

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 30, 2023 – 02:13 AM EDT

PDB ID : 3MRX

Title: Glycogen phosphorylase complexed with 4-methoxybenzaldehyde-4-(2,3,4,6-t

etra-O-acetyl-beta-D-glucopyranosyl)-thiosemicarbazone

Authors : Alexacou, K.-M.

Deposited on : 2010-04-29

Resolution : 1.95 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 (1)) 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

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

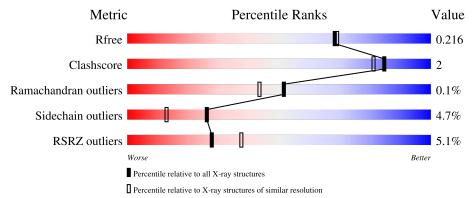
Validation Pipeline (wwPDB-VP) : 2.35

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.95 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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

Mol	Chain	Length	Quality of chain	
			5%	
1	A	842	88%	7% • •



## 2 Entry composition (i)

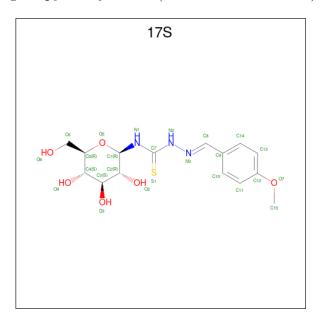
There are 3 unique types of molecules in this entry. The entry contains 7000 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycogen phosphorylase, muscle form.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	811	Total 6626	C 4223	N 1167	O 1206	P 1	S 29	0	3	0

• Molecule 2 is N-( $\{(2E)$ -2-[(4-methoxyphenyl)methylidene]hydrazino $\}$ carbonothioyl)-beta-D-glucopyranosylamine (three-letter code: 17S) (formula:  $C_{15}H_{21}N_3O_6S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	Λ	1	Total	С	N	О	S	0	0
2	Λ	1	25	15	3	6	1	0	
9	Λ	1	Total	С	N	О	S	0	0
	A	1	25	15	3	6	1	U	U

• Molecule 3 is water.

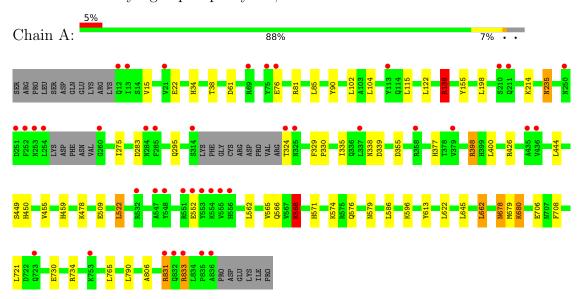
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	324	Total O 324 324	0	0



# 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: Glycogen phosphorylase, muscle form





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	128.31Å 128.31Å 116.05Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.11 - 1.95	Depositor
Resolution (A)	31.12 - 1.95	EDS
% Data completeness	97.4 (31.11-1.95)	Depositor
(in resolution range)	97.4 (31.12-1.95)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.15 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.2.0019, CNS	Depositor
D D.	0.182 , 0.216	Depositor
$R, R_{free}$	0.182 , 0.216	DCC
$R_{free}$ test set	3490 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.3	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 48.3	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.51, < L^2>=0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7000	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.99% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: 17S, LLP

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	Bo	nd angles
MOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.44	0/6760	0.58	3/9148 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	A	138	ARG	NE-CZ-NH2	7.43	124.02	120.30
1	A	138	ARG	NE-CZ-NH1	-6.65	116.97	120.30
1	A	398	ARG	NE-CZ-NH2	5.17	122.88	120.30

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	6626	0	6558	30	0
2	A	50	0	42	0	0
3	A	324	0	0	3	0
All	All	7000	0	6600	30	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 2.



All (30) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${f distance}({ m \AA})$	overlap (Å)
1:A:138:ARG:O	1:A:138:ARG:HD3	1.75	0.87
1:A:76:GLU:HG3	3:A:1167:HOH:O	1.83	0.76
1:A:455:VAL:H	1:A:459:HIS:HD2	1.34	0.74
1:A:730:GLU:O	1:A:734:ARG:HG3	1.90	0.70
1:A:678:ASN:HD22	1:A:679:MET:H	1.41	0.67
1:A:355:ASP:OD1	1:A:398:ARG:HD3	1.96	0.65
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.84	0.60
1:A:450:HIS:HE1	3:A:1107:HOH:O	1.86	0.59
1:A:449:SER:O	1:A:478:LYS:HE2	2.05	0.57
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.86	0.56
1:A:450:HIS:HD2	3:A:934:HOH:O	1.89	0.56
1:A:235:ASN:H	1:A:235:ASN:HD22	1.55	0.53
1:A:81:ARG:HG2	1:A:155:TYR:HE2	1.73	0.52
1:A:85:LEU:HD13	1:A:335:ILE:HG23	1.92	0.51
1:A:680:LLP:O3	1:A:680:LLP:NZ	2.42	0.51
1:A:568:LYS:HG3	1:A:574:LYS:HD3	1.93	0.49
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.94	0.48
1:A:678:ASN:HD22	1:A:679:MET:N	2.10	0.47
1:A:338:ASN:OD1	1:A:377:HIS:NE2	2.47	0.47
1:A:235:ASN:HA	1:A:833:ARG:HG3	1.99	0.45
1:A:562:LEU:HD21	1:A:662:LEU:HB2	1.99	0.45
1:A:214:LYS:HB3	1:A:214:LYS:HE2	1.84	0.44
1:A:678:ASN:ND2	1:A:679:MET:H	2.13	0.43
1:A:566:GLN:HE22	1:A:576:GLN:HA	1.83	0.43
1:A:283:ASP:OD2	1:A:571[B]:HIS:HE1	2.01	0.42
1:A:138:ARG:HD3	1:A:138:ARG:C	2.32	0.42
1:A:275:ILE:O	1:A:295:GLN:HG2	2.20	0.41
1:A:15:VAL:HG12	1:A:509:GLU:HG2	2.02	0.41
1:A:522:LEU:HD13	1:A:806:ALA:CB	2.51	0.41
1:A:235:ASN:HB3	1:A:831:ARG:NH1	2.36	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	807/842 (96%)	784 (97%)	22 (3%)	1 (0%)	51 43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	568	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	703/730 (96%)	670 (95%)	33 (5%)	26 13

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	90	TYR
1	A	102	LEU
1	A	104	LEU
1	A	115	LEU
1	A	122	LEU
1	A	138	ARG
1	A	198	LEU
1	A	235	ASN
1	A	324	THR
1	A	339	ASP
1	A	400	LEU
1	A	426	ARG
1	A	444	LEU
1	A	522	LEU
1	A	552	GLU
1	A	565	VAL
1	A	568	LYS

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Mol	Chain	Res	Type
1	A	579	ASN
1	A	586	LEU
1	A	596	LYS
1	A	613	TYR
1	A	622	LEU
1	A	645	LEU
1	A	662	LEU
1	A	678	ASN
1	A	706	GLU
1	A	708	PHE
1	A	721	LEU
1	A	765	LEU
1	A	790	LEU
1	A	831	ARG
1	A	833	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	235	ASN
1	A	270	ASN
1	A	325	ASN
1	A	390	HIS
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	566	GLN
1	A	579	ASN
1	A	614	HIS
1	A	678	ASN
1	A	727	ASN
1	A	767	HIS

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

1 non-standard protein/DNA/RNA residue is 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	Pog	Link	Bond lengths			Bond angles		
			nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	LLP	A	680	1	23,24,25	1.72	6 (26%)	25,32,34	1.30	4 (16%)

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
1	LLP	A	680	1	-	2/16/17/19	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
1	A	680	LLP	O3-C3	-5.24	1.24	1.37
1	A	680	LLP	C4-C4'	3.03	1.52	1.46
1	A	680	LLP	C4'-NZ	2.18	1.34	1.27
1	A	680	LLP	C2-N1	2.18	1.38	1.33
1	A	680	LLP	P-OP2	-2.17	1.46	1.54
1	A	680	LLP	CE-NZ	2.10	1.51	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
1	A	680	LLP	C4-C4'-NZ	-2.81	111.39	124.31
1	A	680	LLP	OP4-P-OP1	-2.53	99.36	106.47
1	A	680	LLP	C5-C6-N1	-2.39	119.84	123.82
1	A	680	LLP	CE-NZ-C4'	-2.25	112.00	118.90

There are no chirality outliers.

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
1	A	680	LLP	C4-C5-C5'-OP4
1	A	680	LLP	C6-C5-C5'-OP4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	680	LLP	1	0

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

2 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		
MIOI					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	17S	A	920	-	26,26,26	2.34	4 (15%)	35,35,35	1.18	4 (11%)
2	17S	A	998	-	26,26,26	2.31	2 (7%)	35,35,35	1.17	2 (5%)

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	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
2	17S	A	920	-	-	4/14/34/34	0/2/2/2
2	17S	A	998	-	-	1/14/34/34	0/2/2/2

All (6) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	A	998	17S	N2-N3	-11.02	1.24	1.38
2	A	920	17S	N2-N3	-11.01	1.24	1.38
2	A	998	17S	C1-N1	2.66	1.46	1.43
2	A	920	17S	C7-N2	-2.65	1.32	1.36
2	A	920	17S	C8-N3	-2.41	1.25	1.28
2	A	920	17S	C1-N1	2.02	1.45	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
2	A	998	17S	C7-N2-N3	4.72	125.79	120.27
2	A	920	17S	C5-O5-C1	3.10	116.72	112.52
2	A	920	17S	O5-C1-N1	-2.53	103.45	108.01
2	A	920	17S	C2-C1-N1	-2.24	108.67	111.30
2	A	920	17S	C14-C9-C10	2.15	120.82	117.64
2	A	998	17S	O5-C1-C2	-2.03	107.79	109.83

There are no chirality outliers.

All (5) torsion outliers are listed below:

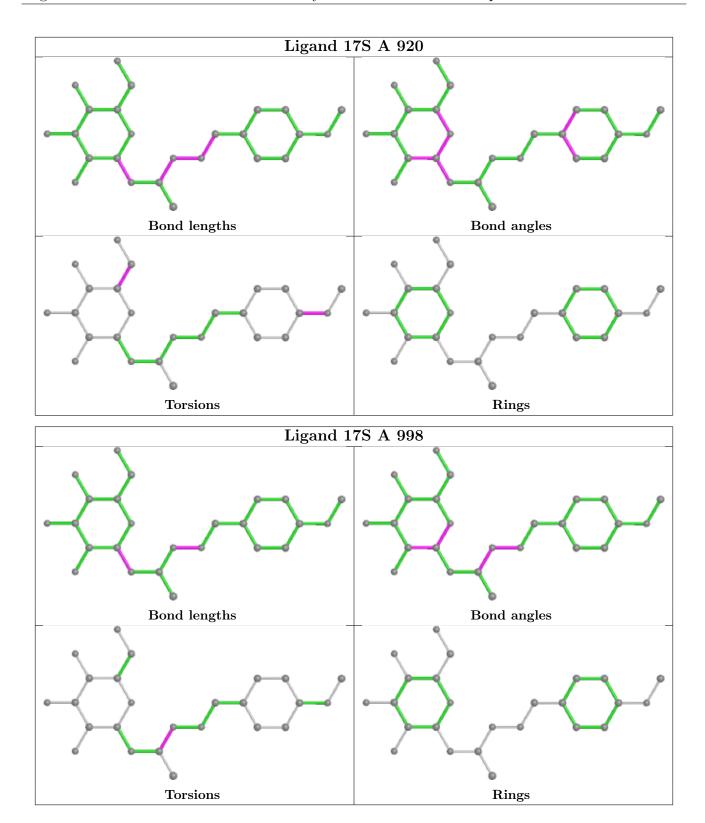
Mol	Chain	Res	Type	Atoms
2	A	920	17S	C4-C5-C6-O6
2	A	920	17S	O5-C5-C6-O6
2	A	920	17S	C11-C12-O7-C15
2	A	920	17S	C13-C12-O7-C15
2	A	998	17S	N1-C7-N2-N3

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.





## 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,  $95^{th}$  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.

Mo	l Chain	Analysed	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ} {>} 2$	2	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	A	810/842 (96%)	0.27	41 (5%) 28	37	17, 27, 45, 65	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	252	PHE	11.1
1	A	324	THR	8.3
1	A	253	ASN	7.2
1	A	435	ALA	6.0
1	A	556	HIS	5.9
1	A	254	LEU	5.5
1	A	211	GLN	5.0
1	A	555	VAL	4.5
1	A	210	SER	3.9
1	A	314	SER	3.7
1	A	69	ARG	3.6
1	A	831	ARG	3.6
1	A	832	GLN	3.6
1	A	285	PHE	3.5
1	A	113	TYR	3.4
1	A	835	PRO	3.3
1	A	75	TYR	3.2
1	A	836	ALA	3.1
1	A	21	VAL	3.0
1	A	12	GLN	3.0
1	A	260	GLY	3.0
1	A	551	ARG	3.0
1	A	436	VAL	3.0
1	A	13	ILE	2.8
1	A	553	TYR	2.7
1	A	284	ASN	2.7
1	A	250	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	753	LYS	2.6
1	A	325	ASN	2.5
1	A	833	ARG	2.5
1	A	358	ARG	2.4
1	A	76	GLU	2.4
1	A	554	LYS	2.4
1	A	251	ASP	2.3
1	A	552	GLU	2.3
1	A	547	ALA	2.3
1	A	337	LEU	2.3
1	A	548	TYR	2.2
1	A	379	VAL	2.2
1	A	532	ARG	2.1
1	A	723	GLN	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	LLP	A	680	24/25	0.98	0.15	16,18,22,25	0

## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

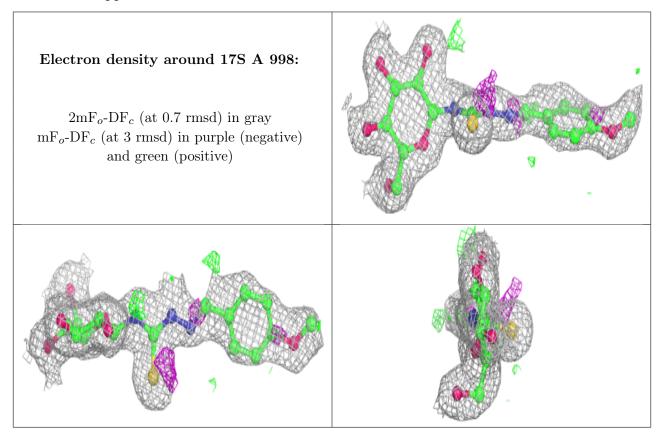
## 6.4 Ligands (i)

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,  $95^{th}$  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.

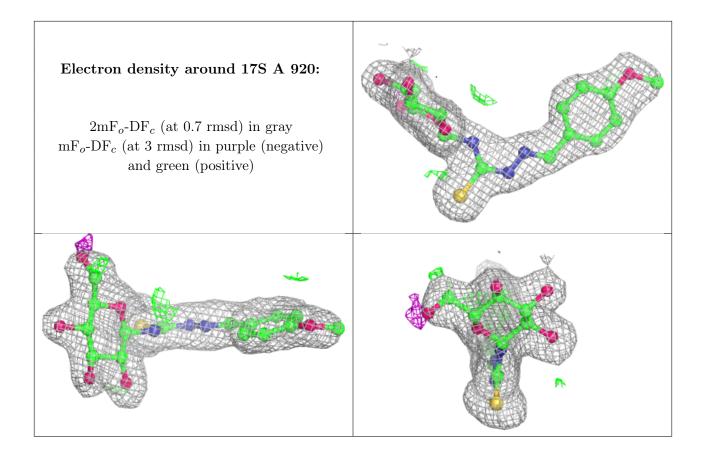
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	17S	A	998	25/25	0.95	0.11	21,24,41,41	0
2	17S	A	920	25/25	0.96	0.11	24,30,34,38	0



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.







## 6.5 Other polymers (i)

There are no such residues in this entry.

