

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

#### Sep 17, 2023 – 02:44 PM EDT

PDB ID	:	4XJ0
Title	:	Crystal structure of ERK2 in complex with an inhibitor 14K
Authors	:	Yin, J.; Wang, W.
Deposited on		
Resolution	:	2.58  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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

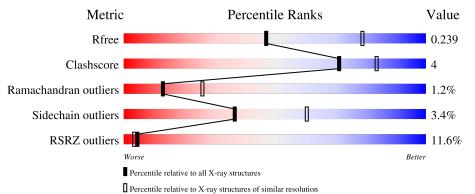
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35.1
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.58 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614(2.60-2.56)

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 <=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	А	349	7%85%	13%	••
1	В	349	16%	11%	•



# 2 Entry composition (i)

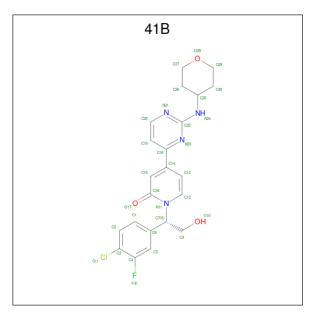
There are 3 unique types of molecules in this entry. The entry contains 5788 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Mitogen-activated protein kinase 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	346		C 1815		-			0	0	0
1	В	339	Total 2775	-		-	Р 1	S 14	0	0	0

• Molecule 2 is 1-[(1S)-1-(4-chloro-3-fluorophenyl)-2-hydroxyethyl]-4-[2-(tetrahydro-2 H-pyran-4-ylamino)pyrimidin-4-yl]pyridin-2(1H)-one (three-letter code: 41B) (formula:  $C_{22}H_{22}ClFN_4O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	А	1	Total 31	-	Cl 1		-	0	0
2	В	1	Total 31	-	Cl 1		-	0	0

• Molecule 3 is water.

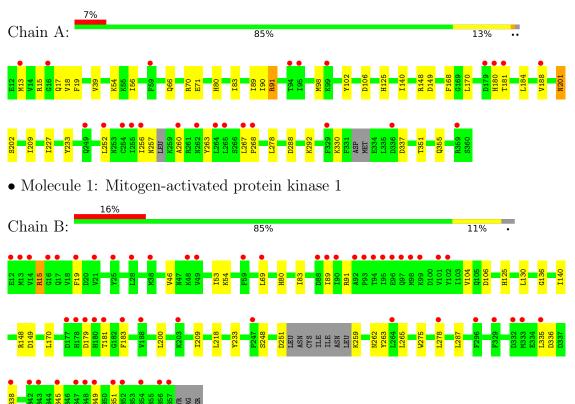


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	78	Total         O           78         78	0	0
3	В	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0



# 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: Mitogen-activated protein kinase 1



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	83.19Å 83.19Å 274.49Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	45.82 - 2.58	Depositor
	44.66 - 2.58	EDS
% Data completeness	99.3 (45.82 - 2.58)	Depositor
(in resolution range)	99.3(44.66-2.58)	EDS
$R_{merge}$	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.54 (at $2.58$ Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
B B.	0.208 , $0.244$	Depositor
$R, R_{free}$	0.205 , $0.239$	DCC
$R_{free}$ test set	1538 reflections $(4.93\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	59.1	Xtriage
Anisotropy	0.525	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33, 59.6	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.51, < L^2>=0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5788	wwPDB-VP
Average B, all atoms $(Å^2)$	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<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: 41B, NEP

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	А	0.48	0/2882	0.65	0/3900	
1	В	0.46	0/2826	0.63	0/3825	
All	All	0.47	0/5708	0.64	0/7725	

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	А	2831	0	2816	22	0
1	В	2775	0	2757	18	0
2	А	31	0	22	1	0
2	В	31	0	22	2	0
3	А	78	0	0	0	0
3	В	42	0	0	0	0
All	All	5788	0	5617	40	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 (40) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:80:HIS:HB3	1:B:83:ILE:HG12	1.80	0.62
1:A:83:ILE:HD12	1:A:140:ILE:HD11	1.81	0.61
1:B:148:ARG:HG2	1:B:209:ILE:HD11	1.82	0.61
1:A:80:HIS:HB3	1:A:83:ILE:HG12	1.82	0.60
1:B:54:LYS:HD3	2:B:401:41B:H1	1.84	0.59
1:B:149:ASP:HB2	1:B:170:LEU:HD12	1.85	0.59
1:B:53:ILE:HG12	1:B:104:VAL:HG22	1.85	0.59
1:A:148:ARG:HG2	1:A:209:ILE:HD11	1.86	0.56
1:A:71:GLU:HG3	1:A:168:PHE:H	1.70	0.56
1:A:149:ASP:HB2	1:A:170:LEU:HD12	1.88	0.55
1:A:106:ASP:O	2:A:401:41B:H5	2.08	0.54
1:B:130:LEU:HD22	1:B:218:LEU:HD13	1.88	0.54
1:A:91:ARG:HG3	1:A:98:MET:SD	2.50	0.52
1:B:148:ARG:HD3	1:B:170:LEU:O	2.09	0.51
1:A:83:ILE:CD1	1:A:140:ILE:HD11	2.42	0.50
1:A:90:ILE:HB	1:A:102:TYR:HB2	1.94	0.50
1:A:148:ARG:HD3	1:A:170:LEU:O	2.12	0.50
1:A:257:ASN:HB3	1:A:260:ALA:HB2	1.94	0.50
1:A:66:GLN:O	1:A:70:ARG:HB2	2.13	0.49
1:B:83:ILE:HD12	1:B:140:ILE:HD11	1.94	0.49
1:B:345:GLU:O	1:B:349:GLU:HG2	2.14	0.48
1:A:89:ILE:HD13	1:A:351:THR:HG22	1.94	0.48
1:A:201:ASN:HB3	1:A:256:ILE:H	1.81	0.46
1:B:69:LEU:HD23	1:B:335:LEU:HD21	1.98	0.46
1:B:275:TRP:HB3	1:B:287:LEU:HD22	1.97	0.46
1:B:89:ILE:HD13	1:B:351:THR:HG22	1.99	0.44
1:A:13:MET:HB3	1:A:18:VAL:HA	1.99	0.44
1:A:257:ASN:HB3	1:A:260:ALA:CB	2.47	0.44
1:A:54:LYS:HD2	1:A:56:ILE:HD11	2.00	0.43
1:A:39:VAL:HG22	1:A:54:LYS:HG2	2.00	0.43
1:B:183:PHE:CZ	1:B:259:LYS:HD3	2.54	0.42
1:B:106:ASP:O	2:B:401:41B:H5	2.19	0.42
1:A:330:LYS:HD2	1:A:330:LYS:HA	1.93	0.42
1:B:335:LEU:HA	1:B:338:LEU:HD12	2.01	0.42
1:A:288:ASP:O	1:A:292:LYS:HG2	2.20	0.41
1:A:267:LEU:HD23	1:A:268:PRO:HD2	2.02	0.41
1:B:262:ASN:HD21	1:B:265:LEU:HG	1.85	0.41
1:B:200:LEU:O	1:B:259:LYS:HB2	2.20	0.40
1:A:91:ARG:NH2	1:A:355:GLN:HG3	2.36	0.40
1:B:136:GLY:O	1:B:140:ILE:HG12	2.20	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	Percenti	les
1	А	339/349~(97%)	320 (94%)	15~(4%)	4 (1%)	13 20	5
1	В	334/349~(96%)	305 (91%)	25~(8%)	4 (1%)	13 20	5
All	All	673/698~(96%)	625~(93%)	40 (6%)	8 (1%)	13 20	5

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	248	SER
1	А	181	THR
1	А	188	VAL
1	В	181	THR
1	А	15	ARG
1	В	15	ARG
1	А	180	HIS
1	В	46	VAL

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	311/315~(99%)	299~(96%)	12 (4%)	32 56		
1	В	304/315~(96%)	295~(97%)	9~(3%)	41 65		



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	615/630~(98%)	594~(97%)	21 (3%)	37 60	

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	17	GLN
1	А	19	PHE
1	А	91	ARG
1	А	184	LEU
1	А	201	ASN
1	А	202	SER
1	А	227	ILE
1	А	233	TYR
1	А	252	LEU
1	А	263	TYR
1	А	278	LEU
1	А	337	ASP
1	В	15	ARG
1	В	19	PHE
1	В	91	ARG
1	В	179	ASP
1	В	233	TYR
1	В	251	ASP
1	В	263	TYR
1	В	278	LEU
1	В	336	ASP

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains 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)

2 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



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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).

Mal	Mol Type Chair	Chain	nain Res	Link	Bo	ond leng	$\mathbf{ths}$	Bond angles		
INIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	NEP	В	125	1	10, 14, 15	2.32	2 (20%)	5,20,22	1.19	0
1	NEP	А	125	1	10,14,15	4.07	3 (30%)	5,20,22	1.74	1 (20%)

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	NEP	В	125	1	-	1/5/12/14	0/1/1/1
1	NEP	А	125	1	-	0/5/12/14	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	А	125	NEP	P-O3P	10.31	1.56	1.47
1	А	125	NEP	P-O1P	-5.77	1.42	1.54
1	В	125	NEP	P-O3P	-5.39	1.42	1.47
1	А	125	NEP	CD2-NE2	-4.37	1.31	1.39
1	В	125	NEP	CD2-NE2	-3.87	1.32	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	125	NEP	O1P-P-O3P	-2.85	107.29	113.44

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	В	125	NEP	CA-CB-CG-ND1

There are no ring outliers.

No monomer is involved in short contacts.



### 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).

Mal	Mol Type Chain Res		Link	Bo	ond leng	$\mathbf{ths}$	Bond angles			
	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
2	41B	В	401	-	34,34,34	0.97	2 (5%)	41,47,47	2.49	14 (34%)
2	41B	А	401	-	34,34,34	0.98	1 (2%)	41,47,47	2.55	15 (36%)

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	41B	В	401	-	-	0/17/26/26	0/4/4/4
2	41B	А	401	-	-	0/17/26/26	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	А	401	41B	C22-N24	4.11	1.40	1.34
2	В	401	41B	C22-N24	4.01	1.39	1.34
2	В	401	41B	C16-N11	-2.17	1.37	1.39

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	401	41B	N21-C22-N23	-7.57	119.38	126.55
2	А	401	41B	C18-N23-C22	7.22	122.64	116.80
2	В	401	41B	N21-C22-N23	-6.93	119.98	126.55
2	В	401	41B	C20-N21-C22	6.90	121.57	115.45



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	401	41B	C20-N21-C22	6.87	121.54	115.45
2	В	401	41B	C18-N23-C22	6.34	121.92	116.80
2	В	401	41B	C6-C7-N11	-4.01	106.99	111.52
2	В	401	41B	C19-C18-N23	-3.73	118.54	122.92
2	А	401	41B	C19-C18-N23	-3.41	118.93	122.92
2	В	401	41B	C7-N11-C16	3.39	121.78	118.78
2	А	401	41B	C6-C7-N11	-3.31	107.78	111.52
2	В	401	41B	C19-C20-N21	-3.16	120.03	123.96
2	А	401	41B	C2-C3-C4	3.10	121.43	118.94
2	А	401	41B	C7-N11-C16	3.02	121.45	118.78
2	В	401	41B	N24-C22-N23	2.95	121.60	117.18
2	В	401	41B	O17-C16-C15	-2.79	118.59	125.72
2	А	401	41B	O17-C16-C15	-2.73	118.74	125.72
2	А	401	41B	N24-C22-N23	2.49	120.92	117.18
2	В	401	41B	C2-C3-C4	2.48	120.93	118.94
2	А	401	41B	C19-C20-N21	-2.44	120.93	123.96
2	В	401	41B	O17-C16-N11	2.31	122.10	119.75
2	А	401	41B	C14-C15-C16	-2.28	119.28	122.61
2	А	401	41B	C15-C16-N11	2.27	119.48	115.47
2	А	401	41B	C5-C4-C3	-2.20	119.59	121.72
2	В	401	41B	C15-C16-N11	2.17	119.30	115.47
2	А	401	41B	C29-O28-C27	2.17	117.13	109.89
2	В	401	41B	C14-C18-N23	2.08	119.72	116.66
2	В	401	41B	C29-O28-C27	2.07	116.81	109.89
2	А	401	41B	O17-C16-N11	2.00	121.78	119.75

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There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

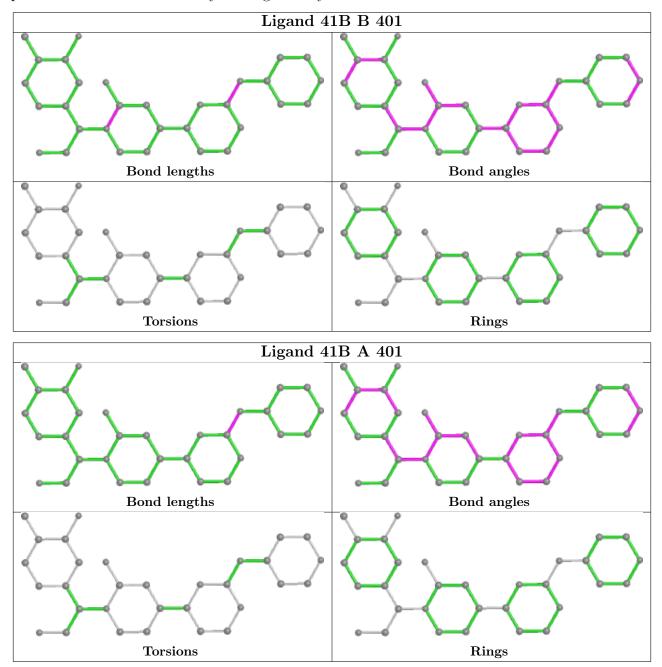
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	401	41B	2	0
2	А	401	41B	1	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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	345/349~(98%)	0.45	24 (6%) 16 13	45, 70, 123, 169	0
1	В	338/349~(96%)	0.78	55 (16%) 1 1	48, 83, 144, 185	0
All	All	683/698~(97%)	0.61	79 (11%) 4 3	45, 77, 138, 185	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	21	VAL	6.1
1	В	333	MET	6.0
1	А	264	LEU	5.9
1	В	13	MET	5.7
1	В	352	ALA	4.7
1	В	180	HIS	4.3
1	В	92	ALA	4.3
1	А	256	ILE	4.3
1	В	93	PRO	4.3
1	В	342	LYS	4.3
1	В	94	THR	4.0
1	В	338	LEU	4.0
1	В	183	PHE	3.9
1	В	99	LYS	3.9
1	В	14	VAL	3.8
1	В	16	GLY	3.7
1	А	265	LEU	3.7
1	В	19	PHE	3.6
1	В	349	GLU	3.6
1	В	95	ILE	3.6
1	В	332	ASP	3.6
1	А	254	CYS	3.4
1	В	296	PHE	3.4
1	В	347	ILE	3.3



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Mol	Chain	Res	Type	RSRZ
1	В	348	PHE	3.3
1	В	17	GLN	3.3
1	А	249	GLN	3.2
1	А	180	HIS	3.2
1	В	25	TYR	3.1
1	В	203	LYS	3.1
1	А	252	LEU	3.1
1	В	28	LEU	3.1
1	В	101	VAL	3.1
1	А	359	ARG	3.1
1	В	49	VAL	3.1
1	В	181	THR	3.1
1	В	12	GLU	3.0
1	В	345	GLU	3.0
1	В	102	TYR	3.0
1	В	264	LEU	3.0
1	В	96	GLU	2.9
1	В	356	PRO	2.9
1	В	59	PHE	2.9
1	А	267	LEU	2.9
1	В	329	PHE	2.8
1	А	179	ASP	2.8
1	В	97	GLN	2.8
1	А	188	VAL	2.8
1	А	13	MET	2.8
1	А	181	THR	2.7
1	В	247	PRO	2.6
1	А	329	PHE	2.6
1	В	90	ILE	2.5
1	В	98	MET	2.5
1	В	343	LEU	2.5
1	В	177	ASP	2.5
1	А	99	LYS	2.5
1	В	188	VAL	2.3
1	В	354	PHE	2.3
1	А	94	THR	2.3
1	В	357	GLY	2.2
1	В	48	LYS	2.2
1	А	262	ASN	2.2
1	В	178	HIS	2.2
1	В	179	ASP	2.2
1	В	89	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	В	351	THR	2.1
1	В	69	LEU	2.1
1	В	278	LEU	2.1
1	В	335	LEU	2.1
1	В	38	MET	2.1
1	А	59	PHE	2.1
1	В	88	ASP	2.1
1	А	95	ILE	2.1
1	А	255	ILE	2.1
1	А	268	PRO	2.1
1	А	336	ASP	2.0
1	А	260	ALA	2.0
1	А	16	GLY	2.0

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#### 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	$B-factors(Å^2)$	Q < 0.9
1	NEP	А	125	14/15	0.97	0.20	$55,\!59,\!66,\!66$	0
1	NEP	В	125	14/15	0.97	0.18	53,62,65,66	0

### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

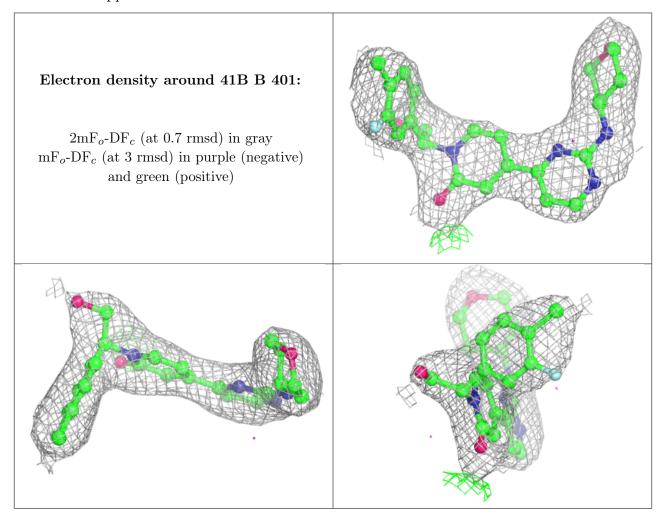
### 6.4 Ligands (i)

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,  $95^{th}$  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.

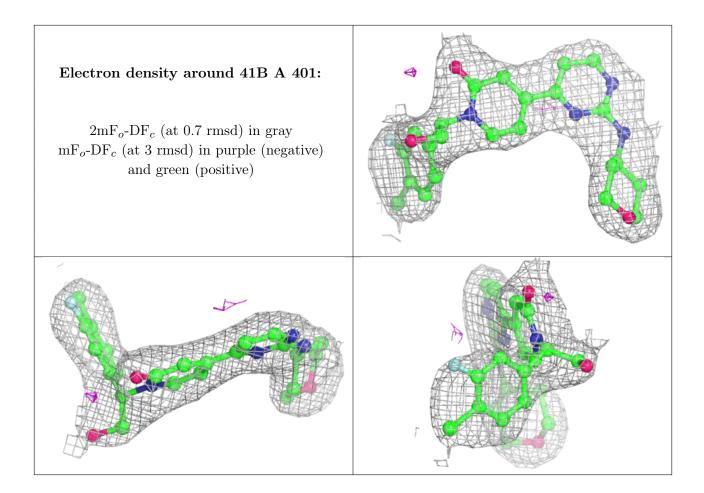
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{\AA}^2)$	Q<0.9
2	41B	В	401	31/31	0.93	0.15	59,74,94,101	0
2	41B	А	401	31/31	0.94	0.17	55,66,98,104	0



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.

