

# Full wwPDB X-ray Structure Validation Report (i)

#### May 22, 2020 – 01:14 am BST

PDB ID : 4V0G

Title: JAK3 in complex with a covalent EGFR inhibitor

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Deposited on : 2014-09-16

Resolution : 3.00 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 (1)) 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)

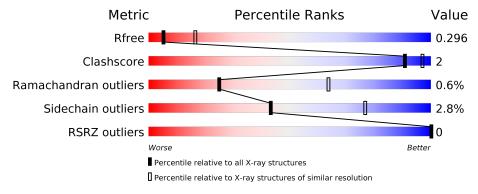
Validation Pipeline (wwPDB-VP) : 2.11

## 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 3.00 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	283	89%	5%	5%			
2	В	283	88%	8%	<del>-</del>			



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4460 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 JAK3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	269	Total 2156	C 1373	N 374	O 393	P 2	S 14	113	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	895	GLU	ARG	conflict	UNP P52333
A	896	PRO	GLN	conflict	UNP P52333
A	1048	SER	CYS	conflict	UNP P52333

• Molecule 2 is a protein called TYROSINE-PROTEIN KINASE JAK3.

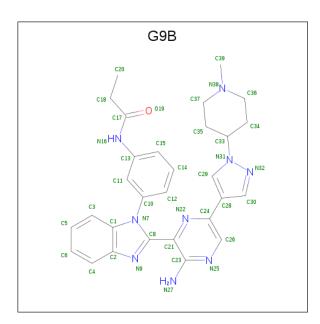
Mo	l Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
2	В	274	Total 2214	C 1405	N 387	O 406	P 2	S 14	87	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	894	GLY	ARG	conflict	UNP P52333
В	895	GLU	GLN	conflict	UNP P52333
В	1039	GLY	CYS	conflict	UNP P52333
В	1048	SER	CYS	conflict	UNP P52333

• Molecule 3 is N-[3-(2-{3-amino-6-[1-(1-methylpiperidin-4-yl)-1H-pyrazol-4-yl]pyrazin-2-yl}-1 H-benzimidazol-1-yl)phenyl|propanamide (three-letter code: G9B) (formula:  $C_{29}H_{31}N_9O$ ).





Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	
3	Δ	1	Total	С	N	О	6	0	
3	3 A	1	39	29	9	1	0		
2	D	1	Total	С	Ν	О	6	0	
) J	Ъ	1	39	29	9	1	0	U	

### • Molecule 4 is water.

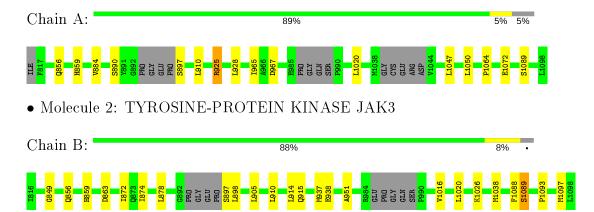
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	6	Total O 6 6	0	0
4	В	6	Total O 6 6	0	0



## 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 JAK3





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	57.14Å 99.03Å 111.37Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.92 - 3.00	Depositor
resolution (A)	48.54 - 3.00	EDS
% Data completeness	99.6 (73.92-3.00)	Depositor
(in resolution range)	99.7 (48.54-3.00)	EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.14 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
P. P.	0.252 , $0.295$	Depositor
$R, R_{free}$	0.246 , $0.296$	DCC
$R_{free}$ test set	593 reflections $(4.51%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.7	Xtriage
Anisotropy	0.635	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.31 , 43.7	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.43, < L^2> = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4460	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	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 44.26 % 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 1.5657e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: G9B, PTR

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	Boı	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.45	2/2170~(0.1%)	0.55	0/2928	
2	В	0.38	0/2229	0.54	0/3006	
All	All	0.42	$2/4399 \ (0.0\%)$	0.55	0/5934	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}( ext{\AA})$
1	A	1072	GLU	CD-OE1	-6.58	1.18	1.25
1	A	1072	GLU	CD-OE2	5.86	1.32	1.25

There are no bond angle outliers.

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	2156	0	2121	4	0
2	В	2214	0	2188	10	0
3	A	39	0	29	0	0
3	В	39	0	29	0	0
4	A	6	0	0	0	0
4	В	6	0	0	0	0
All	All	4460	0	4367	14	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 2.

All (14) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{l}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	Clash overlap (Å)
2:B:910:LEU:HD21	2:B:1020:LEU:HD21	1.91	0.52
2:B:951:ALA:HA	2:B:1016:VAL:HG12	1.92	0.51
2:B:874:ILE:O	2:B:878:LEU:HG	2.12	0.49
1:A:910:LEU:HD21	1:A:1020:LEU:HD21	1.94	0.49
1:A:884:VAL:HG23	1:A:965:ILE:O	2.13	0.48
1:A:925:ARG:HD2	1:A:928:LEU:HD23	1.97	0.47
2:B:937:MET:HB3	2:B:1088:PHE:CE2	2.50	0.46
2:B:872:ILE:HD13	2:B:898:LEU:HD21	1.98	0.44
2:B:1093:PRO:O	2:B:1097:MET:HG3	2.18	0.43
2:B:938:GLU:OE2	2:B:1089:SER:HA	2.19	0.43
2:B:859:HIS:O	2:B:859:HIS:CG	2.72	0.42
2:B:915:GLN:HE22	2:B:1026:LYS:HE3	1.84	0.42
1:A:859:HIS:CG	1:A:859:HIS:O	2.74	0.41
2:B:914:LEU:HD11	2:B:1020:LEU:HD23	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	avoured Allowed		Percentiles		
1	A	$259/283 \ (92\%)$	245 (95%)	12 (5%)	2 (1%)	19 57		
2	В	$267/283 \ (94\%)$	250 (94%)	16 (6%)	1 (0%)	34 72		
All	All	526/566 (93%)	495 (94%)	28 (5%)	3 (1%)	25 64		

All (3) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	967	ASP
2	В	849	GLY
1	A	1064	PRO

#### 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	230/245 (94%)	223 (97%)	7 (3%)	41	75	
2	В	239/245 (98%)	233 (98%)	6 (2%)	47	79	
All	All	469/490 (96%)	456 (97%)	13 (3%)	43	77	

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	856	GLN
1	A	890	SER
1	A	897	SER
1	A	925	ARG
1	A	1047	LEU
1	A	1050	LEU
1	A	1089	SER
2	В	856	GLN
2	В	863	ASP
2	В	897	SER
2	В	905	LEU
2	В	1038	MET
2	В	1089	SER

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

Mol	Chain	Res	Type
1	A	869	GLN
2	В	915	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)

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	Tuna	Chain	Res	Link	Bond lengths			Bond angles		
10101	$\operatorname{ol} \ ig  \ \operatorname{Type} \ ig  \ \operatorname{Chain} \ ig  \ \operatorname{R}$	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
1	PTR	A	980	1	15,16,17	2.01	1 (6%)	19,22,24	0.71	1 (5%)
2	PTR	В	980	2	15,16,17	2.05	1 (6%)	19,22,24	0.64	0
1	PTR	A	981	1	15,16,17	1.94	2 (13%)	19,22,24	0.89	1 (5%)
2	PTR	В	981	2	15,16,17	2.01	1 (6%)	19,22,24	0.62	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PTR	A	980	1	-	0/10/11/13	0/1/1/1
2	PTR	В	980	2	-	0/10/11/13	0/1/1/1
1	PTR	A	981	1	-	0/10/11/13	0/1/1/1
2	PTR	В	981	2	-	4/10/11/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$Ideal(\AA)$
2	В	980	PTR	OH-CZ	-7.73	1.23	1.40
2	В	981	PTR	OH-CZ	-7.49	1.23	1.40
1	A	980	PTR	OH-CZ	-7.36	1.23	1.40
1	A	981	PTR	OH-CZ	-6.81	1.25	1.40
1	A	981	PTR	P-OH	2.70	1.63	1.59



All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	981	PTR	O3P-P-OH	2.11	111.85	105.24
1	A	980	PTR	O3P-P-OH	2.07	111.71	105.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	981	PTR	C-CA-CB-CG
2	В	981	PTR	N-CA-CB-CG
2	В	981	PTR	CA-CB-CG-CD2
2	В	981	PTR	CA-CB-CG-CD1

There are no ring outliers.

No monomer is involved in short contacts.

### 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	Type	Chain	$\operatorname{Res}$	Link	Bond lengths			Bond angles		
IV	101	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
	3	G9B	A	2099	1	41,44,44	1.62	7 (17%)	46,63,63	1.33	5 (10%)
	3	G9B	В	2099	2	41,44,44	1.61	7 (17%)	46,63,63	1.16	4 (8%)

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.



 $^{\prime}\text{-}^{\prime}$  means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	${f Torsions}$	Rings
3	G9B	A	2099	1	-	2/12/32/32	0/6/6/6
3	G9B	В	2099	2	-	0/12/32/32	0/6/6/6

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}( ext{\AA})$
3	В	2099	G9B	C21-C23	-4.82	1.39	1.45
3	A	2099	G9B	C21-C23	-4.77	1.39	1.45
3	В	2099	G9B	C1-N7	-4.17	1.33	1.39
3	В	2099	G9B	C21-N22	3.70	1.40	1.34
3	A	2099	G9B	C21-N22	3.56	1.40	1.34
3	A	2099	G9B	C1-N7	-3.43	1.34	1.39
3	В	2099	G9B	C24-N22	2.99	1.39	1.34
3	A	2099	G9B	C23-N27	2.92	1.41	1.34
3	A	2099	G9B	C24-N22	2.89	1.39	1.34
3	В	2099	G9B	C23-N27	2.62	1.40	1.34
3	В	2099	G9B	C34-C33	2.52	1.58	1.52
3	A	2099	G9B	C10-N7	2.52	1.49	1.45
3	В	2099	G9B	C26-N25	2.49	1.39	1.34
3	A	2099	G9B	C26-N25	2.20	1.39	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
3	A	2099	G9B	C28-C24-N22	3.80	121.42	116.02
3	В	2099	G9B	C28-C24-N22	3.41	120.87	116.02
3	A	2099	G9B	C10-C11-C13	3.03	121.71	118.48
3	A	2099	G9B	C26-N25-C23	2.45	121.22	118.70
3	A	2099	G9B	C12-C10-C11	-2.42	118.88	121.74
3	A	2099	G9B	C13-N16-C17	2.18	131.31	127.50
3	В	2099	G9B	C10-N7-C8	2.12	129.94	125.50
3	В	2099	G9B	C10-N7-C1	-2.03	122.40	125.84
3	В	2099	G9B	C10-C11-C13	2.01	120.62	118.48

There are no chirality outliers.

All (2) torsion outliers are listed below:

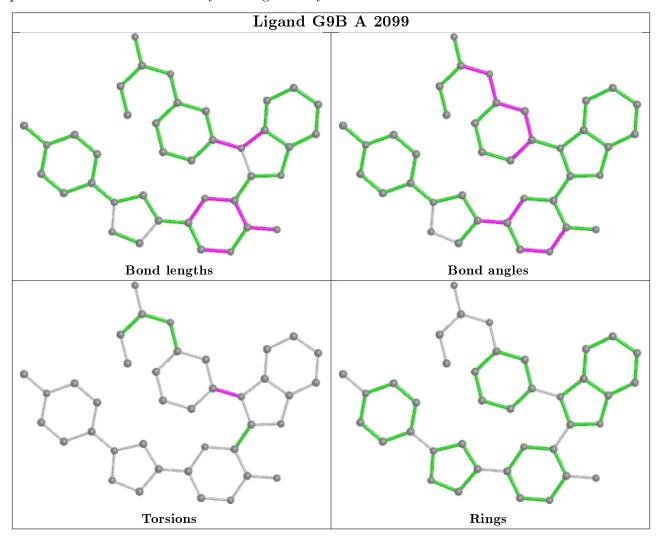
Mol	Chain	Res	Type	Atoms
3	A	2099	G9B	C12-C10-N7-C1
3	A	2099	G9B	C11-C10-N7-C1



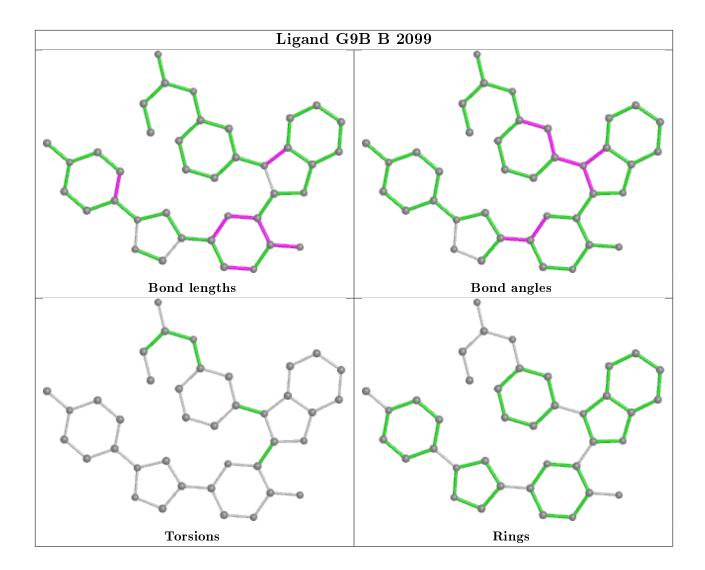
There are no ring outliers.

No monomer is involved in short contacts.

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.







## 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,  $95^{th}$  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 $>$	$\#\mathrm{RSRZ}{>}2$		Z>2	$OWAB(A^2)$	Q < 0.9
1	A	$267/283 \ (94\%)$	-0.44	0	100	100	21, 34, 52, 56	38 (14%)
2	В	$272/283 \ (96\%)$	-0.41	0	100	100	20, 35, 53, 61	31 (11%)
All	All	539/566 (95%)	-0.43	0	100	100	20, 35, 53, 61	69 (12%)

There are no RSRZ outliers to report.

### 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,  $95^{th}$  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	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
1	PTR	A	981	16/17	0.79	0.27	47,52,64,67	0
2	PTR	В	981	16/17	0.82	0.23	45,53,64,68	0
1	PTR	A	980	16/17	0.87	0.22	43,46,56,57	0
2	PTR	В	980	16/17	0.90	0.17	43,46,55,56	0

### 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

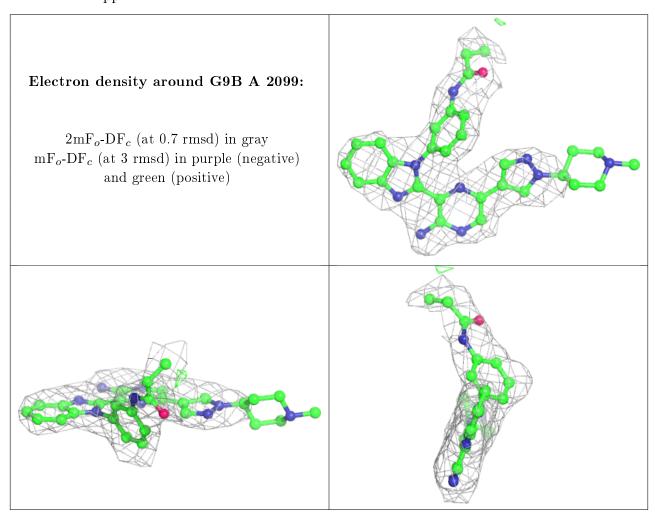
## 6.4 Ligands $\bigcirc$

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  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.

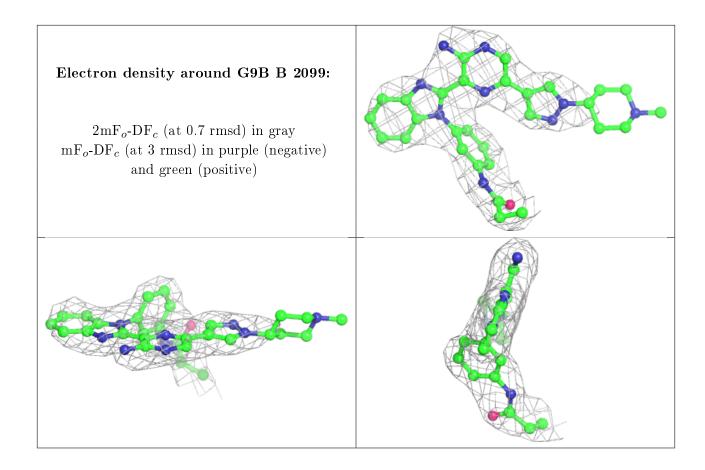


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$oxed{f B-factors({ m \AA}^2)}$	Q<0.9
3	G9B	A	2099	39/39	0.93	0.19	29,33,38,42	6
3	G9B	В	2099	39/39	0.95	0.19	24,29,34,34	6

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.







## 6.5 Other polymers (i)

There are no such residues in this entry.

