



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 31, 2021 – 01:29 PM EDT

PDB ID : 7KHK
Title : Crystal structure of KIT kinase domain with a small molecule inhibitor, PLX9486 (bezuclostinib) in the DFG-in state
Authors : Zhang, Y.
Deposited on : 2020-10-21
Resolution : 2.34 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 : 2.23.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.1

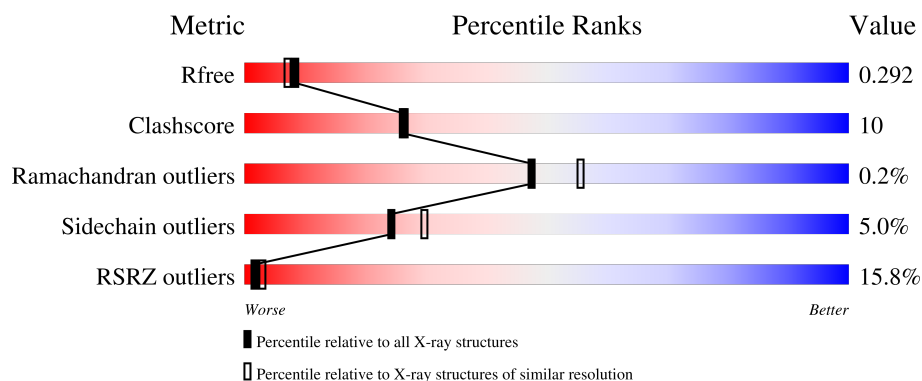
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	335	<div> <div>6%</div> <div>71%</div> <div>16%</div> <div>•</div> <div>13%</div> </div>
1	B	335	<div> <div>20%</div> <div>56%</div> <div>20%</div> <div>•</div> <div>21%</div> </div>

2 Entry composition [i](#)

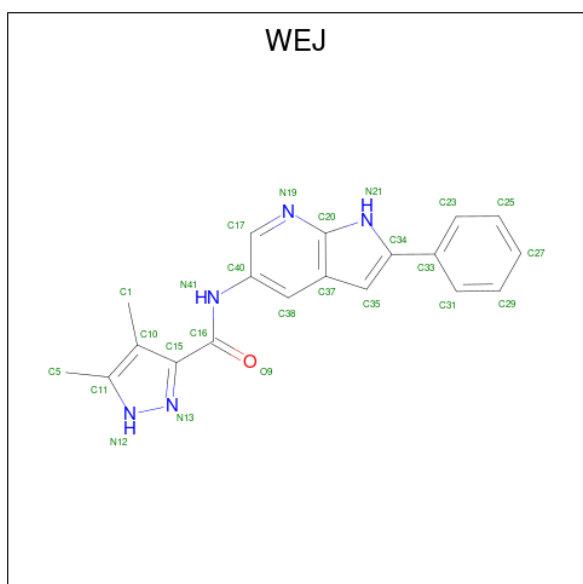
There are 3 unique types of molecules in this entry. The entry contains 4521 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Mast/stem cell growth factor receptor Kit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2321	1487	389	429	16			
1	B	266	Total	C	N	O	S	0	0	0
			2119	1366	350	388	15			

- Molecule 2 is 4,5-dimethyl-N-(2-phenyl-1H-pyrrolo[2,3-b]pyridin-5-yl)-1H-pyrazole-3-carboxamide (three-letter code: WEJ) (formula: C₁₉H₁₇N₅O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			25	19	5	1		
2	B	1	Total	C	N	O	0	0
			25	19	5	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total 31	O 31	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.98Å 61.91Å 206.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.06 – 2.34 46.06 – 2.34	Depositor EDS
% Data completeness (in resolution range)	96.1 (46.06-2.34) 96.1 (46.06-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.245 , 0.285 0.259 , 0.292	Depositor DCC
R_{free} test set	1534 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4521	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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: WEJ

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	0.41	0/2376	0.61	4/3208 (0.1%)
1	B	0.41	2/2167 (0.1%)	0.64	7/2924 (0.2%)
All	All	0.41	2/4543 (0.0%)	0.62	11/6132 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	570	TYR	CD1-CE1	7.39	1.50	1.39
1	B	818	LYS	CD-CE	5.10	1.64	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	570	TYR	CB-CG-CD1	8.14	125.88	121.00
1	B	570	TYR	CB-CG-CD2	-7.88	116.28	121.00
1	A	894	HIS	C-N-CA	-7.59	102.71	121.70
1	A	598	GLY	N-CA-C	-5.68	98.91	113.10
1	B	570	TYR	CZ-CE2-CD2	5.44	124.70	119.80
1	B	570	TYR	CG-CD1-CE1	-5.44	116.95	121.30
1	B	825	ASP	CB-CG-OD2	5.22	122.99	118.30
1	B	615	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	825	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	615	ASP	CB-CG-OD2	5.17	122.95	118.30
1	B	595	LEU	CB-CG-CD1	-5.09	102.34	111.00

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	2321	0	2288	34	0
1	B	2119	0	2102	64	0
2	A	25	0	0	1	0
2	B	25	0	0	4	0
3	A	31	0	0	4	0
All	All	4521	0	4390	92	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 10.

All (92) 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:674:CYS:HB3	1:B:802:HIS:CD2	2.02	0.94
1:B:675:TYR:HB2	1:B:800:LEU:O	1.71	0.91
1:B:887:PHE:CD1	1:B:888:ARG:HG2	2.10	0.87
1:B:602:LYS:HE3	1:B:624:MET:HG3	1.56	0.87
1:A:586:ARG:NH1	1:A:665:PRO:O	2.08	0.87
1:A:774:TYR:OH	3:A:1101:HOH:O	1.96	0.83
1:B:835:TRP:HA	1:B:857:ILE:HD12	1.67	0.76
1:B:809:CYS:HB2	2:B:1001:WEJ:N13	2.00	0.76
1:A:580:HIS:CD2	1:A:662:HIS:HE2	2.04	0.75
1:B:878:LYS:O	1:B:882:MET:HG3	1.88	0.74
1:B:856:GLY:HA3	1:B:907:TRP:HE1	1.51	0.73
1:B:879:PHE:O	1:B:883:ILE:HG12	1.89	0.73
1:B:887:PHE:HD1	1:B:888:ARG:HG2	1.53	0.72
1:B:677:ASP:OD1	1:B:677:ASP:N	2.24	0.70
1:B:586:ARG:NH2	1:B:665:PRO:O	2.23	0.69
1:A:671:GLU:OE2	1:A:807:LYS:NZ	2.29	0.64
1:A:910:ASP:HB3	1:A:913:LYS:HG3	1.79	0.64
1:B:847:THR:H	1:B:850:SER:HB3	1.62	0.64
1:B:887:PHE:HD1	1:B:888:ARG:CG	2.11	0.64
1:A:672:TYR:HE2	1:B:802:HIS:CD2	2.17	0.63
1:B:887:PHE:CD1	1:B:888:ARG:CG	2.83	0.59
1:B:602:LYS:HZ1	1:B:626:LYS:HE2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:675:TYR:HB3	1:B:800:LEU:HB3	1.84	0.59
1:B:800:LEU:HD13	1:B:806:THR:HG23	1.85	0.59
1:A:580:HIS:NE2	1:A:662:HIS:NE2	2.50	0.59
1:A:899:MET:HE1	1:A:902:ILE:HD12	1.84	0.58
1:B:595:LEU:HD13	2:B:1001:WEJ:C35	2.34	0.57
1:A:672:TYR:HE2	1:B:802:HIS:HD2	1.50	0.57
1:A:765:ASP:OD2	1:A:767:GLU:HG2	2.04	0.57
1:A:570:TYR:CD1	1:A:818:LYS:HE2	2.40	0.57
1:A:631:SER:O	1:A:631:SER:OG	2.21	0.57
1:B:832:PRO:O	1:B:836:MET:HG3	2.05	0.56
1:B:660:CYS:HB2	1:B:667:LEU:HB2	1.88	0.56
1:B:802:HIS:ND1	1:B:802:HIS:N	2.53	0.55
1:A:675:TYR:HB2	1:A:800:LEU:O	2.07	0.55
1:A:881:LYS:HE2	1:A:885:GLU:OE2	2.06	0.55
1:A:884:LYS:O	3:A:1102:HOH:O	2.18	0.55
1:B:905:THR:HG23	1:B:915:PRO:HD3	1.89	0.55
1:B:801:THR:HG22	1:B:805:ILE:HB	1.88	0.54
1:B:887:PHE:CE1	1:B:888:ARG:HG2	2.43	0.53
1:B:588:ARG:HD3	1:B:609:GLN:O	2.09	0.53
1:B:673:CYS:O	2:B:1001:WEJ:C31	2.56	0.53
1:A:832:PRO:O	1:A:836:MET:HG3	2.08	0.53
1:A:849:GLU:HG3	1:A:911:PRO:HB3	1.91	0.52
1:B:916:THR:OG1	1:B:919:GLN:HG3	2.09	0.52
1:B:650:HIS:HB3	1:B:653:ILE:HG12	1.92	0.52
1:B:775:GLN:OE1	1:B:805:ILE:HA	2.10	0.51
1:A:847:THR:OG1	1:A:849:GLU:HG2	2.11	0.50
1:B:632:THR:O	1:B:635:GLU:HG2	2.11	0.50
1:B:775:GLN:NE2	1:B:804:ARG:O	2.44	0.50
1:A:623:LYS:NZ	1:A:810:ASP:OD1	2.40	0.50
1:A:923:ASP:OD1	1:A:927:GLN:NE2	2.42	0.50
1:B:672:TYR:CD1	1:B:672:TYR:C	2.85	0.50
1:A:642:LYS:NZ	3:A:1107:HOH:O	2.46	0.49
1:B:573:PRO:HB3	1:B:646:TYR:HB2	1.95	0.49
1:A:878:LYS:O	1:A:882:MET:HG3	2.14	0.48
1:B:782:PHE:O	1:B:785:SER:OG	2.23	0.48
1:A:593:LYS:HG2	1:A:605:GLU:OE2	2.14	0.48
1:B:675:TYR:CB	1:B:800:LEU:HB3	2.42	0.48
1:B:887:PHE:O	1:B:888:ARG:C	2.51	0.48
1:B:603:VAL:HA	1:B:622:VAL:O	2.13	0.47
1:B:602:LYS:HZ1	1:B:626:LYS:CE	2.27	0.47
1:A:672:TYR:CE2	1:B:802:HIS:CD2	3.00	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:801:THR:CG2	1:B:805:ILE:HB	2.45	0.47
1:B:856:GLY:CA	1:B:907:TRP:HE1	2.22	0.47
1:A:674:CYS:HB3	1:B:802:HIS:HD2	1.71	0.47
1:B:675:TYR:HE2	1:B:802:HIS:HA	1.80	0.47
1:B:902:ILE:O	1:B:905:THR:HG22	2.15	0.47
1:A:609:GLN:NE2	1:B:649:ASN:OD1	2.49	0.46
1:A:623:LYS:HB2	2:A:1001:WEJ:C1	2.47	0.45
1:B:876:ASP:OD1	1:B:879:PHE:N	2.37	0.45
1:B:899:MET:HE1	1:B:902:ILE:HD12	1.98	0.45
1:A:631:SER:OG	1:A:634:ARG:HD2	2.17	0.45
1:B:602:LYS:HE3	1:B:624:MET:CG	2.37	0.45
1:B:595:LEU:C	1:B:595:LEU:HD12	2.37	0.44
1:B:576:LEU:O	1:B:642:LYS:HE2	2.18	0.43
1:A:570:TYR:O	1:A:819:ASN:ND2	2.49	0.43
1:A:576:LEU:O	1:A:642:LYS:HE2	2.19	0.43
1:B:682:LEU:H	1:B:682:LEU:HG	1.71	0.42
1:B:778:LYS:HB3	1:B:778:LYS:HE2	1.91	0.42
1:A:765:ASP:CG	1:A:767:GLU:HG2	2.40	0.42
1:B:856:GLY:HA3	1:B:907:TRP:NE1	2.26	0.42
1:B:916:THR:O	1:B:920:ILE:HG13	2.20	0.42
1:B:792:ASP:O	1:B:797:ASN:ND2	2.52	0.41
1:B:853:TRP:CD1	1:B:853:TRP:C	2.92	0.41
1:B:673:CYS:O	2:B:1001:WEJ:N21	2.53	0.41
1:A:774:TYR:CE2	1:A:778:LYS:HD2	2.56	0.41
1:A:796:ARG:HG2	3:A:1112:HOH:O	2.20	0.41
1:B:674:CYS:O	1:B:674:CYS:SG	2.79	0.41
1:B:681:PHE:CE2	1:B:800:LEU:HD23	2.56	0.41
1:B:573:PRO:HG2	1:B:816:VAL:HG21	2.03	0.40
1:B:595:LEU:CD1	1:B:603:VAL:HG23	2.51	0.40

There are no symmetry-related clashes.

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	283/335 (84%)	278 (98%)	4 (1%)	1 (0%)	34	38
1	B	254/335 (76%)	248 (98%)	6 (2%)	0	100	100
All	All	537/670 (80%)	526 (98%)	10 (2%)	1 (0%)	47	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	599	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	253/291 (87%)	245 (97%)	8 (3%)	39	47
1	B	231/291 (79%)	215 (93%)	16 (7%)	15	16
All	All	484/582 (83%)	460 (95%)	24 (5%)	24	30

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	631	SER
1	A	674	CYS
1	A	678	LEU
1	A	688	SER
1	A	690	HIS
1	A	804	ARG
1	A	898	GLU
1	A	930	GLU
1	B	586	ARG
1	B	587	ASN
1	B	612	ILE
1	B	632	THR
1	B	649	ASN
1	B	655	ASN
1	B	671	GLU

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Mol	Chain	Res	Type
1	B	677	ASP
1	B	682	LEU
1	B	770	LEU
1	B	802	HIS
1	B	877	SER
1	B	887	PHE
1	B	888	ARG
1	B	894	HIS
1	B	924	ILE

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	609	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	WEJ	A	1001	-	28,28,28	1.17	2 (7%)	28,40,40	1.10	2 (7%)
2	WEJ	B	1001	-	28,28,28	1.17	2 (7%)	28,40,40	1.10	2 (7%)

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	WEJ	A	1001	-	-	0/8/12/12	0/4/4/4
2	WEJ	B	1001	-	-	0/8/12/12	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	WEJ	C15-C16	-3.03	1.46	1.50
2	A	1001	WEJ	C15-C16	-3.02	1.46	1.50
2	A	1001	WEJ	C17-N19	2.71	1.36	1.31
2	B	1001	WEJ	C17-N19	2.65	1.36	1.31

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	WEJ	C17-N19-C20	-3.38	113.31	116.69
2	A	1001	WEJ	C17-N19-C20	-3.36	113.32	116.69
2	A	1001	WEJ	C40-C17-N19	2.11	126.10	124.49
2	B	1001	WEJ	C40-C17-N19	2.11	126.09	124.49

There are no chirality outliers.

There are no torsion outliers.

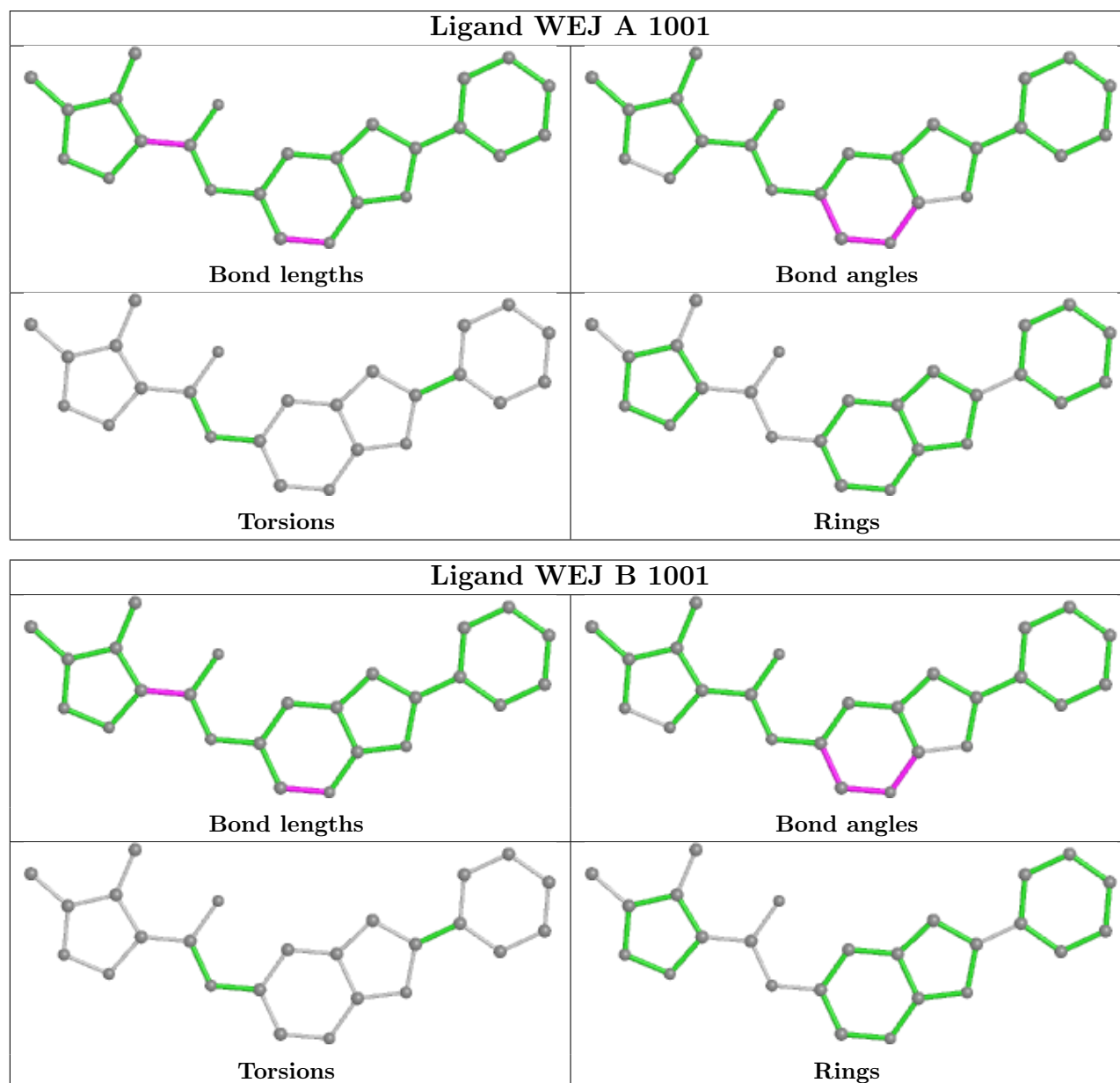
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	WEJ	1	0
2	B	1001	WEJ	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 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	291/335 (86%)	0.61	20 (6%) 16 24	38, 58, 96, 134	0
1	B	266/335 (79%)	1.41	68 (25%) 0 1	54, 100, 126, 158	0
All	All	557/670 (83%)	0.99	88 (15%) 2 3	38, 80, 123, 158	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	865	LEU	9.1
1	B	768	ASP	7.8
1	A	600	PHE	7.7
1	B	926	LYS	7.2
1	B	924	ILE	6.6
1	B	804	ARG	6.6
1	B	679	LEU	6.3
1	B	626	LYS	6.0
1	B	765	ASP	5.7
1	A	598	GLY	5.5
1	B	928	ILE	5.3
1	B	601	GLY	5.1
1	B	862	LEU	4.6
1	B	901	ASP	4.6
1	B	921	VAL	4.5
1	B	663	GLY	4.5
1	B	602	LYS	4.4
1	B	613	LYS	4.3
1	B	662	HIS	4.2
1	A	625	LEU	4.1
1	B	766	LEU	4.1
1	A	665	PRO	3.9
1	B	902	ILE	3.9
1	B	767	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	613	LYS	3.7
1	B	855	TYR	3.6
1	B	886	GLY	3.5
1	B	772	PHE	3.4
1	A	662	HIS	3.3
1	B	899	MET	3.2
1	B	802	HIS	3.1
1	B	922	GLN	3.1
1	B	575	GLN	3.0
1	B	905	THR	3.0
1	A	599	ALA	2.9
1	B	770	LEU	2.9
1	A	626	LYS	2.9
1	B	875	VAL	2.8
1	B	894	HIS	2.8
1	B	863	PHE	2.8
1	B	882	MET	2.8
1	B	868	SER	2.7
1	B	917	PHE	2.7
1	A	597	ALA	2.7
1	B	625	LEU	2.7
1	B	913	LYS	2.7
1	B	570	TYR	2.7
1	B	675	TYR	2.6
1	A	663	GLY	2.5
1	B	681	PHE	2.5
1	B	775	GLN	2.5
1	B	632	THR	2.5
1	B	883	ILE	2.5
1	B	682	LEU	2.4
1	B	808	ILE	2.4
1	A	769	LEU	2.4
1	B	822	ASN	2.4
1	B	800	LEU	2.4
1	B	873	MET	2.3
1	B	860	TRP	2.3
1	B	903	MET	2.3
1	B	591	PHE	2.3
1	A	818	LYS	2.3
1	B	571	ILE	2.3
1	B	867	SER	2.2
1	B	910	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	858	PHE	2.2
1	A	634	ARG	2.2
1	B	923	ASP	2.2
1	A	614	SER	2.2
1	A	675	TYR	2.2
1	B	609	GLN	2.1
1	A	822	ASN	2.1
1	B	830	ARG	2.1
1	B	831	LEU	2.1
1	B	818	LYS	2.1
1	B	848	PHE	2.1
1	B	907	TRP	2.1
1	A	667	LEU	2.1
1	B	912	ASP	2.1
1	A	627	PRO	2.1
1	A	653	ILE	2.1
1	B	596	GLY	2.1
1	B	879	PHE	2.1
1	B	771	SER	2.0
1	B	667	LEU	2.0
1	A	771	SER	2.0
1	B	795	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	WEJ	A	1001	25/25	0.74	0.34	105,105,106,106	0

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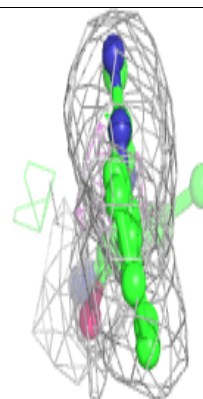
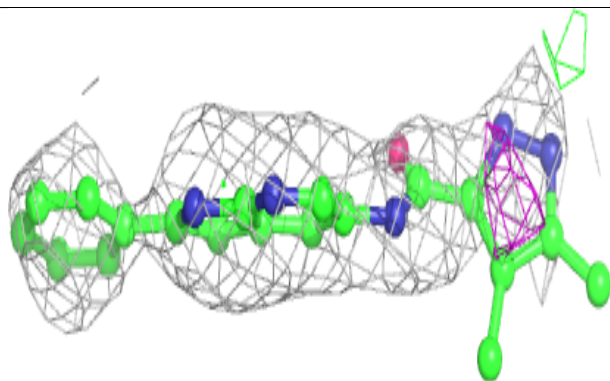
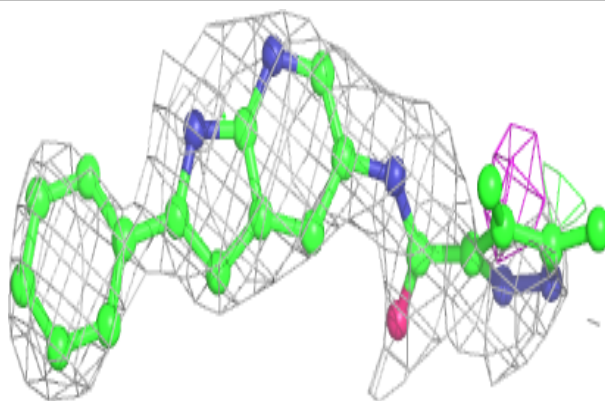
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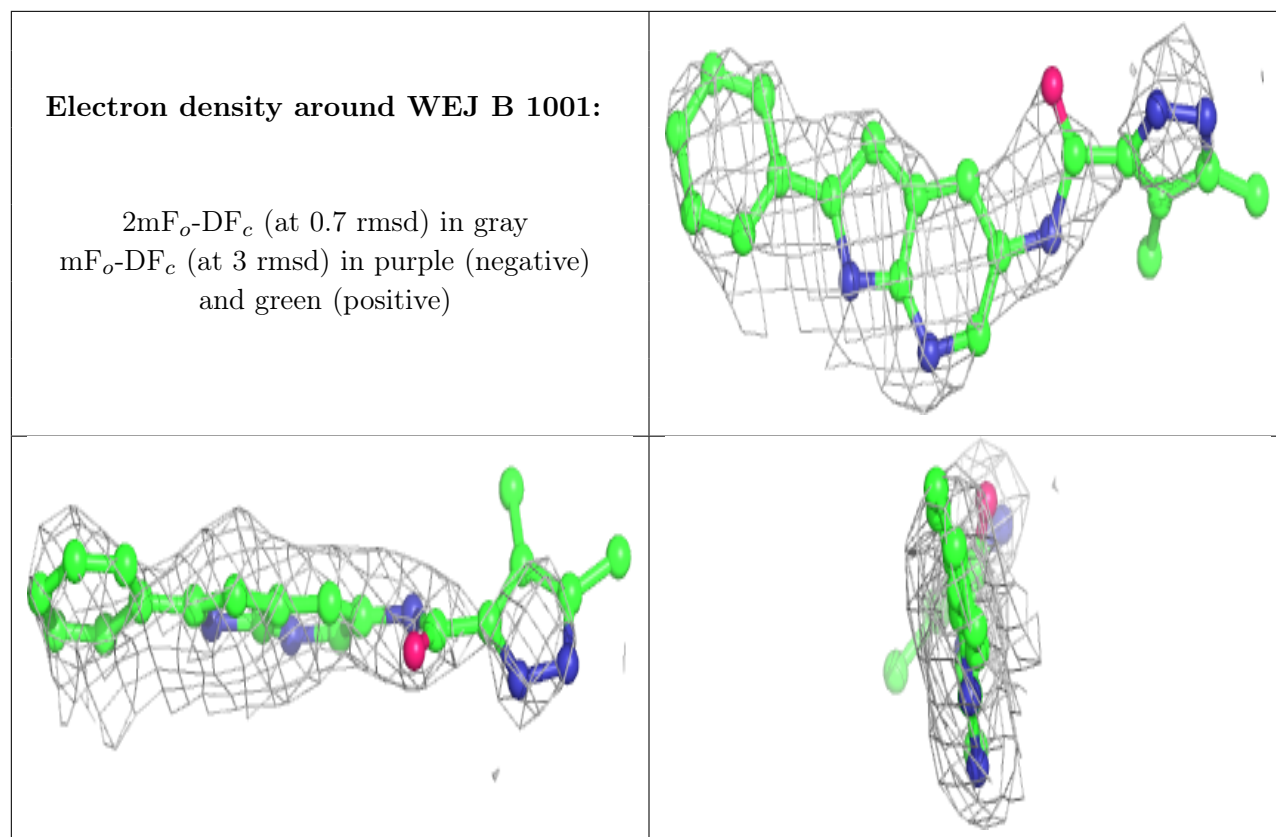
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	WEJ	B	1001	25/25	0.77	0.31	105,106,112,113	0

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 WEJ A 1001:

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.