

Full wwPDB X-ray Structure Validation Report (i)

Oct 10, 2023 – 12:13 PM EDT

PDB ID	:	7KOJ
Title	:	The crystal structure of Papain-Like Protease of SARS CoV-2, C111S mutant,
		in complex with PLP_Snyder494 inhibitor
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		Y.; Zhou, Z.; Azizi, S.A.; Jones, K.; Kathayat, R.; Snyder, S.A.; Dickinson,
		B.C.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases
		(CSGID)
Deposited on	:	2020-11-09
Resolution	:	2.02 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 (i)) were used in the production of this report:

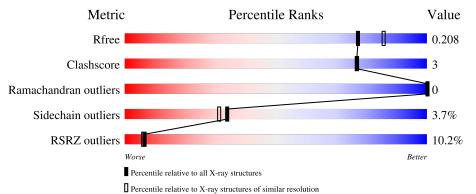
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

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 2.02 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	$10434 \ (2.04-2.00)$
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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		
			10%		
1	А	318	88%	10%	••

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:

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) : 2.35.1



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	UNX	А	512	-	-	-	Х



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2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 2759 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.

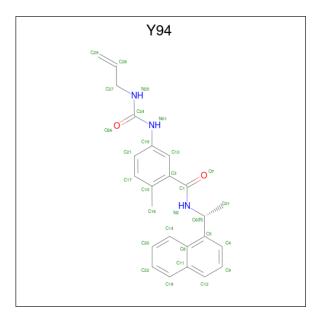
• Molecule 1 is a protein called Papain-like protease.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	313	Total 2513	C 1601	N 418	0 476	S 18	0	5	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-2	SER	-	expression tag	UNP P0DTC1
А	-1	ASN	-	expression tag	UNP P0DTC1
А	0	ALA	-	expression tag	UNP P0DTC1
А	111	SER	CYS	engineered mutation	UNP P0DTC1

• Molecule 2 is 2-methyl-N-[(1R)-1-(naphthalen-1-yl)ethyl]-5-{[(prop-2-en-1-yl)carbamoyl]amino}benzamide (three-letter code: Y94) (formula: C₂₄H₂₅N₃O₂) (labeled as "Ligand of Interest" by depositor).





N	Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
	2	А	1	Total 29	C 24	N 3	O 2	0	0

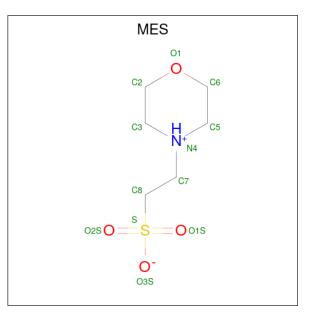
• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	4	Total Zn 5 5	0	1

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	3	Total Cl 3 3	0	0

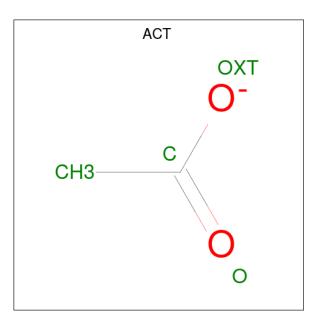
• Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
5	А	1	Total 12	С 6	N 1	0 4	S 1	0	0

• Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).





N	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	6	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
	6	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 7 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	12	Total X 12 12	0	0

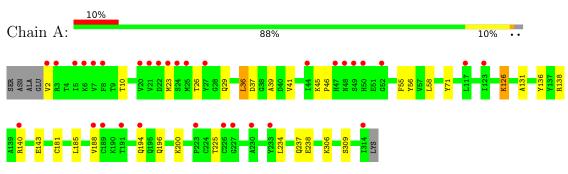
• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	177	Total O 177 177	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: Papain-like protease



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants	113.35Å 113.35Å 220.11Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.41 - 2.02	Depositor
Resolution (A)	45.36 - 2.02	EDS
% Data completeness	99.7 (45.41-2.02)	Depositor
(in resolution range)	99.7 (45.36 - 2.02)	EDS
R _{merge}	0.13	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.73 (at 2.03 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
D D.	0.183 , 0.203	Depositor
R, R_{free}	0.193 , 0.208	DCC
R_{free} test set	2313 reflections (4.94%)	wwPDB-VP
Wilson B-factor $(Å^2)$	51.9	Xtriage
Anisotropy	0.379	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.30 , 57.2	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	0.97	EDS
Total number of atoms	2759	wwPDB-VP
Average B, all atoms $(Å^2)$	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.41% 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: ZN, CL, Y94, ACT, UNX, MES

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	Bo	ond angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.71	0/2587	0.87	2/3508~(0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
1	А	136	TYR	CB-CG-CD2	-8.34	116.00	121.00
1	А	136	TYR	CB-CG-CD1	7.83	125.70	121.00

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	2513	0	2476	15	0
2	А	29	0	0	0	0
3	А	5	0	0	0	0
4	А	3	0	0	0	0
5	А	12	0	13	0	0
6	А	8	0	6	0	0
7	А	12	0	0	0	0
8	А	177	0	0	3	0
All	All	2759	0	2495	15	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.

All (15) 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:26:THR:OG1	1:A:29:GLN:HG3	2.10	0.52
1:A:39:ALA:O	1:A:41:VAL:HG13	2.10	0.52
1:A:188:VAL:HG22	1:A:194:GLN:HG2	1.93	0.50
1:A:140[B]:ARG:HE	1:A:140[B]:ARG:HA	1.79	0.48
1:A:126[A]:LYS:NZ	8:A:605:HOH:O	2.46	0.47
1:A:181:CYS:HA	1:A:238:GLU:O	2.14	0.47
1:A:36:LEU:HG	1:A:55:PHE:CE2	2.49	0.47
1:A:143:GLU:OE1	8:A:601:HOH:O	2.20	0.47
1:A:234:LEU:HD21	1:A:237:GLN:HB2	1.97	0.46
1:A:23:MET:HA	1:A:46:PRO:HG2	2.00	0.44
1:A:185:LEU:O	1:A:196:GLN:HA	2.18	0.43
1:A:71:TYR:CZ	1:A:131:ALA:HA	2.54	0.42
1:A:36:LEU:HD22	1:A:37:ASP:CG	2.41	0.41
1:A:140[B]:ARG:NH2	8:A:613:HOH:O	2.54	0.41
1:A:10:THR:O	1:A:56:TYR:HA	2.21	0.41

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		Percentiles	
1	А	316/318~(99%)	301~(95%)	15~(5%)	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	А	278/277~(100%)	266~(96%)	12~(4%)	29 25	

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	2	VAL
1	А	36	LEU
1	А	45	LYS
1	А	58	LEU
1	А	126[A]	LYS
1	А	126[B]	LYS
1	А	138[A]	ARG
1	А	138[B]	ARG
1	А	200	LYS
1	А	225	THR
1	А	306	LYS
1	А	309	SER

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

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 24 ligands modelled in this entry, 8 are monoatomic and 12 are unknown - leaving 4 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 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	ol Type Chain Res Lin		Link	Bond lengths			Bond angles			
	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	Y94	А	501	-	31,31,31	1.70	8 (25%)	42,42,42	1.69	7 (16%)
6	ACT	А	511	-	3,3,3	1.40	1 (33%)	3,3,3	0.78	0
6	ACT	А	510	-	3,3,3	1.27	0	3,3,3	0.65	0
5	MES	А	509	-	12,12,12	0.81	0	14,16,16	0.49	0

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	Y94	А	501	-	-	6/20/20/20	0/3/3/3
5	MES	А	509	-	-	1/6/14/14	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
2	А	501	Y94	C3-C10	4.08	1.47	1.40
2	А	501	Y94	C19-N01	-3.33	1.34	1.41
2	А	501	Y94	C24-N01	-2.97	1.31	1.37
2	А	501	Y94	C8-C11	2.69	1.47	1.43
2	А	501	Y94	C5-C8	2.51	1.47	1.43
2	А	501	Y94	C6-N2	-2.49	1.42	1.47
2	А	501	Y94	C14-C8	-2.24	1.37	1.42
2	А	501	Y94	C13-C3	-2.20	1.36	1.39
6	А	511	ACT	CH3-C	2.01	1.57	1.49

All (7) bond angle outliers are listed below:



7KOJ

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	501	Y94	C19-N01-C24	4.50	135.83	126.61
2	А	501	Y94	C27-N25-C24	3.73	126.09	120.73
2	А	501	Y94	O7-C1-C3	-3.63	114.38	121.01
2	А	501	Y94	C16-C10-C3	-3.62	117.18	122.79
2	А	501	Y94	C13-C19-N01	-3.57	108.51	120.18
2	А	501	Y94	C21-C19-N01	2.93	130.25	120.40
2	А	501	Y94	C22-C20-C14	2.09	123.38	120.44

There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
5	А	509	MES	C8-C7-N4-C5
2	А	501	Y94	O7-C1-C3-C13
2	А	501	Y94	N2-C1-C3-C13
2	А	501	Y94	C8-C5-C6-C01
2	А	501	Y94	C4-C5-C6-C01
2	А	501	Y94	C8-C5-C6-N2
2	А	501	Y94	C4-C5-C6-N2

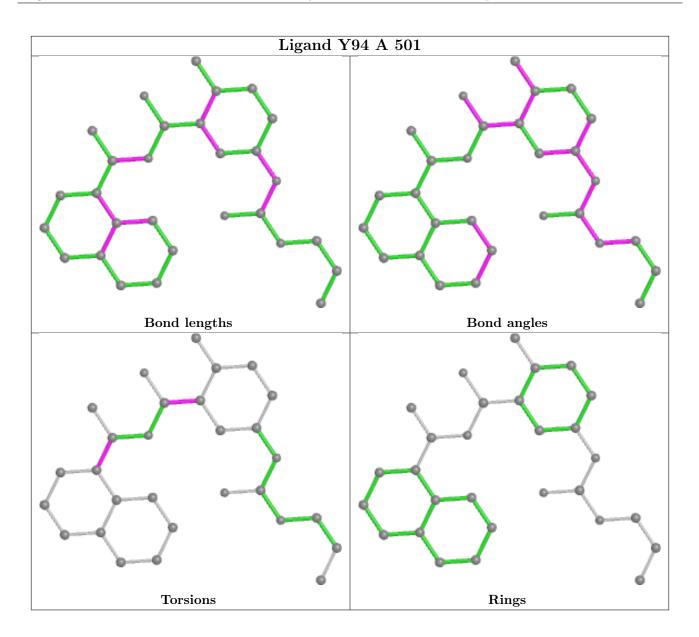
All (7) torsion outliers are listed below:

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	<RSRZ $>$	#RSRZ>2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	А	313/318~(98%)	0.36	32 (10%) 6 6	46, 63, 126, 149	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	21	VAL	5.6
1	А	140[A]	ARG	4.6
1	А	5	ILE	4.4
1	А	3	ARG	4.2
1	А	6	LYS	4.2
1	А	23	MET	4.2
1	А	47	HIS	3.9
1	А	314	ILE	3.8
1	А	233	TYR	3.7
1	А	7	VAL	3.7
1	А	8	PHE	3.7
1	А	50	HIS	3.5
1	А	24	SER	3.0
1	А	2	VAL	2.9
1	А	226	CYS	2.9
1	А	188	VAL	2.9
1	А	52	GLY	2.8
1	А	25	MET	2.7
1	А	230	ALA	2.7
1	А	27	TYR	2.6
1	А	48	ASN	2.6
1	А	194	GLN	2.5
1	А	191	THR	2.4
1	А	223	PRO	2.3
1	А	20	VAL	2.3
1	А	189	CYS	2.3
1	А	44 Continue	ILE	2.3

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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	B-factors(Å ²)	Q<0.9
7	UNX	А	521	1/1	0.65	0.20	79,79,79,79	0
7	UNX	А	513	1/1	0.68	0.22	67,67,67,67	0
5	MES	А	509	12/12	0.69	0.25	104,108,127,128	12
7	UNX	А	516	1/1	0.72	0.35	78,78,78,78	0
7	UNX	А	515	1/1	0.73	0.30	$65,\!65,\!65,\!65$	0
7	UNX	А	523	1/1	0.73	0.12	64,64,64,64	0
7	UNX	А	514	1/1	0.75	0.15	73,73,73,73	0
7	UNX	А	519	1/1	0.78	0.09	73,73,73,73	0
7	UNX	А	512	1/1	0.80	0.47	$69,\!69,\!69,\!69$	0
7	UNX	А	518	1/1	0.83	0.17	70,70,70,70	0
6	ACT	А	511	4/4	0.85	0.17	77,79,84,87	0
3	ZN	А	502	1/1	0.89	0.04	127,127,127,127	0
7	UNX	А	517	1/1	0.94	0.21	70,70,70,70	0
7	UNX	А	522	1/1	0.96	0.08	70,70,70,70	0
2	Y94	А	501	29/29	0.97	0.10	48,54,100,102	0
6	ACT	А	510	4/4	0.97	0.12	$50,\!53,\!54,\!56$	0
3	ZN	А	504[B]	1/1	0.98	0.13	63,63,63,63	1
3	ZN	А	503	1/1	0.98	0.06	97,97,97,97	1

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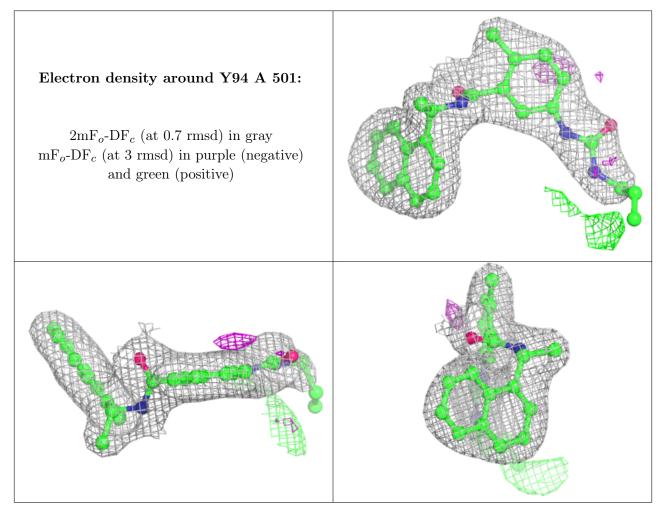
Chain Mol Res Type RSRZ 49SER 2.31 А 1 А 117 LEU 2.21 22ASP А 2.11 А 123ILE 2.11 Α 227 GLY 2.1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
3	ZN	А	504[A]	1/1	0.98	0.13	40,40,40,40	1
4	CL	А	507	1/1	0.99	0.07	57,57,57,57	0
3	ZN	А	505	1/1	0.99	0.11	$57,\!57,\!57,\!57$	0
7	UNX	А	520	1/1	0.99	0.09	58, 58, 58, 58	0
4	CL	А	508	1/1	1.00	0.08	$65,\!65,\!65,\!65$	0
4	CL	А	506	1/1	1.00	0.10	58, 58, 58, 58	0

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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.

