Full wwPDB X-ray Structure Validation Report ⓘ

Jan 7, 2024 – 02:26 am GMT

PDB ID	:	5O9R
Title	:	Crystal structure of ScGas2 in complex with compound 9
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Deposited on	:	2017-06-20
Resolution	:	1.70 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:

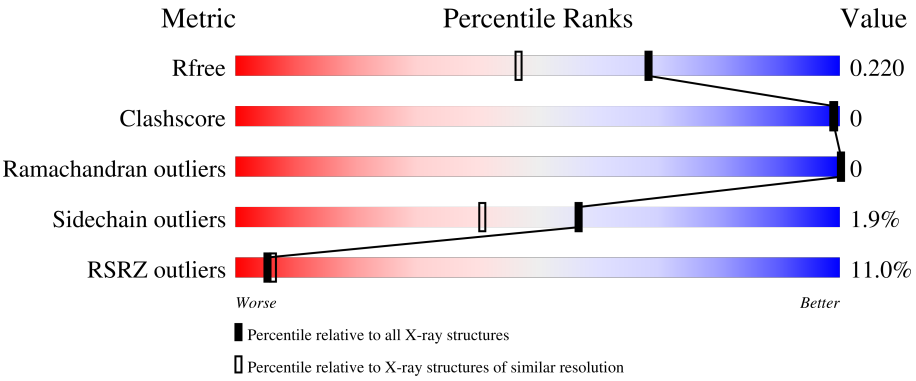
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	555	8%, 75%, 23%
2	B	3	33%, 67%

2 Entry composition (i)

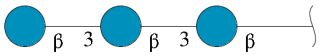
There are 6 unique types of molecules in this entry. The entry contains 3872 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1,3-beta-glucanosyltransferase GAS2.

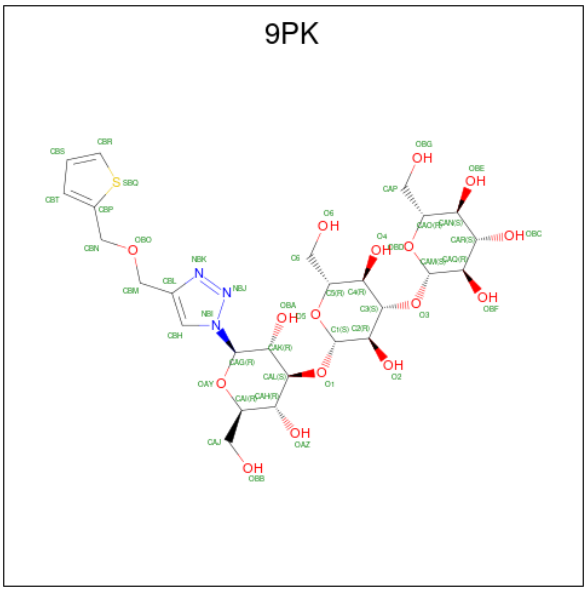
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	429	3418	2179	551	665	23	11	0	0

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose.



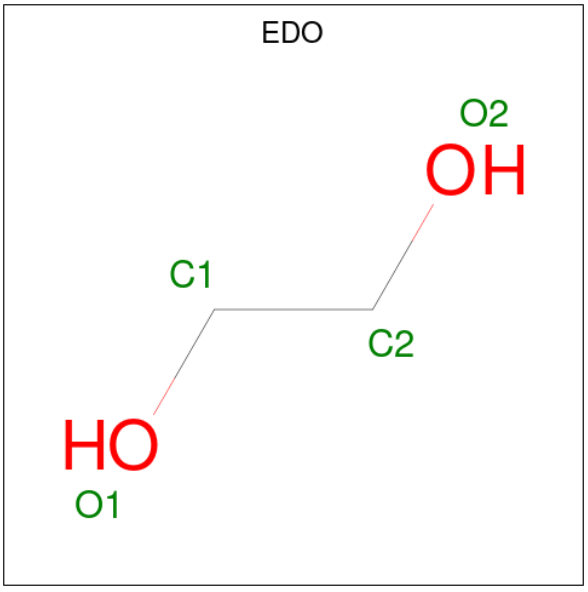
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	O				
2	B	3	34	18	16		0	0	0

- Molecule 3 is (2 {R},3 {S},4 {S},5 {R},6 {S})-2-(hydroxymethyl)-6-[(2 {R},3 {R},4 {S},5 {R},6 {S})-2-(hydroxymethyl)-6-[(2 {R},3 {R},4 {S},5 {R},6 {R})-2-(hydroxymethyl)-3,5-bis(oxidanyl)-6-[4-(thiophen-2-ylmethoxymethyl)-1,2,3-triazol-1-yl]oxan-4-yl]oxy-3,5-bis(oxidanyl)oxan-4-yl]oxy-oxane-3,4,5-triol (three-letter code: 9PK) (formula: $C_{26}H_{39}N_3O_{16}S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			46	26	3	16	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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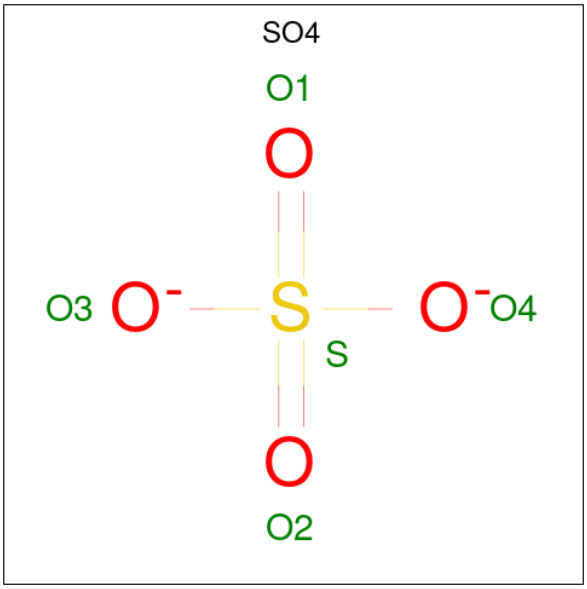
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0

- Molecule 6 is water.

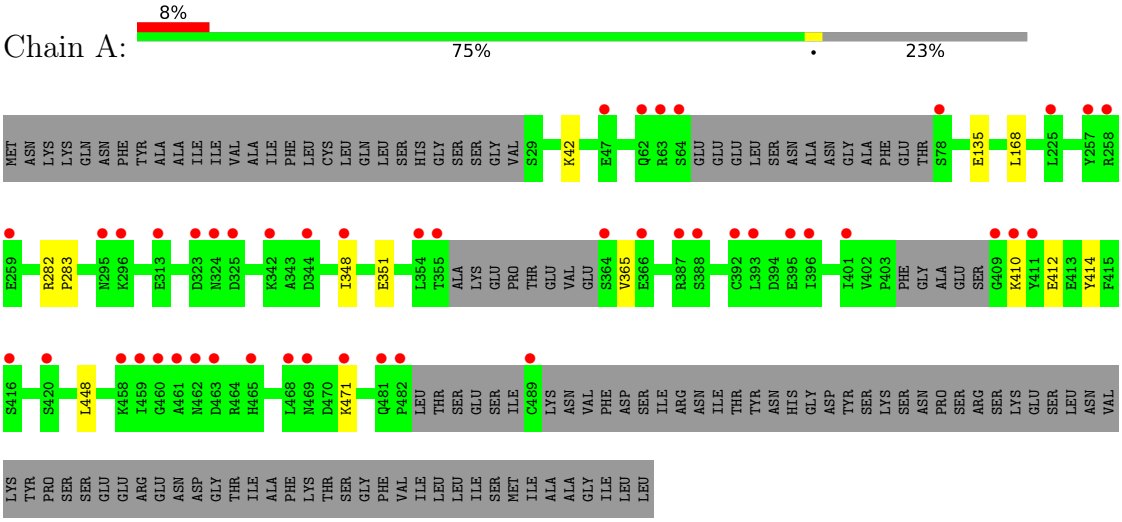
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	328	Total O 328 328	0	0

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: 1,3-beta-glucanosyltransferase GAS2

Chain A:



• Molecule 2: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	50.20Å 71.20Å 150.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	150.44 – 1.70 19.79 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (150.44-1.70) 99.6 (19.79-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.42 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.195 , 0.212 0.204 , 0.220	Depositor DCC
R_{free} test set	1832 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å^2)	22.0	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 46.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3872	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BGC, 9PK, EDO, SO4

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	0.49	2/3500 (0.1%)	0.69	4/4733 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	414	TYR	CB-CG	15.24	1.74	1.51
1	A	412	GLU	CB-CG	13.14	1.77	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	414	TYR	CB-CG-CD1	17.64	131.58	121.00
1	A	414	TYR	CB-CG-CD2	-17.47	110.52	121.00
1	A	414	TYR	CA-CB-CG	-8.14	97.94	113.40
1	A	412	GLU	CA-CB-CG	-5.12	102.13	113.40

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	3418	0	3257	2	0
2	B	34	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	46	0	0	0	0
4	A	36	0	54	0	0
5	A	10	0	0	0	0
6	A	328	0	0	0	0
All	All	3872	0	3341	2	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 0.

All (2) 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:42:LYS:HE3	1:A:348:ILE:HD11	1.97	0.47
1:A:282:ARG:HA	1:A:283:PRO:C	2.39	0.43

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	420/555 (76%)	412 (98%)	8 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	377/485 (78%)	370 (98%)	7 (2%)	57 41

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	GLU
1	A	168	LEU
1	A	351	GLU
1	A	365	VAL
1	A	410	LYS
1	A	448	LEU
1	A	471	LYS

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)

3 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	$\#\|Z\| > 2$
2	BGC	B	1	2	12,12,12	0.58	0	17,17,17	1.69	5 (29%)
2	BGC	B	2	2	11,11,12	0.43	0	15,15,17	1.35	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	BGC	B	3	2	11,11,12	0.30	0	15,15,17	0.85	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
2	BGC	B	1	2	-	0/2/22/22	0/1/1/1
2	BGC	B	2	2	-	0/2/19/22	0/1/1/1
2	BGC	B	3	2	-	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})
2	B	1	BGC	O3-C3-C2	4.05	119.72	110.35
2	B	2	BGC	C1-C2-C3	4.02	114.60	109.67
2	B	1	BGC	O3-C3-C4	2.58	116.30	110.35
2	B	1	BGC	C4-C3-C2	-2.47	106.52	110.82
2	B	1	BGC	C1-C2-C3	-2.31	105.53	110.31
2	B	1	BGC	C3-C4-C5	-2.19	106.34	110.24

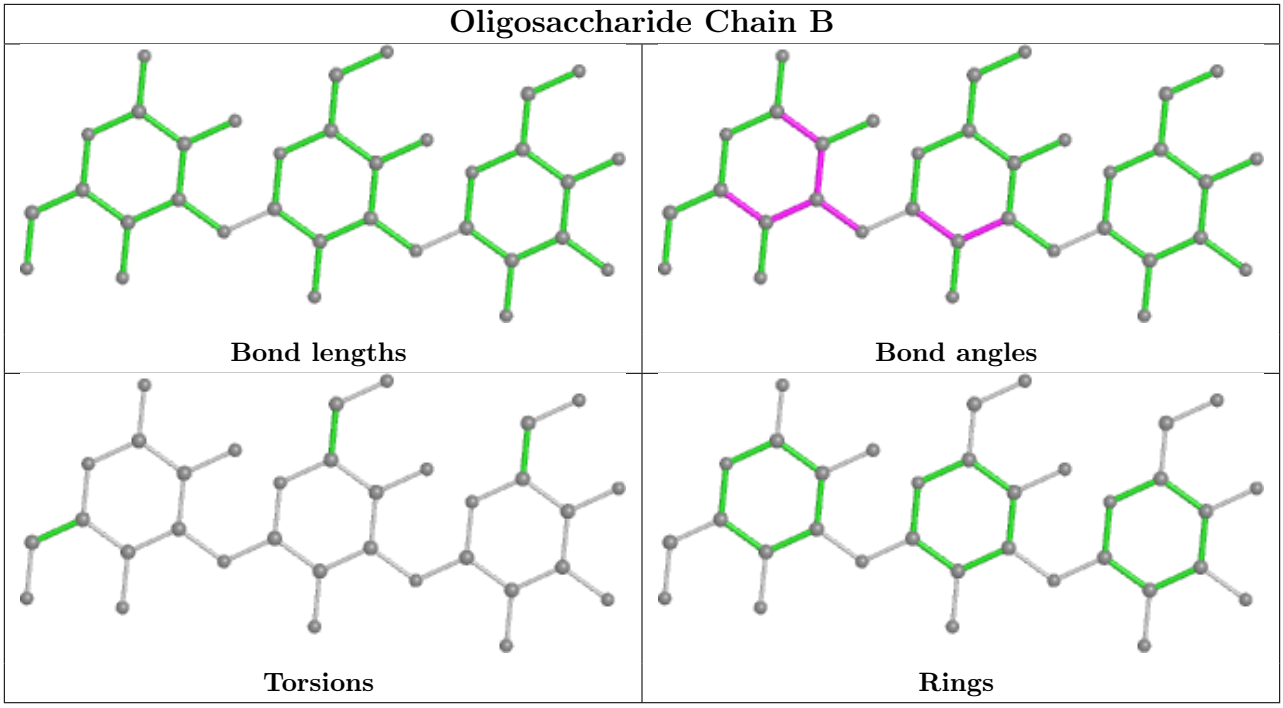
There are no chirality outliers.

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.



5.6 Ligand geometry (i)

12 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	$\#\|Z\| > 2$
4	EDO	A	613	-	3,3,3	0.36	0	2,2,2	0.36	0
4	EDO	A	609	-	3,3,3	0.48	0	2,2,2	0.25	0
5	SO4	A	614	-	4,4,4	0.32	0	6,6,6	0.07	0
5	SO4	A	615	-	4,4,4	0.33	0	6,6,6	0.06	0
4	EDO	A	607	-	3,3,3	0.45	0	2,2,2	0.28	0
4	EDO	A	608	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	A	612	-	3,3,3	0.45	0	2,2,2	0.16	0
3	9PK	A	604	-	48,50,50	1.62	6 (12%)	57,72,72	1.45	6 (10%)
4	EDO	A	606	-	3,3,3	0.48	0	2,2,2	0.26	0
4	EDO	A	611	-	3,3,3	0.46	0	2,2,2	0.24	0
4	EDO	A	605	-	3,3,3	0.49	0	2,2,2	0.19	0
4	EDO	A	610	-	3,3,3	0.45	0	2,2,2	0.34	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
4	EDO	A	613	-	-	0/1/1/1	-
4	EDO	A	609	-	-	1/1/1/1	-
4	EDO	A	607	-	-	0/1/1/1	-
4	EDO	A	608	-	-	0/1/1/1	-
4	EDO	A	612	-	-	1/1/1/1	-
3	9PK	A	604	-	-	6/16/84/84	0/5/5/5
4	EDO	A	606	-	-	1/1/1/1	-
4	EDO	A	611	-	-	1/1/1/1	-
4	EDO	A	605	-	-	1/1/1/1	-
4	EDO	A	610	-	-	0/1/1/1	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	604	9PK	NBK-NBJ	-6.41	1.22	1.34
3	A	604	9PK	CBP-SBQ	-5.62	1.62	1.73
3	A	604	9PK	NBJ-NBI	-4.66	1.26	1.34
3	A	604	9PK	CBH-CBL	-2.59	1.32	1.36
3	A	604	9PK	CBN-CBP	2.58	1.53	1.50
3	A	604	9PK	CBH-NBI	-2.23	1.33	1.35

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	604	9PK	CBS-CBR-SBQ	-7.32	107.04	112.98
3	A	604	9PK	CAM-O3-C3	-3.42	109.50	117.96
3	A	604	9PK	C1-O1-CAL	-3.40	109.55	117.96
3	A	604	9PK	CBL-CBH-NBI	-2.48	103.52	107.35
3	A	604	9PK	CAM-OBD-CAO	-2.14	109.48	113.69
3	A	604	9PK	C1-O5-C5	-2.14	109.49	113.69

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	605	EDO	O1-C1-C2-O2
4	A	606	EDO	O1-C1-C2-O2

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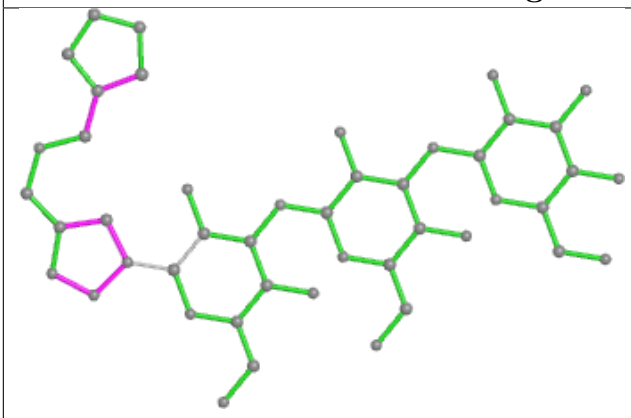
Mol	Chain	Res	Type	Atoms
4	A	611	EDO	O1-C1-C2-O2
4	A	609	EDO	O1-C1-C2-O2
3	A	604	9PK	C2-C1-O1-CAL
3	A	604	9PK	O5-C1-O1-CAL
3	A	604	9PK	OAY-CAI-CAJ-OBB
3	A	604	9PK	CAH-CAI-CAJ-OBB
4	A	612	EDO	O1-C1-C2-O2
3	A	604	9PK	CAQ-CAM-O3-C3
3	A	604	9PK	OBD-CAM-O3-C3

There are no ring outliers.

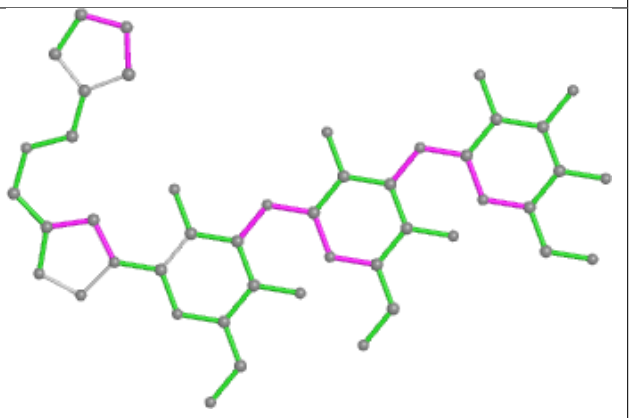
No monomer is involved in short contacts.

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

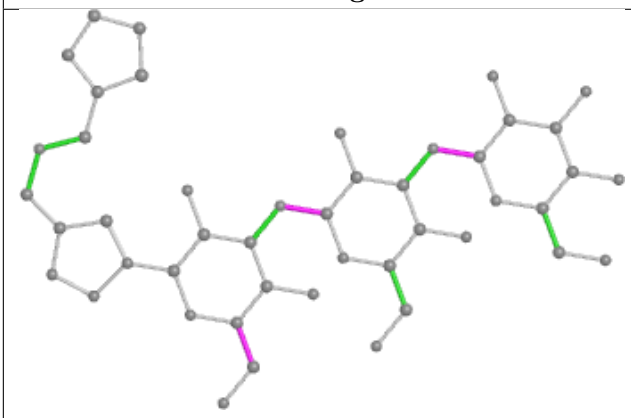
Ligand 9PK A 604



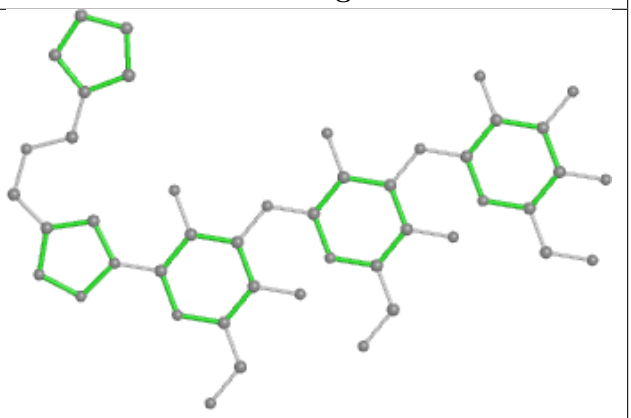
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	429/555 (77%)	0.60	47 (10%)	5 6	14, 23, 42, 53	6 (1%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	64	SER	9.5
1	A	489	CYS	6.9
1	A	482	PRO	6.0
1	A	323	ASP	5.2
1	A	355	THR	5.0
1	A	460	GLY	4.8
1	A	462	ASN	4.4
1	A	63	ARG	4.4
1	A	324	ASN	4.3
1	A	364	SER	4.3
1	A	313	GLU	3.9
1	A	461	ALA	3.9
1	A	295	ASN	3.7
1	A	62	GLN	3.7
1	A	344	ASP	3.6
1	A	387	ARG	3.4
1	A	465	HIS	3.4
1	A	410	LYS	3.2
1	A	409	GLY	3.2
1	A	354	LEU	3.1
1	A	481	GLN	2.8
1	A	396	ILE	2.6
1	A	257	TYR	2.6
1	A	47	GLU	2.6
1	A	395	GLU	2.6
1	A	458	LYS	2.5
1	A	366	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	259	GLU	2.5
1	A	342	LYS	2.5
1	A	348	ILE	2.4
1	A	459	ILE	2.4
1	A	258	ARG	2.4
1	A	392	CYS	2.3
1	A	416	SER	2.3
1	A	463	ASP	2.3
1	A	78	SER	2.3
1	A	225	LEU	2.1
1	A	468	LEU	2.1
1	A	325	ASP	2.1
1	A	401	ILE	2.1
1	A	420	SER	2.1
1	A	471	LYS	2.1
1	A	296	LYS	2.0
1	A	411	TYR	2.0
1	A	388	SER	2.0
1	A	393	LEU	2.0
1	A	469	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)

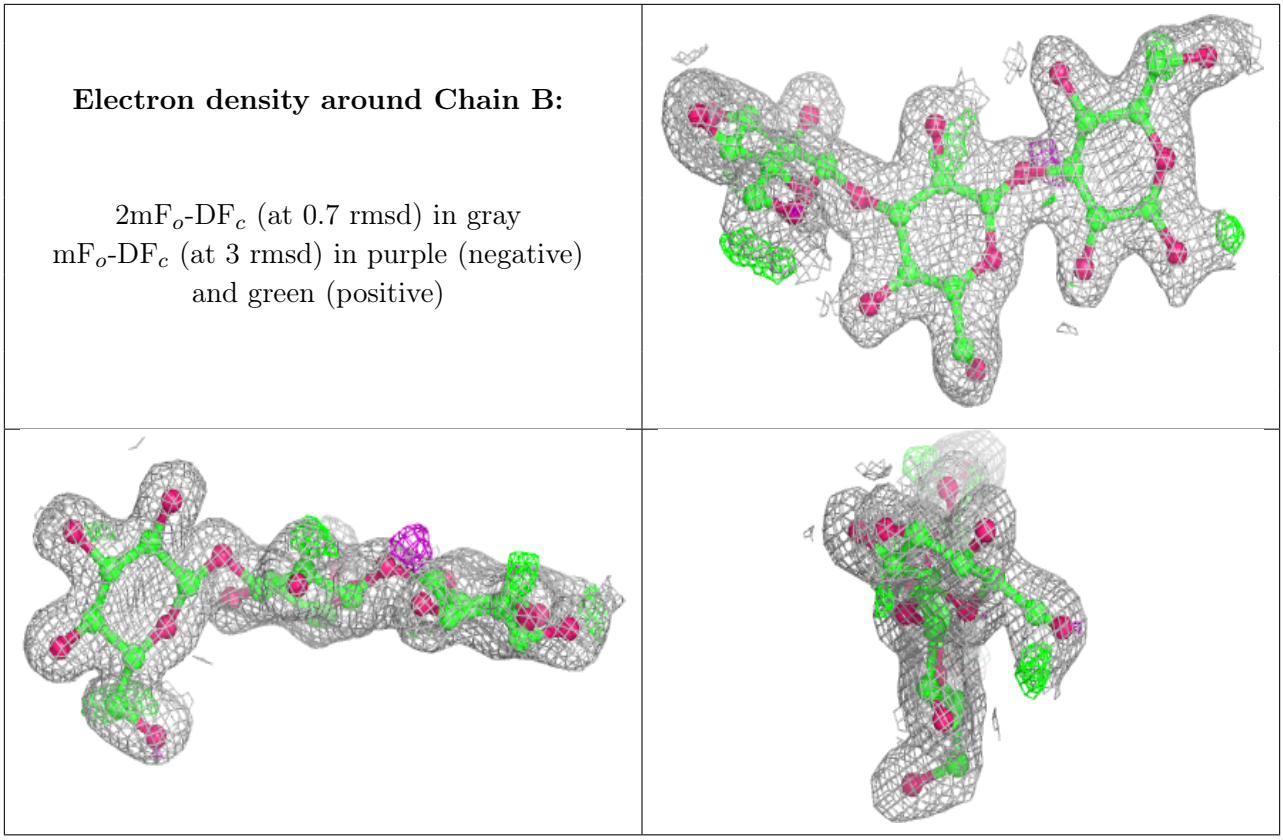
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	BGC	B	1	12/12	0.86	0.22	31,34,35,35	0
2	BGC	B	3	11/12	0.89	0.18	25,26,27,28	0
2	BGC	B	2	11/12	0.93	0.13	27,29,30,30	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 B:

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



6.4 Ligands

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, 95^{th} 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.

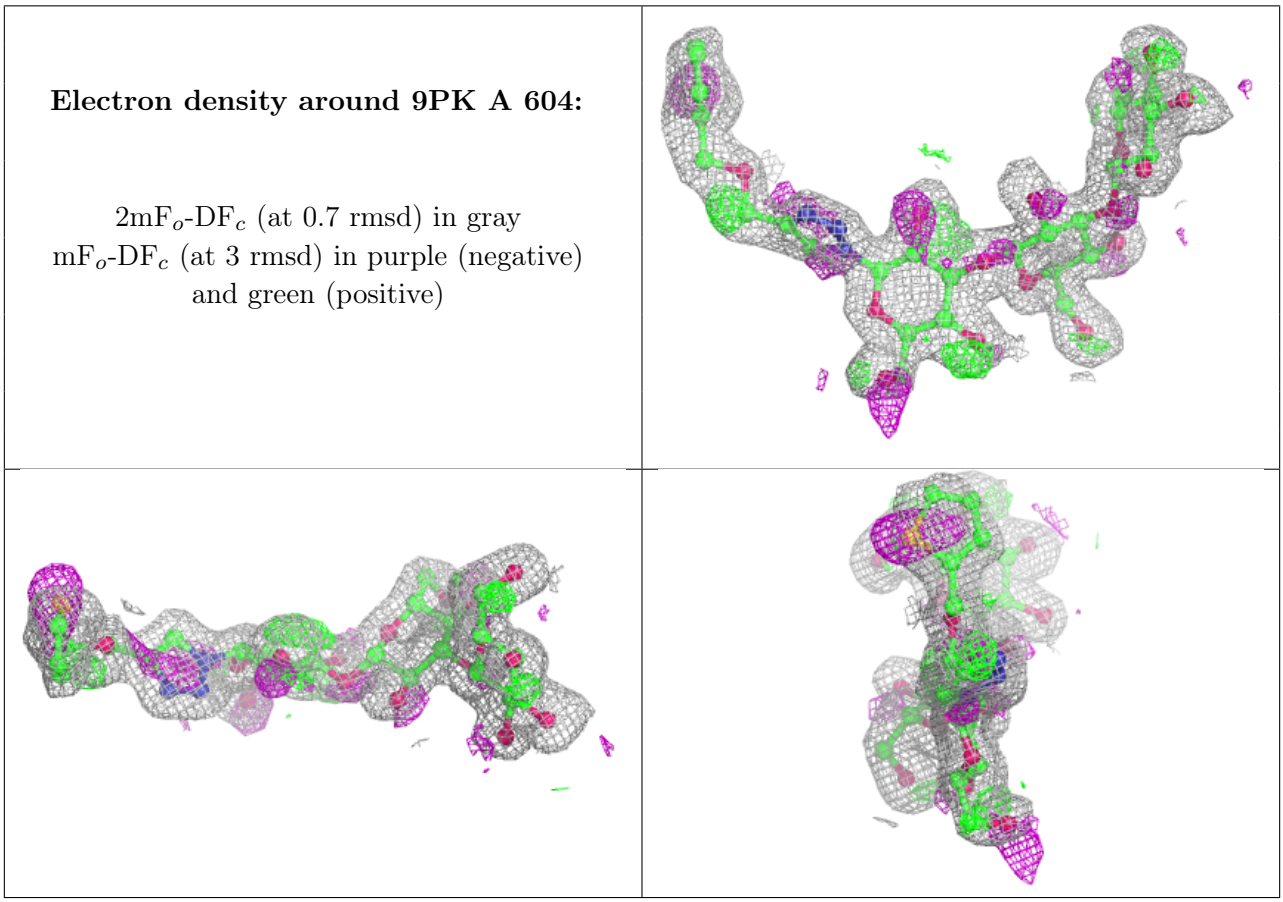
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	EDO	A	609	4/4	0.42	0.30	50,51,52,52	0
4	EDO	A	605	4/4	0.54	0.24	49,50,50,50	0
4	EDO	A	606	4/4	0.66	0.31	43,44,44,45	0
4	EDO	A	611	4/4	0.74	0.34	35,36,36,37	0
3	9PK	A	604	46/46	0.77	0.18	21,24,37,40	0
4	EDO	A	613	4/4	0.79	0.34	29,30,30,32	0
4	EDO	A	612	4/4	0.82	0.16	30,31,31,31	0
4	EDO	A	610	4/4	0.82	0.20	42,42,42,42	0
4	EDO	A	607	4/4	0.83	0.32	54,55,55,55	0
4	EDO	A	608	4/4	0.86	0.37	43,43,43,43	0
5	SO4	A	615	5/5	0.95	0.33	68,68,69,69	0
5	SO4	A	614	5/5	0.96	0.24	58,59,59,59	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 9PK A 604:

$2mF_o$-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.