

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

May 17, 2020 – 04:58 am BST

PDB ID : 4P7S

Title : Crystal structure of PfMIF in complex with 4-(3-methoxy-5-methylphenoxy)-

2-(4-methoxyphenyl)-6-methylpyridine

Authors : Pantouris, G.; Lolis, E.

Deposited on : 2014-03-27

Resolution : 2.87 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)

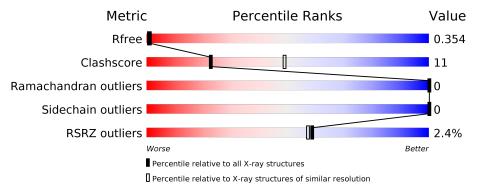
Validation Pipeline (wwPDB-VP) : 2.11

### 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 2.87 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	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

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	114	79%	12%	9%
1	В	114	77%	11%	12%
1	С	114	72%	10%	18%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	2OK	В	201	-	-	X	-
2	20K	С	201	-	-	X	X



## 2 Entry composition (i)

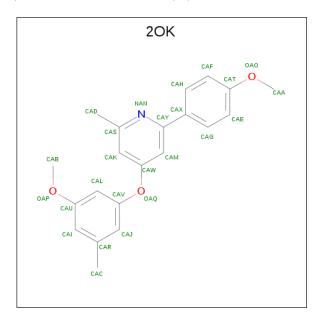
There are 2 unique types of molecules in this entry. The entry contains 2136 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Macrophage migration inhibitory factor-like protein.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	104	Total	С	N	О	S	0	0	0
1	Λ	104	751	468	126	152	5	0	U	
1	D	100	Total	С	N	О	S	0	0	0
1	Б	100	681	423	119	134	5	0	0	0
1	С	93	Total	С	N	О	S	0	0	0
1		90	654	405	112	133	4	0	0	0

• Molecule 2 is 4-(3-methoxy-5-methylphenoxy)-2-(4-methoxyphenyl)-6-methylpyridine (three-letter code: 2OK) (formula:  $C_{21}H_{21}NO_3$ ).



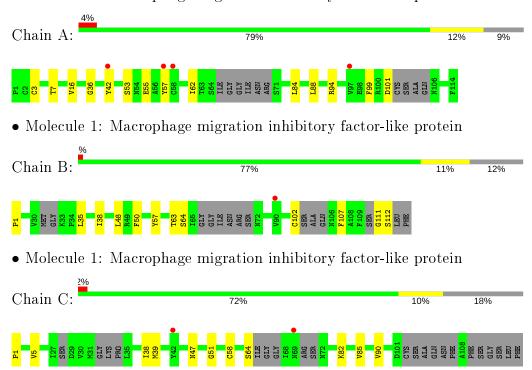
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	С	Ν	О	0	0
	Ъ	1	25	21	1	3	0	
9	С	1	Total	С	N	О	0	0
		1	25	21	1	3	0	U



## 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: Macrophage migration inhibitory factor-like protein





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	79.55Å 80.14Å 97.66Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	48.83 - 2.87	Depositor
rtesolution (A)	48.83 - 2.87	EDS
% Data completeness	98.5 (48.83-2.87)	Depositor
(in resolution range)	98.6 (48.83-2.87)	EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.84~({\rm at}~2.86{\rm \AA})$	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
$R, R_{free}$	0.287 , $0.345$	Depositor
$\Pi, \Pi free$	0.292 , $0.354$	DCC
$R_{free}$ test set	334  reflections  (4.59%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.1	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	$0.35\;,60.1$	EDS
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.020 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.83	EDS
Total number of atoms	2136	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.36% of the height of the origin peak. No significant pseudotranslation is detected.

<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: 20K

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).

Mal	Mol Chain		lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.58	0/758	0.68	0/1027	
1	В	0.56	0/685	0.66	0/929	
1	С	0.66	0/657	0.67	0/891	
All	All	0.60	0/2100	0.67	0/2847	

There are no bond length outliers.

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	751	0	688	10	0
1	В	681	0	583	23	0
1	С	654	0	559	16	0
2	В	25	0	21	12	0
2	С	25	0	21	15	0
All	All	2136	0	1872	46	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 11.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

	<b>A</b> 4 0	Interatomic	Clash
Atom-1	Atom-2	${f distance} \; ({f \mathring{A}})$	overlap (Å)
1:C:1:PRO:N	2:C:201:2OK:H11	1.27	1.47
1:C:1:PRO:H3	2:C:201:2OK:CAK	1.57	1.16
1:B:1:PRO:CD	2:B:201:20K:CAV	2.28	1.09
1:C:1:PRO:N	2:C:201:2OK:CAK	2.15	1.03
1:B:1:PRO:HD3	2:B:201:20K:OAQ	1.66	0.95
1:B:1:PRO:HD2	2:B:201:20K:CAV	2.02	0.90
1:B:1:PRO:CD	2:B:201:2OK:OAQ	2.19	0.90
1:B:1:PRO:HD3	2:B:201:20K:CAV	2.04	0.82
1:C:64:SER:OG	2:C:201:2OK:H13	1.82	0.80
1:C:1:PRO:CD	2:C:201:2OK:H11	2.13	0.76
1:B:57:TYR:OH	2:C:201:2OK:H7	1.86	0.75
1:C:1:PRO:H2	2:C:201:2OK:H11	1.51	0.75
1:C:5:VAL:HG13	1:C:58:CYS:SG	2.32	0.69
1:B:1:PRO:CD	2:B:201:20K:CAL	2.71	0.68
1:B:1:PRO:HD2	2:B:201:20K:CAL	2.25	0.66
1:B:1:PRO:N	2:B:201:2OK:OAQ	2.29	0.65
1:B:50:PHE:CD1	2:C:201:2OK:H8	2.33	0.64
1:B:50:PHE:HA	1:C:38:ILE:O	1.98	0.62
1:C:1:PRO:CD	2:C:201:2OK:CAK	2.76	0.61
1:B:57:TYR:OH	2:C:201:2OK:CAC	2.49	0.60
1:B:35:LEU:O	1:B:38:ILE:HG22	2.03	0.59
1:B:1:PRO:HD3	2:B:201:20K:CAL	2.31	0.59
1:B:63:THR:HG22	1:B:64:SER:OG	2.03	0.58
1:B:1:PRO:N	2:B:201:20K:CAV	2.67	0.56
1:C:85:VAL:HG23	1:C:90:VAL:O	2.05	0.55
1:B:50:PHE:CE1	2:C:201:2OK:CAI	2.92	0.53
1:A:99:PHE:O	2:B:201:2OK:H16	2.10	0.52
1:A:36:GLY:O	1:C:51:GLY:HA2	2.10	0.51
1:A:3:CYS:SG	1:A:62:ILE:CD1	2.98	0.51
1:B:111:GLY:O	1:B:112:SER:C	2.50	0.49
1:B:50:PHE:CE1	2:C:201:2OK:H8	2.49	0.48
1:C:1:PRO:H2	2:C:201:2OK:CAK	2.12	0.47
1:C:5:VAL:CG1	1:C:58:CYS:SG	3.03	0.46
1:B:48:LEU:HD11	1:C:39:MET:CE	2.46	0.46
1:B:1:PRO:H2	2:B:201:20K:CAJ	2.29	0.45
1:A:57:TYR:HD1	1:A:94:ARG:HB3	1.83	0.44
1:A:7:THR:HG21	1:A:42:TYR:CZ	2.53	0.43
1:B:107:PHE:CD1	1:B:107:PHE:N	2.86	0.43
1:A:53:SER:OG	1:A:55:GLU:HG3	2.19	0.43
1:A:101:ASP:O	1:B:102:CYS:SG	2.78	0.42
1:A:84:LEU:O	1:A:88:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	$egin{array}{c}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:A:57:TYR:CD1	1:A:94:ARG:O	2.74	0.41
1:A:16:VAL:HG11	1:C:47:ASN:CG	2.41	0.41
2:C:201:2OK:H4	2:C:201:2OK:CAM	2.49	0.41
1:C:82:LYS:HA	1:C:85:VAL:HG12	2.01	0.41
2:C:201:20K:CAM	2:C:201:20K:CAL	2.95	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	Perce	$_{ m ntiles}$
1	A	98/114 (86%)	95 (97%)	3 (3%)	0	100	100
1	В	90/114 (79%)	86 (96%)	4 (4%)	0	100	100
1	С	82/114 (72%)	81 (99%)	1 (1%)	0	100	100
All	All	270/342 (79%)	262 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	78/101 (77%)	78 (100%)	0	100 100
1	В	63/101 (62%)	63 (100%)	0	100 100

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Mol	Chain	Analysed	Analysed Rotameric Outliers		Percentiles		
1	С	62/101 (61%)	62 (100%)	0	100	100	
All	All	203/303 (67%)	203 (100%)	0	100	100	

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	73	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)

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

#### 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).

1	/[a]	Type	Type Chain		$\operatorname{Res} \left  \operatorname{Link} \right $	Bond lengths			Bond angles		
1	Mol Type C	Chain	1165	Counts		RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
	2	2OK	С	201	_	27,27,27	2.58	8 (29%)	37,37,37	1.48	10 (27%)
	2	2OK	В	201	_	27,27,27	2.00	6 (22%)	37,37,37	1.64	11 (29%)



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.

$\mathbf{Mol}$	Type	Chain	$\operatorname{Res}$	Link	Chirals	${f Torsions}$	Rings
2	2OK	С	201	-	-	6/12/12/12	0/3/3/3
2	2OK	В	201	-	-	8/12/12/12	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	В	201	2OK	CAX-CAY	-7.34	1.37	1.48
2	С	201	2OK	CAX-CAY	-6.94	1.38	1.48
2	С	201	2OK	CAD-CAS	-5.70	1.36	1.50
2	С	201	2OK	CAC-CAR	-5.18	1.32	1.51
2	С	201	2OK	OAQ-CAV	-3.69	1.31	1.39
2	В	201	2OK	CAD-CAS	-3.61	1.41	1.50
2	В	201	2OK	CAC-CAR	-3.51	1.38	1.51
2	С	201	2OK	OAQ-CAW	-3.47	1.32	1.39
2	С	201	2OK	CAJ-CAR	-3.24	1.33	1.39
2	С	201	2OK	CAY-NAN	-2.86	1.30	1.34
2	С	201	2OK	CAI-CAR	-2.82	1.34	1.39
2	В	201	2OK	CAJ-CAV	2.37	1.43	1.38
2	В	201	2OK	CAK-CAW	2.24	1.42	1.38
2	В	201	2OK	CAK-CAS	2.09	1.42	1.38

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	${\bf Observed}({}^o)$	$\mathbf{Ideal}(^o)$
2	С	201	20K	CAY-NAN-CAS	3.46	122.02	118.45
2	С	201	20K	CAW-OAQ-CAV	3.07	125.98	118.80
2	В	201	20K	OAQ-CAW-CAK	2.97	128.41	119.10
2	В	201	20K	CAB-OAP-CAU	-2.78	111.48	117.51
2	С	201	20K	CAI-CAU-CAL	-2.72	116.64	120.98
2	В	201	2OK	CAK-CAW-CAM	-2.68	116.71	120.98
2	В	201	20K	CAK-CAS-NAN	-2.63	117.67	121.49
2	В	201	20K	CAC-CAR-CAI	-2.47	117.29	120.94
2	В	201	2OK	CAF-CAH-CAX	-2.44	117.63	121.13
2	С	201	20K	OAQ-CAW-CAM	2.43	126.73	119.10
2	С	201	2OK	CAM-CAY-NAN	-2.33	119.59	122.35
2	С	201	2OK	CAD-CAS-NAN	2.27	120.18	116.56
2	С	201	2OK	CAJ-CAR-CAI	2.27	120.79	118.09
2	В	201	2OK	CAH-CAX-CAG	2.25	122.08	117.59

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Mol	Chain	Res	Type	${f Atoms}$	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	В	201	2OK	CAY-NAN-CAS	2.23	120.75	118.45
2	С	201	20K	CAU-CAI-CAR	2.19	121.98	119.64
2	В	201	2OK	CAW-CAK-CAS	2.18	122.08	118.36
2	С	201	20K	CAD-CAS-CAK	-2.10	118.61	121.81
2	В	201	2OK	CAM-CAY-CAX	-2.07	119.10	121.85
2	В	201	20K	CAV-CAL-CAU	2.04	121.54	118.48
2	С	201	20K	CAC-CAR-CAI	-2.03	117.93	120.94

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	201	2OK	CAI-CAU-OAP-CAB
2	С	201	2OK	CAG-CAX-CAY-CAM
2	В	201	2OK	CAL-CAU-OAP-CAB
2	С	201	2OK	CAG-CAX-CAY-NAN
2	С	201	2OK	CAH-CAX-CAY-CAM
2	С	201	2OK	CAF-CAT-OAO-CAA
2	С	201	2OK	CAE-CAT-OAO-CAA
2	С	201	2OK	CAH-CAX-CAY-NAN
2	В	201	2OK	CAH-CAX-CAY-NAN
2	В	201	2OK	CAG-CAX-CAY-NAN
2	В	201	2OK	CAH-CAX-CAY-CAM
2	В	201	2OK	CAE-CAT-OAO-CAA
2	В	201	2OK	CAF-CAT-OAO-CAA
2	В	201	2OK	CAG-CAX-CAY-CAM

There are no ring outliers.

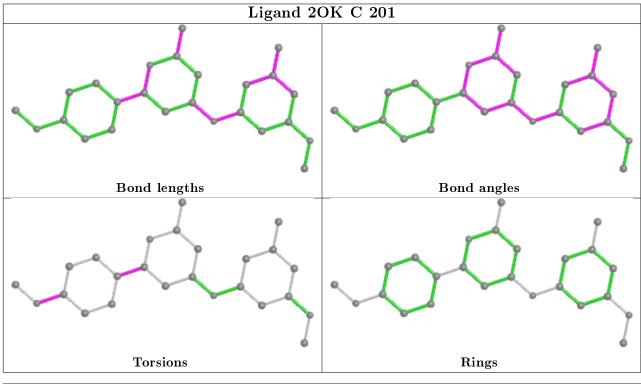
2 monomers are involved in 27 short contacts:

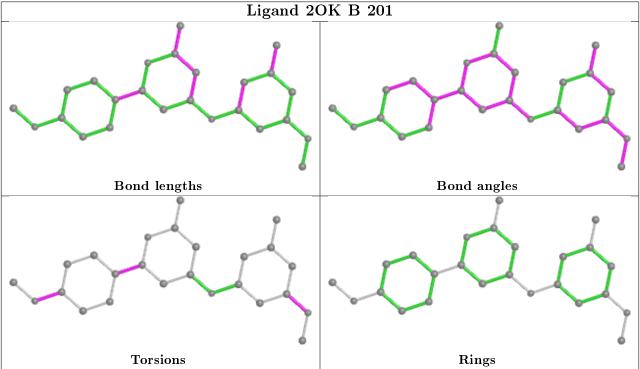
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	С	201	2OK	15	0
2	В	201	20K	12	0

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.







## 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></rsrz>	$\# \mathrm{RSRZ} {>} 2$	$OWAB(A^2)$	Q<0.9
1	A	104/114 (91%)	0.17	4 (3%) 40 36	26, 42, 58, 62	2 (1%)
1	В	100/114 (87%)	0.30	1 (1%) 82 82	29, 54, 80, 85	1 (1%)
1	С	93/114 (81%)	0.14	2 (2%) 62 60	24, 40, 57, 70	4 (4%)
All	All	297/342 (86%)	0.20	7 (2%) 59 57	24, 44, 73, 85	7 (2%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	69	ASN	3.7
1	A	58	CYS	3.1
1	A	97	VAL	2.5
1	A	42	TYR	2.4
1	С	42	TYR	2.3
1	A	57	TYR	2.1
1	В	90	VAL	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 carbohydrates in this entry.

### 6.4 Ligands (i)

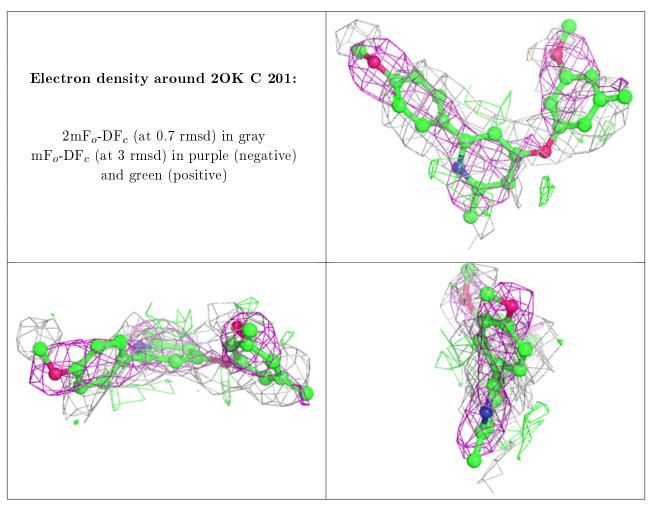
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



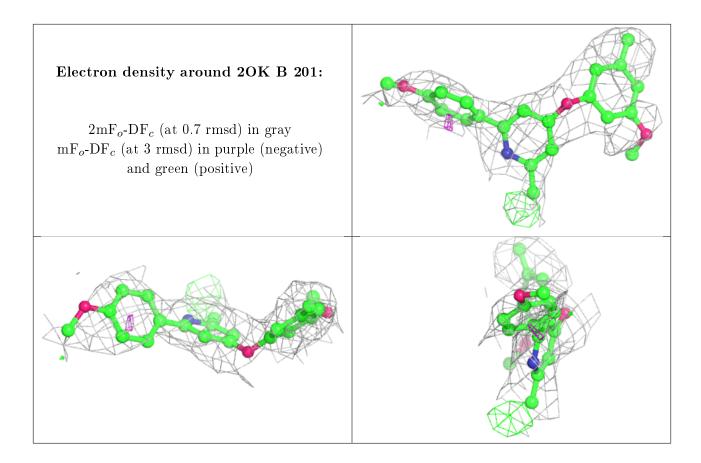
median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B\text{-factors}}({f \AA}^2)$	Q<0.9
2	2OK	С	201	25/25	0.54	0.51	20,20,20,20	0
2	20K	В	201	25/25	0.69	0.31	48,59,75,84	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.

