28	2	20	0	0	0

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	L	1	Total	O	S	0	0
			5	4	1		

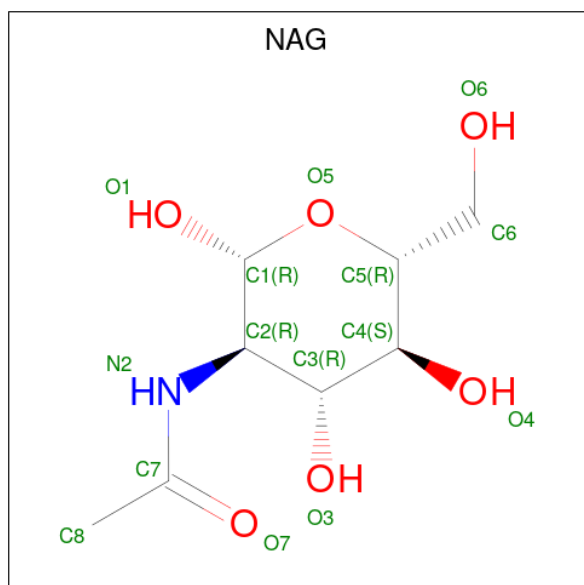
- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	4	Total	Ca	0	0
			4	4		
9	C	4	Total	Ca	0	0
			4	4		

- Molecule 10 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

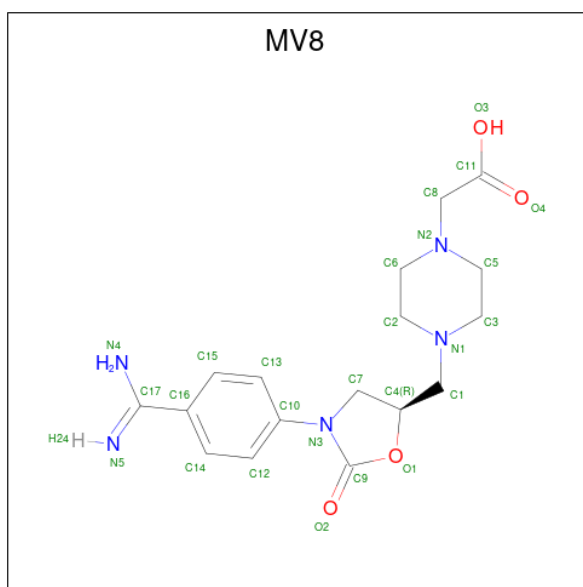
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	3	Total	Mn	0	0
			3	3		
10	D	3	Total	Mn	0	0
			3	3		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 12 is (4-{{(5R)-3-(4-carbamimidoylphenyl)-2-oxo-1,3-oxazolidin-5-yl}methyl}piperazin-1-yl)acetic acid (three-letter code: MV8) (formula: C₁₇H₂₃N₅O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	1	Total	C	N	O	0	0
			26	17	5	4		
12	D	1	Total	C	N	O	0	0
			26	17	5	4		

- Molecule 13 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	C	1	Total	Cl	0	0
			1	1		
13	D	1	Total	Cl	0	0
			1	1		

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	448	Total	O	0	0
			448	448		
14	B	283	Total	O	0	0
			283	283		
14	C	224	Total	O	0	0
			224	224		
14	D	197	Total	O	0	0
			197	197		
14	E	18	Total	O	0	0
			18	18		

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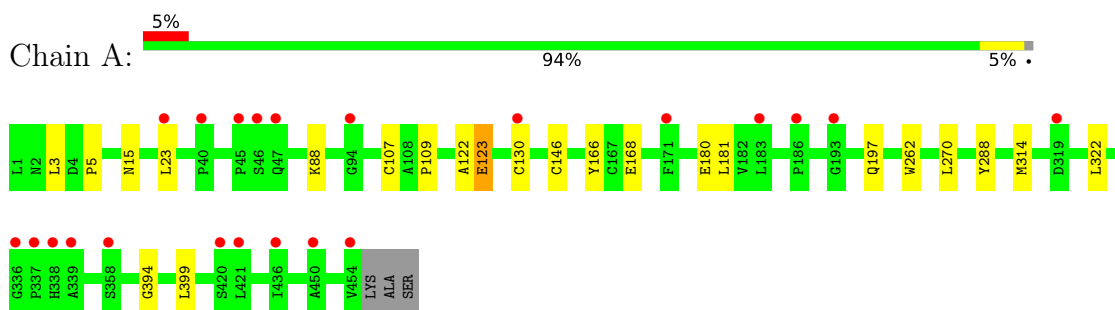
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	F	18	Total O 18 18	0	0
14	H	36	Total O 36 36	0	0
14	L	57	Total O 57 57	0	0

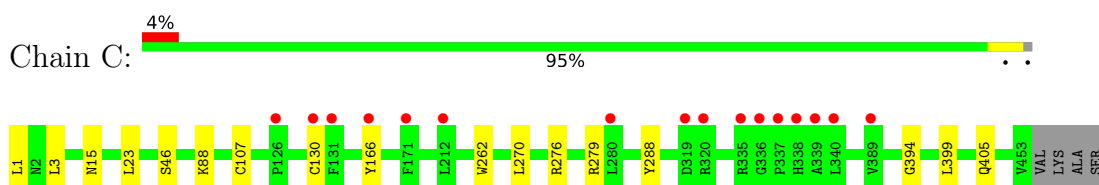
3 Residue-property plots

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.

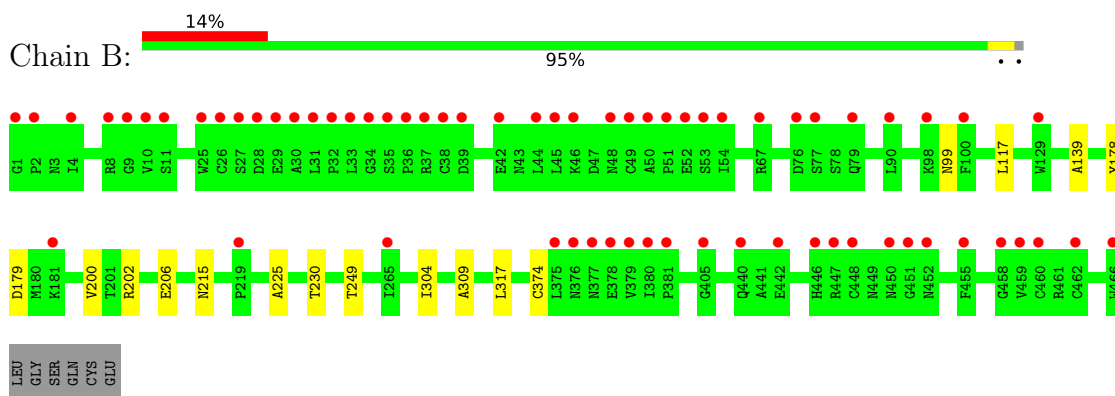
- Molecule 1: Integrin alpha-IIb heavy chain



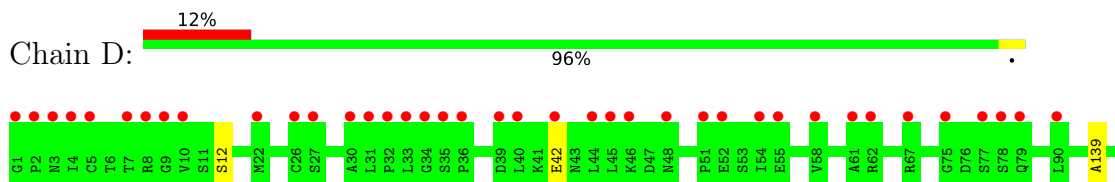
- Molecule 1: Integrin alpha-IIb heavy chain

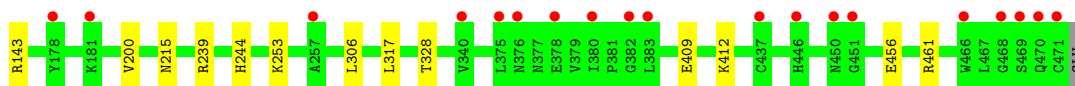


- Molecule 2: Isoform Beta-3C of Integrin beta-3

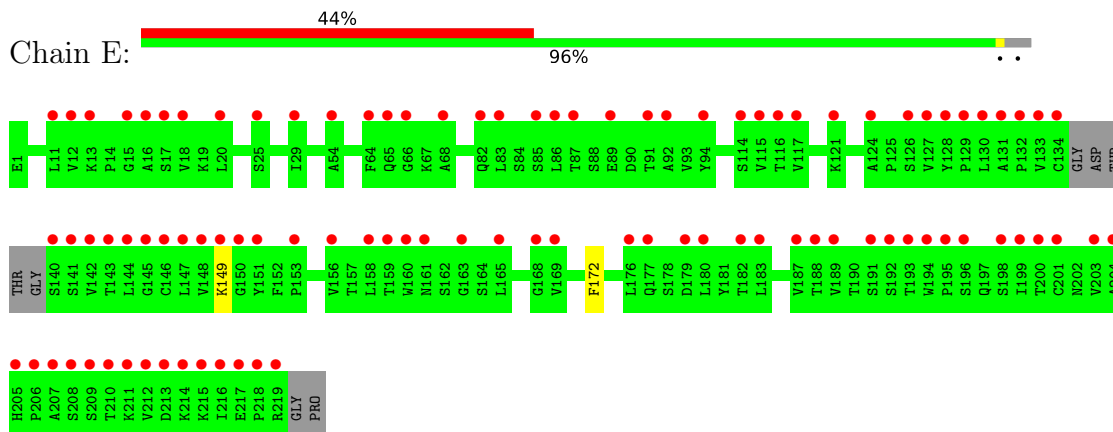


- Molecule 2: Isoform Beta-3C of Integrin beta-3

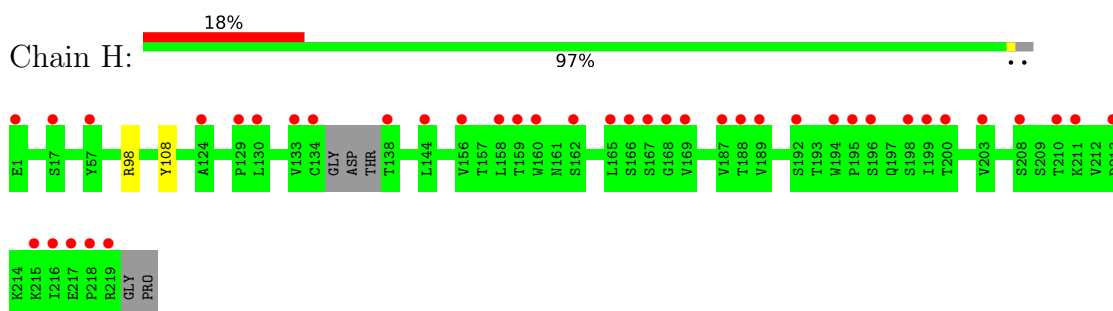




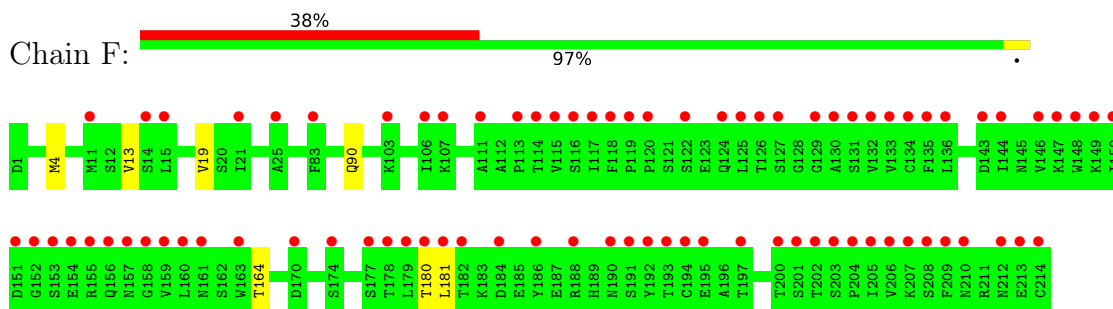
- Molecule 3: 10E5 Fab heavy chain



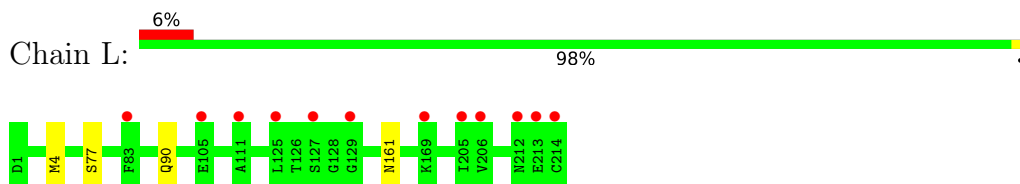
- Molecule 3: 10E5 Fab heavy chain



- Molecule 4: 10E5 Fab light chain



- Molecule 4: 10E5 Fab light chain



- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  40% 60%


MAG1
MAG2
BMA3
MAN4
MAN5

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

Chain I:  100%


MAG1
MAG2

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

Chain K:  100%


MAG1
MAG2

- Molecule 7: 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 J:  50% 50%


MAG1
MAG2
BMA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	258.55Å 144.46Å 105.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.98 – 2.35 48.98 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.98-2.35) 99.5 (48.98-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 2.34Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.221 , 0.231 0.221 , 0.231	Depositor DCC
R_{free} test set	1995 reflections (1.22%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtrriage
Anisotropy	0.267	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	22418	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, MV8, CA, SO4, MN, NAG, CL, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.26	0/3618	0.48	0/4931
1	C	0.25	0/3617	0.46	0/4928
2	B	0.24	0/3694	0.45	0/5008
2	D	0.24	0/3699	0.44	0/5015
3	E	0.24	0/1673	0.45	0/2290
3	H	0.24	0/1684	0.46	0/2305
4	F	0.24	0/1673	0.44	0/2269
4	L	0.24	0/1673	0.45	0/2269
All	All	0.25	0/21331	0.45	0/29015

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3512	0	3350	12	0
1	C	3514	0	3342	9	0
2	B	3624	0	3537	8	0
2	D	3632	0	3547	9	0
3	E	1631	0	1590	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1642	0	1600	1	0
4	F	1637	0	1553	4	0
4	L	1637	0	1553	2	0
5	G	61	0	52	0	0
6	I	28	0	25	0	0
6	K	28	0	25	0	0
7	J	50	0	43	0	0
8	A	20	0	0	0	0
8	C	20	0	0	0	0
8	L	5	0	0	0	0
9	A	4	0	0	0	0
9	C	4	0	0	0	0
10	B	3	0	0	0	0
10	D	3	0	0	0	0
11	B	14	0	13	0	0
11	D	14	0	13	0	0
12	B	26	0	0	0	0
12	D	26	0	0	0	0
13	C	1	0	0	0	0
13	D	1	0	0	0	0
14	A	448	0	0	3	2
14	B	283	0	0	1	0
14	C	224	0	0	3	2
14	D	197	0	0	0	0
14	E	18	0	0	0	0
14	F	18	0	0	0	0
14	H	36	0	0	0	0
14	L	57	0	0	1	0
All	All	22418	0	20243	42	2

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 1.

All (42) 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:146:CYS:SG	14:A:798:HOH:O	2.36	0.83
2:B:99:ASN:OD1	14:B:2101:HOH:O	2.11	0.69
1:C:46[B]:SER:OG	14:C:601:HOH:O	2.15	0.63
4:L:4:MET:HE2	4:L:90:GLN:HB3	1.86	0.57
1:C:3:LEU:O	1:C:405:GLN:NE2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:161:ASN:ND2	14:L:402:HOH:O	2.44	0.50
4:F:4:MET:HE2	4:F:90:GLN:HB3	1.93	0.49
2:B:202:ARG:NH2	2:B:206:GLU:OE2	2.47	0.48
1:A:88:LYS:NZ	14:A:608:HOH:O	2.36	0.47
2:D:306:LEU:HB3	2:D:328:THR:HG22	1.96	0.47
1:A:15[A]:ASN:ND2	14:A:607:HOH:O	2.36	0.47
2:B:117:LEU:HD11	2:B:225:ALA:HB1	1.96	0.46
3:E:172:PHE:CD2	4:F:164:THR:HG23	2.50	0.46
1:A:122:ALA:O	1:A:123:GLU:HB2	2.15	0.46
1:C:107:CYS:HA	1:C:130:CYS:HA	1.98	0.45
1:A:262:TRP:HB3	2:B:317:LEU:HD13	1.99	0.45
1:C:394:GLY:HA2	1:C:399:LEU:HD23	1.98	0.44
4:F:13:VAL:HG11	4:F:19:VAL:HG11	1.99	0.44
2:D:139:ALA:HB2	2:D:200:VAL:HG11	1.99	0.44
2:B:139:ALA:HB2	2:B:200:VAL:HG11	2.00	0.44
2:B:230:THR:HG23	2:B:304:ILE:HG13	2.00	0.44
1:A:394:GLY:HA2	1:A:399:LEU:HD23	2.00	0.44
1:A:180:GLU:HG2	1:A:197:GLN:NE2	2.33	0.43
1:A:107:CYS:HA	1:A:130:CYS:HA	1.99	0.43
2:B:249:THR:HA	2:B:309:ALA:O	2.18	0.43
1:A:314:MET:HB3	1:A:322:LEU:HB3	2.01	0.43
1:C:1:LEU:N	14:C:619:HOH:O	2.51	0.43
1:C:262:TRP:HB3	2:D:317:LEU:HD13	2.01	0.43
1:A:109:PRO:O	1:A:168:GLU:HA	2.18	0.42
1:C:276:ARG:HD2	1:C:279:ARG:HB2	2.02	0.42
2:D:409:GLU:HB2	2:D:412:LYS:HE2	2.02	0.42
1:C:88:LYS:NZ	14:C:608:HOH:O	2.38	0.41
1:A:181:LEU:O	1:A:197:GLN:HA	2.20	0.41
2:D:42:GLU:OE2	2:D:42:GLU:N	2.52	0.41
2:D:239:ARG:O	2:D:244:HIS:NE2	2.46	0.41
3:E:149:LYS:NZ	4:F:180:THR:HG21	2.35	0.41
3:H:98:ARG:HG3	3:H:108:TYR:HB2	2.03	0.41
2:D:12:SER:HB3	2:D:461:ARG:HD3	2.03	0.41
1:A:3:LEU:O	1:A:5:PRO:HD3	2.21	0.40
2:B:178:TYR:CG	2:B:179:ASP:N	2.89	0.40
1:C:262:TRP:CD1	2:D:253:LYS:HE2	2.57	0.40
2:D:456:GLU:OE2	2:D:461:ARG:NH1	2.55	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:A:825:HOH:O	14:C:793:HOH:O[1_554]	2.19	0.01
14:A:825:HOH:O	14:C:767:HOH:O[1_554]	2.19	0.01

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	457/457 (100%)	444 (97%)	12 (3%)	1 (0%)	47	55
1	C	457/457 (100%)	440 (96%)	17 (4%)	0	100	100
2	B	469/472 (99%)	449 (96%)	20 (4%)	0	100	100
2	D	470/472 (100%)	450 (96%)	20 (4%)	0	100	100
3	E	210/221 (95%)	195 (93%)	15 (7%)	0	100	100
3	H	212/221 (96%)	199 (94%)	13 (6%)	0	100	100
4	F	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
4	L	212/214 (99%)	203 (96%)	8 (4%)	1 (0%)	29	31
All	All	2699/2728 (99%)	2581 (96%)	116 (4%)	2 (0%)	51	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
4	L	77	SER

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	367/364 (101%)	363 (99%)	4 (1%)	73	83
1	C	367/364 (101%)	362 (99%)	5 (1%)	67	78
2	B	417/417 (100%)	415 (100%)	2 (0%)	88	93
2	D	417/417 (100%)	415 (100%)	2 (0%)	88	93
3	E	186/190 (98%)	186 (100%)	0	100	100
3	H	187/190 (98%)	187 (100%)	0	100	100
4	F	188/188 (100%)	187 (100%)	1 (0%)	88	93
4	L	188/188 (100%)	188 (100%)	0	100	100
All	All	2317/2318 (100%)	2303 (99%)	14 (1%)	86	92

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

Mol	Chain	Res	Type
1	A	23	LEU
1	A	166	TYR
1	A	270	LEU
1	A	288	TYR
2	B	215	ASN
2	B	374	CYS
1	C	15	ASN
1	C	23	LEU
1	C	166	TYR
1	C	270	LEU
1	C	288	TYR
2	D	143	ARG
2	D	215	ASN
4	F	181	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	197	GLN
2	D	301	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

13 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	G	1	2,5	14,14,15	0.29	0	17,19,21	0.53	0
5	NAG	G	2	5	14,14,15	0.20	0	17,19,21	0.41	0
5	BMA	G	3	5	11,11,12	1.12	2 (18%)	15,15,17	1.24	2 (13%)
5	MAN	G	4	5	11,11,12	0.88	0	15,15,17	0.98	1 (6%)
5	MAN	G	5	5	11,11,12	0.80	1 (9%)	15,15,17	1.05	2 (13%)
6	NAG	I	1	6,2	14,14,15	0.50	0	17,19,21	0.46	0
6	NAG	I	2	6	14,14,15	0.35	0	17,19,21	0.46	0
7	NAG	J	1	2,7	14,14,15	0.22	0	17,19,21	0.58	0
7	NAG	J	2	7	14,14,15	0.40	0	17,19,21	0.49	0
7	BMA	J	3	7	11,11,12	1.35	2 (18%)	15,15,17	1.26	2 (13%)
7	MAN	J	4	7	11,11,12	1.04	1 (9%)	15,15,17	1.00	2 (13%)
6	NAG	K	1	6,2	14,14,15	0.27	0	17,19,21	0.37	0
6	NAG	K	2	6	14,14,15	0.17	0	17,19,21	0.44	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
5	NAG	G	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	MAN	G	4	5	-	2/2/19/22	0/1/1/1
5	MAN	G	5	5	-	1/2/19/22	0/1/1/1

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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	3	BMA	C4-C3	2.59	1.58	1.52
5	G	3	BMA	C4-C5	2.58	1.58	1.53
7	J	4	MAN	C1-C2	2.42	1.57	1.52
7	J	3	BMA	C4-C5	2.41	1.58	1.53
5	G	3	BMA	C4-C3	2.07	1.57	1.52
5	G	5	MAN	C1-C2	2.00	1.56	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	3	BMA	C3-C4-C5	2.86	115.35	110.24
7	J	3	BMA	C3-C4-C5	2.75	115.15	110.24
5	G	5	MAN	C1-O5-C5	2.61	115.72	112.19
7	J	4	MAN	O2-C2-C3	-2.36	105.41	110.14
5	G	3	BMA	O5-C1-C2	-2.23	107.32	110.77
5	G	4	MAN	O2-C2-C3	-2.19	105.75	110.14
7	J	4	MAN	C1-O5-C5	2.16	115.11	112.19
7	J	3	BMA	C2-C3-C4	2.07	114.47	110.89
5	G	5	MAN	O2-C2-C3	-2.05	106.03	110.14

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	I	2	NAG	O5-C5-C6-O6
7	J	3	BMA	C4-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2

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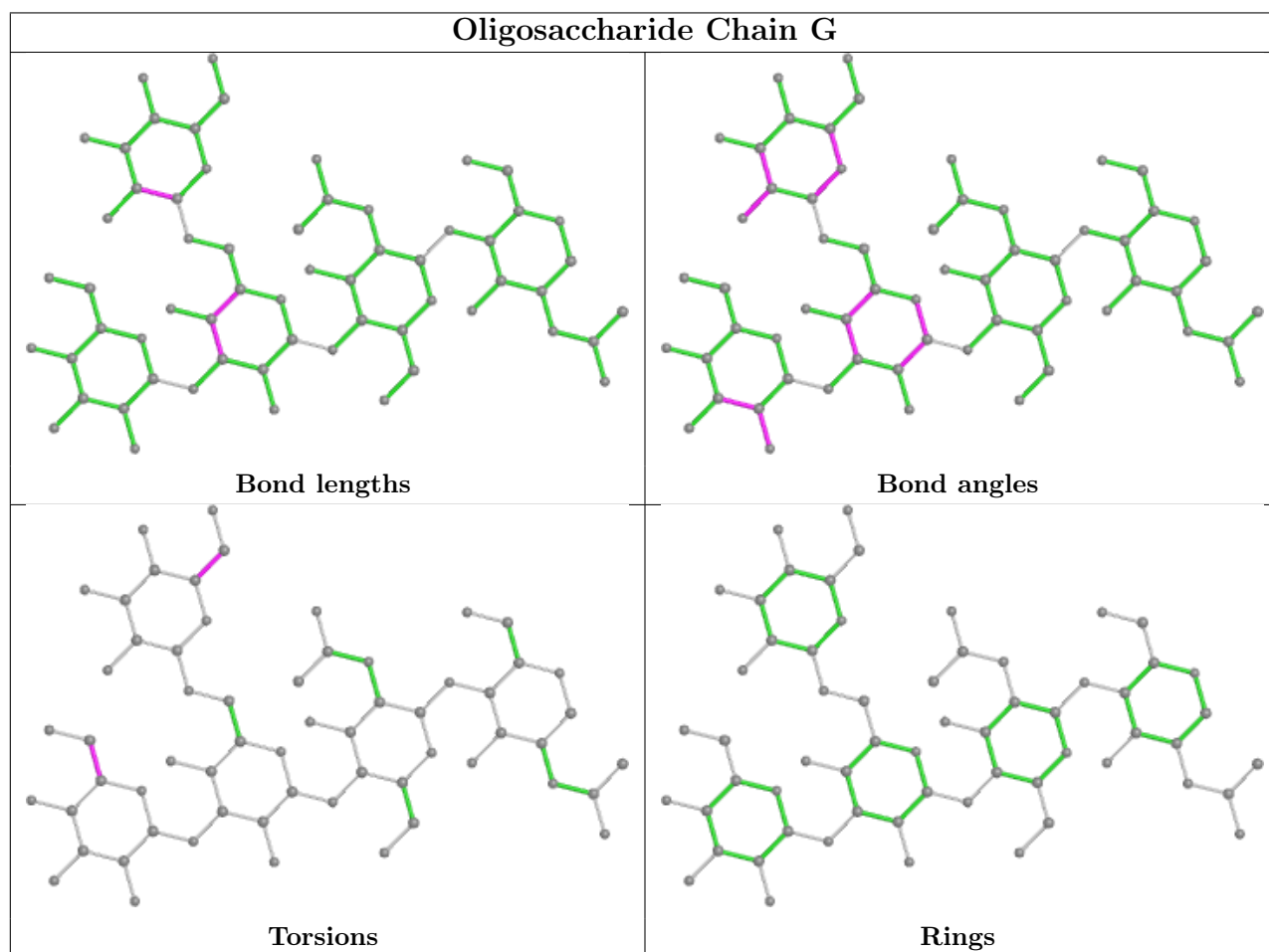
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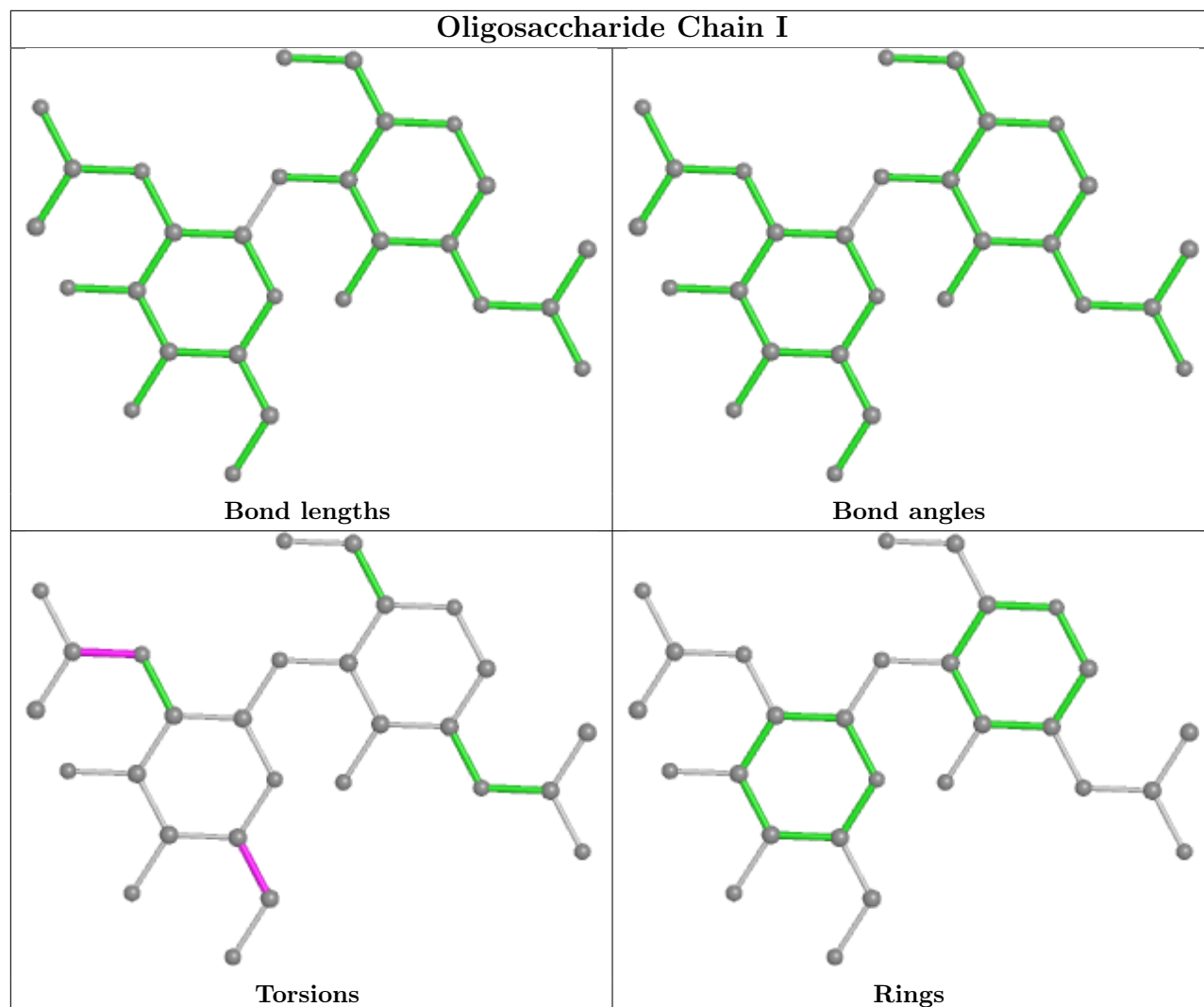
Mol	Chain	Res	Type	Atoms
6	K	2	NAG	C8-C7-N2-C2
6	K	2	NAG	O7-C7-N2-C2
5	G	5	MAN	O5-C5-C6-O6
7	J	3	BMA	O5-C5-C6-O6
6	K	2	NAG	C4-C5-C6-O6
6	K	1	NAG	O5-C5-C6-O6
6	I	2	NAG	C4-C5-C6-O6
6	K	1	NAG	C4-C5-C6-O6
7	J	2	NAG	C4-C5-C6-O6
6	K	2	NAG	O5-C5-C6-O6
5	G	4	MAN	C4-C5-C6-O6
7	J	2	NAG	O5-C5-C6-O6
5	G	4	MAN	O5-C5-C6-O6

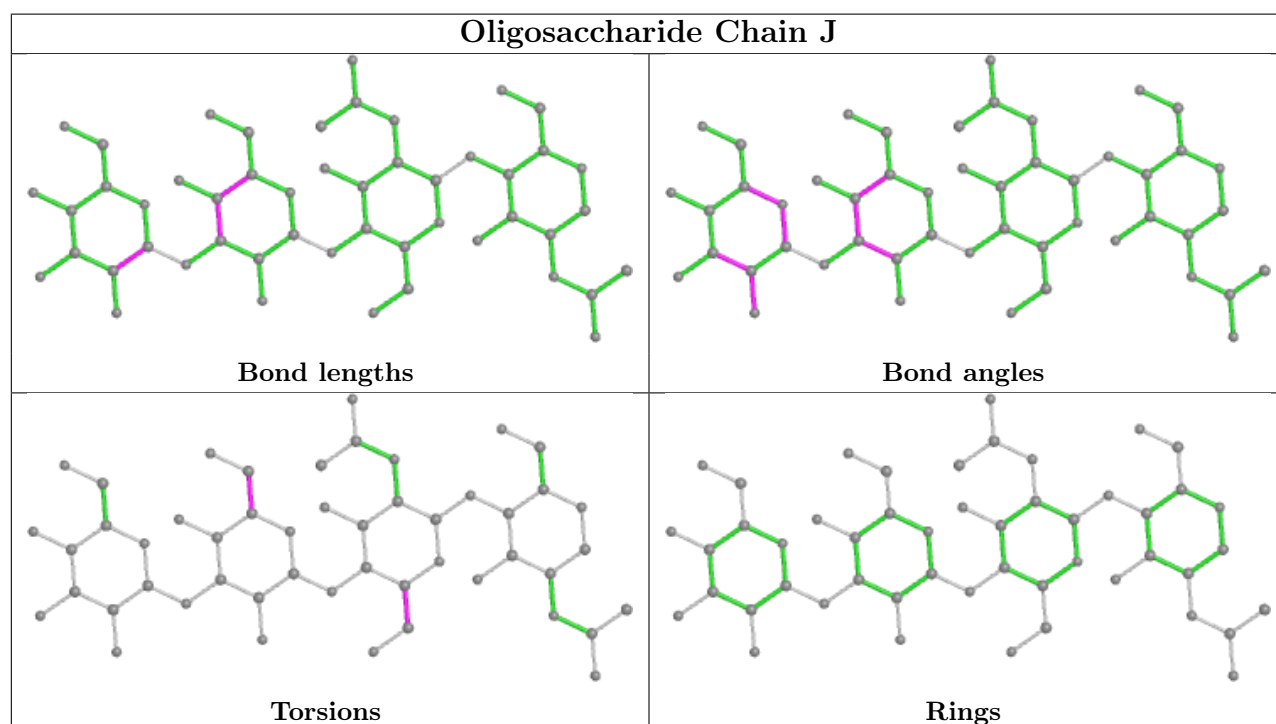
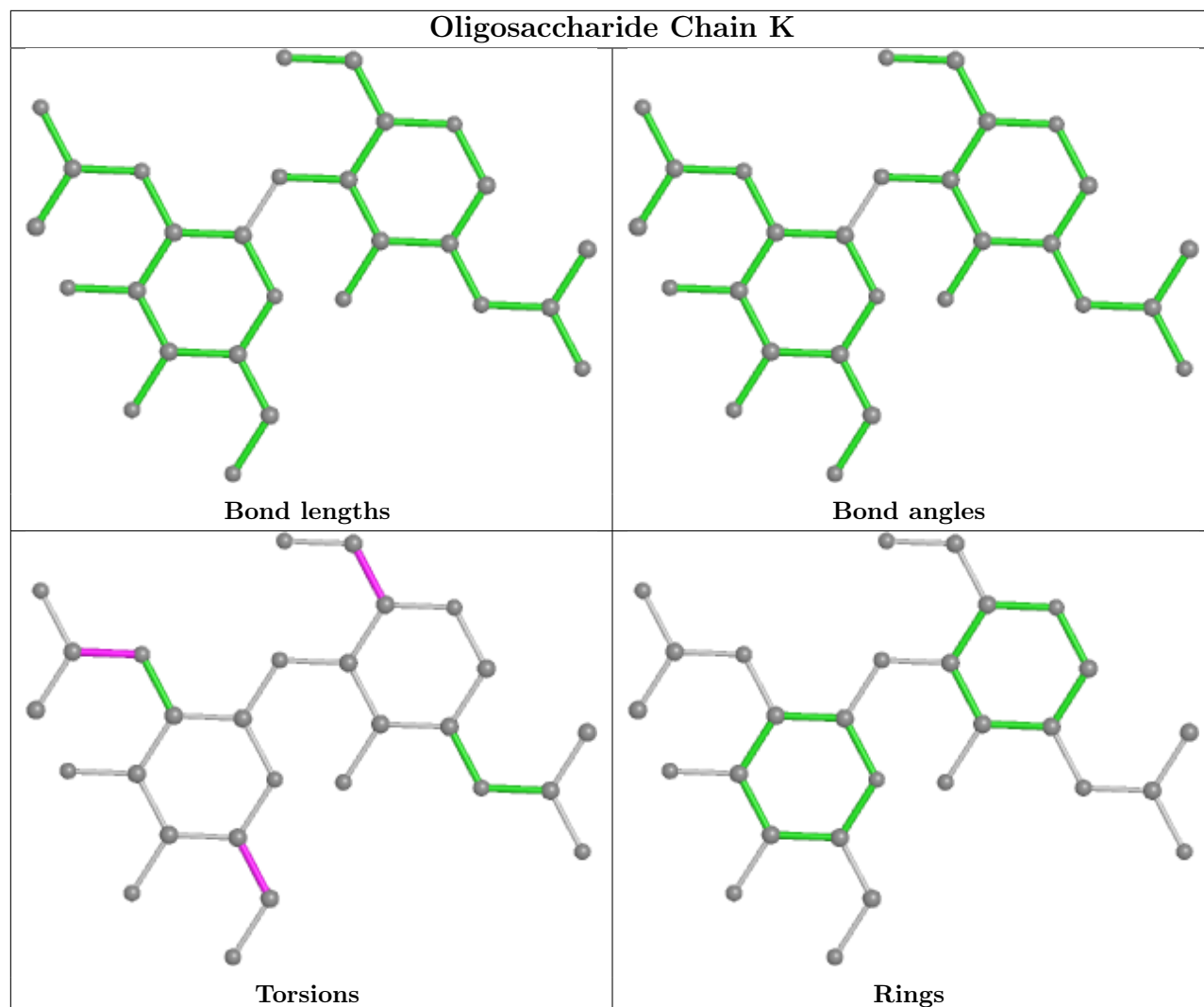
There are no ring outliers.

No monomer is involved in short contacts.

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







5.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 16 are monoatomic - leaving 13 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	SO4	C	501	-	4,4,4	0.17	0	6,6,6	0.19	0
12	MV8	B	2005	10	28,28,28	1.30	2 (7%)	34,39,39	1.76	5 (14%)
11	NAG	B	2004	2	14,14,15	0.48	0	17,19,21	0.58	0
8	SO4	L	301	-	4,4,4	0.18	0	6,6,6	0.13	0
8	SO4	A	508	-	4,4,4	0.16	0	6,6,6	0.19	0
12	MV8	D	2006	10	28,28,28	1.31	2 (7%)	34,39,39	1.72	5 (14%)
8	SO4	C	503	-	4,4,4	0.18	0	6,6,6	0.18	0
8	SO4	A	502	-	4,4,4	0.15	0	6,6,6	0.08	0
8	SO4	A	501	-	4,4,4	0.16	0	6,6,6	0.13	0
8	SO4	A	507	-	4,4,4	0.22	0	6,6,6	0.12	0
8	SO4	C	509	-	4,4,4	0.16	0	6,6,6	0.12	0
8	SO4	C	502	-	4,4,4	0.17	0	6,6,6	0.13	0
11	NAG	D	2004	2	14,14,15	0.38	0	17,19,21	0.69	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	MV8	D	2006	10	-	2/16/38/38	0/3/3/3
12	MV8	B	2005	10	-	4/16/38/38	0/3/3/3
11	NAG	B	2004	2	-	2/6/23/26	0/1/1/1
11	NAG	D	2004	2	-	1/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	2005	MV8	C9-N3	3.13	1.39	1.36
12	B	2005	MV8	O1-C4	-3.08	1.42	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	D	2006	MV8	C9-N3	3.05	1.39	1.36
12	D	2006	MV8	O1-C4	-2.77	1.42	1.46

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	2005	MV8	C4-O1-C9	6.97	115.64	110.15
12	D	2006	MV8	C4-O1-C9	6.78	115.50	110.15
12	B	2005	MV8	O1-C9-N3	-4.73	106.57	109.83
12	D	2006	MV8	O1-C9-N3	-4.55	106.70	109.83
12	B	2005	MV8	O1-C4-C7	-2.69	101.86	104.57
12	D	2006	MV8	O1-C4-C7	-2.51	102.04	104.57
11	D	2004	NAG	C1-O5-C5	2.36	115.39	112.19
12	B	2005	MV8	C8-N2-C5	2.30	114.66	111.09
12	D	2006	MV8	C16-C17-N4	2.16	121.31	118.05
12	D	2006	MV8	C4-C7-N3	2.15	103.97	101.81
12	B	2005	MV8	C16-C17-N4	2.07	121.17	118.05

There are no chirality outliers.

All (9) torsion outliers are listed below:

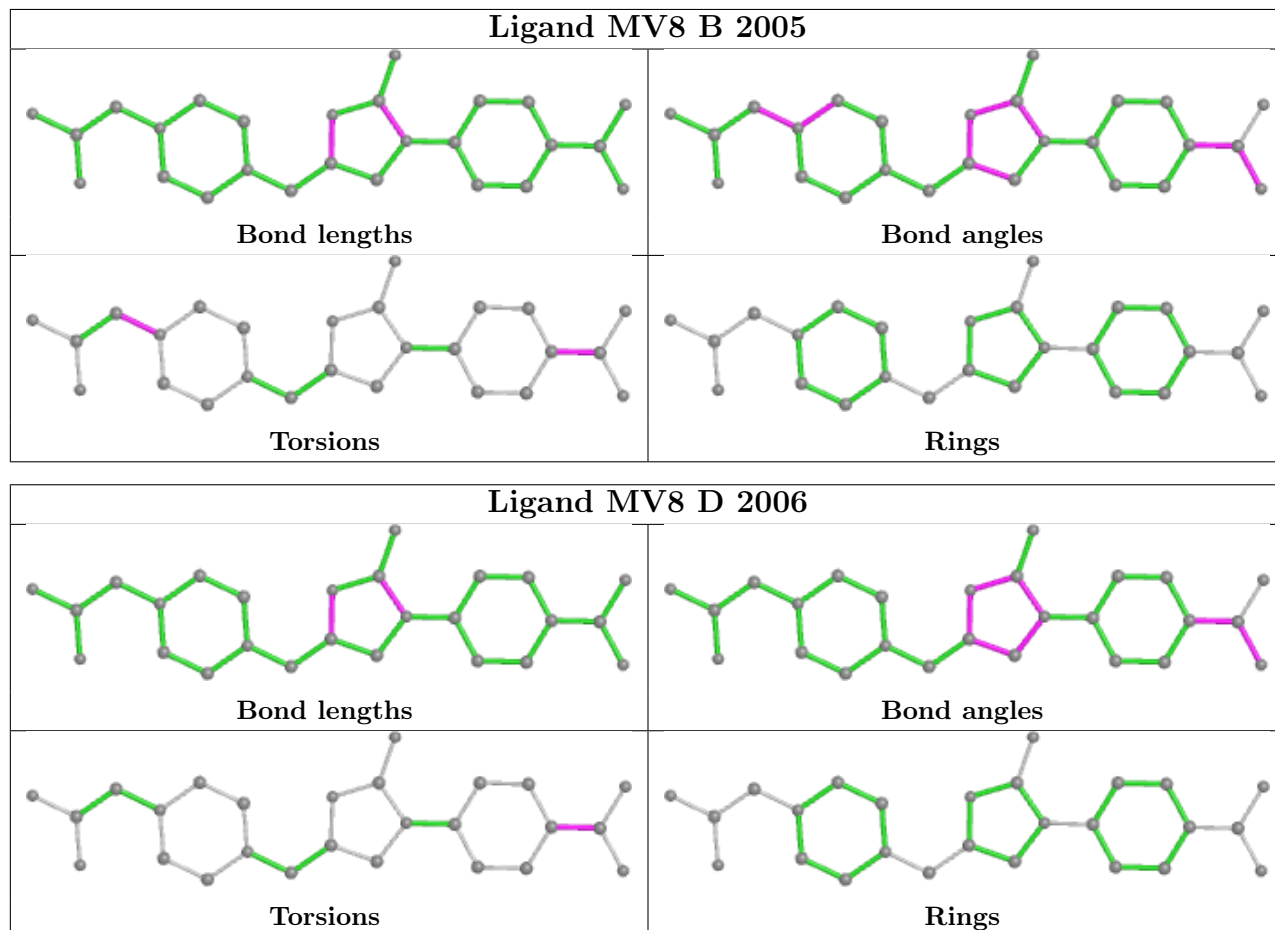
Mol	Chain	Res	Type	Atoms
12	B	2005	MV8	C14-C16-C17-N4
12	B	2005	MV8	C15-C16-C17-N4
12	B	2005	MV8	C11-C8-N2-C6
12	D	2006	MV8	C14-C16-C17-N4
12	D	2006	MV8	C15-C16-C17-N4
11	B	2004	NAG	O5-C5-C6-O6
11	B	2004	NAG	C4-C5-C6-O6
11	D	2004	NAG	O5-C5-C6-O6
12	B	2005	MV8	C15-C16-C17-N5

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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 [\(i\)](#)

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	454/457 (99%)	0.80	22 (4%) 30 41	30, 43, 64, 94	0
1	C	453/457 (99%)	0.64	16 (3%) 44 54	36, 56, 78, 106	0
2	B	466/472 (98%)	1.03	66 (14%) 2 4	30, 64, 133, 152	0
2	D	471/472 (99%)	0.88	58 (12%) 4 7	38, 72, 124, 142	0
3	E	214/221 (96%)	2.30	97 (45%) 0 0	69, 118, 172, 186	0
3	H	216/221 (97%)	0.98	40 (18%) 1 2	52, 92, 139, 151	0
4	F	214/214 (100%)	1.96	82 (38%) 0 0	73, 119, 162, 182	0
4	L	214/214 (100%)	0.70	12 (5%) 24 33	56, 83, 104, 134	0
All	All	2702/2728 (99%)	1.04	393 (14%) 2 4	30, 70, 145, 186	0

All (393) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	201	CYS	12.9
3	E	133	VAL	11.6
3	E	212	VAL	11.5
2	B	33	LEU	10.9
4	L	214	CYS	10.9
3	E	194	TRP	10.8
3	E	147	LEU	10.8
4	F	181	LEU	10.7
4	F	206	VAL	10.4
2	D	471	CYS	9.3
3	E	156	VAL	9.3
3	E	134	CYS	9.0
4	F	115	VAL	8.8
4	F	214	CYS	8.8
3	E	160	TRP	8.5
1	A	454	VAL	8.3

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Mol	Chain	Res	Type	RSRZ
2	D	469	SER	8.3
3	E	216	ILE	7.8
4	F	125	LEU	7.7
4	F	130	ALA	7.7
4	F	180	THR	7.6
2	D	375	LEU	7.6
3	E	142	VAL	7.5
2	B	34	GLY	7.4
2	B	49	CYS	7.0
3	E	219	ARG	7.0
2	B	77	SER	6.9
3	E	127	VAL	6.8
4	F	193	THR	6.6
3	E	200	THR	6.6
3	E	144	LEU	6.5
4	F	148	TRP	6.5
4	F	135	PHE	6.5
3	E	165	LEU	6.4
3	E	196	SER	6.4
4	F	179	LEU	6.3
4	F	132	VAL	6.2
4	F	209	PHE	6.2
2	B	44	LEU	6.1
2	B	54	ILE	6.1
3	E	198	SER	6.1
3	E	129	PRO	6.0
2	D	470	GLN	6.0
3	E	11	LEU	6.0
2	B	10	VAL	5.9
2	B	36	PRO	5.9
4	L	212	ASN	5.9
4	F	178	THR	5.8
2	B	2	PRO	5.8
3	E	199	ILE	5.8
3	E	203	VAL	5.8
4	F	159	VAL	5.8
2	D	44	LEU	5.7
2	B	466	TRP	5.6
3	E	183	LEU	5.6
4	F	120	PRO	5.5
2	B	32	PRO	5.5
2	D	2	PRO	5.4

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Mol	Chain	Res	Type	RSRZ
3	E	205	HIS	5.4
3	H	165	LEU	5.3
2	D	181	LYS	5.3
4	F	194	CYS	5.3
3	E	215	LYS	5.3
4	F	195	GLU	5.2
4	F	160	LEU	5.2
3	E	176	LEU	5.2
4	F	117	ILE	5.2
4	F	144	ILE	5.2
4	F	126	THR	5.2
4	F	190	ASN	5.1
3	E	140	SER	5.1
2	B	51	PRO	5.1
3	E	146	CYS	5.1
3	E	217	GLU	5.1
2	B	375	LEU	5.0
4	F	134	CYS	5.0
2	B	452	ASN	5.0
4	L	125	LEU	4.9
3	E	195	PRO	4.9
4	F	204	PRO	4.9
4	F	205	ILE	4.9
2	B	28	ASP	4.9
4	F	213	GLU	4.8
4	F	136	LEU	4.8
4	L	205	ILE	4.8
3	E	131	ALA	4.8
2	B	451	GLY	4.8
1	A	337	PRO	4.7
4	F	191	SER	4.6
3	E	12	VAL	4.6
3	H	144	LEU	4.6
3	E	143	THR	4.6
2	D	39	ASP	4.6
3	E	132	PRO	4.6
3	H	196	SER	4.6
3	H	133	VAL	4.5
3	E	130	LEU	4.5
3	H	134	CYS	4.5
4	L	206	VAL	4.5
2	B	8	ARG	4.5

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Mol	Chain	Res	Type	RSRZ
4	F	15	LEU	4.5
4	F	156	GLN	4.4
2	B	458	GLY	4.4
3	E	128	TYR	4.4
2	B	31	LEU	4.4
2	B	53	SER	4.4
1	C	339	ALA	4.4
2	B	4	ILE	4.4
4	F	116	SER	4.3
3	H	216	ILE	4.3
4	F	201	SER	4.3
2	D	1	GLY	4.3
3	E	218	PRO	4.3
3	E	204	ALA	4.3
3	H	189	VAL	4.2
2	D	42	GLU	4.2
4	F	83	PHE	4.2
4	F	150	ILE	4.2
4	F	118	PHE	4.2
4	F	146	VAL	4.1
3	E	116	THR	4.1
4	F	152	GLY	4.1
3	E	86	LEU	4.1
2	D	52	GLU	4.1
2	D	466	TRP	4.0
4	F	147	LYS	4.0
3	E	210	THR	4.0
3	H	198	SER	3.9
2	D	35	SER	3.9
3	E	115	VAL	3.9
3	H	195	PRO	3.9
4	F	212	ASN	3.8
2	B	1	GLY	3.8
1	A	339	ALA	3.8
2	D	36	PRO	3.8
2	D	46	LYS	3.8
3	H	158	LEU	3.8
2	D	32	PRO	3.8
4	F	203	SER	3.8
4	F	158	GLY	3.8
3	H	203	VAL	3.8
2	D	33	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
2	D	8	ARG	3.7
2	B	50	ALA	3.7
2	D	380	ILE	3.7
3	E	191	SER	3.7
3	E	192	SER	3.7
4	F	197	THR	3.7
3	H	130	LEU	3.7
4	F	107	LYS	3.7
2	B	9	GLY	3.7
2	B	440	GLN	3.6
3	E	187	VAL	3.6
3	E	82	GLN	3.6
3	E	16	ALA	3.6
4	F	157	ASN	3.6
2	D	468	GLY	3.6
2	B	30	ALA	3.6
1	C	337	PRO	3.6
2	B	76	ASP	3.6
2	B	181	LYS	3.5
3	E	148	VAL	3.5
2	D	31	LEU	3.5
1	C	340	LEU	3.5
3	E	85	SER	3.5
1	C	335	ARG	3.5
4	F	192	TYR	3.5
2	B	67	ARG	3.4
3	E	25	SER	3.4
2	D	378	GLU	3.4
2	D	376	ASN	3.4
3	E	124	ALA	3.4
4	F	210	ASN	3.4
2	B	29	GLU	3.4
3	E	65	GLN	3.3
3	E	189	VAL	3.3
4	F	207	LYS	3.3
3	E	209	SER	3.3
3	H	188	THR	3.3
3	E	17	SER	3.3
2	B	381	PRO	3.3
4	F	14	SER	3.3
2	B	460	CYS	3.3
3	E	15	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
4	F	208	SER	3.3
4	F	182	THR	3.3
2	D	61	ALA	3.3
2	D	383	LEU	3.3
3	E	206	PRO	3.3
3	H	219	ARG	3.2
2	D	451	GLY	3.2
2	D	51	PRO	3.2
2	B	46	LYS	3.2
4	F	186	TYR	3.2
2	B	26	CYS	3.2
3	H	208	SER	3.2
3	H	192	SER	3.1
2	D	79	GLN	3.1
4	F	129	GLY	3.1
4	L	105	GLU	3.1
2	B	459	VAL	3.1
3	H	217	GLU	3.1
2	B	52	GLU	3.1
3	E	114	SER	3.1
4	F	114	THR	3.1
2	D	4	ILE	3.1
2	B	37	ARG	3.1
3	E	149	LYS	3.0
2	D	26	CYS	2.9
3	E	141	SER	2.9
2	B	455	PHE	2.9
4	F	151	ASP	2.9
2	B	442	GLU	2.9
3	E	163	GLY	2.9
4	F	202	THR	2.9
2	D	58	VAL	2.9
2	D	34	GLY	2.9
2	B	376	ASN	2.9
2	D	40	LEU	2.9
2	B	45	LEU	2.9
4	F	149	LYS	2.9
4	F	113	PRO	2.9
4	L	213	GLU	2.8
3	E	207	ALA	2.8
1	C	130	CYS	2.8
1	C	320	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
3	E	117	VAL	2.8
2	B	98	LYS	2.8
2	D	48	ASN	2.8
2	D	30	ALA	2.7
4	F	188	ARG	2.8
4	L	111	ALA	2.7
2	D	75	GLY	2.7
3	E	66	GLY	2.7
2	B	27	SER	2.7
3	E	92	ALA	2.7
3	E	169	VAL	2.7
4	F	119	PRO	2.7
3	H	166	SER	2.7
2	B	129	TRP	2.7
2	B	11	SER	2.7
3	E	18	VAL	2.7
1	A	338	HIS	2.7
3	E	177	GLN	2.7
2	D	9	GLY	2.7
1	A	46	SER	2.6
4	F	163	TRP	2.6
3	H	199	ILE	2.6
3	H	218	PRO	2.6
1	C	336	GLY	2.6
3	E	83	LEU	2.6
1	A	436	ILE	2.6
4	F	200	THR	2.6
4	F	131	SER	2.6
2	D	340	VAL	2.6
3	E	188	THR	2.6
4	F	154	GLU	2.6
3	E	180	LEU	2.6
2	D	7	THR	2.5
3	E	179	ASP	2.5
3	H	213	ASP	2.5
2	D	178	TYR	2.5
3	E	68	ALA	2.5
2	D	45	LEU	2.5
3	E	168	GLY	2.5
1	C	389	VAL	2.5
2	B	39	ASP	2.5
2	B	380	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	446	HIS	2.5
2	D	22	MET	2.5
3	H	1	GLU	2.5
2	B	35	SER	2.5
4	L	169	LYS	2.5
3	E	91	THR	2.5
2	D	54	ILE	2.5
2	D	3	ASN	2.5
2	D	27	SER	2.4
2	B	379	VAL	2.4
2	B	48	ASN	2.4
2	B	450	ASN	2.4
2	D	437	CYS	2.4
4	F	122	SER	2.4
2	B	377	ASN	2.4
3	E	159	THR	2.4
3	E	182	THR	2.4
2	B	448	CYS	2.4
1	A	47	GLN	2.4
2	B	79	GLN	2.4
3	H	187	VAL	2.4
3	H	194	TRP	2.4
3	H	211	LYS	2.4
1	C	319	ASP	2.4
4	F	143	ASP	2.4
3	E	13	LYS	2.4
3	E	211	LYS	2.4
3	E	208	SER	2.4
3	H	160	TRP	2.4
4	F	106	ILE	2.4
2	D	90	LEU	2.4
2	B	405	GLY	2.4
3	E	121	LYS	2.4
1	A	45	PRO	2.4
2	D	257	ALA	2.4
3	E	150	GLY	2.4
1	A	420	SER	2.4
3	E	20	LEU	2.3
3	E	126	SER	2.3
1	A	421	LEU	2.3
1	A	319	ASP	2.3
1	C	131	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	10	VAL	2.3
4	F	170	ASP	2.3
2	B	42	GLU	2.3
1	A	193	GLY	2.3
1	C	338	HIS	2.3
1	A	130	CYS	2.3
1	C	212	LEU	2.3
3	H	124	ALA	2.3
2	D	55	GLU	2.3
4	F	177	SER	2.3
1	A	171	PHE	2.3
2	B	447	ARG	2.3
2	D	77	SER	2.3
3	H	162	SER	2.3
4	F	21	ILE	2.3
3	E	54	ALA	2.3
2	B	90	LEU	2.3
3	H	200	THR	2.3
3	E	94	TYR	2.3
4	F	184	ASP	2.3
3	H	129	PRO	2.3
2	B	378	GLU	2.2
2	D	446	HIS	2.2
2	D	62	ARG	2.2
3	E	87	THR	2.2
3	H	168	GLY	2.2
3	E	151	TYR	2.2
4	F	133	VAL	2.2
1	C	171	PHE	2.2
4	F	111	ALA	2.2
2	B	265	ILE	2.2
4	F	103	LYS	2.2
1	A	94	GLY	2.2
4	L	83	PHE	2.2
2	B	25	TRP	2.2
2	D	78	SER	2.2
3	E	213	ASP	2.2
2	B	100	PHE	2.2
1	A	183	LEU	2.2
4	F	153	SER	2.2
3	E	89	GLU	2.1
2	B	38	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
3	E	161	ASN	2.1
4	L	129	GLY	2.1
3	E	158	LEU	2.1
1	A	450	ALA	2.1
3	E	193	THR	2.1
3	E	214	LYS	2.1
3	H	138	THR	2.1
3	H	159	THR	2.1
1	A	186	PRO	2.1
1	A	358	SER	2.1
4	F	155	ARG	2.1
1	C	280	LEU	2.1
4	F	11	MET	2.1
3	H	169	VAL	2.1
4	F	25	ALA	2.1
2	D	67	ARG	2.1
3	E	64	PHE	2.1
1	A	336	GLY	2.1
2	B	219	PRO	2.1
3	E	153	PRO	2.1
2	B	462	CYS	2.1
2	D	450	ASN	2.1
2	D	382	GLY	2.1
3	H	57	TYR	2.1
3	H	215	LYS	2.1
4	F	174	SER	2.1
4	L	127	SER	2.1
1	A	23	LEU	2.1
2	D	5	CYS	2.1
4	F	161	ASN	2.0
3	H	17	SER	2.0
4	F	127	SER	2.0
1	C	126	PRO	2.0
4	F	124	GLN	2.0
1	C	166	TYR	2.0
3	E	145	GLY	2.0
1	A	40	PRO	2.0
3	H	156	VAL	2.0
3	E	29	ILE	2.0
3	H	167	SER	2.0
3	H	210	THR	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](#)

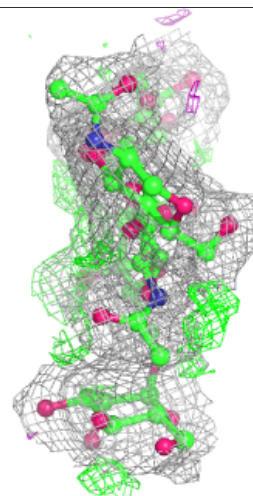
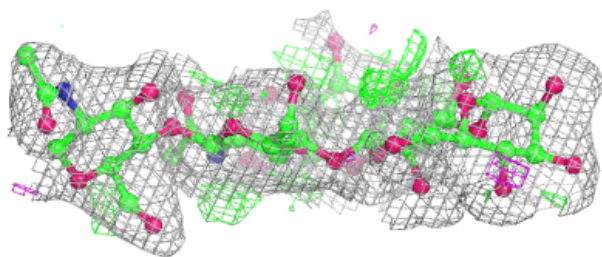
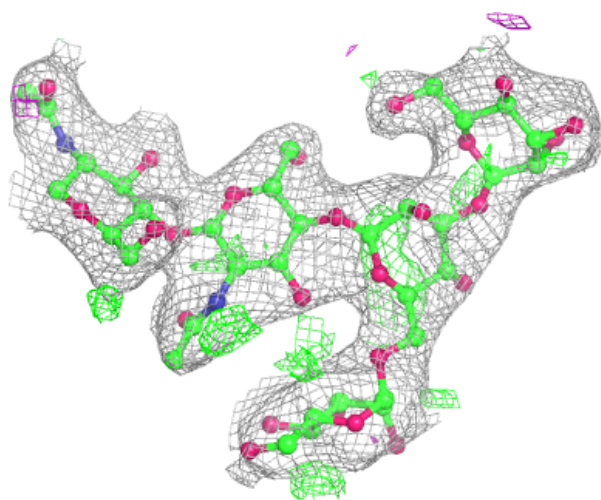
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	BMA	J	3	11/12	0.73	0.28	89,89,89,89	0
7	MAN	J	4	11/12	0.82	0.26	88,88,88,88	0
5	MAN	G	5	11/12	0.83	0.15	89,89,89,89	0
6	NAG	I	2	14/15	0.83	0.22	96,96,96,96	0
5	BMA	G	3	11/12	0.85	0.13	81,81,81,81	0
7	NAG	J	2	14/15	0.87	0.20	77,77,77,77	0
5	MAN	G	4	11/12	0.89	0.12	77,77,77,77	0
6	NAG	I	1	14/15	0.90	0.20	94,94,94,94	0
5	NAG	G	2	14/15	0.90	0.14	66,66,66,66	0
6	NAG	K	1	14/15	0.90	0.21	96,96,96,96	0
7	NAG	J	1	14/15	0.91	0.14	63,63,63,63	0
6	NAG	K	2	14/15	0.91	0.27	99,99,99,99	0
5	NAG	G	1	14/15	0.95	0.14	49,49,49,49	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.

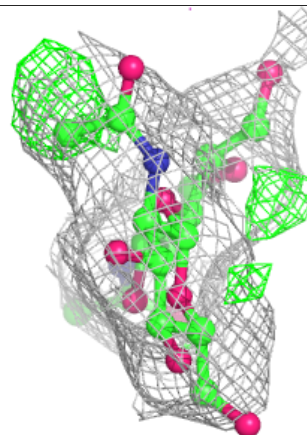
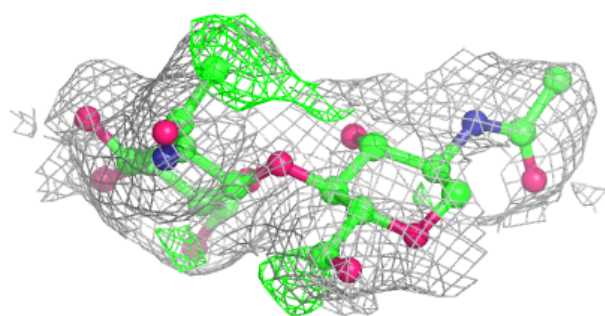
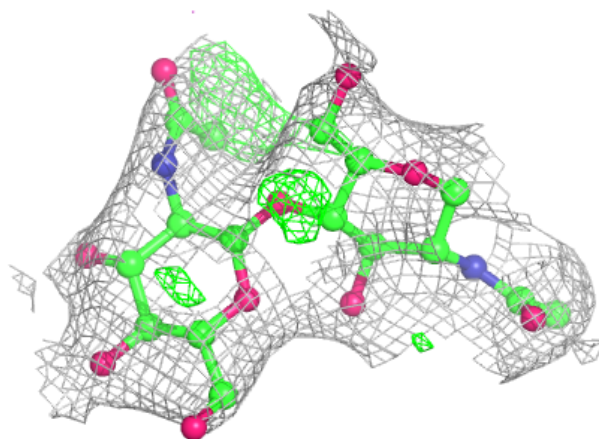
Electron density around Chain G:

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

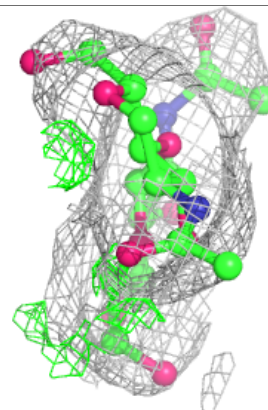
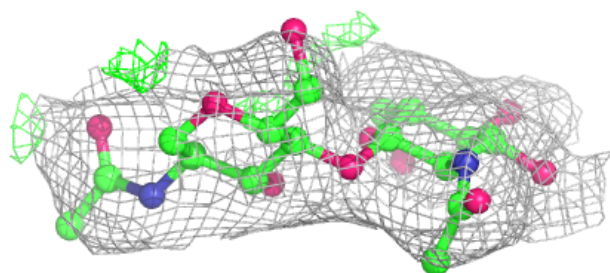
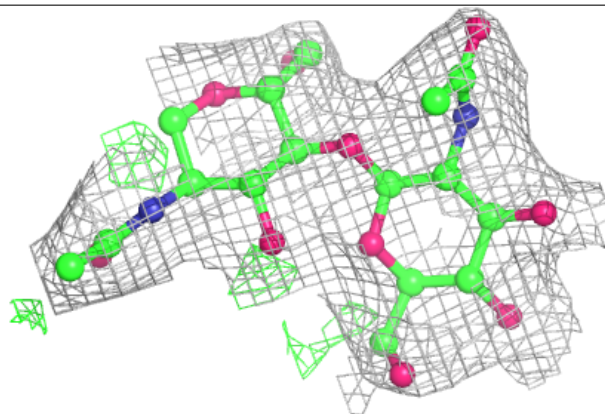


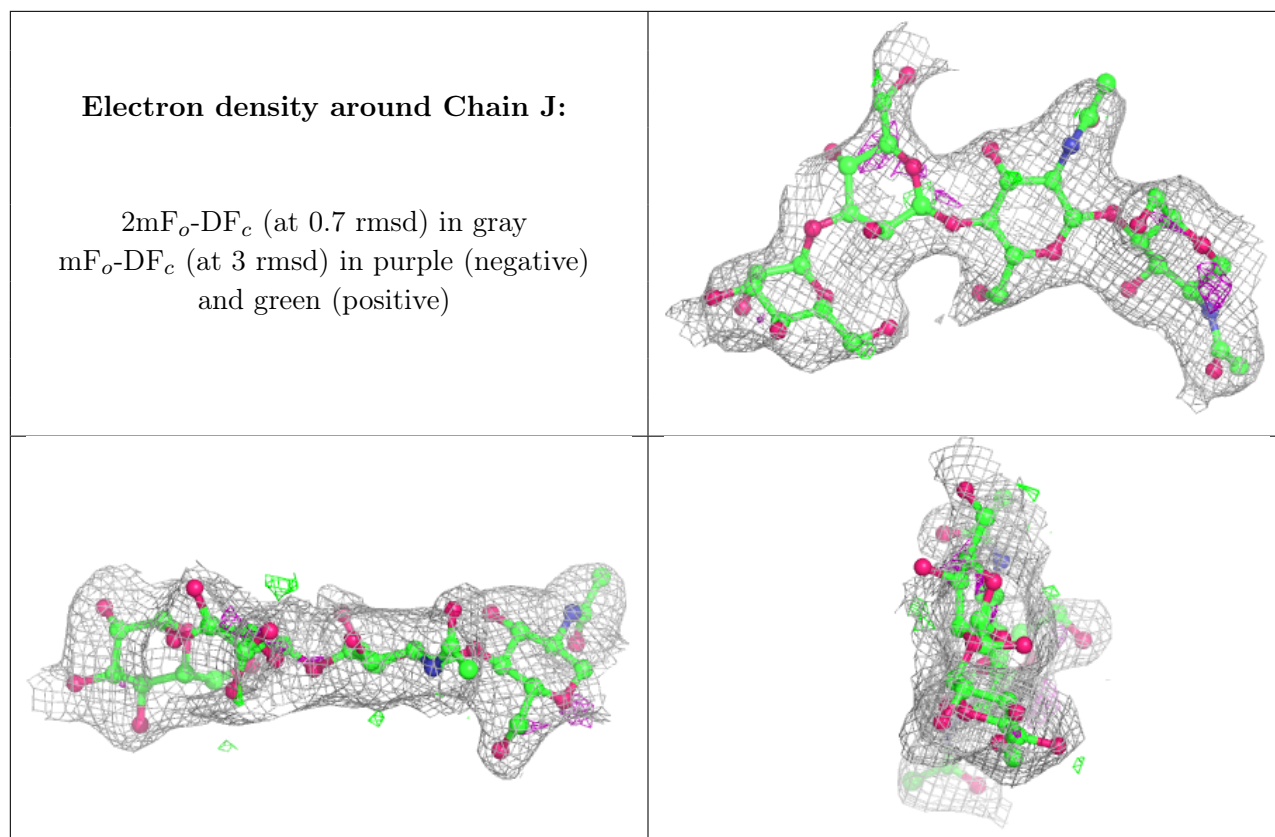
Electron density around Chain I:

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

**Electron density around Chain K:**

$2mF_o-DF_c$ (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.

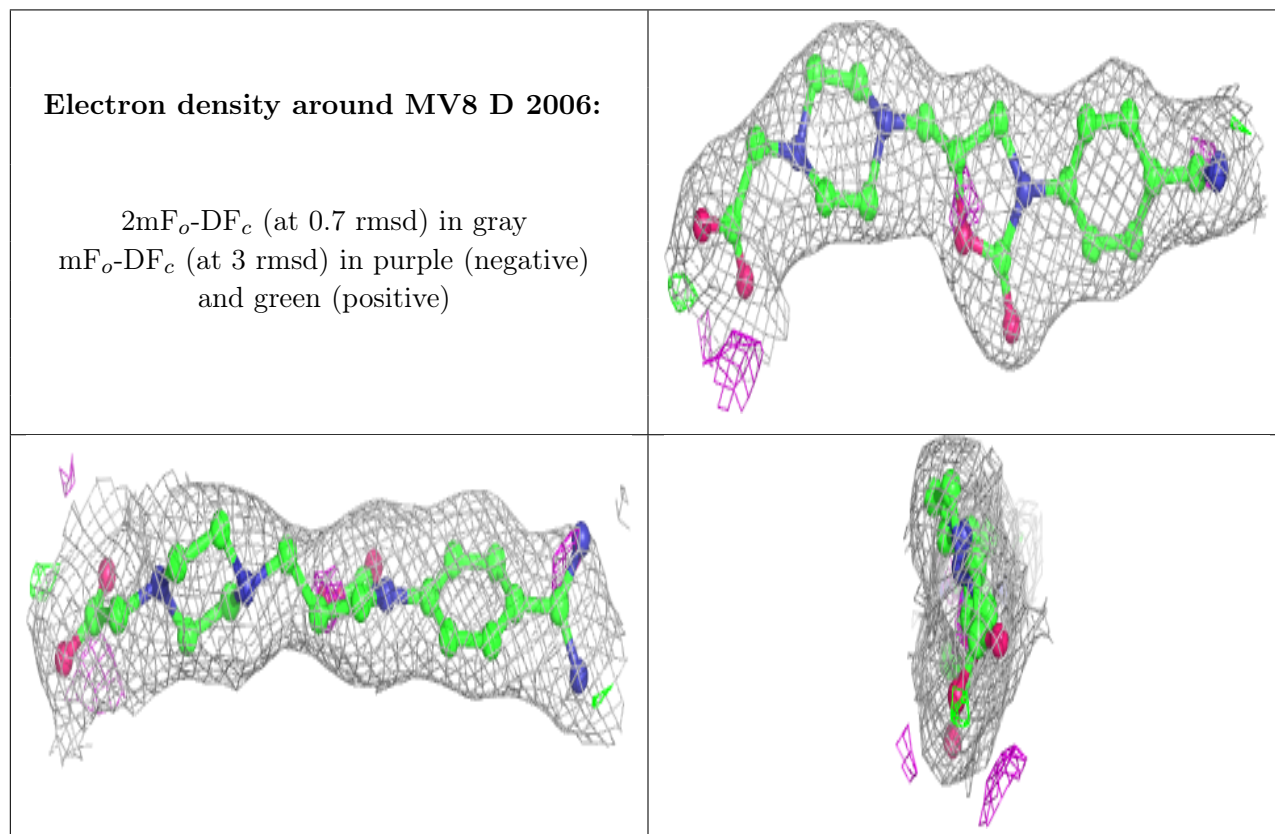
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	CA	C	505	1/1	0.75	0.07	75,75,75,75	0
8	SO4	A	507	5/5	0.81	0.21	76,76,76,76	0
11	NAG	D	2004	14/15	0.83	0.24	89,89,89,89	0
10	MN	B	2002	1/1	0.84	0.07	71,71,71,71	0
11	NAG	B	2004	14/15	0.86	0.31	97,97,97,97	0
13	CL	D	2005	1/1	0.88	0.11	82,82,82,82	0
8	SO4	C	502	5/5	0.89	0.15	86,86,86,86	0
13	CL	C	504	1/1	0.91	0.26	67,67,67,67	0
9	CA	C	507	1/1	0.92	0.15	54,54,54,54	0
8	SO4	C	503	5/5	0.92	0.21	89,89,89,89	0
8	SO4	A	508	5/5	0.92	0.14	79,79,79,79	0
9	CA	A	504	1/1	0.93	0.10	35,35,35,35	0
8	SO4	A	501	5/5	0.93	0.13	65,65,65,65	0
12	MV8	D	2006	26/26	0.93	0.17	52,52,52,52	0

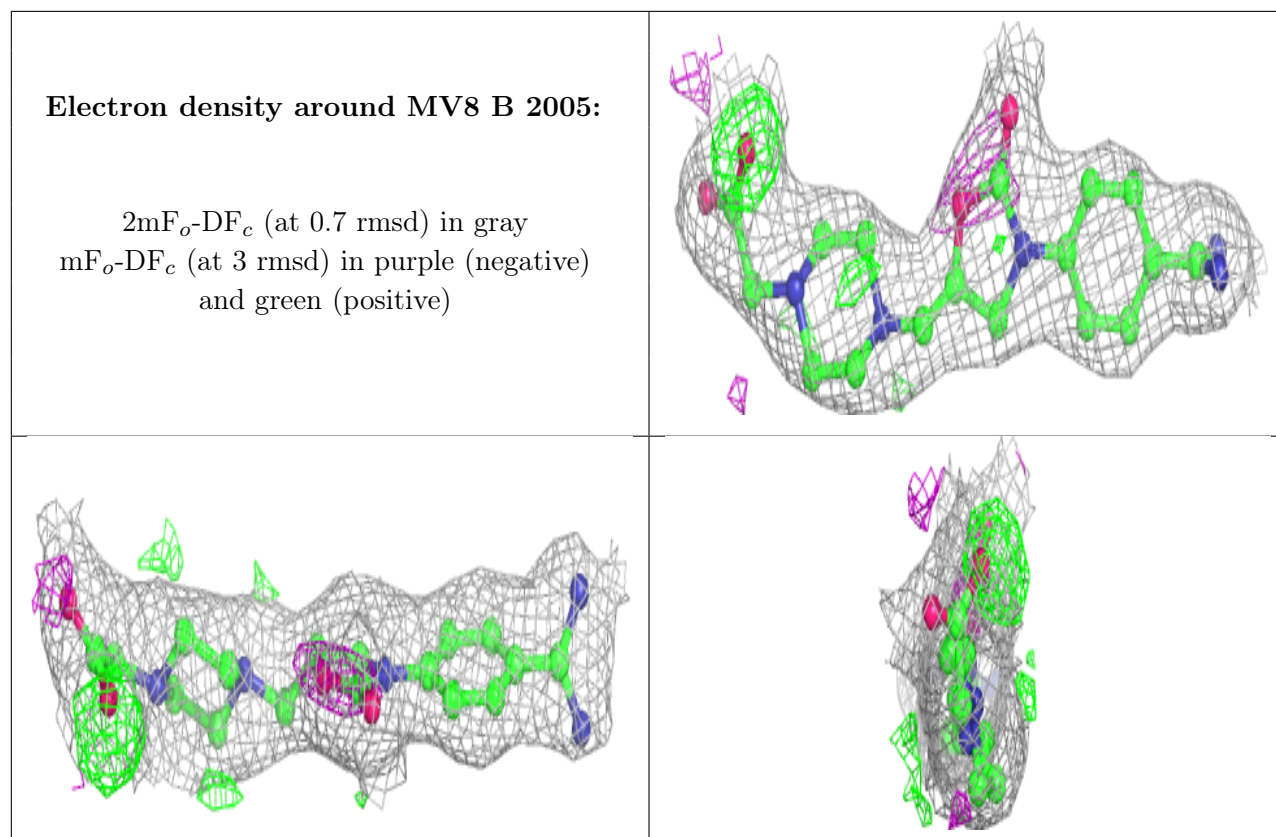
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	SO4	C	501	5/5	0.93	0.20	78,78,78,78	0
8	SO4	C	509	5/5	0.93	0.13	85,85,85,85	0
12	MV8	B	2005	26/26	0.94	0.18	42,42,42,42	0
9	CA	C	506	1/1	0.94	0.04	64,64,64,64	0
9	CA	A	503	1/1	0.95	0.08	50,50,50,50	0
9	CA	A	506	1/1	0.95	0.16	36,36,36,36	0
8	SO4	L	301	5/5	0.96	0.15	86,86,86,86	0
10	MN	D	2001	1/1	0.96	0.14	46,46,46,46	0
9	CA	C	508	1/1	0.96	0.14	50,50,50,50	0
10	MN	B	2001	1/1	0.96	0.17	33,33,33,33	0
8	SO4	A	502	5/5	0.97	0.14	56,56,56,56	0
10	MN	D	2002	1/1	0.97	0.10	58,58,58,58	0
10	MN	D	2003	1/1	0.97	0.14	47,47,47,47	0
9	CA	A	505	1/1	0.98	0.18	33,33,33,33	0
10	MN	B	2003	1/1	0.99	0.16	37,37,37,37	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.