wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2020 – 09:22 PM BST

PDB ID	:	4IT0
Title	:	Structure of the RNA ligase RtcB-GMP/Mn(II) complex
Authors	:	Desai, K.K.; Bingman, C.A.; Phillips Jr., G.N.; Raines, R.T.
Deposited on	:	2013-01-17
Resolution	:	2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references (i)) were used in the production of this report:

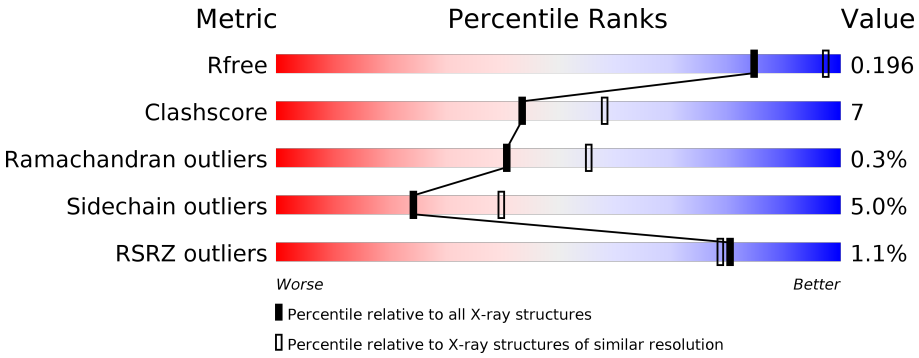
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 on 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	481	% 83% 15% .
1	B	481	% 87% 12% .
2	C	2	50% 50%
2	D	2	50% 50%

2 Entry composition

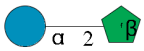
There are 6 unique types of molecules in this entry. The entry contains 15871 atoms, of which 7634 are hydrogens and 0 are deuteriums.

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 tRNA-splicing ligase RtcB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	480	Total	C	H	N	O	S	0	0	0
			7548	2370	3789	693	680	16			
1	B	480	Total	C	H	N	O	S	0	0	0
			7549	2370	3790	693	680	16			

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

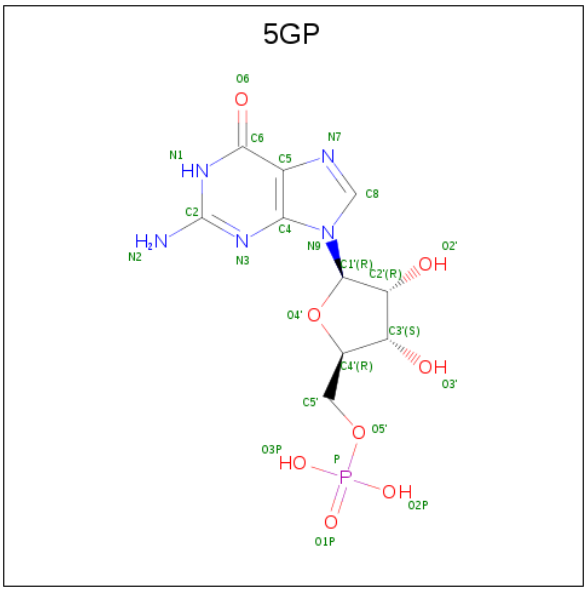


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	H	O	0	0	0
			45	12	22	11			
2	D	2	Total	C	H	O	0	0	0
			44	12	21	11			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

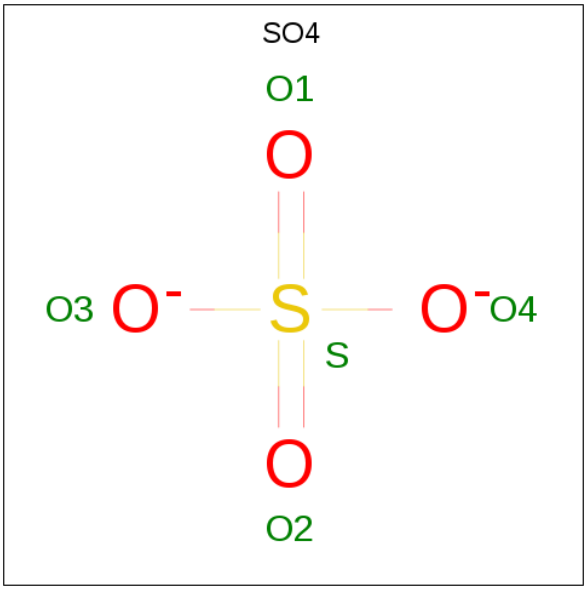
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mn	0	0
			2	2		
3	A	2	Total	Mn	0	0
			2	2		

- Molecule 4 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	P	0	0
			35	10	12	5	7	1		

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



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

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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
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0

- Molecule 6 is water.

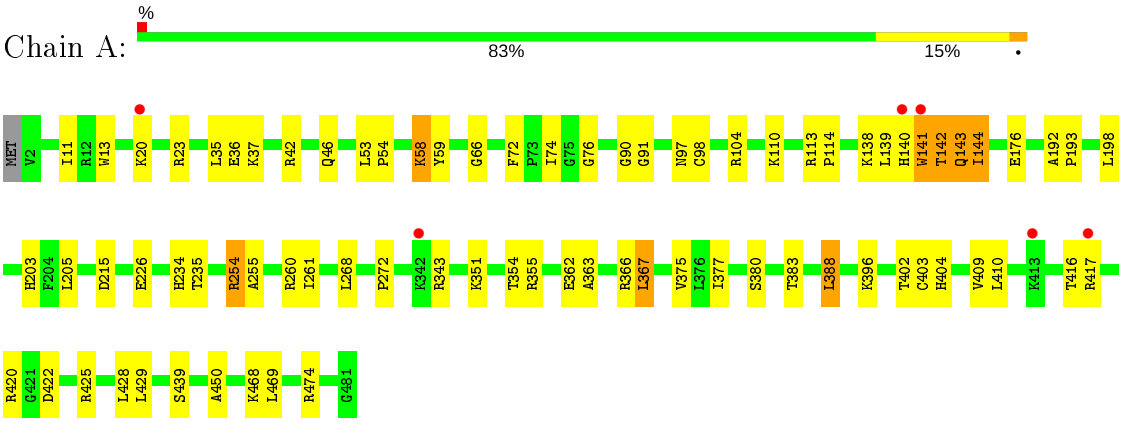
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	265	Total O 265 265	0	0
6	B	286	Total O 286 286	0	0

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.

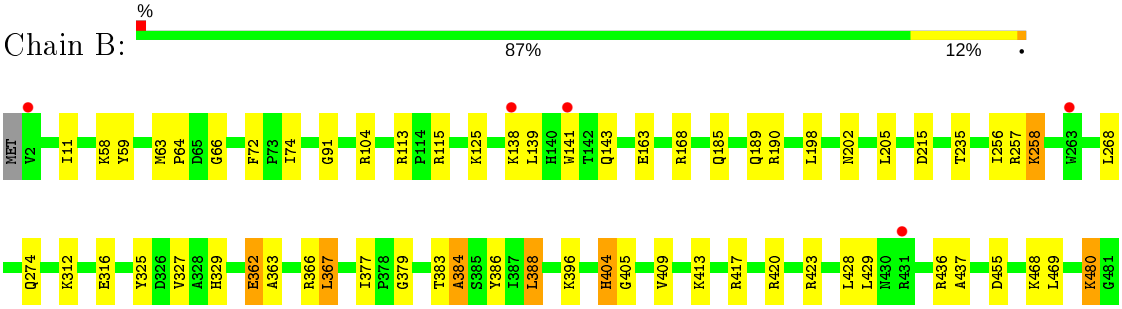
- Molecule 1: tRNA-splicing ligase RtcB

Chain A:



- Molecule 1: tRNA-splicing ligase RtcB

Chain B:



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain C:

- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.11Å 138.91Å 149.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.75 – 2.40 49.75 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.75-2.40) 94.5 (49.75-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.35 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.152 , 0.192 0.156 , 0.196	Depositor DCC
R_{free} test set	2024 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å^2)	35.3	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 49.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	15871	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: GLC, MN, SO4, FRU, 5GP

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	0.64	2/3836 (0.1%)	0.73	2/5175 (0.0%)
1	B	0.64	0/3836	0.72	1/5175 (0.0%)
All	All	0.64	2/7672 (0.0%)	0.72	3/10350 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	CYS	CB-SG	-5.87	1.72	1.81
1	A	36	GLU	CG-CD	5.29	1.59	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	367	LEU	CA-CB-CG	5.87	128.81	115.30
1	A	23	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	A	205	LEU	CB-CG-CD2	-5.00	102.49	111.00

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	3759	3789	3782	59	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3759	3790	3782	45	0
2	C	23	22	21	0	0
2	D	23	21	21	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	23	12	11	4	0
5	A	45	0	0	3	0
5	B	50	0	0	2	0
6	A	265	0	0	12	0
6	B	286	0	0	16	2
All	All	8237	7634	7617	102	2

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 7.

The worst 5 of 102 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:404:HIS:NE2	4:A:503:5GP:P	2.07	1.26
1:A:139:LEU:HA	1:A:143:GLN:OE1	1.80	0.82
5:B:508:SO4:O1	6:B:606:HOH:O	1.97	0.81
1:A:254:ARG:HG2	1:A:255:ALA:N	2.03	0.74
1:B:143:GLN:O	6:B:806:HOH:O	2.06	0.73

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ARG:NH1	6:B:768:HOH:O[1_455]	1.94	0.26
1:A:260:ARG:HH12	6:B:768:HOH:O[1_455]	1.42	0.18

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	478/481 (99%)	462 (97%)	14 (3%)	2 (0%)	34	48
1	B	478/481 (99%)	463 (97%)	14 (3%)	1 (0%)	47	62
All	All	956/962 (99%)	925 (97%)	28 (3%)	3 (0%)	41	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	384	ALA
1	A	141	TRP
1	A	58	LYS

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	389/390 (100%)	370 (95%)	19 (5%)	25	40
1	B	389/390 (100%)	369 (95%)	20 (5%)	24	39
All	All	778/780 (100%)	739 (95%)	39 (5%)	24	40

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	439	SER
1	B	104	ARG
1	B	428	LEU
1	A	474	ARG
1	B	11	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

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	$\#\|Z\| > 2$
2	GLC	C	1	2	11,11,12	0.62	0	15,15,17	1.11	2 (13%)
2	FRU	C	2	2	11,12,12	0.85	0	10,18,18	0.82	0
2	GLC	D	1	2	11,11,12	0.63	0	15,15,17	1.90	5 (33%)
2	FRU	D	2	2	11,12,12	0.78	0	10,18,18	1.11	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	GLC	C	1	2	-	0/2/19/22	0/1/1/1
2	FRU	C	2	2	-	0/5/24/24	0/1/1/1
2	GLC	D	1	2	-	2/2/19/22	0/1/1/1
2	FRU	D	2	2	-	3/5/24/24	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1	GLC	C1-O5-C5	4.36	118.11	112.19
2	D	1	GLC	O2-C2-C3	3.20	116.56	110.14
2	C	1	GLC	O5-C5-C6	2.66	111.37	107.20
2	D	1	GLC	O3-C3-C2	2.53	114.83	109.99
2	D	1	GLC	C2-C3-C4	-2.19	107.10	110.89

There are no chirality outliers.

All (5) torsion outliers are listed below:

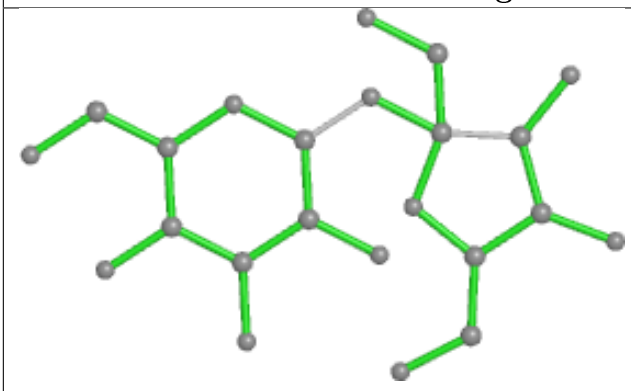
Mol	Chain	Res	Type	Atoms
2	D	1	GLC	O5-C5-C6-O6
2	D	1	GLC	C4-C5-C6-O6
2	D	2	FRU	O1-C1-C2-O2
2	D	2	FRU	O1-C1-C2-O5
2	D	2	FRU	O1-C1-C2-C3

There are no ring outliers.

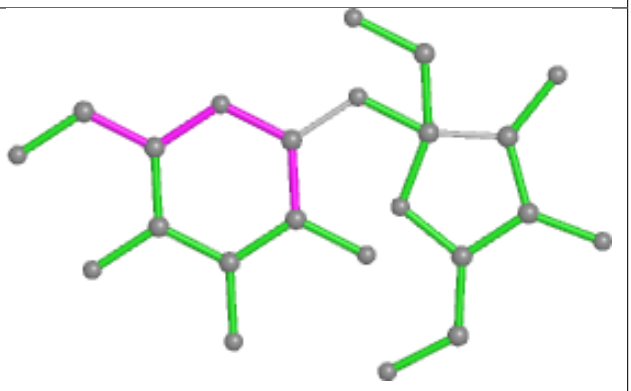
No monomer is involved in short contacts.

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

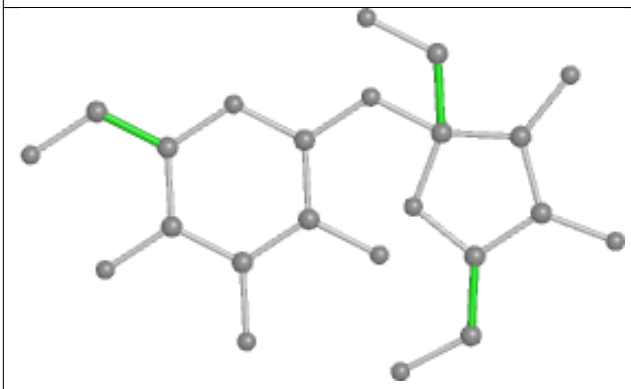
Oligosaccharide Chain C



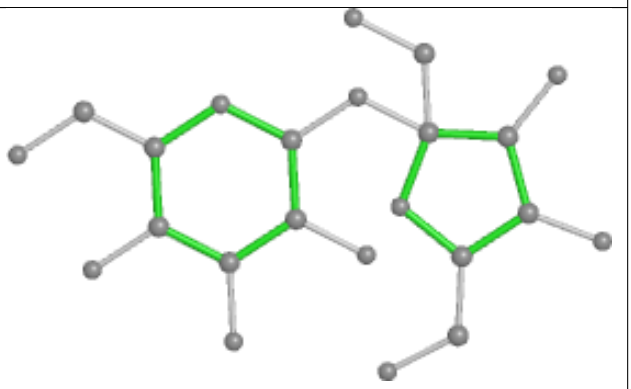
Bond lengths



Bond angles

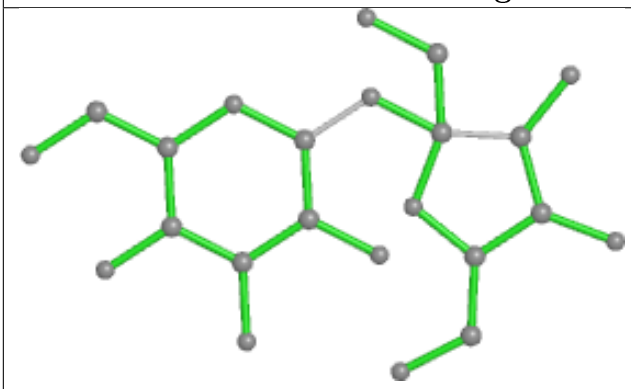


Torsions

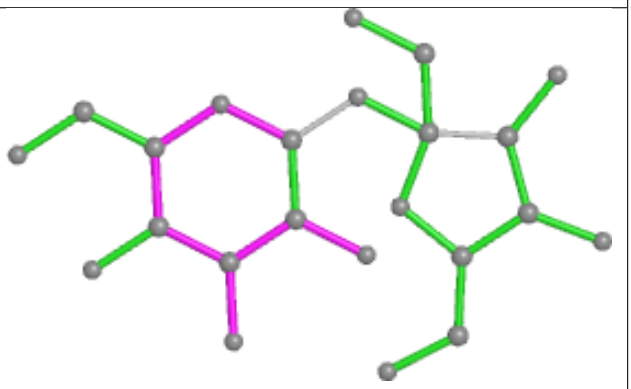


Rings

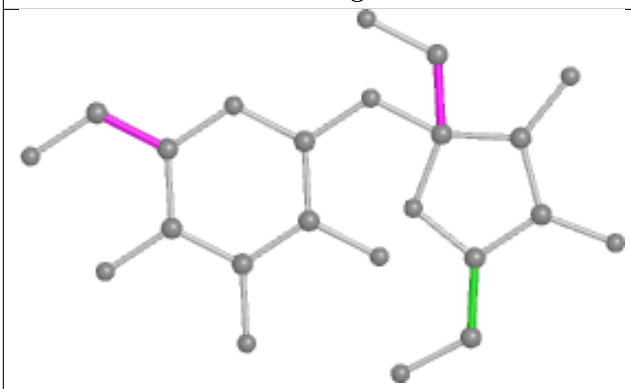
Oligosaccharide Chain D



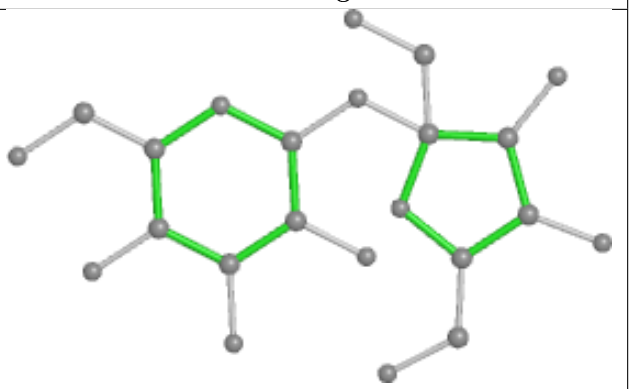
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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	$\#\|Z\| > 2$
5	SO4	A	504	-	4,4,4	0.08	0	6,6,6	0.71	0
5	SO4	B	510	-	4,4,4	0.31	0	6,6,6	1.16	1 (16%)
5	SO4	A	512	-	4,4,4	0.12	0	6,6,6	0.81	0
5	SO4	A	508	-	4,4,4	0.27	0	6,6,6	0.40	0
5	SO4	B	508	-	4,4,4	0.21	0	6,6,6	0.57	0
5	SO4	B	512	-	4,4,4	0.28	0	6,6,6	0.41	0
5	SO4	A	505	-	4,4,4	0.12	0	6,6,6	0.56	0
5	SO4	A	511	-	4,4,4	0.30	0	6,6,6	0.50	0
5	SO4	A	510	-	4,4,4	0.25	0	6,6,6	0.50	0
5	SO4	A	506	-	4,4,4	0.21	0	6,6,6	0.27	0
4	5GP	A	503	3	18,25,26	0.66	0	20,37,40	2.12	8 (40%)
5	SO4	B	504	-	4,4,4	0.21	0	6,6,6	0.34	0
5	SO4	A	507	-	4,4,4	0.21	0	6,6,6	0.35	0
5	SO4	B	503	-	4,4,4	0.22	0	6,6,6	0.61	0
5	SO4	B	506	-	4,4,4	0.19	0	6,6,6	0.40	0
5	SO4	A	509	-	4,4,4	0.18	0	6,6,6	0.15	0
5	SO4	B	507	-	4,4,4	0.40	0	6,6,6	1.50	1 (16%)
5	SO4	B	505	-	4,4,4	0.18	0	6,6,6	0.29	0
5	SO4	B	509	-	4,4,4	0.06	0	6,6,6	0.25	0
5	SO4	B	511	-	4,4,4	0.11	0	6,6,6	0.60	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	5GP	A	503	3	-	2/3/25/26	0/3/3/3

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	503	5GP	N3-C2-N1	-4.64	121.03	127.22
4	A	503	5GP	C6-N1-C2	3.91	122.14	115.93
4	A	503	5GP	C5-C6-N1	-3.37	118.82	123.43
5	B	507	SO4	O4-S-O3	-3.07	95.95	109.06
4	A	503	5GP	C1'-N9-C4	-2.83	121.66	126.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	5GP	O4'-C4'-C5'-O5'
4	A	503	5GP	C3'-C4'-C5'-O5'

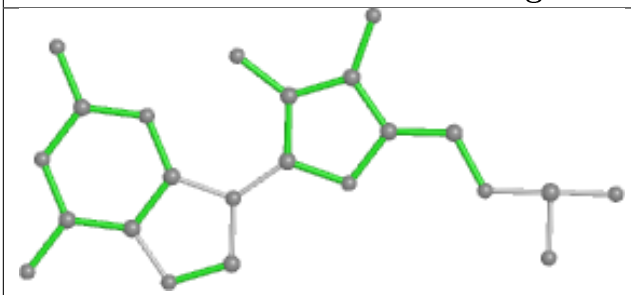
There are no ring outliers.

6 monomers are involved in 9 short contacts:

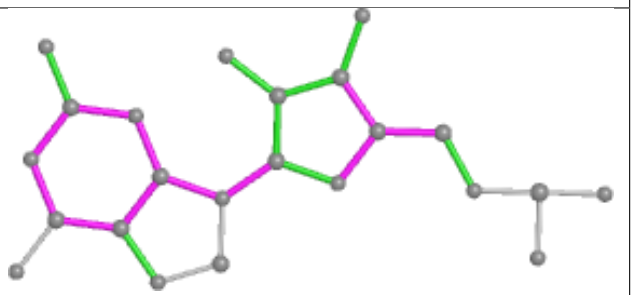
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	508	SO4	1	0
5	A	511	SO4	1	0
5	A	510	SO4	1	0
4	A	503	5GP	4	0
5	A	509	SO4	1	0
5	B	509	SO4	1	0

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.

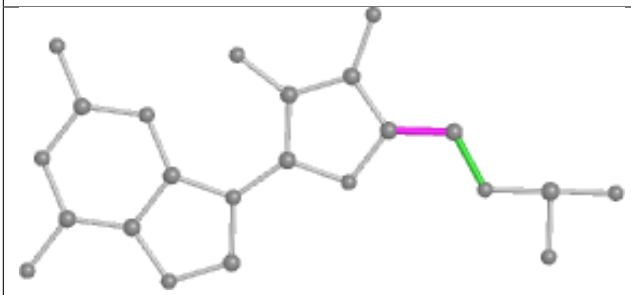
Ligand 5GP A 503



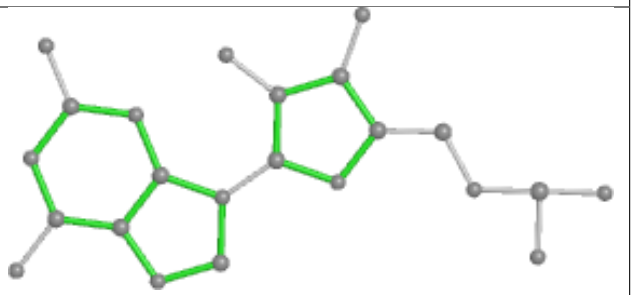
Bond lengths



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	480/481 (99%)	-0.45	6 (1%)	77	75	20, 30, 57, 91	0
1	B	480/481 (99%)	-0.44	5 (1%)	82	80	21, 30, 58, 82	0
All	All	960/962 (99%)	-0.44	11 (1%)	80	79	20, 30, 58, 91	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	HIS	3.7
1	A	141	TRP	3.4
1	B	263	TRP	2.9
1	A	417	ARG	2.9
1	A	342	LYS	2.3

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

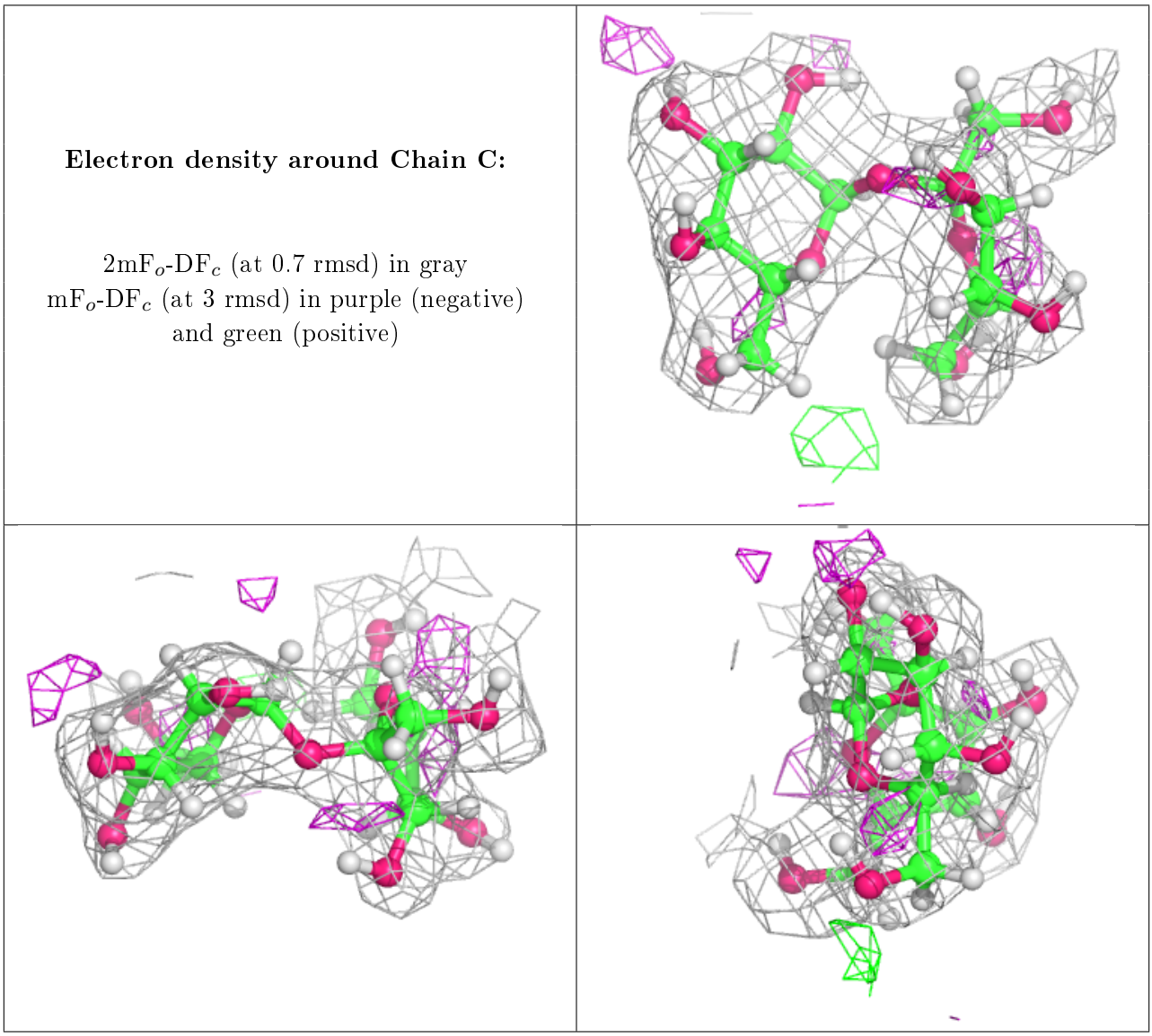
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	FRU	D	2	12/12	0.89	0.29	43,56,68,76	0
2	GLC	D	1	11/12	0.90	0.34	47,63,73,77	0
2	GLC	C	1	11/12	0.94	0.26	44,60,72,78	0
2	FRU	C	2	12/12	0.94	0.28	34,53,65,69	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.

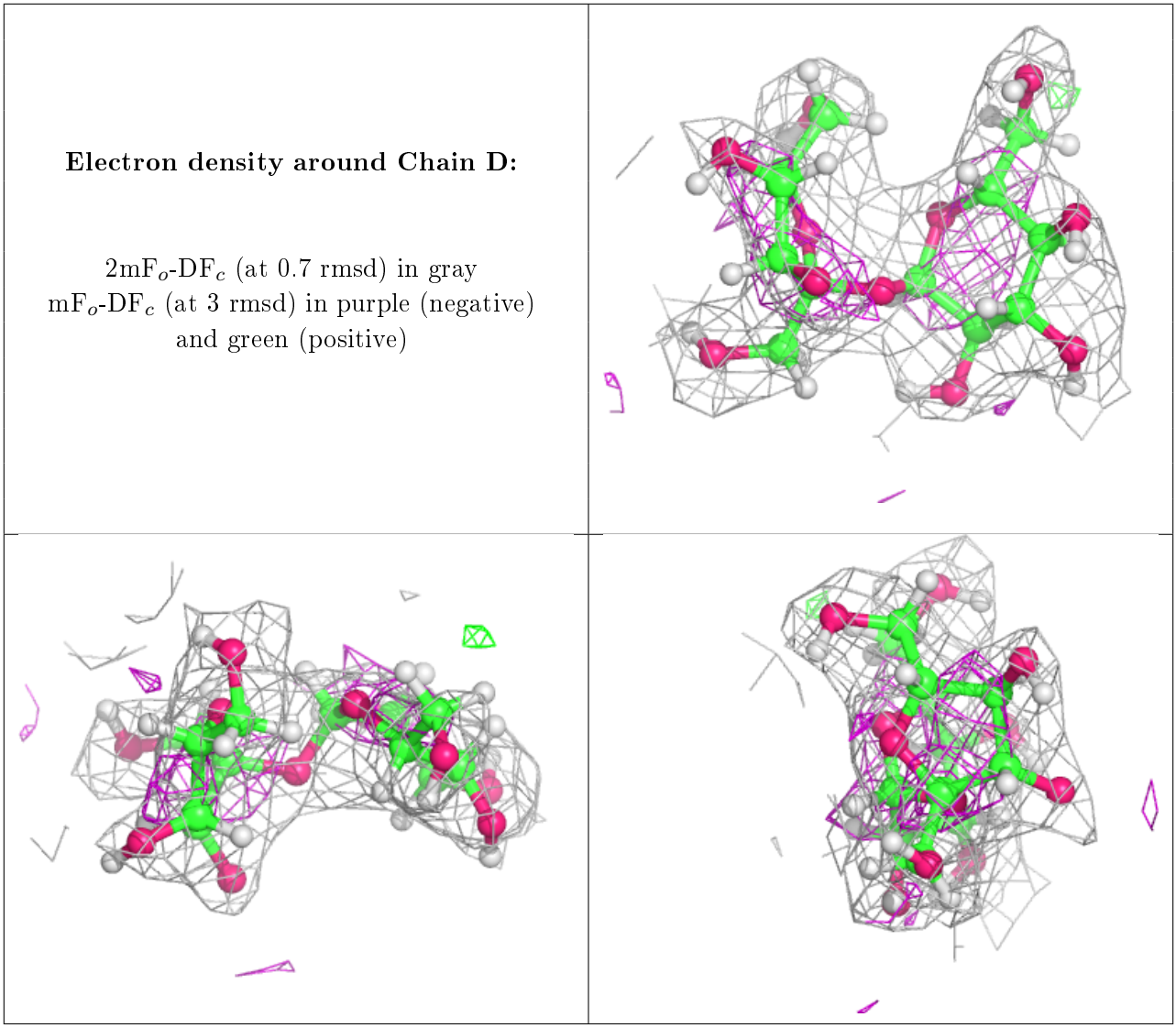
Electron density around Chain C:

$2mF_o$-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 D:

$2mF_o$-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
5	SO4	B	510	5/5	0.77	0.30	40,43,58,62	5
5	SO4	B	512	5/5	0.84	0.20	42,42,48,79	5
5	SO4	B	511	5/5	0.90	0.31	38,43,49,69	5
5	SO4	B	509	5/5	0.91	0.18	47,48,56,66	5
3	MN	A	502	1/1	0.93	0.29	51,51,51,51	1
5	SO4	A	507	5/5	0.93	0.19	69,69,71,83	0
4	5GP	A	503	23/24	0.93	0.22	37,45,51,60	35

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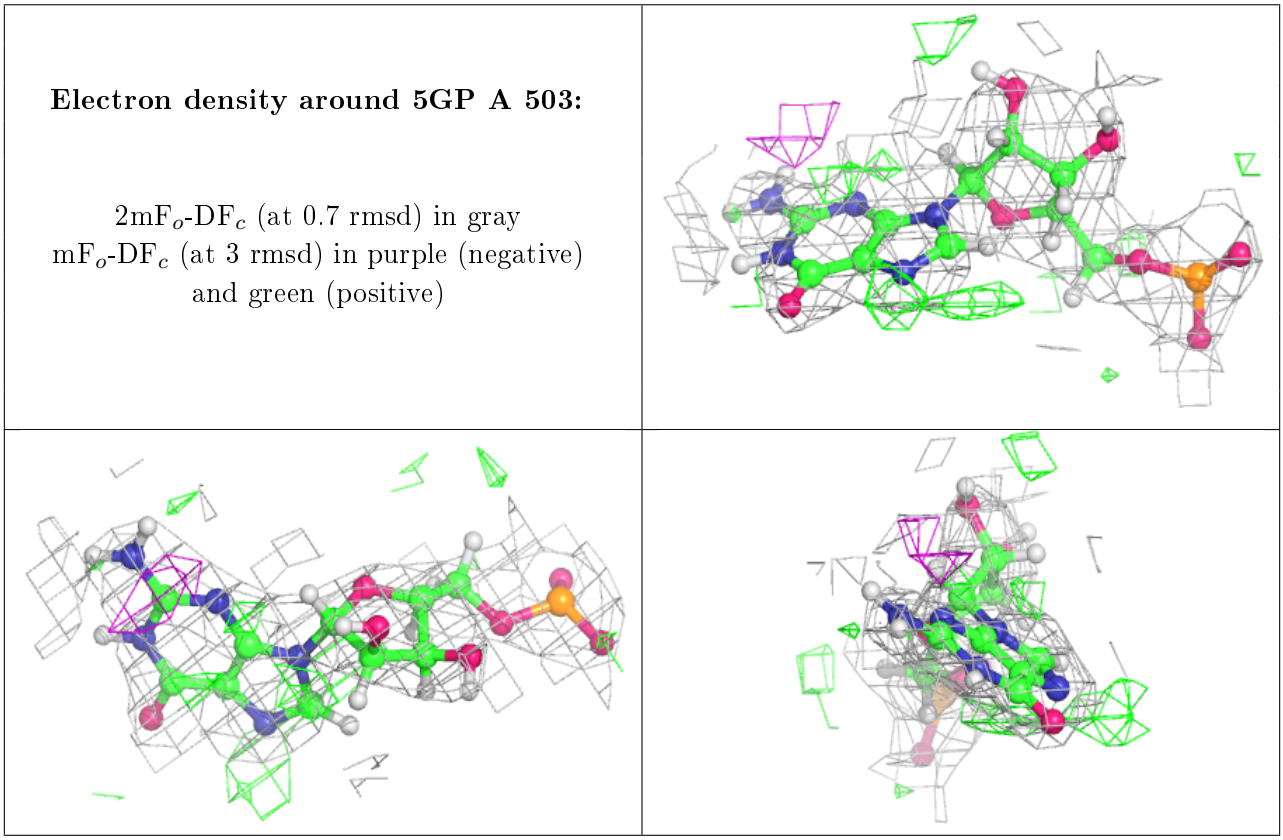
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	SO4	A	511	5/5	0.93	0.31	35,44,54,55	5
5	SO4	B	504	5/5	0.94	0.25	60,64,72,85	0
5	SO4	A	509	5/5	0.94	0.37	50,52,57,63	5
5	SO4	B	508	5/5	0.94	0.15	37,49,55,70	5
3	MN	B	502	1/1	0.94	0.25	48,48,48,48	1
5	SO4	A	506	5/5	0.94	0.22	55,59,77,84	0
5	SO4	B	505	5/5	0.95	0.27	60,69,76,85	0
5	SO4	B	507	5/5	0.95	0.17	25,42,62,69	0
5	SO4	A	510	5/5	0.95	0.13	40,49,51,51	5
5	SO4	A	508	5/5	0.95	0.10	39,42,58,59	5
5	SO4	B	506	5/5	0.97	0.10	53,62,68,70	0
5	SO4	A	512	5/5	0.98	0.18	38,41,47,49	5
5	SO4	B	503	5/5	0.99	0.20	33,40,47,49	0
5	SO4	A	505	5/5	0.99	0.15	27,32,46,54	0
5	SO4	A	504	5/5	0.99	0.11	26,38,41,49	0
3	MN	A	501	1/1	0.99	0.14	41,41,41,41	1
3	MN	B	501	1/1	0.99	0.18	53,53,53,53	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 5GP 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)



6.5 Other polymers (i)

There are no such residues in this entry.