



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2023 – 10:32 PM EDT

PDB ID : 7TMZ
Title : Integrin alaphIIBbeta3 complex with BMS compound 4
Authors : Zhu, J.; Lin, F.-Y.; Zhu, J.; Springer, T.A.
Deposited on : 2022-01-20
Resolution : 2.20 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

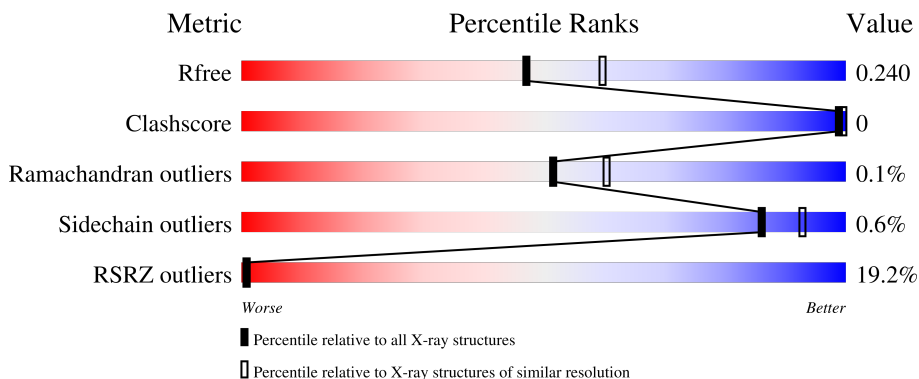
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.



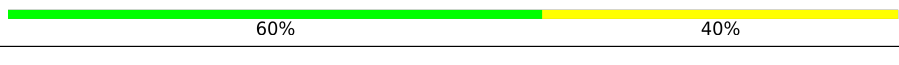
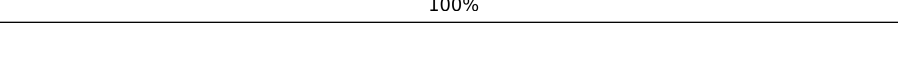
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	454	 11% (poor fit), 98% (0 outliers), 1% (not modelled)
1	C	454	 10% (poor fit), 97% (0 outliers), 1% (not modelled)
2	B	471	 17% (poor fit), 97% (0 outliers), 2% (not modelled)
2	D	471	 15% (poor fit), 97% (0 outliers), 1% (not modelled)
3	E	216	 54% (poor fit), 98% (0 outliers), 2% (not modelled)

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Mol	Chain	Length	Quality of chain
3	H	216	 22% 100%
4	F	214	 44% 100%
4	L	214	 8% 100%
5	G	5	 60% 40%
6	I	2	 100%
6	K	2	 100%
7	J	4	 100%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 42485 atoms, of which 20311 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	454	6846	2226	3347	601	664	8	2	6	0
1	C	453	6840	2224	3338	604	666	8	0	6	0

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	466	7138	2245	3534	615	710	34	7	6	0
2	D	471	7167	2255	3544	619	715	34	10	1	0

- Molecule 3 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	E	214	3221	1035	1590	264	326	6	0	0	0
3	H	216	3242	1041	1600	266	329	6	0	0	0

- Molecule 4 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
4	F	214	3190	1019	1553	268	341	9	0	0	0
4	L	214	3190	1019	1553	268	341	9	0	0	0

- 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	H	N	O			
5	G	5	118	34	57	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	H	N	O			
6	I	2	55	16	27	2	10	0	0	0
6	K	2	55	16	27	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	H	N	O			
7	J	4	97	28	47	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 5 4 1	0	0
8	A	1	Total O S 5 4 1	0	0
8	A	1	Total O S 5 4 1	0	0
8	A	1	Total O S 5 4 1	0	0
8	A	1	Total O S 5 4 1	0	0
8	C	1	Total O S 5 4 1	0	0
8	C	1	Total O S 5 4 1	0	0
8	C	1	Total O S 5 4 1	0	0
8	C	1	Total O S 5 4 1	0	0
8	L	1	Total O S 5 4 1	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	4	Total Ca 4 4	0	0
9	B	2	Total Ca 2 2	0	0

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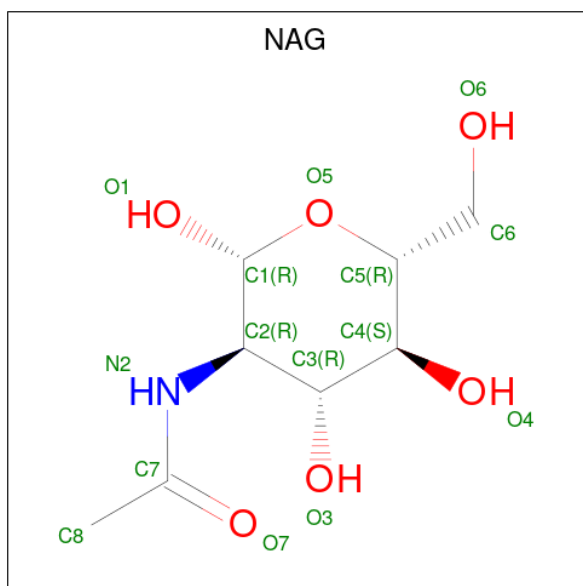
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	4	Total Ca 4 4	0	0
9	D	2	Total Ca 2 2	0	0

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

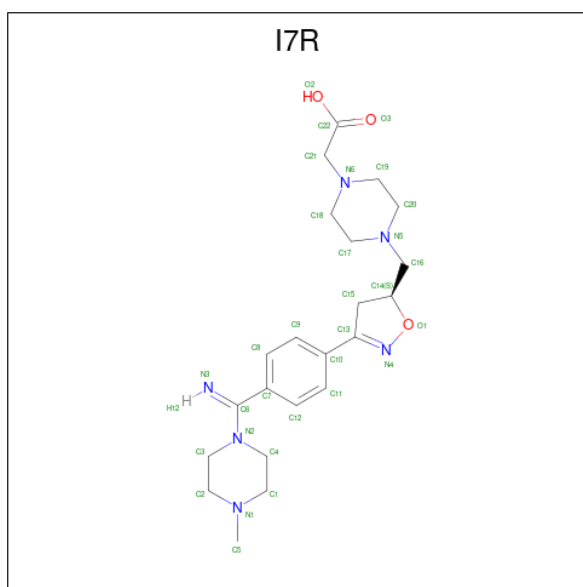
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total Mg 1 1	0	0
10	D	1	Total Mg 1 1	0	0

- 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 H N O 28 8 14 1 5	0	0
11	D	1	Total C H N O 28 8 14 1 5	0	0

- Molecule 12 is (4-{(5S)-3-{4-[(E)-imino(4-methylpiperazin-1-yl)methyl]phenyl}-4,5-dihydro-1,2-oxazol-5-yl)methyl}piperazin-1-yl)acetic acid (three-letter code: I7R) (formula: C₂₂H₃₂N₆O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
12	B	1	Total	C	H	N	O	0	0
			64	22	33	6	3		
12	D	1	Total	C	H	N	O	0	0
			64	22	33	6	3		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	C	2	Total	Cl	0	0
			2	2		
13	D	1	Total	Cl	0	0
			1	1		

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	410	Total	O	0	0
			410	410		
14	B	230	Total	O	0	0
			230	230		
14	C	187	Total	O	0	0
			187	187		
14	D	150	Total	O	0	0
			150	150		
14	E	15	Total	O	0	0
			15	15		

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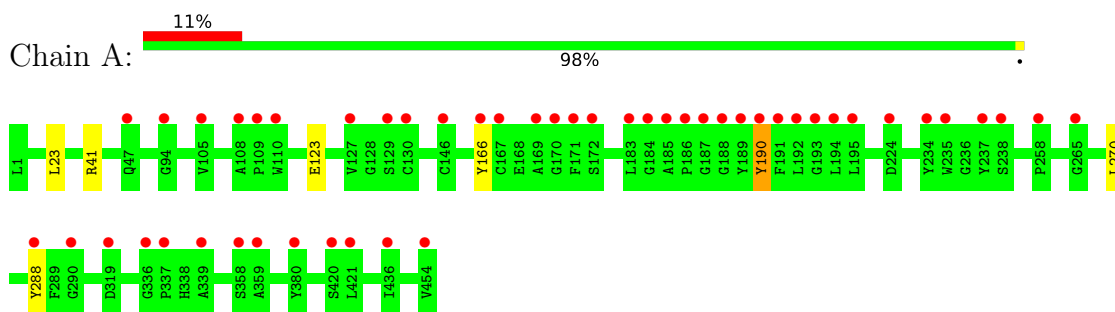
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	F	6	Total O 6 6	0	0
14	H	33	Total O 33 33	0	0
14	L	44	Total O 44 44	0	0

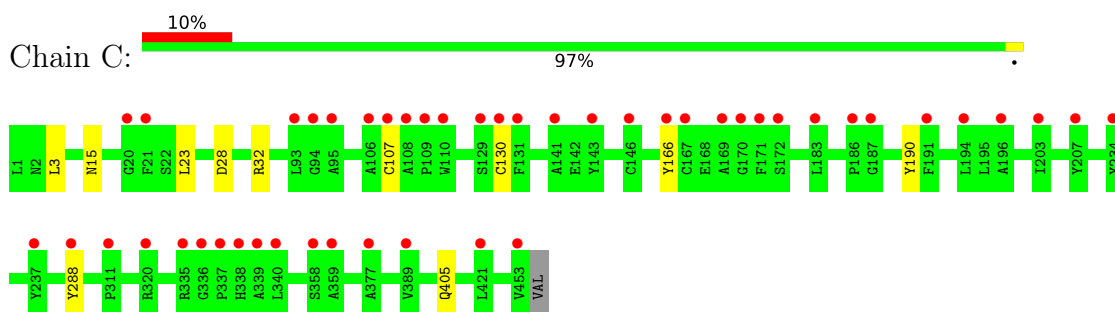
3 Residue-property plots [i](#)

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.

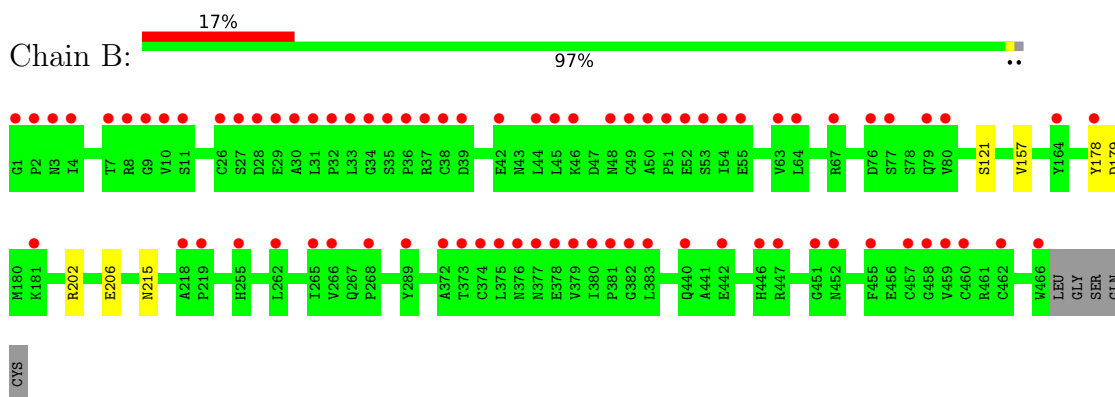
- Molecule 1: Integrin alpha-IIb



- Molecule 1: Integrin alpha-IIb

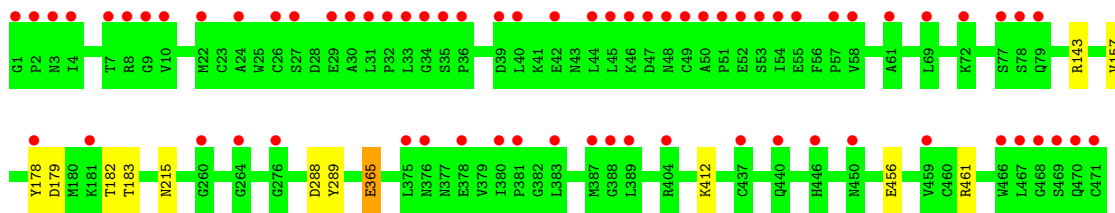


- Molecule 2: Integrin beta-3

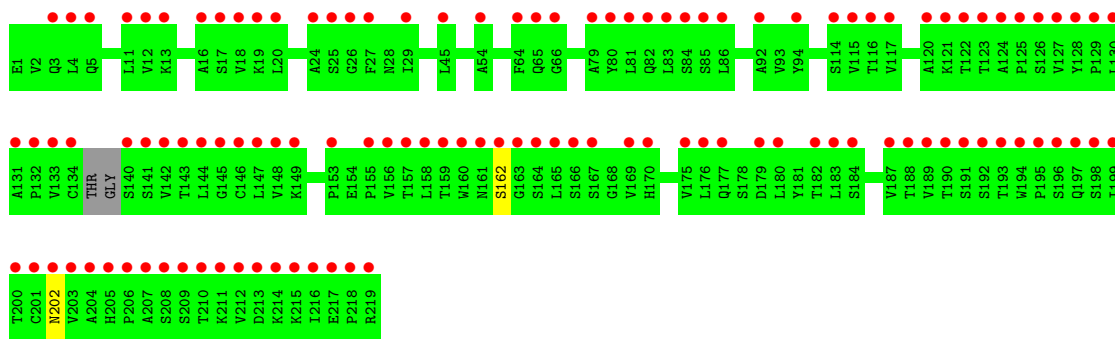


- Molecule 2: Integrin beta-3

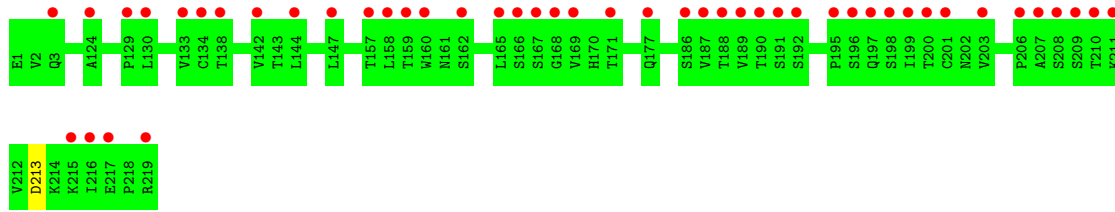




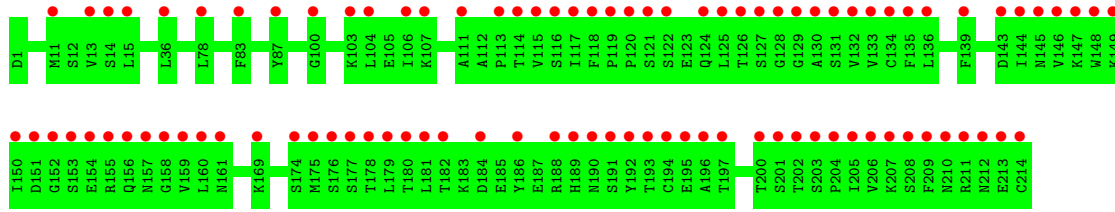
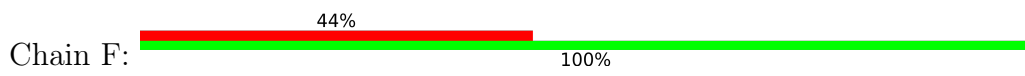
● Molecule 3: Fab heavy chain



● Molecule 3: Fab heavy chain



● Molecule 4: Fab light chain



● Molecule 4: 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:  60% 40%

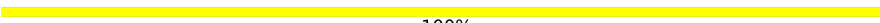
MAG1
MAG2
EMG3
MAN4
MAN5

- 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:  100%

MAG1
MAG2
EMG3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	258.89Å 144.21Å 105.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.38 – 2.20 49.38 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.1 (49.38-2.20) 98.9 (49.38-2.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.214 , 0.241 0.214 , 0.240	Depositor DCC
R_{free} test set	2000 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å ²)	51.2	Xtrriage
Anisotropy	0.233	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	42485	wwPDB-VP
Average B, all atoms (Å ²)	66.0	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: SO4, I7R, NAG, BMA, MAN, CA, MG, CL

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	0.29	0/3620	0.47	0/4935
1	C	0.26	0/3618	0.42	0/4930
2	B	0.26	0/3710	0.43	0/5030
2	D	0.24	0/3702	0.40	0/5019
3	E	0.22	0/1673	0.38	0/2290
3	H	0.23	0/1684	0.40	0/2305
4	F	0.22	0/1673	0.37	0/2269
4	L	0.23	0/1673	0.39	0/2269
All	All	0.25	0/21353	0.42	0/29047

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	3499	3347	3331	2	0
1	C	3502	3338	3320	3	0
2	B	3604	3534	3495	3	0
2	D	3623	3544	3532	5	0
3	E	1631	1590	1590	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1642	1600	1600	1	0
4	F	1637	1553	1553	0	0
4	L	1637	1553	1553	0	0
5	G	61	57	52	0	0
6	I	28	27	25	0	0
6	K	28	27	25	1	0
7	J	50	47	43	0	0
8	A	25	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	B	2	0	0	0	0
9	C	4	0	0	0	0
9	D	2	0	0	0	0
10	B	1	0	0	0	0
10	D	1	0	0	0	0
11	B	14	14	13	0	0
11	D	14	14	13	0	0
12	B	31	33	0	2	0
12	D	31	33	0	1	0
13	C	2	0	0	0	0
13	D	1	0	0	0	0
14	A	410	0	0	1	1
14	B	230	0	0	0	0
14	C	187	0	0	0	0
14	D	150	0	0	1	1
14	E	15	0	0	0	0
14	F	6	0	0	0	0
14	H	33	0	0	0	0
14	L	44	0	0	0	0
All	All	22174	20311	20145	17	1

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 0.

All (17) 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:D:456:GLU:OE2	2:D:461:ARG:NH1	2.30	0.64
6:K:1:NAG:O4	6:K:2:NAG:H83	2.02	0.60
1:C:3:LEU:O	1:C:405:GLN:NE2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:182:THR:OG1	2:D:183:THR:N	2.41	0.54
1:A:41:ARG:NH1	14:A:609:HOH:O	2.39	0.51
2:D:365:GLU:OE2	2:D:412:LYS:NZ	2.46	0.49
2:B:202:ARG:NH2	2:B:206:GLU:OE2	2.48	0.47
1:A:190:TYR:CE1	12:B:2005:I7R:C15	2.98	0.46
2:B:121:SER:HB2	12:B:2005:I7R:O3	2.15	0.45
2:D:178:TYR:CG	2:D:179:ASP:N	2.85	0.45
3:E:162:SER:N	3:E:202:ASN:OD1	2.50	0.44
1:C:107:CYS:HA	1:C:130:CYS:HA	1.99	0.44
3:H:213:ASP:OD1	3:H:213:ASP:N	2.51	0.44
2:D:288:ASP:OD1	2:D:289:TYR:N	2.52	0.42
12:D:2006:I7R:C18	14:D:2150:HOH:O	2.68	0.41
2:B:178:TYR:CG	2:B:179:ASP:N	2.89	0.40
1:C:28:ASP:OD1	1:C:32:ARG:N	2.53	0.40

All (1) 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:894:HOH:O	14:D:2175:HOH:O[1_554]	2.16	0.04

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	458/454 (101%)	442 (96%)	15 (3%)	1 (0%)	47 55
1	C	457/454 (101%)	439 (96%)	18 (4%)	0	100 100
2	B	470/471 (100%)	455 (97%)	14 (3%)	1 (0%)	47 55
2	D	470/471 (100%)	452 (96%)	17 (4%)	1 (0%)	47 55
3	E	210/216 (97%)	194 (92%)	16 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	H	212/216 (98%)	201 (95%)	11 (5%)	0	100	100
4	F	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
4	L	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
All	All	2701/2710 (100%)	2589 (96%)	109 (4%)	3 (0%)	51	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
2	B	157	VAL
2	D	157	VAL

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	367/362 (101%)	362 (99%)	5 (1%)	67	80
1	C	366/362 (101%)	361 (99%)	5 (1%)	67	80
2	B	418/416 (100%)	417 (100%)	1 (0%)	93	97
2	D	417/416 (100%)	414 (99%)	3 (1%)	84	91
3	E	186/187 (100%)	186 (100%)	0	100	100
3	H	187/187 (100%)	187 (100%)	0	100	100
4	F	188/188 (100%)	188 (100%)	0	100	100
4	L	188/188 (100%)	188 (100%)	0	100	100
All	All	2317/2306 (100%)	2303 (99%)	14 (1%)	86	93

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	190	TYR

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Mol	Chain	Res	Type
1	A	270	LEU
1	A	288	TYR
2	B	215	ASN
1	C	15	ASN
1	C	23	LEU
1	C	166	TYR
1	C	190	TYR
1	C	288	TYR
2	D	143	ARG
2	D	215	ASN
2	D	365	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	0.20	0	17,19,21	0.44	0
5	NAG	G	2	5	14,14,15	0.30	0	17,19,21	0.37	0
5	BMA	G	3	5	11,11,12	0.78	0	15,15,17	0.78	0
5	MAN	G	4	5	11,11,12	0.90	0	15,15,17	1.08	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MAN	G	5	5	11,11,12	1.05	1 (9%)	15,15,17	1.22	1 (6%)
6	NAG	I	1	2,6	14,14,15	0.37	0	17,19,21	0.37	0
6	NAG	I	2	6	14,14,15	0.20	0	17,19,21	0.48	0
7	NAG	J	1	2,7	14,14,15	0.35	0	17,19,21	0.70	0
7	NAG	J	2	7	14,14,15	0.33	0	17,19,21	0.66	0
7	BMA	J	3	7	11,11,12	0.30	0	15,15,17	0.69	0
7	MAN	J	4	7	11,11,12	0.27	0	15,15,17	0.63	0
6	NAG	K	1	2,6	14,14,15	0.35	0	17,19,21	0.69	0
6	NAG	K	2	6	14,14,15	0.25	0	17,19,21	0.74	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	-	2/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
5	MAN	G	5	5	-	1/2/19/22	0/1/1/1
6	NAG	I	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	3/6/23/26	0/1/1/1
7	NAG	J	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	0/6/23/26	0/1/1/1
7	BMA	J	3	7	-	2/2/19/22	0/1/1/1
7	MAN	J	4	7	-	2/2/19/22	0/1/1/1
6	NAG	K	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	5	MAN	C4-C5	2.18	1.57	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	5	MAN	C1-O5-C5	3.57	117.03	112.19
5	G	4	MAN	C1-O5-C5	2.33	115.35	112.19
5	G	4	MAN	O2-C2-C3	-2.03	106.08	110.14

There are no chirality outliers.

All (12) torsion outliers are listed below:

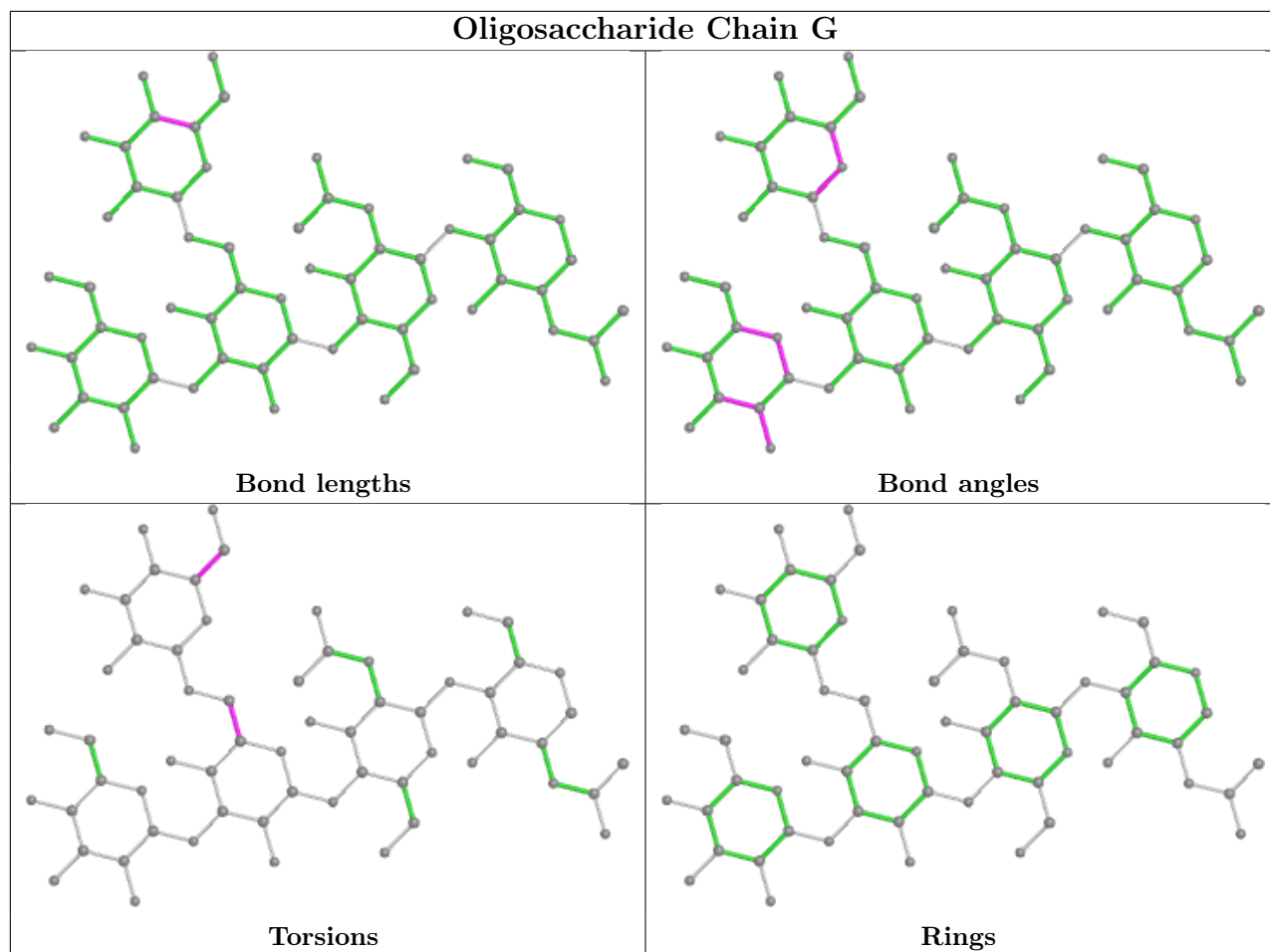
Mol	Chain	Res	Type	Atoms
7	J	4	MAN	O5-C5-C6-O6
7	J	3	BMA	O5-C5-C6-O6
5	G	3	BMA	C4-C5-C6-O6
7	J	3	BMA	C4-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2
6	K	2	NAG	C8-C7-N2-C2
6	K	2	NAG	O7-C7-N2-C2
5	G	3	BMA	O5-C5-C6-O6
7	J	4	MAN	C4-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6
5	G	5	MAN	C4-C5-C6-O6

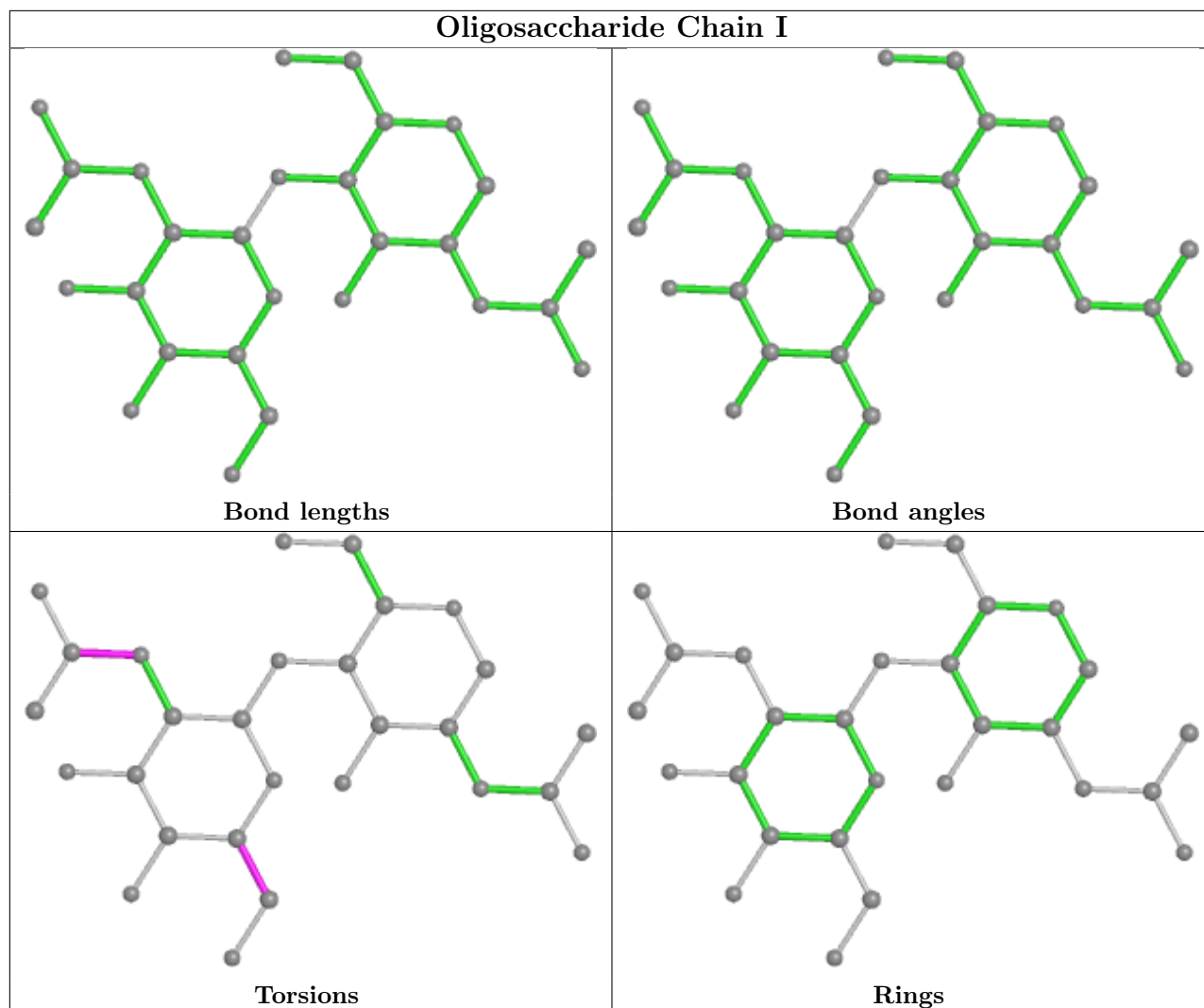
There are no ring outliers.

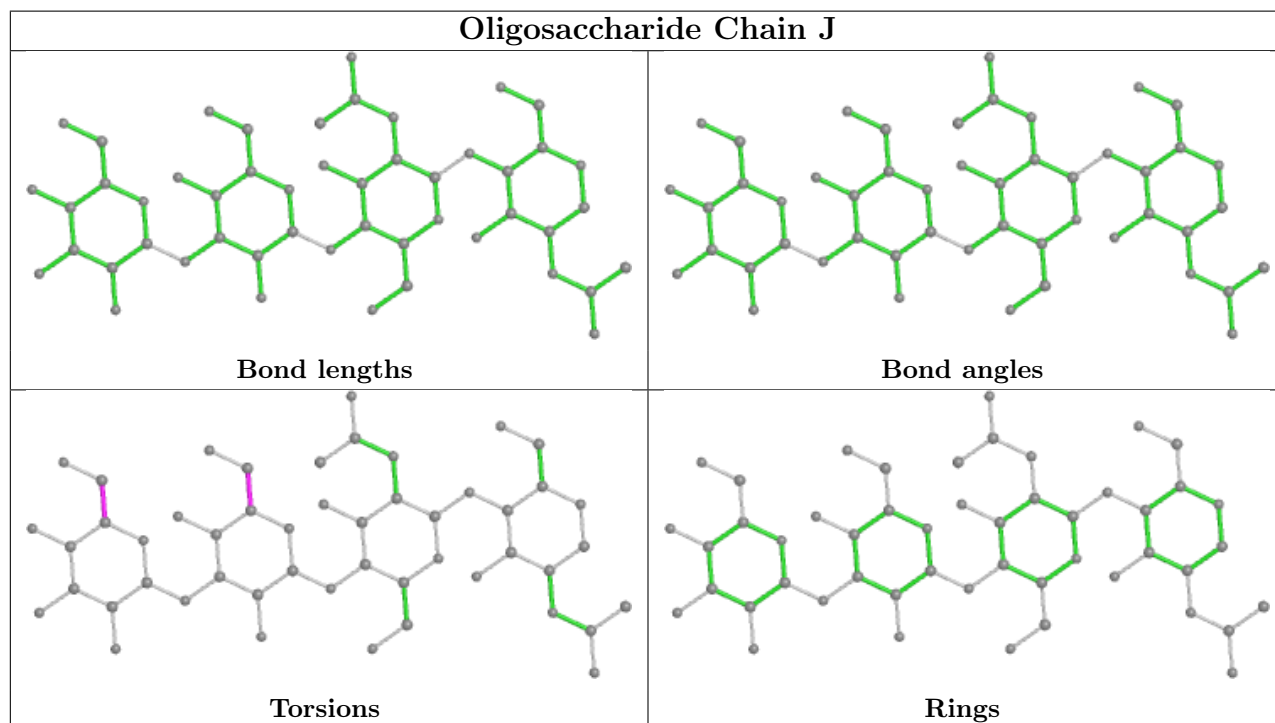
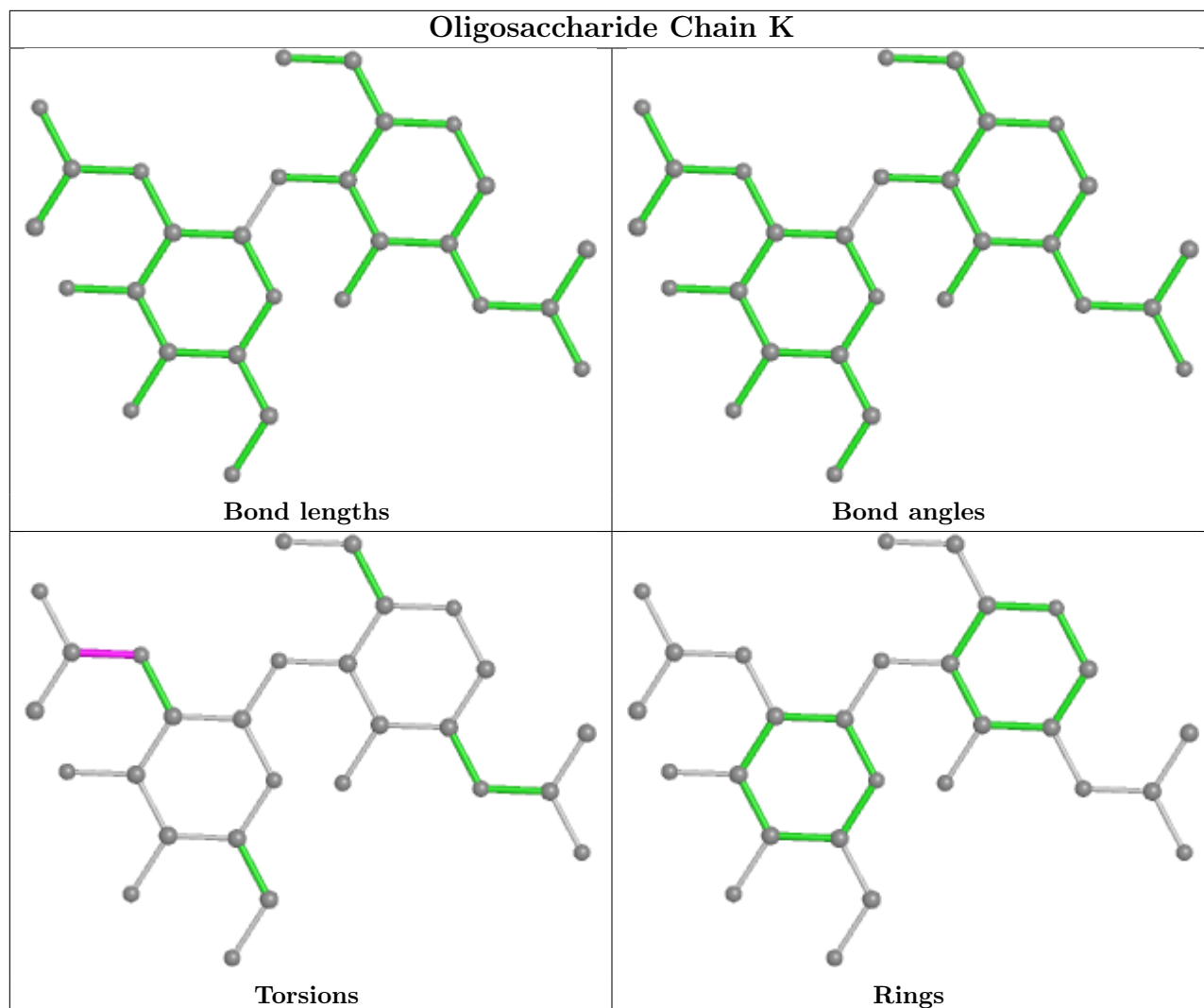
2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	2	NAG	1	0
6	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](#)

Of 31 ligands modelled in this entry, 17 are monoatomic - leaving 14 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	A	501	-	4,4,4	0.14	0	6,6,6	0.07	0
8	SO4	C	503	-	4,4,4	0.14	0	6,6,6	0.05	0
8	SO4	C	510	-	4,4,4	0.14	0	6,6,6	0.07	0
11	NAG	B	2004	2	14,14,15	0.20	0	17,19,21	0.53	0
8	SO4	A	502	-	4,4,4	0.14	0	6,6,6	0.08	0
8	SO4	A	509	-	4,4,4	0.15	0	6,6,6	0.12	0
11	NAG	D	2004	2	14,14,15	0.39	0	17,19,21	0.46	0
8	SO4	A	507	-	4,4,4	0.15	0	6,6,6	0.05	0
8	SO4	A	508	-	4,4,4	0.14	0	6,6,6	0.06	0
12	I7R	B	2005	10	34,34,34	1.06	2 (5%)	44,47,47	0.93	1 (2%)
8	SO4	C	501	-	4,4,4	0.14	0	6,6,6	0.07	0
8	SO4	L	301	-	4,4,4	0.14	0	6,6,6	0.05	0
8	SO4	C	502	-	4,4,4	0.14	0	6,6,6	0.06	0
12	I7R	D	2006	10	34,34,34	1.24	4 (11%)	44,47,47	1.06	3 (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
12	I7R	B	2005	10	-	5/18/49/49	0/4/4/4
11	NAG	B	2004	2	-	2/6/23/26	0/1/1/1
11	NAG	D	2004	2	-	0/6/23/26	0/1/1/1
12	I7R	D	2006	10	-	6/18/49/49	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	D	2006	I7R	O1-C14	-4.05	1.41	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	2005	I7R	C6-N3	2.84	1.34	1.27
12	B	2005	I7R	O1-C14	-2.74	1.42	1.46
12	D	2006	I7R	O2-C22	-2.57	1.22	1.30
12	D	2006	I7R	C6-N3	2.42	1.33	1.27
12	D	2006	I7R	C15-C13	-2.06	1.47	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	D	2006	I7R	C4-C1-N1	-2.86	107.58	110.80
12	D	2006	I7R	C17-C18-N6	2.43	115.64	110.64
12	D	2006	I7R	C14-C15-C13	2.16	102.83	100.85
12	B	2005	I7R	C14-C15-C13	2.04	102.72	100.85

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	B	2005	I7R	C15-C14-C16-N5
12	B	2005	I7R	O1-C14-C16-N5
12	D	2006	I7R	C15-C14-C16-N5
12	D	2006	I7R	O1-C14-C16-N5
11	B	2004	NAG	O5-C5-C6-O6
11	B	2004	NAG	C4-C5-C6-O6
12	B	2005	I7R	C7-C6-N2-C3
12	B	2005	I7R	C14-C16-N5-C20
12	D	2006	I7R	C22-C21-N6-C18
12	D	2006	I7R	N3-C6-C7-C8
12	D	2006	I7R	C7-C6-N2-C3
12	B	2005	I7R	N3-C6-C7-C8
12	D	2006	I7R	N3-C6-C7-C12

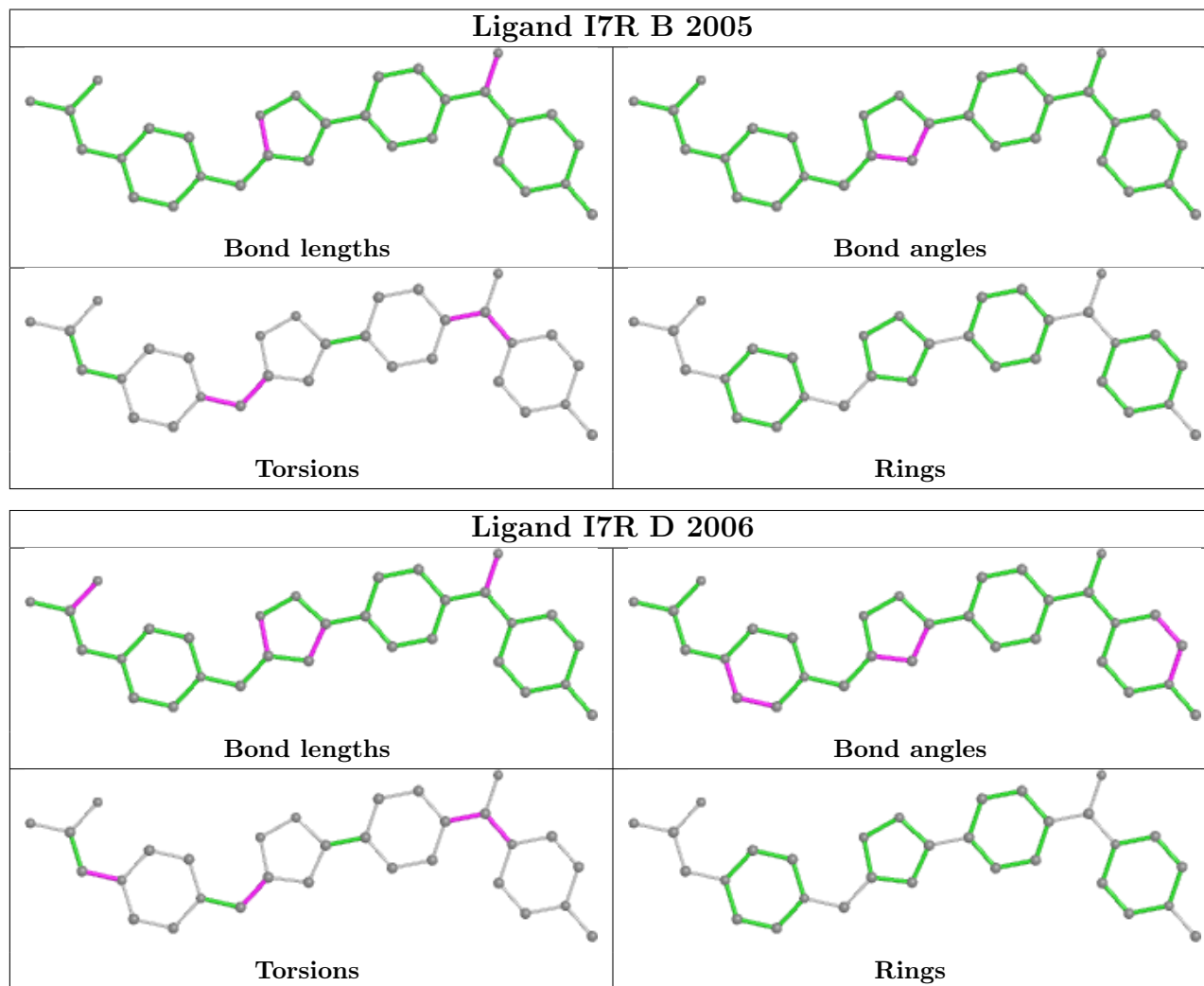
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	B	2005	I7R	2	0
12	D	2006	I7R	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	134:CYS	C	138:THR	N	7.08

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	454/454 (100%)	0.93	49 (10%) 5 5	34, 48, 78, 125	0
1	C	453/454 (99%)	0.77	47 (10%) 6 5	44, 66, 98, 131	0
2	B	466/471 (98%)	1.03	78 (16%) 1 1	34, 72, 153, 182	1 (0%)
2	D	471/471 (100%)	0.92	69 (14%) 2 2	45, 84, 140, 166	1 (0%)
3	E	214/216 (99%)	3.18	117 (54%) 0 0	81, 137, 218, 228	0
3	H	216/216 (100%)	1.16	47 (21%) 0 0	57, 105, 163, 181	0
4	F	214/214 (100%)	2.53	94 (43%) 0 0	82, 131, 196, 218	0
4	L	214/214 (100%)	0.69	18 (8%) 11 9	61, 96, 124, 158	0
All	All	2702/2710 (99%)	1.22	519 (19%) 1 1	34, 81, 171, 228	2 (0%)

All (519) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	201	CYS	15.8
3	E	212	VAL	14.8
3	E	165	LEU	13.9
3	E	142	VAL	12.7
2	B	33	LEU	12.5
4	F	206	VAL	11.9
2	D	375	LEU	11.8
3	E	216	ILE	11.7
3	E	133	VAL	11.6
4	F	125	LEU	11.2
2	D	471	CYS	11.0
4	F	193	THR	10.4
4	L	214	CYS	10.3
3	E	199	ILE	10.1
3	E	194	TRP	10.1
3	E	156	VAL	10.0

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Mol	Chain	Res	Type	RSRZ
3	E	219	ARG	9.9
4	F	181	LEU	9.8
4	F	132	VAL	9.8
3	E	160	TRP	9.7
3	E	200	THR	9.6
3	E	144	LEU	9.6
4	F	179	LEU	9.6
4	F	115	VAL	9.5
4	F	122	SER	9.4
3	E	129	PRO	9.4
3	E	198	SER	9.2
2	B	77	SER	9.2
3	E	134	CYS	9.1
1	A	454	VAL	9.0
2	D	469	SER	8.9
4	F	126	THR	8.8
3	E	196	SER	8.7
4	F	148	TRP	8.7
2	D	33	LEU	8.3
4	F	117	ILE	8.3
4	F	130	ALA	8.3
3	E	147	LEU	8.2
3	E	203	VAL	8.1
4	F	147	LYS	8.1
3	E	127	VAL	7.9
3	E	131	ALA	7.9
2	B	10	VAL	7.6
4	F	209	PHE	7.6
3	E	215	LYS	7.6
3	E	169	VAL	7.5
3	E	132	PRO	7.5
4	F	205	ILE	7.4
4	F	194	CYS	7.4
4	F	133	VAL	7.3
2	D	468	GLY	7.2
4	F	214	CYS	7.0
3	E	218	PRO	7.0
3	E	130	LEU	6.9
3	E	128	TYR	6.9
3	E	195	PRO	6.9
2	B	34	GLY	6.8
3	E	217	GLU	6.8

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Mol	Chain	Res	Type	RSRZ
4	F	136	LEU	6.7
4	F	144	ILE	6.7
4	F	180	THR	6.6
3	E	210	THR	6.6
3	H	158	LEU	6.6
4	F	152	GLY	6.5
3	H	189	VAL	6.4
3	H	211	LYS	6.4
3	E	183	LEU	6.3
4	F	202	THR	6.3
2	D	380	ILE	6.2
3	E	143	THR	6.2
4	F	159	VAL	6.2
2	B	1	GLY	6.1
4	F	195	GLU	6.1
4	F	213	GLU	6.1
3	E	11	LEU	6.0
2	D	181	LYS	6.0
2	B	466	TRP	6.0
3	E	146	CYS	5.9
4	F	160	LEU	5.9
3	H	203	VAL	5.9
4	F	178	THR	5.9
3	E	191	SER	5.8
3	H	216	ILE	5.8
3	E	145	GLY	5.8
2	B	2	PRO	5.8
3	E	206	PRO	5.7
2	B	49	CYS	5.7
4	F	208	SER	5.7
2	B	30	ALA	5.7
3	H	198	SER	5.7
3	E	167	SER	5.7
3	H	209	SER	5.7
4	F	204	PRO	5.7
2	D	46	LYS	5.7
3	H	134	CYS	5.6
3	E	189	VAL	5.6
4	F	146	VAL	5.6
2	B	31	LEU	5.6
3	E	141	SER	5.6
2	B	54	ILE	5.5

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Mol	Chain	Res	Type	RSRZ
3	E	211	LYS	5.5
2	B	9	GLY	5.5
3	E	193	THR	5.5
3	E	214	LYS	5.5
4	F	150	ILE	5.4
3	H	165	LEU	5.4
2	B	76	ASP	5.4
3	E	187	VAL	5.4
4	L	212	ASN	5.3
3	E	54	ALA	5.3
2	B	36	PRO	5.3
4	F	157	ASN	5.3
4	F	129	GLY	5.3
4	F	156	GLN	5.3
2	B	4	ILE	5.2
4	F	118	PHE	5.2
4	F	191	SER	5.1
2	B	8	ARG	5.1
3	E	12	VAL	5.1
3	E	205	HIS	5.1
3	H	208	SER	5.1
2	D	48	ASN	5.0
3	E	140	SER	5.0
4	F	182	THR	5.0
2	B	32	PRO	5.0
2	B	375	LEU	5.0
3	E	158	LEU	5.0
3	E	204	ALA	4.9
3	E	155	PRO	4.9
2	D	2	PRO	4.9
4	F	120	PRO	4.9
2	D	52	GLU	4.8
4	F	149	LYS	4.8
4	F	135	PHE	4.8
4	F	186	TYR	4.8
2	D	35	SER	4.8
3	E	20	LEU	4.8
3	H	169	VAL	4.7
2	D	376	ASN	4.7
2	B	51	PRO	4.6
2	D	34	GLY	4.6
3	E	16	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
2	B	35	SER	4.6
3	H	166	SER	4.6
2	B	44	LEU	4.6
4	F	158	GLY	4.6
4	F	134	CYS	4.6
3	H	217	GLU	4.5
2	D	44	LEU	4.5
3	E	209	SER	4.5
3	H	196	SER	4.5
3	E	126	SER	4.5
4	F	192	TYR	4.5
2	D	51	PRO	4.5
2	D	32	PRO	4.5
4	F	201	SER	4.4
1	C	340	LEU	4.4
3	H	187	VAL	4.4
4	F	177	SER	4.4
3	E	17	SER	4.4
3	E	82	GLN	4.3
3	E	121	LYS	4.3
1	A	337	PRO	4.3
2	B	451	GLY	4.3
4	F	212	ASN	4.3
4	F	151	ASP	4.3
4	F	207	LYS	4.3
4	F	197	THR	4.3
2	D	9	GLY	4.3
3	E	161	ASN	4.3
3	E	29	ILE	4.2
4	F	128	GLY	4.2
4	F	211	ARG	4.2
3	E	197	GLN	4.1
2	D	470	GLN	4.1
4	F	210	ASN	4.1
2	D	27	SER	4.1
4	F	155	ARG	4.1
3	E	202	ASN	4.1
3	H	201	CYS	4.1
3	E	18	VAL	4.1
2	B	29	GLU	4.0
3	E	213	ASP	4.0
4	L	205	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
3	E	117	VAL	4.0
3	E	85	SER	4.0
3	E	192	SER	4.0
3	E	190	THR	3.9
2	B	28	ASP	3.9
4	L	206	VAL	3.9
2	D	42	GLU	3.9
3	H	133	VAL	3.9
4	F	119	PRO	3.9
4	F	83	PHE	3.8
2	B	440	GLN	3.8
2	B	380	ILE	3.8
4	F	114	THR	3.8
2	B	46	LYS	3.8
4	F	116	SER	3.8
3	E	162	SER	3.8
3	E	5	GLN	3.8
1	A	336	GLY	3.7
2	D	54	ILE	3.7
3	E	166	SER	3.7
4	F	190	ASN	3.7
2	B	50	ALA	3.7
1	C	337	PRO	3.7
2	D	31	LEU	3.7
3	E	124	ALA	3.7
3	E	115	VAL	3.7
3	E	148	VAL	3.7
3	H	197	GLN	3.7
3	E	176	LEU	3.6
4	F	106	ILE	3.6
2	B	458	GLY	3.6
2	D	467	LEU	3.6
4	L	125	LEU	3.6
3	H	162	SER	3.6
2	B	372	ALA	3.6
2	D	36	PRO	3.6
3	E	116	THR	3.6
3	H	206	PRO	3.6
2	B	45	LEU	3.5
3	E	175	VAL	3.5
2	D	378	GLU	3.5
4	F	111	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
4	L	13	VAL	3.5
2	D	178	TYR	3.5
2	B	26	CYS	3.5
2	D	8	ARG	3.5
4	F	203	SER	3.5
4	F	169	LYS	3.4
3	H	144	LEU	3.4
1	C	131	PHE	3.4
3	H	160	TRP	3.4
3	H	188	THR	3.4
4	F	14	SER	3.4
4	L	150	ILE	3.4
2	B	379	VAL	3.4
4	F	103	LYS	3.4
1	C	338	HIS	3.4
2	D	53	SER	3.4
3	H	130	LEU	3.4
1	C	143	TYR	3.4
2	B	52	GLU	3.4
3	H	199	ILE	3.4
4	F	154	GLU	3.4
4	F	78	LEU	3.4
2	D	437	CYS	3.4
2	D	79	GLN	3.3
3	E	153	PRO	3.3
3	H	195	PRO	3.3
4	F	113	PRO	3.3
2	B	11	SER	3.3
4	F	174	SER	3.3
3	E	207	ALA	3.3
2	B	48	ASN	3.3
3	E	180	LEU	3.3
3	E	157	THR	3.3
4	F	124	GLN	3.3
2	B	452	ASN	3.3
3	E	86	LEU	3.3
2	D	22	MET	3.2
2	B	53	SER	3.2
3	E	122	THR	3.2
3	E	163	GLY	3.2
2	D	389	LEU	3.2
2	B	374	CYS	3.2

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Mol	Chain	Res	Type	RSRZ
3	H	207	ALA	3.2
1	A	171	PHE	3.1
3	E	27	PHE	3.1
4	F	100	GLY	3.1
2	D	55	GLU	3.1
3	H	124	ALA	3.1
3	H	219	ARG	3.1
1	A	146	CYS	3.1
1	A	167	CYS	3.1
1	C	109	PRO	3.1
3	E	177	GLN	3.1
2	D	404	ARG	3.1
3	H	167	SER	3.1
4	F	153	SER	3.1
3	E	83	LEU	3.1
2	B	27	SER	3.0
3	E	19	LYS	3.0
4	L	169	LYS	3.0
4	F	13	VAL	3.0
2	D	77	SER	3.0
3	H	192	SER	3.0
4	F	200	THR	3.0
2	B	42	GLU	3.0
1	C	130	CYS	3.0
3	E	123	THR	3.0
2	B	181	LYS	3.0
3	E	149	LYS	3.0
2	D	40	LEU	3.0
1	C	191	PHE	3.0
1	C	453	VAL	3.0
1	C	336	GLY	2.9
2	B	381	PRO	2.9
1	A	47	GLN	2.9
1	A	193	GLY	2.9
2	D	45	LEU	2.9
1	C	335	ARG	2.9
4	L	213	GLU	2.9
1	C	171	PHE	2.9
3	H	200	THR	2.9
2	B	383	LEU	2.9
1	A	235	TRP	2.9
3	E	188	THR	2.9

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Mol	Chain	Res	Type	RSRZ
3	E	25	SER	2.9
2	B	462	CYS	2.9
2	D	383	LEU	2.9
3	E	208	SER	2.8
3	H	138	THR	2.8
3	E	64	PHE	2.8
1	C	196	ALA	2.8
2	B	378	GLU	2.8
3	E	182	THR	2.8
2	D	58	VAL	2.8
1	A	185	ALA	2.8
1	C	339	ALA	2.8
2	B	460	CYS	2.8
3	E	164	SER	2.8
2	D	39	ASP	2.8
2	B	459	VAL	2.8
4	L	19	VAL	2.8
3	E	24	ALA	2.8
3	E	79	ALA	2.8
1	A	186	PRO	2.8
3	H	159	THR	2.8
3	E	65	GLN	2.8
4	F	15	LEU	2.8
2	D	7	THR	2.8
1	A	190	TYR	2.8
2	B	442	GLU	2.8
4	F	188	ARG	2.7
1	C	108	ALA	2.7
2	D	78	SER	2.7
3	H	168	GLY	2.7
2	D	466	TRP	2.7
4	F	131	SER	2.7
1	C	146	CYS	2.7
1	C	110	TRP	2.7
2	B	373	THR	2.7
2	D	3	ASN	2.7
2	D	1	GLY	2.7
3	E	45	LEU	2.7
2	D	49	CYS	2.7
1	C	187	GLY	2.7
1	C	320	ARG	2.7
3	E	84	SER	2.7

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Mol	Chain	Res	Type	RSRZ
3	H	190	THR	2.7
2	B	37	ARG	2.6
2	B	38	CYS	2.6
4	F	145	ASN	2.6
1	A	183	LEU	2.6
2	B	455	PHE	2.6
3	E	13	LYS	2.6
1	A	319	ASP	2.6
4	L	21	ILE	2.6
1	A	189	TYR	2.6
1	C	186	PRO	2.6
1	A	169	ALA	2.6
2	D	50	ALA	2.6
2	B	79	GLN	2.6
1	C	183	LEU	2.6
2	D	381	PRO	2.6
3	E	4	LEU	2.6
1	A	184	GLY	2.6
2	D	24	ALA	2.6
3	E	92	ALA	2.6
3	E	114	SER	2.6
2	D	57	PRO	2.5
1	A	192	LEU	2.5
4	F	139	PHE	2.5
1	C	106	ALA	2.5
1	C	167	CYS	2.5
2	D	26	CYS	2.5
1	C	234	TYR	2.5
1	C	237	TYR	2.5
2	B	376	ASN	2.5
3	E	80	TYR	2.5
1	A	191	PHE	2.5
1	A	421	LEU	2.5
4	F	11	MET	2.5
2	B	63	VAL	2.5
2	D	47	ASP	2.5
4	F	196	ALA	2.5
2	B	67	ARG	2.5
3	H	157	THR	2.5
4	F	176	SER	2.4
1	A	339	ALA	2.4
1	C	169	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	187	GLY	2.4
3	E	3	GLN	2.4
3	E	94	TYR	2.4
3	E	179	ASP	2.4
1	A	110	TRP	2.4
1	C	172	SER	2.4
1	A	130	CYS	2.4
2	D	10	VAL	2.4
2	B	164	TYR	2.4
2	B	289	TYR	2.4
1	A	194	LEU	2.4
1	A	188	GLY	2.4
2	D	30	ALA	2.4
1	C	107	CYS	2.4
1	A	234	TYR	2.4
1	A	288	TYR	2.4
1	C	207	TYR	2.4
3	H	210	THR	2.4
3	H	177	GLN	2.4
4	F	161	ASN	2.4
1	A	109	PRO	2.3
2	B	219	PRO	2.3
3	E	120	ALA	2.3
4	F	104	LEU	2.3
2	D	450	ASN	2.3
4	L	127	SER	2.3
1	A	170	GLY	2.3
2	B	7	THR	2.3
2	D	4	ILE	2.3
3	E	159	THR	2.3
4	F	184	ASP	2.3
3	H	191	SER	2.3
4	F	175	MET	2.3
1	C	170	GLY	2.3
2	B	382	GLY	2.3
1	A	436	ILE	2.3
2	B	457	CYS	2.3
2	B	255	HIS	2.3
4	F	189	HIS	2.3
2	B	377	ASN	2.3
3	E	184	SER	2.3
2	B	64	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	94	GLY	2.2
1	C	389	VAL	2.2
1	A	359	ALA	2.2
1	C	95	ALA	2.2
2	D	264	GLY	2.2
2	D	29	GLU	2.2
2	B	3	ASN	2.2
2	B	178	TYR	2.2
2	D	72	LYS	2.2
1	C	129	SER	2.2
1	C	20	GLY	2.2
1	C	94	GLY	2.2
2	D	260	GLY	2.2
2	D	276	GLY	2.2
4	L	103	LYS	2.2
1	C	358[A]	SER	2.2
1	A	265	GLY	2.2
3	E	66	GLY	2.2
4	L	128	GLY	2.2
1	A	195	LEU	2.2
1	C	93	LEU	2.2
2	B	262	LEU	2.2
2	B	268	PRO	2.2
3	E	125	PRO	2.2
3	H	142	VAL	2.2
4	F	107	LYS	2.2
3	E	81	LEU	2.2
1	A	380	TYR	2.1
1	A	358	SER	2.1
3	H	129	PRO	2.1
2	D	387	MET	2.1
3	E	26	GLY	2.1
2	B	447	ARG	2.1
1	C	21	PHE	2.1
4	L	196	ALA	2.1
3	H	215	LYS	2.1
4	L	184	ASP	2.1
1	A	238	SER	2.1
1	C	194	LEU	2.1
1	C	311	PRO	2.1
1	C	421	LEU	2.1
1	A	290	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	127	VAL	2.1
1	A	237	TYR	2.1
2	D	459	VAL	2.1
4	F	87	TYR	2.1
4	L	118	PHE	2.1
1	A	258	PRO	2.1
1	C	203	ILE	2.1
2	D	69	LEU	2.1
2	D	440	GLN	2.1
1	A	105	VAL	2.1
1	C	288	TYR	2.1
4	L	210	ASN	2.1
3	H	147	LEU	2.1
4	F	36	LEU	2.1
3	H	3	GLN	2.1
1	C	141	ALA	2.1
1	C	359	ALA	2.1
2	B	266	VAL	2.1
3	E	170	HIS	2.1
4	F	127	SER	2.1
1	A	166	TYR	2.1
1	C	166	TYR	2.1
2	B	39	ASP	2.0
2	D	446	HIS	2.0
1	A	172	SER	2.0
4	F	121	SER	2.0
2	B	446	HIS	2.0
2	B	265	ILE	2.0
2	D	388	GLY	2.0
3	H	171	THR	2.0
1	A	129	SER	2.0
1	A	420	SER	2.0
1	C	377	ALA	2.0
2	B	218	ALA	2.0
2	D	61	ALA	2.0
1	A	224	ASP	2.0
2	B	80	VAL	2.0
2	B	55	GLU	2.0
3	H	186	SER	2.0
4	F	143	ASP	2.0
1	A	108	ALA	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](#)

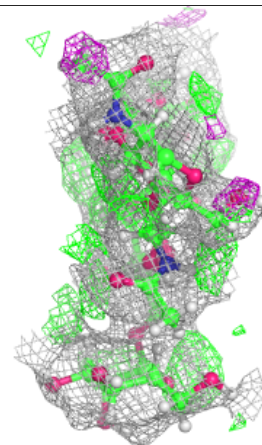
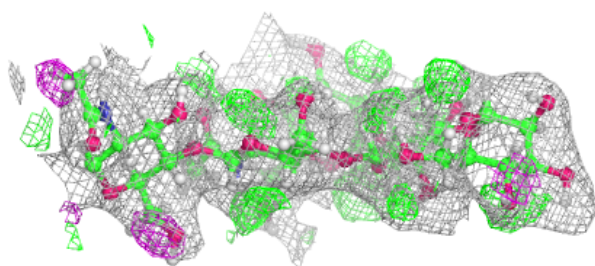
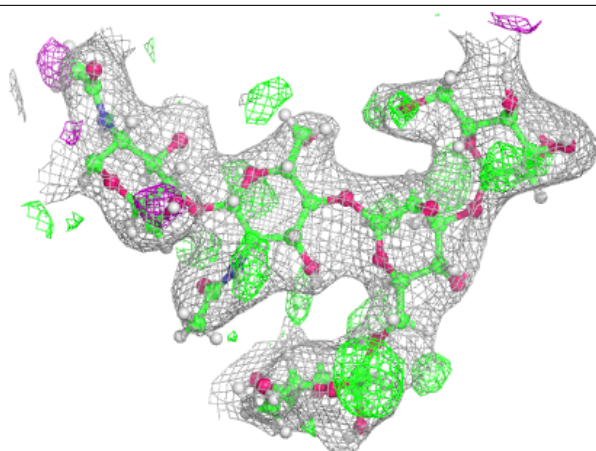
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	K	1	14/15	0.71	0.20	45,45,118,118	0
5	BMA	G	3	11/12	0.75	0.14	45,97,97,97	0
6	NAG	I	1	14/15	0.76	0.25	45,45,113,113	0
5	MAN	G	5	11/12	0.77	0.19	45,45,106,106	0
7	BMA	J	3	11/12	0.77	0.30	45,45,109,109	0
5	MAN	G	4	11/12	0.81	0.12	45,45,94,94	0
7	MAN	J	4	11/12	0.81	0.29	45,45,111,111	0
6	NAG	K	2	14/15	0.83	0.26	45,45,124,124	0
7	NAG	J	2	14/15	0.86	0.22	45,45,89,89	0
5	NAG	G	2	14/15	0.87	0.12	45,45,73,73	0
6	NAG	I	2	14/15	0.87	0.22	45,45,119,119	0
7	NAG	J	1	14/15	0.87	0.13	45,45,72,72	0
5	NAG	G	1	14/15	0.89	0.17	45,45,54,54	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.

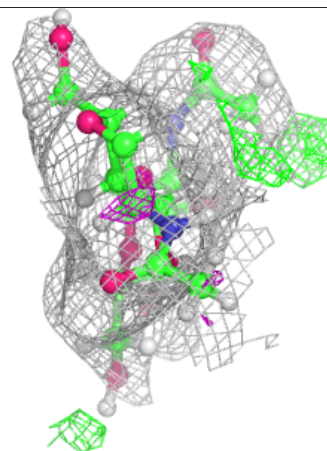
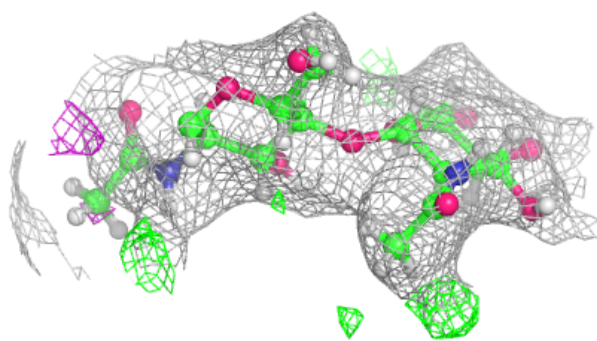
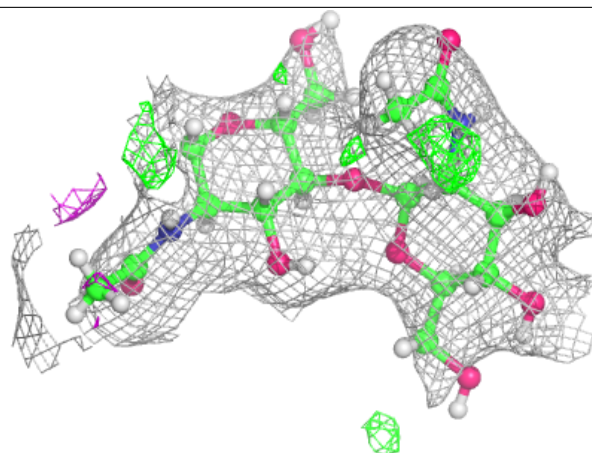
Electron density around Chain G:

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



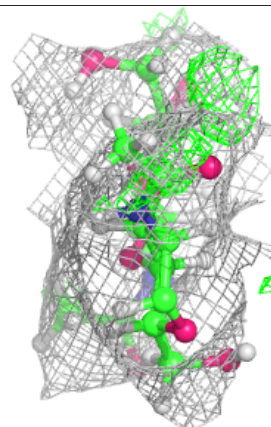
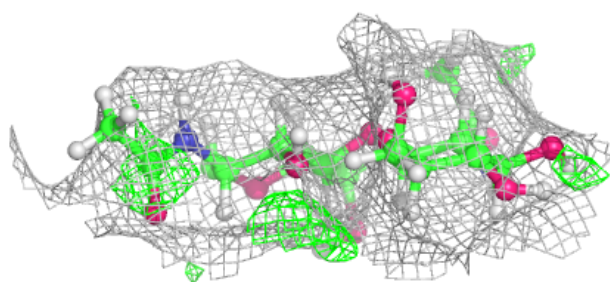
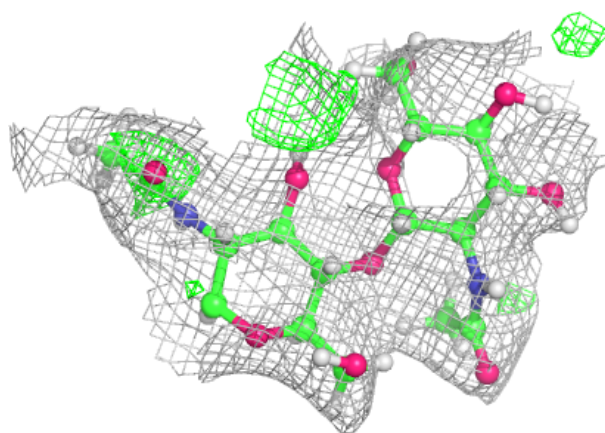
Electron density around Chain I:

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

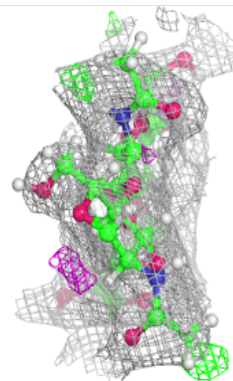
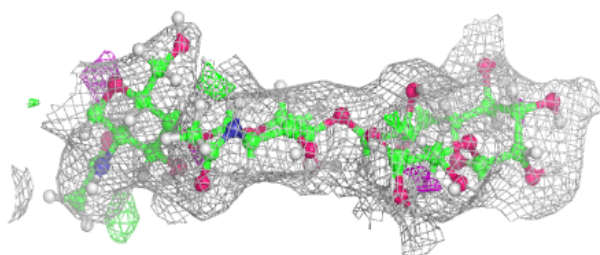
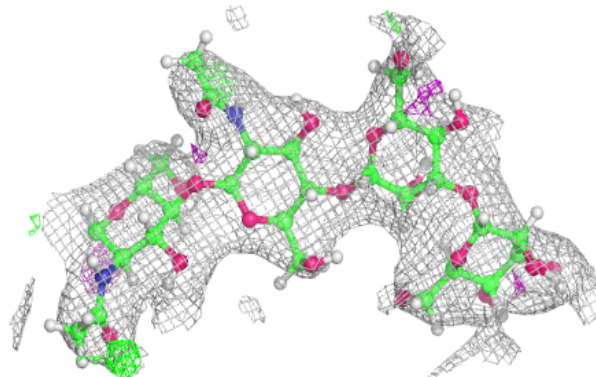


Electron density around Chain K:

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

**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)

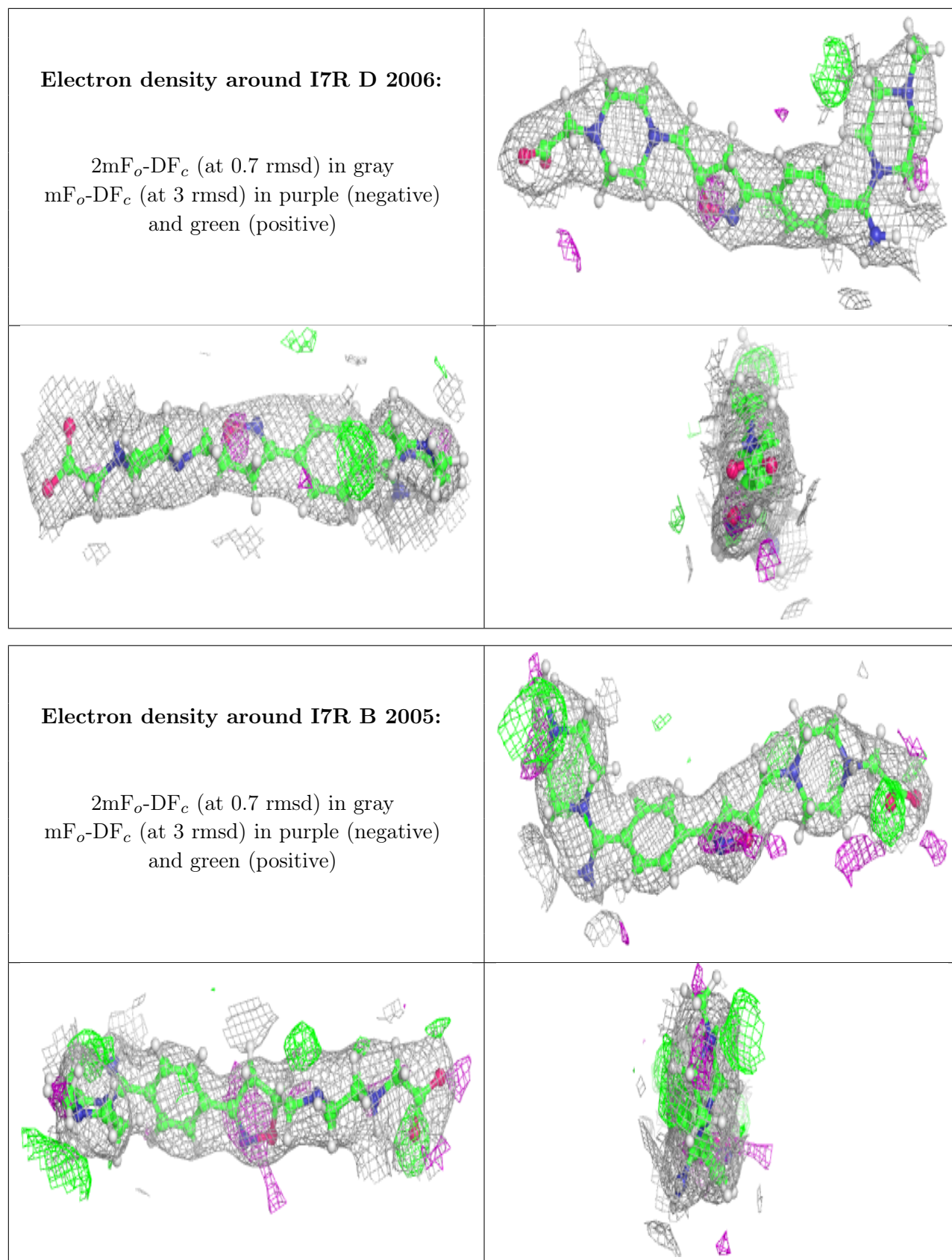


6.4 Ligands [i](#)

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
13	CL	C	505	1/1	0.66	0.16	98,98,98,98	0
11	NAG	D	2004	14/15	0.77	0.24	45,45,114,114	0
8	SO4	A	507	5/5	0.80	0.17	97,97,97,97	0
8	SO4	A	508	5/5	0.81	0.17	101,101,101,101	0
11	NAG	B	2004	14/15	0.81	0.30	45,45,120,120	0
13	CL	D	2005	1/1	0.82	0.26	99,99,99,99	0
8	SO4	C	502	5/5	0.87	0.15	110,110,110,110	0
12	I7R	D	2006	31/31	0.87	0.17	45,45,68,68	0
8	SO4	C	510	5/5	0.88	0.17	107,107,107,107	0
12	I7R	B	2005	31/31	0.90	0.23	45,45,54,54	0
13	CL	C	504	1/1	0.90	0.44	78,78,78,78	0
8	SO4	C	501	5/5	0.92	0.14	102,102,102,102	0
8	SO4	C	503	5/5	0.92	0.13	110,110,110,110	0
8	SO4	A	501	5/5	0.93	0.13	81,81,81,81	0
9	CA	C	506	1/1	0.94	0.05	89,89,89,89	0
9	CA	A	503	1/1	0.94	0.11	56,56,56,56	0
9	CA	D	2003	1/1	0.95	0.20	51,51,51,51	0
8	SO4	A	509	5/5	0.95	0.18	75,75,75,75	0
9	CA	C	507	1/1	0.95	0.07	71,71,71,71	0
9	CA	C	509	1/1	0.95	0.15	58,58,58,58	0
10	MG	D	2001	1/1	0.96	0.16	44,44,44,44	0
8	SO4	L	301	5/5	0.96	0.17	100,100,100,100	0
9	CA	C	508	1/1	0.97	0.14	59,59,59,59	0
9	CA	A	504	1/1	0.98	0.15	45,45,45,45	0
10	MG	B	2001	1/1	0.98	0.25	26,26,26,26	0
8	SO4	A	502	5/5	0.99	0.16	68,68,68,68	0
9	CA	A	505	1/1	0.99	0.21	38,38,38,38	0
9	CA	A	506	1/1	0.99	0.19	43,43,43,43	0
9	CA	B	2002	1/1	0.99	0.17	55,55,55,55	0
9	CA	D	2002	1/1	0.99	0.21	62,62,62,62	0
9	CA	B	2003	1/1	1.00	0.23	41,41,41,41	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.