Full wwPDB X-ray Structure Validation Report (i)

May 14, 2020 – 12:16 pm BST

PDB ID	:	3Q32
Title	:	Structure of Janus kinase 2 with a pyrrolotriazine inhibitor
Authors	:	Sack, J.S.
Deposited on	:	2010-12-21
Resolution	:	2.50 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 (i) symbol.

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

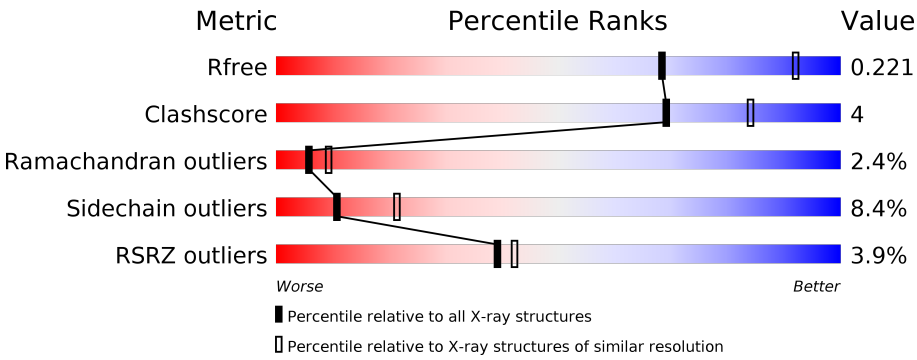
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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	301	5% 80% 15% • • •
1	B	301	3% 82% 14% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5039 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.

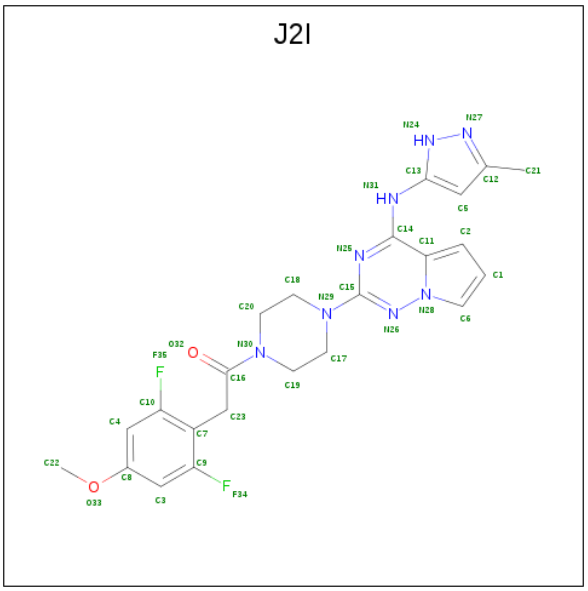
- Molecule 1 is a protein called Tyrosine-protein kinase JAK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	293	2425	1536	421	452	2	14	0	0	0
1	B	296	2454	1553	429	455	2	15	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	838	MET	-	INITIATING METHIONINE	UNP O60674
A	1133	HIS	-	EXPRESSION TAG	UNP O60674
A	1134	HIS	-	EXPRESSION TAG	UNP O60674
A	1135	HIS	-	EXPRESSION TAG	UNP O60674
A	1136	HIS	-	EXPRESSION TAG	UNP O60674
A	1137	HIS	-	EXPRESSION TAG	UNP O60674
A	1138	HIS	-	EXPRESSION TAG	UNP O60674
B	838	MET	-	INITIATING METHIONINE	UNP O60674
B	1133	HIS	-	EXPRESSION TAG	UNP O60674
B	1134	HIS	-	EXPRESSION TAG	UNP O60674
B	1135	HIS	-	EXPRESSION TAG	UNP O60674
B	1136	HIS	-	EXPRESSION TAG	UNP O60674
B	1137	HIS	-	EXPRESSION TAG	UNP O60674
B	1138	HIS	-	EXPRESSION TAG	UNP O60674

- Molecule 2 is 2-(2,6-difluoro-4-methoxyphenyl)-1-(4-{4-[(3-methyl-1H-pyrazol-5-yl)amino]pyrrolo[2,1-f][1,2,4]triazin-2-yl}piperazin-1-yl)ethanone (three-letter code: J2I) (formula: $C_{23}H_{24}F_2N_8O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			35	23	2	8	2		
2	B	1	Total	C	F	N	O	0	0
			35	23	2	8	2		

- Molecule 3 is water.

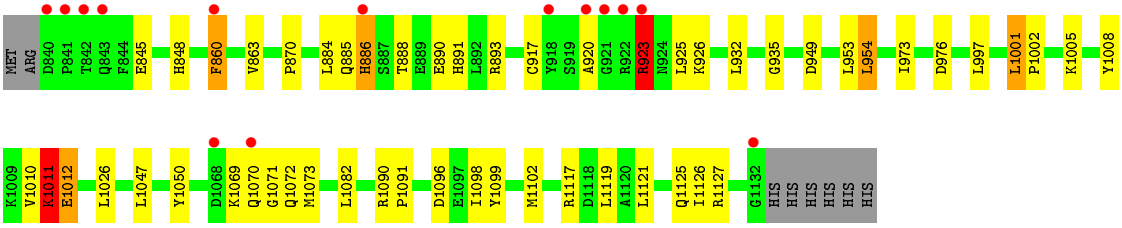
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	42	Total	O	0	0
			42	42		
3	B	48	Total	O	0	0
			48	48		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

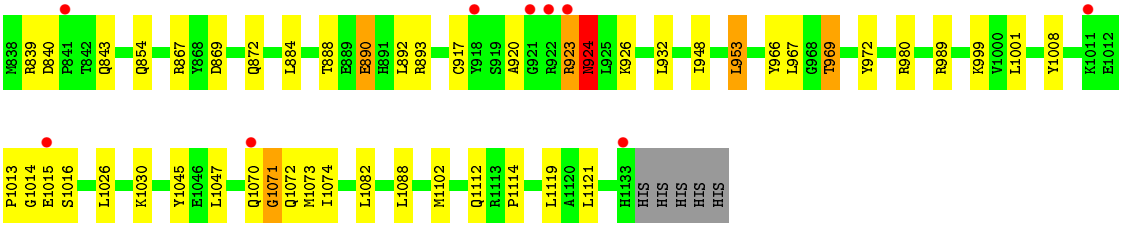
- Molecule 1: Tyrosine-protein kinase JAK2

Chain A:



- Molecule 1: Tyrosine-protein kinase JAK2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	110.59Å 110.59Å 69.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.46 – 2.50 49.46 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.46-2.50) 100.0 (49.46-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.36 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.9.7, AUTOBUSTER	Depositor
R, R_{free}	0.178 , 0.210 0.185 , 0.221	Depositor DCC
R_{free} test set	649 reflections (2.21%)	wwPDB-VP
Wilson B-factor (Å^2)	43.7	Xtriage
Anisotropy	0.554	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.046 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5039	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[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, J2I

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	0.51	0/2443	0.73	0/3287
1	B	0.50	0/2473	0.75	1/3326 (0.0%)
All	All	0.50	0/4916	0.74	1/6613 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	923	ARG	C-N-CA	5.75	136.08	121.70

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	2425	0	2396	21	0
1	B	2454	0	2425	15	0
2	A	35	0	24	4	0
2	B	35	0	24	1	0
3	A	42	0	0	0	0
3	B	48	0	0	0	0
All	All	5039	0	4869	36	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (36) 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:932:LEU:H	2:B:2:J2I:HN24	1.15	0.92
1:A:932:LEU:H	2:A:1:J2I:HN24	1.28	0.78
1:A:917:CYS:HB3	1:A:926:LYS:HB2	1.77	0.66
1:A:1011:LYS:H	1:A:1011:LYS:HD3	1.62	0.64
1:A:1008:PTR:HE1	1:A:1010:VAL:HB	1.86	0.57
1:B:917:CYS:HB3	1:B:926:LYS:HB2	1.88	0.55
1:A:888:THR:HG23	1:A:891:HIS:HB2	1.89	0.55
1:B:888:THR:HG22	1:B:890:GLU:H	1.74	0.52
1:A:935:GLY:HA2	2:A:1:J2I:C11	2.40	0.51
1:B:1071:GLY:HA2	1:B:1074:ILE:HD12	1.92	0.51
1:A:1002:PRO:HG2	1:A:1005:LYS:HB2	1.91	0.51
1:B:1045:TYR:HB2	1:B:1102:MET:HE3	1.93	0.51
1:A:920:ALA:H	1:A:923:ARG:HB3	1.76	0.50
1:B:966:TYR:O	1:B:969:THR:HB	2.12	0.49
1:A:845:GLU:HB3	1:A:848:HIS:HD2	1.78	0.48
1:A:860:PHE:H	1:A:860:PHE:HD1	1.61	0.48
1:A:863:VAL:HG23	2:A:1:J2I:O33	2.14	0.47
1:B:840:ASP:HB3	1:B:843:GLN:HG2	1.97	0.47
1:B:999:LYS:HD2	1:B:1008:PTR:HE1	1.97	0.46
1:A:886:HIS:HB3	1:A:888:THR:HG22	2.00	0.44
1:A:1098:ILE:HD11	1:A:1126:ILE:HG21	2.00	0.43
1:A:1050:TYR:CD2	1:B:1112:GLN:HG3	2.53	0.43
1:A:976:ASP:HB2	1:A:997:LEU:HD12	2.00	0.43
1:A:954:LEU:HB3	1:A:1127:ARG:CG	2.49	0.43
1:B:867:ARG:HG2	1:B:869:ASP:HB2	2.02	0.42
2:A:1:J2I:H20	2:A:1:J2I:C7	2.49	0.42
1:A:1090:ARG:HG3	1:A:1099:TYR:HB2	2.02	0.41
1:B:1114:PRO:HG2	1:B:1119:LEU:HD21	2.03	0.41
1:B:923:ARG:HG2	1:B:924:ASN:N	2.36	0.41
1:A:1008:PTR:C	1:A:1008:PTR:HD1	2.51	0.41
1:B:948:ILE:CG2	1:B:953:LEU:HD13	2.51	0.41
1:A:848:HIS:CG	1:A:870:PRO:HA	2.55	0.41
1:B:923:ARG:O	1:B:924:ASN:HB3	2.21	0.40
1:B:967:LEU:HG	1:B:972:TYR:HB2	2.04	0.40
1:A:973:ILE:HG12	1:A:1001:LEU:HD13	2.04	0.40
1:A:1091:PRO:HD3	1:A:1102:MET:HE1	2.03	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	289/301 (96%)	270 (93%)	13 (4%)	6 (2%)	7 11
1	B	292/301 (97%)	275 (94%)	9 (3%)	8 (3%)	5 7
All	All	581/602 (96%)	545 (94%)	22 (4%)	14 (2%)	6 9

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1011	LYS
1	A	1070	GLN
1	B	920	ALA
1	B	924	ASN
1	B	1070	GLN
1	A	925	LEU
1	A	1012	GLU
1	A	1071	GLY
1	B	1013	PRO
1	B	1015	GLU
1	B	1071	GLY
1	A	923	ARG
1	B	1016	SER
1	B	1014	GLY

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	265/273 (97%)	241 (91%)	24 (9%)	9 18
1	B	268/273 (98%)	247 (92%)	21 (8%)	12 24
All	All	533/546 (98%)	488 (92%)	45 (8%)	11 21

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	860	PHE
1	A	884	LEU
1	A	885	GLN
1	A	886	HIS
1	A	890	GLU
1	A	893	ARG
1	A	923	ARG
1	A	949	ASP
1	A	953	LEU
1	A	954	LEU
1	A	1001	LEU
1	A	1011	LYS
1	A	1012	GLU
1	A	1026	LEU
1	A	1047	LEU
1	A	1069	LYS
1	A	1072	GLN
1	A	1073	MET
1	A	1082	LEU
1	A	1096	ASP
1	A	1117	ARG
1	A	1119	LEU
1	A	1121	LEU
1	A	1125	GLN
1	B	839	ARG
1	B	854	GLN
1	B	872	GLN
1	B	884	LEU
1	B	890	GLU
1	B	892	LEU
1	B	893	ARG
1	B	924	ASN
1	B	953	LEU
1	B	969	THR
1	B	980	ARG

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Mol	Chain	Res	Type
1	B	989	ARG
1	B	1001	LEU
1	B	1026	LEU
1	B	1030	LYS
1	B	1047	LEU
1	B	1072	GLN
1	B	1073	MET
1	B	1082	LEU
1	B	1088	LEU
1	B	1121	LEU

Some 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	B	1008	1	15,16,17	1.27	2 (13%)	19,22,24	1.42	3 (15%)
1	PTR	A	1008	1	15,16,17	1.44	3 (20%)	19,22,24	1.67	4 (21%)
1	PTR	A	1007	1	15,16,17	1.42	2 (13%)	19,22,24	1.35	2 (10%)
1	PTR	B	1007	1	15,16,17	1.20	0	19,22,24	1.15	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	B	1008	1	-	1/10/11/13	0/1/1/1
1	PTR	A	1008	1	-	1/10/11/13	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

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1007	PTR	CE2-CZ	3.02	1.44	1.38
1	A	1008	PTR	CE2-CZ	2.79	1.44	1.38
1	B	1008	PTR	CE2-CZ	2.77	1.44	1.38
1	A	1008	PTR	P-OH	-2.48	1.55	1.59
1	A	1008	PTR	CE2-CD2	2.40	1.43	1.38
1	A	1007	PTR	CE1-CZ	2.16	1.43	1.38
1	B	1008	PTR	CE2-CD2	2.08	1.42	1.38

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1007	PTR	O3P-P-OH	3.70	116.80	105.24
1	A	1008	PTR	CB-CA-C	3.38	117.80	111.47
1	A	1008	PTR	OH-CZ-CE2	3.29	129.01	119.23
1	A	1007	PTR	CG-CB-CA	-3.22	107.57	114.10
1	A	1007	PTR	O3P-P-OH	3.22	115.31	105.24
1	A	1008	PTR	O3P-P-OH	3.02	114.68	105.24
1	B	1008	PTR	CB-CA-C	2.80	116.72	111.47
1	B	1007	PTR	P-OH-CZ	-2.50	115.73	123.75
1	B	1008	PTR	P-OH-CZ	-2.46	115.85	123.75
1	A	1008	PTR	OH-CZ-CE1	-2.43	112.00	119.23
1	B	1008	PTR	CE2-CZ-CE1	-2.15	116.87	120.18

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1008	PTR	CZ-OH-P-O1P
1	A	1008	PTR	CZ-OH-P-O3P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1008	PTR	1	0
1	A	1008	PTR	2	0

5.5 Carbohydrates (i)

There are no carbohydrates 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	J2I	B	2	-	34,39,39	1.13	1 (2%)	43,56,56	1.88	8 (18%)
2	J2I	A	1	-	34,39,39	1.20	4 (11%)	43,56,56	2.21	14 (32%)

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	J2I	B	2	-	-	4/16/28/28	0/5/5/5
2	J2I	A	1	-	-	2/16/28/28	0/5/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	J2I	C15-N25	3.74	1.41	1.34
2	A	1	J2I	C15-N25	2.97	1.39	1.34
2	A	1	J2I	C16-N30	2.38	1.40	1.35
2	A	1	J2I	C3-C9	2.18	1.41	1.37
2	A	1	J2I	C12-N27	2.09	1.36	1.34

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1	J2I	C4-C10-C7	-6.42	120.08	124.59
2	A	1	J2I	C3-C9-C7	-6.28	120.18	124.59
2	B	2	J2I	C4-C10-C7	-5.76	120.55	124.59
2	B	2	J2I	C3-C9-C7	-5.13	120.99	124.59
2	B	2	J2I	N31-C14-N25	4.13	122.54	118.66
2	A	1	J2I	C10-C7-C9	3.77	119.76	114.51
2	A	1	J2I	F35-C10-C7	3.62	121.95	117.63
2	A	1	J2I	C13-C5-C12	-3.08	104.05	107.23
2	B	2	J2I	F35-C10-C7	3.07	121.29	117.63
2	B	2	J2I	C5-C12-N27	-3.06	105.26	110.81
2	A	1	J2I	C23-C7-C9	-3.02	116.97	123.14
2	A	1	J2I	N31-C14-N25	2.89	121.37	118.66
2	A	1	J2I	C18-C20-N30	2.76	116.35	110.44
2	A	1	J2I	C20-N30-C19	2.70	117.81	112.62
2	B	2	J2I	C10-C7-C9	2.69	118.26	114.51
2	A	1	J2I	C5-C12-N27	-2.67	105.96	110.81
2	B	2	J2I	C20-N30-C19	2.61	117.65	112.62
2	A	1	J2I	C1-C6-N28	2.46	108.24	106.78
2	A	1	J2I	O32-C16-C23	-2.34	117.79	121.60
2	B	2	J2I	C13-C5-C12	-2.33	104.83	107.23
2	A	1	J2I	C21-C12-C5	2.07	134.56	129.06
2	A	1	J2I	N26-C15-N25	-2.01	123.19	125.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	J2I	C3-C8-O33-C22
2	A	1	J2I	C4-C8-O33-C22
2	B	2	J2I	C3-C8-O33-C22
2	B	2	J2I	C4-C8-O33-C22
2	B	2	J2I	C16-C23-C7-C9
2	B	2	J2I	C16-C23-C7-C10

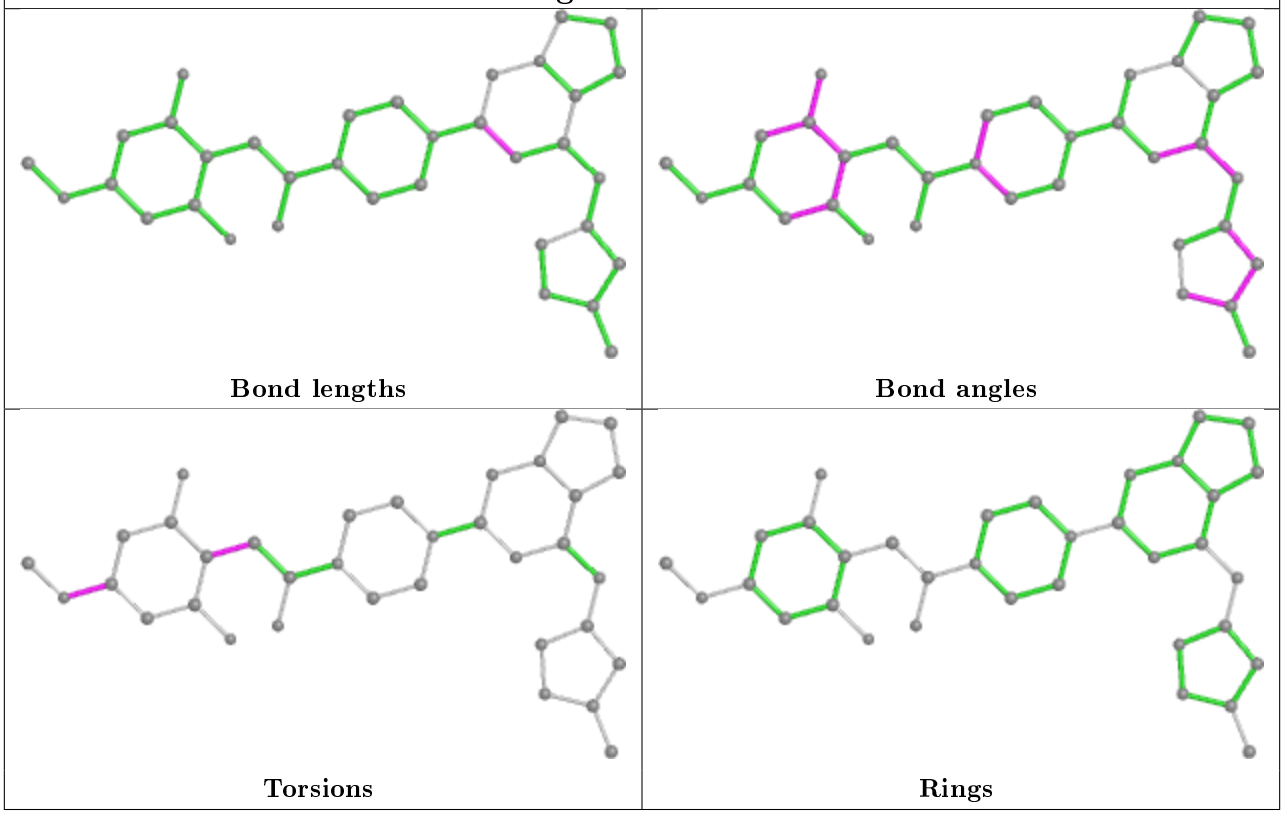
There are no ring outliers.

2 monomers are involved in 5 short contacts:

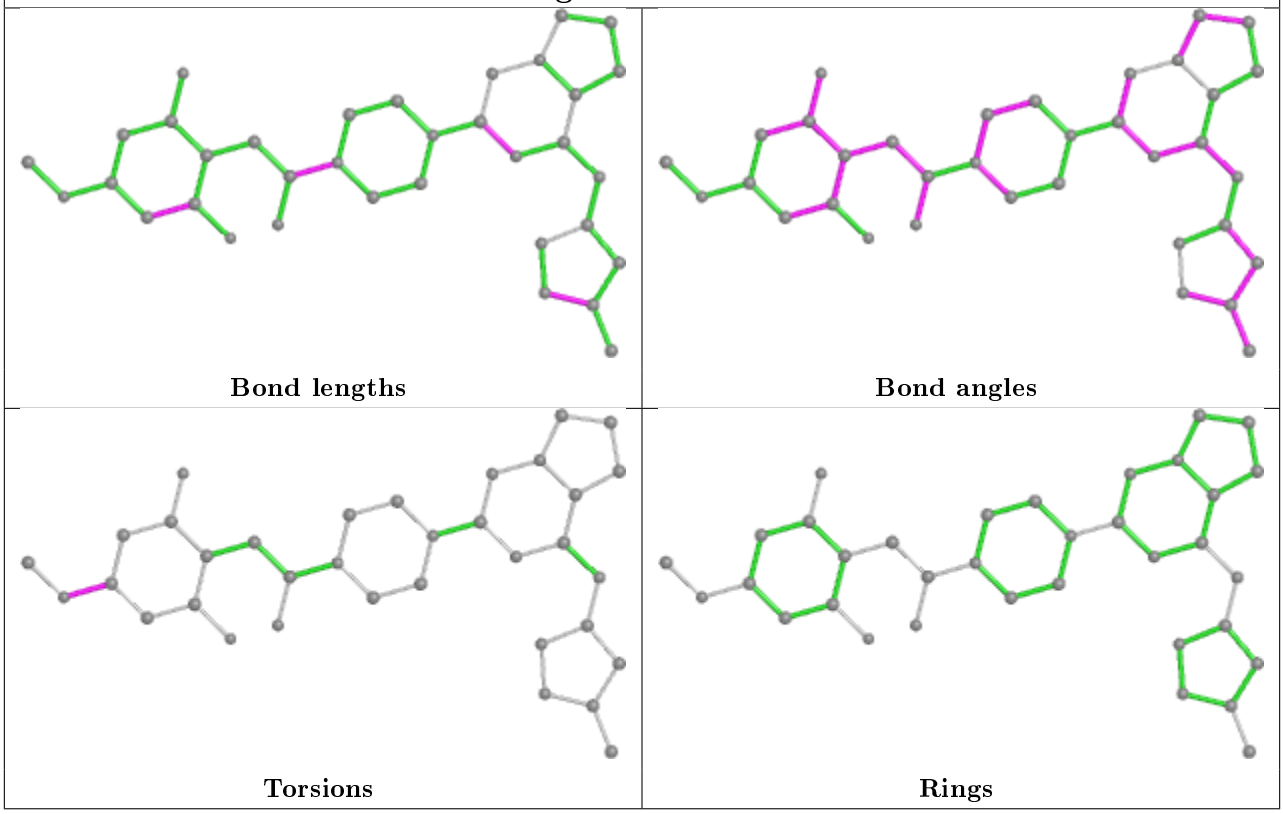
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	J2I	1	0
2	A	1	J2I	4	0

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 J2I B 2



Ligand J2I A 1



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	291/301 (96%)	0.01	14 (4%)	30	32	30, 49, 99, 128	0
1	B	294/301 (97%)	-0.02	9 (3%)	49	52	33, 51, 89, 114	0
All	All	585/602 (97%)	-0.01	23 (3%)	39	42	30, 50, 95, 128	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	840	ASP	8.3
1	A	921	GLY	7.0
1	A	841	PRO	6.6
1	A	842	THR	5.9
1	A	922	ARG	4.9
1	B	922	ARG	4.4
1	B	918	TYR	4.2
1	B	923	ARG	4.1
1	A	920	ALA	3.9
1	A	1132	GLY	3.2
1	A	918	TYR	3.1
1	A	886	HIS	3.1
1	B	1070	GLN	3.0
1	B	1011	LYS	2.9
1	B	921	GLY	2.8
1	A	843	GLN	2.7
1	A	1070	GLN	2.7
1	A	1068	ASP	2.6
1	B	841	PRO	2.5
1	A	923	ARG	2.4
1	B	1133	HIS	2.3
1	A	860	PHE	2.2
1	B	1015	GLU	2.0

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	B	1008	16/17	0.88	0.17	63,78,89,90	0
1	PTR	B	1007	16/17	0.92	0.15	66,73,84,84	0
1	PTR	A	1008	16/17	0.94	0.13	43,55,73,73	0
1	PTR	A	1007	16/17	0.96	0.10	43,48,65,65	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

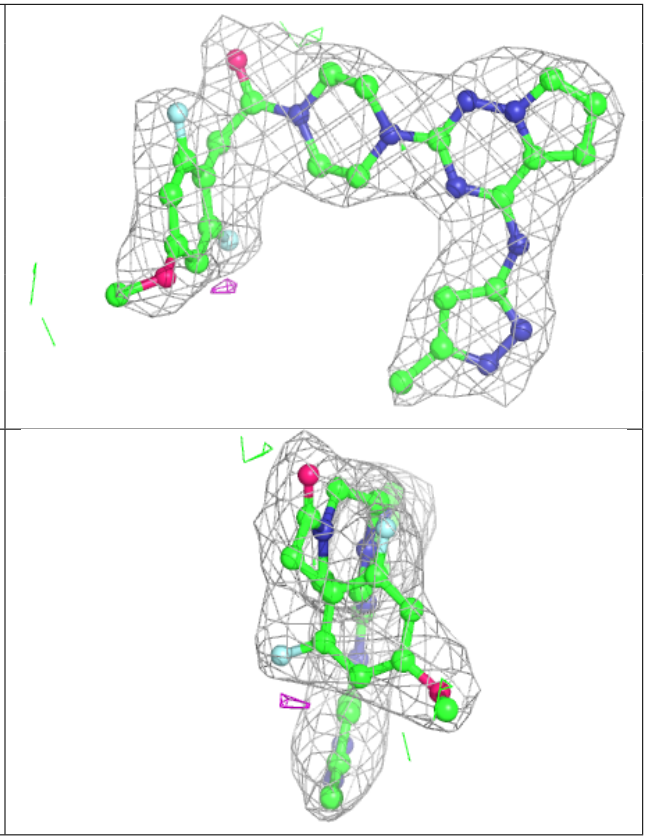
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	J2I	A	1	35/35	0.97	0.14	31,39,54,56	0
2	J2I	B	2	35/35	0.98	0.15	30,40,53,58	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.

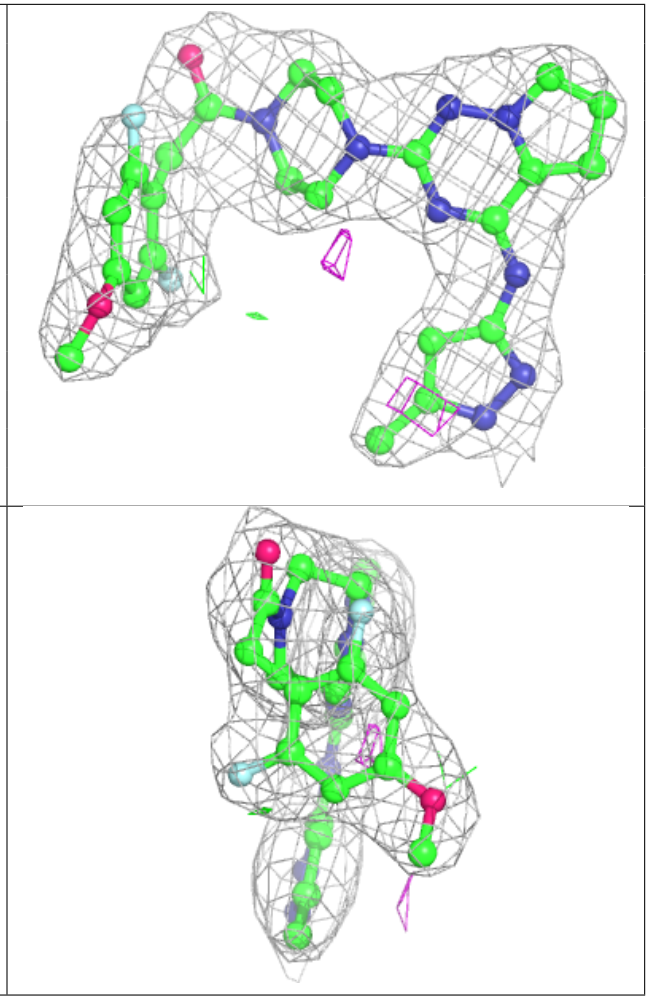
Electron density around J2I A 1:

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



Electron density around J2I B 2:

$2mF_o$-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.