WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Apr 15, 2024 – 04:35 PM EDT

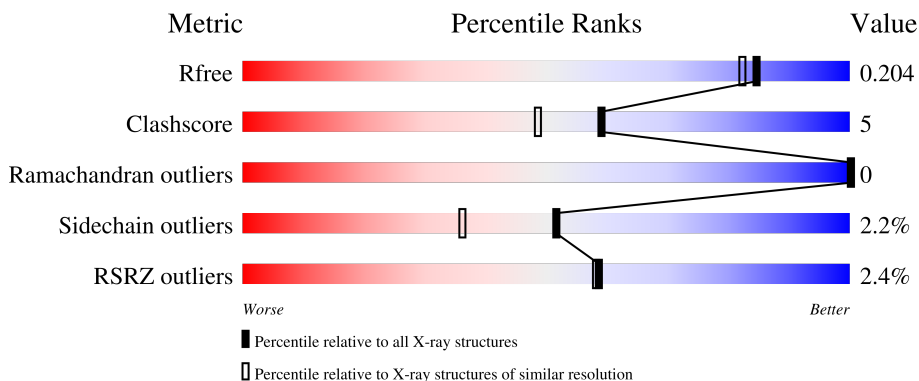|		
PDB ID	:	8SIG
Title	:	Crystal Structure of PRMT4 with Compound YD1-288
Authors	:	Song, X.; Dong, A.; Deng, Y.; Huang, R.; Arrowsmith, C.H.; Edwards, A.M.; Min, J.; Structural Genomics Consortium (SGC)
Deposited on	:	2023-04-16
Resolution	:	1.78 Å(reported)

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 1.78 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	Percentile Ranks	Value
Rfree		0.204
Clashscore		5
Ramachandran outliers		0
Sidechain outliers		2.2%
RSRZ outliers		2.4%

Worse ... *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	359	2% / 85% / 8% / 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	UNX	A	505	-	-	-	X

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 3074 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 Histone-arginine methyltransferase CARM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	333	2779	1797	456	509	17	0	18	1

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	MET	-	initiating methionine	UNP Q86X55
A	123	HIS	-	expression tag	UNP Q86X55
A	124	HIS	-	expression tag	UNP Q86X55
A	125	HIS	-	expression tag	UNP Q86X55
A	126	HIS	-	expression tag	UNP Q86X55
A	127	HIS	-	expression tag	UNP Q86X55
A	128	HIS	-	expression tag	UNP Q86X55
A	129	SER	-	expression tag	UNP Q86X55
A	130	SER	-	expression tag	UNP Q86X55
A	131	GLY	-	expression tag	UNP Q86X55
A	132	ARG	-	expression tag	UNP Q86X55
A	133	GLU	-	expression tag	UNP Q86X55
A	134	ASN	-	expression tag	UNP Q86X55
A	135	LEU	-	expression tag	UNP Q86X55
A	136	TYR	-	expression tag	UNP Q86X55
A	137	PHE	-	expression tag	UNP Q86X55
A	138	GLN	-	expression tag	UNP Q86X55
A	139	GLY	-	expression tag	UNP Q86X55

- Molecule 2 is 5'-{(3-aminopropyl)[2-(benzylcarbamamido)ethyl]amino}-5'-deoxyadenosine (three-letter code: GWU) (formula: $C_{23}H_{33}N_9O_4$) (labeled as "Ligand of Interest" by depositor).

GWU
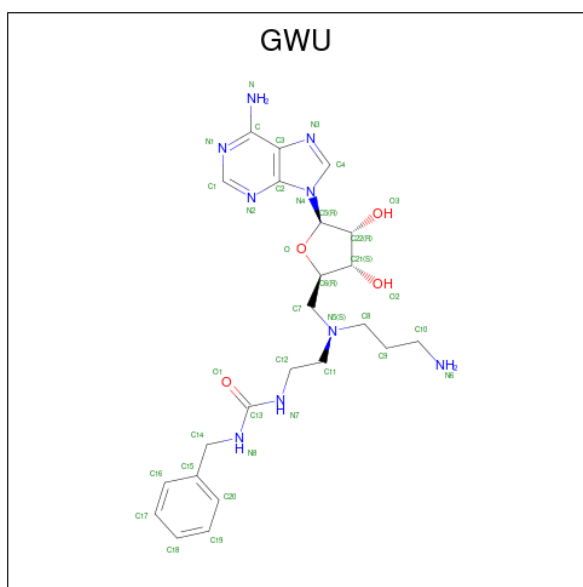
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	36	23	9	4	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
3	A	1	1	1	0	0

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	X		
4	A	7	7	7	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	248	251	251	0	3

3 Residue-property plots ⓘ

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: Histone-arginine methyltransferase CARM1
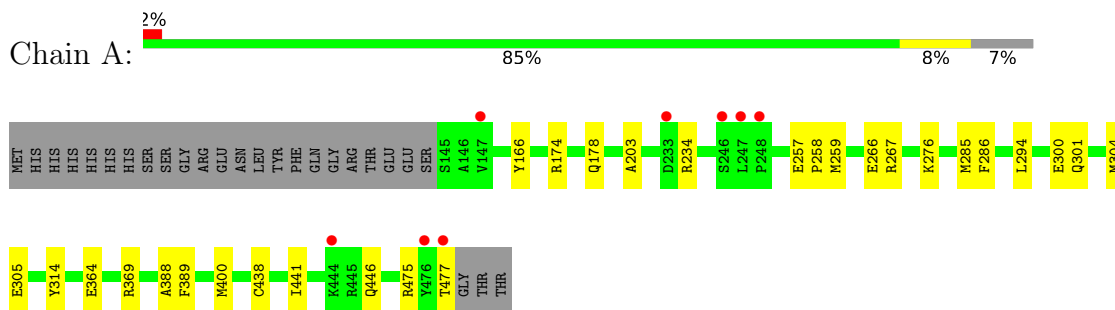
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	84.89Å 84.89Å 130.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.91 – 1.78 48.86 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.91-1.78) 99.9 (48.86-1.78)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.78 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.183 , 0.199 0.195 , 0.204	Depositor DCC
R_{free} test set	1035 reflections (1.95%)	wwPDB-VP
Wilson B-factor (Å^2)	27.7	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.8	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3074	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: UNX, GWU, NA

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	0.69	0/2852	0.72	0/3868

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2779	0	2668	26	0
2	A	36	0	0	0	0
3	A	1	0	0	0	0
4	A	7	0	0	0	0
5	A	251	0	0	2	0
All	All	3074	0	2668	26	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 5.

All (26) 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:300:GLU:CG	1:A:304[B]:MET:HE2	2.04	0.86
1:A:300:GLU:CG	1:A:304[B]:MET:CE	2.65	0.74
1:A:300:GLU:HG3	1:A:304[B]:MET:HE2	1.71	0.73
1:A:300:GLU:HG2	1:A:304[B]:MET:CE	2.20	0.71
1:A:174[B]:ARG:NH2	5:A:601:HOH:O	2.28	0.66
1:A:300:GLU:HG3	1:A:304[B]:MET:CE	2.26	0.65
1:A:300:GLU:HG2	1:A:304[B]:MET:HE2	1.81	0.62
1:A:369[A]:ARG:HG3	1:A:441:ILE:CD1	2.29	0.62
1:A:294[B]:LEU:HD23	1:A:294[B]:LEU:N	2.14	0.61
1:A:178[A]:GLN:HA	1:A:178[A]:GLN:OE1	2.05	0.56
1:A:178[B]:GLN:OE1	1:A:400:MET:SD	2.64	0.55
1:A:364[A]:GLU:HG2	5:A:602:HOH:O	2.07	0.55
1:A:276:LYS:HD3	1:A:285[A]:MET:SD	2.48	0.54
1:A:294[A]:LEU:CD2	1:A:438[A]:CYS:SG	2.96	0.53
1:A:294[B]:LEU:HD23	1:A:294[B]:LEU:H	1.77	0.49
1:A:294[B]:LEU:HA	1:A:388:ALA:O	2.15	0.47
1:A:300:GLU:O	1:A:304[B]:MET:HG3	2.14	0.47
1:A:294[A]:LEU:HD23	1:A:438[A]:CYS:SG	2.55	0.47
1:A:301:GLN:O	1:A:305[A]:GLU:HG3	2.16	0.46
1:A:203:ALA:O	1:A:234[B]:ARG:NH2	2.44	0.45
1:A:294[A]:LEU:HG	1:A:389:PHE:CE2	2.51	0.45
1:A:294[A]:LEU:HD21	1:A:438[A]:CYS:SG	2.57	0.45
1:A:369[A]:ARG:HG3	1:A:441:ILE:HD13	1.99	0.44
1:A:305[A]:GLU:CD	1:A:475:ARG:HH11	2.21	0.42
1:A:267:ARG:NH2	1:A:446:GLN:CB	2.84	0.41
1:A:258:PRO:HD2	1:A:259:MET:SD	2.61	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	349/359 (97%)	340 (97%)	9 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	293/312 (94%)	287 (98%)	6 (2%)	55	40

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	TYR
1	A	257	GLU
1	A	266	GLU
1	A	286	PHE
1	A	314	TYR
1	A	477	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	160	GLN
1	A	164	GLN

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 1 is monoatomic and 7 are unknown - leaving 1 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	#$|Z| > 2$
2	GWU	A	501	-	36,39,39	0.76	1 (2%)	39,53,53	0.85	3 (7%)

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	GWU	A	501	-	-	5/19/39/39	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	GWU	C7-N5	-2.94	1.41	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	GWU	C8-N5-C7	-2.84	105.18	111.96
2	A	501	GWU	O-C6-C7	-2.16	105.33	108.90
2	A	501	GWU	C3-C-N	2.14	123.60	120.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GWU	O-C6-C7-N5
2	A	501	GWU	C21-C6-C7-N5
2	A	501	GWU	C6-C7-N5-C11

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Mol	Chain	Res	Type	Atoms
2	A	501	GWU	C12-C11-N5-C7
2	A	501	GWU	N6-C10-C9-C8

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 GWU A 501

Bond lengths   Bond angles

Torsions   Rings
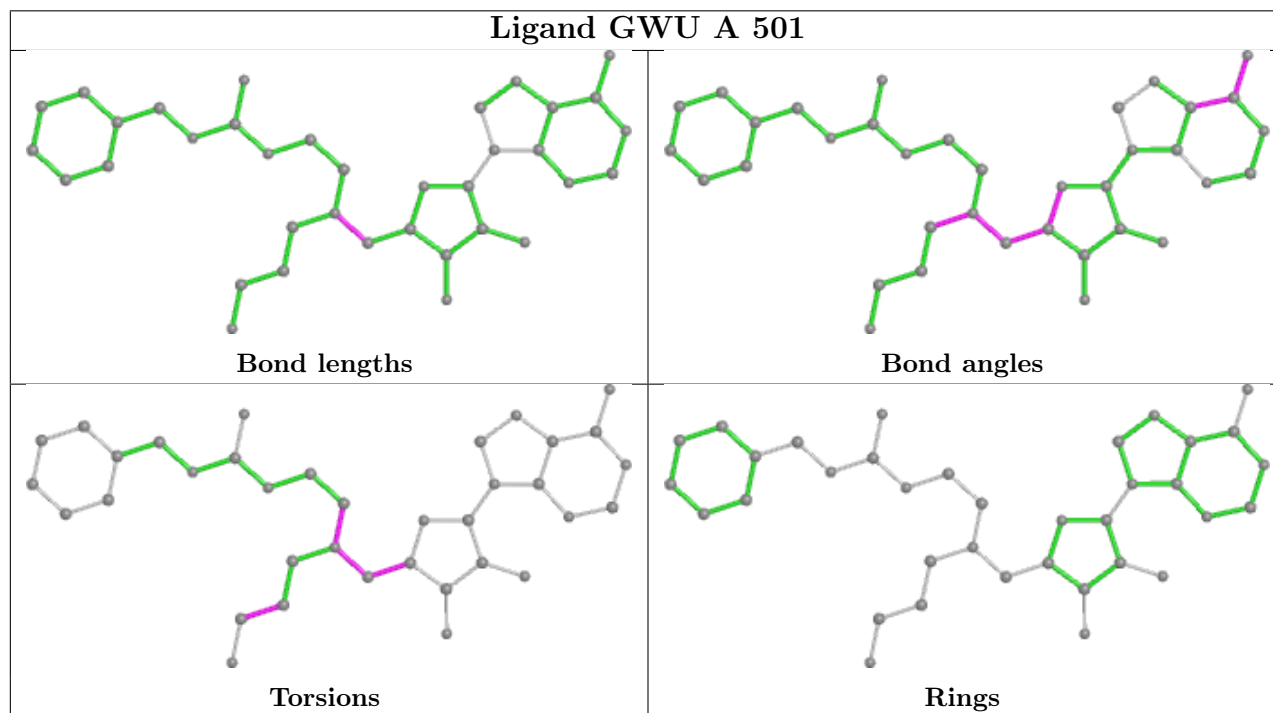
5.7 Other polymers ⓘ

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 ⓘ

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, 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	333/359 (92%)	-0.12	8 (2%)	59	58	19, 28, 42, 69	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	476[A]	TYR	3.4
1	A	477	THR	3.2
1	A	233	ASP	2.5
1	A	248	PRO	2.3
1	A	444	LYS	2.3
1	A	147	VAL	2.3
1	A	246	SER	2.3
1	A	247	LEU	2.1

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

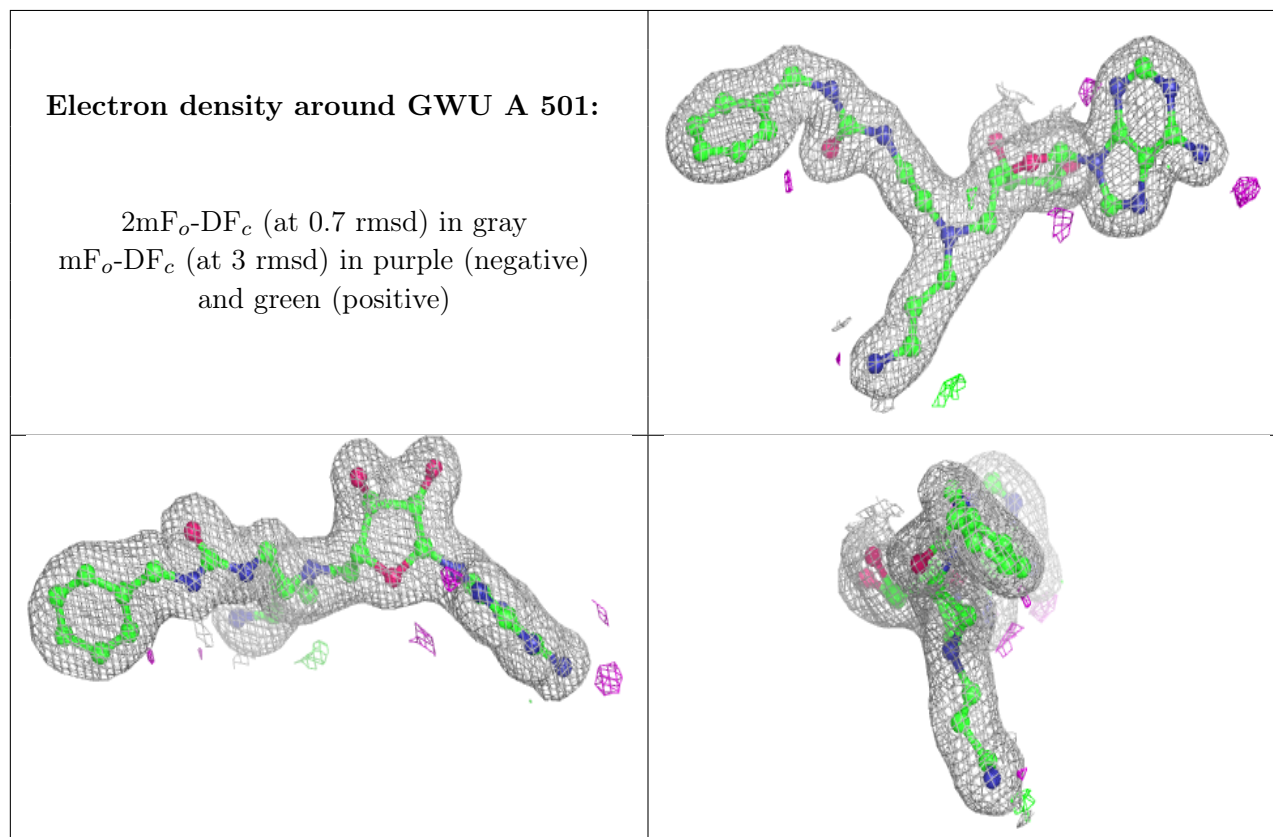There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
4	UNX	A	505	1/1	0.69	0.49	40,40,40,40	0
4	UNX	A	509	1/1	0.77	0.20	38,38,38,38	0
4	UNX	A	503	1/1	0.80	0.30	32,32,32,32	0
4	UNX	A	504	1/1	0.86	0.23	28,28,28,28	0
4	UNX	A	506	1/1	0.92	0.47	43,43,43,43	0
4	UNX	A	508	1/1	0.93	0.17	44,44,44,44	0
2	GWU	A	501	36/36	0.94	0.08	20,27,31,32	0
4	UNX	A	507	1/1	0.95	0.28	20,20,20,20	0
3	NA	A	502	1/1	0.98	0.06	23,23,23,23	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 GWU A 501:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.