

wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 09:16 AM EDT

PDB ID 6NZP : Title CRYSTAL STRUCTURE OF TYROSINE KINASE 2 JH2 (PSEUDO KI-: NASE DOMAIN) COMPLEXED WITH COMPOUND-11 AKA 6-CYCLOP ROPANEAMIDO-4-{[2-METHOXY-3-(1-METHYL-1H-1,2,4-TRI AZOL-3-YL)PHENYL]AMINO}-N-(?H?)METHYLPYRIDAZINE-3-CARBOXAMID Е Authors Khan, J.A. : Deposited on 2019-02-14 Resolution 2.35 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* 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 (i)) were used in the production of this report:

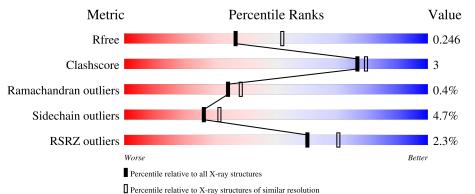
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

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 2.35 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	$1164 \ (2.36-2.36)$
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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	317	% 74%	8%	18%			
1	В	317	3% 75%	6% •	18%			

Ideal geometry (DNA, RNA) : Parkinson et al. (1996) Validation Pipeline (wwPDB-VP) : 2.36.2



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4208 atoms, of which 44 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	259	Total	С	Ν	0	\mathbf{S}	0	2	0
	A	239	2009	1275	359	363	12	0		
1	В	260	Total	С	Ν	0	S	0	1	0
	D	200	2016	1278	362	364	12	0	1	0

• Molecule 1 is a protein called Non-receptor tyrosine-protein kinase TYK2.

Chain	Residue	Modelled	Actual	Comment	Reference
А	553	MET	-	expression tag	UNP P29597
А	554	GLY	-	expression tag	UNP P29597
А	555	SER	-	expression tag	UNP P29597
А	556	SER	-	expression tag	UNP P29597
А	557	HIS	-	expression tag	UNP P29597
А	558	HIS	-	expression tag	UNP P29597
А	559	HIS	-	expression tag	UNP P29597
A	560	HIS	-	expression tag	UNP P29597
А	561	HIS	-	expression tag	UNP P29597
A	562	HIS	-	expression tag	UNP P29597
А	563	SER	-	expression tag	UNP P29597
А	564	SER	-	expression tag	UNP P29597
А	565	GLY	-	expression tag	UNP P29597
А	566	GLU	-	expression tag	UNP P29597
А	567	THR	-	expression tag	UNP P29597
А	568	VAL	-	expression tag	UNP P29597
А	569	ARG	-	expression tag	UNP P29597
А	570	PHE	-	expression tag	UNP P29597
А	571	GLN	-	expression tag	UNP P29597
А	572	GLY	-	expression tag	UNP P29597
А	573	HIS	-	expression tag	UNP P29597
А	574	MET	-	expression tag	UNP P29597
В	553	MET	-	expression tag	UNP P29597
В	554	GLY	-	expression tag	UNP P29597
В	555	SER	-	expression tag	UNP P29597

There are 44 discrepancies between the modelled and reference sequences:

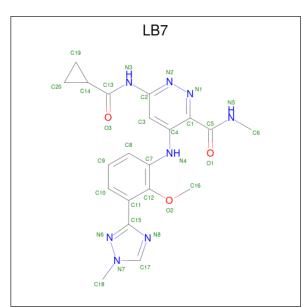
Continued on next page...



Chain	Residue	Modelled	Actual	Comment	Reference
В	556	SER	-	expression tag	UNP P29597
В	557	HIS	_	expression tag	UNP P29597
В	558	HIS	-	expression tag	UNP P29597
В	559	HIS	-	expression tag	UNP P29597
В	560	HIS	-	expression tag	UNP P29597
В	561	HIS	-	expression tag	UNP P29597
В	562	HIS	-	expression tag	UNP P29597
В	563	SER	-	expression tag	UNP P29597
В	564	SER	-	expression tag	UNP P29597
В	565	GLY	-	expression tag	UNP P29597
В	566	GLU	-	expression tag	UNP P29597
В	567	THR	-	expression tag	UNP P29597
В	568	VAL	-	expression tag	UNP P29597
В	569	ARG	-	expression tag	UNP P29597
В	570	PHE	-	expression tag	UNP P29597
В	571	GLN	-	expression tag	UNP P29597
В	572	GLY	-	expression tag	UNP P29597
В	573	HIS	-	expression tag	UNP P29597
В	574	MET	-	expression tag	UNP P29597

Continued from previous page...

• Molecule 2 is 6-[(cyclopropanecarbonyl)amino]-4-{[2-methoxy-3-(1-methyl-1H-1,2,4-triazol-3-yl)phenyl]amino}-N-methylpyridazine-3-carboxamide (three-letter code: LB7) (formula: $C_{20}H_{22}N_8O_3$).



Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
2	Δ	1	Total	С	Η	Ν	0	<u> </u>	0
	2 A	1	53	20	22	8	3		0

Continued on next page...



Continued from previous page...

Mol	Chain	Residues		Ate	\mathbf{oms}			ZeroOcc	AltConf
0	В	1	Total	С	Η	Ν	Ο	22	0
	D		53	20	22	8	3	22	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total Cl 1 1	0	0

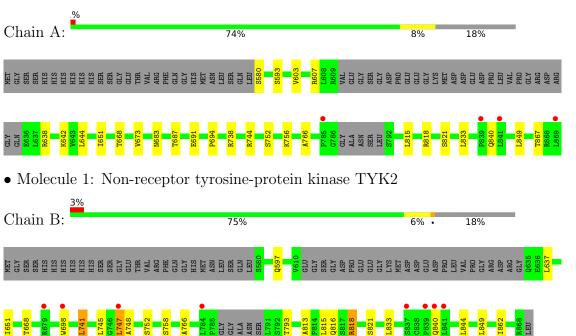
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	39	Total O 39 39	0	0
4	В	37	Total O 37 37	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: Non-receptor tyrosine-protein kinase TYK2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	71.63Å 66.97 Å 75.10 Å	Depositor
a, b, c, α , β , γ	90.00° 113.34° 90.00°	Depositor
Resolution (Å)	48.04 - 2.35	Depositor
Resolution (A)	48.04 - 2.35	EDS
% Data completeness	60.9(48.04-2.35)	Depositor
(in resolution range)	60.9(48.04-2.35)	EDS
R_{merge}	0.09	Depositor
R _{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	$1.13 (at 2.34 \text{\AA})$	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.189 , 0.238	Depositor
It, Itfree	0.194 , 0.246	DCC
R_{free} test set	783 reflections (4.69%)	wwPDB-VP
Wilson B-factor $(Å^2)$	45.6	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35 , 53.8	EDS
L-test for $twinning^2$	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.009 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4208	wwPDB-VP
Average B, all atoms $(Å^2)$	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 12.51% 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: LB7, $\rm CL$

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		lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.51	0/2064	0.70	0/2805	
1	В	0.52	0/2068	0.70	0/2810	
All	All	0.52	0/4132	0.70	0/5615	

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	2009	0	1974	11	0
1	В	2016	0	1976	13	0
2	А	31	22	0	0	0
2	В	31	22	0	0	0
3	В	1	0	0	0	0
4	А	39	0	0	0	0
4	В	37	0	0	0	0
All	All	4164	44	3950	24	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 3.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:815:LEU:HA	1:A:818:ARG:HD3	1.57	0.87
1:B:815:LEU:HD23	1:B:818:ARG:HE	1.59	0.67
1:A:815:LEU:HA	1:A:818:ARG:CD	2.27	0.64
1:B:818:ARG:H	1:B:818:ARG:HD3	1.63	0.63
1:B:818:ARG:HD3	1:B:818:ARG:N	2.15	0.61

The worst 5 of 24 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	ntiles
1	А	255/317~(80%)	246 (96%)	8(3%)	1 (0%)	34	38
1	В	255/317~(80%)	245~(96%)	9~(4%)	1 (0%)	34	38
All	All	510/634~(80%)	491 (96%)	17 (3%)	2~(0%)	34	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	748	ALA
1	А	691	GLU

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	215/273 (79%)	206~(96%)	9~(4%)	30 36		
1	В	215/273 (79%)	204 (95%)	11 (5%)	24 27		
All	All	430/546~(79%)	410 (95%)	20~(5%)	26 31		

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	747	LEU
1	В	818	ARG
1	В	840	GLN
1	В	821	SER
1	А	821	SER

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

Mol	Chain	Res	Type
1	А	597	GLN
1	А	602	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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



			1				0 (0 /		
Mol	Iol Type Chain Res Link		Timle	Bond lengths			Bond angles			
IVIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	LB7	А	901	-	32,34,34	0.56	0	37,48,48	0.65	1 (2%)
2	LB7	В	901	-	32,34,34	0.58	0	37,48,48	0.78	1 (2%)

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).

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	LB7	А	901	-	-	0/24/26/26	0/4/4/4
2	LB7	В	901	-	-	0/24/26/26	0/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	901	LB7	C7-N4-C4	2.41	132.96	125.36
2	А	901	LB7	C7-N4-C4	2.26	132.50	125.36

There are no chirality outliers.

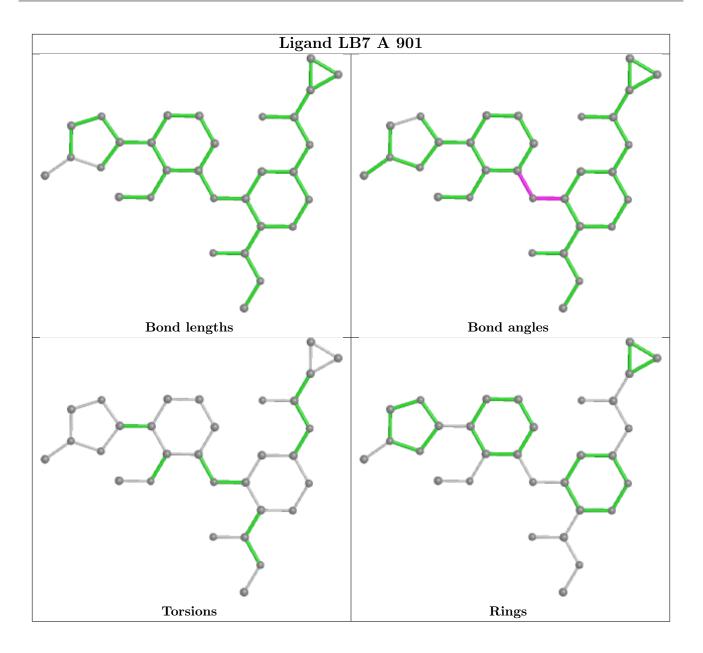
There are no torsion outliers.

There are no ring outliers.

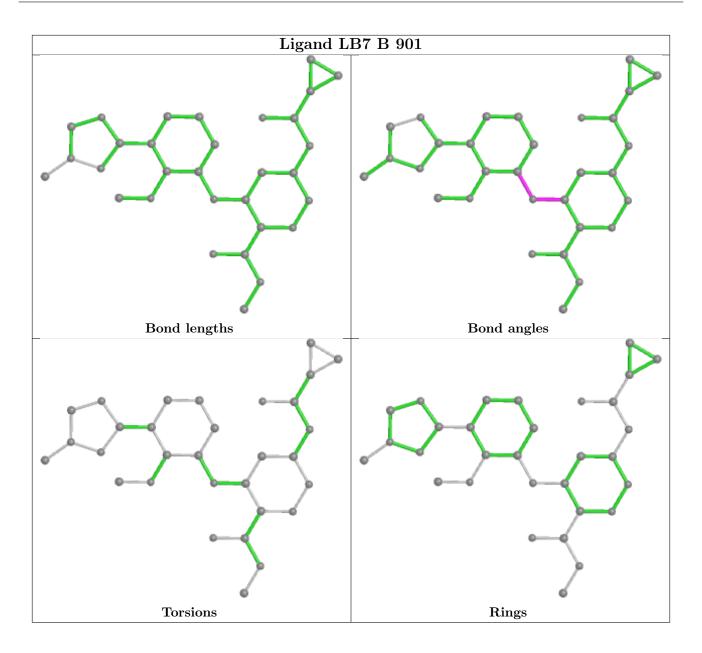
No monomer is involved in short contacts.

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 sufficient 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	$OWAB(Å^2)$	Q<0.9
1	А	259/317~(81%)	0.05	4 (1%) 73 81	27, 46, 75, 94	0
1	В	260/317~(82%)	0.10	8 (3%) 49 61	27, 45, 68, 84	0
All	All	519/634~(81%)	0.08	12 (2%) 60 70	27, 46, 69, 94	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	839	PRO	4.2
1	А	869	LEU	3.6
1	А	839	PRO	3.3
1	В	841	LEU	3.1
1	А	841	LEU	2.8

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.

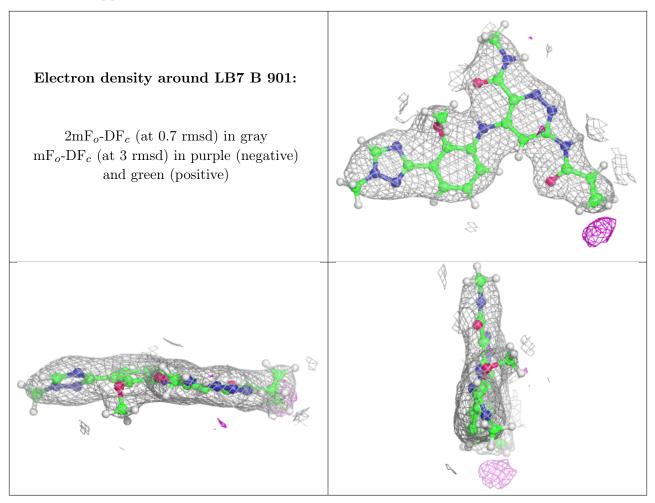
6.4 Ligands (i)

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.

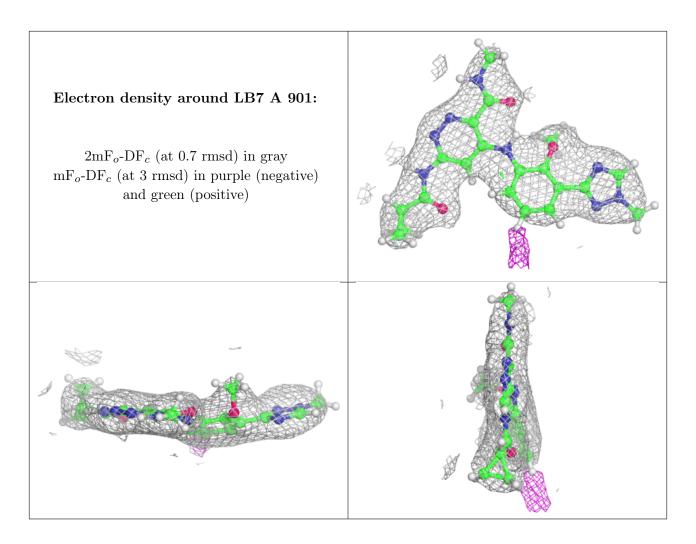


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	CL	В	902	1/1	0.96	0.36	$55,\!55,\!55,\!55$	0
2	LB7	В	901	31/31	0.97	0.15	39,43,43,44	22
2	LB7	А	901	31/31	0.98	0.15	36,43,43,45	22

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.

