



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2024 – 10:57 pm BST

PDB ID : 8P1Q  
Title : USP28 in complex with FT206  
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Deposited on : 2023-05-12  
Resolution : 2.79 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36.2  
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) : 2.36.2

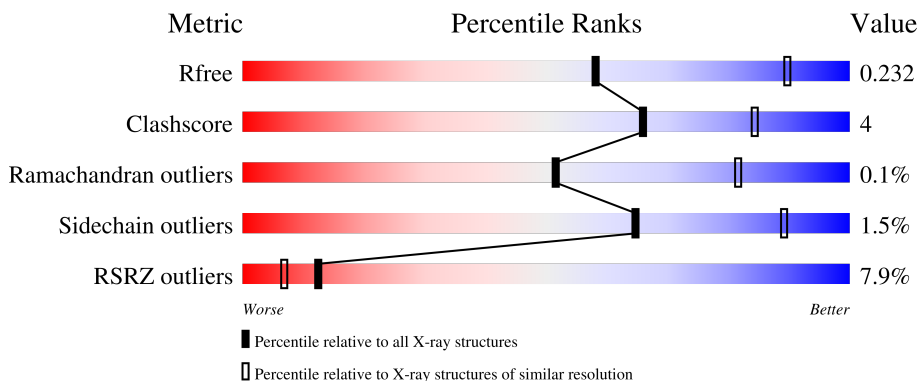
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.79 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	494	 4% 77% 11% 11%
1	B	494	 9% 74% 8% 18%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6782 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 Ubiquitin carboxyl-terminal hydrolase 28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	439	3534	2264	592	657	21	0	2	0
1	B	405	3121	2003	516	583	19	0	1	0

There are 10 discrepancies between the modelled and reference sequences:

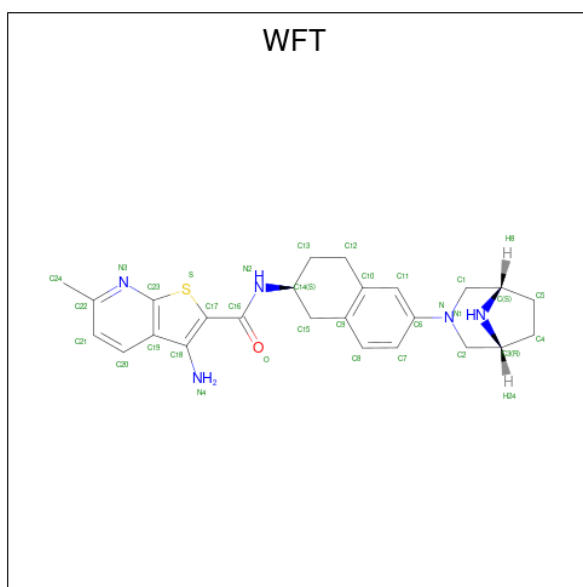
Chain	Residue	Modelled	Actual	Comment	Reference
A	148	GLY	-	expression tag	UNP Q96RU2
A	525	SER	-	linker	UNP Q96RU2
A	526	GLY	-	linker	UNP Q96RU2
A	527	SER	-	linker	UNP Q96RU2
A	528	GLY	-	linker	UNP Q96RU2
B	148	GLY	-	expression tag	UNP Q96RU2
B	525	SER	-	linker	UNP Q96RU2
B	526	GLY	-	linker	UNP Q96RU2
B	527	SER	-	linker	UNP Q96RU2
B	528	GLY	-	linker	UNP Q96RU2

- Molecule 2 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

- Molecule 3 is 3-azanyl-N-[(2S)-6-[(1S,5R)-3,8-diazabicyclo[3.2.1]octan-3-yl]-1,2,3,4-tetrahydro naphthalen-2-yl]-6-methyl-thieno[2,3-b]pyridine-2-carboxamide (three-letter code: WFT) (formula: C<sub>25</sub>H<sub>29</sub>N<sub>5</sub>OS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			32	25	5	1	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	B	1	32	25	5	1	1	0	0

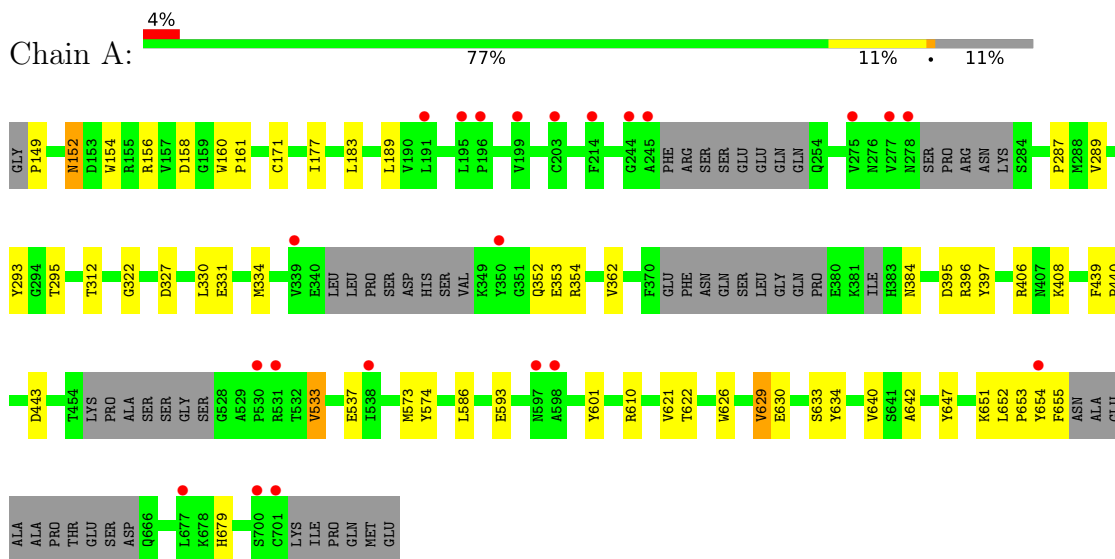
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	43	Total	O	0	0
			43	43		
4	B	12	Total	O	0	0
			12	12		

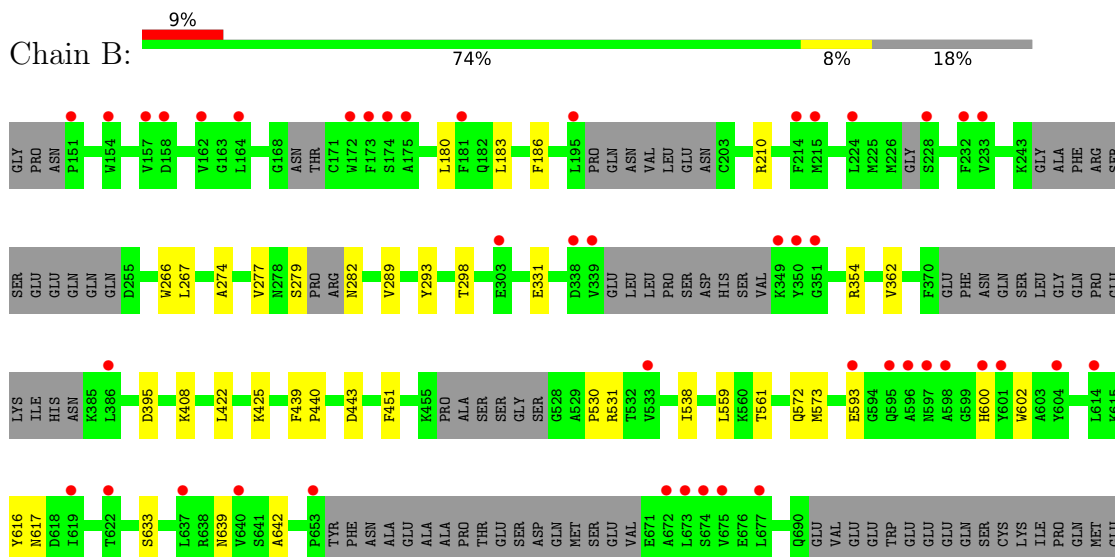
### 3 Residue-property plots [i](#)

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: Ubiquitin carboxyl-terminal hydrolase 28



- Molecule 1: Ubiquitin carboxyl-terminal hydrolase 28



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.44Å 105.54Å 178.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.09 – 2.79 46.09 – 2.79	Depositor EDS
% Data completeness (in resolution range)	72.0 (46.09-2.79) 72.0 (46.09-2.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 2.77Å)	Xtrriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, $R_{free}$	0.212 , 0.235 0.210 , 0.232	Depositor DCC
$R_{free}$ test set	1216 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	79.9	Xtrriage
Anisotropy	0.133	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 69.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.020 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6782	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	101.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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: DMS, WFT

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	0.25	0/3625	0.45	0/4917
1	B	0.25	0/3191	0.45	0/4339
All	All	0.25	0/6816	0.45	0/9256

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	3534	0	3315	33	0
1	B	3121	0	2868	23	0
2	A	8	0	12	0	0
3	A	32	0	0	1	0
3	B	32	0	0	0	0
4	A	43	0	0	2	0
4	B	12	0	0	0	0
All	All	6782	0	6195	52	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 4.



All (52) 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:B:279:SER:HG	1:B:282:ASN:N	1.63	0.96
1:B:279:SER:OG	1:B:282:ASN:N	2.28	0.64
1:A:633:SER:HB3	1:A:642:ALA:HB2	1.80	0.63
1:B:298:THR:HG23	1:B:354:ARG:HG3	1.82	0.62
1:A:295:THR:HG22	1:A:312:THR:HG22	1.82	0.62
1:B:633:SER:HB3	1:B:642:ALA:HB2	1.81	0.60
1:A:396[B]:ARG:HH21	1:A:574:TYR:HB2	1.69	0.58
1:A:161:PRO:HB2	1:A:621:VAL:HG11	1.86	0.57
1:A:353:GLU:OE1	1:A:406:ARG:NH1	2.37	0.57
1:A:327:ASP:OD1	1:A:396[B]:ARG:NH1	2.37	0.57
1:A:183:LEU:HD21	1:A:362:VAL:HG21	1.89	0.55
1:A:630:GLU:HG2	1:A:634:TYR:CZ	2.41	0.54
1:A:152:ASN:O	1:A:152:ASN:ND2	2.41	0.54
1:A:156:ARG:HD2	1:A:160:TRP:O	2.09	0.53
1:A:154:TRP:HH2	1:B:561:THR:HG22	1.73	0.53
1:A:440:PRO:HG2	1:A:443:ASP:HB2	1.91	0.52
1:A:352:GLN:OE1	1:A:354:ARG:NH1	2.43	0.52
1:A:322:GLY:H	1:A:384:ASN:HD22	1.57	0.52
1:B:439:PHE:CG	1:B:440:PRO:HD2	2.45	0.52
1:A:652:LEU:O	1:A:654:TYR:N	2.40	0.52
1:A:149:PRO:HG3	1:B:559:LEU:HD23	1.94	0.50
1:B:183:LEU:HD21	1:B:362:VAL:HG21	1.94	0.49
1:A:439:PHE:CG	1:A:440:PRO:HD2	2.47	0.49
1:B:210:ARG:HD2	1:B:266:TRP:CH2	2.48	0.49
1:A:593:GLU:HB2	1:A:640:VAL:HG22	1.94	0.49
1:A:396[B]:ARG:HD2	1:A:397:TYR:CZ	2.48	0.49
1:A:601:TYR:HE2	3:A:802:WFT:C5	2.26	0.49
1:A:334:MET:HE1	1:A:397:TYR:HB3	1.94	0.48
1:A:610:ARG:NH2	4:A:901:HOH:O	2.46	0.48
1:B:440:PRO:HG2	1:B:443:ASP:HB2	1.95	0.48
1:B:600:HIS:NE2	1:B:617:ASN:OD1	2.46	0.48
1:B:289:VAL:HA	1:B:293:TYR:CD1	2.52	0.45
1:A:189:LEU:HD13	1:A:287:PRO:HB2	2.00	0.44
1:A:408:LYS:HD3	1:A:573:MET:HG3	1.98	0.44
1:A:289:VAL:HA	1:A:293:TYR:CD1	2.53	0.44
1:A:622:THR:HA	1:B:572[A]:GLN:NE2	2.33	0.44
1:A:533:VAL:HG13	1:A:537:GLU:HB3	2.00	0.44
1:A:651:LYS:NZ	4:A:902:HOH:O	2.51	0.43
1:B:180:LEU:HB3	1:B:186:PHE:CE2	2.53	0.43
1:B:593:GLU:HA	1:B:639:ASN:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:422:LEU:O	1:B:425:LYS:HB2	2.19	0.43
1:A:626:TRP:HA	1:A:629:VAL:HG13	2.00	0.43
1:A:177:ILE:HD13	1:A:177:ILE:HA	1.90	0.42
1:B:602:TRP:HB2	1:B:616:TYR:O	2.19	0.42
1:B:408:LYS:HD3	1:B:573:MET:HG3	1.99	0.42
1:A:158:ASP:OD2	1:B:408:LYS:NZ	2.53	0.41
1:B:186:PHE:HZ	1:B:267:LEU:HD13	1.85	0.41
1:B:274:ALA:O	1:B:277:VAL:HG22	2.21	0.41
1:B:451:PHE:CZ	1:B:530:PRO:HB3	2.55	0.41
1:B:531:ARG:HA	1:B:538:ILE:HD11	2.03	0.41
1:A:586:LEU:HD13	1:A:647:TYR:CZ	2.56	0.40
1:A:330:LEU:O	1:A:334:MET:HG2	2.22	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	425/494 (86%)	415 (98%)	9 (2%)	1 (0%)	47	78
1	B	386/494 (78%)	373 (97%)	13 (3%)	0	100	100
All	All	811/988 (82%)	788 (97%)	22 (3%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	653	PRO

### 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	370/449 (82%)	362 (98%)	8 (2%)	52	83
1	B	313/449 (70%)	311 (99%)	2 (1%)	86	96
All	All	683/898 (76%)	673 (98%)	10 (2%)	65	89

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	ASN
1	A	171	CYS
1	A	331	GLU
1	A	395	ASP
1	A	533	VAL
1	A	629	VAL
1	A	655	PHE
1	A	679	HIS
1	B	331	GLU
1	B	395	ASP

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

### 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](#)

4 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	WFT	B	801	-	34,37,37	0.60	0	39,55,55	1.47	3 (7%)
2	DMS	A	803	-	3,3,3	0.66	0	3,3,3	0.46	0
2	DMS	A	801	-	3,3,3	0.66	0	3,3,3	0.49	0
3	WFT	A	802	-	34,37,37	0.65	0	39,55,55	1.45	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
3	WFT	B	801	-	-	0/8/38/38	0/6/6/6
3	WFT	A	802	-	-	0/8/38/38	0/6/6/6

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	WFT	C20-C19-C18	-6.97	131.53	135.53
3	A	802	WFT	C20-C19-C18	-6.73	131.67	135.53
3	B	801	WFT	C18-C19-C23	3.77	111.79	107.47
3	A	802	WFT	C18-C19-C23	3.65	111.64	107.47
3	B	801	WFT	C4-C3-C2	2.57	113.98	111.63
3	A	802	WFT	C1-N-C2	2.05	119.12	113.42

There are no chirality outliers.

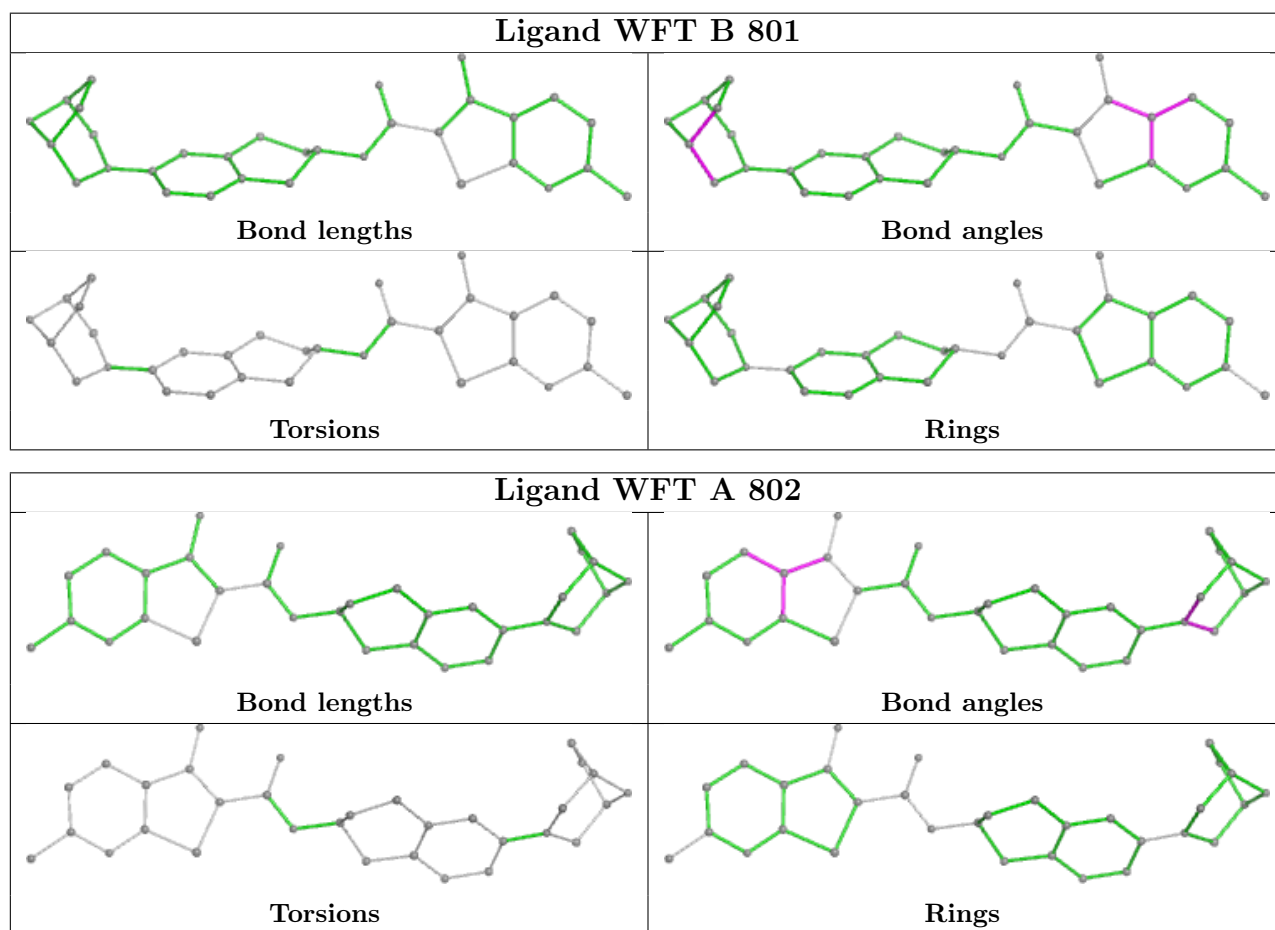
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	WFT	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 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

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	439/494 (88%)	0.31	22 (5%) 28 19	39, 86, 156, 244	0
1	B	405/494 (81%)	0.64	45 (11%) 5 3	44, 115, 197, 234	0
All	All	844/988 (85%)	0.47	67 (7%) 12 7	39, 95, 191, 244	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	195	LEU	4.7
1	B	224	LEU	4.7
1	B	677	LEU	4.4
1	B	154	TRP	4.0
1	B	622	THR	4.0
1	B	597	ASN	3.9
1	B	351	GLY	3.8
1	B	619	ILE	3.8
1	A	195	LEU	3.7
1	A	244	GLY	3.7
1	B	598	ALA	3.7
1	B	675	VAL	3.7
1	A	598	ALA	3.7
1	A	701	CYS	3.6
1	A	277	VAL	3.6
1	A	245	ALA	3.5
1	B	604	TYR	3.5
1	A	597	ASN	3.5
1	B	164	LEU	3.2
1	B	640	VAL	3.2
1	A	530	PRO	3.2
1	A	350	TYR	3.1
1	B	228	SER	3.1
1	B	350	TYR	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	677	LEU	3.0
1	B	151	PRO	3.0
1	B	596	ALA	2.9
1	B	157	VAL	2.8
1	A	214	PHE	2.8
1	B	338	ASP	2.8
1	B	175	ALA	2.8
1	B	601	TYR	2.8
1	B	595	GLN	2.7
1	B	386	LEU	2.7
1	A	203	CYS	2.7
1	B	232	PHE	2.7
1	A	654	TYR	2.6
1	B	162	VAL	2.6
1	B	614	LEU	2.6
1	B	303	GLU	2.6
1	A	199	VAL	2.6
1	B	215	MET	2.6
1	B	174	SER	2.6
1	B	672	ALA	2.5
1	B	172	TRP	2.5
1	A	339	VAL	2.5
1	B	674	SER	2.4
1	B	173	PHE	2.4
1	B	181	PHE	2.4
1	B	673	LEU	2.4
1	A	538	ILE	2.3
1	B	349	LYS	2.3
1	B	600	HIS	2.3
1	A	700	SER	2.3
1	B	233	VAL	2.3
1	A	191	LEU	2.2
1	B	214	PHE	2.2
1	B	533	VAL	2.2
1	A	531	ARG	2.1
1	B	158	ASP	2.1
1	A	196	PRO	2.0
1	B	653	PRO	2.0
1	B	593	GLU	2.0
1	A	275	VAL	2.0
1	A	278	ASN	2.0
1	B	637	LEU	2.0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	339	VAL	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](#)

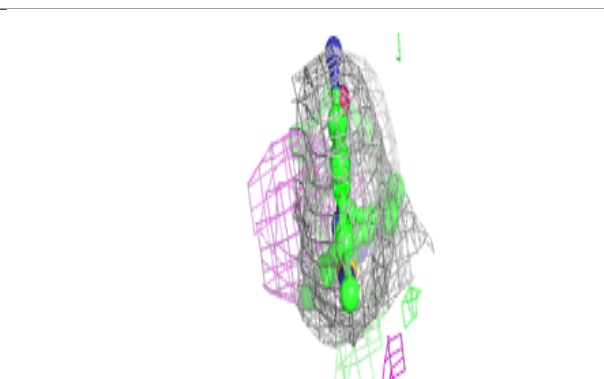
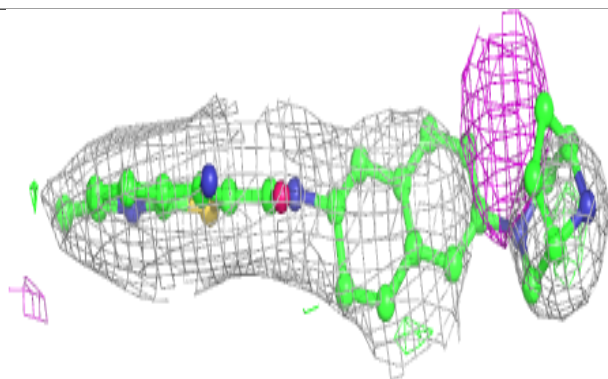
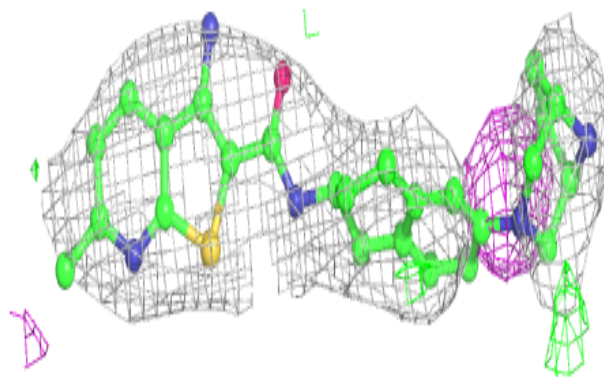
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	DMS	A	803	4/4	0.85	0.28	66,72,75,143	0
3	WFT	B	801	32/32	0.85	0.28	74,108,158,165	0
3	WFT	A	802	32/32	0.95	0.26	46,74,102,107	0
2	DMS	A	801	4/4	0.98	0.16	38,60,72,73	0

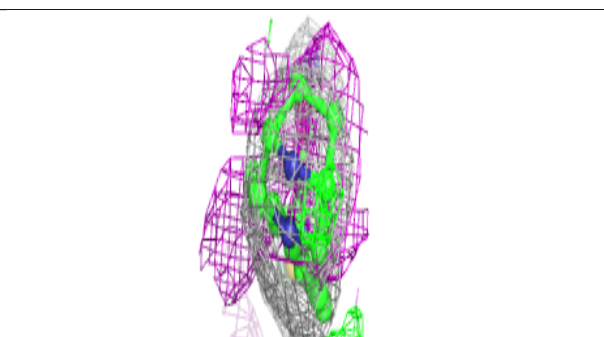
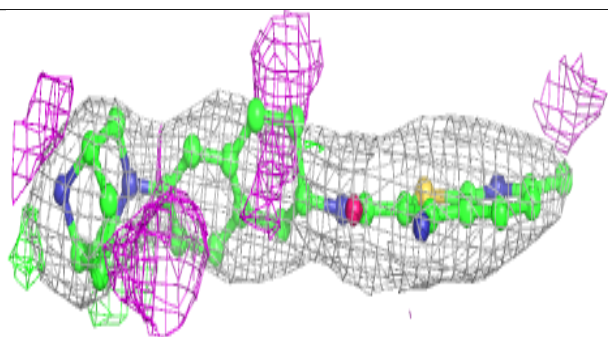
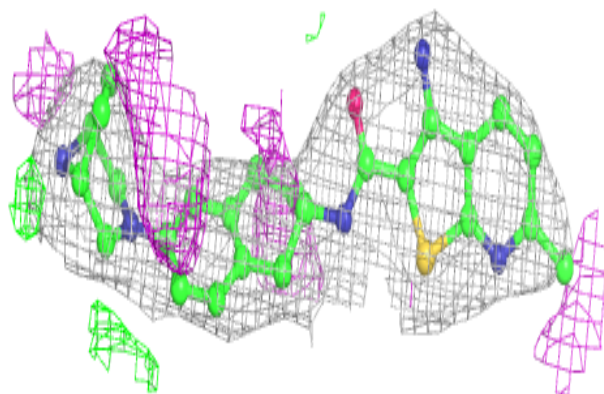
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around WFT B 801:**

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

**Electron density around WFT A 802:**

$2mF_o-DF_c$  (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.