Full wwPDB X-ray Structure Validation Report (i)

Aug 23, 2023 – 10:00 AM EDT

PDB ID	:	3EHU
Title	:	Crystal structure of the extracellular domain of human corticotropin releasing factor receptor type 1 (CRFR1) in complex with CRF
Authors	:	Pioszak, A.A.; Xu, H.E.
Deposited on	:	2008-09-14
Resolution	:	1.96 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

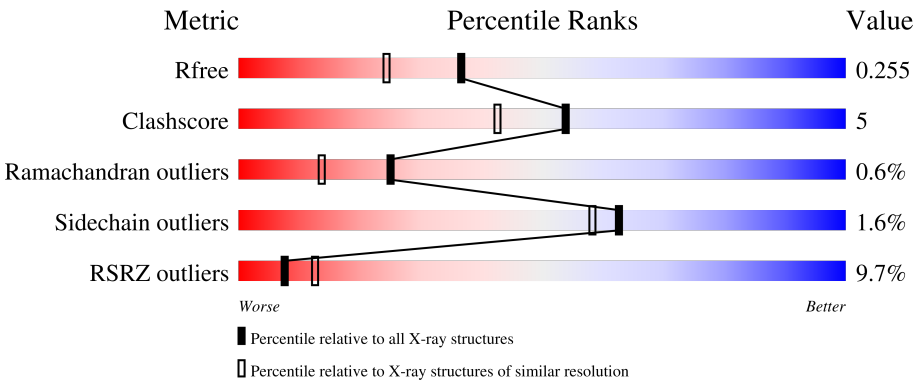
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	476	8%; 84%; 8% • 7%
1	B	476	8%; 83%; 8% • 7%
2	C	21	38%; 62%; 19%; 19%
2	D	21	38%; 81%; 19%
3	E	2	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	2	50% 50%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7584 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 FUSION PROTEIN OF CRFR1 EXTRACELLULAR DOMAIN AND MBP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	441	3399	2173	561	654	11	0	0	0
1	B	441	3399	2173	561	654	11	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-350	MET	-	initiating methionine	UNP P0AEX9
A	-25	GLU	ALA	engineered mutation	UNP P0AEX9
A	18	ASN	-	linker	UNP P0AEX9
A	19	ALA	-	linker	UNP P0AEX9
A	20	ALA	-	linker	UNP P0AEX9
A	21	ALA	-	linker	UNP P0AEX9
A	22	GLU	-	linker	UNP P0AEX9
A	23	PHE	-	linker	UNP P0AEX9
A	120	HIS	-	expression tag	UNP P34998
A	121	HIS	-	expression tag	UNP P34998
A	122	HIS	-	expression tag	UNP P34998
A	123	HIS	-	expression tag	UNP P34998
A	124	HIS	-	expression tag	UNP P34998
A	125	HIS	-	expression tag	UNP P34998
B	-350	MET	-	initiating methionine	UNP P0AEX9
B	-25	GLU	ALA	engineered mutation	UNP P0AEX9
B	18	ASN	-	linker	UNP P0AEX9
B	19	ALA	-	linker	UNP P0AEX9
B	20	ALA	-	linker	UNP P0AEX9
B	21	ALA	-	linker	UNP P0AEX9
B	22	GLU	-	linker	UNP P0AEX9
B	23	PHE	-	linker	UNP P0AEX9
B	120	HIS	-	expression tag	UNP P34998
B	121	HIS	-	expression tag	UNP P34998

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	122	HIS	-	expression tag	UNP P34998
B	123	HIS	-	expression tag	UNP P34998
B	124	HIS	-	expression tag	UNP P34998
B	125	HIS	-	expression tag	UNP P34998

- Molecule 2 is a protein called Corticoliberin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	17	123	76	25	21	1	0	0	1
2	D	17	123	76	25	21	1	0	0	1

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	42	NH2	-	amidation	UNP P06850
D	42	NH2	-	amidation	UNP P06850

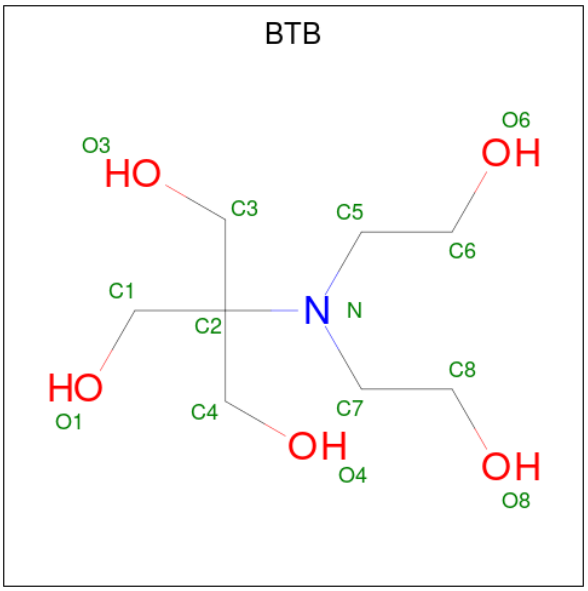
- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	E	2	23	12	11	0	0	0
3	F	2	23	12	11	0	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

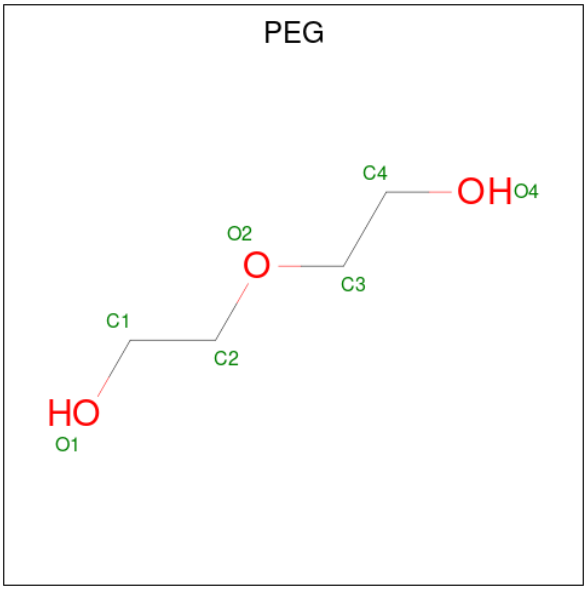
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	A	1	1	1	0	0
4	B	1	1	1	0	0

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
6	A	1	7	4	3		0	0
6	B	1	7	4	3		0	0

- Molecule 7 is water.

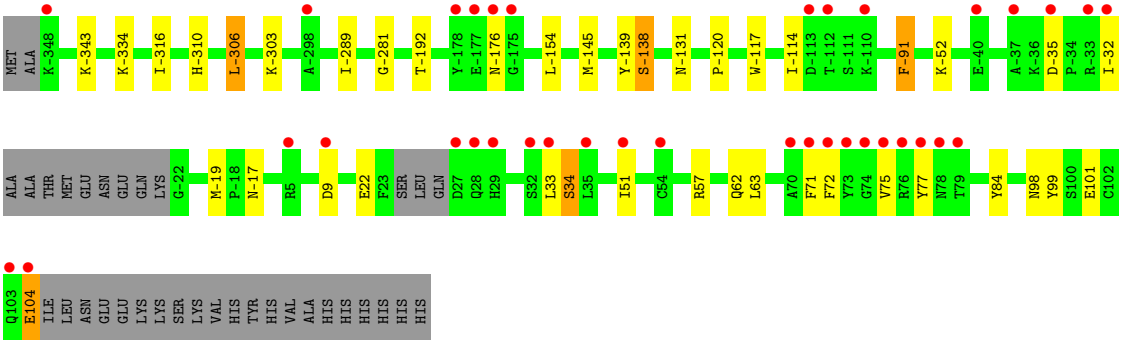
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	216	Total O 216 216	0	0
7	B	225	Total O 225 225	0	0
7	C	5	Total O 5 5	0	0
7	D	4	Total O 4 4	0	0

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.

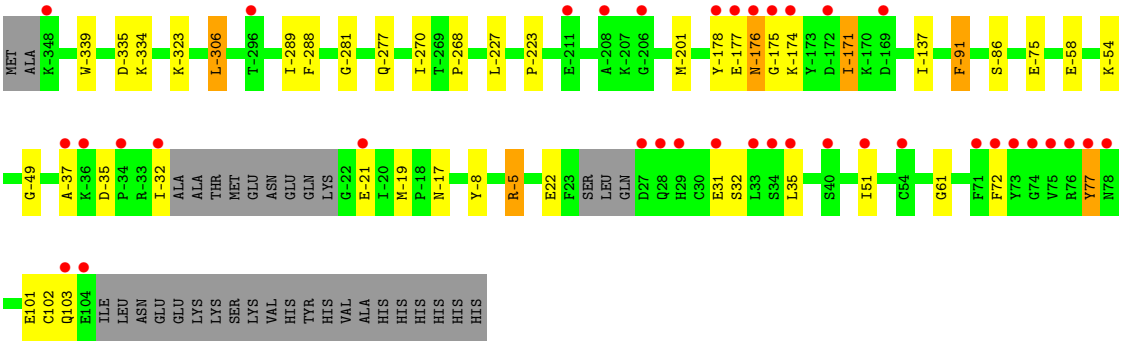
• Molecule 1: FUSION PROTEIN OF CRFR1 EXTRACELLULAR DOMAIN AND MBP

Chain A:



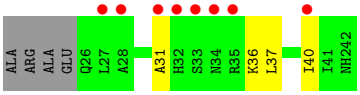
• Molecule 1: FUSION PROTEIN OF CRFR1 EXTRACELLULAR DOMAIN AND MBP

Chain B:



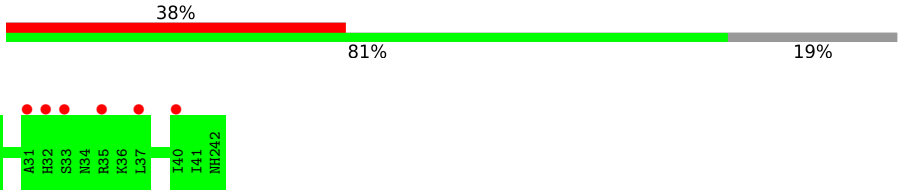
• Molecule 2: Corticoliberin

Chain C:



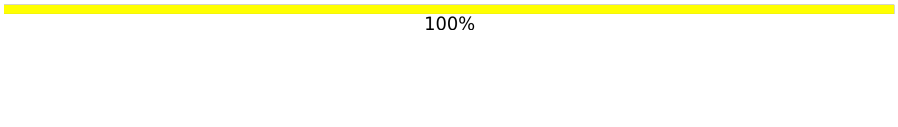
• Molecule 2: Corticoliberin

Chain D:



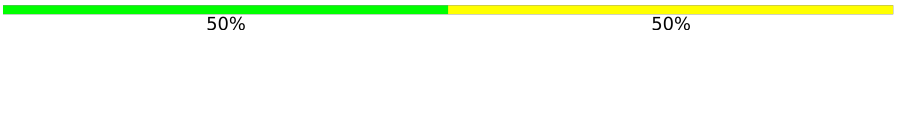
- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain E:



- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	49.20Å 63.48Å 85.88Å 99.75° 106.28° 101.67°	Depositor
Resolution (Å)	39.50 – 1.96 39.49 – 1.95	Depositor EDS
% Data completeness (in resolution range)	94.9 (39.50-1.96) 94.4 (39.49-1.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.256 0.209 , 0.255	Depositor DCC
R_{free} test set	3270 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	22.6	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 50.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7584	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.30 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8890e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, BTB, PEG, GLC, NH2

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	0.72	4/3480 (0.1%)	0.61	2/4729 (0.0%)
1	B	0.55	2/3480 (0.1%)	0.59	0/4729
2	C	0.33	0/122	0.44	0/162
2	D	0.42	0/122	0.53	0/162
All	All	0.63	6/7204 (0.1%)	0.60	2/9782 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	104	GLU	C-O	20.55	1.62	1.23
1	A	77	TYR	CE2-CZ	11.72	1.53	1.38
1	A	77	TYR	CG-CD1	10.97	1.53	1.39
1	A	77	TYR	CG-CD2	8.01	1.49	1.39
1	B	103	GLN	C-O	5.42	1.33	1.23
1	B	77	TYR	CE2-CZ	5.28	1.45	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	104	GLU	CA-C-O	-7.68	103.98	120.10
1	A	77	TYR	CD1-CE1-CZ	-6.23	114.19	119.80

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	3399	0	3314	35	0
1	B	3399	0	3314	35	0
2	C	123	0	124	3	0
2	D	123	0	124	0	0
3	E	23	0	21	0	0
3	F	23	0	21	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	14	0	15	5	0
5	B	14	0	15	3	0
6	A	7	0	10	0	0
6	B	7	0	10	1	0
7	A	216	0	0	11	0
7	B	225	0	0	13	0
7	C	5	0	0	0	0
7	D	4	0	0	0	0
All	All	7584	0	6968	74	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (74) 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:-52:LYS:HE2	7:A:555:HOH:O	1.61	1.00
1:B:101:GLU:HB3	7:B:711:HOH:O	1.71	0.90
1:B:-8:TYR:HD2	7:B:633:HOH:O	1.56	0.87
1:B:-339:TRP:HE3	7:B:718:HOH:O	1.63	0.81
1:A:101:GLU:HB3	7:A:600:HOH:O	1.82	0.80
1:B:-306:LEU:HB2	7:B:718:HOH:O	1.80	0.79
1:A:-334:LYS:NZ	7:A:718:HOH:O	2.16	0.78
1:A:-310:HIS:HE1	7:A:707:HOH:O	1.67	0.76
1:B:-339:TRP:CE3	7:B:718:HOH:O	2.40	0.70
1:A:-35:ASP:HB3	1:A:-32:ILE:HB	1.75	0.68
1:B:-201:MET:HE1	1:B:-137:ILE:HG22	1.76	0.67
1:A:101:GLU:OE2	1:B:-5:ARG:NH2	2.28	0.66
1:A:34:SER:HB3	7:A:549:HOH:O	1.97	0.65
1:B:-35:ASP:HB3	1:B:-32:ILE:HD12	1.78	0.64
1:B:-201:MET:CE	1:B:-137:ILE:HG22	2.28	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:-171:ILE:HD12	1:B:22:GLU:OE2	1.97	0.64
1:A:-334:LYS:HE3	7:A:718:HOH:O	1.97	0.63
1:A:-334:LYS:CE	7:A:718:HOH:O	2.46	0.63
1:B:101:GLU:HB2	7:B:580:HOH:O	1.98	0.63
1:A:-154:LEU:HD12	1:A:-145:MET:HE1	1.82	0.62
1:A:51:ILE:HD12	1:A:99:TYR:CE1	2.40	0.57
5:A:501:BTB:H11	7:A:701:HOH:O	2.03	0.57
1:B:-335:ASP:OD1	1:B:-334:LYS:NZ	2.37	0.57
1:A:-192:THR:HG23	7:A:703:HOH:O	2.04	0.57
1:A:-154:LEU:CD1	1:A:-145:MET:HE1	2.35	0.56
1:A:-131:ASN:OD1	1:A:-114:ILE:HA	2.06	0.55
1:B:-306:LEU:HD13	7:B:718:HOH:O	2.07	0.55
1:B:-49:GLY:O	1:B:-32:ILE:HD13	2.07	0.54
1:A:-32:ILE:HG21	7:A:704:HOH:O	2.06	0.54
1:B:-281:GLY:HA3	1:B:-17:ASN:O	2.08	0.53
1:B:-5:ARG:NH1	7:B:588:HOH:O	2.32	0.52
5:B:501:BTB:H11	7:B:710:HOH:O	2.10	0.52
1:A:104:GLU:OE1	2:C:31:ALA:HB1	2.11	0.51
1:A:71:PHE:HA	1:A:75:VAL:O	2.11	0.51
1:B:-174:LYS:HG3	7:B:619:HOH:O	2.12	0.50
1:B:-270:ILE:HD12	1:B:-268:PRO:HD3	1.95	0.48
5:A:501:BTB:H62	5:A:501:BTB:C1	2.44	0.48
1:A:33:LEU:O	1:A:34:SER:HB2	2.14	0.48
1:A:57:ARG:HH11	1:A:57:ARG:HG3	1.79	0.48
1:B:-323:LYS:HD2	6:B:502:PEG:H41	1.95	0.48
1:A:98:ASN:ND2	1:B:-8:TYR:OH	2.46	0.47
1:B:32:SER:HA	1:B:35:LEU:HG	1.97	0.46
1:B:-75:GLU:HG2	7:B:713:HOH:O	2.14	0.46
1:B:72:PHE:HB3	1:B:77:TYR:CE1	2.50	0.46
1:A:63:LEU:HD11	1:A:84:TYR:HB3	1.98	0.46
1:A:-303:LYS:NZ	7:A:619:HOH:O	2.48	0.45
1:B:72:PHE:HB3	1:B:77:TYR:HE1	1.80	0.45
2:C:36:LYS:HE2	2:C:40:ILE:HD11	1.99	0.45
1:B:-306:LEU:C	1:B:-306:LEU:HD12	2.36	0.45
1:A:-281:GLY:HA3	1:A:-17:ASN:O	2.17	0.44
1:B:-288:PHE:HA	1:B:-86:SER:O	2.17	0.44
1:B:-91:PHE:CG	1:B:-19:MET:HG2	2.53	0.44
1:A:-306:LEU:HD12	1:A:-306:LEU:C	2.37	0.44
1:A:-139:TYR:CG	1:A:-138:SER:N	2.86	0.44
1:A:-91:PHE:CG	1:A:-19:MET:HG2	2.53	0.43
1:A:-139:TYR:CD1	5:A:501:BTB:H41	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:GLN:NE2	1:B:-277:GLN:OE1	2.47	0.43
5:A:501:BTB:H71	5:A:501:BTB:H32	1.57	0.43
1:A:22:GLU:HB2	1:B:61:GLY:HA2	2.01	0.43
1:A:72:PHE:HZ	2:C:37:LEU:HD23	1.83	0.43
5:B:501:BTB:H32	5:B:501:BTB:H71	1.78	0.43
1:B:-227:LEU:HD21	1:B:-223:PRO:HD3	2.01	0.42
1:A:33:LEU:O	1:A:34:SER:CB	2.67	0.42
1:B:-58:GLU:HG3	1:B:-54:LYS:HE3	2.00	0.42
1:A:57:ARG:HG3	1:A:57:ARG:NH1	2.34	0.42
1:B:-21:GLU:HG2	7:B:604:HOH:O	2.20	0.42
1:B:-178:TYR:OH	1:B:-175:GLY:HA2	2.19	0.42
1:A:-343:LYS:HA	1:A:-316:ILE:HG23	2.03	0.41
5:A:501:BTB:H62	5:A:501:BTB:H12	2.02	0.41
5:B:501:BTB:H62	5:B:501:BTB:O1	2.20	0.41
1:A:-117:TRP:HA	1:A:-114:ILE:HD12	2.01	0.41
1:B:-8:TYR:CD2	7:B:633:HOH:O	2.46	0.41
1:B:-177:GLU:O	1:B:-176:ASN:C	2.58	0.41
1:A:-120:PRO:HA	1:A:-117:TRP:CE2	2.56	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	435/476 (91%)	426 (98%)	8 (2%)	1 (0%)	47 38
1	B	435/476 (91%)	420 (97%)	11 (2%)	4 (1%)	17 8
2	C	15/21 (71%)	15 (100%)	0	0	100 100
2	D	15/21 (71%)	15 (100%)	0	0	100 100
All	All	900/994 (90%)	876 (97%)	19 (2%)	5 (1%)	25 14

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	SER
1	B	-176	ASN
1	B	31	GLU
1	B	-37	ALA
1	B	102	CYS

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	352/386 (91%)	346 (98%)	6 (2%)	60	55
1	B	352/386 (91%)	346 (98%)	6 (2%)	60	55
2	C	12/16 (75%)	12 (100%)	0	100	100
2	D	12/16 (75%)	12 (100%)	0	100	100
All	All	728/804 (90%)	716 (98%)	12 (2%)	62	58

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

Mol	Chain	Res	Type
1	A	-306	LEU
1	A	-289	ILE
1	A	-176	ASN
1	A	-138	SER
1	A	-91	PHE
1	A	9	ASP
1	B	-306	LEU
1	B	-289	ILE
1	B	-171	ILE
1	B	-91	PHE
1	B	-5	ARG
1	B	51	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-176	ASN
1	A	62	GLN
1	A	81	ASN
1	A	103	GLN
1	B	-277	GLN
1	B	-115	ASN
1	B	38	ASN

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)

4 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	$\#\|Z\| > 2$
3	GLC	E	1	3	12,12,12	0.61	0	17,17,17	1.51	3 (17%)
3	GLC	E	2	3	11,11,12	0.62	0	15,15,17	1.24	2 (13%)
3	GLC	F	1	3	12,12,12	0.57	0	17,17,17	1.06	0
3	GLC	F	2	3	11,11,12	0.54	0	15,15,17	1.11	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLC	E	1	3	-	0/2/22/22	0/1/1/1
3	GLC	E	2	3	-	0/2/19/22	0/1/1/1
3	GLC	F	1	3	-	0/2/22/22	0/1/1/1
3	GLC	F	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	1	GLC	O5-C1-C2	3.98	117.38	110.28
3	F	2	GLC	C1-O5-C5	3.34	116.72	112.19
3	E	1	GLC	C1-O5-C5	3.29	119.87	113.66
3	E	2	GLC	C1-O5-C5	3.21	116.54	112.19
3	E	1	GLC	O3-C3-C2	-2.19	105.29	110.35
3	E	2	GLC	O4-C4-C3	-2.09	105.53	110.35

There are no chirality outliers.

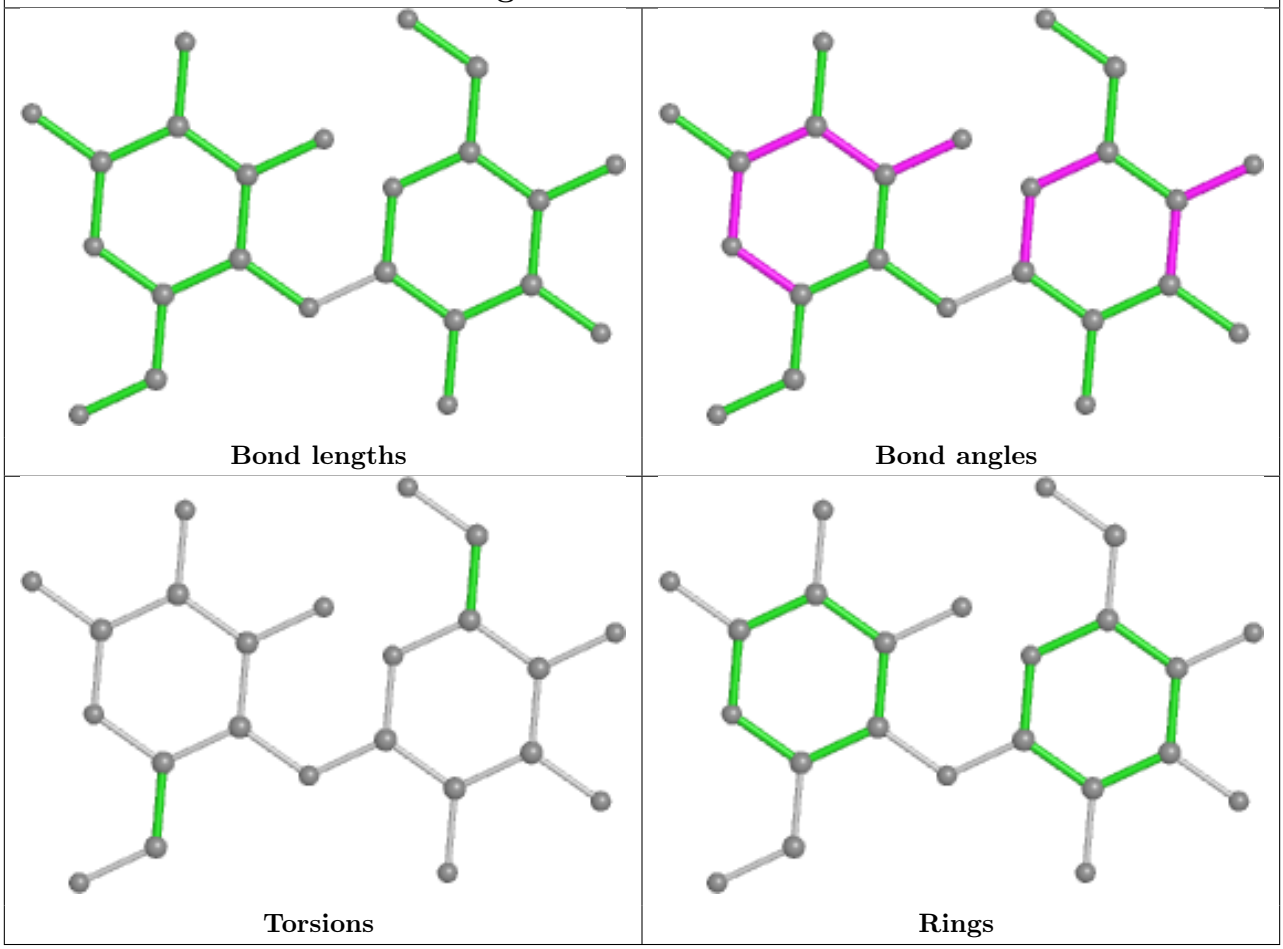
There are no torsion outliers.

There are no ring outliers.

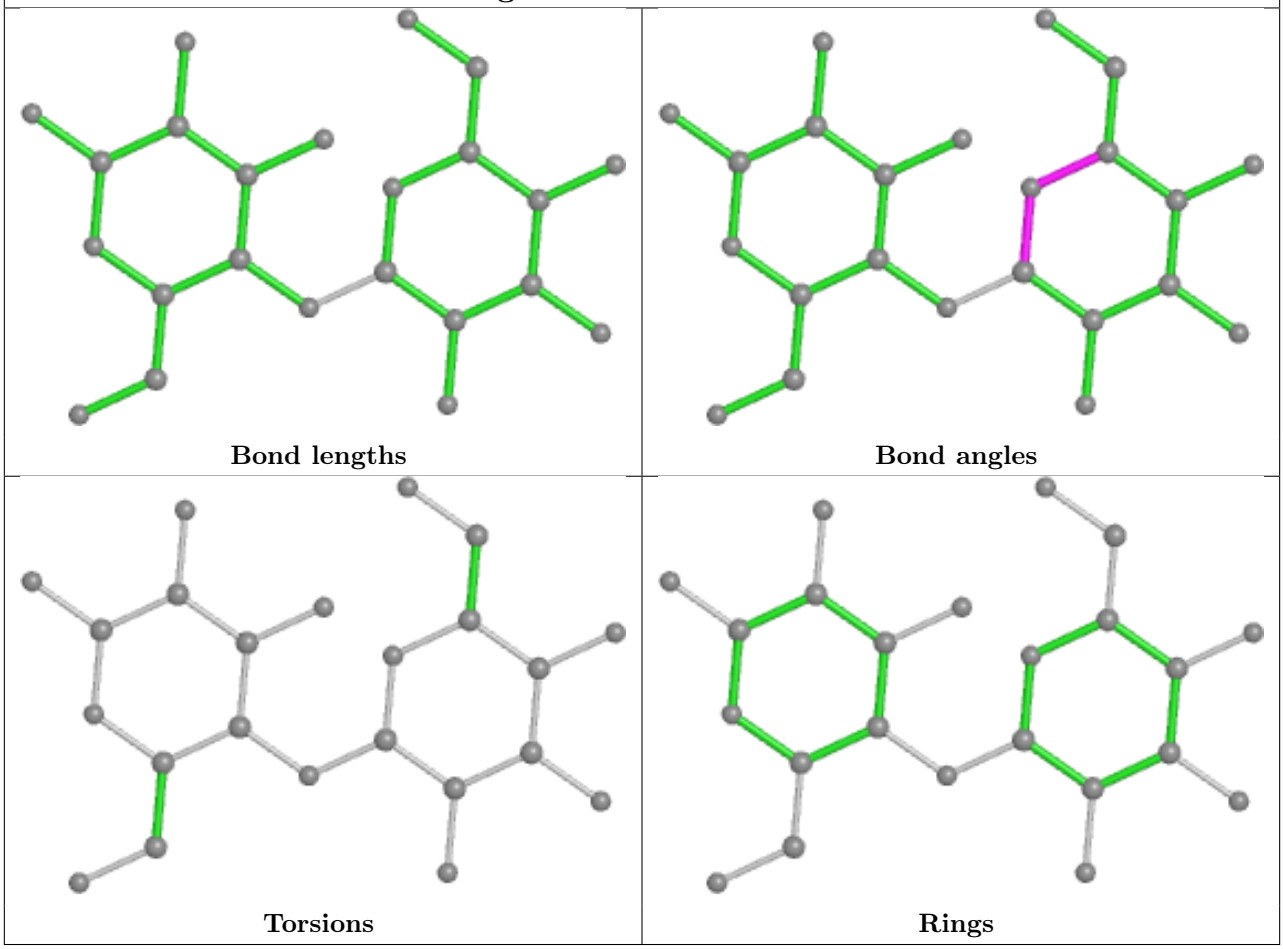
No monomer is involved in short contacts.

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

Oligosaccharide Chain E



Oligosaccharide Chain F



5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
6	PEG	B	502	-	6,6,6	0.46	0	5,5,5	0.19	0
5	BTB	A	501	4	13,13,13	0.58	0	7,16,16	1.11	0
6	PEG	A	502	-	6,6,6	0.40	0	5,5,5	0.33	0
5	BTB	B	501	4	13,13,13	0.35	0	7,16,16	0.83	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
6	PEG	B	502	-	-	3/4/4/4	-
5	BTB	A	501	4	-	2/21/21/21	-
6	PEG	A	502	-	-	2/4/4/4	-
5	BTB	B	501	4	-	4/21/21/21	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	BTB	C3-C2-N-C7
6	A	502	PEG	O2-C3-C4-O4
6	B	502	PEG	O2-C3-C4-O4
5	B	501	BTB	C8-C7-N-C5
5	A	501	BTB	C6-C5-N-C2
5	B	501	BTB	C6-C5-N-C2
5	B	501	BTB	C3-C2-N-C7
6	B	502	PEG	C4-C3-O2-C2
6	A	502	PEG	C4-C3-O2-C2
6	B	502	PEG	O1-C1-C2-O2
5	B	501	BTB	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	502	PEG	1	0
5	A	501	BTB	5	0
5	B	501	BTB	3	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	441/476 (92%)	0.68	36 (8%)	11	18	20, 28, 40, 58	0
1	B	441/476 (92%)	0.62	37 (8%)	11	17	21, 28, 40, 61	0
2	C	16/21 (76%)	2.36	8 (50%)	0	0	27, 38, 40, 41	0
2	D	16/21 (76%)	2.39	8 (50%)	0	0	26, 32, 36, 36	0
All	All	914/994 (91%)	0.71	89 (9%)	7	12	20, 28, 40, 61	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	75	VAL	8.0
1	B	-175	GLY	7.2
1	A	73	TYR	7.1
2	C	31	ALA	6.6
1	B	73	TYR	6.2
1	A	78	ASN	6.1
1	A	76	ARG	6.1
1	A	-37	ALA	5.9
2	D	31	ALA	5.7
1	A	-178	TYR	5.7
2	C	32	HIS	5.6
1	B	-176	ASN	5.5
1	B	33	LEU	5.5
1	B	-178	TYR	5.4
1	A	72	PHE	5.3
1	A	33	LEU	5.1
1	B	75	VAL	4.9
2	D	27	LEU	4.8
2	C	27	LEU	4.8
1	A	71	PHE	4.6
1	B	103	GLN	4.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	29	HIS	4.5
1	A	74	GLY	4.5
1	A	35	LEU	4.4
1	B	-34	PRO	4.3
1	B	-32	ILE	4.2
1	A	-175	GLY	4.2
1	B	104	GLU	4.1
1	B	28	GLN	4.1
1	A	77	TYR	3.9
2	C	33	SER	3.9
1	B	31	GLU	3.9
1	A	70	ALA	3.8
1	A	32	SER	3.8
2	D	32	HIS	3.8
1	B	-37	ALA	3.6
1	A	103	GLN	3.5
1	A	-176	ASN	3.4
1	B	78	ASN	3.4
1	A	-35	ASP	3.4
1	B	35	LEU	3.4
2	C	35	ARG	3.4
1	B	-177	GLU	3.4
1	A	-177	GLU	3.3
1	B	72	PHE	3.3
1	B	74	GLY	3.3
1	B	-296	THR	3.2
1	B	34	SER	3.2
2	D	35	ARG	3.1
1	A	27	ASP	3.1
2	D	28	ALA	2.9
1	B	27	ASP	2.9
2	D	33	SER	2.9
1	A	51	ILE	2.9
2	D	40	ILE	2.8
1	B	77	TYR	2.8
1	A	29	HIS	2.7
1	A	-32	ILE	2.7
1	B	76	ARG	2.7
2	C	28	ALA	2.7
1	B	-206	GLY	2.6
1	B	40	SER	2.6
1	A	-40	GLU	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	-110	LYS	2.5
1	B	-174	LYS	2.5
1	A	104	GLU	2.5
1	B	-211	GLU	2.5
1	A	28	GLN	2.4
1	B	-172	ASP	2.4
1	A	79	THR	2.4
1	A	-298	ALA	2.4
2	D	37	LEU	2.3
1	B	-21	GLU	2.3
1	A	-33	ARG	2.3
1	A	-112	THR	2.3
2	C	40	ILE	2.3
1	A	-113	ASP	2.3
1	A	5	ARG	2.3
1	B	71	PHE	2.2
1	B	51	ILE	2.2
1	A	-348	LYS	2.2
1	B	54	CYS	2.2
1	A	54	CYS	2.1
1	B	-348	LYS	2.1
1	B	-169	ASP	2.1
1	A	9	ASP	2.0
1	B	-208	ALA	2.0
1	B	-36	LYS	2.0
2	C	34	ASN	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
3	GLC	F	1	12/12	0.94	0.13	28,31,34,39	0
3	GLC	E	1	12/12	0.95	0.15	27,30,35,37	0

Continued on next page...

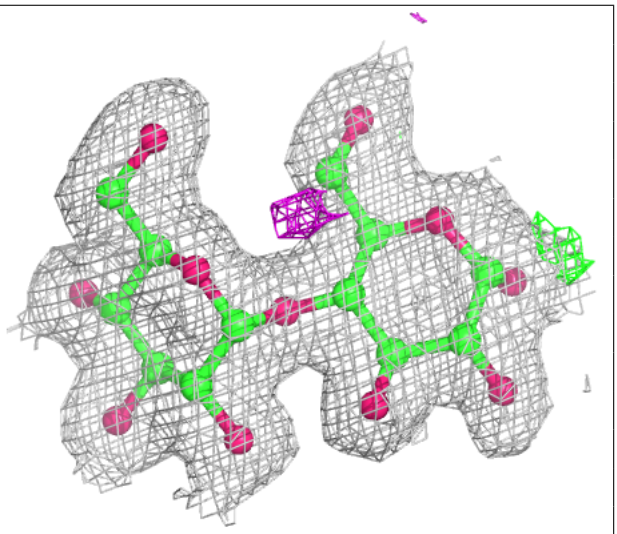
Continued from previous page...

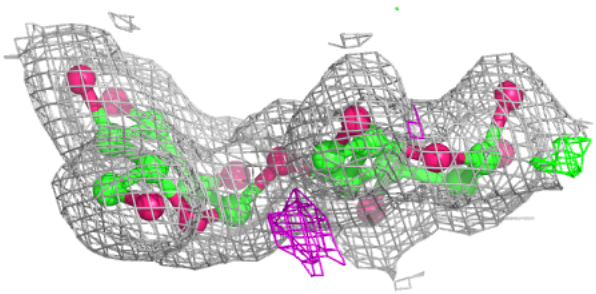
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GLC	E	2	11/12	0.96	0.17	25,25,27,27	0
3	GLC	F	2	11/12	0.97	0.12	23,25,27,27	0

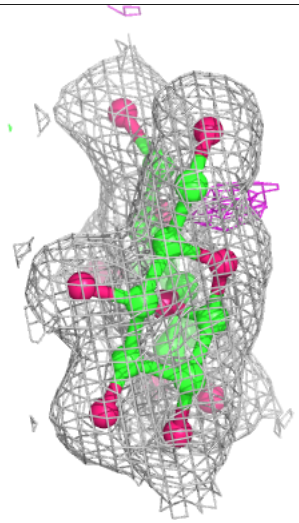
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

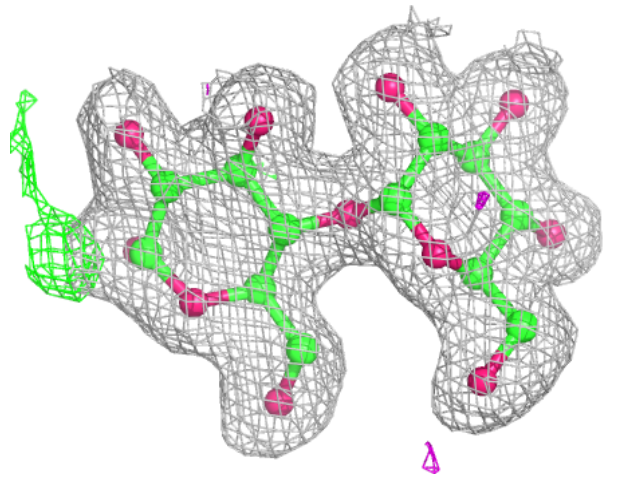


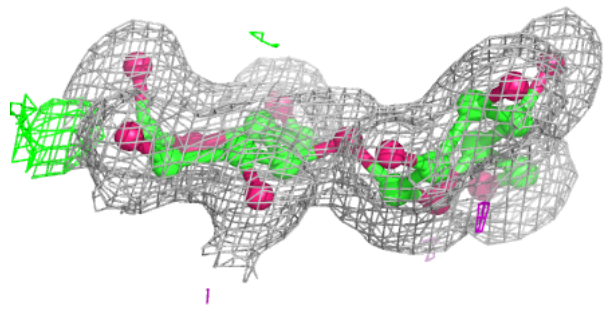


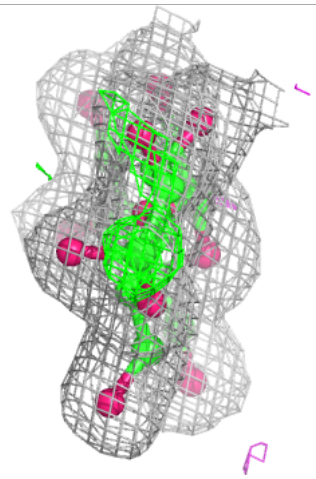


Electron density around Chain F:

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







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
6	PEG	B	502	7/7	0.88	0.09	38,40,44,45	0
5	BTB	A	501	14/14	0.89	0.15	21,26,28,33	0
6	PEG	A	502	7/7	0.90	0.11	36,38,39,41	0
5	BTB	B	501	14/14	0.93	0.13	14,22,25,31	0
4	CA	B	500	1/1	0.99	0.08	17,17,17,17	0
4	CA	A	500	1/1	1.00	0.08	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.