

Full wwPDB X-ray Structure Validation Report (i)

Dec 3, 2020 - 09:05 AM GMT

PDB ID	:	7AK0
Title	:	Human MALT1(329-729) in complex with a chromane urea containing in-
		hibitor
Authors	:	Renatus, M.
Deposited on	:	2020-09-29
Resolution	:	2.32 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:

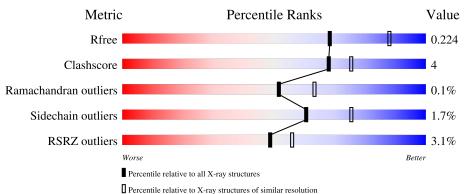
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541 be (2020)
$\mathbf{Xtriage} \ (\mathbf{Phenix})$:	1.13
EDS	:	2.14.6
buster-report		
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\operatorname{CCP4}$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)		Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

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 2.32 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R _{free}	130704	5974(2.34-2.30)
Clashscore	141614	6604(2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855(2.34-2.30)

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	А	404	2% 78 %	9%	12%
1	В	404	81%	8%	10%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6026 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 Mucosa-associated lymphoid tissue lymphoma translocation protein 1.

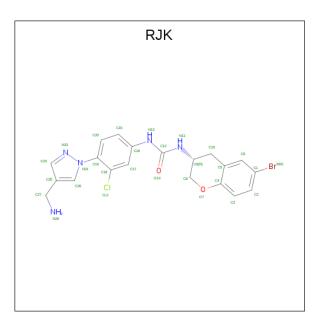
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	355	Total 2819	C 1807	N 458	O 533	S 21	0	0	0
1	В	363	Total 2882	C 1847	N 466	0 548	S 21	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	GLY	-	expression tag	UNP Q9UDY8
A	326	PRO	-	expression tag	UNP Q9UDY8
A	327	GLY	-	expression tag	UNP Q9UDY8
A	328	SER	-	expression tag	UNP Q9UDY8
В	325	GLY	-	expression tag	UNP Q9UDY8
В	326	PRO	-	expression tag	UNP Q9UDY8
В	327	GLY	-	expression tag	UNP Q9UDY8
В	328	SER	-	expression tag	UNP Q9UDY8

There are 8 discrepancies between the modelled and reference sequences:

• Molecule 2 is 1-[4-[4-(aminomethyl)pyrazol-1-yl]-3-chloranyl-phenyl]-3-[(3 {R})-6-bromanyl-3,4-dihydro-2 {H}-chromen-3-yl]urea (three-letter code: RJK) (formula: C₂₀H₁₉BrClN₅O₂) (labeled as "Ligand of Interest" by author).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
2	Λ	1	Total	Br	С	Cl	Ν	0	0	0
	1	29	1	20	1	5	2	0	0	
2	В	1	Total	Br	С	Cl	Ν	Ο	0	0
	D	L	29	1	20	1	5	2	0	U

• Molecule 3 is water.

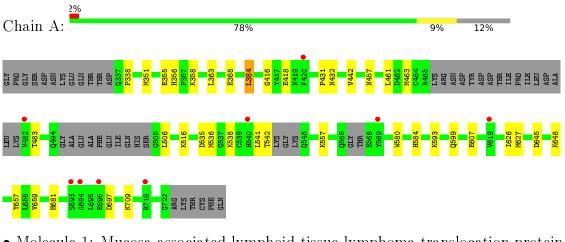
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	144	Total O 144 144	0	0
3	В	123	Total O 123 123	0	0



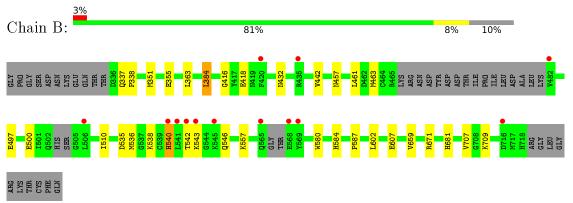
3 Residue-property plots (i)

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: Mucosa-associated lymphoid tissue lymphoma translocation protein 1



 \bullet Molecule 1: Mucosa-associated lymphoid tissue lymphoma translocation protein 1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	62.25Å 104.82Å 73.28Å	Depositor
a, b, c, α , β , γ	90.00° 111.14° 90.00°	Depositor
Resolution (Å)	68.35 - 2.32	Depositor
Resolution (A)	68.35 - 2.32	EDS
% Data completeness	93.3 (68.35-2.32)	Depositor
(in resolution range)	$93.3\ (68.35 - 2.32)$	EDS
R _{merge}	0.06	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.35 (at 2.32 \text{\AA})$	Xtriage
Refinement program	BUSTER	Depositor
D D	0.182 , 0.220	Depositor
R, R_{free}	0.184 , 0.224	DCC
R_{free} test set	1814 reflections (5.08%)	wwPDB-VP
Wilson B-factor $(Å^2)$	41.2	Xtriage
Anisotropy	0.573	Xtriage
Bulk solvent $k_{sol}(e/A^3)$, $B_{sol}(A^2)$	0.34 , 46.5	EDS
L-test for $twinning^2$	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6026	wwPDB-VP
Average B, all atoms $(Å^2)$	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.31% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities 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: RJK

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.41	0/2868	0.58	0/3874	
1	В	0.41	0/2933	0.59	0/3962	
All	All	0.41	0/5801	0.58	0/7836	

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	2819	0	2840	22	0
1	В	2882	0	2897	22	0
2	А	29	0	0	0	0
2	В	29	0	0	0	0
3	А	144	0	0	2	0
3	В	123	0	0	3	0
All	All	6026	0	5737	44	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 (44) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:356:HIS:HE1	1:A:432:ASN:HD22	1.18	0.87
1:A:356:HIS:CE1	1:A:432:ASN:HD22	2.03	0.76
1:B:540:HIS:ND1	1:B:543:LYS:NZ	2.36	0.74
1:A:506:LEU:HD23	1:A:657:TYR:CE2	2.23	0.73
1:A:368:GLU:HB3	3:A:974:HOH:O	1.92	0.69
1:A:442:VAL:HG21	1:A:461:LEU:HD11	1.75	0.68
1:B:442:VAL:HG21	1:B:461:LEU:HD11	1.75	0.68
1:B:659:VAL:HG12	3:B:913:HOH:O	1.95	0.65
1:B:536:MET:HB3	1:B:542:THR:HG21	1.81	0.62
1:B:542:THR:HG23	1:B:546:GLN:HB3	1.81	0.62
1:B:510:ILE:HB	1:B:546:GLN:HE21	1.71	0.56
1:B:607:GLU:OE1	1:B:671:ARG:NH1	2.38	0.53
1:B:363:LEU:HD12	1:B:384:LEU:HD21	1.90	0.52
1:A:363:LEU:HD12	1:A:384:LEU:HD21	1.91	0.52
1:B:338:PRO:HG2	1:B:557:LYS:O	2.11	0.51
1:B:355:GLU:HB3	1:B:432:ASN:HB2	1.93	0.50
1:B:416:GLY:HA3	1:B:463:MET:SD	2.51	0.50
1:B:671:ARG:NH2	3:B:901:HOH:O	2.28	0.49
1:A:416:GLY:HA3	1:A:463:MET:SD	2.53	0.49
1:A:593:LYS:HG2	1:A:599:GLN:HG2	1.93	0.49
1:A:356:HIS:CE1	1:A:432:ASN:ND2	2.79	0.48
1:B:497:GLU:HB2	1:B:500:GLU:HB2	1.94	0.48
1:A:338:PRO:HG2	1:A:557:LYS:O	2.14	0.47
1:A:535:ASP:HA	1:A:538:LYS:HE2	1.96	0.47
1:A:351:MET:SD	1:A:363:LEU:HB2	2.55	0.47
1:A:626:ILE:HG23	1:A:627:MET:HG2	1.97	0.47
1:B:463:MET:HE2	3:B:997:HOH:O	2.14	0.47
1:A:536:MET:O	1:A:542:THR:OG1	2.30	0.46
1:A:355:GLU:HG3	1:A:431:PRO:HA	1.98	0.45
1:A:607:GLU:HG3	1:A:659:VAL:HG13	1.99	0.45
1:B:535:ASP:HA	1:B:538:LYS:CE	2.46	0.45
1:A:535:ASP:HA	1:A:538:LYS:CE	2.47	0.44
1:B:607:GLU:HG3	1:B:659:VAL:HG13	2.00	0.44
1:A:645:ASP:HA	1:A:648:LYS:HE2	2.00	0.44
1:B:535:ASP:HA	1:B:538:LYS:HE2	2.00	0.43
1:B:580:TRP:O	1:B:584:HIS:HD2	2.02	0.42
1:B:337:GLN:HA	1:B:338:PRO:HD3	1.90	0.41
1:B:351:MET:SD	1:B:363:LEU:HB2	2.60	0.41
1:A:506:LEU:HD23	1:A:657:TYR:CZ	2.56	0.41
1:A:580:TRP:NE1	1:A:584:HIS:CE1	2.88	0.41
1:B:681:HIS:HD2	1:B:709:LYS:HG3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:PRO:HB3	1:B:707:VAL:HB	2.01	0.41
1:A:516:LYS:NZ	3:A:916:HOH:O	2.52	0.41
1:A:681:HIS:HD2	1:A:709:LYS:HG3	1.86	0.40

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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	\mathbf{n} tiles
1	А	345/404~(85%)	338~(98%)	6 (2%)	1 (0%)	41	50
1	В	355/404~(88%)	345~(97%)	10 (3%)	0	100	100
All	All	700/808~(87%)	683~(98%)	16 (2%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	483	THR

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	А	316/357~(88%)	310~(98%)	6(2%)	57 73
1	В	322/357~(90%)	317~(98%)	5(2%)	62 77

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Mol	Chain	in Analysed Rotameric Outliers		Percentiles	
All	All	638/714 (89%)	627~(98%)	11 (2%)	60 75

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	358	LYS
1	А	384	LEU
1	А	418	GLU
1	А	457	ASN
1	А	541	LEU
1	А	697	ASP
1	В	384	LEU
1	В	418	GLU
1	В	457	ASN
1	В	540	HIS
1	В	602	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	352	ASN
1	А	356	HIS
1	А	457	ASN
1	А	485	ASN
1	А	508	ASN
1	А	681	HIS
1	В	393	ASN
1	В	438	ASN
1	В	457	ASN
1	В	485	ASN
1	В	508	ASN
1	В	546	GLN
1	В	565	GLN
1	В	577	ASN
1	В	681	HIS

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).

Mal	Mol Type Chain	Chain	\mathbf{Res}	Link	Bo	ond leng	\mathbf{ths}	B	ond ang	les	
	туре	Chain	nes	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	RJK	В	801	-	30,32,32	1.64	7 (23%)	37,45,45	2.74	6 (16%)	
2	RJK	А	801	-	30,32,32	1.59	6 (20%)	37,45,45	2.46	5 (13%)	

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	RJK	В	801	-	-	1/10/23/23	0/4/4/4
2	RJK	А	801	-	-	1/10/23/23	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	А	801	RJK	C8-C9	4.78	1.56	1.51
2	В	801	RJK	C8-C9	4.68	1.56	1.51
2	А	801	RJK	C10-C9	4.05	1.55	1.52
2	В	801	RJK	C10-C9	3.57	1.55	1.52
2	В	801	RJK	C24-C25	3.47	1.46	1.37
2	А	801	RJK	C24-C25	3.39	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
2	В	801	RJK	BR2-C1	-2.84	1.84	1.90
2	В	801	RJK	O7-C4	2.70	1.40	1.37
2	А	801	RJK	C24-N23	-2.27	1.27	1.33
2	В	801	RJK	C19-C18	2.26	1.41	1.39
2	А	801	RJK	BR2-C1	-2.09	1.86	1.90
2	А	801	RJK	O7-C4	2.05	1.39	1.37
2	В	801	RJK	C24-N23	-2.03	1.27	1.33

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All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	801	RJK	C24-N23-N21	11.70	112.22	103.70
2	А	801	RJK	C24-N23-N21	10.86	111.60	103.70
2	В	801	RJK	C19-N21-N23	8.06	125.80	118.79
2	А	801	RJK	C19-N21-N23	6.40	124.36	118.79
2	В	801	RJK	C26-N21-N23	-5.05	107.58	112.72
2	А	801	RJK	C26-N21-N23	-4.70	107.93	112.72
2	А	801	RJK	C17-C18-C19	3.46	121.77	118.93
2	В	801	RJK	C17-C18-C19	3.07	121.45	118.93
2	А	801	RJK	O7-C4-C5	-2.89	120.27	122.38
2	В	801	RJK	O7-C4-C5	-2.75	120.37	122.38
2	В	801	RJK	C17-C18-CL2	-2.70	114.13	118.49

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	801	RJK	C20-C19-N21-N23
2	А	801	RJK	C20-C19-N21-N23

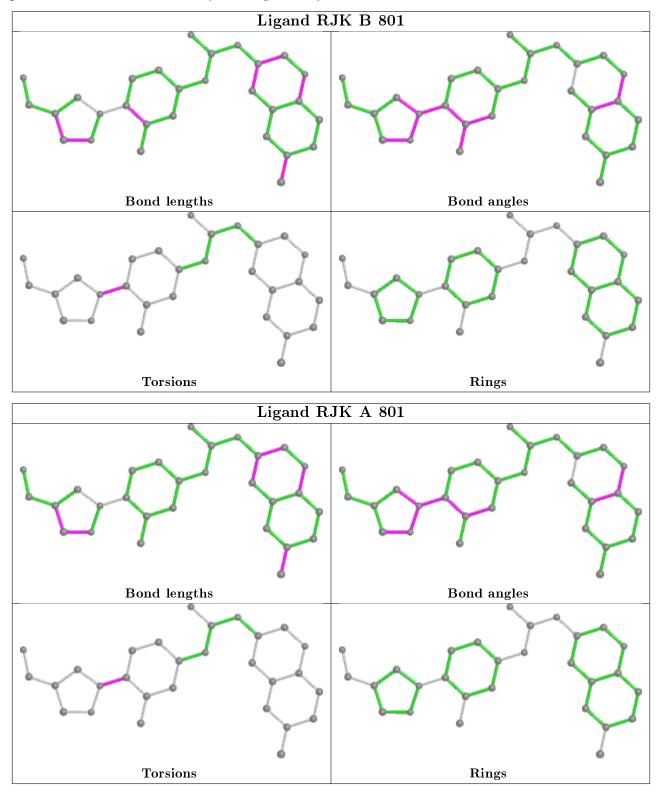
There are no ring outliers.

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 $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	355/404~(87%)	0.14	9 (2%) 57 64	30, 47, 79, 99	0
1	В	363/404~(89%)	0.14	13 (3%) 42 49	30, 47, 81, 96	0
All	All	718/808~(88%)	0.14	22 (3%) 49 56	30, 47, 80, 99	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	В	540	HIS	5.5	
1	А	619	VAL	5.4	
1	В	569	TYR	4.8	
1	А	569	TYR	4.5	
1	В	541	LEU	3.8	
1	В	716	ASP	3.8	
1	А	719	ARG	3.6	
1	В	482	VAL	3.6	
1	А	693	SER	3.3	
1	В	543	LYS	3.2	
1	А	420	PHE	2.9	
1	А	694	GLY	2.9	
1	В	545	LYS	2.8	
1	А	540	HIS	2.6	
1	А	696	GLU	2.5	
1	В	568	GLU	2.4	
1	В	420	PHE	2.4	
1	В	506	LEU	2.4	
1	А	482	VAL	2.3	
1	В	565	GLN	2.2	
1	В	542	THR	2.1	
1	В	435	ARG	2.1	



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.

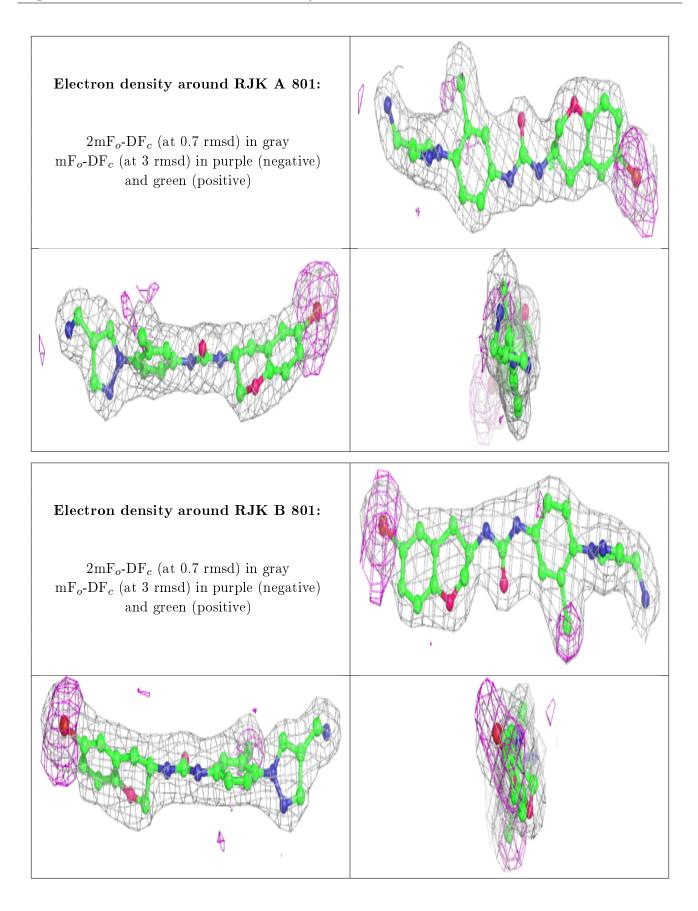
6.4 Ligands (i)

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, 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	${f B} ext{-factors}({f A}^2)$	$Q{<}0.9$
2	RJK	А	801	29/29	0.95	0.13	$38,\!39,\!49,\!57$	0
2	RJK	В	801	29/29	0.96	0.12	$38,\!41,\!46,\!55$	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.

