



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 12, 2021 – 10:05 AM EDT

PDB ID : 7KID  
Title : PRMT5:MEP50 Complexed with 5,5-Bicyclic Inhibitor Compound 72  
Authors : Palte, R.L.  
Deposited on : 2020-10-23  
Resolution : 2.50 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.18  
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) : 2.18

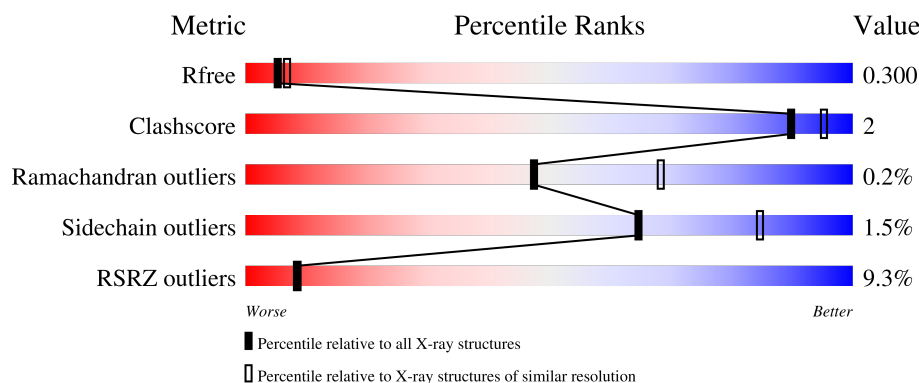
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	645	 6% 89% 8% .
2	B	350	 14% 85% . 11%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7750 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 Protein arginine N-methyltransferase 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	625	Total	C	N	O	S	0	3	0
			5086	3251	873	937	25			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP O14744
A	-6	ASP	-	expression tag	UNP O14744
A	-5	TYR	-	expression tag	UNP O14744
A	-4	LYS	-	expression tag	UNP O14744
A	-3	ASP	-	expression tag	UNP O14744
A	-2	ASP	-	expression tag	UNP O14744
A	-1	ASP	-	expression tag	UNP O14744
A	0	ASP	-	expression tag	UNP O14744
A	1	LYS	-	expression tag	UNP O14744

- Molecule 2 is a protein called Methylosome protein 50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	311	Total	C	N	O	S	0	1	0
			2353	1475	403	460	15			

There are 9 discrepancies between the modelled and reference sequences:

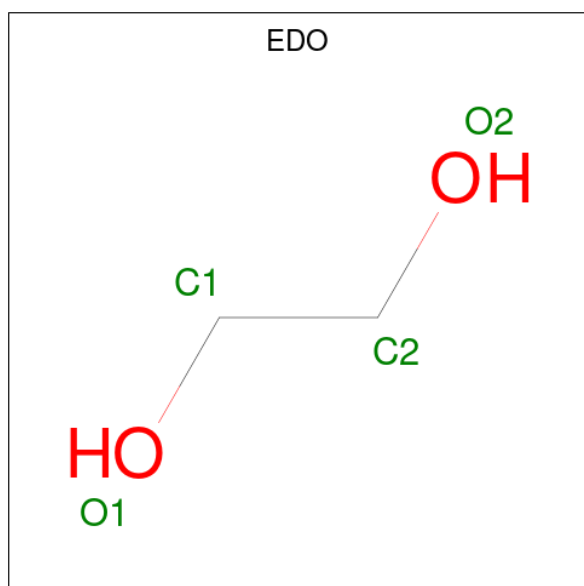
Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	MET	-	initiating methionine	UNP Q9BQA1
B	-6	HIS	-	expression tag	UNP Q9BQA1
B	-5	HIS	-	expression tag	UNP Q9BQA1
B	-4	HIS	-	expression tag	UNP Q9BQA1
B	-3	HIS	-	expression tag	UNP Q9BQA1
B	-2	HIS	-	expression tag	UNP Q9BQA1
B	-1	HIS	-	expression tag	UNP Q9BQA1

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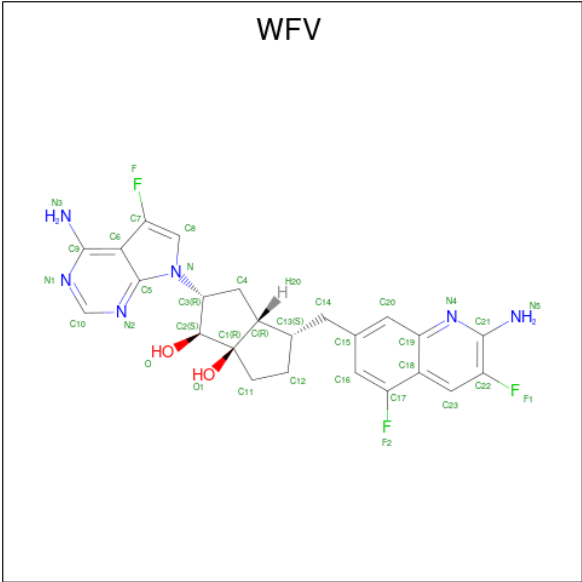
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	HIS	-	expression tag	UNP Q9BQA1
B	1	HIS	-	expression tag	UNP Q9BQA1

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 4 is (1S,2R,3aR,4S,6aR)-4-[(2-amino-3,5-difluoroquinolin-7-yl)methyl]-2-(4-amino-5-fluoro-7H-pyrrolo[2,3-d]pyrimidin-7-yl)hexahydropentalene-1,6a(1H)-diol (three-letter code: WFV) (formula: C<sub>24</sub>H<sub>23</sub>F<sub>3</sub>N<sub>6</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			35	24	3	6	2		

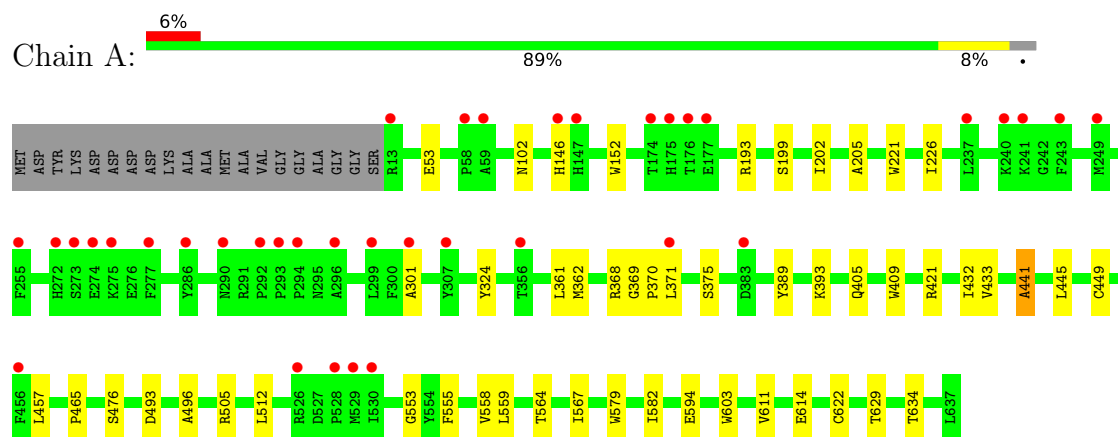
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	223	Total	O	0	0
			223	223		
5	B	37	Total	O	0	0
			37	37		

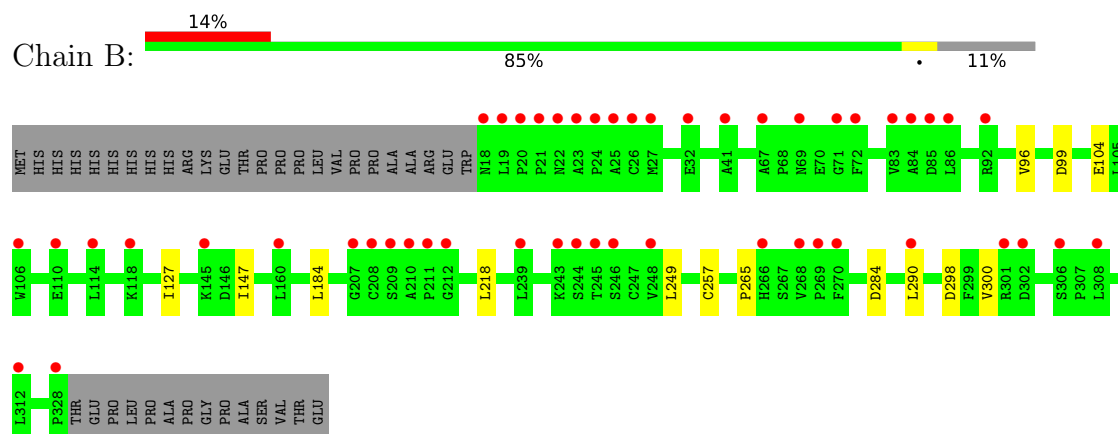
### 3 Residue-property plots [i](#)

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: Protein arginine N-methyltransferase 5



- Molecule 2: Methylosome protein 50



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.68Å 139.18Å 178.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.79 – 2.50 33.54 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (34.79-2.50) 98.3 (33.54-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, $R_{free}$	0.259 , 0.279 0.273 , 0.300	Depositor DCC
$R_{free}$ test set	2257 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.2	Xtriage
Anisotropy	0.891	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 35.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	7750	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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: EDO, WFV

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	0.70	0/5228	0.41	0/7111
2	B	0.71	0/2410	0.43	0/3294
All	All	0.70	0/7638	0.42	0/10405

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 [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	5086	0	4970	23	0
2	B	2353	0	2266	4	0
3	A	16	0	24	0	0
4	A	35	0	0	0	0
5	A	223	0	0	0	0
5	B	37	0	0	0	0
All	All	7750	0	7260	27	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 (27) 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:362:MET:HG2	1:A:389:TYR:HB2	1.88	0.55
1:A:152:TRP:HB3	1:A:205:ALA:HB2	1.89	0.54
1:A:199:SER:HB3	1:A:202:ILE:HD12	1.93	0.51
1:A:445:LEU:HD11	1:A:611:VAL:HB	1.92	0.51
1:A:405:GLN:HA	1:A:409:TRP:HB2	1.92	0.50
1:A:301:ALA:HB1	1:A:505:ARG:HG2	1.93	0.50
1:A:369:GLY:N	1:A:370:PRO:HD3	2.26	0.50
1:A:493:ASP:HB3	1:A:496:ALA:HB2	1.94	0.49
1:A:432:ILE:HG12	1:A:457:LEU:HD13	1.95	0.49
1:A:567:ILE:HG21	1:A:579:TRP:HB2	1.94	0.49
1:A:369:GLY:H	1:A:370:PRO:HD3	1.78	0.48
1:A:603:TRP:HB2	1:A:614:GLU:HB2	1.96	0.48
1:A:221:TRP:HB3	1:A:226:ILE:HD11	1.95	0.48
1:A:371:LEU:HD13	1:A:433:VAL:HG12	1.98	0.46
1:A:53:GLU:HA	1:A:102[B]:ASN:HD21	1.80	0.46
2:B:96:VAL:HB	2:B:104:GLU:HB2	1.99	0.45
1:A:324:TYR:CB	1:A:368:ARG:HD2	2.47	0.45
1:A:553:GLY:HA3	1:A:582:ILE:HG22	1.98	0.45
1:A:476:SER:HB2	1:A:512:LEU:HD21	1.99	0.43
1:A:465:PRO:HB3	1:A:559:LEU:HD23	2.00	0.43
1:A:441:ALA:HB2	1:A:555:PHE:HB2	1.99	0.43
2:B:184:LEU:HB3	2:B:218:LEU:HD13	1.99	0.43
2:B:99:ASP:HA	2:B:127:ILE:HG23	2.00	0.43
1:A:421:ARG:HD2	1:A:449:CYS:HA	2.00	0.43
1:A:558:VAL:HA	1:A:564:THR:HG22	2.02	0.41
1:A:361:LEU:HD13	1:A:375:SER:HB3	2.01	0.41
2:B:284:ASP:HB3	2:B:290:LEU:HD11	2.03	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	626/645 (97%)	605 (97%)	20 (3%)	1 (0%)	47	68
2	B	310/350 (89%)	298 (96%)	11 (4%)	1 (0%)	41	61
All	All	936/995 (94%)	903 (96%)	31 (3%)	2 (0%)	47	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	147	ILE
1	A	441	ALA

### 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	561/570 (98%)	554 (99%)	7 (1%)	71	88
2	B	265/298 (89%)	260 (98%)	5 (2%)	57	80
All	All	826/868 (95%)	814 (98%)	12 (2%)	65	85

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	193	ARG
1	A	393	LYS
1	A	594	GLU
1	A	622	CYS
1	A	629	THR
1	A	634	THR
2	B	249	LEU
2	B	257	CYS
2	B	265	PRO
2	B	298	ASP
2	B	300	VAL

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	525	ASN
2	B	22	ASN

### 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](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

5 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	EDO	A	701	-	3,3,3	0.56	0	2,2,2	0.33	0
3	EDO	A	702	-	3,3,3	0.61	0	2,2,2	0.30	0
4	WFV	A	705	-	37,40,40	0.80	1 (2%)	40,63,63	1.28	3 (7%)
3	EDO	A	703	-	3,3,3	0.52	0	2,2,2	0.37	0
3	EDO	A	704	-	3,3,3	0.52	0	2,2,2	0.33	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
3	EDO	A	701	-	-	0/1/1/1	-
3	EDO	A	702	-	-	0/1/1/1	-
4	WFV	A	705	-	-	0/4/38/38	0/6/6/6
3	EDO	A	703	-	-	0/1/1/1	-
3	EDO	A	704	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	705	WFV	C21-C22	3.18	1.42	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	705	WFV	C16-C17-C18	-6.28	121.07	124.07
4	A	705	WFV	C7-C8-N	2.19	110.63	108.22
4	A	705	WFV	C12-C11-C1	2.19	106.41	102.57

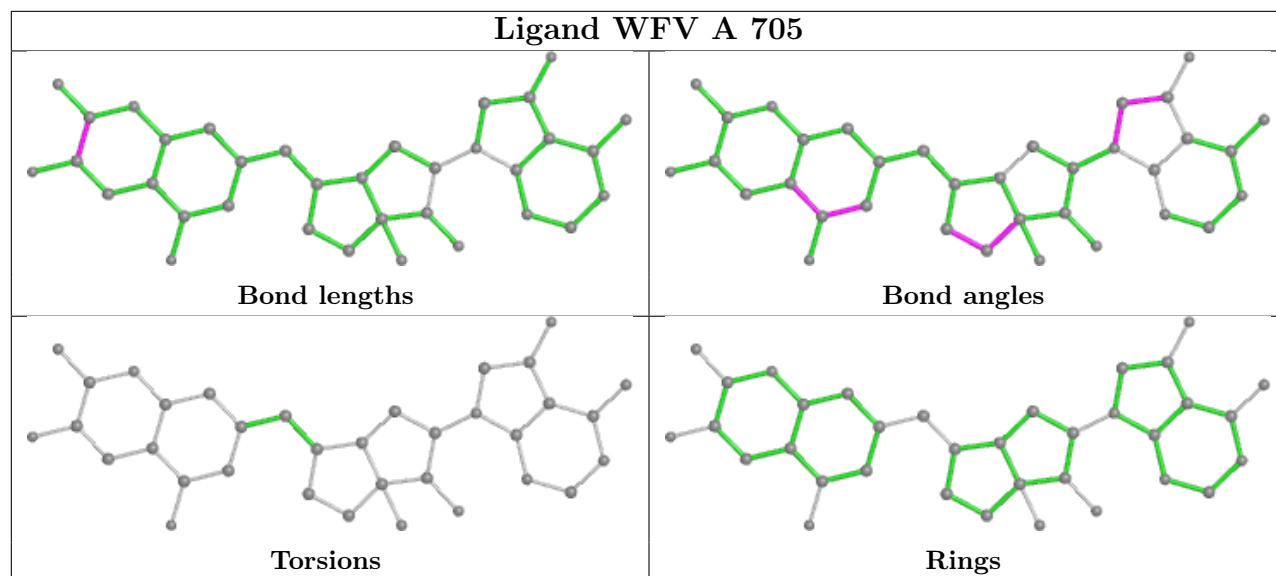
There are no chirality outliers.

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 than 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

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	625/645 (96%)	0.49	37 (5%) 22 23	20, 40, 72, 93	0
2	B	311/350 (88%)	1.20	50 (16%) 1 1	37, 58, 79, 114	0
All	All	936/995 (94%)	0.73	87 (9%) 8 8	20, 47, 75, 114	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	209	SER	6.0
1	A	296	ALA	5.9
1	A	176	THR	5.9
2	B	22	ASN	5.7
1	A	273	SER	5.6
2	B	208	CYS	5.5
2	B	18	ASN	5.4
2	B	248	VAL	5.4
2	B	210	ALA	5.3
1	A	294	PRO	5.2
1	A	274	GLU	5.0
2	B	21	PRO	5.0
1	A	175	HIS	4.9
1	A	243	PHE	4.9
2	B	23	ALA	4.7
1	A	299	LEU	4.3
1	A	146	HIS	4.3
2	B	243	LYS	4.2
2	B	19	LEU	4.2
1	A	529	MET	4.2
1	A	277	PHE	4.2
1	A	293	PRO	3.9
2	B	211	PRO	3.9
2	B	212	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	290	LEU	3.9
1	A	272	HIS	3.8
2	B	24	PRO	3.8
2	B	114	LEU	3.8
2	B	245	THR	3.8
1	A	528	PRO	3.7
2	B	312	LEU	3.6
2	B	71	GLY	3.6
2	B	308	LEU	3.5
2	B	72	PHE	3.4
1	A	356	THR	3.4
1	A	526	ARG	3.3
2	B	118	LYS	3.3
2	B	25	ALA	3.2
1	A	174	THR	3.1
2	B	270	PHE	3.1
2	B	67	ALA	3.1
1	A	275	LYS	3.0
2	B	26	CYS	3.0
2	B	86	LEU	3.0
1	A	292	PRO	2.9
1	A	255	PHE	2.8
2	B	110	GLU	2.7
1	A	383	ASP	2.7
2	B	84	ALA	2.7
1	A	249	MET	2.7
2	B	302	ASP	2.6
2	B	306	SER	2.5
2	B	244	SER	2.5
1	A	177	GLU	2.5
1	A	237	LEU	2.5
1	A	307	TYR	2.5
2	B	27	MET	2.5
2	B	160	LEU	2.4
2	B	20	PRO	2.4
1	A	301	ALA	2.4
2	B	266	HIS	2.3
1	A	530	ILE	2.3
1	A	240	LYS	2.3
1	A	456	PHE	2.3
2	B	41	ALA	2.3
2	B	246	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	241	LYS	2.3
1	A	147	HIS	2.3
2	B	268	VAL	2.3
1	A	13	ARG	2.3
2	B	106	TRP	2.2
1	A	286	TYR	2.2
2	B	32	GLU	2.2
2	B	69	ASN	2.2
2	B	207	GLY	2.2
2	B	301	ARG	2.2
2	B	239	LEU	2.1
2	B	85	ASP	2.1
1	A	290	ASN	2.1
2	B	83	VAL	2.1
2	B	92	ARG	2.1
2	B	269	PRO	2.0
2	B	328	PRO	2.0
1	A	371	LEU	2.0
2	B	145	LYS	2.0
1	A	59	ALA	2.0
1	A	58	PRO	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 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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	EDO	A	701	4/4	0.77	0.25	40,40,41,41	0
3	EDO	A	704	4/4	0.81	0.22	57,57,57,57	0

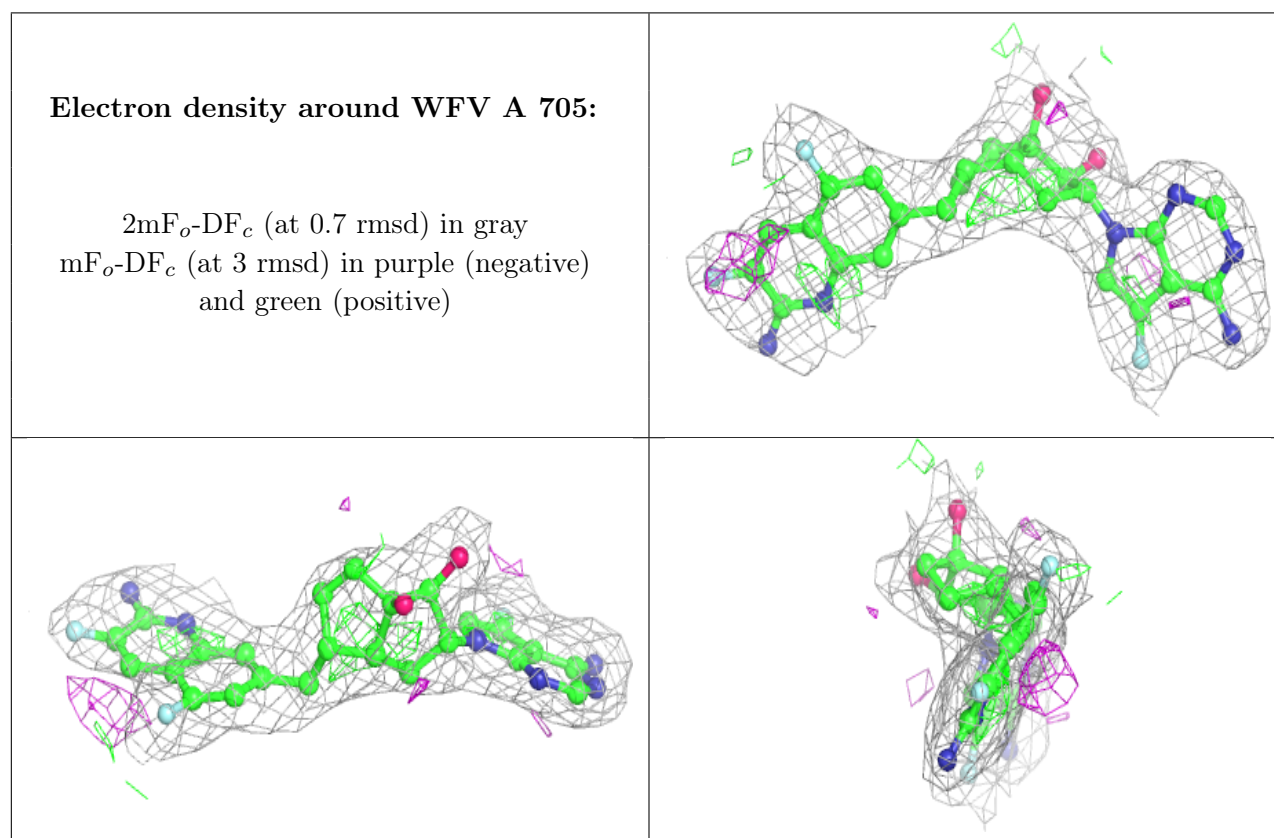
*Continued on next page...*



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	A	703	4/4	0.82	0.23	48,48,48,48	0
3	EDO	A	702	4/4	0.88	0.24	36,36,36,36	0
4	WFV	A	705	35/35	0.92	0.18	29,32,33,34	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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.