



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 11, 2024 – 03:05 PM EDT

PDB ID : 6MJJ
Title : Crystal structure of the mCD1d/xxm (JJ290) /iNKTcr ternary complex
Authors : Zajonc, D.M.; Bitra, A.; Janssens, J.
Deposited on : 2018-09-21
Resolution : 1.93 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	:	2.36.2
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)	:	2.36.2

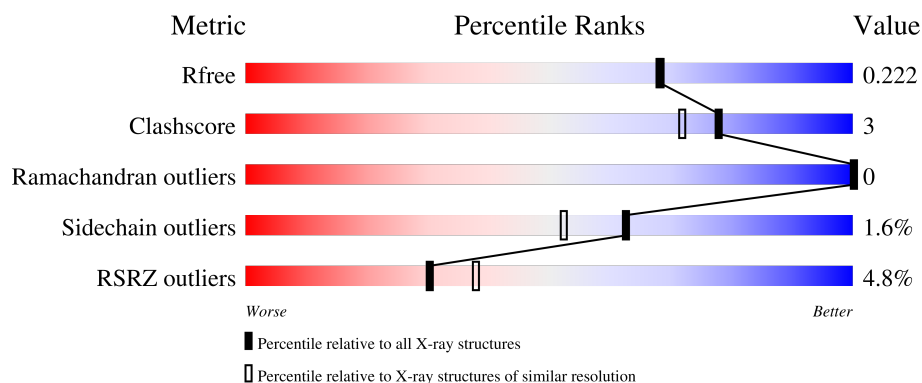
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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	C	209	<div> <div>5%</div> <div>90%</div> <div>6%</div> <div>.</div> </div>
2	D	241	<div> <div>%</div> <div>95%</div> <div>.</div> <div>.</div> </div>
3	A	285	<div> <div>8%</div> <div>86%</div> <div>10%</div> <div>.</div> </div>
4	B	99	<div> <div>3%</div> <div>92%</div> <div>5%</div> <div>.</div> <div>.</div> </div>
5	E	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
6	F	3	 33% 67%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7333 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 T cell receptor alpha variable 11,T cell receptor alpha variable 11,T cell receptor alpha joining 18,Human nkt tcr alpha chain, CHIMERIC PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	201	Total	C	N	O	S	0	4	0
			1563	973	268	314	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	initiating methionine	UNP A0A0B4J1J9
C	113	ILE	-	linker	UNP A0A0B4J1J9

- Molecule 2 is a protein called Beta-chain,Tcell receptor chain,T cell receptor beta constant 2, CHIMERIC PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	239	Total	C	N	O	S	0	1	0
			1870	1174	331	359	6			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	95	ASP	-	linker	UNP A2NTY6
D	96	GLU	-	linker	UNP A2NTY6
D	97	GLY	-	linker	UNP A2NTY6
D	98	TYR	-	linker	UNP A2NTY6
D	130	ALA	ALA	linker	UNP A0N8J3
D	168	CYS	SER	variant	UNP A0A5B9
D	186	SER	CYS	variant	UNP A0A5B9

- Molecule 3 is a protein called Antigen-presenting glycoprotein CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	273	Total	C	N	O	S	0	4	0
			2201	1404	376	408	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	280	HIS	-	expression tag	UNP A0A0R4J090
A	281	HIS	-	expression tag	UNP A0A0R4J090
A	282	HIS	-	expression tag	UNP A0A0R4J090
A	283	HIS	-	expression tag	UNP A0A0R4J090
A	284	HIS	-	expression tag	UNP A0A0R4J090
A	285	HIS	-	expression tag	UNP A0A0R4J090

- Molecule 4 is a protein called Beta-2-microglobulin.

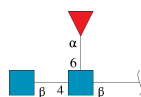
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	97	Total	C	N	O	S	0	1	0
			779	497	131	144	7			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O		0	0	0
			28	16	2	10				

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	3	Total	C	N	O		0	0	0
			38	22	2	14				

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

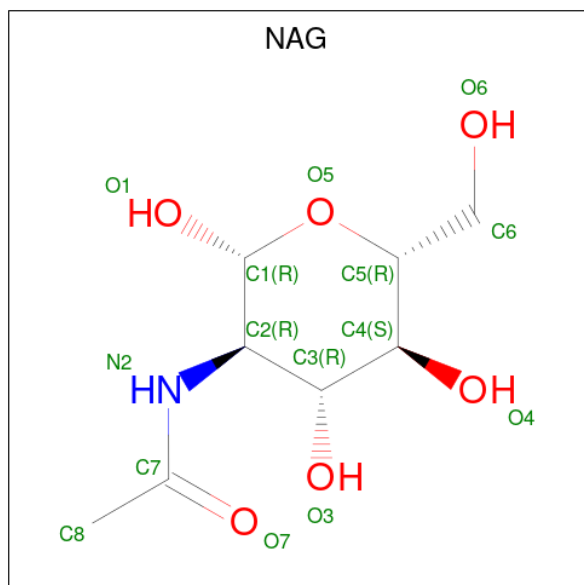
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	5	Total	Na	0	0
			5	5		
8	D	3	Total	Na	0	0
			3	3		

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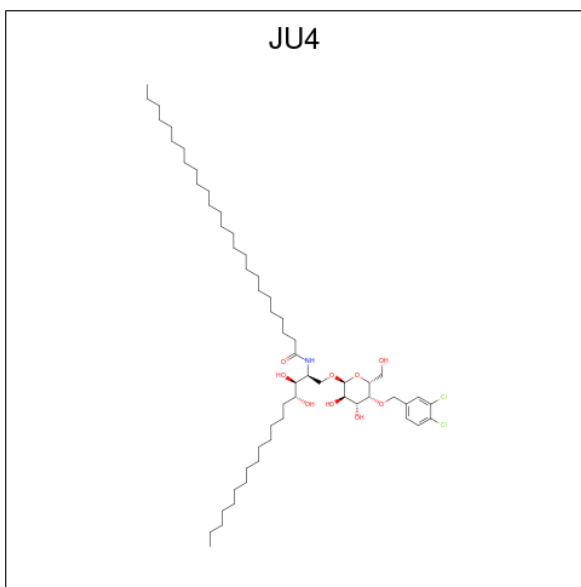
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	Na		0	0
			1	1			

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 10 is N-[(2S,3S,4R)-1-({4-O-[(3,4-dichlorophenyl)methyl]-alpha-D-galactopyranosyl}oxy)-3,4-dihydroxyoctadecan-2-yl]hexacosanamide (three-letter code: JU4) (formula: $C_{57}H_{103}Cl_2NO_9$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	Cl	N	O	0	0
			69	57	2	1	9		

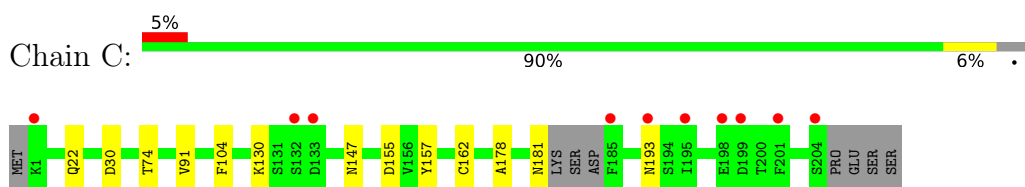
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	C	156	Total	O	0	0
			156	156		
11	D	254	Total	O	0	0
			254	254		
11	A	215	Total	O	0	0
			215	215		
11	B	77	Total	O	0	0
			77	77		

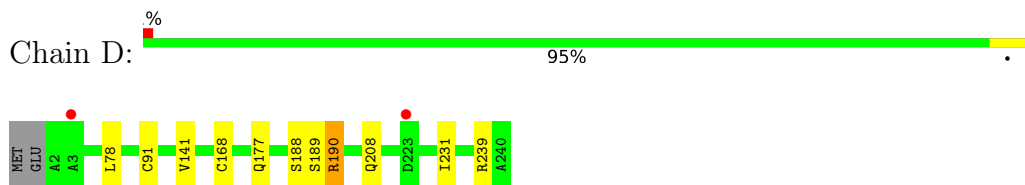
3 Residue-property plots

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.

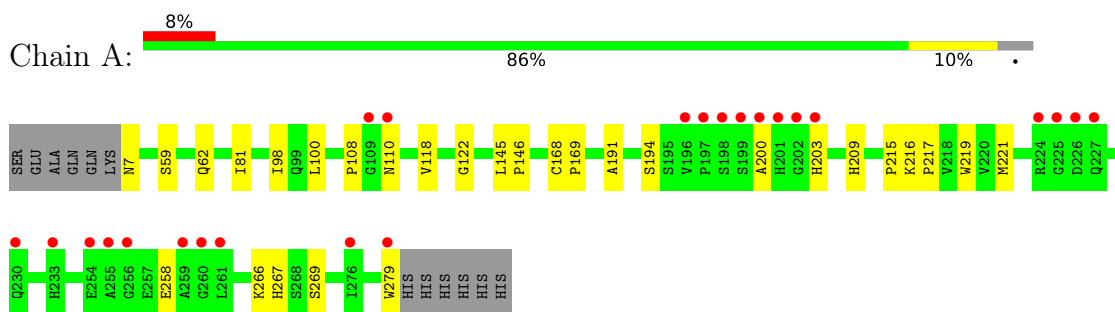
- Molecule 1: T cell receptor alpha variable 11,T cell receptor alpha variable 11,T cell receptor alpha joining 18,Human nkt tcr alpha chain, CHIMERIC PROTEIN



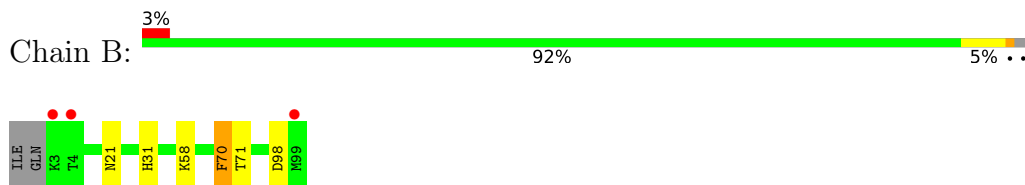
- Molecule 2: Beta-chain,Tcell receptor chain,T cell receptor beta constant 2, CHIMERIC PROTEIN



- Molecule 3: Antigen-presenting glycoprotein CD1d1



- Molecule 4: Beta-2-microglobulin




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

Chain E:  100%

MAG1
MAG2

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  33% 67%

MAG1
MAG2
FUC3

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	79.00Å 191.28Å 151.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.87 – 1.93 47.82 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.87-1.93) 99.7 (47.82-1.93)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.184 , 0.216 0.193 , 0.222	Depositor DCC
R_{free} test set	4229 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7333	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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: GOL, FUC, JU4, NA, NAG

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	C	0.30	0/1594	0.55	0/2169
2	D	0.31	0/1921	0.53	0/2621
3	A	0.31	0/2271	0.49	0/3090
4	B	0.30	0/805	0.53	0/1102
All	All	0.31	0/6591	0.52	0/8982

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	C	1563	0	1488	7	0
2	D	1870	0	1762	10	0
3	A	2201	0	2102	20	0
4	B	779	0	719	4	0
5	E	28	0	25	0	0
6	F	38	0	34	0	0
7	A	6	0	8	0	0
7	B	18	0	24	4	0
7	C	30	0	40	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	6	0	8	0	0
8	A	1	0	0	0	0
8	C	5	0	0	0	0
8	D	3	0	0	0	0
9	A	14	0	13	0	0
10	A	69	0	0	0	0
11	A	215	0	0	0	0
11	B	77	0	0	0	0
11	C	156	0	0	1	0
11	D	254	0	0	1	0
All	All	7333	0	6223	37	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 3.

All (37) 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:C:162:CYS:SG	2:D:190:ARG:NH1	2.63	0.71
2:D:91:CYS:HB3	11:D:482:HOH:O	1.97	0.63
3:A:59:SER:H	3:A:62:GLN:HE21	1.48	0.61
3:A:215:PRO:O	3:A:267:HIS:HE1	1.86	0.58
3:A:191:ALA:HA	3:A:209:HIS:O	2.08	0.53
3:A:258:GLU:HB3	3:A:279:TRP:CD1	2.44	0.53
3:A:168:CYS:HB3	3:A:169:PRO:HD3	1.92	0.52
3:A:267:HIS:HD2	3:A:269:SER:OG	1.94	0.50
3:A:145:LEU:HB3	3:A:146:PRO:HD3	1.94	0.49
3:A:219:TRP:CH2	3:A:221:MET:HB2	2.48	0.49
1:C:22[A]:GLN:OE1	1:C:74:THR:HG22	2.13	0.49
3:A:59:SER:H	3:A:62:GLN:NE2	2.11	0.48
2:D:78:LEU:HD12	2:D:78:LEU:N	2.29	0.48
3:A:122:GLY:CA	7:B:103:GOL:H31	2.44	0.48
3:A:168:CYS:HB3	3:A:169:PRO:CD	2.44	0.47
2:D:188:SER:OG	2:D:190:ARG:NH2	2.46	0.47
3:A:219:TRP:HB3	3:A:266:LYS:HB2	1.97	0.47
3:A:122:GLY:HA2	7:B:103:GOL:H31	1.97	0.46
2:D:177:GLN:HE21	2:D:177:GLN:HA	1.80	0.46
3:A:7:ASN:HD21	3:A:108:PRO:HD3	1.82	0.45
4:B:31:HIS:HB2	7:B:103:GOL:H2	1.99	0.45
3:A:81:ILE:HD12	3:A:98:ILE:CD1	2.48	0.44
2:D:189:SER:C	2:D:190:ARG:HD3	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:162:CYS:CB	2:D:190:ARG:HH11	2.33	0.42
2:D:208:GLN:HG3	2:D:231:ILE:HG23	2.01	0.42
1:C:30:ASP:HB2	11:C:815:HOH:O	2.19	0.42
3:A:100:LEU:HG	3:A:118:VAL:HG22	2.01	0.42
1:C:162:CYS:CB	2:D:190:ARG:NH1	2.83	0.41
1:C:157:TYR:O	1:C:178:ALA:HA	2.20	0.41
3:A:194:SER:HB2	4:B:98:ASP:HA	2.02	0.41
2:D:141:VAL:HG22	2:D:190:ARG:HG3	2.01	0.41
4:B:58:LYS:HA	7:B:101:GOL:H2	2.02	0.41
1:C:91[B]:VAL:HG12	1:C:104:PHE:CD2	2.57	0.41
4:B:21:ASN:HB3	4:B:70:PHE:CE1	2.56	0.41
3:A:216:LYS:N	3:A:217:PRO:CD	2.84	0.40
3:A:219:TRP:CZ2	3:A:221:MET:HG3	2.56	0.40
3:A:200:ALA:HB3	3:A:203:HIS:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	C	201/209 (96%)	194 (96%)	7 (4%)	0	100	100
2	D	238/241 (99%)	235 (99%)	3 (1%)	0	100	100
3	A	275/285 (96%)	270 (98%)	5 (2%)	0	100	100
4	B	96/99 (97%)	96 (100%)	0	0	100	100
All	All	810/834 (97%)	795 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	C	177/188 (94%)	172 (97%)	5 (3%)	43	29
2	D	201/208 (97%)	198 (98%)	3 (2%)	65	56
3	A	239/249 (96%)	238 (100%)	1 (0%)	91	91
4	B	85/93 (91%)	82 (96%)	3 (4%)	36	21
All	All	702/738 (95%)	690 (98%)	12 (2%)	62	49

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	130	LYS
1	C	147	ASN
1	C	155	ASP
1	C	181	ASN
1	C	193	ASN
2	D	168	CYS
2	D	190	ARG
2	D	239	ARG
3	A	110	ASN
4	B	70	PHE
4	B	71[A]	THR
4	B	71[B]	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	181	ASN
2	D	24	ASN
2	D	177	GLN
2	D	217	ASN
2	D	230	GLN
3	A	7	ASN
3	A	62	GLN

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Mol	Chain	Res	Type
3	A	110	ASN
3	A	267	HIS

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 ⓘ

5 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	E	1	5,3	14,14,15	0.36	0	17,19,21	0.63	0
5	NAG	E	2	5	14,14,15	0.29	0	17,19,21	0.65	0
6	NAG	F	1	3,6	14,14,15	0.24	0	17,19,21	0.97	1 (5%)
6	NAG	F	2	6	14,14,15	0.26	0	17,19,21	0.82	1 (5%)
6	FUC	F	3	6	10,10,11	0.47	0	14,14,16	0.62	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	E	1	5,3	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	0/6/23/26	0/1/1/1
6	NAG	F	1	3,6	-	0/6/23/26	0/1/1/1
6	NAG	F	2	6	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	FUC	F	3	6	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	1	NAG	O5-C5-C6	3.04	111.96	107.20
6	F	2	NAG	C1-O5-C5	2.36	115.38	112.19

There are no chirality outliers.

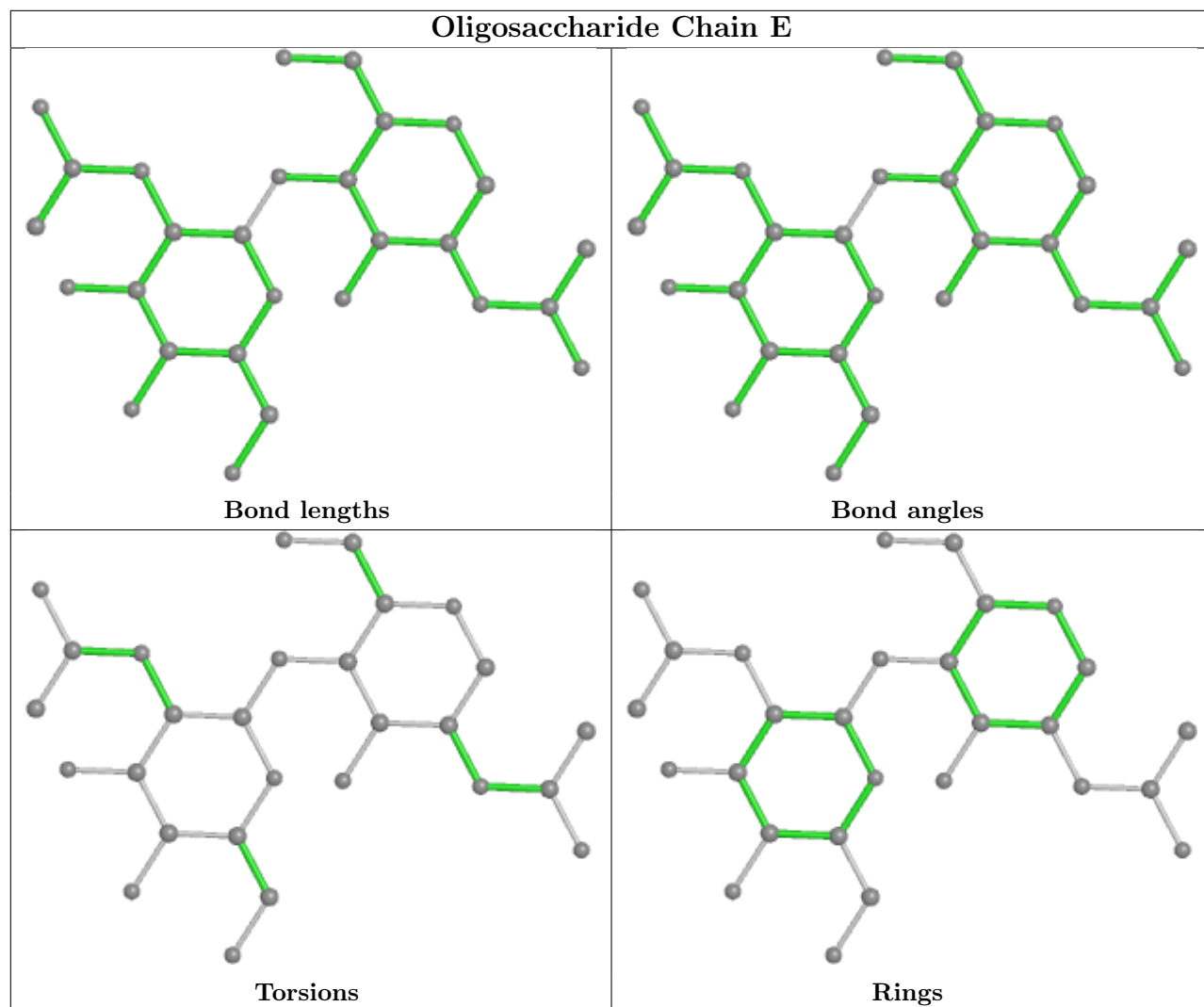
All (1) torsion outliers are listed below:

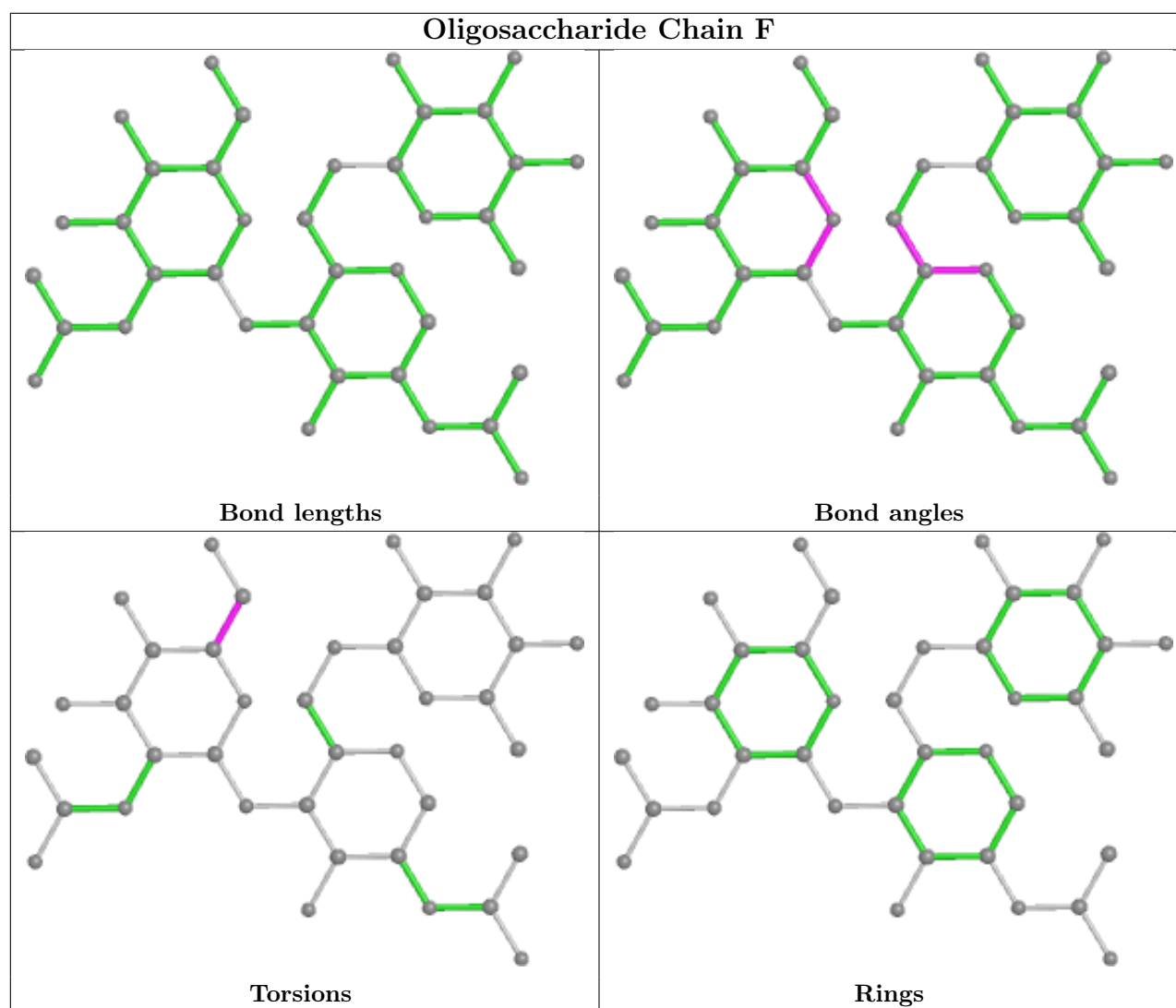
Mol	Chain	Res	Type	Atoms
6	F	2	NAG	O5-C5-C6-O6

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 21 ligands modelled in this entry, 9 are monoatomic - leaving 12 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	$\# Z > 2$
7	GOL	C	601	-	5,5,5	0.31	0	5,5,5	0.19	0
10	JU4	A	308	-	70,70,70	0.77	1 (1%)	79,83,83	0.84	0
7	GOL	C	603	-	5,5,5	0.43	0	5,5,5	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GOL	A	301	-	5,5,5	0.34	0	5,5,5	0.18	0
7	GOL	C	604	-	5,5,5	0.33	0	5,5,5	0.15	0
7	GOL	C	609	8	5,5,5	0.31	0	5,5,5	0.18	0
7	GOL	B	103	-	5,5,5	0.33	0	5,5,5	0.36	0
7	GOL	C	602	-	5,5,5	0.38	0	5,5,5	0.65	0
7	GOL	B	102	-	5,5,5	0.29	0	5,5,5	0.14	0
7	GOL	B	101	-	5,5,5	0.41	0	5,5,5	0.42	0
9	NAG	A	304	3	14,14,15	0.41	0	17,19,21	0.92	0
7	GOL	D	301	-	5,5,5	0.38	0	5,5,5	0.27	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
7	GOL	C	601	-	-	2/4/4/4	-
10	JU4	A	308	-	-	11/63/83/83	0/2/2/2
7	GOL	C	603	-	-	3/4/4/4	-
7	GOL	A	301	-	-	1/4/4/4	-
7	GOL	C	604	-	-	2/4/4/4	-
7	GOL	C	609	8	-	0/4/4/4	-
7	GOL	B	103	-	-	4/4/4/4	-
7	GOL	C	602	-	-	1/4/4/4	-
7	GOL	B	102	-	-	3/4/4/4	-
7	GOL	B	101	-	-	2/4/4/4	-
9	NAG	A	304	3	-	0/6/23/26	0/1/1/1
7	GOL	D	301	-	-	3/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	308	JU4	CAT-CAU	-4.36	1.40	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	601	GOL	C1-C2-C3-O3
7	C	603	GOL	C1-C2-C3-O3
7	C	604	GOL	O1-C1-C2-C3
7	B	101	GOL	O1-C1-C2-C3
7	B	102	GOL	C1-C2-C3-O3
7	B	103	GOL	O1-C1-C2-C3
7	B	103	GOL	C1-C2-C3-O3
7	C	603	GOL	O2-C2-C3-O3
10	A	308	JU4	CCG-CCH-CCI-CCJ
10	A	308	JU4	CCK-CCL-CCM-CCN
7	D	301	GOL	O1-C1-C2-C3
10	A	308	JU4	CBZ-CCA-CCB-CCC
10	A	308	JU4	CCD-CCE-CCF-CCG
10	A	308	JU4	CBP-CBQ-CBR-CBS
7	B	103	GOL	O2-C2-C3-O3
10	A	308	JU4	O6-C2-C3-O2
10	A	308	JU4	CCN-CCO-CCP-CCQ
7	C	601	GOL	O2-C2-C3-O3
7	C	604	GOL	O1-C1-C2-O2
7	B	101	GOL	O1-C1-C2-O2
7	B	102	GOL	O2-C2-C3-O3
10	A	308	JU4	CCL-CCM-CCN-CCO
7	C	603	GOL	O1-C1-C2-C3
7	C	602	GOL	O2-C2-C3-O3
7	D	301	GOL	C1-C2-C3-O3
7	B	103	GOL	O1-C1-C2-O2
10	A	308	JU4	CBK-CBL-CBM-CBN
7	B	102	GOL	O1-C1-C2-C3
10	A	308	JU4	CBX-CBY-CBZ-CCA
7	D	301	GOL	O2-C2-C3-O3
10	A	308	JU4	CCC-CCD-CCE-CCF
7	A	301	GOL	C1-C2-C3-O3

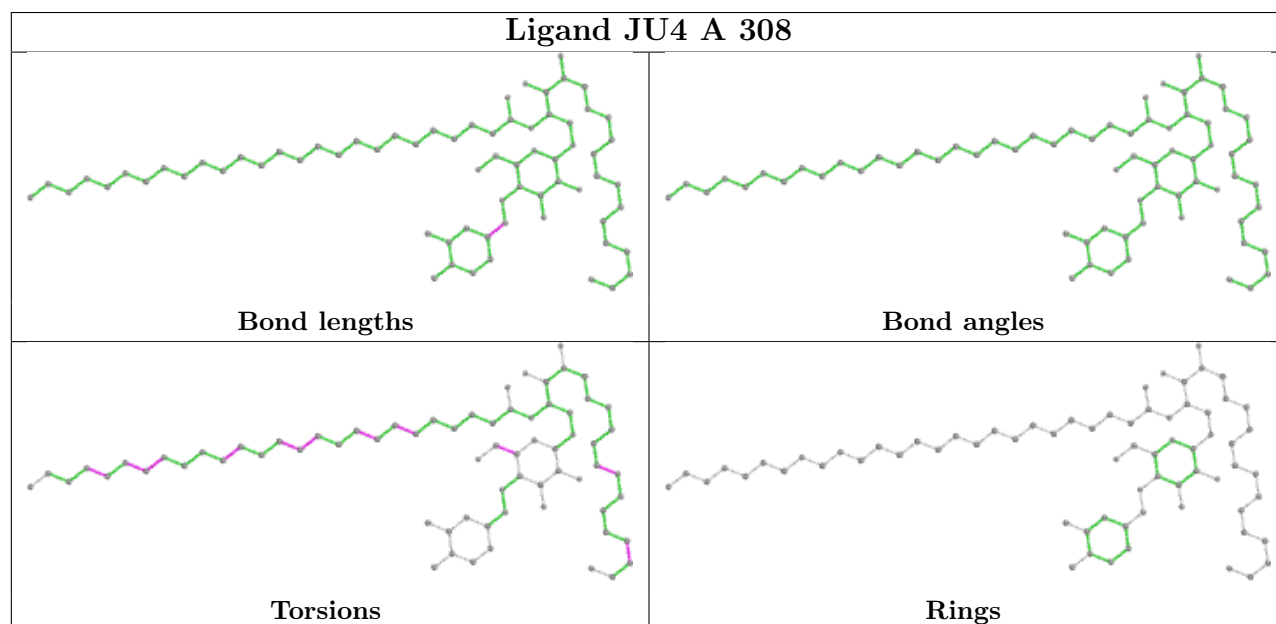
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	103	GOL	3	0
7	B	101	GOL	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 [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	C	201/209 (96%)	0.50	10 (4%) 28 36	17, 28, 61, 72	0
2	D	239/241 (99%)	0.18	2 (0%) 86 89	16, 26, 41, 57	0
3	A	273/285 (95%)	0.49	24 (8%) 10 15	17, 27, 67, 89	0
4	B	97/99 (97%)	0.22	3 (3%) 49 56	21, 33, 53, 69	0
All	All	810/834 (97%)	0.37	39 (4%) 30 38	16, 28, 58, 89	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	197	PRO	4.5
3	A	200	ALA	4.5
3	A	255	ALA	4.4
3	A	199	SER	4.4
4	B	99	MET	4.4
1	C	132	SER	4.2
3	A	110	ASN	4.1
1	C	133	ASP	3.8
3	A	276	ILE	3.6
3	A	109	GLY	3.4
3	A	201	HIS	3.3
3	A	202	GLY	3.3
3	A	279	TRP	3.3
3	A	259	ALA	3.2
2	D	223	ASP	3.0
1	C	204	SER	3.0
3	A	203	HIS	3.0
3	A	226	ASP	2.9
3	A	256	GLY	2.9
3	A	198	SER	2.9
1	C	185	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
3	A	260	GLY	2.8
1	C	1	LYS	2.7
3	A	227	GLN	2.6
1	C	199	ASP	2.6
3	A	261	LEU	2.5
4	B	4	THR	2.5
1	C	198	GLU	2.5
3	A	225	GLY	2.4
1	C	193	ASN	2.4
2	D	3	ALA	2.4
3	A	196	VAL	2.3
1	C	201	PHE	2.3
4	B	3	LYS	2.3
1	C	195	ILE	2.2
3	A	233	HIS	2.2
3	A	254	GLU	2.1
3	A	224	ARG	2.1
3	A	230	GLN	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](#)

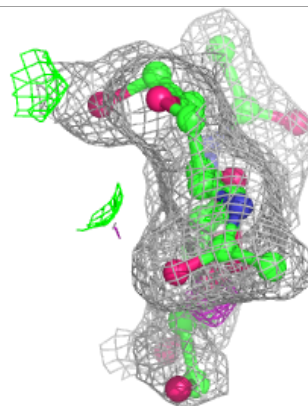
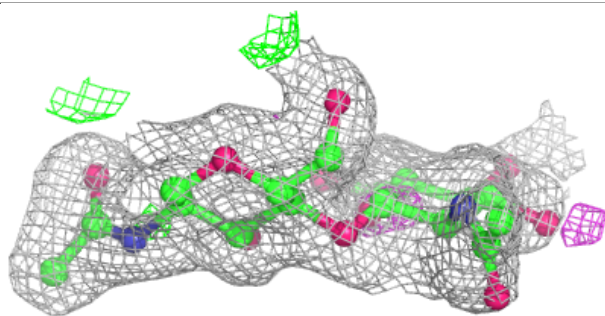
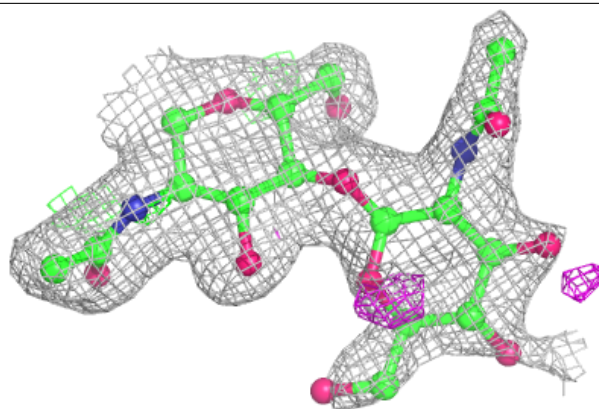
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

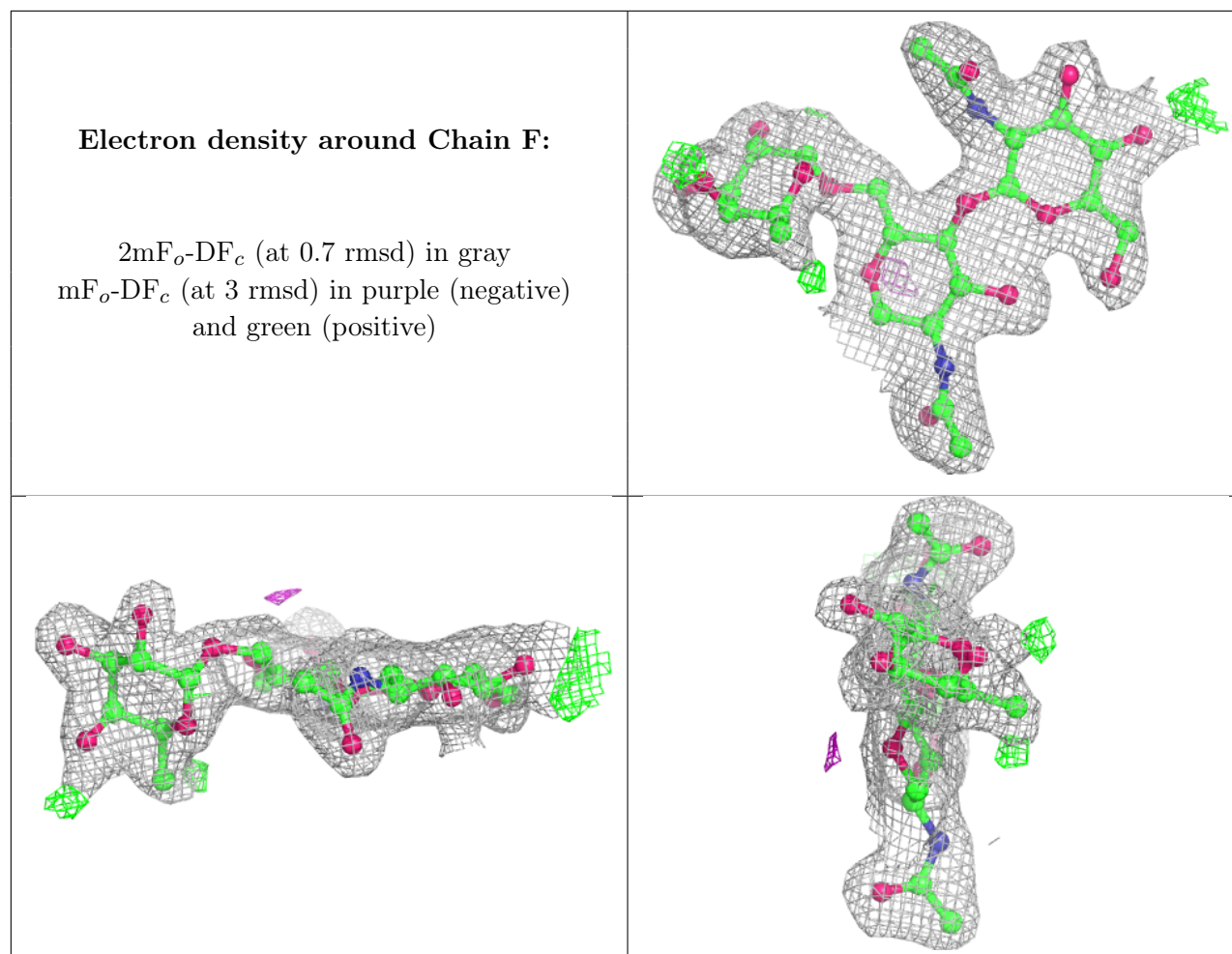
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	E	2	14/15	0.75	0.28	51,58,63,63	0
6	FUC	F	3	10/11	0.84	0.19	41,43,44,44	0
6	NAG	F	2	14/15	0.92	0.15	37,40,43,44	0
5	NAG	E	1	14/15	0.94	0.10	29,32,36,43	0
6	NAG	F	1	14/15	0.95	0.11	29,31,34,38	0

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 E:

$2mF_o-DF_c$ (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	NA	D	304	1/1	0.53	0.16	63,63,63,63	0
7	GOL	C	603	6/6	0.62	0.29	58,59,60,61	0
7	GOL	C	604	6/6	0.65	0.21	65,67,68,69	0
7	GOL	B	101	6/6	0.67	0.39	47,53,54,54	0
7	GOL	A	301	6/6	0.74	0.31	52,57,59,59	0
7	GOL	C	609	6/6	0.78	0.22	63,65,66,66	0
8	NA	D	303	1/1	0.79	0.16	62,62,62,62	0
7	GOL	D	301	6/6	0.80	0.20	37,44,47,52	0
7	GOL	B	103	6/6	0.81	0.35	49,50,51,51	0
7	GOL	B	102	6/6	0.82	0.27	64,65,66,67	0

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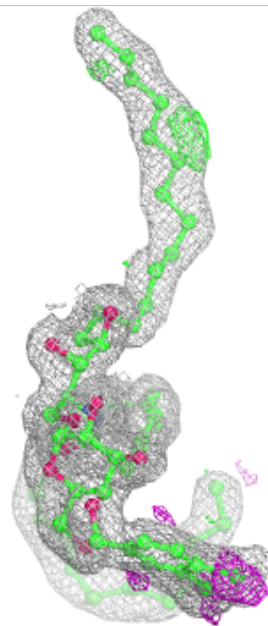
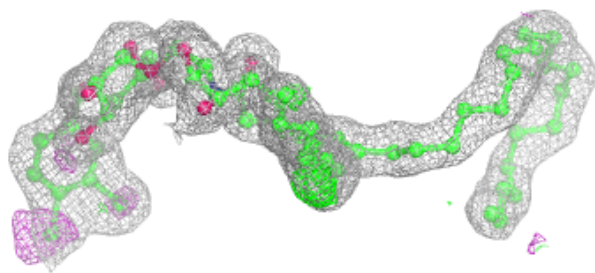
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	NAG	A	304	14/15	0.82	0.20	48,52,58,58	0
8	NA	C	607	1/1	0.85	0.21	47,47,47,47	0
7	GOL	C	602	6/6	0.85	0.21	33,37,38,39	0
7	GOL	C	601	6/6	0.90	0.18	38,45,47,50	0
8	NA	C	605	1/1	0.90	0.14	40,40,40,40	0
10	JU4	A	308	69/69	0.92	0.14	18,28,37,51	0
8	NA	C	606	1/1	0.94	0.31	47,47,47,47	0
8	NA	A	309	1/1	0.95	0.14	28,28,28,28	0
8	NA	C	608	1/1	0.95	0.11	41,41,41,41	0
8	NA	D	302	1/1	0.95	0.13	32,32,32,32	0
8	NA	C	610	1/1	0.98	0.08	27,27,27,27	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 JU4 A 308:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.