



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2023 – 12:14 PM EDT

PDB ID : 8TB6  
Title : TYK2 JH2 bound to Compound14  
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Deposited on : 2023-06-28  
Resolution : 1.96 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

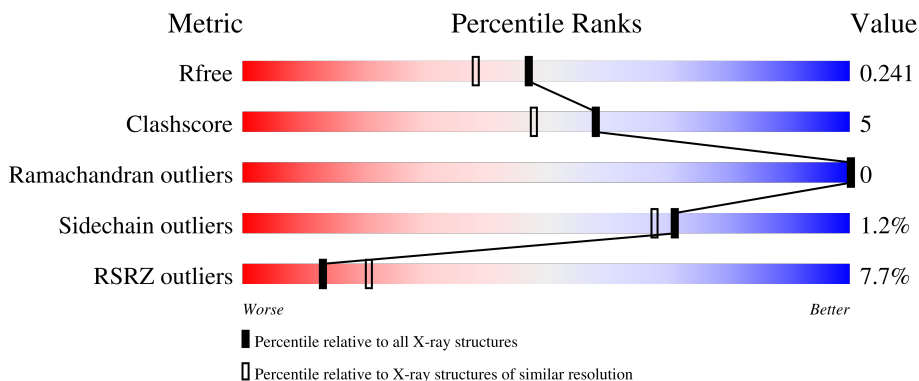
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.96 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	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  $\geq 3$ , 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	326	 5% 72% 8% 19%
1	B	326	 7% 71% 7% 22%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 4327 atoms, of which 42 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 Non-receptor tyrosine-protein kinase TYK2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	263	2031	1291	367	362	11	0	1	0
1	B	254	1958	1246	350	351	11	0	1	0

There are 42 discrepancies between the modelled and reference sequences:

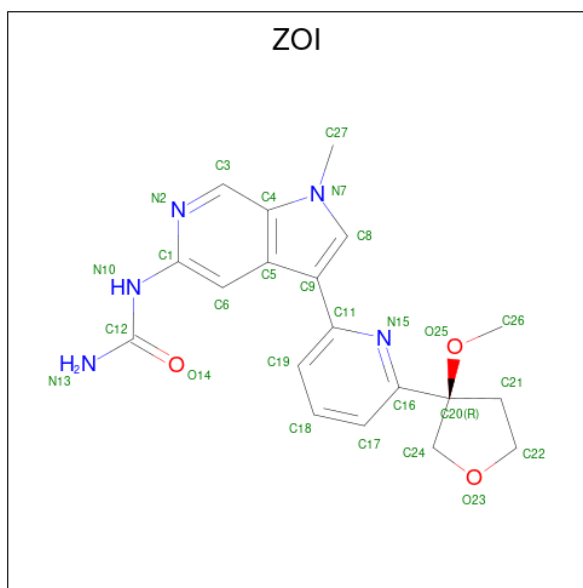
Chain	Residue	Modelled	Actual	Comment	Reference
A	545	ALA	-	expression tag	UNP P29597
A	546	HIS	-	expression tag	UNP P29597
A	547	HIS	-	expression tag	UNP P29597
A	548	HIS	-	expression tag	UNP P29597
A	549	HIS	-	expression tag	UNP P29597
A	550	HIS	-	expression tag	UNP P29597
A	551	HIS	-	expression tag	UNP P29597
A	552	HIS	-	expression tag	UNP P29597
A	553	HIS	-	expression tag	UNP P29597
A	554	HIS	-	expression tag	UNP P29597
A	555	HIS	-	expression tag	UNP P29597
A	556	GLY	-	expression tag	UNP P29597
A	557	ALA	-	expression tag	UNP P29597
A	558	LEU	-	expression tag	UNP P29597
A	559	GLU	-	expression tag	UNP P29597
A	560	VAL	-	expression tag	UNP P29597
A	561	LEU	-	expression tag	UNP P29597
A	562	PHE	-	expression tag	UNP P29597
A	563	GLN	-	expression tag	UNP P29597
A	564	GLY	-	expression tag	UNP P29597
A	565	PRO	-	expression tag	UNP P29597
B	545	ALA	-	expression tag	UNP P29597
B	546	HIS	-	expression tag	UNP P29597
B	547	HIS	-	expression tag	UNP P29597
B	548	HIS	-	expression tag	UNP P29597

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Chain	Residue	Modelled	Actual	Comment	Reference
B	549	HIS	-	expression tag	UNP P29597
B	550	HIS	-	expression tag	UNP P29597
B	551	HIS	-	expression tag	UNP P29597
B	552	HIS	-	expression tag	UNP P29597
B	553	HIS	-	expression tag	UNP P29597
B	554	HIS	-	expression tag	UNP P29597
B	555	HIS	-	expression tag	UNP P29597
B	556	GLY	-	expression tag	UNP P29597
B	557	ALA	-	expression tag	UNP P29597
B	558	LEU	-	expression tag	UNP P29597
B	559	GLU	-	expression tag	UNP P29597
B	560	VAL	-	expression tag	UNP P29597
B	561	LEU	-	expression tag	UNP P29597
B	562	PHE	-	expression tag	UNP P29597
B	563	GLN	-	expression tag	UNP P29597
B	564	GLY	-	expression tag	UNP P29597
B	565	PRO	-	expression tag	UNP P29597

- Molecule 2 is N-[(3M)-3-{6-[(3R)-3-methoxyoxolan-3-yl]pyridin-2-yl}-1-methyl-1H-pyrrolo[2,3-c]pyridin-5-yl]urea (three-letter code: ZOI) (formula: C<sub>19</sub>H<sub>21</sub>N<sub>5</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	N			O
2	A	1	Total	C	H	N	O	0	0
			48	19	21	5	3		
2	B	1	Total	C	H	N	O	0	0
			48	19	21	5	3		

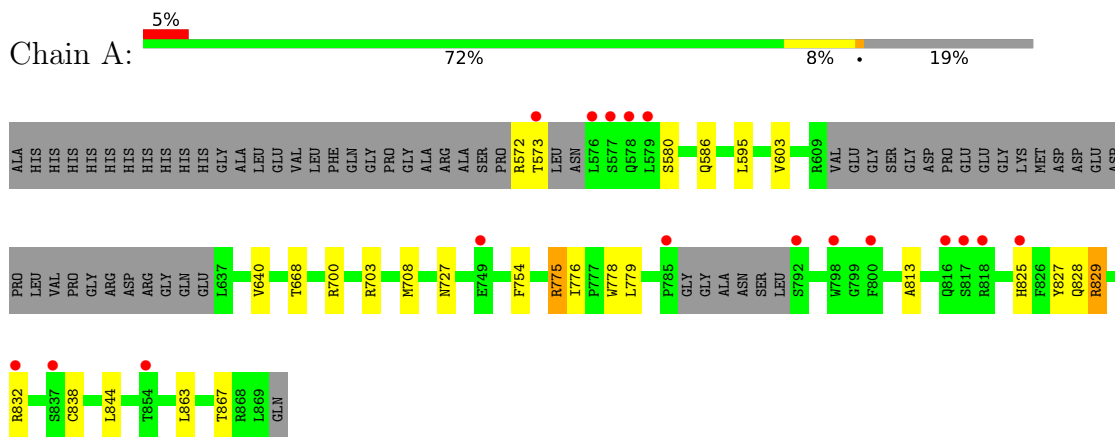
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	128	Total 128	O 128	0	0
3	B	114	Total 114	O 114	0	0

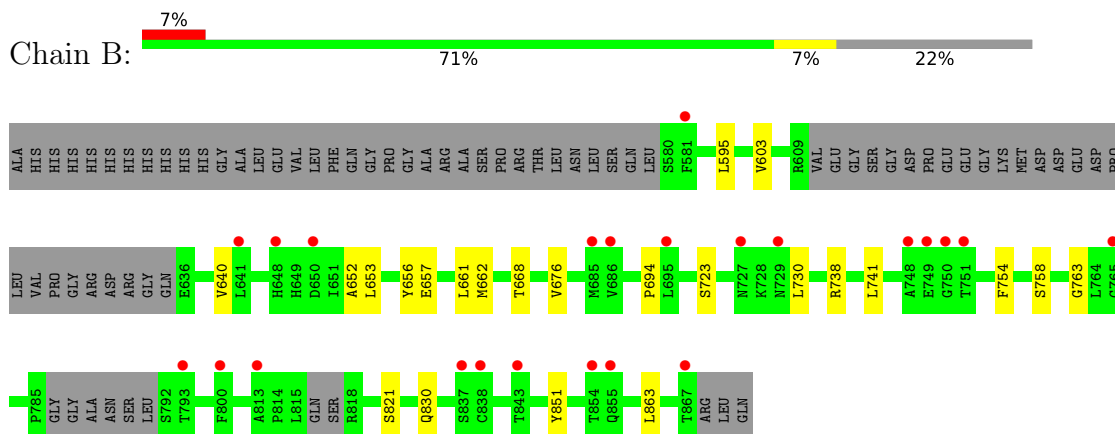
### 3 Residue-property plots [i](#)

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: Non-receptor tyrosine-protein kinase TYK2



- Molecule 1: Non-receptor tyrosine-protein kinase TYK2



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.47Å 47.72Å 119.31Å 90.00° 91.08° 90.00°	Depositor
Resolution (Å)	19.76 – 1.96 19.76 – 1.96	Depositor EDS
% Data completeness (in resolution range)	98.3 (19.76-1.96) 98.3 (19.76-1.96)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 1.96Å)	Xtrriage
Refinement program	BUSTER, PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.193 , 0.236 0.200 , 0.241	Depositor DCC
$R_{free}$ test set	2067 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.1	Xtrriage
Anisotropy	0.106	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.054 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4327	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.85% 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: ZOI

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	0.36	0/2077	0.58	0/2825
1	B	0.37	0/2003	0.57	0/2725
All	All	0.36	0/4080	0.58	0/5550

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	2031	0	1996	21	0
1	B	1958	0	1916	17	0
2	A	27	21	0	0	0
2	B	27	21	0	1	0
3	A	128	0	0	2	0
3	B	114	0	0	2	0
All	All	4285	42	3912	38	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 (38) 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:727:ASN:ND2	3:A:1001:HOH:O	2.05	0.84
1:B:661:LEU:HD23	1:B:662:MET:CE	2.23	0.69
1:B:694:PRO:HB3	1:B:738:ARG:HD3	1.76	0.66
1:A:708:MET:HG2	1:A:838:CYS:SG	2.37	0.65
1:A:700:ARG:HB3	1:A:703:ARG:HH21	1.63	0.64
1:B:661:LEU:HD23	1:B:662:MET:HE3	1.85	0.59
1:A:700:ARG:CB	1:A:703:ARG:HH21	2.17	0.57
1:B:668:THR:HG22	1:B:754:PHE:HZ	1.69	0.57
1:A:700:ARG:HB3	1:A:703:ARG:NH2	2.19	0.57
1:B:656:TYR:CE1	1:B:676:VAL:HG11	2.40	0.56
1:B:668:THR:HG22	1:B:754:PHE:CZ	2.43	0.53
1:A:586:GLN:HG2	3:A:1076:HOH:O	2.09	0.52
1:B:603[A]:VAL:HG13	1:B:640:VAL:CG1	2.41	0.51
1:B:668:THR:CG2	1:B:754:PHE:HZ	2.23	0.51
1:B:640:VAL:HG21	2:B:901:ZOI:C1	2.41	0.51
1:B:653:LEU:O	1:B:657:GLU:HG3	2.13	0.48
1:B:661:LEU:HD11	1:B:730:LEU:HD22	1.95	0.48
1:A:825:HIS:O	1:A:829:ARG:HD2	2.14	0.48
1:B:830:GLN:HA	1:B:851:TYR:CZ	2.49	0.47
1:A:863:LEU:O	1:A:867:THR:HG23	2.15	0.47
1:B:741:LEU:HD11	1:B:758:SER:HB2	1.97	0.46
1:B:821:SER:HB2	3:B:1085:HOH:O	2.15	0.46
1:A:776:ILE:HG12	1:A:827:TYR:CE2	2.52	0.45
1:B:652:ALA:O	1:B:656:TYR:HD2	2.01	0.44
1:A:603[A]:VAL:HG13	1:A:640:VAL:CG1	2.47	0.44
1:A:668:THR:HG22	1:A:754:PHE:CZ	2.52	0.44
1:A:832:ARG:HE	1:A:832:ARG:HB3	1.66	0.44
1:A:775:ARG:HB3	1:A:779:LEU:HB2	1.99	0.44
1:A:825:HIS:HB3	1:A:829:ARG:NH1	2.32	0.43
1:A:778:TRP:CZ2	1:A:813:ALA:HB2	2.53	0.43
1:A:595:LEU:HB2	1:A:603[B]:VAL:HG23	2.01	0.43
1:B:595:LEU:HB2	1:B:603[B]:VAL:HG23	2.01	0.43
1:A:825:HIS:HD2	1:A:828:GLN:HE22	1.66	0.42
1:A:572:ARG:O	1:A:573:THR:O	2.37	0.42
1:A:572:ARG:O	1:A:573:THR:C	2.57	0.42
1:B:763:GLY:HA3	3:B:1016:HOH:O	2.20	0.41
1:A:668:THR:HG22	1:A:754:PHE:HZ	1.86	0.40
1:A:844:LEU:HD12	1:A:844:LEU:HA	1.80	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	256/326 (78%)	253 (99%)	3 (1%)	0	100	100
1	B	247/326 (76%)	241 (98%)	6 (2%)	0	100	100
All	All	503/652 (77%)	494 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	215/278 (77%)	212 (99%)	3 (1%)	67	62
1	B	207/278 (74%)	205 (99%)	2 (1%)	76	74
All	All	422/556 (76%)	417 (99%)	5 (1%)	71	68

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	580	SER
1	A	775	ARG
1	A	829	ARG
1	B	723	SER
1	B	863	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	586	GLN
1	A	727	ASN
1	A	729	ASN
1	A	825	HIS
1	A	828	GLN
1	A	830	GLN
1	B	729	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](#)

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		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	ZOI	A	901	-	26,30,30	1.00	1 (3%)	32,44,44	2.22	6 (18%)
2	ZOI	B	901	-	26,30,30	1.05	1 (3%)	32,44,44	2.00	4 (12%)

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	ZOI	A	901	-	-	5/13/26/26	0/4/4/4
2	ZOI	B	901	-	-	4/13/26/26	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	ZOI	C9-C11	-3.50	1.44	1.49
2	B	901	ZOI	C9-C11	-3.50	1.44	1.49

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	ZOI	N13-C12-N10	-7.70	106.83	115.49
2	B	901	ZOI	N13-C12-N10	-7.11	107.48	115.49
2	A	901	ZOI	O14-C12-N10	7.09	130.12	122.36
2	B	901	ZOI	O14-C12-N10	6.45	129.42	122.36
2	A	901	ZOI	C11-C9-C5	3.87	131.46	123.90
2	B	901	ZOI	C11-C9-C5	3.08	129.93	123.90
2	A	901	ZOI	C26-O25-C20	-2.99	112.34	115.96
2	B	901	ZOI	C26-O25-C20	-2.54	112.89	115.96
2	A	901	ZOI	C3-N2-C1	2.27	120.11	117.81
2	A	901	ZOI	C8-C9-C11	-2.10	120.62	127.25

There are no chirality outliers.

All (9) torsion outliers are listed below:

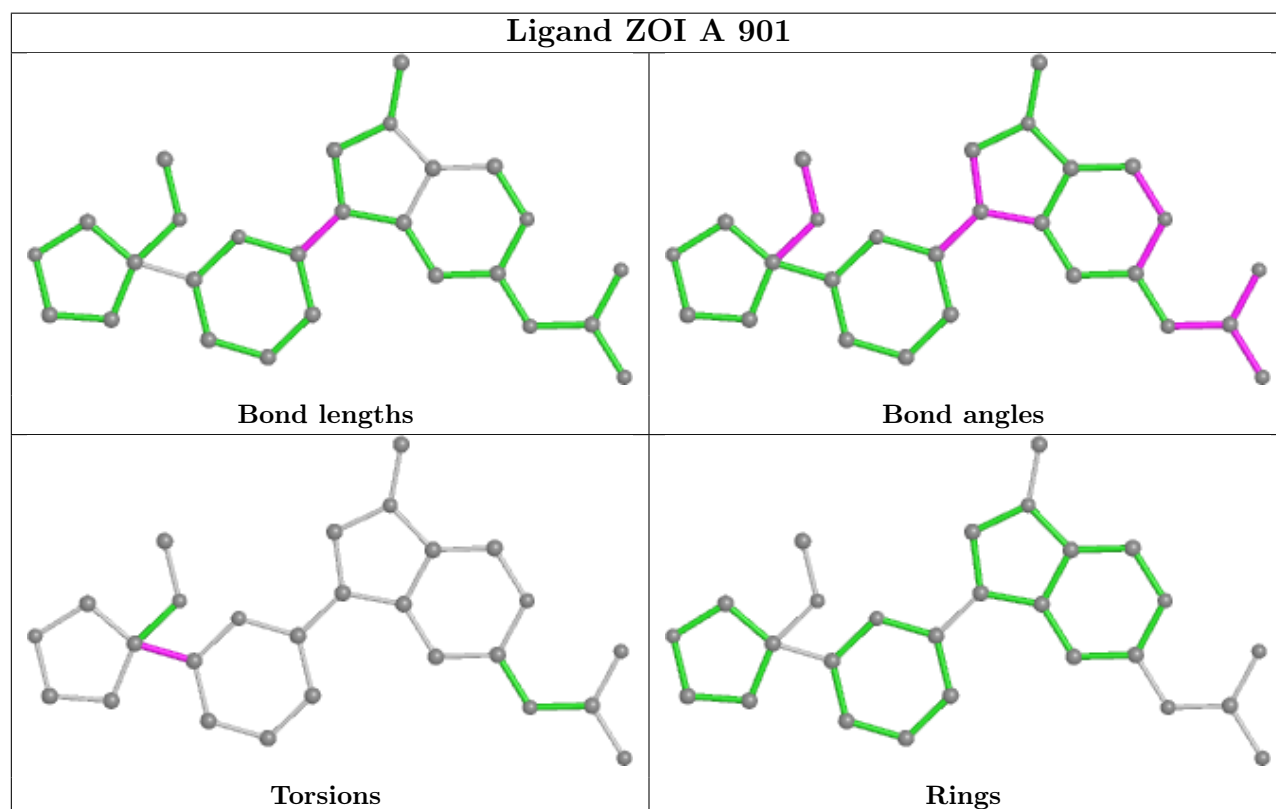
Mol	Chain	Res	Type	Atoms
2	A	901	ZOI	C17-C16-C20-O25
2	A	901	ZOI	N15-C16-C20-C24
2	A	901	ZOI	N15-C16-C20-O25
2	B	901	ZOI	C17-C16-C20-O25
2	B	901	ZOI	N15-C16-C20-O25
2	A	901	ZOI	N15-C16-C20-C21
2	B	901	ZOI	N15-C16-C20-C24
2	A	901	ZOI	C17-C16-C20-C21
2	B	901	ZOI	N15-C16-C20-C21

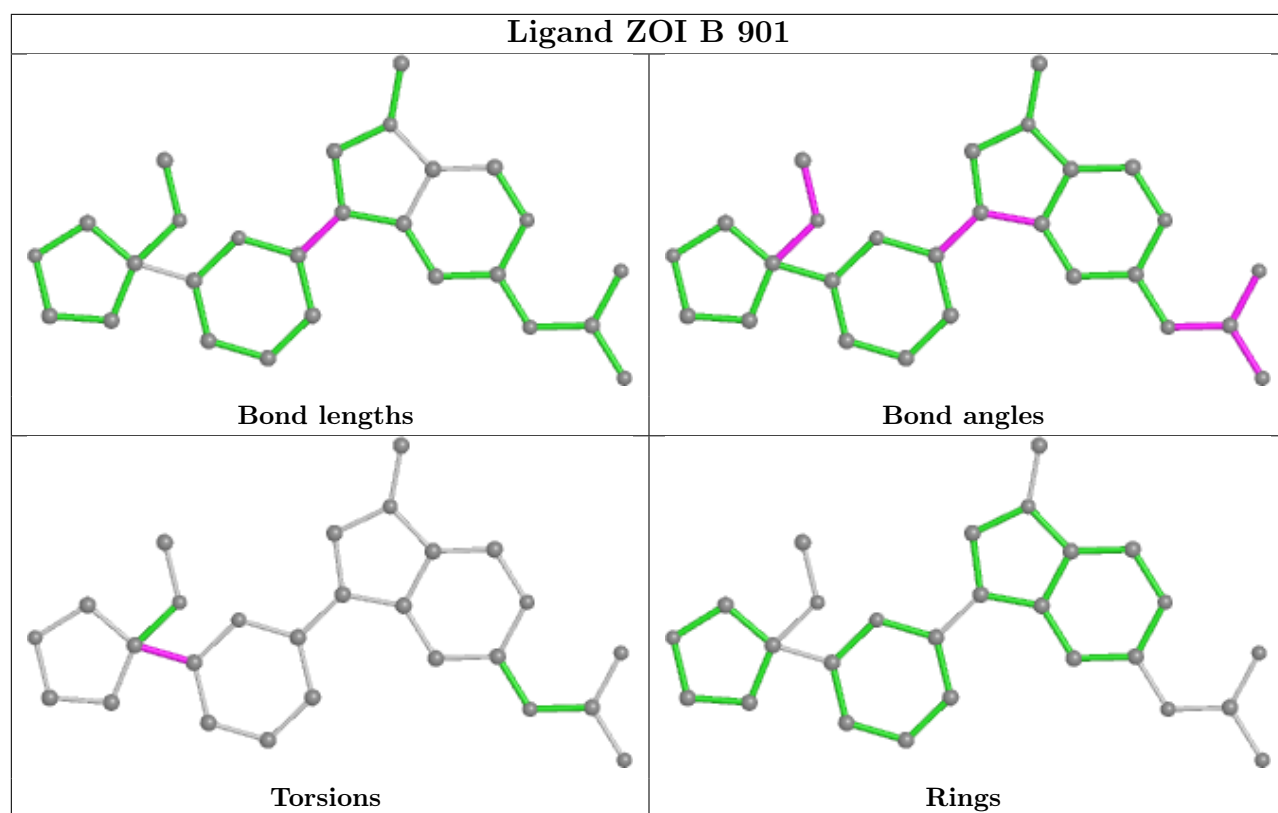
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	ZOI	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 [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	263/326 (80%)	0.42	17 (6%) 18 27	15, 26, 42, 61	0
1	B	254/326 (77%)	0.50	23 (9%) 9 15	18, 30, 44, 55	0
All	All	517/652 (79%)	0.46	40 (7%) 13 21	15, 28, 43, 61	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	750	GLY	6.5
1	A	577	SER	5.9
1	B	838	CYS	4.6
1	A	578	GLN	4.5
1	A	817	SER	4.3
1	B	748	ALA	3.9
1	B	837	SER	3.8
1	B	813	ALA	3.6
1	B	843	THR	3.3
1	B	751	THR	3.1
1	A	825	HIS	3.0
1	B	855	GLN	3.0
1	B	867	THR	2.7
1	B	686	VAL	2.4
1	A	854	THR	2.4
1	B	749	GLU	2.4
1	A	576	LEU	2.4
1	A	798	TRP	2.4
1	A	785	PRO	2.4
1	B	650	ASP	2.3
1	B	648	HIS	2.3
1	A	749	GLU	2.3
1	B	641	LEU	2.3
1	A	818	ARG	2.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	800	PHE	2.3
1	B	581	PHE	2.2
1	A	816	GLN	2.2
1	A	837	SER	2.2
1	B	729	ASN	2.2
1	B	765	GLY	2.2
1	B	695	LEU	2.2
1	A	573	THR	2.2
1	A	832	ARG	2.1
1	B	727	ASN	2.1
1	A	579	LEU	2.1
1	B	793	THR	2.0
1	B	685	MET	2.0
1	B	854	THR	2.0
1	A	800	PHE	2.0
1	A	792	SER	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.

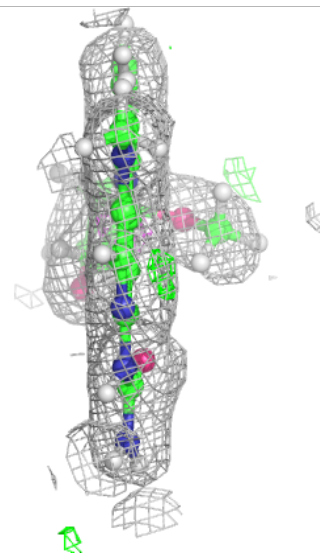
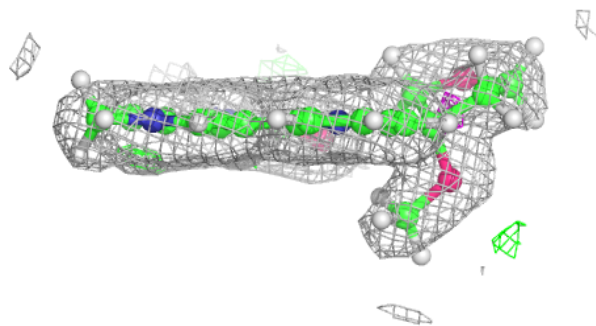
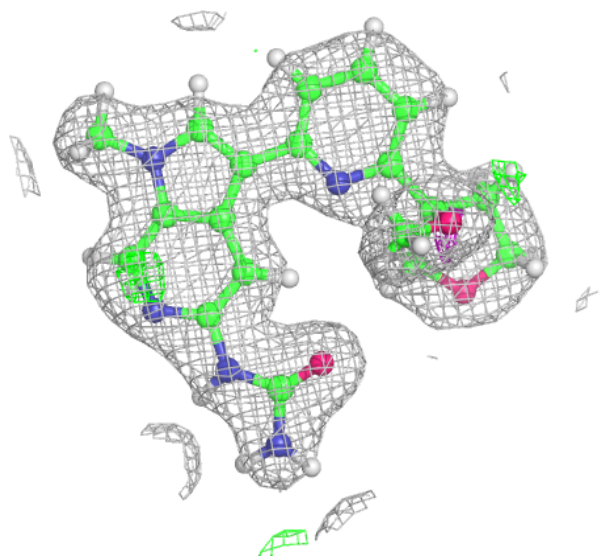
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZOI	A	901	27/27	0.94	0.11	15,20,24,24	0
2	ZOI	B	901	27/27	0.95	0.10	18,22,27,28	0

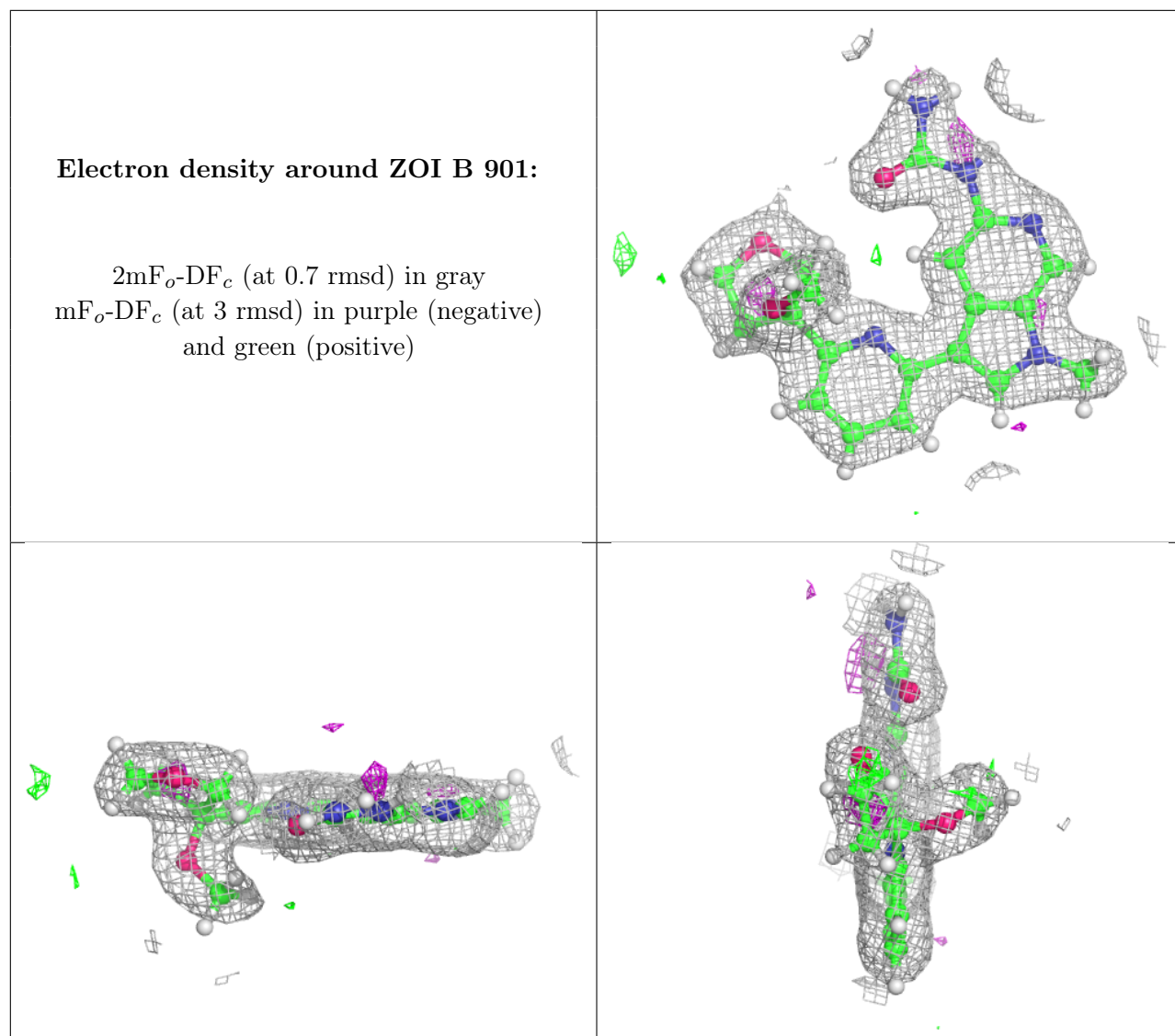
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



**Electron density around ZOI A 901:**

$2mF_o-DF_c$  (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.