



# wwPDB X-ray Structure Validation Summary Report

Mar 1, 2026 – 02:34 AM UTC

PDB ID : 5CF6 / pdb\_00005cf6  
Title : CRYSTAL STRUCTURE OF JANUS KINASE 2 IN COMPLEX WITH N,N-DICYCLOPROPYL-10-[(2S)-2,3-DIHYDROXYPROPYL]-3-METHYL-7-(METHYLAMINO)-3,5,8,10-TETRAAZATRICYCLO [7.3.0.02,6]DODECA-1(9),2(6),4,7,11-PENTAENE-11-CARBOXAMIDE  
Authors : Sack, J.S.  
Deposited on : 2015-07-08  
Resolution : 2.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

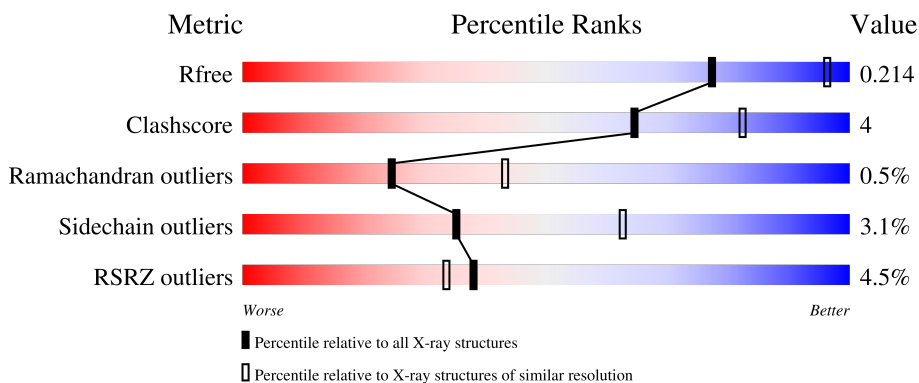
# 1 Overall quality at a glance i

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))
$R_{free}$	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	321	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 11%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">5%      75%      13%      • 11%</p>
1	B	321	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 78%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">3%      78%      12%      • 9%</p>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4992 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	287	2339	1485	399	439	2	14	0	0	0
1	B	292	2384	1512	411	444	2	15	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

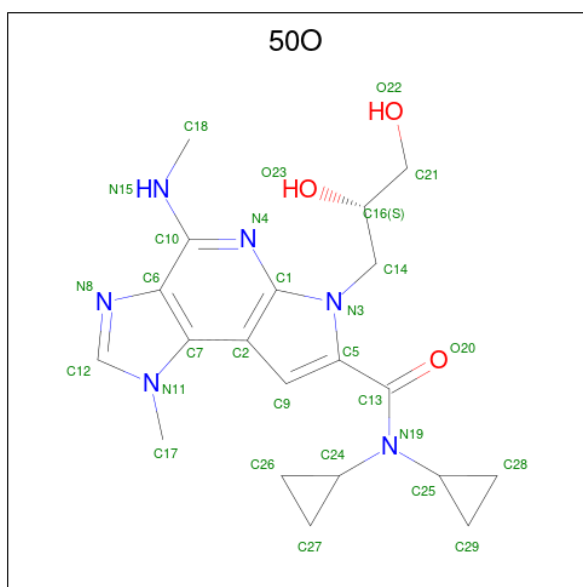
Chain	Residue	Modelled	Actual	Comment	Reference
A	818	MET	-	initiating methionine	UNP O60674
A	819	GLY	-	expression tag	UNP O60674
A	820	SER	-	expression tag	UNP O60674
A	821	SER	-	expression tag	UNP O60674
A	822	HIS	-	expression tag	UNP O60674
A	823	HIS	-	expression tag	UNP O60674
A	824	HIS	-	expression 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	SER	-	expression tag	UNP O60674
A	829	SER	-	expression tag	UNP O60674
A	830	GLY	-	expression tag	UNP O60674
A	831	LEU	-	expression tag	UNP O60674
A	832	VAL	-	expression tag	UNP O60674
A	833	PRO	-	expression tag	UNP O60674
A	834	ARG	-	expression tag	UNP O60674
A	835	GLY	-	expression tag	UNP O60674
A	836	SER	-	expression tag	UNP O60674
A	837	HIS	-	expression tag	UNP O60674
A	838	MET	-	expression tag	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

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1137	HIS	-	expression tag	UNP O60674
A	1138	HIS	-	expression tag	UNP O60674
B	818	MET	-	initiating methionine	UNP O60674
B	819	GLY	-	expression tag	UNP O60674
B	820	SER	-	expression tag	UNP O60674
B	821	SER	-	expression tag	UNP O60674
B	822	HIS	-	expression tag	UNP O60674
B	823	HIS	-	expression tag	UNP O60674
B	824	HIS	-	expression tag	UNP O60674
B	825	HIS	-	expression tag	UNP O60674
B	826	HIS	-	expression tag	UNP O60674
B	827	HIS	-	expression tag	UNP O60674
B	828	SER	-	expression tag	UNP O60674
B	829	SER	-	expression tag	UNP O60674
B	830	GLY	-	expression tag	UNP O60674
B	831	LEU	-	expression tag	UNP O60674
B	832	VAL	-	expression tag	UNP O60674
B	833	PRO	-	expression tag	UNP O60674
B	834	ARG	-	expression tag	UNP O60674
B	835	GLY	-	expression tag	UNP O60674
B	836	SER	-	expression tag	UNP O60674
B	837	HIS	-	expression tag	UNP O60674
B	838	MET	-	expression tag	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 N,N-dicyclopropyl-6-[(2S)-2,3-dihydroxypropyl]-1-methyl-4-(methylamino)-1,6-dihydroimidazo[4,5-d]pyrrolo[2,3-b]pyridine-7-carboxamide (CCD ID: 500) (formula: C<sub>20</sub>H<sub>26</sub>N<sub>6</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
2	A	1	Total	C	N	O	0	0
			29	20	6	3		
2	B	1	Total	C	N	O	0	0
			29	20	6	3		

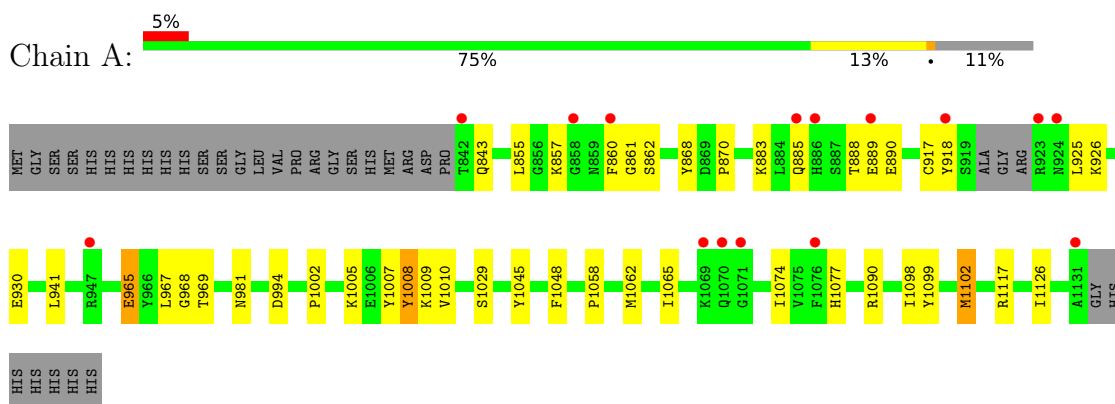
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	103	Total	O	0	0
			103	103		
3	B	108	Total	O	0	0
			108	108		

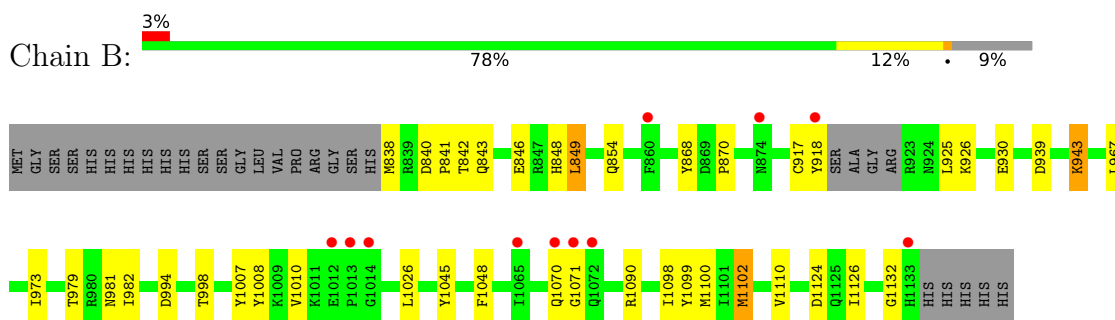
### 3 Residue-property plots [i](#)

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 i

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.64Å 111.64Å 70.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.93 – 2.50 49.93 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.93-2.50) 99.3 (49.93-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.93 (at 2.51Å)	Xtrriage
Refinement program	BUSTER 2.11.6	Depositor
R, $R_{free}$	0.186 , 0.214 0.184 , 0.214	Depositor DCC
$R_{free}$ test set	650 reflections (2.17%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.2	Xtrriage
Anisotropy	0.464	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.035 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4992	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PTR, 500

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	0.86	1/2353 (0.0%)	1.32	7/3171 (0.2%)
1	B	0.89	1/2401 (0.0%)	1.34	9/3234 (0.3%)
All	All	0.87	2/4754 (0.0%)	1.33	16/6405 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1102	MET	SD-CE	-8.00	1.59	1.79
1	A	1102	MET	SD-CE	-7.90	1.59	1.79

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	846	GLU	CA-C-N	7.37	130.47	120.38
1	B	846	GLU	C-N-CA	7.37	130.47	120.38
1	B	841	PRO	CA-C-N	6.28	132.14	121.14
1	B	841	PRO	C-N-CA	6.28	132.14	121.14
1	A	941	LEU	CA-C-N	6.21	129.22	120.28

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	2339	0	2282	20	0
1	B	2384	0	2315	17	0
2	A	29	0	26	5	0
2	B	29	0	26	4	0
3	A	103	0	0	0	0
3	B	108	0	0	0	0
All	All	4992	0	4649	37	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.

The worst 5 of 37 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:1002:PRO:HG2	1:A:1005:LYS:HB2	1.77	0.67
1:B:994:ASP:HB2	2:B:4000:50O:C27	2.26	0.66
1:A:994:ASP:HB2	2:A:4000:50O:C27	2.28	0.64
1:B:979:THR:HA	1:B:982:ILE:HD12	1.82	0.60
1:B:840:ASP:HB3	1:B:843:GLN:HG2	1.82	0.60

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	281/321 (88%)	271 (96%)	9 (3%)	1 (0%)	30	49
1	B	286/321 (89%)	277 (97%)	7 (2%)	2 (1%)	18	34
All	All	567/642 (88%)	548 (97%)	16 (3%)	3 (0%)	24	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	860	PHE
1	B	1070	GLN
1	B	1071	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	252/290 (87%)	246 (98%)	6 (2%)	43 70
1	B	256/290 (88%)	246 (96%)	10 (4%)	28 55
All	All	508/580 (88%)	492 (97%)	16 (3%)	35 62

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1100	MET
1	B	1026	LEU
1	B	849	LEU
1	B	1010	VAL
1	B	842	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	848	HIS
1	B	885	GLN
1	B	950	HIS
1	B	1111	ASN

### 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	1007	1	15,16,17	1.71	5 (33%)	17,22,24	1.48	2 (11%)
1	PTR	A	1008	1	15,16,17	2.25	3 (20%)	17,22,24	2.56	5 (29%)
1	PTR	A	1007	1	15,16,17	1.50	3 (20%)	17,22,24	1.41	3 (17%)
1	PTR	B	1008	1	15,16,17	1.66	4 (26%)	17,22,24	2.47	3 (17%)

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

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1008	PTR	CE2-CZ	5.38	1.48	1.38
1	A	1008	PTR	P-OH	-4.97	1.50	1.59
1	B	1008	PTR	P-OH	-4.23	1.51	1.59
1	B	1007	PTR	CD2-CG	3.16	1.45	1.38
1	B	1007	PTR	CE1-CZ	3.11	1.44	1.38

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1008	PTR	OH-CZ-CE2	6.61	139.03	119.22
1	A	1008	PTR	OH-CZ-CE1	-6.32	100.27	119.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1008	PTR	OH-CZ-CE1	6.23	137.89	119.22
1	B	1008	PTR	OH-CZ-CE2	-5.81	101.78	119.22
1	B	1007	PTR	O2P-P-OH	3.61	116.00	105.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	1007	PTR	CZ-OH-P-O2P
1	A	1008	PTR	CZ-OH-P-O3P

There are no ring outliers.

1 monomer is involved in 1 short contact:

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	50O	B	4000	-	33,33,33	0.49	0	39,50,50	1.13	4 (10%)
2	50O	A	4000	-	33,33,33	0.40	0	39,50,50	1.32	4 (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
2	50O	B	4000	-	-	7/24/28/28	0/5/5/5
2	50O	A	4000	-	-	10/24/28/28	0/5/5/5

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4000	50O	C24-N19-C13	-4.45	114.67	121.31
2	A	4000	50O	C7-C2-C9	3.02	139.89	132.62
2	B	4000	50O	C7-C2-C9	2.97	139.77	132.62
2	A	4000	50O	C25-N19-C13	2.92	125.67	121.31
2	A	4000	50O	C10-C6-N8	-2.86	129.32	132.43

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	4000	50O	C26-C24-N19-C13
2	A	4000	50O	C26-C24-N19-C25
2	A	4000	50O	C16-C14-N3-C1
2	A	4000	50O	C28-C25-N19-C13
2	A	4000	50O	C29-C25-N19-C13

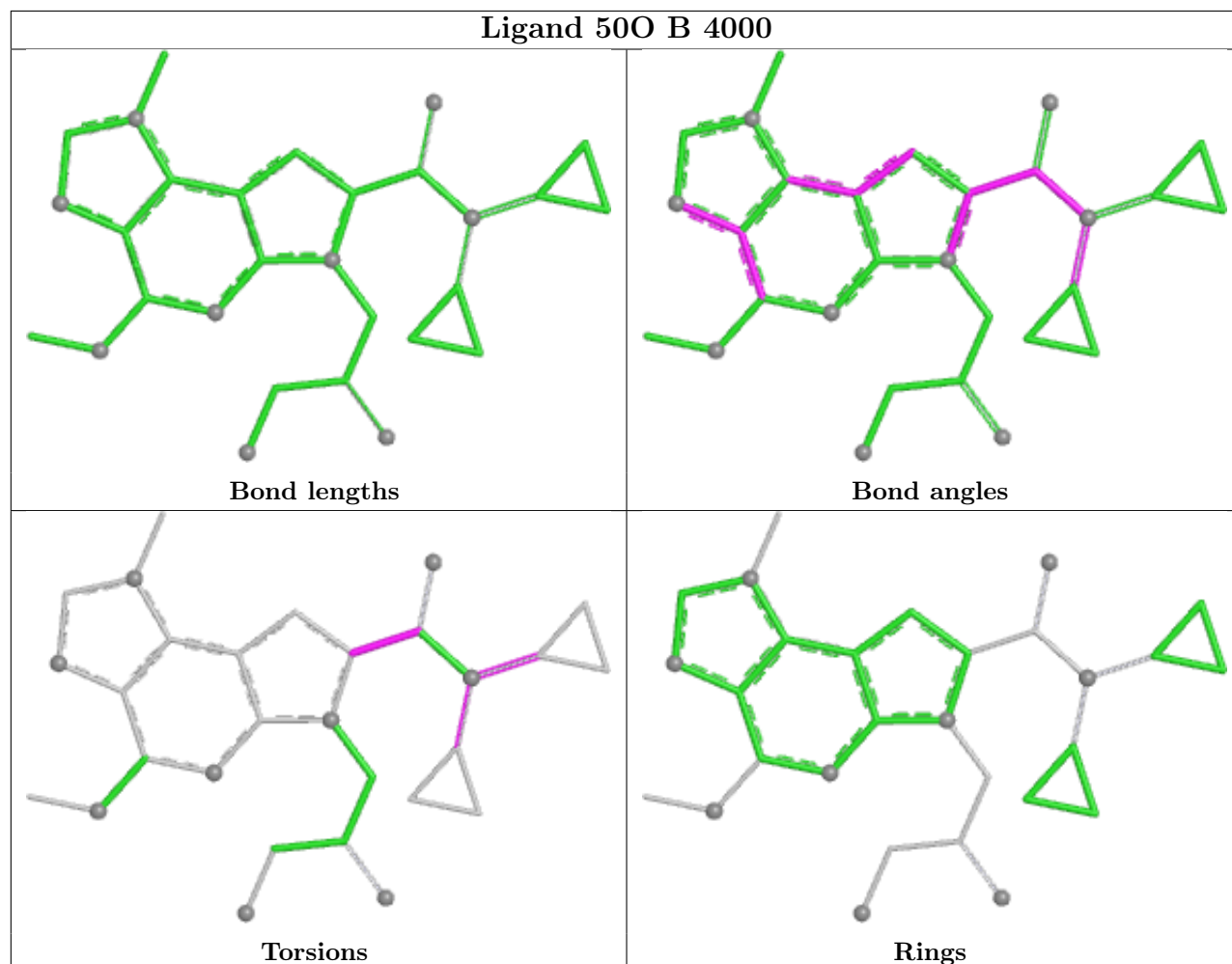
There are no ring outliers.

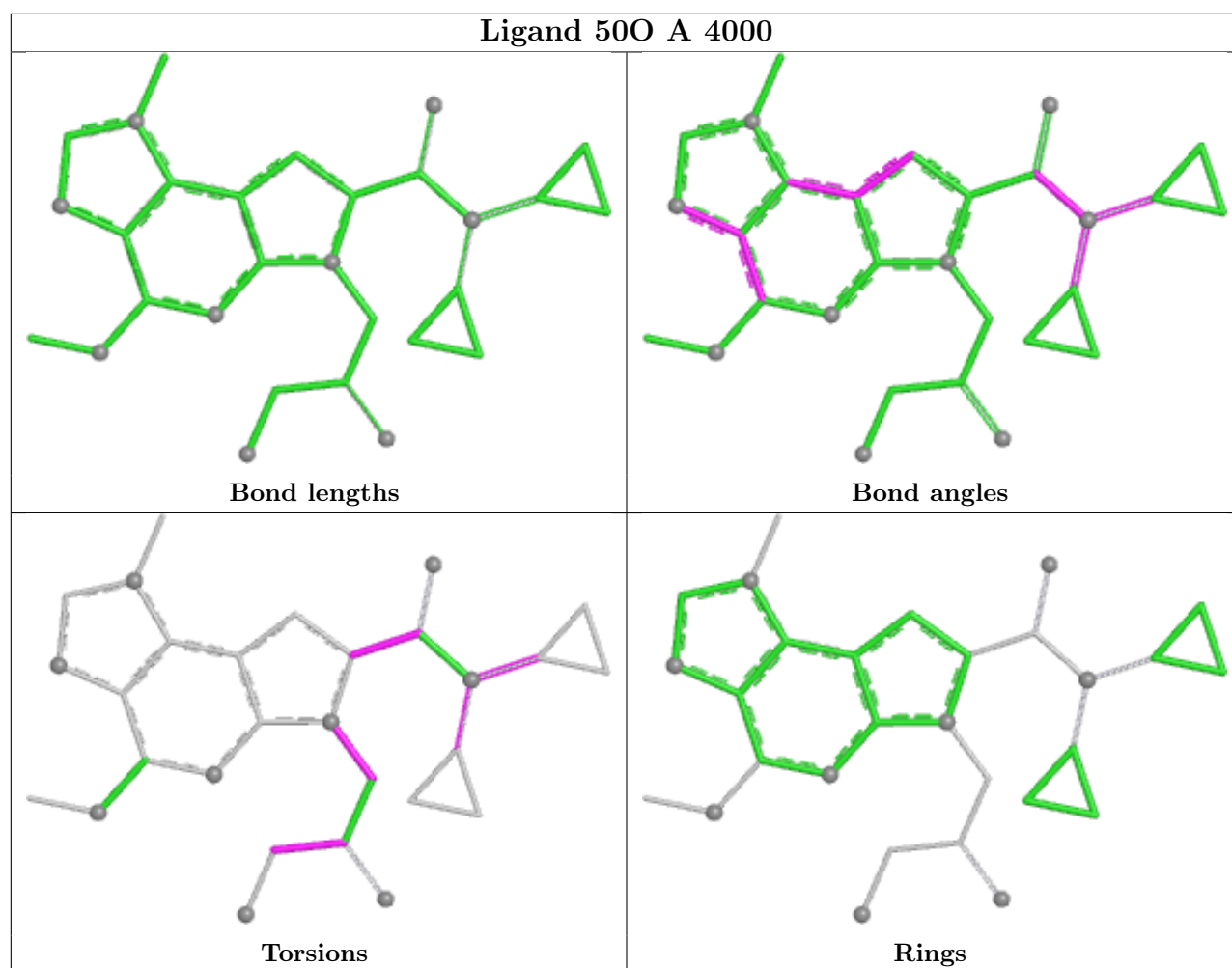
2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4000	50O	4	0
2	A	4000	50O	5	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	285/321 (88%)	0.10	15 (5%) 32 28	26, 42, 85, 106	0
1	B	290/321 (90%)	0.14	11 (3%) 44 39	27, 44, 74, 92	0
All	All	575/642 (89%)	0.12	26 (4%) 38 33	26, 44, 78, 106	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	918	TYR	5.2
1	A	1069	LYS	4.3
1	B	1133	HIS	4.2
1	A	918	TYR	3.9
1	B	1013	PRO	3.7

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PTR	B	1008	16/17	0.92	0.13	58,68,78,79	0
1	PTR	B	1007	16/17	0.94	0.10	57,63,72,74	0
1	PTR	A	1007	16/17	0.94	0.09	39,44,65,66	0
1	PTR	A	1008	16/17	0.95	0.08	38,49,70,70	0

### 6.3 Carbohydrates [i](#)

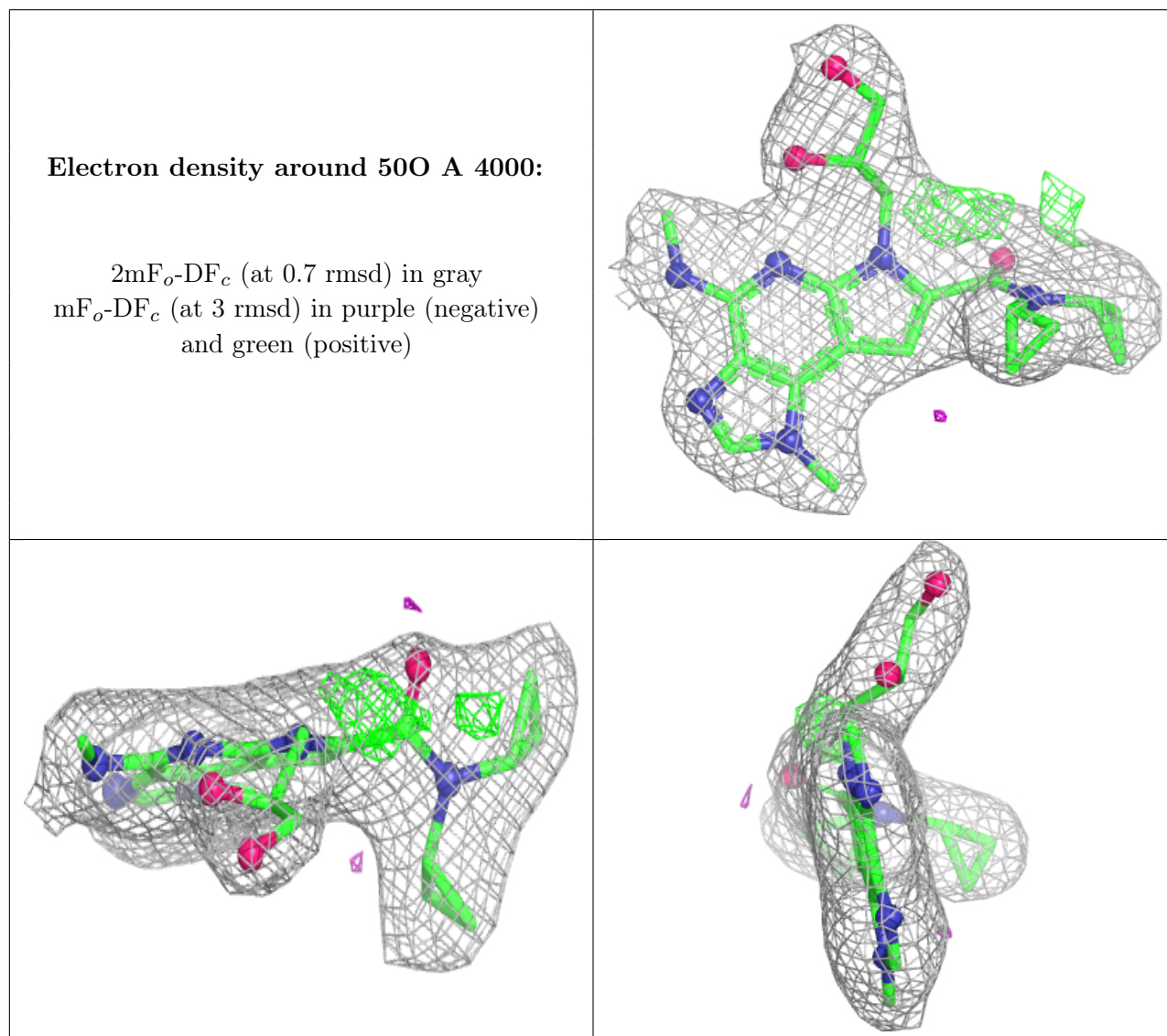
There are no oligosaccharides in this entry.

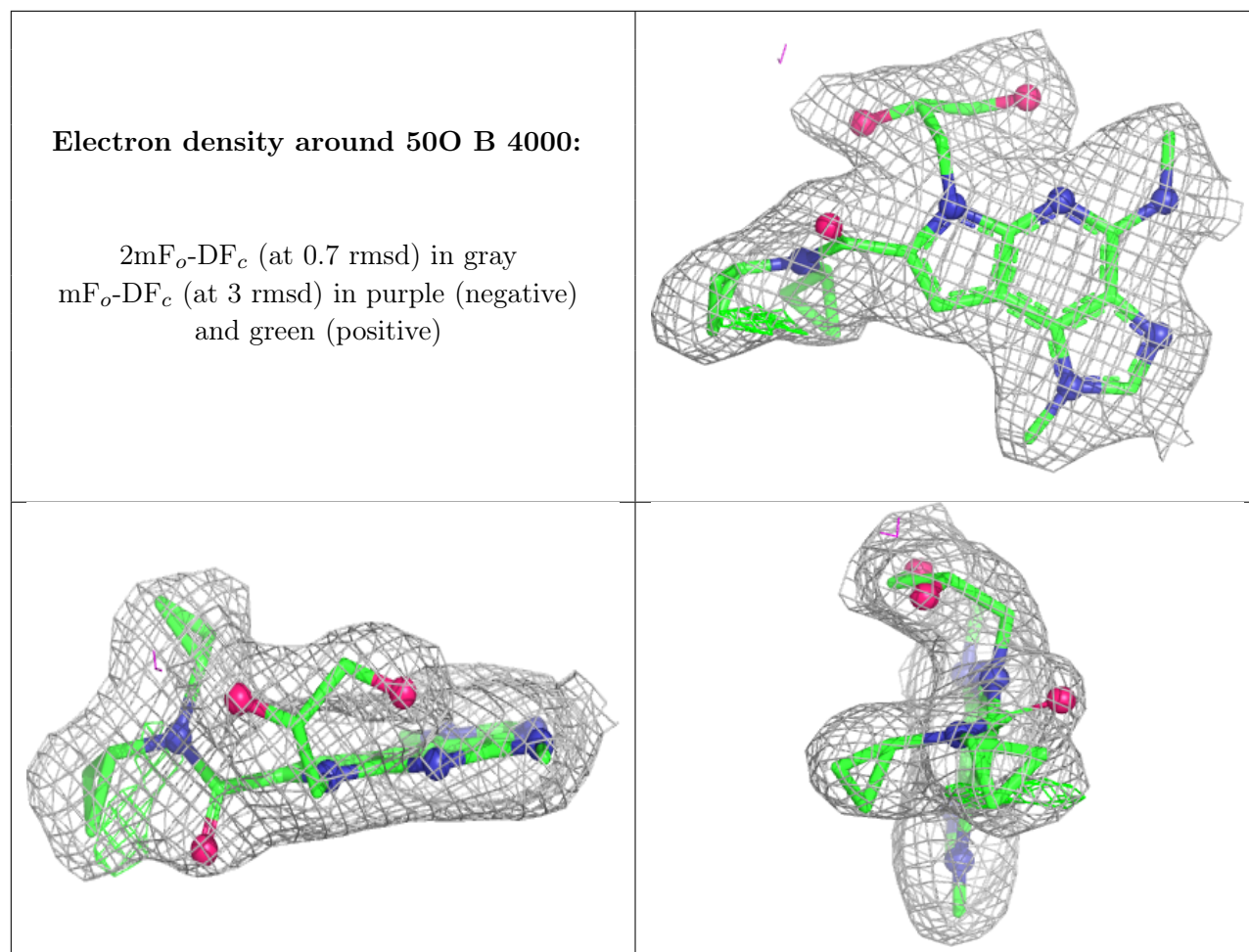
## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	500	A	4000	29/29	0.95	0.09	24,34,44,49	0
2	500	B	4000	29/29	0.95	0.08	30,36,49,51	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.