



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 19, 2025 – 08:14 PM JST

PDB ID : 9VMK / pdb_00009vmk
Title : Crystal structure of TeGH116 from *Thermosynechococcus elongatus* with glucose
Authors : Beagbandee, C.; Charoenwattanasatien, R.; Pengthaisong, S.; Kurisu, G.; Ketudat Cairns, J.R.
Deposited on : 2025-06-28
Resolution : 2.00 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	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

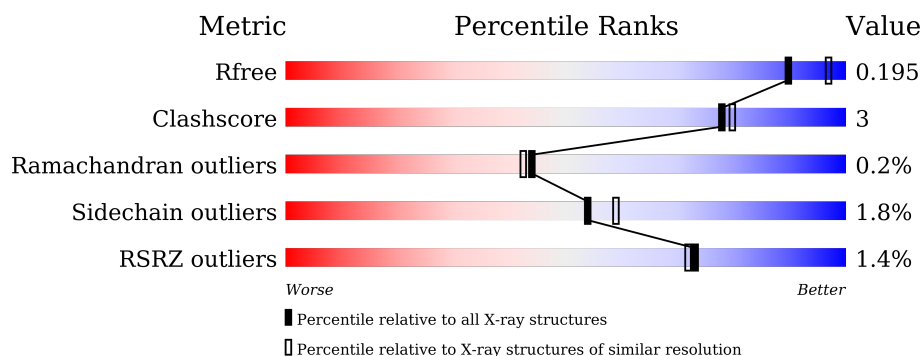
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	809	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 89% 8% ... </div> </div>
1	B	809	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 86% 10% ... </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13216 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.

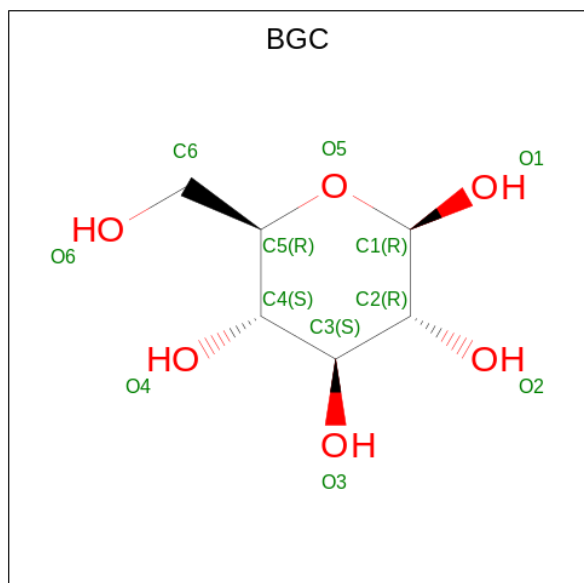
- Molecule 1 is a protein called Tlr0193 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	785	Total	C	N	O	S	0	1	0
			6248	4023	1061	1138	26			
1	B	785	Total	C	N	O	S	0	1	0
			6251	4025	1062	1138	26			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	-	expression tag	UNP Q8DMC7
A	3	MET	-	expression tag	UNP Q8DMC7
A	4	ALA	-	expression tag	UNP Q8DMC7
B	2	ALA	-	expression tag	UNP Q8DMC7
B	3	MET	-	expression tag	UNP Q8DMC7
B	4	ALA	-	expression tag	UNP Q8DMC7

- Molecule 2 is beta-D-glucopyranose (CCD ID: BGC) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).

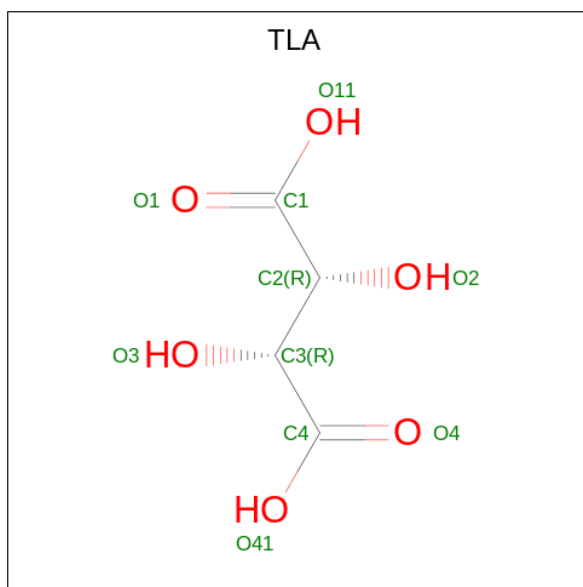


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 5 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 10 4 6	0	0
5	B	1	Total C O 10 4 6	0	0

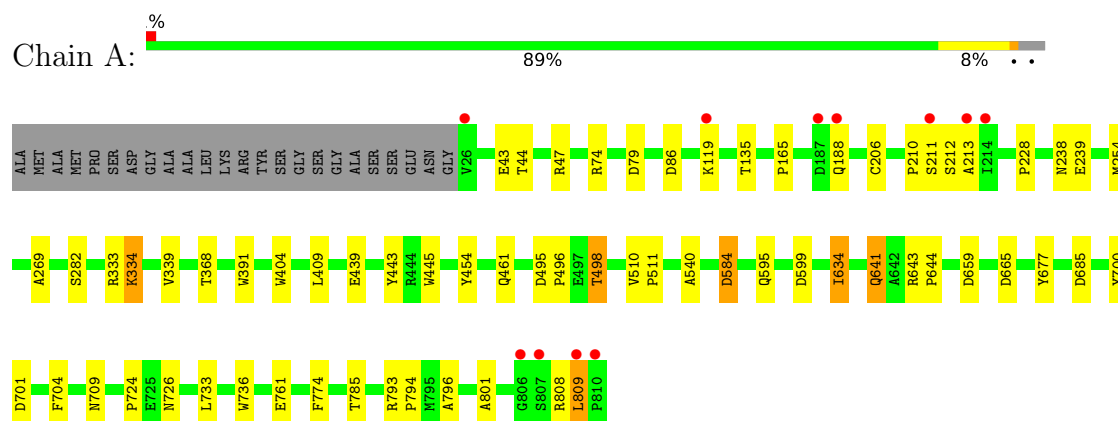
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	312	Total O 312 312	0	0
6	B	305	Total O 305 305	0	0

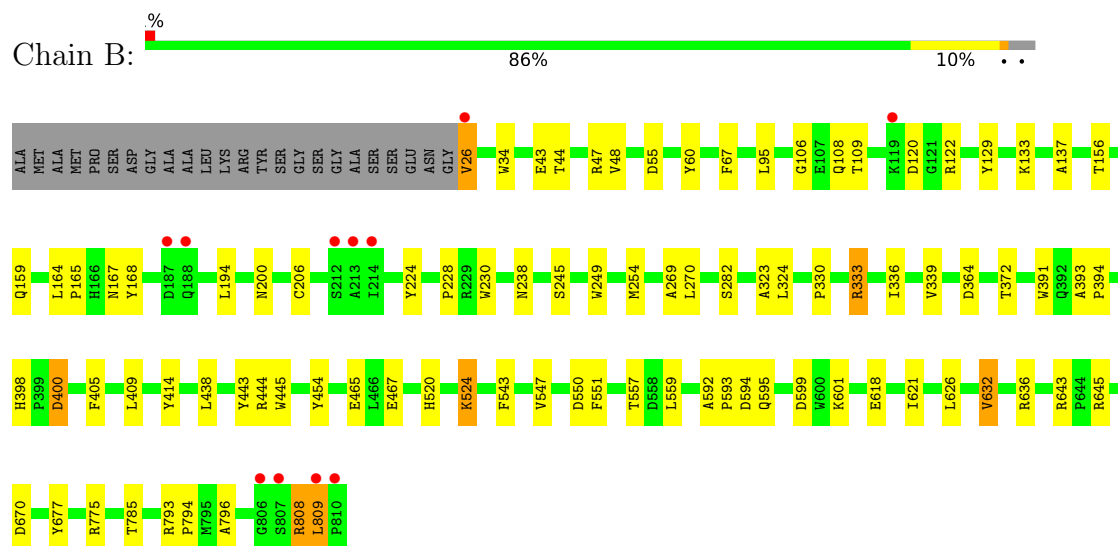
3 Residue-property plots [i](#)

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: Tlr0193 protein



• Molecule 1: Tlr0193 protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	269.00Å 55.09Å 182.00Å 90.00° 131.86° 90.00°	Depositor
Resolution (Å)	26.54 – 2.00 26.54 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.9 (26.54-2.00) 97.9 (26.54-2.00)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.169 , 0.189 0.175 , 0.195	Depositor DCC
R_{free} test set	6491 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	16.5	Xtriage
Anisotropy	0.177	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.006 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13216	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TLA, GOL, CA, BGC

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	0.87	0/6459	1.20	16/8832 (0.2%)
1	B	0.90	1/6462 (0.0%)	1.23	14/8835 (0.2%)
All	All	0.88	1/12921 (0.0%)	1.22	30/17667 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	245	SER	CA-CB	-5.38	1.45	1.53

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	670	ASP	CA-CB-CG	7.75	120.36	112.60
1	B	372	THR	CA-CB-OG1	-7.68	98.09	109.60
1	B	645	ARG	N-CA-CB	-6.46	100.62	110.12
1	A	584	ASP	CA-CB-CG	6.33	118.93	112.60
1	B	67	PHE	CA-CB-CG	6.30	120.10	113.80
1	B	364	ASP	CA-CB-CG	5.97	118.57	112.60
1	A	86	ASP	CA-CB-CG	5.93	118.53	112.60
1	A	498	THR	CA-CB-OG1	-5.93	100.71	109.60
1	B	594	ASP	CA-CB-CG	5.89	118.49	112.60
1	B	108	GLN	N-CA-CB	-5.72	102.18	110.70
1	A	43	GLU	CB-CA-C	5.67	119.69	110.96
1	A	44	THR	CA-CB-OG1	-5.57	101.25	109.60
1	B	599	ASP	CA-CB-CG	5.53	118.13	112.60
1	A	665	ASP	CA-CB-CG	-5.44	107.16	112.60
1	A	685	ASP	CA-CB-CG	5.39	117.99	112.60
1	A	188	GLN	N-CA-CB	-5.37	101.67	110.43
1	A	774	PHE	CA-CB-CG	-5.34	108.46	113.80
1	B	557	THR	CA-CB-OG1	-5.31	101.64	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	636	ARG	CG-CD-NE	-5.31	100.32	112.00
1	A	511	PRO	CB-CA-C	5.25	117.86	110.98
1	A	368	THR	CA-C-O	-5.23	114.36	120.53
1	A	599	ASP	CA-CB-CG	5.23	117.83	112.60
1	A	135	THR	CA-CB-OG1	-5.18	101.83	109.60
1	B	400	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	701	ASP	CA-CB-CG	5.15	117.75	112.60
1	B	601	LYS	CB-CA-C	5.11	118.16	109.84
1	B	106	GLY	CA-C-N	5.10	127.89	120.79
1	B	106	GLY	C-N-CA	5.10	127.89	120.79
1	A	641	GLN	N-CA-CB	5.04	117.59	110.13
1	A	239	GLU	CB-CA-C	5.04	119.91	109.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	6248	0	5892	29	0
1	B	6251	0	5901	38	0
2	A	12	0	12	2	0
2	B	12	0	12	0	0
3	A	36	0	48	0	0
3	B	18	0	24	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	10	0	4	0	0
5	B	10	0	4	0	0
6	A	312	0	0	1	0
6	B	305	0	0	0	0
All	All	13216	0	11897	67	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 (67) 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:206:CYS:O	1:B:228:PRO:HA	1.92	0.68
1:A:808:ARG:O	1:A:809:LEU:HD12	1.98	0.63
1:B:621:ILE:HA	1:B:632:VAL:HG22	1.82	0.62
1:A:443:TYR:HB3	1:A:445:TRP:CZ2	2.35	0.61
1:A:584:ASP:OD1	6:A:1001:HOH:O	2.16	0.61
1:B:238:ASN:HB2	1:B:282:SER:O	2.01	0.61
1:B:443:TYR:HB3	1:B:445:TRP:CZ2	2.37	0.58
1:A:238:ASN:HB2	1:A:282:SER:O	2.04	0.58
1:B:224:TYR:O	3:B:902:GOL:H31	2.05	0.56
1:A:206:CYS:O	1:A:228:PRO:HA	2.07	0.55
1:A:724:PRO:HB3	1:A:733:LEU:HD21	1.89	0.55
1:B:333:ARG:HG2	1:B:333:ARG:HH11	1.71	0.55
1:B:551:PHE:CZ	1:B:626:LEU:CD2	2.90	0.55
1:A:409:LEU:HD11	1:A:801:ALA:HB2	1.90	0.54
1:B:520:HIS:HB3	1:B:524:LYS:HG3	1.90	0.54
1:A:510:VAL:HG21	1:A:540:ALA:HA	1.90	0.54
1:B:269:ALA:HA	1:B:339:VAL:O	2.10	0.52
1:A:495:ASP:OD2	1:A:498:THR:HB	2.08	0.52
1:A:454[A]:TYR:HB3	1:A:796:ALA:HB2	1.91	0.52
1:B:165:PRO:HD2	1:B:391:TRP:CD1	2.45	0.52
1:B:793:ARG:N	1:B:794:PRO:HD2	2.25	0.51
1:B:324:LEU:HD23	1:B:336:ILE:HD13	1.92	0.50
1:B:454[B]:TYR:HB3	1:B:796:ALA:HB2	1.95	0.49
1:A:165:PRO:HD2	1:A:391:TRP:CD1	2.49	0.48
1:A:726:ASN:OD1	1:A:726:ASN:C	2.57	0.48
1:B:60:TYR:CE1	1:B:775:ARG:HD3	2.50	0.47
1:A:700:TYR:O	1:A:704:PHE:HB3	2.13	0.47
1:A:269:ALA:HA	1:A:339:VAL:O	2.16	0.45
1:B:47:ARG:O	1:B:785:THR:HA	2.16	0.45
1:A:659:ASP:OD1	1:A:659:ASP:C	2.59	0.45
1:B:438:LEU:HD13	1:B:444:ARG:HD3	1.99	0.45
1:B:95:LEU:HD21	1:B:230:TRP:CZ2	2.52	0.45
1:B:269:ALA:O	1:B:270:LEU:HD23	2.16	0.45
1:B:414:TYR:C	1:B:414:TYR:CD2	2.93	0.45
1:A:793:ARG:N	1:A:794:PRO:HD2	2.31	0.44
1:B:120:ASP:OD2	1:B:122:ARG:NH2	2.49	0.44
1:A:210:PRO:O	1:A:211:SER:C	2.60	0.44
1:A:736:TRP:CH2	2:A:901:BGC:H6C2	2.54	0.43
1:B:194:LEU:O	1:B:323:ALA:HA	2.19	0.43
1:B:26:VAL:HG11	1:B:156:THR:OG1	2.19	0.43
1:A:808:ARG:O	1:A:809:LEU:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:LYS:HE2	1:A:334:LYS:HB2	1.92	0.43
1:A:643:ARG:N	1:A:644:PRO:HD2	2.34	0.42
1:A:47:ARG:O	1:A:785:THR:HA	2.19	0.42
1:A:808:ARG:O	1:A:809:LEU:CB	2.67	0.42
1:B:467:GLU:OE2	1:B:550:ASP:OD2	2.37	0.42
1:A:634:ILE:HD12	1:A:634:ILE:N	2.35	0.42
1:B:200:ASN:OD1	1:B:200:ASN:C	2.62	0.42
1:B:543:PHE:O	1:B:547:VAL:HG23	2.20	0.42
1:B:592:ALA:O	1:B:593:PRO:C	2.63	0.42
1:B:618:GLU:OE2	1:B:643:ARG:NH1	2.51	0.42
1:A:212:SER:O	1:A:213:ALA:C	2.63	0.42
1:B:48:VAL:HB	1:B:55:ASP:HB2	2.01	0.42
1:B:168:TYR:CZ	1:B:465:GLU:HB2	2.55	0.41
1:B:393:ALA:N	1:B:394:PRO:HD2	2.35	0.41
1:A:439:GLU:OE2	2:A:901:BGC:H1	2.21	0.41
1:B:398:HIS:CD2	1:B:808:ARG:HD2	2.56	0.41
1:A:74:ARG:HA	1:A:79:ASP:O	2.21	0.41
1:A:254:MET:HE3	1:A:254:MET:HB3	1.81	0.41
1:B:34:TRP:O	1:B:137:ALA:HA	2.20	0.41
1:B:120:ASP:OD1	1:B:120:ASP:C	2.63	0.41
1:B:43:GLU:HG2	1:B:44:THR:HG23	2.04	0.40
1:B:254:MET:HB3	1:B:254:MET:HE3	1.76	0.40
1:A:404:TRP:CZ2	1:A:761:GLU:HB2	2.56	0.40
1:B:129:TYR:CE2	1:B:133:LYS:HB2	2.56	0.40
1:B:405:PHE:O	1:B:409:LEU:HB2	2.21	0.40
1:B:164:LEU:O	1:B:167:ASN:HB3	2.21	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	A	784/809 (97%)	757 (97%)	26 (3%)	1 (0%)	48	47
1	B	784/809 (97%)	758 (97%)	24 (3%)	2 (0%)	37	35
All	All	1568/1618 (97%)	1515 (97%)	50 (3%)	3 (0%)	44	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	809	LEU
1	B	808	ARG
1	B	809	LEU

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	A	635/650 (98%)	625 (98%)	10 (2%)	58	64
1	B	636/650 (98%)	623 (98%)	13 (2%)	50	55
All	All	1271/1300 (98%)	1248 (98%)	23 (2%)	54	59

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	LYS
1	A	333	ARG
1	A	334	LYS
1	A	461	GLN
1	A	496	PRO
1	A	595	GLN
1	A	634	ILE
1	A	641	GLN
1	A	677	TYR
1	A	709	ASN
1	B	26	VAL
1	B	109	THR
1	B	159	GLN

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Mol	Chain	Res	Type
1	B	249	TRP
1	B	330	PRO
1	B	333	ARG
1	B	400	ASP
1	B	524	LYS
1	B	559	LEU
1	B	595	GLN
1	B	632	VAL
1	B	677	TYR
1	B	809	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	723	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 2 are monoatomic - leaving 13 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	907	-	5,5,5	0.36	0	5,5,5	0.94	0
2	BGC	B	901	-	12,12,12	0.59	0	17,17,17	0.94	0
3	GOL	B	904	-	5,5,5	0.27	0	5,5,5	0.61	0
3	GOL	A	902	-	5,5,5	0.29	0	5,5,5	0.82	0
3	GOL	A	904	-	5,5,5	0.30	0	5,5,5	0.82	0
3	GOL	B	902	-	5,5,5	0.24	0	5,5,5	0.74	0
2	BGC	A	901	-	12,12,12	0.46	0	17,17,17	0.96	0
5	TLA	A	909	-	9,9,9	1.01	0	12,12,12	1.06	0
3	GOL	A	905	-	5,5,5	0.26	0	5,5,5	0.53	0
3	GOL	A	906	-	5,5,5	0.27	0	5,5,5	0.43	0
3	GOL	B	903	-	5,5,5	0.39	0	5,5,5	1.03	0
5	TLA	B	906	-	9,9,9	0.99	0	12,12,12	1.14	0
3	GOL	A	903	-	5,5,5	0.22	0	5,5,5	0.51	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
3	GOL	A	907	-	-	0/4/4/4	-
2	BGC	B	901	-	-	0/2/22/22	0/1/1/1
3	GOL	B	904	-	-	3/4/4/4	-
3	GOL	A	902	-	-	2/4/4/4	-
3	GOL	A	904	-	-	1/4/4/4	-
3	GOL	B	902	-	-	2/4/4/4	-
2	BGC	A	901	-	-	0/2/22/22	0/1/1/1
5	TLA	A	909	-	-	0/12/12/12	-
3	GOL	A	905	-	-	2/4/4/4	-
3	GOL	A	906	-	-	2/4/4/4	-
3	GOL	B	903	-	-	1/4/4/4	-
5	TLA	B	906	-	-	0/12/12/12	-
3	GOL	A	903	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

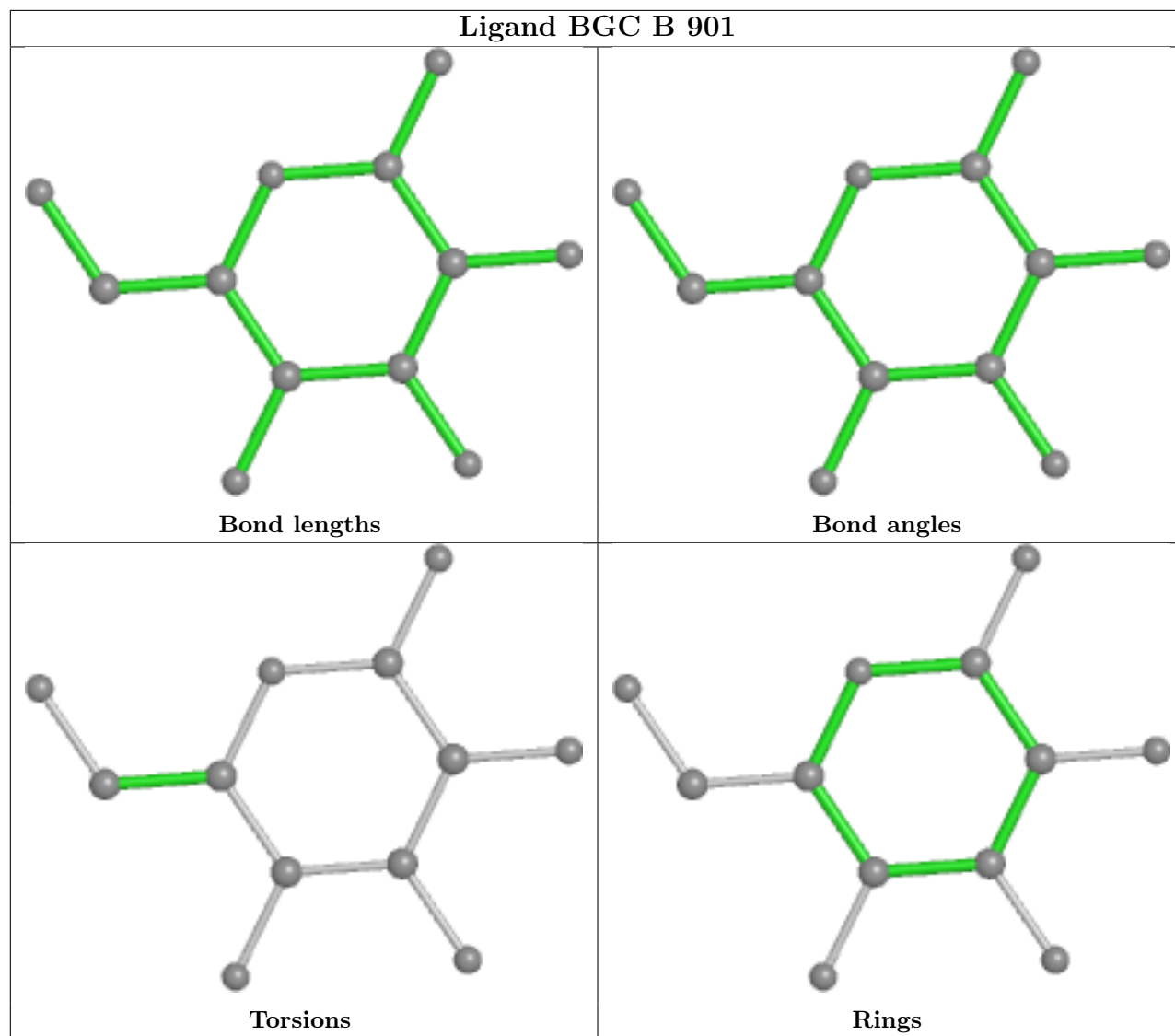
Mol	Chain	Res	Type	Atoms
3	A	902	GOL	C1-C2-C3-O3
3	A	902	GOL	O2-C2-C3-O3
3	B	902	GOL	O1-C1-C2-C3
3	B	904	GOL	O2-C2-C3-O3
3	A	905	GOL	O1-C1-C2-C3
3	A	906	GOL	O1-C1-C2-C3
3	B	903	GOL	C1-C2-C3-O3
3	B	904	GOL	C1-C2-C3-O3
3	A	905	GOL	O1-C1-C2-O2
3	A	906	GOL	O1-C1-C2-O2
3	A	904	GOL	O1-C1-C2-C3
3	B	904	GOL	O1-C1-C2-O2
3	B	902	GOL	O1-C1-C2-O2

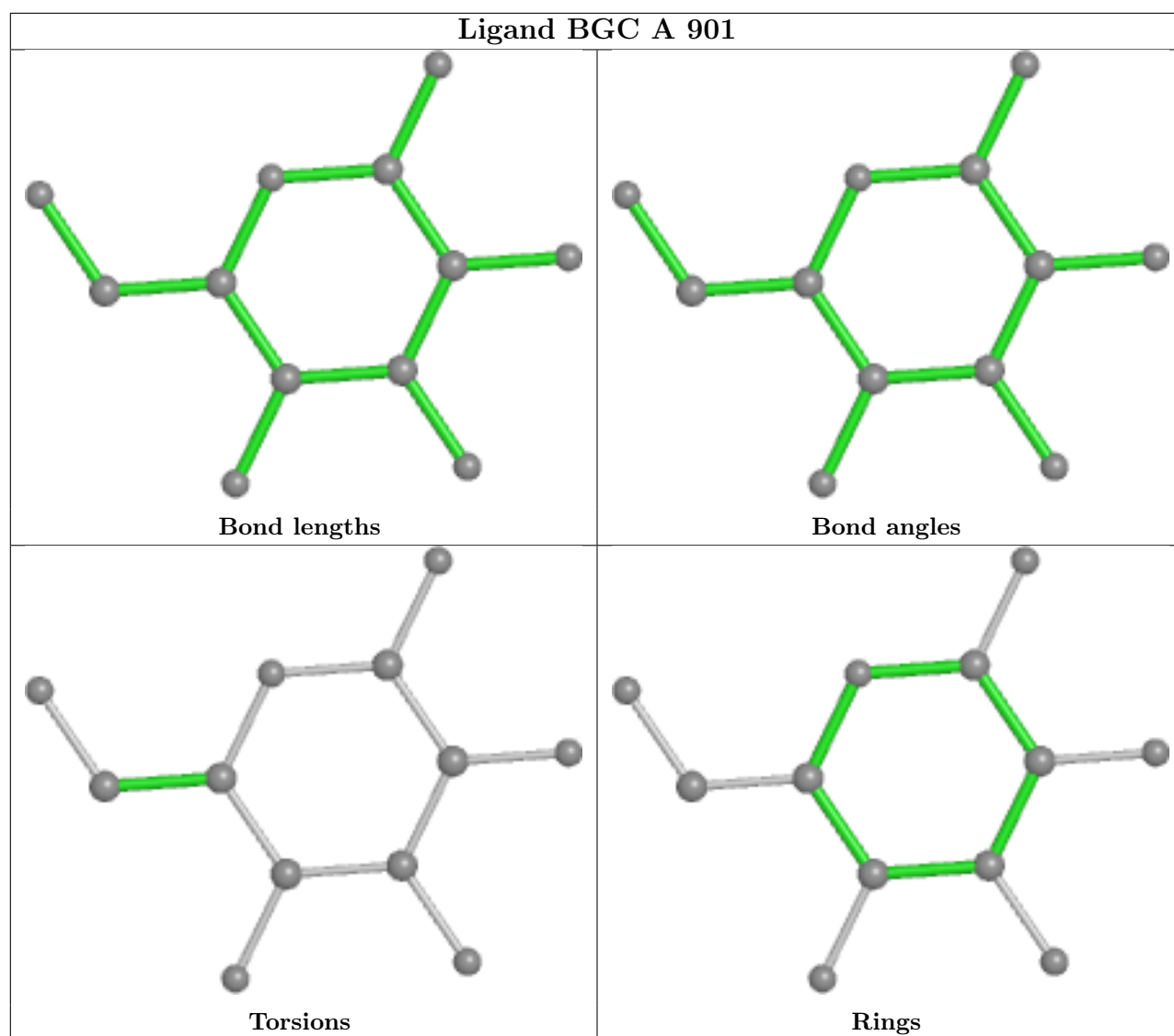
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	902	GOL	1	0
2	A	901	BGC	2	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 [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	785/809 (97%)	-0.49	11 (1%)	73 72	6, 17, 37, 84	1 (0%)
1	B	785/809 (97%)	-0.48	11 (1%)	73 72	6, 17, 35, 67	1 (0%)
All	All	1570/1618 (97%)	-0.48	22 (1%)	73 72	6, 17, 36, 84	2 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	ALA	4.5
1	A	188	GLN	4.0
1	B	809	LEU	3.7
1	B	26	VAL	3.6
1	B	212	SER	3.5
1	A	26	VAL	3.5
1	B	807	SER	3.5
1	B	806	GLY	3.4
1	A	807	SER	3.3
1	B	187	ASP	3.1
1	A	806	GLY	3.0
1	A	213	ALA	2.9
1	A	214	ILE	2.6
1	A	809	LEU	2.4
1	A	810	PRO	2.4
1	B	188	GLN	2.4
1	A	187	ASP	2.3
1	B	214	ILE	2.3
1	B	810	PRO	2.3
1	A	119	LYS	2.2
1	A	211	SER	2.2
1	B	119	LYS	2.1

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

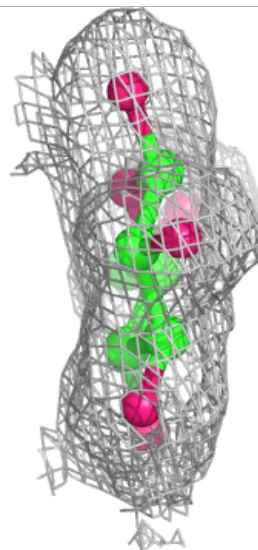
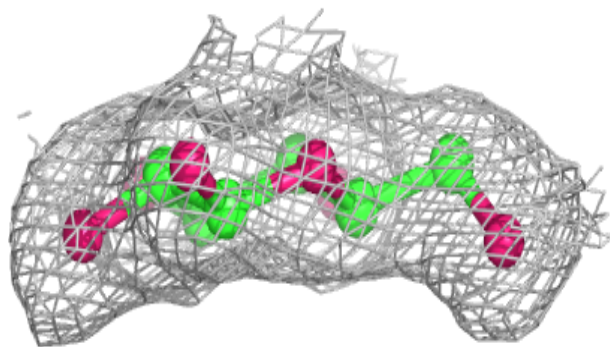
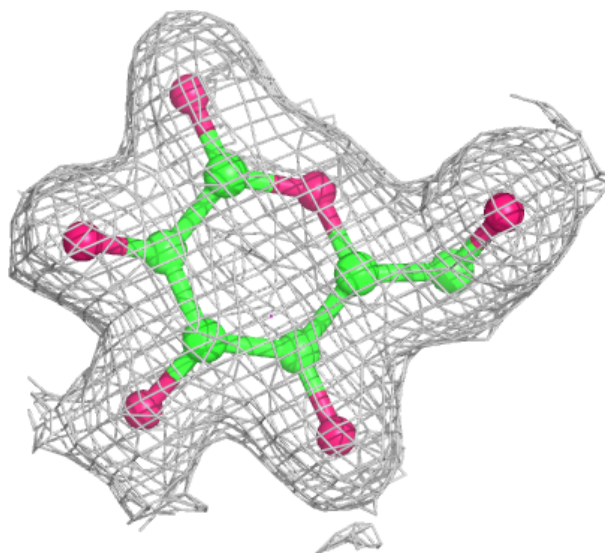
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	A	906	6/6	0.76	0.18	37,38,41,44	0
3	GOL	A	903	6/6	0.80	0.16	44,51,54,56	0
3	GOL	B	903	6/6	0.84	0.12	34,36,41,42	0
3	GOL	A	905	6/6	0.89	0.14	29,40,46,49	0
3	GOL	B	904	6/6	0.89	0.14	19,35,39,48	0
3	GOL	A	904	6/6	0.90	0.13	39,45,47,49	0
3	GOL	B	902	6/6	0.90	0.13	34,36,38,45	0
3	GOL	A	902	6/6	0.92	0.10	20,24,31,34	0
5	TLA	A	909	10/10	0.92	0.08	33,36,40,43	0
5	TLA	B	906	10/10	0.92	0.09	35,37,41,42	0
3	GOL	A	907	6/6	0.93	0.11	22,31,36,42	0
4	CA	A	908	1/1	0.99	0.06	18,18,18,18	0
2	BGC	B	901	12/12	0.99	0.03	8,8,10,11	0
2	BGC	A	901	12/12	0.99	0.04	10,11,12,13	0
4	CA	B	905	1/1	1.00	0.03	22,22,22,22	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.

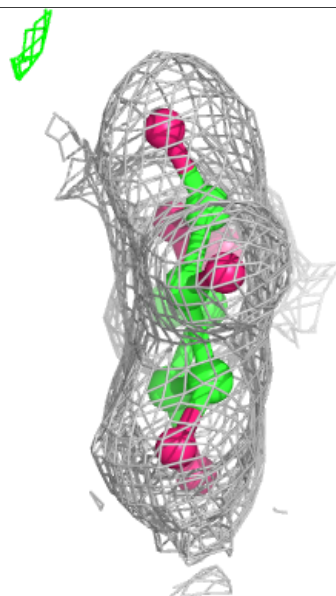
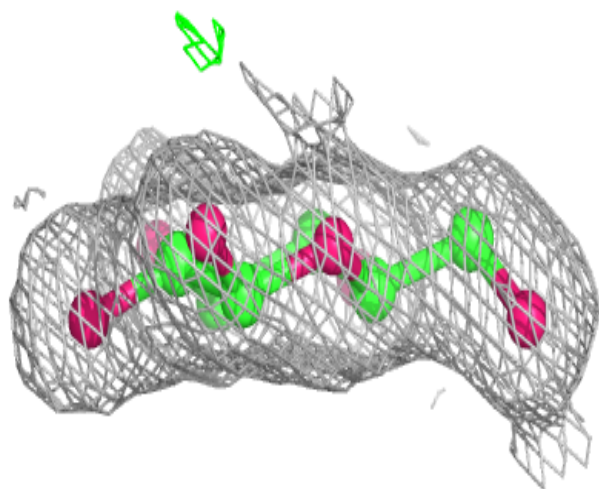
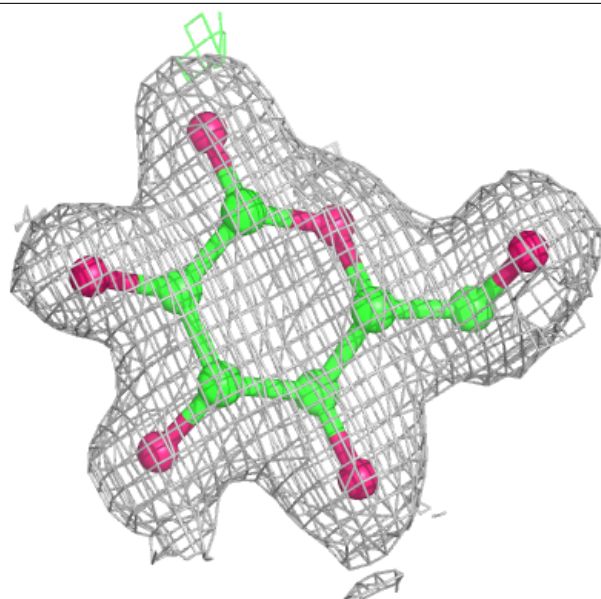
Electron density around BGC B 901:

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



Electron density around BGC A 901:

$2mF_o-DF_c$ (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.