



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 8, 2021 – 06:02 PM EST

PDB ID : 6VNE  
Title : JAK2 JH1 in complex with Fedratinib  
Authors : Davis, R.R.; Schonbrunn, E.  
Deposited on : 2020-01-29  
Resolution : 2.32 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 : 2.17  
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) : 2.17

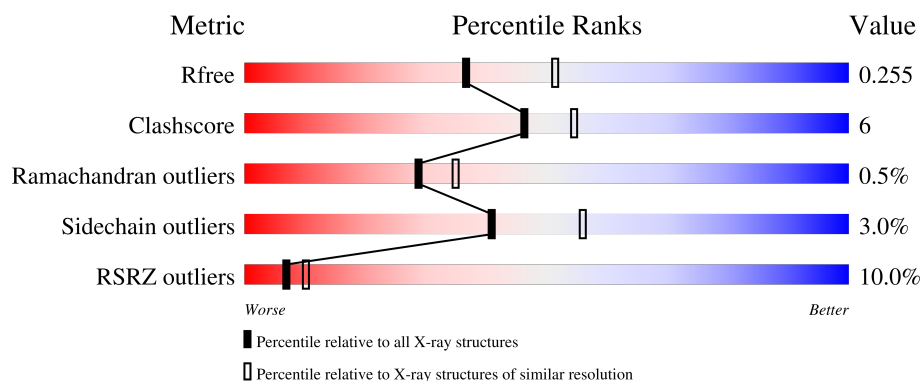
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.32 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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	308	<div> <div>10%</div> <div>78%</div> <div>15%</div> <div>• 5%</div> </div>
1	B	308	<div> <div>9%</div> <div>77%</div> <div>16%</div> <div>6%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4920 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 Tyrosine-protein kinase JAK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	289	Total	C	N	O	P	S	0	0	0
			2395	1521	417	442	1	14			
1	A	292	Total	C	N	O	P	S	0	0	0
			2417	1534	420	448	1	14			

There are 30 discrepancies between the modelled and reference sequences:

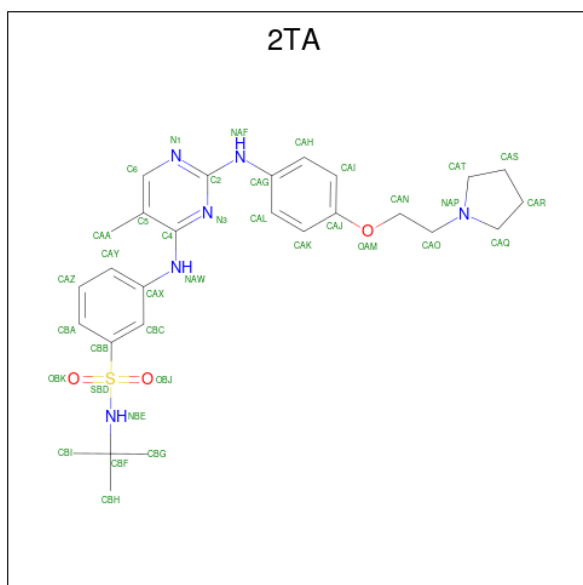
Chain	Residue	Modelled	Actual	Comment	Reference
B	825	HIS	-	expression tag	UNP O60674
B	826	HIS	-	expression tag	UNP O60674
B	827	HIS	-	expression tag	UNP O60674
B	828	HIS	-	expression tag	UNP O60674
B	829	HIS	-	expression tag	UNP O60674
B	830	HIS	-	expression tag	UNP O60674
B	831	HIS	-	expression tag	UNP O60674
B	832	HIS	-	expression tag	UNP O60674
B	833	GLU	-	expression tag	UNP O60674
B	834	ASN	-	expression tag	UNP O60674
B	835	LEU	-	expression tag	UNP O60674
B	836	TYR	-	expression tag	UNP O60674
B	837	PHE	-	expression tag	UNP O60674
B	838	GLN	-	expression tag	UNP O60674
B	839	GLY	-	expression tag	UNP O60674
A	825	HIS	-	expression tag	UNP O60674
A	826	HIS	-	expression tag	UNP O60674
A	827	HIS	-	expression tag	UNP O60674
A	828	HIS	-	expression tag	UNP O60674
A	829	HIS	-	expression tag	UNP O60674
A	830	HIS	-	expression tag	UNP O60674
A	831	HIS	-	expression tag	UNP O60674
A	832	HIS	-	expression tag	UNP O60674
A	833	GLU	-	expression tag	UNP O60674
A	834	ASN	-	expression tag	UNP O60674

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Chain	Residue	Modelled	Actual	Comment	Reference
A	835	LEU	-	expression tag	UNP O60674
A	836	TYR	-	expression tag	UNP O60674
A	837	PHE	-	expression tag	UNP O60674
A	838	GLN	-	expression tag	UNP O60674
A	839	GLY	-	expression tag	UNP O60674

- Molecule 2 is N-tert-butyl-3-{{[5-methyl-2-({4-[2-(pyrrolidin-1-yl)ethoxy]phenyl}amino)pyrimidin-4-yl]amino}benzenesulfonamide (three-letter code: 2TA) (formula: C<sub>27</sub>H<sub>36</sub>N<sub>6</sub>O<sub>3</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			37	27	6	3	1		
2	A	1	Total	C	N	O	S	0	0
			37	27	6	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	20	Total	O	0	0
			20	20		
3	A	14	Total	O	0	0
			14	14		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.24Å 114.24Å 70.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.48 – 2.32 44.48 – 2.32	Depositor EDS
% Data completeness (in resolution range)	96.3 (44.48-2.32) 99.7 (44.48-2.32)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.50 (at 2.32Å)	Xtriage
Refinement program	PHENIX 1.14-3260_3260	Depositor
R, $R_{free}$	0.217 , 0.256 0.216 , 0.255	Depositor DCC
$R_{free}$ test set	1087 reflections (2.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.6	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4920	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PTR, 2TA

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	0.47	0/2452	0.68	5/3300 (0.2%)
1	B	0.42	0/2429	0.58	0/3267
All	All	0.44	0/4881	0.63	5/6567 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	922	ARG	CG-CD-NE	7.83	128.24	111.80
1	A	1011	LYS	C-N-CA	6.79	138.68	121.70
1	A	864	GLU	CA-CB-CG	5.67	125.88	113.40
1	A	864	GLU	OE1-CD-OE2	-5.65	116.52	123.30
1	A	922	ARG	NE-CZ-NH1	-5.15	117.72	120.30

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	2417	0	2395	34	0
1	B	2395	0	2377	25	2
2	A	37	0	36	2	0
2	B	37	0	36	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	14	0	0	1	0
3	B	20	0	0	1	0
All	All	4920	0	4844	61	2

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 6.

All (61) 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:896:GLU:OE1	1:A:922:ARG:NH1	1.93	1.00
1:A:896:GLU:CD	1:A:922:ARG:HH12	1.75	0.90
1:A:864:GLU:OE1	1:A:883:LYS:NZ	2.18	0.76
1:A:857:LYS:HG3	1:A:862:SER:HB2	1.68	0.74
1:A:857:LYS:HG3	1:A:862:SER:CB	2.26	0.65
1:B:1018:ILE:HD13	1:B:1075:VAL:HG22	1.78	0.65
1:A:922:ARG:O	1:A:923:ARG:HB2	1.99	0.62
1:B:951:ILE:H	1:B:951:ILE:HD12	1.64	0.61
1:B:845:GLU:OE1	1:B:847:ARG:NH1	2.35	0.60
1:A:925:LEU:HD12	1:A:926:LYS:H	1.67	0.59
1:A:954:LEU:HD12	1:A:1130:MET:HE1	1.85	0.58
1:B:989:ARG:NH2	1:B:991:LYS:NZ	2.53	0.57
1:B:881:VAL:HG22	1:B:928:ILE:HD12	1.86	0.57
1:B:977:LEU:HD11	1:B:982:ILE:HD11	1.89	0.55
1:B:989:ARG:HH21	1:B:991:LYS:NZ	2.05	0.54
1:B:989:ARG:NH2	1:B:991:LYS:HZ1	2.06	0.53
1:A:952:LYS:NZ	1:A:988:ASN:OD1	2.42	0.53
1:A:860:PHE:CD1	1:A:860:PHE:N	2.77	0.52
1:B:848:HIS:CG	1:B:870:PRO:HA	2.44	0.52
1:B:960:ILE:HG12	1:B:982:ILE:HD12	1.93	0.51
1:A:1012:GLU:O	1:A:1012:GLU:OE1	2.28	0.51
1:A:859:ASN:HB3	1:A:860:PHE:CD1	2.45	0.50
1:A:919:SER:OG	1:A:924:ASN:ND2	2.44	0.50
1:B:1009:LYS:HA	1:B:1029:SER:O	2.12	0.49
1:A:975:ARG:HG3	1:A:1031:PHE:CD2	2.47	0.49
1:B:1125:GLN:HG3	1:B:1125:GLN:O	2.13	0.49
1:A:924:ASN:N	1:A:924:ASN:OD1	2.44	0.48
1:B:971:ARG:NH2	1:B:1002:PRO:O	2.45	0.48
1:A:930:GLU:O	2:A:1201:2TA:H19	2.14	0.47
1:A:999:LYS:HD3	1:A:999:LYS:HA	1.64	0.47
1:A:1035:SER:HB3	3:A:1303:HOH:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1083:LYS:HB3	1:A:1083:LYS:HE2	1.66	0.47
1:A:911:VAL:HG22	1:A:992:ILE:O	2.15	0.46
1:A:1110:VAL:HG12	1:A:1113:ARG:NH1	2.31	0.46
1:B:1035:SER:OG	3:B:1301:HOH:O	2.21	0.45
1:A:848:HIS:HA	1:A:850:LYS:HE2	1.98	0.45
1:A:918:TYR:HD2	1:A:925:LEU:HD13	1.80	0.45
1:A:1090:ARG:NH1	1:A:1094:CYS:O	2.45	0.45
1:B:902:LEU:HG	1:B:913:TYR:HB2	1.98	0.44
1:A:892:LEU:HD23	1:A:892:LEU:HA	1.72	0.44
1:A:860:PHE:N	1:A:860:PHE:HD1	2.16	0.44
1:A:859:ASN:C	1:A:860:PHE:HD1	2.21	0.44
1:B:1027:THR:HG22	1:B:1079:ILE:HD13	2.00	0.43
1:A:978:ALA:HA	1:A:1043:VAL:HG22	1.99	0.43
1:B:989:ARG:HH21	1:B:991:LYS:HZ1	1.62	0.43
1:A:893:ARG:HD3	1:A:893:ARG:HA	1.75	0.43
1:B:857:LYS:HE3	1:B:885:GLN:HE22	1.84	0.43
1:B:952:LYS:NZ	1:B:988:ASN:OD1	2.51	0.43
1:B:1090:ARG:HD2	1:B:1094:CYS:O	2.19	0.43
1:B:965:GLU:O	1:B:969:THR:HG23	2.18	0.43
1:A:945:LYS:HE2	1:A:945:LYS:HB2	1.75	0.43
1:B:1045:TYR:O	1:B:1049:THR:HG23	2.19	0.42
1:A:921:GLY:O	1:A:922:ARG:HB2	2.19	0.42
2:A:1201:2TA:N3	2:A:1201:2TA:H17	2.34	0.42
1:A:925:LEU:HD12	1:A:926:LYS:N	2.32	0.42
1:B:999:LYS:HG2	1:B:1008:TYR:CZ	2.54	0.42
1:B:1069:LYS:HE3	1:B:1077:HIS:CE1	2.55	0.41
1:A:976:ASP:HB2	1:A:997:LEU:HD12	2.02	0.41
1:B:1038:TRP:CE3	1:B:1106:TRP:HA	2.56	0.40
2:B:1201:2TA:OAM	2:B:1201:2TA:H7	2.20	0.40
1:A:1044:LEU:HD21	1:A:1098:ILE:HG23	2.02	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:883:LYS:NZ	1:B:1007:PTR:O3P[2_654]	1.30	0.90
1:B:883:LYS:NZ	1:B:1007:PTR:P[2_654]	2.10	0.10

## 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	289/308 (94%)	275 (95%)	12 (4%)	2 (1%)	22	26
1	B	286/308 (93%)	278 (97%)	7 (2%)	1 (0%)	41	50
All	All	575/616 (93%)	553 (96%)	19 (3%)	3 (0%)	29	35

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	923	ARG
1	A	920	ALA
1	B	920	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	266/280 (95%)	258 (97%)	8 (3%)	41	56
1	B	263/280 (94%)	255 (97%)	8 (3%)	41	56
All	All	529/560 (94%)	513 (97%)	16 (3%)	41	56

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	843	GLN
1	B	917	CYS
1	B	923	ARG

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Mol	Chain	Res	Type
1	B	936	SER
1	B	1012	GLU
1	B	1061	PHE
1	B	1062	MET
1	B	1122	ARG
1	A	840	ASP
1	A	917	CYS
1	A	936	SER
1	A	980	ARG
1	A	981	ASN
1	A	1011	LYS
1	A	1012	GLU
1	A	1128	ASP

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

Mol	Chain	Res	Type
1	B	885	GLN
1	A	942	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	PTR	A	1007	1	15,16,17	1.30	1 (6%)	19,22,24	0.53	0
1	PTR	B	1007	1	15,16,17	1.32	1 (6%)	19,22,24	0.49	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
1	PTR	A	1007	1	-	0/10/11/13	0/1/1/1
1	PTR	B	1007	1	-	0/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1007	PTR	OH-CZ	-4.35	1.30	1.40
1	A	1007	PTR	OH-CZ	-3.86	1.31	1.40

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1007	PTR	0	2

## 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	2TA	A	1201	-	39,40,40	3.36	12 (30%)	55,57,57	2.80	11 (20%)
2	2TA	B	1201	-	39,40,40	3.27	13 (33%)	55,57,57	2.70	12 (21%)

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	2TA	A	1201	-	-	5/26/33/33	0/4/4/4
2	2TA	B	1201	-	-	0/26/33/33	0/4/4/4

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	2TA	CAO-NAP	-11.37	1.21	1.47
2	B	1201	2TA	CAO-NAP	-11.29	1.21	1.47
2	A	1201	2TA	CAQ-NAP	-10.32	1.28	1.47
2	B	1201	2TA	CAQ-NAP	-10.20	1.28	1.47
2	A	1201	2TA	SBD-NBE	9.04	1.75	1.61
2	B	1201	2TA	SBD-NBE	8.74	1.74	1.61
2	A	1201	2TA	C4-NAW	4.99	1.45	1.36
2	A	1201	2TA	C2-NAF	4.28	1.45	1.36
2	A	1201	2TA	CBB-SBD	4.24	1.83	1.76
2	B	1201	2TA	C2-NAF	4.22	1.45	1.36
2	B	1201	2TA	C4-NAW	3.84	1.43	1.36
2	B	1201	2TA	CBB-SBD	3.29	1.81	1.76
2	B	1201	2TA	CAS-CAR	-3.20	1.26	1.48
2	B	1201	2TA	CAR-CAQ	3.14	1.62	1.51
2	A	1201	2TA	CAS-CAR	-3.10	1.26	1.48
2	A	1201	2TA	CAR-CAQ	3.03	1.62	1.51
2	A	1201	2TA	OBK-SBD	2.94	1.46	1.43
2	A	1201	2TA	OBJ-SBD	2.84	1.46	1.43
2	B	1201	2TA	OBJ-SBD	2.81	1.46	1.43
2	B	1201	2TA	OBK-SBD	2.68	1.46	1.43
2	B	1201	2TA	CAG-NAF	2.58	1.46	1.40
2	A	1201	2TA	CAG-NAF	2.58	1.46	1.40
2	A	1201	2TA	CAT-NAP	2.38	1.52	1.47
2	B	1201	2TA	CAT-NAP	2.29	1.52	1.47
2	B	1201	2TA	C5-C4	-2.09	1.38	1.41

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	2TA	OBK-SBD-OBJ	-16.61	99.13	119.55
2	B	1201	2TA	OBK-SBD-OBJ	-15.29	100.75	119.55
2	A	1201	2TA	C5-C6-N1	-5.80	119.18	125.11
2	B	1201	2TA	N1-C2-N3	-5.22	121.60	126.55
2	B	1201	2TA	C5-C6-N1	-5.14	119.86	125.11
2	A	1201	2TA	N1-C2-N3	-4.41	122.37	126.55
2	B	1201	2TA	CAA-C5-C4	-3.56	118.87	121.97
2	B	1201	2TA	OBJ-SBD-NBE	3.43	115.14	107.32
2	A	1201	2TA	CAT-NAP-CAQ	3.39	107.34	104.04
2	A	1201	2TA	CBB-SBD-NBE	3.21	113.48	108.17
2	B	1201	2TA	CAT-NAP-CAQ	3.19	107.14	104.04
2	A	1201	2TA	C6-N1-C2	3.11	120.58	115.88
2	B	1201	2TA	C6-N1-C2	3.09	120.55	115.88
2	A	1201	2TA	C5-C4-N3	-2.88	120.08	123.37
2	A	1201	2TA	OBK-SBD-CBB	2.81	111.43	107.97
2	B	1201	2TA	CAA-C5-C6	2.67	124.51	120.01
2	B	1201	2TA	CAX-NAW-C4	-2.66	122.71	129.39
2	B	1201	2TA	NAW-C4-N3	2.64	123.05	119.12
2	B	1201	2TA	C5-C4-NAW	-2.64	115.25	119.22
2	A	1201	2TA	OBK-SBD-NBE	2.53	113.09	107.32
2	B	1201	2TA	CBB-SBD-NBE	2.37	112.09	108.17
2	A	1201	2TA	CBI-CBF-CBH	-2.30	104.61	109.94
2	A	1201	2TA	CAA-C5-C4	-2.11	120.13	121.97

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	2TA	CAN-CAO-NAP-CAT
2	A	1201	2TA	OAM-CAN-CAO-NAP
2	A	1201	2TA	CBF-NBE-SBD-OBK
2	A	1201	2TA	CAK-CAJ-OAM-CAN
2	A	1201	2TA	CAI-CAJ-OAM-CAN

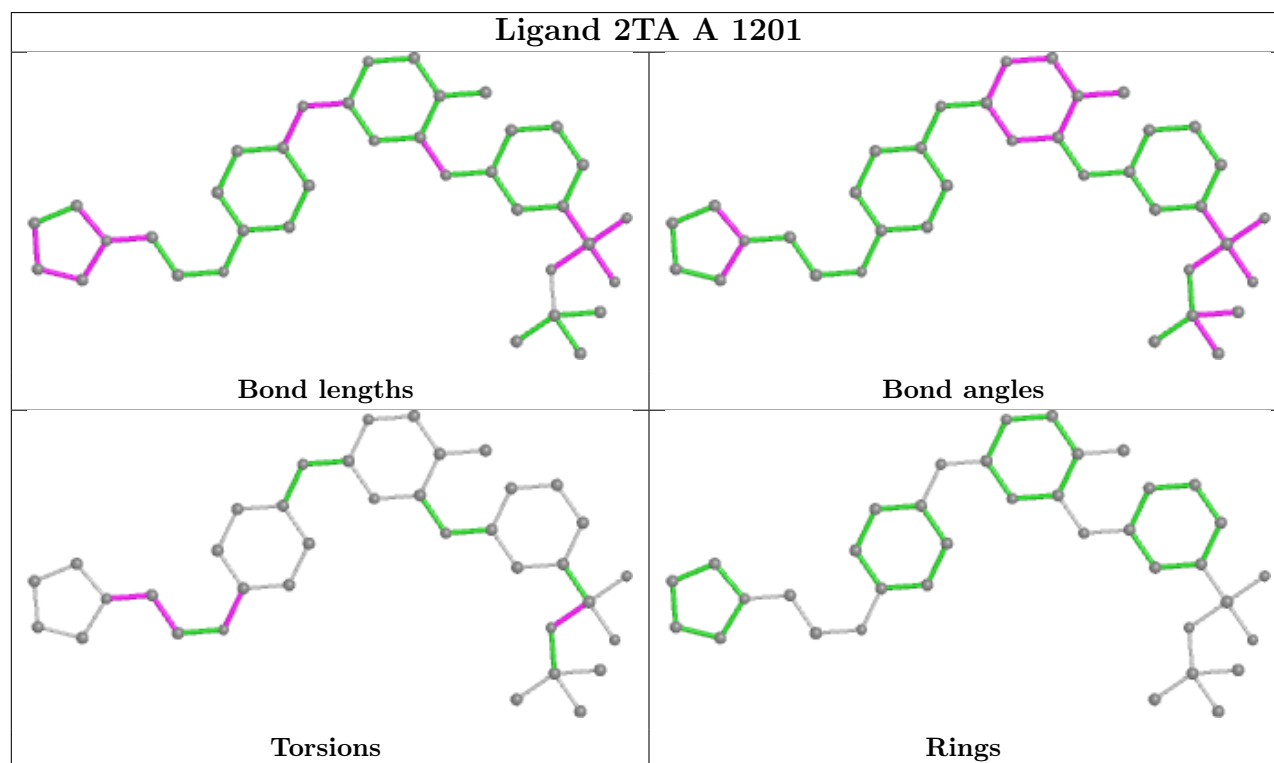
There are no ring outliers.

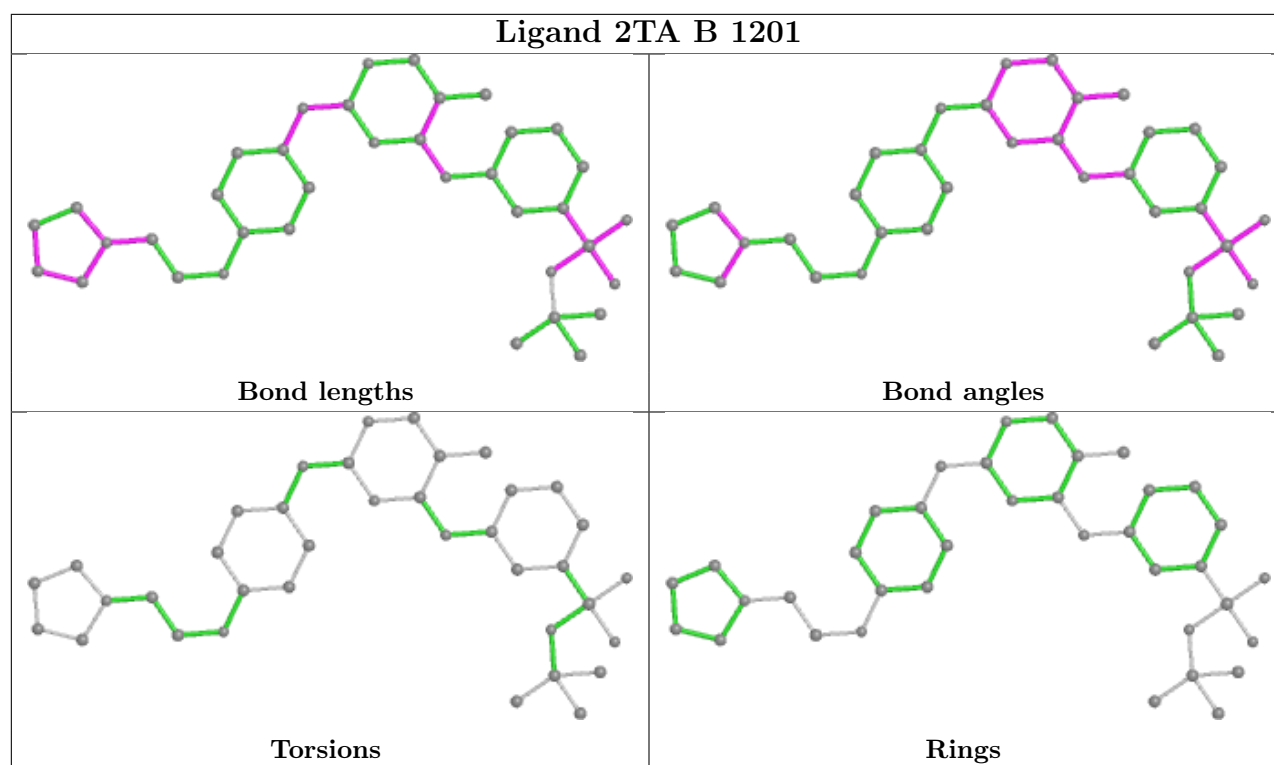
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	2TA	2	0
2	B	1201	2TA	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	291/308 (94%)	0.95	30 (10%) 6 9	49, 72, 113, 150	0
1	B	288/308 (93%)	0.96	28 (9%) 7 11	47, 69, 116, 142	0
All	All	579/616 (93%)	0.96	58 (10%) 7 10	47, 71, 116, 150	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	920	ALA	9.7
1	B	1068	ASP	8.1
1	B	922	ARG	6.3
1	B	1067	ASN	6.0
1	B	1070	GLN	5.9
1	B	921	GLY	5.6
1	A	922	ARG	5.4
1	A	923	ARG	5.0
1	A	1068	ASP	4.1
1	B	919	SER	4.1
1	B	1074	ILE	4.0
1	B	1078	LEU	3.4
1	A	1066	GLY	3.4
1	A	921	GLY	3.3
1	A	840	ASP	3.3
1	B	1013	PRO	3.3
1	B	1014	GLY	3.3
1	B	918	TYR	3.2
1	B	1015	GLU	3.2
1	A	1011	LYS	3.2
1	A	864	GLU	2.9
1	A	935	GLY	2.9
1	B	873	ASP	2.8
1	A	932	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	860	PHE	2.8
1	A	841	PRO	2.8
1	B	1073	MET	2.7
1	A	1012	GLU	2.7
1	A	1064	MET	2.6
1	A	1052	GLU	2.6
1	A	1067	ASN	2.6
1	A	1071	GLY	2.6
1	A	1016	SER	2.6
1	B	906	GLN	2.5
1	A	890	GLU	2.4
1	B	1069	LYS	2.4
1	A	855	LEU	2.4
1	B	1076	PHE	2.4
1	A	893	ARG	2.4
1	A	918	TYR	2.4
1	B	1075	VAL	2.4
1	A	1002	PRO	2.3
1	B	844	PHE	2.3
1	A	1065	ILE	2.3
1	B	886	HIS	2.3
1	B	1125	GLN	2.3
1	B	984	VAL	2.3
1	B	940	TYR	2.2
1	B	1131	ALA	2.2
1	B	1012	GLU	2.2
1	A	1069	LYS	2.2
1	B	888	THR	2.1
1	A	1070	GLN	2.1
1	B	1128	ASP	2.1
1	A	1089	PRO	2.1
1	A	981	ASN	2.1
1	A	879	VAL	2.1
1	A	1101	ILE	2.0

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

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
1	PTR	A	1007	16/17	0.87	0.14	76,98,149,149	0
1	PTR	B	1007	16/17	0.89	0.19	51,81,137,140	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

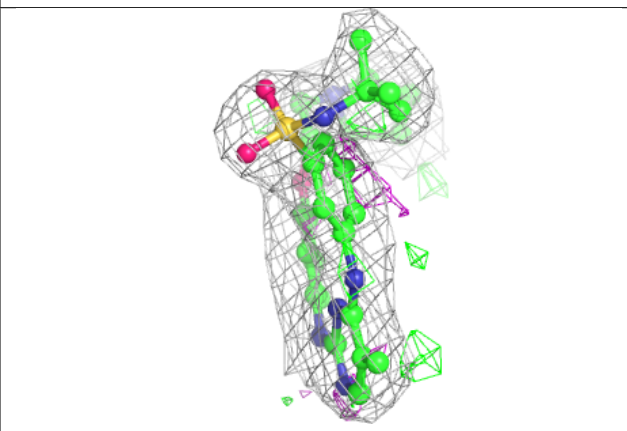
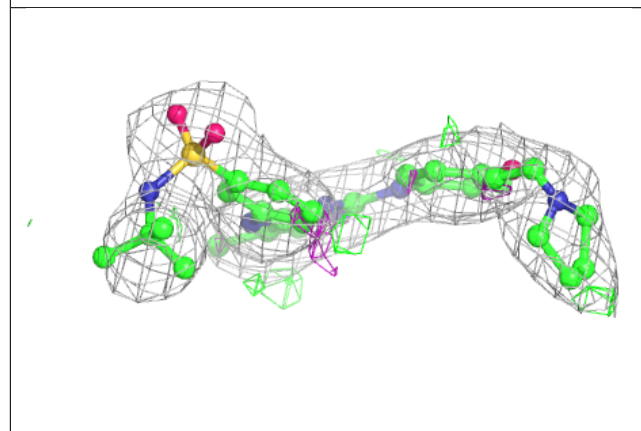
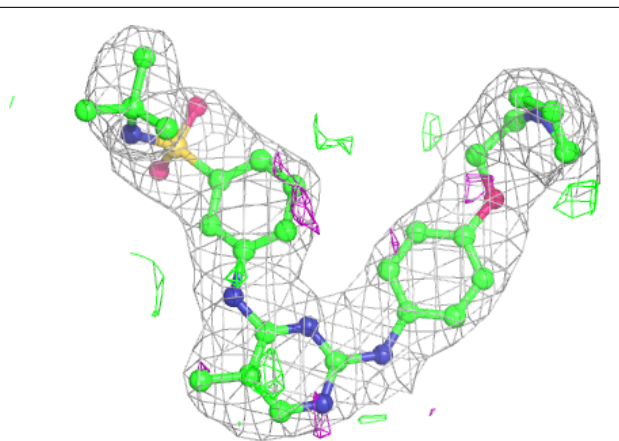
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	2TA	B	1201	37/37	0.92	0.17	33,53,93,95	0
2	2TA	A	1201	37/37	0.92	0.24	49,64,98,107	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.

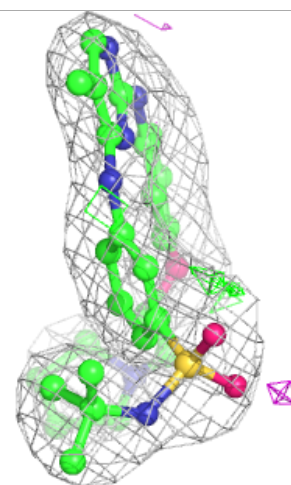
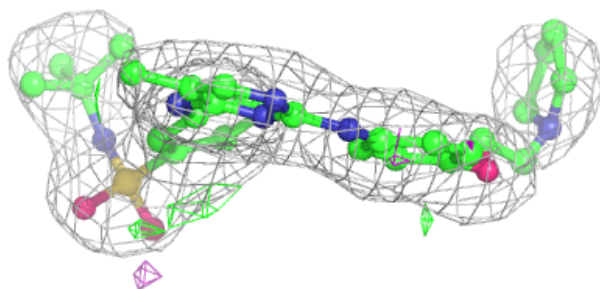
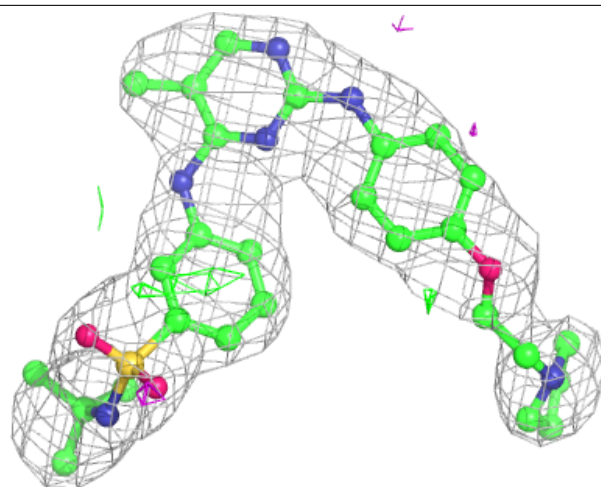
**Electron density around 2TA B 1201:**

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



**Electron density around 2TA A 1201:**

$2mF_o-DF_c$  (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.