Full wwPDB X-ray Structure Validation Report (i)

Oct 8, 2023 – 09:28 AM EDT

PDB ID	:	6E9N
Title	:	E. coli D-galactonate:proton symporter in the inward open form
Authors	:	Leano, J.B.; Edwards, R.H.; Stroud, R.M.
Deposited on	:	2018-08-01
Resolution	:	2.92 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:

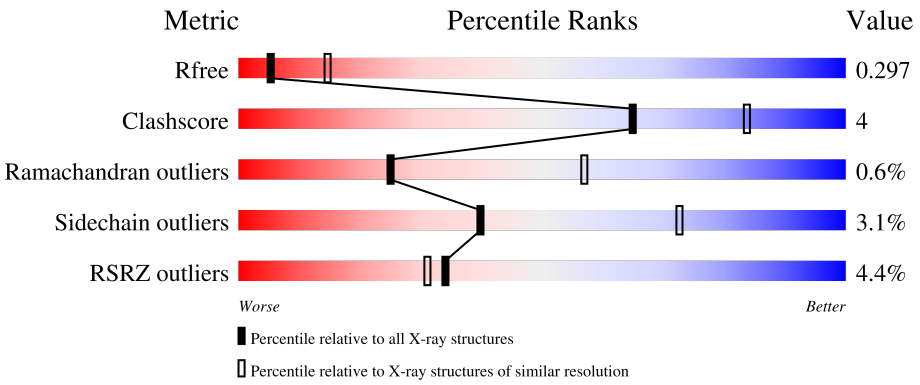
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.92 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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	460	5% 78% 11% 11%
1	B	460	3% 76% 12% 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6472 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 D-galactonate transport.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	409	3177	2125	508	527	17	0	0	0
1	B	409	3177	2125	508	527	17	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	446	SER	-	expression tag	UNP J7QAK3
A	447	LEU	-	expression tag	UNP J7QAK3
A	448	VAL	-	expression tag	UNP J7QAK3
A	449	PRO	-	expression tag	UNP J7QAK3
A	450	ARG	-	expression tag	UNP J7QAK3
A	451	GLY	-	expression tag	UNP J7QAK3
A	452	SER	-	expression tag	UNP J7QAK3
A	453	GLY	-	expression tag	UNP J7QAK3
A	454	SER	-	expression tag	UNP J7QAK3
A	455	HIS	-	expression tag	UNP J7QAK3
A	456	HIS	-	expression tag	UNP J7QAK3
A	457	HIS	-	expression tag	UNP J7QAK3
A	458	HIS	-	expression tag	UNP J7QAK3
A	459	HIS	-	expression tag	UNP J7QAK3
A	460	HIS	-	expression tag	UNP J7QAK3
B	446	SER	-	expression tag	UNP J7QAK3
B	447	LEU	-	expression tag	UNP J7QAK3
B	448	VAL	-	expression tag	UNP J7QAK3
B	449	PRO	-	expression tag	UNP J7QAK3
B	450	ARG	-	expression tag	UNP J7QAK3
B	451	GLY	-	expression tag	UNP J7QAK3
B	452	SER	-	expression tag	UNP J7QAK3
B	453	GLY	-	expression tag	UNP J7QAK3
B	454	SER	-	expression tag	UNP J7QAK3
B	455	HIS	-	expression tag	UNP J7QAK3

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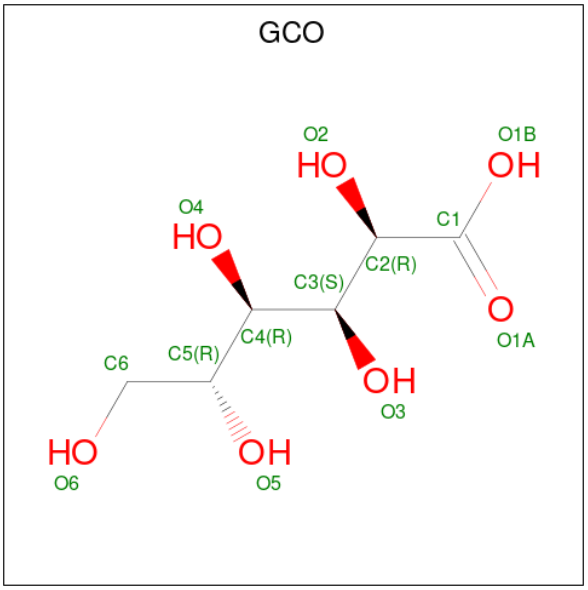
Chain	Residue	Modelled	Actual	Comment	Reference
B	456	HIS	-	expression tag	UNP J7QAK3
B	457	HIS	-	expression tag	UNP J7QAK3
B	458	HIS	-	expression tag	UNP J7QAK3
B	459	HIS	-	expression tag	UNP J7QAK3
B	460	HIS	-	expression tag	UNP J7QAK3

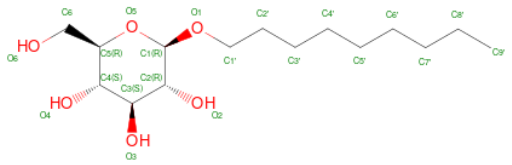
- Molecule 2 is D-gluconic acid (three-letter code: GCO) (formula: $C_6H_{12}O_7$).



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

- Molecule 3 is nonyl beta-D-glucopyranoside (three-letter code: BNG) (formula: $C_{15}H_{30}O_6$).

BNG



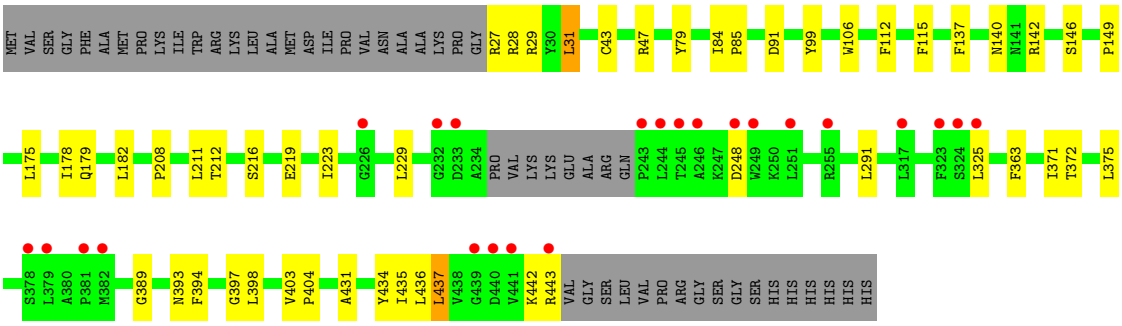
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	21	15	6	0	0
			Total	C	O		
3	A	1	21	15	6	0	0
			Total	C	O		
3	B	1	21	15	6	0	0
			Total	C	O		
3	B	1	21	15	6	0	0
			Total	C	O		
3	B	1	21	15	6	0	0

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.

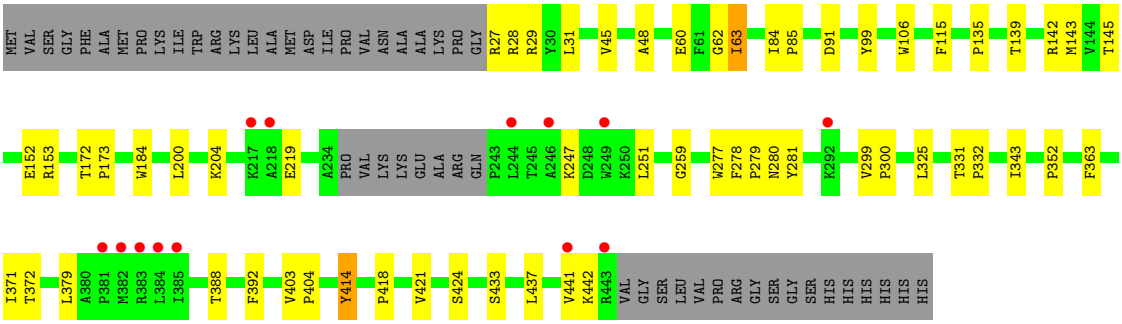
- Molecule 1: D-galactonate transport

Chain A:



- Molecule 1: D-galactonate transport

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.70Å 107.63Å 103.21Å 90.00° 108.32° 90.00°	Depositor
Resolution (Å)	48.28 – 2.92 48.28 – 2.91	Depositor EDS
% Data completeness (in resolution range)	60.5 (48.28-2.92) 60.5 (48.28-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.87 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, R_{free}	0.243 , 0.297 0.249 , 0.297	Depositor DCC
R_{free} test set	1256 reflections (5.95%)	wwPDB-VP
Wilson B-factor (Å^2)	69.1	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.23 , 25.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	6472	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: BNG, GCO

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	0.25	0/3270	0.42	0/4451
1	B	0.25	0/3270	0.40	0/4451
All	All	0.25	0/6540	0.41	0/8902

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	3177	0	3238	28	0
1	B	3177	0	3238	28	0
2	A	13	0	11	2	0
3	A	42	0	60	1	0
3	B	63	0	90	0	0
All	All	6472	0	6637	54	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (54) 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:B:60:GLU:OE1	1:B:184:TRP:NE1	2.23	0.71
1:B:91:ASP:OD1	1:B:142:ARG:NH2	2.28	0.66
1:B:247:LYS:O	1:B:251:LEU:N	2.32	0.62
1:B:28:ARG:N	1:B:219:GLU:OE2	2.33	0.61
1:A:115:PHE:O	1:B:204:LYS:NZ	2.38	0.56
1:A:137:PHE:HB2	2:A:501:GCO:H62	1.89	0.55
1:A:435:ILE:HG23	1:A:436:LEU:HD23	1.88	0.54
1:A:47:ARG:NH2	1:A:79:TYR:OH	2.40	0.54
1:A:91:ASP:OD1	1:A:142:ARG:NH2	2.41	0.52
1:A:371:ILE:HA	3:A:502:BNG:H4	1.92	0.52
1:A:389:GLY:O	1:A:393:ASN:ND2	2.43	0.52
1:A:372:THR:O	1:A:375:LEU:N	2.43	0.51
1:A:442:LYS:O	1:A:443:ARG:HB2	2.11	0.51
1:B:139:THR:O	1:B:143:MET:N	2.41	0.50
1:B:29:ARG:NH1	1:B:152:GLU:OE1	2.42	0.50
1:B:277:TRP:O	1:B:281:TYR:N	2.43	0.49
1:B:27:ARG:N	1:B:219:GLU:OE2	2.45	0.49
1:B:388:THR:O	1:B:392:PHE:N	2.41	0.49
1:A:178:ILE:O	1:A:182:LEU:N	2.46	0.47
1:B:84:ILE:N	1:B:85:PRO:HD2	2.29	0.47
1:A:137:PHE:HB2	2:A:501:GCO:C6	2.45	0.47
1:A:112:PHE:CZ	1:B:200:LEU:HB2	2.49	0.46
1:B:278:PHE:HB3	1:B:279:PRO:HD3	1.99	0.45
1:A:28:ARG:HH11	1:A:31:LEU:HB3	1.81	0.45
1:B:331:THR:HB	1:B:332:PRO:HD3	1.99	0.45
1:A:146:SER:OG	1:A:229:LEU:O	2.32	0.44
1:B:45:VAL:O	1:B:48:ALA:N	2.51	0.44
1:B:259:GLY:HA2	1:B:437:LEU:HD12	2.00	0.44
1:A:84:ILE:N	1:A:85:PRO:CD	2.81	0.44
1:A:394:PHE:O	1:A:398:LEU:N	2.49	0.43
1:A:137:PHE:O	1:A:140:ASN:N	2.52	0.43
1:A:27:ARG:N	1:A:219:GLU:OE2	2.51	0.43
1:B:84:ILE:HG23	1:B:85:PRO:HD3	2.01	0.43
1:B:172:THR:N	1:B:173:PRO:CD	2.82	0.42
1:B:299:VAL:HB	1:B:300:PRO:HD3	2.00	0.42
1:A:208:PRO:O	1:A:212:THR:OG1	2.31	0.42
1:B:62:GLY:O	1:B:63:ILE:C	2.57	0.42
1:A:84:ILE:HG12	1:A:85:PRO:HD3	2.02	0.42
1:A:29:ARG:HG2	1:A:223:ILE:HD11	2.02	0.42
1:A:248:ASP:OD1	1:A:248:ASP:N	2.53	0.42
1:A:393:ASN:O	1:A:397:GLY:N	2.42	0.42
1:A:403:VAL:CG1	1:A:404:PRO:HD3	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:ALA:O	1:A:435:ILE:HG22	2.20	0.42
1:B:414:TYR:CD2	1:B:414:TYR:N	2.87	0.42
1:B:418:PRO:O	1:B:421:VAL:N	2.50	0.41
1:B:403:VAL:N	1:B:404:PRO:CD	2.83	0.41
1:A:84:ILE:CG1	1:A:85:PRO:HD3	2.50	0.41
1:B:145:THR:HA	1:B:153:ARG:HE	1.85	0.41
1:B:259:GLY:O	1:B:433:SER:OG	2.36	0.41
1:B:379:LEU:HA	1:B:442:LYS:O	2.21	0.40
1:A:175:LEU:O	1:A:179:GLN:N	2.42	0.40
1:A:436:LEU:HB2	1:A:437:LEU:HD23	2.04	0.40
1:B:343:ILE:HG22	1:B:424:SER:OG	2.21	0.40
1:B:135:PRO:O	1:B:139:THR:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	405/460 (88%)	383 (95%)	21 (5%)	1 (0%)	47	77
1	B	405/460 (88%)	389 (96%)	12 (3%)	4 (1%)	15	43
All	All	810/920 (88%)	772 (95%)	33 (4%)	5 (1%)	25	57

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	441	VAL
1	B	63	ILE
1	B	352	PRO
1	A	149	PRO
1	B	371	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	325/366 (89%)	314 (97%)	11 (3%)	37	69
1	B	325/366 (89%)	316 (97%)	9 (3%)	43	75
All	All	650/732 (89%)	630 (97%)	20 (3%)	40	72

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	43	CYS
1	A	99	TYR
1	A	106	TRP
1	A	211	LEU
1	A	216	SER
1	A	291	LEU
1	A	325	LEU
1	A	363	PHE
1	A	434	TYR
1	A	437	LEU
1	B	31	LEU
1	B	99	TYR
1	B	106	TRP
1	B	115	PHE
1	B	280	ASN
1	B	325	LEU
1	B	363	PHE
1	B	372	THR
1	B	414	TYR

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)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	BNG	A	503	-	21,21,21	1.11	1 (4%)	26,26,26	0.83	0
2	GCO	A	501	-	12,12,12	0.98	0	16,16,16	1.14	1 (6%)
3	BNG	B	503	-	21,21,21	1.15	2 (9%)	26,26,26	0.92	2 (7%)
3	BNG	B	502	-	21,21,21	1.07	2 (9%)	26,26,26	0.83	0
3	BNG	B	501	-	21,21,21	1.04	1 (4%)	26,26,26	1.16	3 (11%)
3	BNG	A	502	-	21,21,21	1.06	1 (4%)	26,26,26	0.90	1 (3%)

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	BNG	A	503	-	-	8/12/32/32	0/1/1/1
2	GCO	A	501	-	-	14/18/18/18	-
3	BNG	B	503	-	-	8/12/32/32	0/1/1/1
3	BNG	B	502	-	-	5/12/32/32	0/1/1/1
3	BNG	B	501	-	-	5/12/32/32	0/1/1/1
3	BNG	A	502	-	-	10/12/32/32	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	BNG	O5-C1	3.56	1.50	1.41
3	A	503	BNG	O5-C1	3.53	1.50	1.41
3	B	502	BNG	O5-C1	3.38	1.50	1.41
3	A	502	BNG	O5-C1	3.37	1.50	1.41
3	B	501	BNG	O5-C1	3.34	1.50	1.41
3	B	503	BNG	O1-C1	-2.10	1.36	1.40
3	B	502	BNG	O1-C1	-2.04	1.36	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	501	BNG	C1-C2-C3	2.69	115.60	110.00
3	B	503	BNG	O5-C5-C4	2.41	114.07	109.69
2	A	501	GCO	O1B-C1-C2	2.33	119.58	113.27
3	B	503	BNG	C1'-O1-C1	2.29	117.63	113.84
3	B	501	BNG	C1-O5-C5	-2.26	109.24	113.69
3	A	502	BNG	C1-O5-C5	-2.18	109.42	113.69
3	B	501	BNG	C4-C3-C2	2.11	114.51	110.82

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GCO	C1-C2-C3-C4
2	A	501	GCO	C1-C2-C3-O3
2	A	501	GCO	O2-C2-C3-C4
2	A	501	GCO	O2-C2-C3-O3
2	A	501	GCO	O5-C5-C6-O6
3	A	502	BNG	C2-C1-O1-C1'
3	A	502	BNG	O5-C1-O1-C1'
3	A	503	BNG	C2'-C1'-O1-C1
3	B	502	BNG	C2-C1-O1-C1'
3	B	502	BNG	O5-C1-O1-C1'
3	B	503	BNG	C2-C1-O1-C1'
3	B	503	BNG	O5-C1-O1-C1'
2	A	501	GCO	O1A-C1-C2-O2
2	A	501	GCO	O1B-C1-C2-O2
3	A	503	BNG	O5-C5-C6-O6
2	A	501	GCO	C4-C5-C6-O6
3	B	503	BNG	O5-C5-C6-O6
3	A	503	BNG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	A	503	BNG	C2-C1-O1-C1'
3	B	503	BNG	C2'-C3'-C4'-C5'
3	B	501	BNG	C5'-C6'-C7'-C8'
3	A	503	BNG	C5'-C6'-C7'-C8'
3	B	502	BNG	C4'-C5'-C6'-C7'
3	A	503	BNG	C3'-C4'-C5'-C6'
3	A	502	BNG	O1-C1'-C2'-C3'
3	B	501	BNG	C1'-C2'-C3'-C4'
3	B	503	BNG	C4-C5-C6-O6
3	A	502	BNG	C1'-C2'-C3'-C4'
2	A	501	GCO	O1A-C1-C2-C3
3	B	501	BNG	O5-C5-C6-O6
3	B	503	BNG	C4'-C5'-C6'-C7'
3	B	503	BNG	C5'-C6'-C7'-C8'
3	A	502	BNG	O5-C5-C6-O6
3	A	502	BNG	C4'-C5'-C6'-C7'
2	A	501	GCO	O1B-C1-C2-C3
2	A	501	GCO	O3-C3-C4-O4
3	A	503	BNG	C1'-C2'-C3'-C4'
3	A	503	BNG	O1-C1'-C2'-C3'
3	A	502	BNG	C2'-C1'-O1-C1
3	B	503	BNG	C2'-C1'-O1-C1
3	B	502	BNG	C1'-C2'-C3'-C4'
3	A	502	BNG	C6'-C7'-C8'-C9'
2	A	501	GCO	O3-C3-C4-C5
2	A	501	GCO	C2-C3-C4-C5
3	B	502	BNG	O1-C1'-C2'-C3'
3	A	502	BNG	C3'-C4'-C5'-C6'
2	A	501	GCO	C2-C3-C4-O4
3	B	501	BNG	C6'-C7'-C8'-C9'
3	A	502	BNG	C5'-C6'-C7'-C8'
3	B	501	BNG	C2'-C1'-O1-C1

There are no ring outliers.

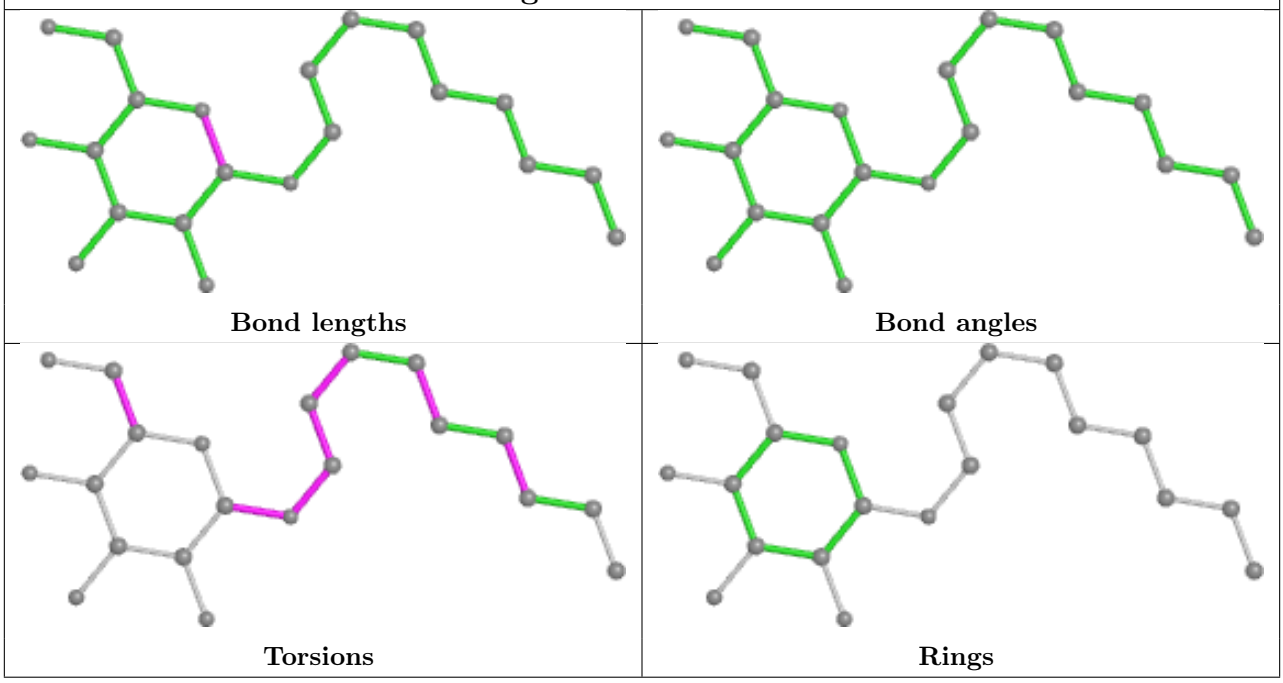
2 monomers are involved in 3 short contacts:

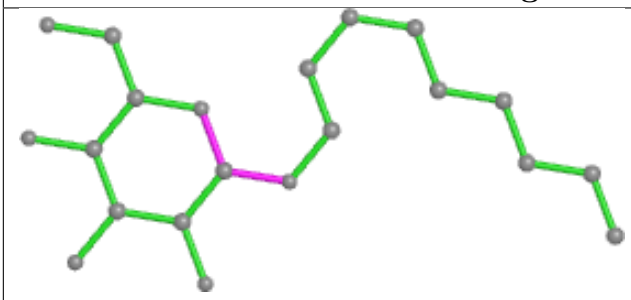
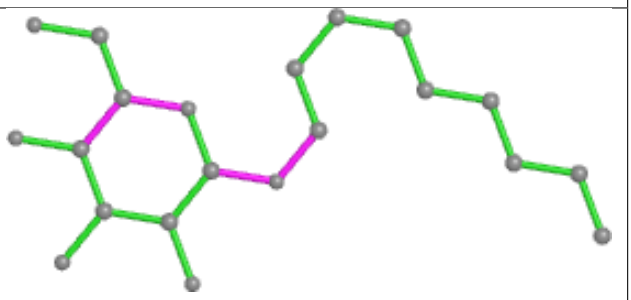
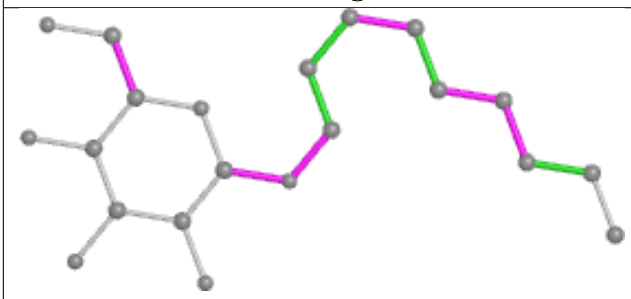
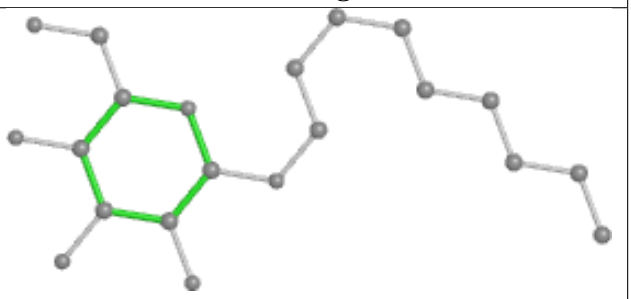
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	GCO	2	0
3	A	502	BNG	1	0

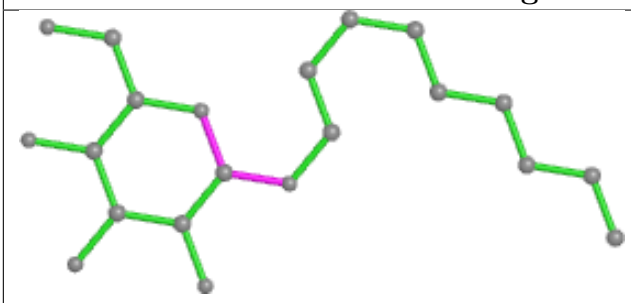
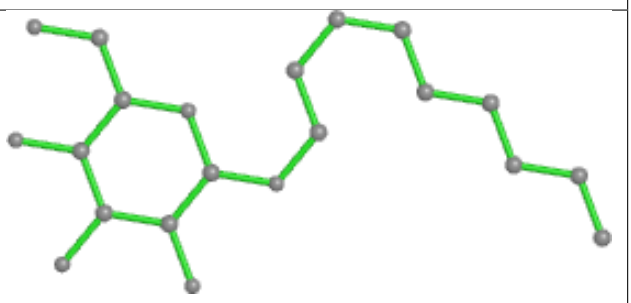
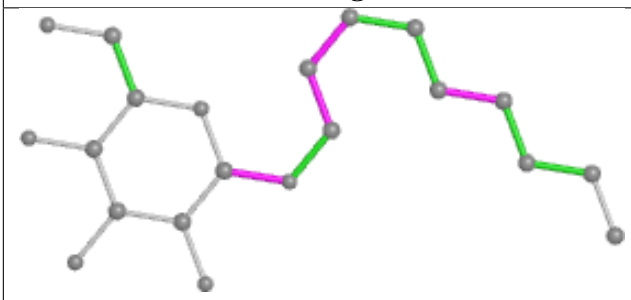
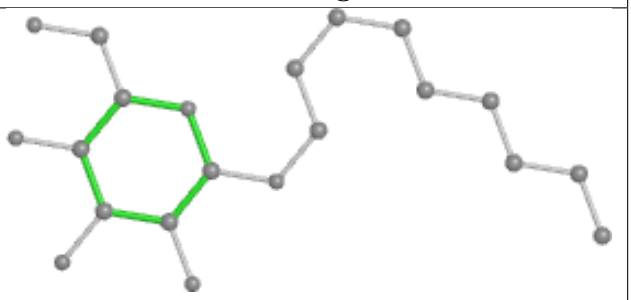
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

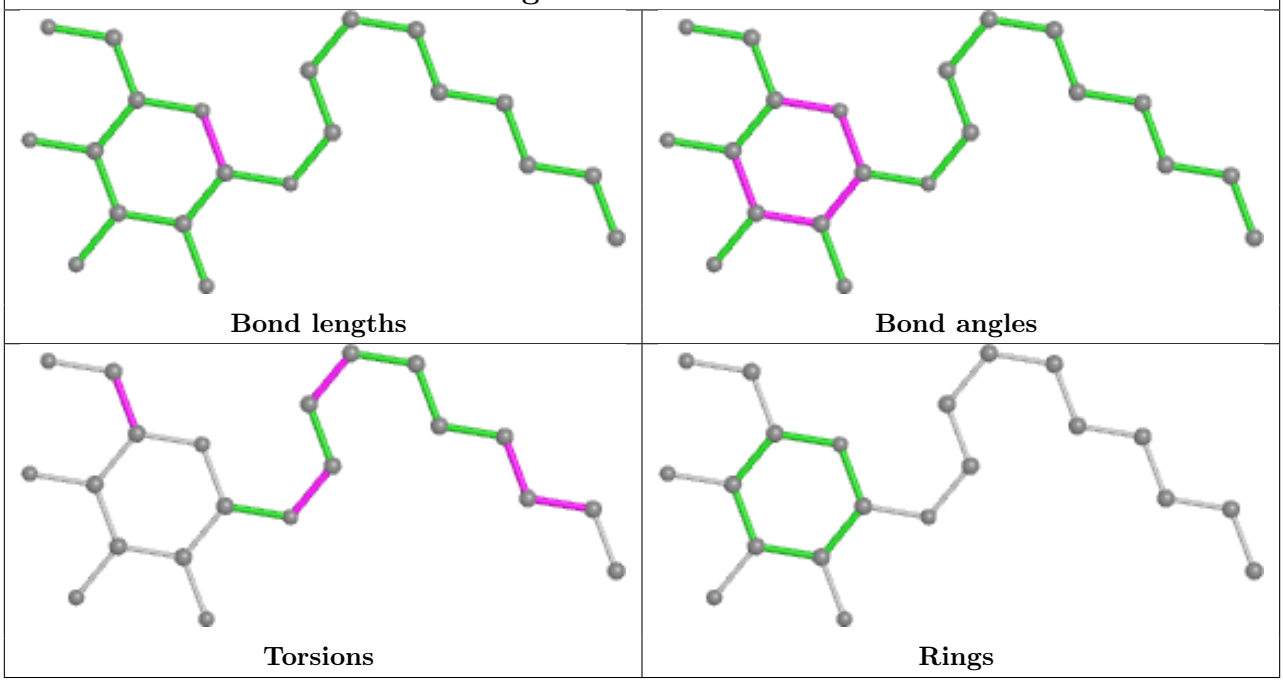
Ligand BNG A 503



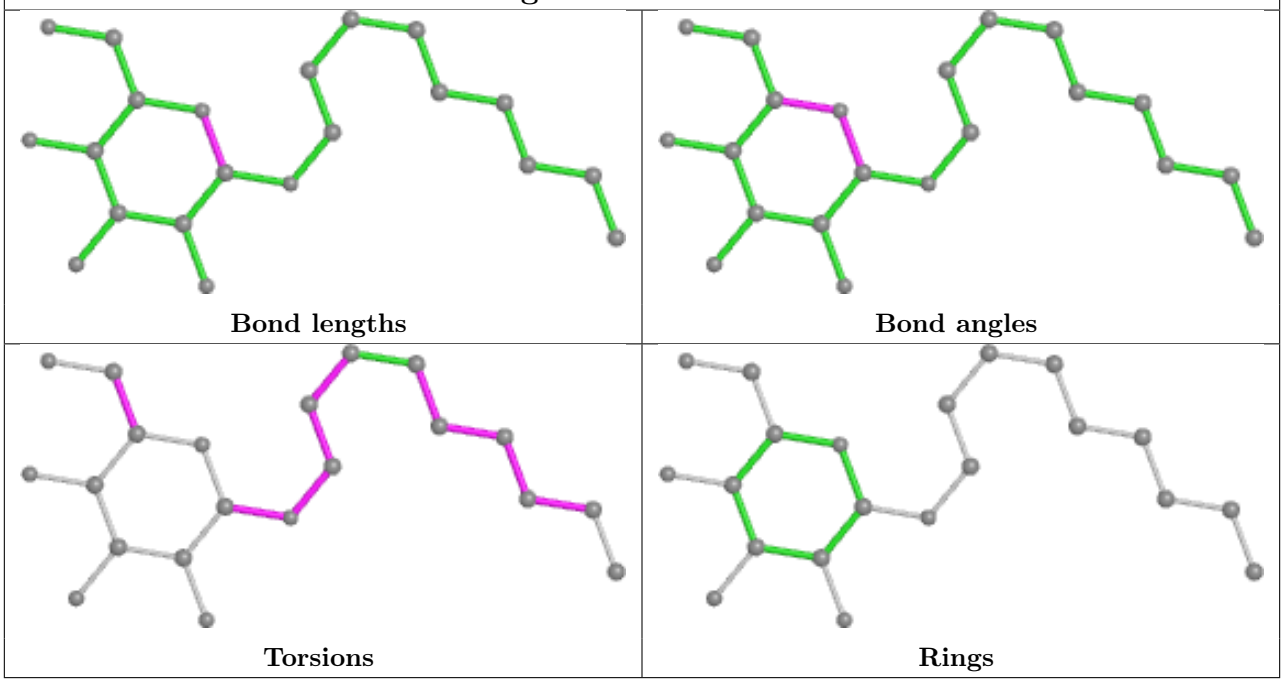
Ligand BNG B 503	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand BNG B 502	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand BNG B 501



Ligand BNG A 502



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	409/460 (88%)	-0.05	23 (5%)	24	21	24, 50, 100, 153	0
1	B	409/460 (88%)	-0.22	13 (3%)	47	44	25, 56, 86, 127	0
All	All	818/920 (88%)	-0.14	36 (4%)	34	31	24, 54, 94, 153	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	PRO	11.1
1	A	244	LEU	10.9
1	B	382	MET	6.0
1	A	245	THR	5.4
1	A	443	ARG	5.4
1	A	249	TRP	5.1
1	B	443	ARG	4.2
1	A	248	ASP	4.1
1	A	441	VAL	4.0
1	B	381	PRO	3.9
1	B	383	ARG	3.9
1	B	218	ALA	3.6
1	A	323	PHE	3.3
1	A	378	SER	3.3
1	B	385	ILE	3.3
1	A	439	GLY	3.2
1	A	440	ASP	3.2
1	B	384	LEU	3.1
1	B	244	LEU	2.8
1	B	217	LYS	2.8
1	A	325	LEU	2.8
1	A	251	LEU	2.5
1	A	232	GLY	2.5
1	B	249	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	246	ALA	2.5
1	A	233	ASP	2.3
1	A	382	MET	2.3
1	A	379	LEU	2.3
1	B	292	LYS	2.3
1	A	324	SER	2.2
1	A	226	GLY	2.1
1	A	317	LEU	2.1
1	A	246	ALA	2.1
1	A	381	PRO	2.1
1	A	255	ARG	2.1
1	B	441	VAL	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)

There are no monosaccharides in this entry.

6.4 Ligands (i)

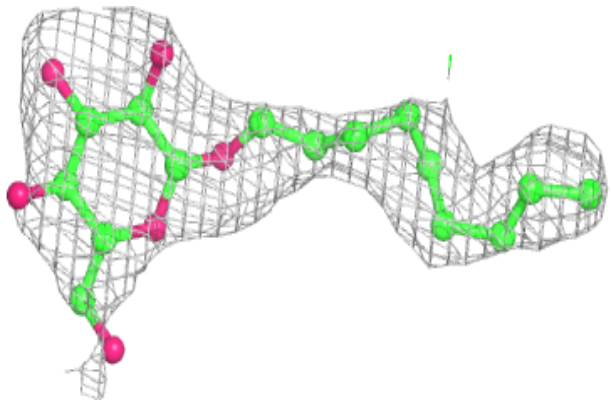
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

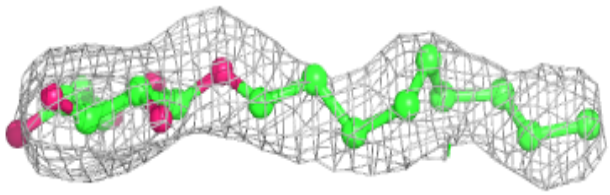
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GCO	A	501	13/13	0.79	0.30	69,91,98,105	0
3	BNG	B	502	21/21	0.80	0.35	69,83,98,100	0
3	BNG	A	503	21/21	0.84	0.53	37,58,95,103	0
3	BNG	B	503	21/21	0.84	0.26	45,77,102,105	0
3	BNG	A	502	21/21	0.85	0.26	46,79,97,110	0
3	BNG	B	501	21/21	0.87	0.26	45,66,78,104	0

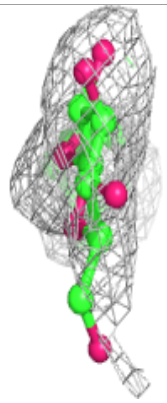
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around BNG B 502:

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

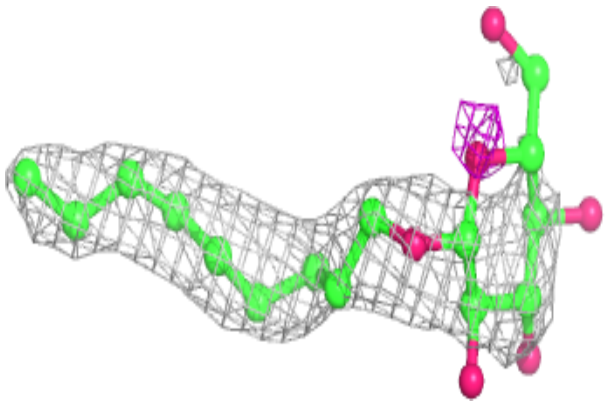


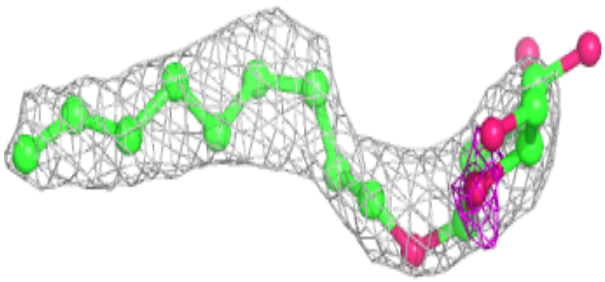


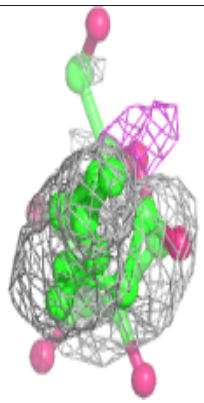


Electron density around BNG A 503:

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

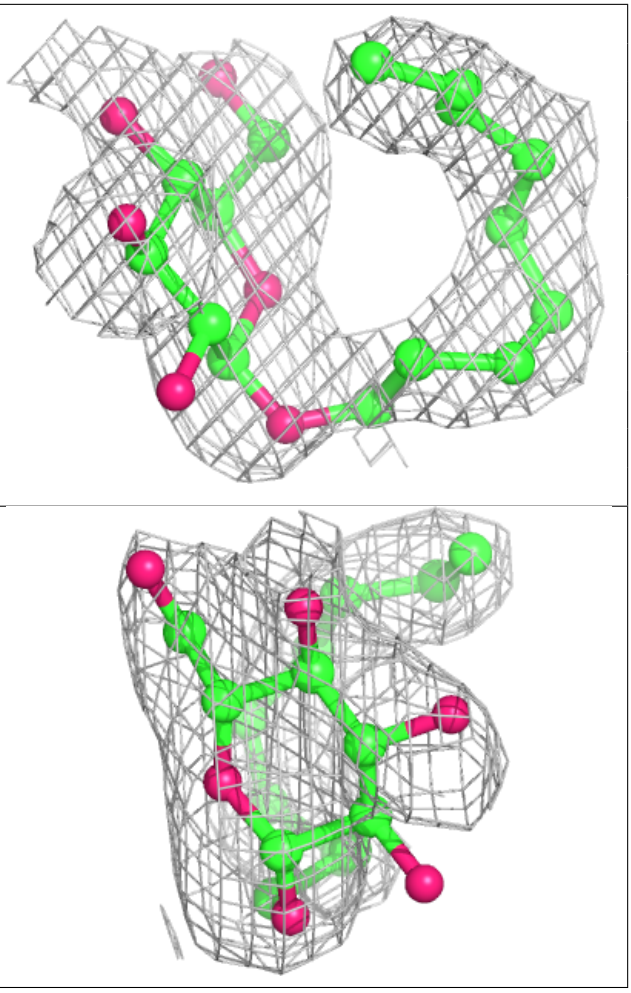






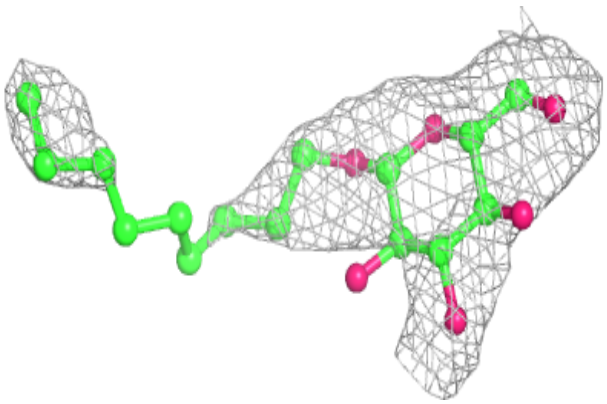
Electron density around BNG B 503:

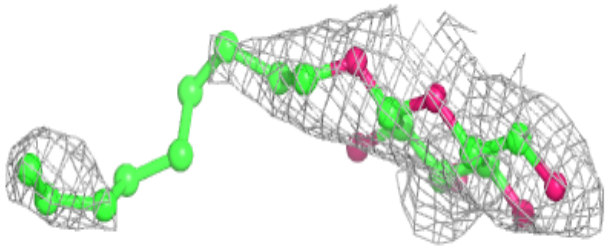
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

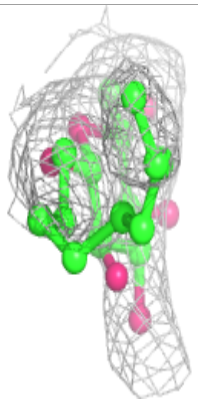


Electron density around BNG A 502:

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

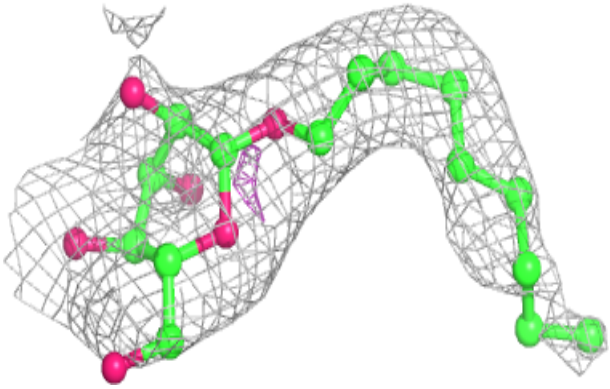


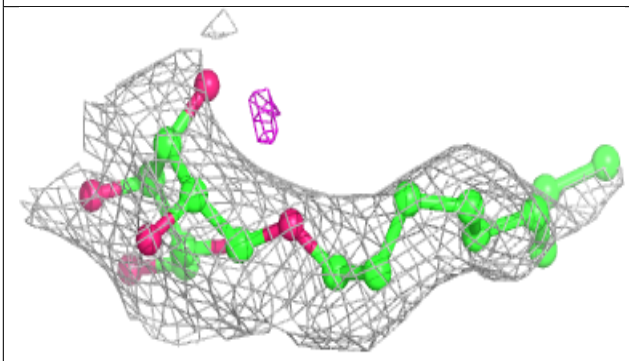


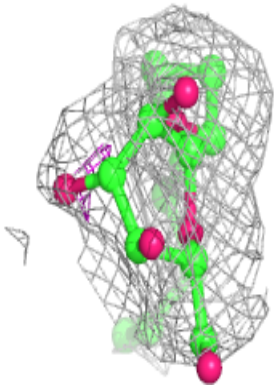


Electron density around BNG B 501:

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







6.5 Other polymers (i)

There are no such residues in this entry.