Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2026 – 08:20 PM JST

PDB ID	:	9VS9 / pdb_00009vs9
Title	:	Small molecule 3-127 targeting YTHDC1
Authors	:	Fu, S.; Wang, M.; Chen, S.
Deposited on	:	2025-07-08
Resolution	:	1.82 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

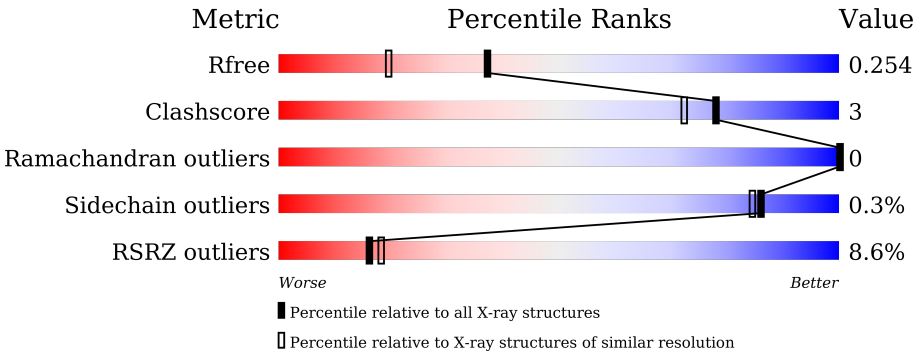
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 1.82 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}	180053	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	187	8% 79% 9% 12%
1	B	187	7% 82% 5% • 13%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2769 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 YTH domain-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	164	Total	C	N	O	S	0	1	0
			1312	843	233	230	6			
1	B	163	Total	C	N	O	S	0	0	0
			1300	836	231	227	6			

There are 42 discrepancies between the modelled and reference sequences:

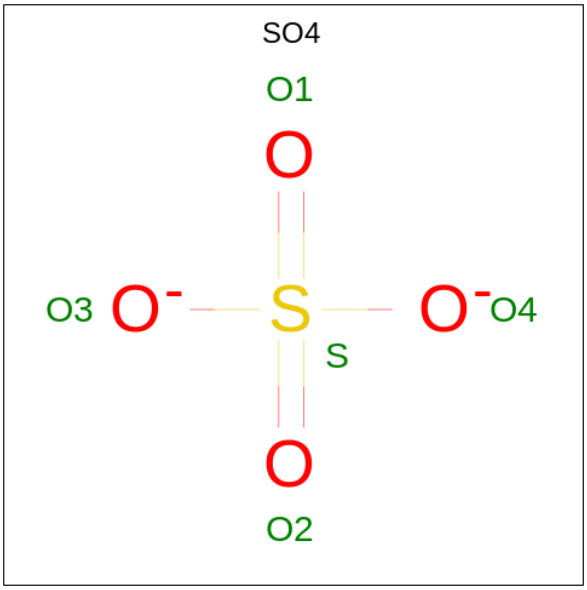
Chain	Residue	Modelled	Actual	Comment	Reference
A	323	MET	-	initiating methionine	UNP Q96MU7
A	324	GLY	-	expression tag	UNP Q96MU7
A	325	SER	-	expression tag	UNP Q96MU7
A	326	SER	-	expression tag	UNP Q96MU7
A	327	HIS	-	expression tag	UNP Q96MU7
A	328	HIS	-	expression tag	UNP Q96MU7
A	329	HIS	-	expression tag	UNP Q96MU7
A	330	HIS	-	expression tag	UNP Q96MU7
A	331	HIS	-	expression tag	UNP Q96MU7
A	332	HIS	-	expression tag	UNP Q96MU7
A	333	SER	-	expression tag	UNP Q96MU7
A	334	SER	-	expression tag	UNP Q96MU7
A	335	GLY	-	expression tag	UNP Q96MU7
A	336	LEU	-	expression tag	UNP Q96MU7
A	337	VAL	-	expression tag	UNP Q96MU7
A	338	PRO	-	expression tag	UNP Q96MU7
A	339	ARG	-	expression tag	UNP Q96MU7
A	340	GLY	-	expression tag	UNP Q96MU7
A	341	SER	-	expression tag	UNP Q96MU7
A	342	HIS	-	expression tag	UNP Q96MU7
A	343	MET	-	expression tag	UNP Q96MU7
B	323	MET	-	initiating methionine	UNP Q96MU7
B	324	GLY	-	expression tag	UNP Q96MU7
B	325	SER	-	expression tag	UNP Q96MU7
B	326	SER	-	expression tag	UNP Q96MU7

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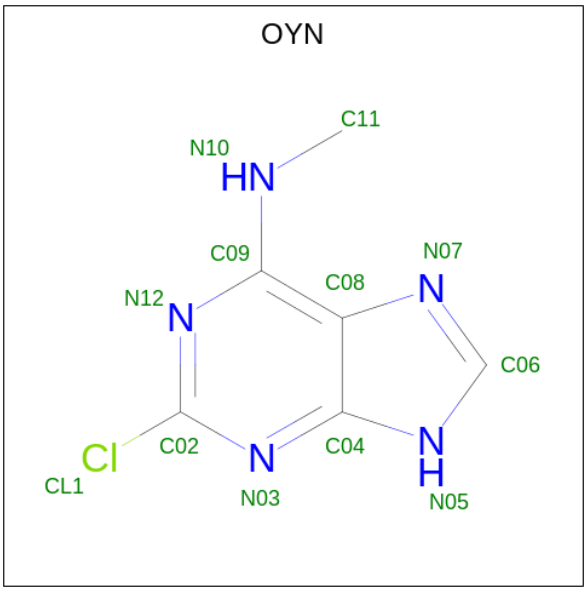
Chain	Residue	Modelled	Actual	Comment	Reference
B	327	HIS	-	expression tag	UNP Q96MU7
B	328	HIS	-	expression tag	UNP Q96MU7
B	329	HIS	-	expression tag	UNP Q96MU7
B	330	HIS	-	expression tag	UNP Q96MU7
B	331	HIS	-	expression tag	UNP Q96MU7
B	332	HIS	-	expression tag	UNP Q96MU7
B	333	SER	-	expression tag	UNP Q96MU7
B	334	SER	-	expression tag	UNP Q96MU7
B	335	GLY	-	expression tag	UNP Q96MU7
B	336	LEU	-	expression tag	UNP Q96MU7
B	337	VAL	-	expression tag	UNP Q96MU7
B	338	PRO	-	expression tag	UNP Q96MU7
B	339	ARG	-	expression tag	UNP Q96MU7
B	340	GLY	-	expression tag	UNP Q96MU7
B	341	SER	-	expression tag	UNP Q96MU7
B	342	HIS	-	expression tag	UNP Q96MU7
B	343	MET	-	expression tag	UNP Q96MU7

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

- Molecule 3 is 2-chloranyl- {N}-methyl-9 {H}-purin-6-amine (CCD ID: OYN) (formula: $C_6H_6ClN_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C Cl N 12 6 1 5	0	0
3	B	1	Total C Cl N 12 6 1 5	0	0

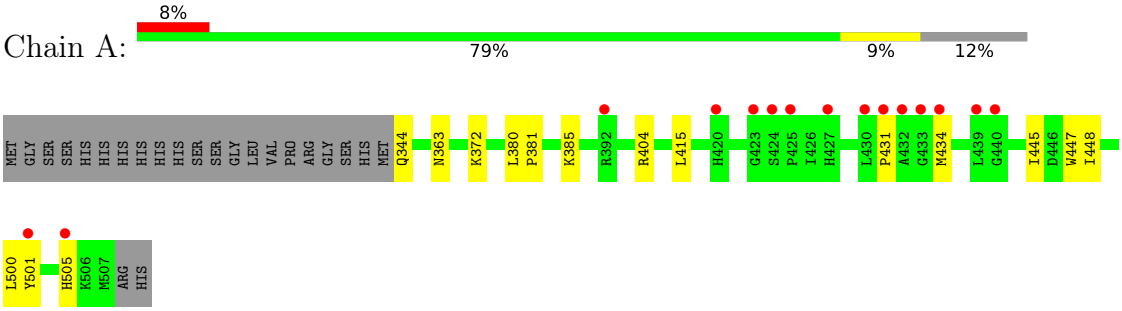
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	75	Total O 75 75	0	0
4	B	53	Total O 53 53	0	0

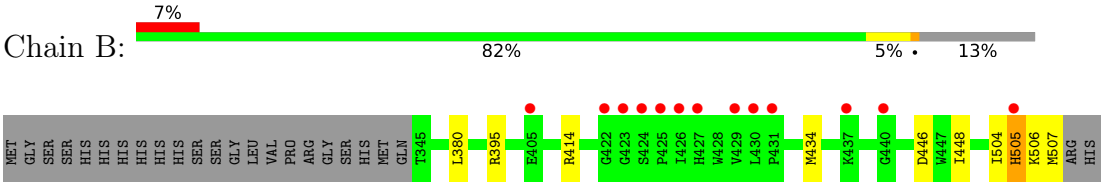
3 Residue-property plots (i)

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: YTH domain-containing protein 1



• Molecule 1: YTH domain-containing protein 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	39.86Å 103.28Å 41.86Å 90.00° 104.42° 90.00°	Depositor
Resolution (Å)	40.54 – 1.82 40.54 – 1.82	Depositor EDS
% Data completeness (in resolution range)	97.3 (40.54-1.82) 97.3 (40.54-1.82)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.18 (at 1.82Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.217 , 0.253 0.218 , 0.254	Depositor DCC
R_{free} test set	1989 reflections (6.81%)	wwPDB-VP
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 36.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.049 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2769	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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: SO4, OYN

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	0.38	0/1348	0.60	0/1818
1	B	0.38	0/1333	0.59	0/1798
All	All	0.38	0/2681	0.60	0/3616

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	1312	0	1332	9	0
1	B	1300	0	1319	6	0
2	A	5	0	0	0	0
3	A	12	0	0	0	0
3	B	12	0	0	0	0
4	A	75	0	0	1	0
4	B	53	0	0	1	0
All	All	2769	0	2651	15	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (15) 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:431:PRO:HD2	1:A:434:MET:HE3	1.81	0.61
1:A:448:ILE:HG23	1:A:500:LEU:HD21	1.91	0.53
1:B:380:LEU:HD21	1:B:434:MET:HE2	1.91	0.53
1:A:381:PRO:O	1:A:385:LYS:HG3	2.09	0.52
1:B:505:HIS:HB3	4:B:753:HOH:O	2.12	0.49
1:B:504:ILE:O	1:B:507:MET:HG3	2.14	0.47
1:B:446:ASP:OD2	1:B:506:LYS:HD3	2.15	0.47
1:A:501:TYR:CE1	1:A:505:HIS:CE1	3.04	0.46
1:A:363:ASN:OD1	1:A:404:ARG:HD2	2.17	0.45
1:B:414:ARG:HB2	1:B:448:ILE:HD11	2.00	0.43
1:A:344:GLN:HG3	4:A:724:HOH:O	2.18	0.42
1:B:395:ARG:HH11	1:B:395:ARG:HG2	1.84	0.42
1:A:380:LEU:HD23	1:A:380:LEU:HA	1.82	0.42
1:A:415:LEU:HD23	1:A:445:ILE:HG22	2.02	0.41
1:A:372:LYS:HA	1:A:447:TRP:NE1	2.36	0.41

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	163/187 (87%)	162 (99%)	1 (1%)	0	100	100
1	B	161/187 (86%)	158 (98%)	3 (2%)	0	100	100
All	All	324/374 (87%)	320 (99%)	4 (1%)	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	145/164 (88%)	145 (100%)	0	100	100
1	B	143/164 (87%)	142 (99%)	1 (1%)	76	70
All	All	288/328 (88%)	287 (100%)	1 (0%)	86	84

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	505	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	365	HIS
1	A	505	HIS
1	B	353	GLN
1	B	468	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

3 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	$\#\|Z\| > 2$
3	OYN	A	602	-	13,13,13	0.34	0	17,18,18	1.16	1 (5%)
2	SO4	A	601	-	4,4,4	0.23	0	6,6,6	0.19	0
3	OYN	B	601	-	13,13,13	0.35	0	17,18,18	1.17	1 (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	Res	Link	Chirals	Torsions	Rings
3	OYN	A	602	-	-	0/2/2/2	0/2/2/2
3	OYN	B	601	-	-	0/2/2/2	0/2/2/2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	601	OYN	C02-N03-C04	-3.95	111.50	116.73
3	A	602	OYN	C02-N03-C04	-3.90	111.56	116.73

There are no chirality outliers.

There are no torsion outliers.

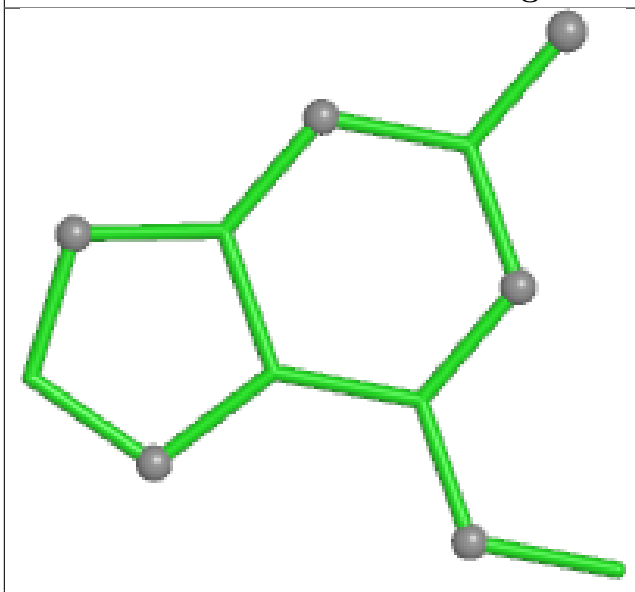
There are no ring outliers.

No monomer is involved in short contacts.

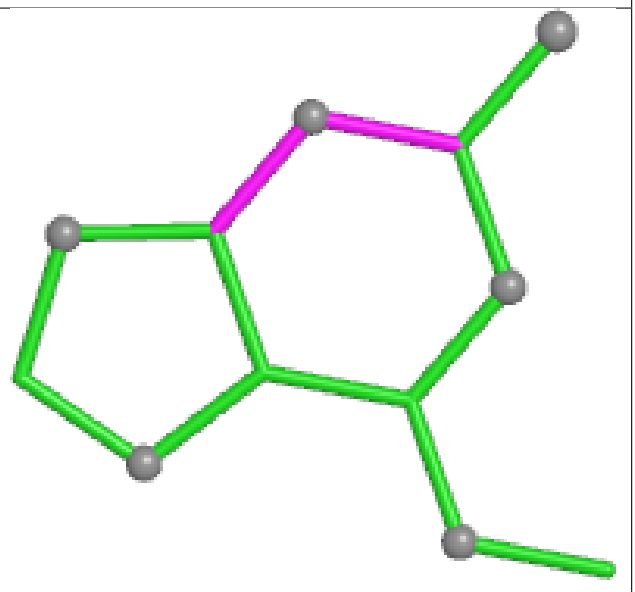
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

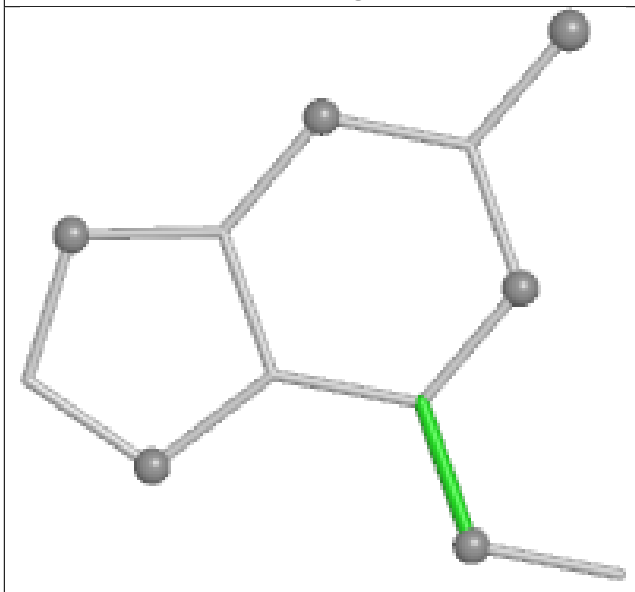
Ligand OYN A 602



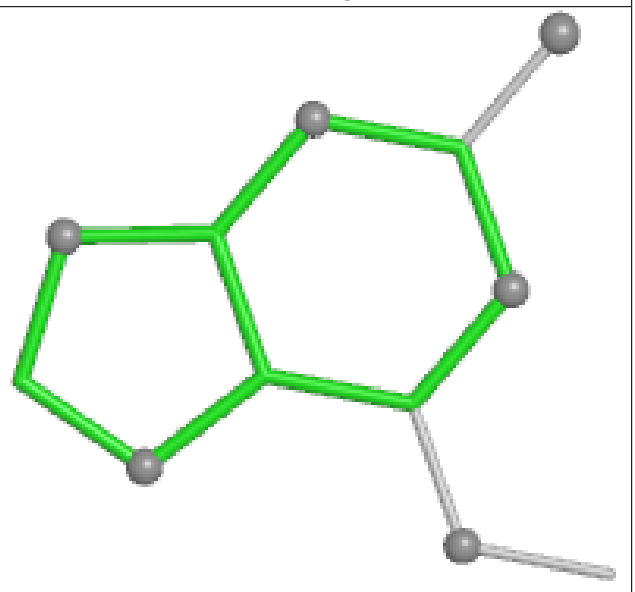
Bond lengths



Bond angles

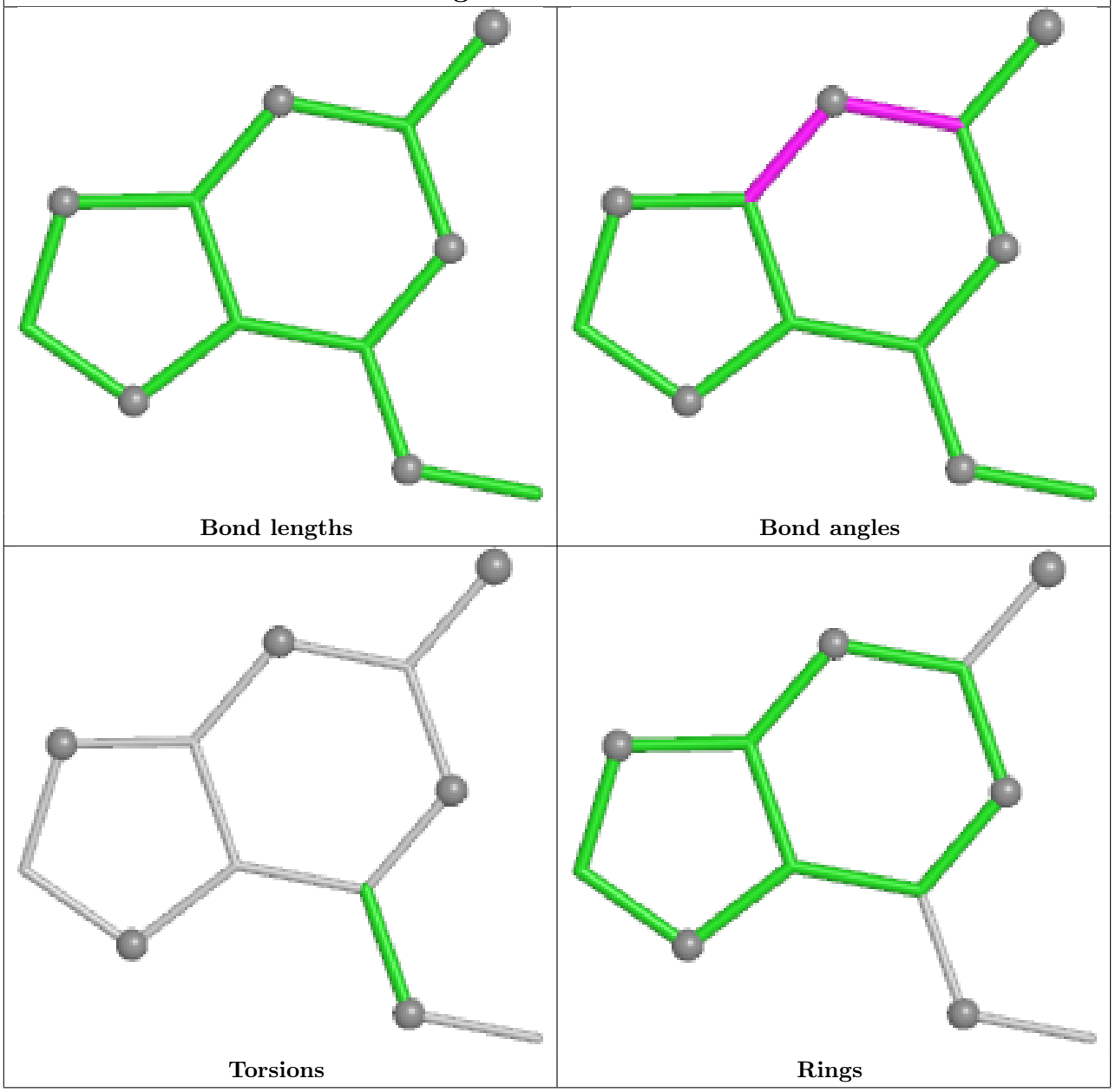


Torsions



Rings

Ligand OYN B 601



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

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	164/187 (87%)	0.43	15 (9%)	15	16	12, 23, 48, 60	1 (0%)
1	B	163/187 (87%)	0.47	13 (7%)	18	20	15, 25, 58, 63	0
All	All	327/374 (87%)	0.45	28 (8%)	16	18	12, 24, 54, 63	1 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	422	GLY	4.8
1	A	427	HIS	4.5
1	B	429	VAL	3.8
1	B	423	GLY	3.5
1	A	424	SER	3.5
1	A	505	HIS	3.5
1	A	433	GLY	3.5
1	B	505	HIS	3.0
1	A	434	MET	2.9
1	B	430	LEU	2.7
1	A	425	PRO	2.6
1	B	425	PRO	2.6
1	A	420	HIS	2.6
1	B	440	GLY	2.5
1	B	424	SER	2.5
1	B	427	HIS	2.5
1	A	432	ALA	2.4
1	A	423	GLY	2.4
1	B	431	PRO	2.3
1	A	430	LEU	2.3
1	A	392	ARG	2.3
1	A	440	GLY	2.2
1	A	431	PRO	2.2
1	A	501	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	405	GLU	2.1
1	A	439	LEU	2.0
1	B	437	LYS	2.0
1	B	426	ILE	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)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

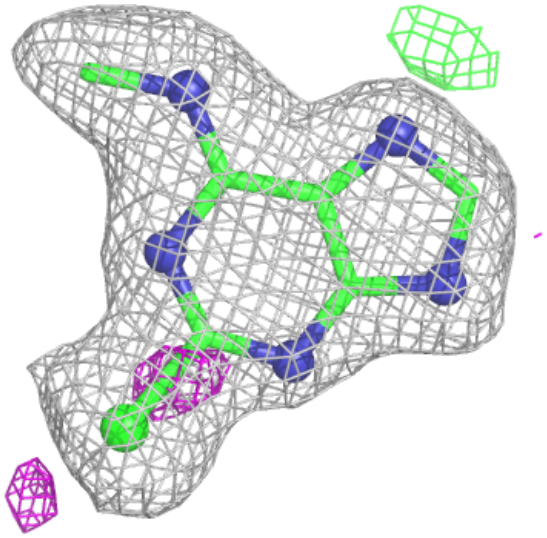
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

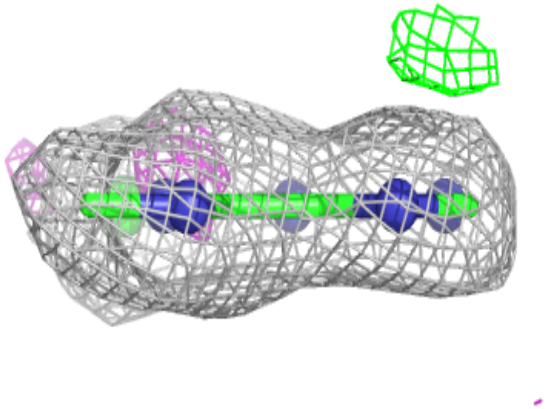
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	OYN	B	601	12/12	0.89	0.10	29,35,40,43	0
3	OYN	A	602	12/12	0.96	0.06	22,24,28,28	0
2	SO4	A	601	5/5	0.97	0.07	28,29,32,34	0

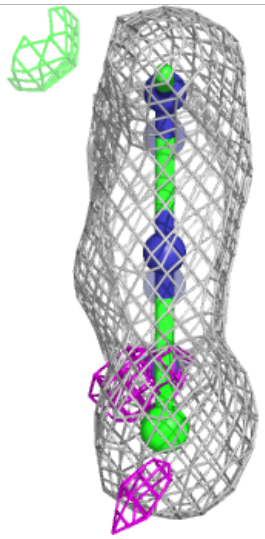
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around OYN B 601:

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

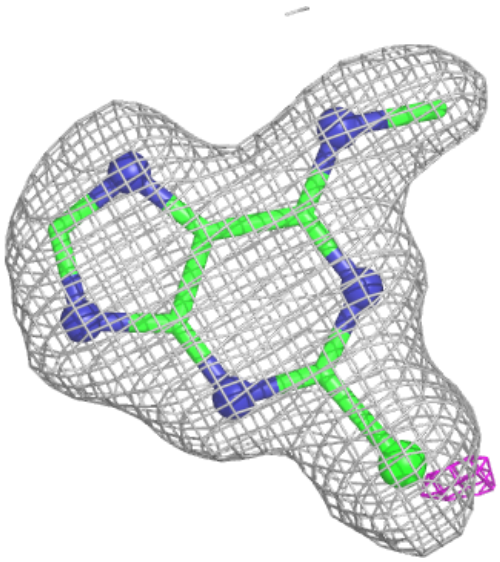


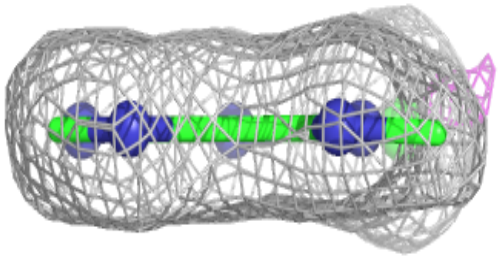


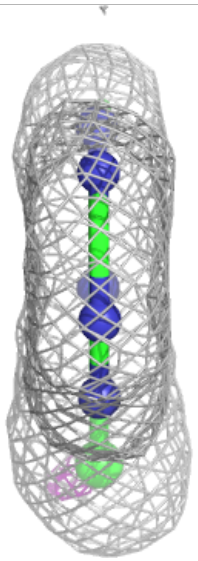


Electron density around OYN A 602:

$2mF_o$-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.