



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 8, 2021 – 06:02 PM EST

PDB ID : 6VN8
Title : JAK2 JH1 in complex with baricitinib
Authors : Davis, R.R.; Schonbrunn, E.
Deposited on : 2020-01-29
Resolution : 1.90 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

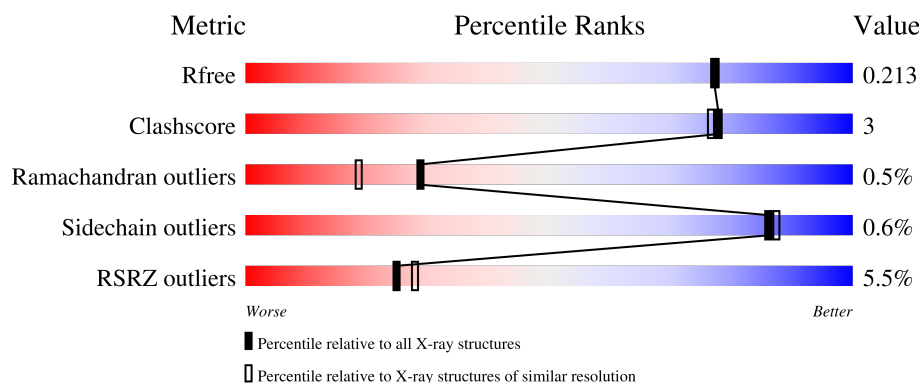
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 $\leq 5\%$. 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>6%</div> <div>89%</div> <div>8%</div> <div>.</div> </div>
1	B	308	<div> <div>5%</div> <div>88%</div> <div>6%</div> <div>6%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5179 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	298	Total	C	N	O	P	S	0	0	0
			2465	1567	427	456	1	14			

There are 30 discrepancies between the modelled and reference sequences:

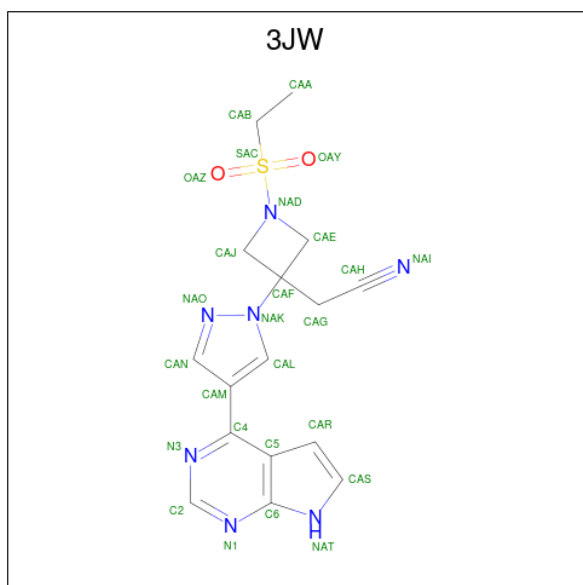
Chain	Residue	Modelled	Actual	Comment	Reference
B	825	HIS	-	expression tag	UNP O60674
B	826	HIS	-	expression tag	UNP O60674
B	827	HIS	-	expression tag	UNP O60674
B	828	HIS	-	expression tag	UNP O60674
B	829	HIS	-	expression tag	UNP O60674
B	830	HIS	-	expression tag	UNP O60674
B	831	HIS	-	expression tag	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 Baricitinib (three-letter code: 3JW) (formula: C₁₆H₁₇N₇O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			26	16	7	2	1		
2	A	1	Total	C	N	O	S	0	0
			26	16	7	2	1		

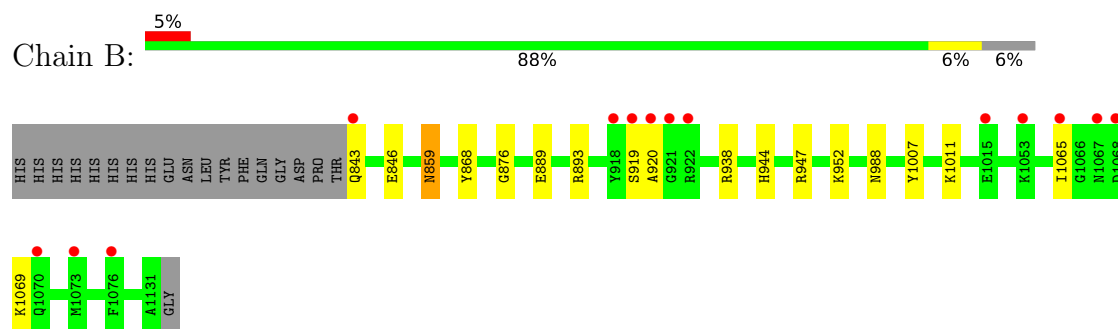
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	118	Total	O	0	0
			118	118		
3	A	149	Total	O	0	0
			149	149		

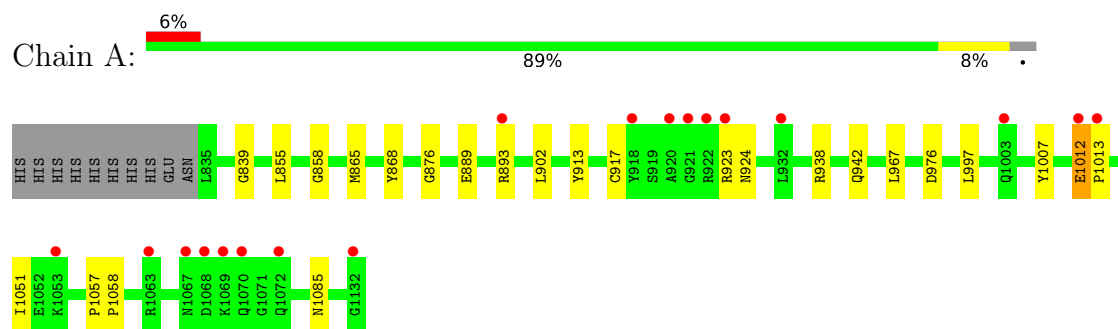
3 Residue-property plots [i](#)

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



- Molecule 1: Tyrosine-protein kinase JAK2



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	112.20Å 112.20Å 71.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.04 – 1.90 44.04 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (44.04-1.90) 100.0 (44.04-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.14-3260_3260	Depositor
R, R_{free}	0.184 , 0.215 0.182 , 0.213	Depositor DCC
R_{free} test set	1492 reflections (2.14%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5179	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, 3JW

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	0.61	1/2502 (0.0%)	0.71	0/3367
1	B	0.58	0/2429	0.68	0/3267
All	All	0.59	1/4931 (0.0%)	0.70	0/6634

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	917	CYS	CB-SG	-7.24	1.70	1.82

There are no bond angle outliers.

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	2465	0	2439	15	0
1	B	2395	0	2377	13	0
2	A	26	0	17	1	0
2	B	26	0	17	0	0
3	A	149	0	0	2	1
3	B	118	0	0	5	1
All	All	5179	0	4850	28	1

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.

All (28) 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:843:GLN:OE1	3:B:1301:HOH:O	2.07	0.72
1:B:846:GLU:OE2	1:B:919:SER:OG	2.08	0.71
1:B:952:LYS:NZ	1:B:988:ASN:OD1	2.26	0.69
1:B:938:ARG:NH2	3:B:1305:HOH:O	2.25	0.69
1:A:942:GLN:HG2	1:A:1051:ILE:HB	1.76	0.68
1:A:1085:ASN:ND2	3:A:1302:HOH:O	2.28	0.66
1:A:1012:GLU:OE1	3:A:1301:HOH:O	2.13	0.65
1:B:859:ASN:O	3:B:1303:HOH:O	2.14	0.64
1:A:889:GLU:OE2	1:A:893:ARG:NH1	2.30	0.64
1:A:1012:GLU:HB3	1:A:1013:PRO:C	2.22	0.60
1:A:1012:GLU:HB3	1:A:1013:PRO:CA	2.34	0.56
1:B:868:TYR:O	1:B:876:GLY:HA3	2.07	0.55
1:B:938:ARG:HD3	3:B:1302:HOH:O	2.06	0.55
1:B:944:HIS:HB3	1:B:947:ARG:HD3	1.92	0.51
1:B:944:HIS:O	1:B:947:ARG:HG2	2.13	0.49
1:A:923:ARG:NH2	1:A:924:ASN:HD21	2.12	0.48
1:B:938:ARG:NH1	3:B:1302:HOH:O	2.14	0.48
1:B:889:GLU:OE1	1:B:893:ARG:NH1	2.45	0.47
1:A:858:GLY:HA3	2:A:1201:3JW:H4	1.97	0.46
1:B:1065:ILE:O	1:B:1069:LYS:HE3	2.16	0.46
1:A:868:TYR:O	1:A:876:GLY:HA3	2.16	0.46
1:A:938:ARG:O	1:A:942:GLN:HG3	2.17	0.44
1:A:976:ASP:HB2	1:A:997:LEU:HD12	2.00	0.44
1:A:855:LEU:HD21	1:A:865:MET:CE	2.48	0.44
1:A:923:ARG:NH2	1:A:924:ASN:ND2	2.65	0.44
1:B:944:HIS:ND1	1:B:947:ARG:HD3	2.34	0.42
1:A:902:LEU:HG	1:A:913:TYR:HB2	2.02	0.41
1:A:1057:PRO:HB2	1:A:1058:PRO:HD3	2.03	0.41

All (1) 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)
3:B:1365:HOH:O	3:A:1383:HOH:O[4_655]	1.92	0.28

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	295/308 (96%)	287 (97%)	6 (2%)	2 (1%)	22	12
1	B	286/308 (93%)	277 (97%)	8 (3%)	1 (0%)	41	31
All	All	581/616 (94%)	564 (97%)	14 (2%)	3 (0%)	29	18

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	920	ALA
1	A	839	GLY
1	A	1012	GLU

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	270/280 (96%)	269 (100%)	1 (0%)	91	91
1	B	263/280 (94%)	261 (99%)	2 (1%)	81	82
All	All	533/560 (95%)	530 (99%)	3 (1%)	86	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	859	ASN
1	B	1011	LYS
1	A	967	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	924	ASN

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	B	1007	1	15,16,17	1.28	1 (6%)	19,22,24	0.67	1 (5%)
1	PTR	A	1007	1	15,16,17	1.19	1 (6%)	19,22,24	0.66	1 (5%)

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	B	1007	1	-	0/10/11/13	0/1/1/1
1	PTR	A	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	-4.00	1.31	1.40
1	A	1007	PTR	OH-CZ	-3.71	1.32	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1007	PTR	O2P-P-OH	2.65	113.53	105.24
1	B	1007	PTR	O2P-P-OH	2.35	112.58	105.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	3JW	B	1201	-	21,29,29	2.25	9 (42%)	23,44,44	4.13	11 (47%)
2	3JW	A	1201	-	21,29,29	2.13	9 (42%)	23,44,44	4.14	13 (56%)

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	3JW	B	1201	-	-	7/7/33/33	0/4/4/4
2	3JW	A	1201	-	-	6/7/33/33	0/4/4/4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	3JW	CAG-CAH	4.64	1.52	1.46
2	B	1201	3JW	OAY-SAC	4.51	1.48	1.43
2	A	1201	3JW	CAG-CAH	4.44	1.51	1.46
2	B	1201	3JW	CAB-SAC	3.78	1.81	1.76
2	A	1201	3JW	CAJ-NAD	-3.75	1.46	1.49
2	B	1201	3JW	SAC-NAD	3.61	1.67	1.63
2	A	1201	3JW	OAY-SAC	3.44	1.47	1.43
2	B	1201	3JW	CAL-NAK	-3.10	1.32	1.35
2	A	1201	3JW	OAZ-SAC	3.08	1.46	1.43
2	A	1201	3JW	CAL-NAK	-3.01	1.32	1.35
2	A	1201	3JW	C6-NAT	2.59	1.39	1.34
2	B	1201	3JW	C5-C6	-2.35	1.36	1.43
2	B	1201	3JW	C6-NAT	2.33	1.39	1.34
2	A	1201	3JW	CAE-NAD	-2.29	1.47	1.49
2	A	1201	3JW	C5-C6	-2.10	1.37	1.43
2	B	1201	3JW	OAZ-SAC	2.09	1.45	1.43
2	B	1201	3JW	CAJ-NAD	-2.06	1.47	1.49
2	A	1201	3JW	SAC-NAD	2.02	1.65	1.63

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1201	3JW	OAZ-SAC-OAY	-14.22	104.39	118.98
2	A	1201	3JW	OAZ-SAC-OAY	-11.37	107.31	118.98
2	A	1201	3JW	OAZ-SAC-CAB	7.97	122.31	108.55
2	A	1201	3JW	CAA-CAB-SAC	-7.58	102.25	112.93
2	B	1201	3JW	CAA-CAB-SAC	-6.38	103.94	112.93
2	B	1201	3JW	CAG-CAH-NAI	-6.03	170.13	178.11
2	A	1201	3JW	C5-C4-N3	-5.70	119.29	123.04
2	A	1201	3JW	N1-C2-N3	-5.45	120.17	128.68
2	B	1201	3JW	N1-C2-N3	-4.67	121.37	128.68
2	B	1201	3JW	OAY-SAC-CAB	4.17	115.75	108.55
2	B	1201	3JW	CAN-NAO-NAK	4.08	108.47	104.23
2	A	1201	3JW	CAN-NAO-NAK	3.57	107.95	104.23
2	A	1201	3JW	CAL-NAK-CAF	3.57	126.89	124.18
2	B	1201	3JW	C2-N1-C6	3.48	121.60	113.45
2	A	1201	3JW	C2-N1-C6	3.44	121.51	113.45
2	B	1201	3JW	C5-C4-N3	-3.38	120.81	123.04
2	A	1201	3JW	CAJ-NAD-SAC	3.05	129.55	122.96
2	A	1201	3JW	C2-N3-C4	2.87	122.11	117.69
2	B	1201	3JW	CAL-NAK-CAF	2.85	126.35	124.18
2	A	1201	3JW	OAY-SAC-NAD	-2.69	104.95	107.23
2	A	1201	3JW	OAZ-SAC-NAD	-2.55	105.07	107.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1201	3JW	CAE-NAD-SAC	2.25	127.82	122.96
2	B	1201	3JW	OAZ-SAC-NAD	2.13	109.03	107.23
2	A	1201	3JW	CAG-CAH-NAI	-2.01	175.46	178.11

There are no chirality outliers.

All (13) torsion outliers are listed below:

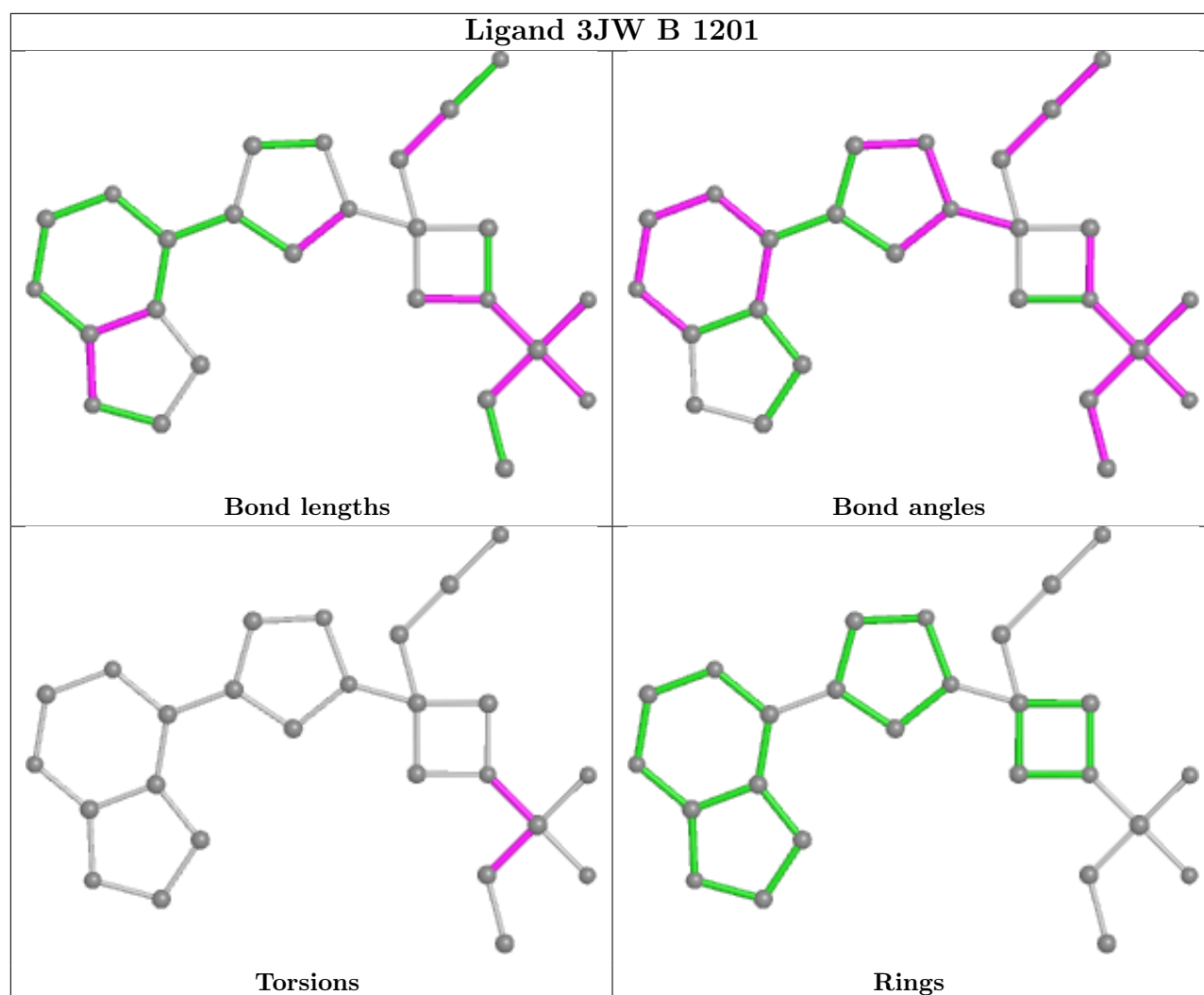
Mol	Chain	Res	Type	Atoms
2	B	1201	3JW	CAA-CAB-SAC-OAY
2	B	1201	3JW	CAA-CAB-SAC-OAZ
2	B	1201	3JW	CAA-CAB-SAC-NAD
2	B	1201	3JW	CAE-NAD-SAC-OAZ
2	A	1201	3JW	CAA-CAB-SAC-OAY
2	A	1201	3JW	CAA-CAB-SAC-OAZ
2	A	1201	3JW	CAA-CAB-SAC-NAD
2	A	1201	3JW	CAE-NAD-SAC-OAZ
2	B	1201	3JW	CAJ-NAD-SAC-OAZ
2	A	1201	3JW	CAJ-NAD-SAC-OAZ
2	B	1201	3JW	CAJ-NAD-SAC-OAY
2	A	1201	3JW	CAJ-NAD-SAC-OAY
2	B	1201	3JW	CAE-NAD-SAC-OAY

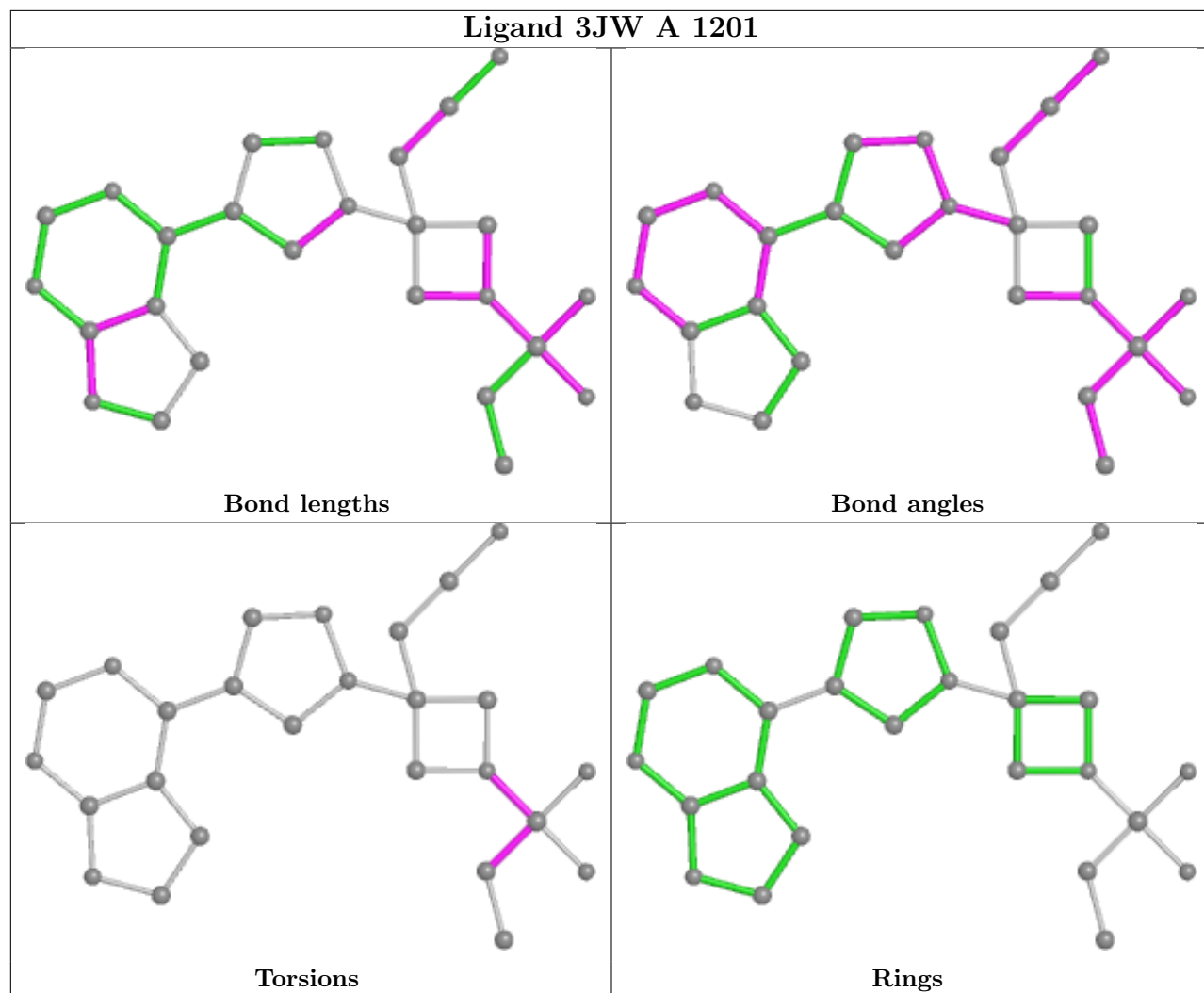
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	3JW	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 [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	297/308 (96%)	0.17	18 (6%) 21 24	33, 47, 81, 114	0
1	B	288/308 (93%)	0.04	14 (4%) 29 33	30, 45, 82, 115	0
All	All	585/616 (94%)	0.11	32 (5%) 25 28	30, 46, 82, 115	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	921	GLY	6.1
1	A	922	ARG	5.0
1	A	923	ARG	4.7
1	B	920	ALA	4.6
1	B	922	ARG	4.1
1	B	1067	ASN	4.0
1	A	920	ALA	4.0
1	A	921	GLY	3.8
1	B	1068	ASP	3.5
1	B	918	TYR	3.5
1	A	1068	ASP	3.3
1	B	1070	GLN	3.1
1	A	1067	ASN	2.9
1	A	1132	GLY	2.8
1	B	919	SER	2.8
1	B	1053	LYS	2.8
1	A	1053	LYS	2.7
1	A	918	TYR	2.7
1	B	843	GLN	2.6
1	B	1073	MET	2.6
1	A	1003	GLN	2.4
1	A	1069	LYS	2.4
1	A	1013	PRO	2.4
1	B	1065	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	1070	GLN	2.3
1	B	1076	PHE	2.3
1	B	1015	GLU	2.3
1	A	1072	GLN	2.2
1	A	893	ARG	2.1
1	A	1012	GLU	2.1
1	A	932	LEU	2.1
1	A	1063	ARG	2.1

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(\AA^2)	Q<0.9
1	PTR	B	1007	16/17	0.93	0.13	42,57,121,167	0
1	PTR	A	1007	16/17	0.95	0.10	42,57,89,94	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

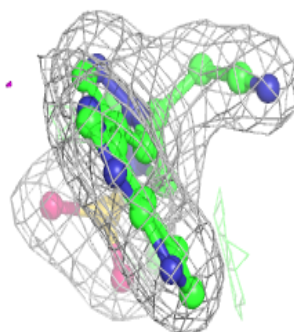
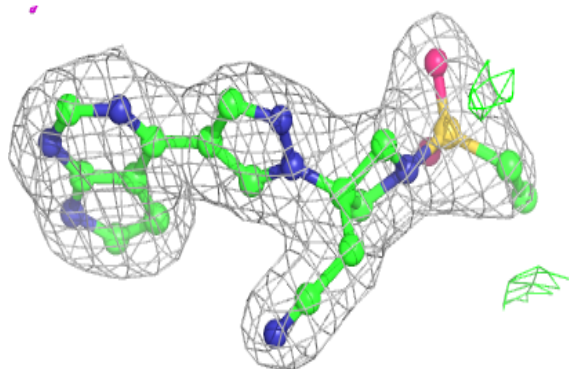
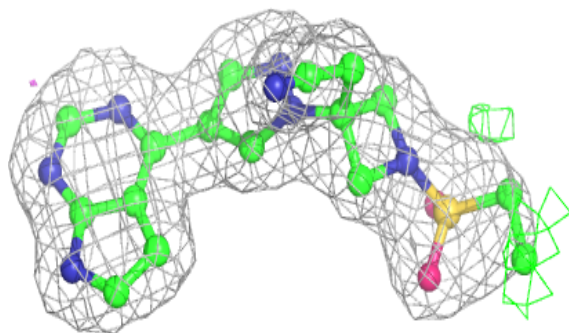
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	3JW	A	1201	26/26	0.98	0.15	31,38,46,60	0
2	3JW	B	1201	26/26	0.99	0.11	30,36,49,70	0

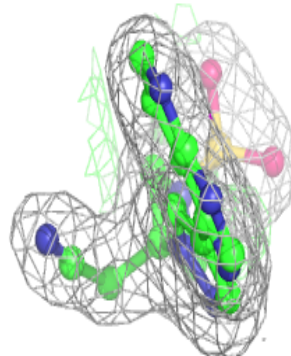
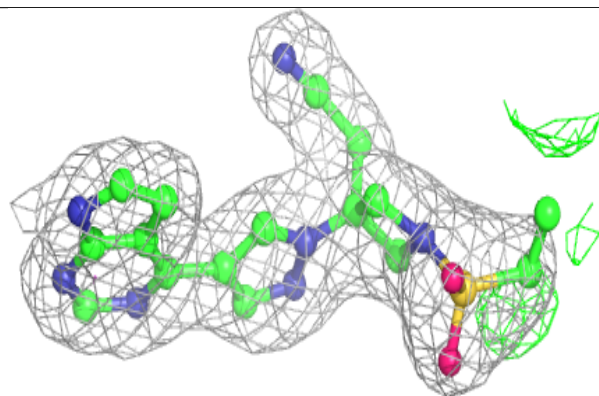
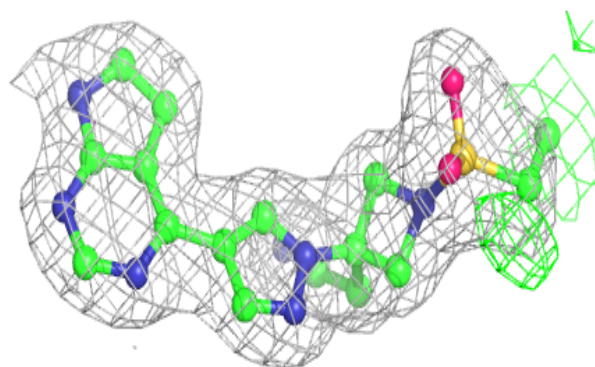
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 3JW 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)

**Electron density around 3JW 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.