wwPDB X-ray Structure Validation Summary Report (i)

Nov 20, 2023 – 03:15 pm GMT

PDB ID	:	8BPW
Title	:	Crystal structure of JAK2 JH1 in complex with lestaurtinib
Authors	:	Miao, Y.; Haikarainen, T.
Deposited on	:	2022-11-18
Resolution	:	1.80 Å(reported)

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

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

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

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

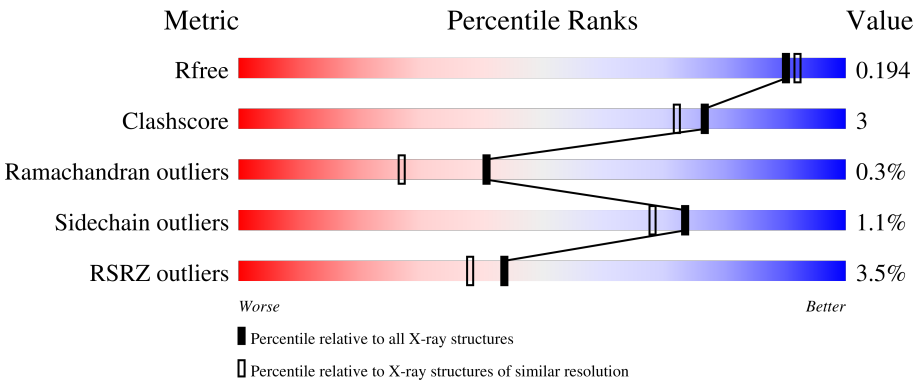
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	317	3% 84% 10% 5%
1	B	317	3% 88% 6% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10477 atoms, of which 4901 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
			Total	C	H	N	O	P	S			
1	A	300	4918	1580	2431	425	465	2	15	0	5	0
1	B	300	4916	1578	2428	426	467	2	15	0	4	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	816	MET	-	initiating methionine	UNP O60674
A	817	GLY	-	expression tag	UNP O60674
A	818	HIS	-	expression tag	UNP O60674
A	819	HIS	-	expression tag	UNP O60674
A	820	HIS	-	expression tag	UNP O60674
A	821	HIS	-	expression tag	UNP O60674
A	822	HIS	-	expression tag	UNP O60674
A	823	HIS	-	expression tag	UNP O60674
A	824	SER	-	expression tag	UNP O60674
A	825	SER	-	expression tag	UNP O60674
A	826	GLY	-	expression tag	UNP O60674
A	827	VAL	-	expression tag	UNP O60674
A	828	ASP	-	expression tag	UNP O60674
A	829	LEU	-	expression tag	UNP O60674
A	830	GLY	-	expression tag	UNP O60674
A	831	THR	-	expression tag	UNP O60674
A	832	GLU	-	expression tag	UNP O60674
A	833	ASN	-	expression tag	UNP O60674
A	834	LEU	-	expression tag	UNP O60674
A	835	TYR	-	expression tag	UNP O60674
A	836	PHE	-	expression tag	UNP O60674
A	837	GLN	-	expression tag	UNP O60674
A	838	SER	-	expression tag	UNP O60674
A	839	MET	-	expression tag	UNP O60674
B	816	MET	-	initiating methionine	UNP O60674

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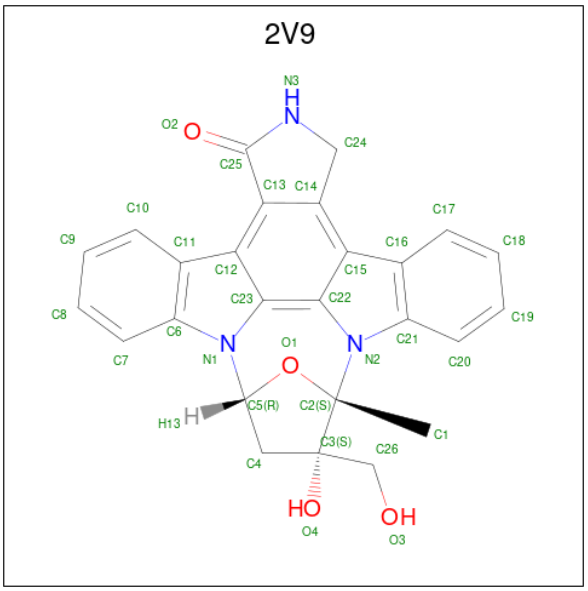
Chain	Residue	Modelled	Actual	Comment	Reference
B	817	GLY	-	expression tag	UNP O60674
B	818	HIS	-	expression tag	UNP O60674
B	819	HIS	-	expression tag	UNP O60674
B	820	HIS	-	expression tag	UNP O60674
B	821	HIS	-	expression tag	UNP O60674
B	822	HIS	-	expression tag	UNP O60674
B	823	HIS	-	expression tag	UNP O60674
B	824	SER	-	expression tag	UNP O60674
B	825	SER	-	expression tag	UNP O60674
B	826	GLY	-	expression tag	UNP O60674
B	827	VAL	-	expression tag	UNP O60674
B	828	ASP	-	expression tag	UNP O60674
B	829	LEU	-	expression tag	UNP O60674
B	830	GLY	-	expression tag	UNP O60674
B	831	THR	-	expression tag	UNP O60674
B	832	GLU	-	expression tag	UNP O60674
B	833	ASN	-	expression tag	UNP O60674
B	834	LEU	-	expression tag	UNP O60674
B	835	TYR	-	expression tag	UNP O60674
B	836	PHE	-	expression tag	UNP O60674
B	837	GLN	-	expression tag	UNP O60674
B	838	SER	-	expression tag	UNP O60674
B	839	MET	-	expression tag	UNP O60674

- Molecule 2 is Lestaurtinib (three-letter code: 2V9) (formula: $C_{26}H_{21}N_3O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	A	1	54	26	21	3	4	0	0
			Total	C	H	N	O		
2	B	1	54	26	21	3	4	0	0

- Molecule 3 is water.

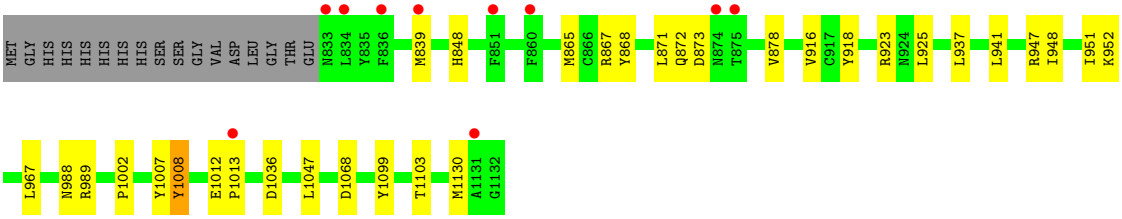
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	265	270	270	0	5
			Total	O		
3	B	261	265	265	0	4

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.

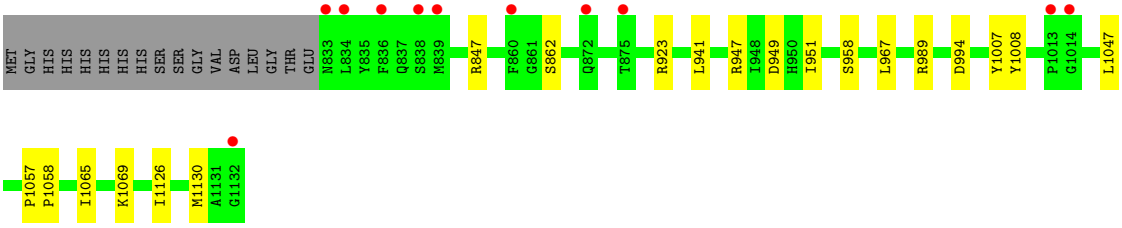
- Molecule 1: Tyrosine-protein kinase JAK2

Chain A:



- Molecule 1: Tyrosine-protein kinase JAK2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	99.53Å 69.51Å 110.89Å 90.00° 98.70° 90.00°	Depositor
Resolution (Å)	68.26 – 1.80 68.26 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (68.26-1.80) 99.9 (68.26-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.02 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.161 , 0.197 0.160 , 0.194	Depositor DCC
R_{free} test set	3462 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	20.6	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 53.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10477	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 74.90 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4009e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PTR, 2V9

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	0.52	0/2516	0.71	2/3390 (0.1%)
1	B	0.53	1/2514 (0.0%)	0.72	1/3386 (0.0%)
All	All	0.52	1/5030 (0.0%)	0.71	3/6776 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	958	SER	CB-OG	-5.75	1.34	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	967	LEU	CB-CG-CD1	-6.40	100.12	111.00
1	B	967	LEU	CB-CG-CD1	-5.73	101.26	111.00
1	A	1036	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	923	ARG	Sidechain
1	B	923	ARG	Sidechain

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	2487	2431	2437	18	0
1	B	2488	2428	2431	8	0
2	A	33	21	19	2	0
2	B	33	21	19	2	0
3	A	270	0	0	2	0
3	B	265	0	0	1	0
All	All	5576	4901	4906	30	0

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

The worst 5 of 30 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:1103[A]:THR:HG22	3:A:1469:HOH:O	1.70	0.91
2:B:1201:2V9:H12	2:B:1201:2V9:H9	1.70	0.71
2:A:1201:2V9:H12	2:A:1201:2V9:H9	1.73	0.68
1:B:951[A]:ILE:HD11	1:B:1130:MET:HB2	1.81	0.61
1:A:952:LYS:NZ	1:A:988:ASN:OD1	2.34	0.59

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	301/317 (95%)	289 (96%)	11 (4%)	1 (0%)	41	27
1	B	300/317 (95%)	287 (96%)	11 (4%)	2 (1%)	22	10
All	All	601/634 (95%)	576 (96%)	22 (4%)	3 (0%)	41	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	994[A]	ASP
1	B	994[B]	ASP
1	A	872	GLN

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	270/286 (94%)	267 (99%)	3 (1%)	73	68
1	B	270/286 (94%)	267 (99%)	3 (1%)	73	68
All	All	540/572 (94%)	534 (99%)	6 (1%)	73	68

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	862	SER
1	B	947	ARG
1	B	989	ARG
1	A	989	ARG
1	A	867	ARG

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)

4 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	1008	1	15,16,17	1.22	1 (6%)	19,22,24	1.01	1 (5%)
1	PTR	A	1007	1	15,16,17	1.31	2 (13%)	19,22,24	0.98	2 (10%)
1	PTR	B	1007	1	15,16,17	1.34	1 (6%)	19,22,24	0.55	1 (5%)
1	PTR	B	1008	1	15,16,17	1.19	1 (6%)	19,22,24	1.04	2 (10%)

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	1008	1	-	0/10/11/13	0/1/1/1
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
1	PTR	B	1008	1	-	1/10/11/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1008	PTR	OH-CZ	-4.27	1.31	1.40
1	B	1007	PTR	OH-CZ	-4.10	1.31	1.40
1	A	1008	PTR	OH-CZ	-4.01	1.31	1.40
1	A	1007	PTR	OH-CZ	-3.92	1.31	1.40
1	A	1007	PTR	P-OH	2.67	1.63	1.59

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1008	PTR	P-OH-CZ	2.84	132.84	123.75
1	B	1008	PTR	O3P-P-OH	2.71	113.71	105.24
1	A	1007	PTR	O3P-P-OH	2.54	113.18	105.24
1	B	1008	PTR	P-OH-CZ	2.49	131.73	123.75
1	A	1007	PTR	O2P-P-OH	2.38	112.69	105.24

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1008	PTR	CZ-OH-P-O1P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1008	PTR	1	0

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	2V9	B	1201	-	30,40,40	2.42	9 (30%)	30,67,67	2.29	8 (26%)
2	2V9	A	1201	-	30,40,40	2.06	8 (26%)	30,67,67	2.13	8 (26%)

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	2V9	B	1201	-	-	0/3/41/41	-
2	2V9	A	1201	-	-	0/3/41/41	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	2V9	C25-N3	7.96	1.41	1.35
2	A	1201	2V9	C25-N3	6.15	1.40	1.35
2	A	1201	2V9	C4-C3	-5.26	1.47	1.54
2	B	1201	2V9	C24-C14	-5.17	1.46	1.50
2	B	1201	2V9	C12-C23	-3.96	1.37	1.42

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1201	2V9	O1-C2-C1	-6.05	97.98	109.04
2	A	1201	2V9	C14-C24-N3	6.02	107.89	101.76
2	B	1201	2V9	C14-C24-N3	5.85	107.71	101.76
2	B	1201	2V9	C24-N3-C25	-5.64	108.43	113.85
2	A	1201	2V9	O1-C2-C1	-4.77	100.32	109.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

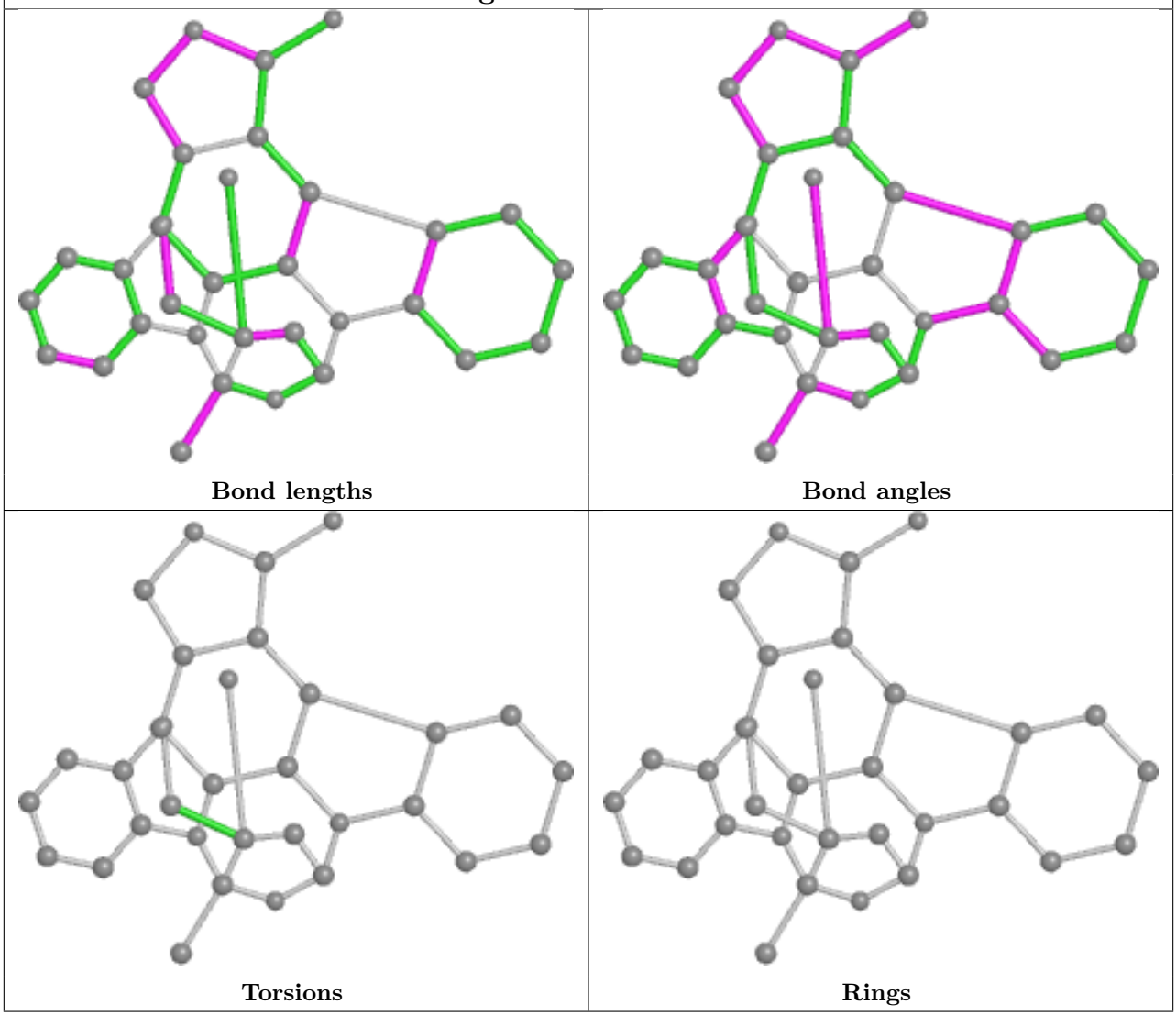
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1201	2V9	2	0
2	A	1201	2V9	2	0

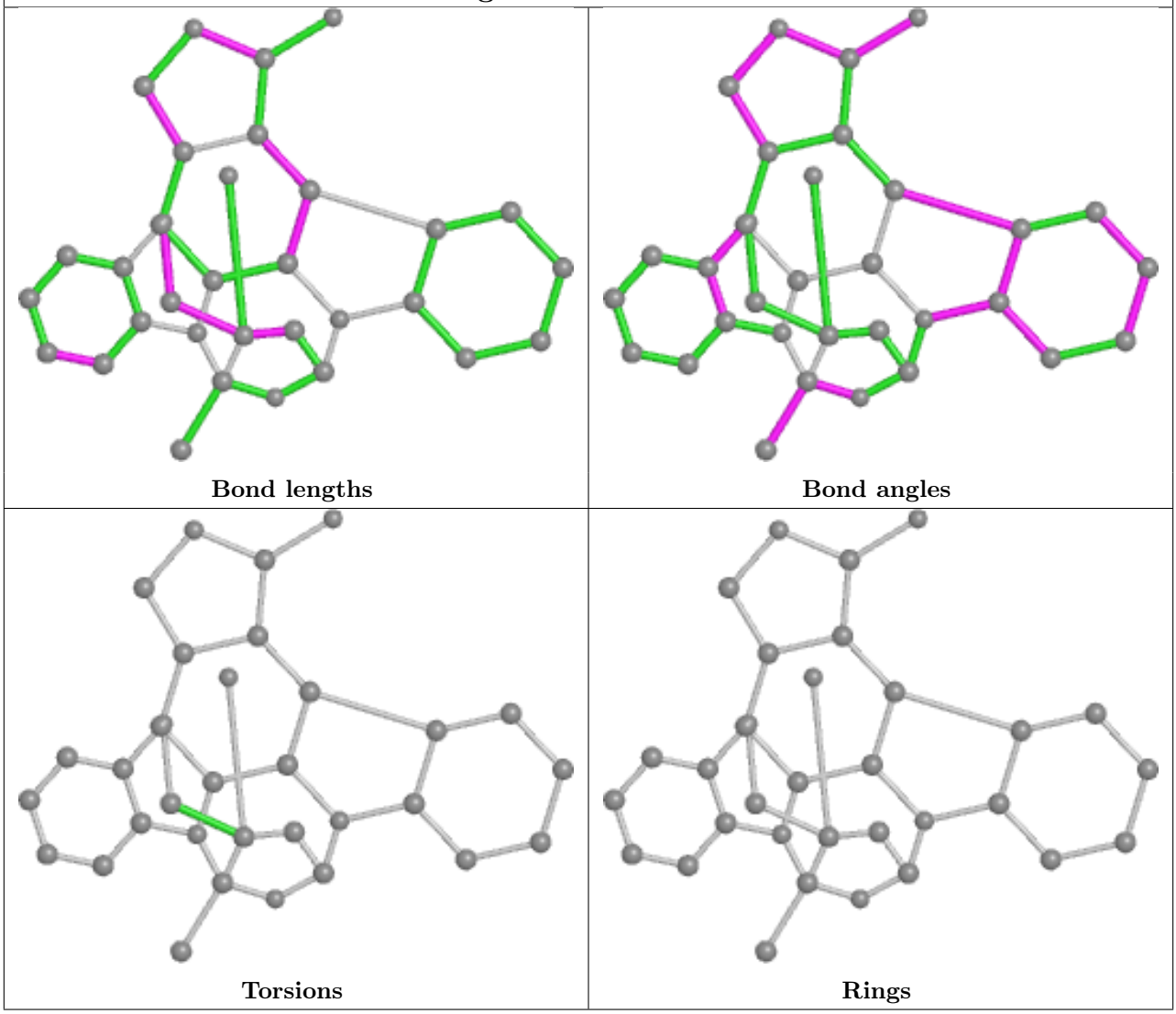
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand 2V9 B 1201



Ligand 2V9 A 1201



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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	298/317 (94%)	-0.06	10 (3%)	45	39	15, 24, 58, 79	0
1	B	298/317 (94%)	-0.04	11 (3%)	41	36	15, 24, 67, 86	0
All	All	596/634 (94%)	-0.05	21 (3%)	44	38	15, 24, 62, 86	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	834	LEU	4.7
1	A	833	ASN	3.7
1	A	874	ASN	3.6
1	B	836	PHE	3.6
1	B	1132	GLY	3.5

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	PTR	A	1007	16/17	0.93	0.11	25,37,64,78	0
1	PTR	B	1007	16/17	0.93	0.12	26,41,70,77	0
1	PTR	B	1008	16/17	0.94	0.12	20,32,77,79	0
1	PTR	A	1008	16/17	0.95	0.15	21,36,73,92	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

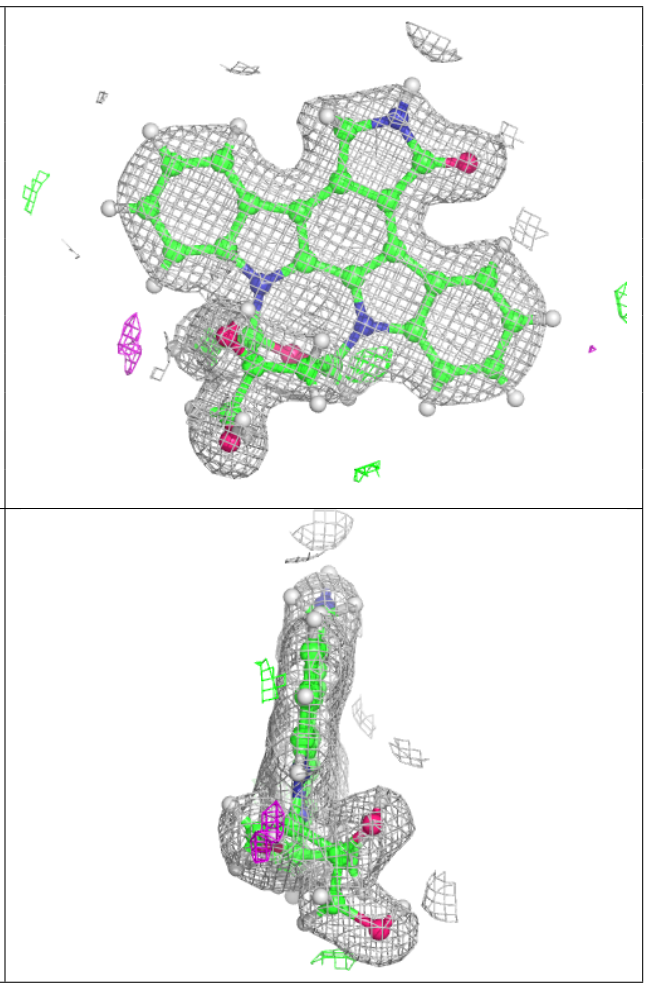
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	2V9	B	1201	33/33	0.95	0.10	16,21,29,31	0
2	2V9	A	1201	33/33	0.96	0.10	15,20,25,27	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.

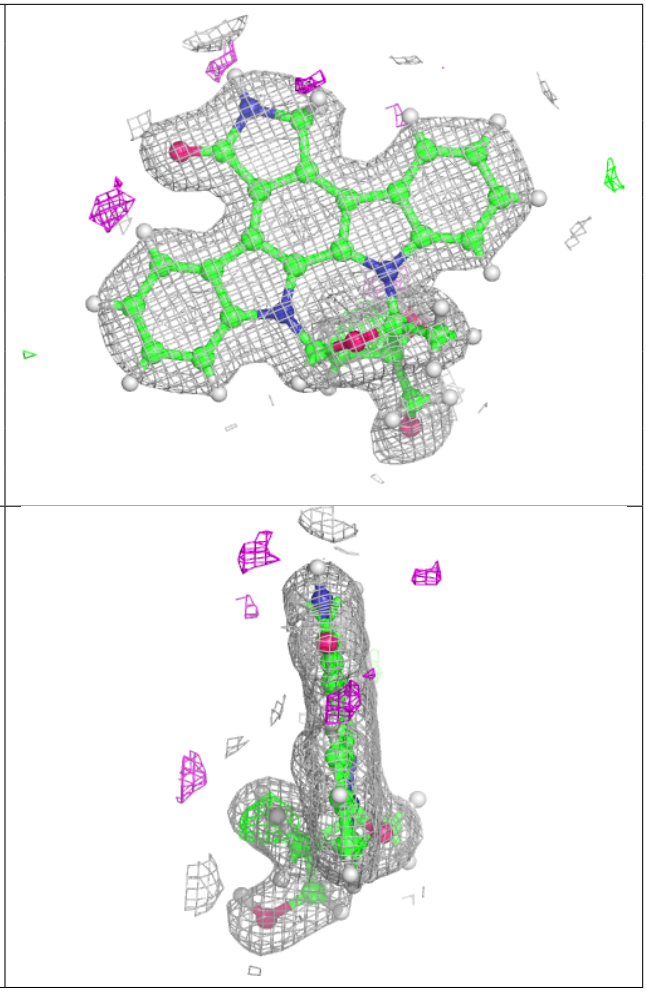
Electron density around 2V9 B 1201:

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 2V9 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.