

Full wwPDB X-ray Structure Validation Report (i)

Apr 12, 2022 – 07:15 pm BST

PDB ID	:	70UZ
Title	:	Human OMPD-domain of UMPS in complex with 6-hydroxy-UMP at 0.9
		Angstroms resolution, crystal 1
Authors	:	Rindfleisch, S.; Tittmann, K.
Deposited on		
Resolution	:	0.90 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:

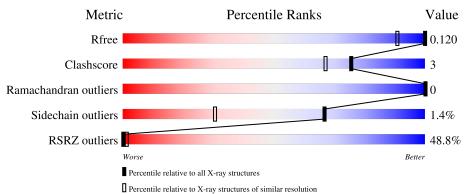
MolProbity	:	4.02b-467
•		1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 0.90 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	1061 (1.04-0.76)
Clashscore	141614	1132 (1.04-0.76)
Ramachandran outliers	138981	1055 (1.04-0.76)
Sidechain outliers	138945	1056 (1.04-0.76)
RSRZ outliers	127900	1028 (1.04-0.76)

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	
			49%	
1	А	257	93%	6%



70UZ

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5148 atoms, of which 2435 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.

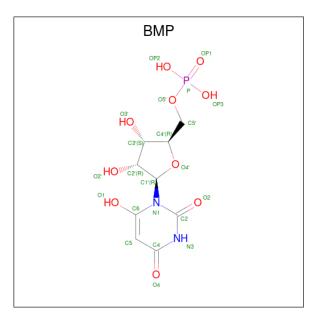
• Molecule 1 is a protein called Uridine 5'-monophosphate synthase.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	А	257	Total 4755	C 1484	Н 2410	N 402	O 443	S 16	0	80	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	223	MET	-	initiating methionine	UNP P11172

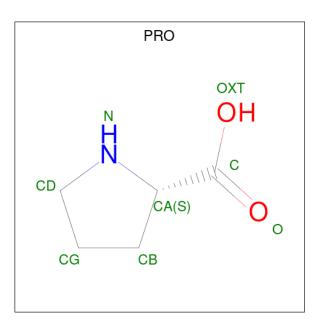
• Molecule 2 is 6-HYDROXYURIDINE-5'-PHOSPHATE (three-letter code: BMP) (formula: $C_9H_{13}N_2O_{10}P$) (labeled as "Ligand of Interest" by depositor).



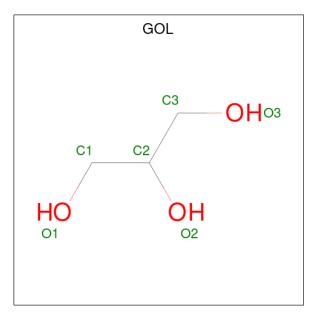
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	А	1	Total 31	С 9	Н 9	N 2	O 10	Р 1	0	0

• Molecule 3 is PROLINE (three-letter code: PRO) (formula: $C_5H_9NO_2$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total C 8 5		$\begin{array}{c} 0\\2\end{array}$	0	0



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	А	1	Total 28	C 6	Н 16	O 6	0	1

• Molecule 5 is water.

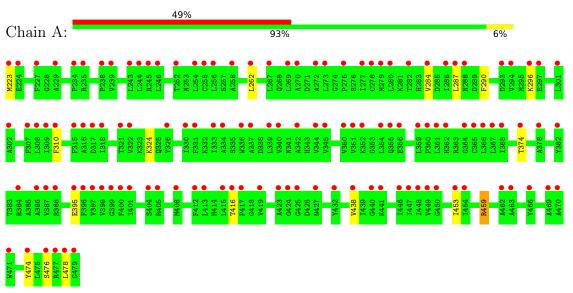


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	321	Total O 326 326	0	6



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: Uridine 5'-monophosphate synthase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	77.90Å 116.42Å 61.97Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.30 - 0.90	Depositor
Resolution (A)	30.30 - 0.90	EDS
% Data completeness	96.8 (30.30-0.90)	Depositor
(in resolution range)	96.8 (30.30-0.90)	EDS
R _{merge}	0.04	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.17 (at 0.90 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
B B.	0.110 , 0.120	Depositor
R, R_{free}	0.110 , 0.120	DCC
R_{free} test set	9883 reflections (4.93%)	wwPDB-VP
Wilson B-factor $(Å^2)$	8.1	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	5148	wwPDB-VP
Average B, all atoms $(Å^2)$	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.77% 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: GOL, CSS, BMP

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.46	0/2645	0.71	0/3562	

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	2345	2410	2102	15	0
2	А	22	9	10	0	0
3	А	8	0	7	0	0
4	А	12	16	16	0	3
5	А	326	0	0	6	3
All	All	2713	2435	2135	15	3

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:416:THR:HG21	1:A:438[B]:VAL:CG1	2.33	0.57
1:A:416:THR:HG21	1:A:438[B]:VAL:HG11	1.87	0.57
1:A:287[B]:LEU:HG	5:A:734:HOH:O	2.06	0.55
1:A:416:THR:CG2	1:A:438[B]:VAL:HG11	2.40	0.51
1:A:374[B]:THR:HG21	5:A:736:HOH:O	2.12	0.49
1:A:284[B]:VAL:CG2	1:A:290:PHE:CD1	2.97	0.47
1:A:453:ILE:O	1:A:459:ARG:HG3	2.16	0.45
1:A:310[B]:PHE:C	1:A:310[B]:PHE:CD1	2.90	0.45
1:A:474:TYR:CZ	1:A:478[B]:LEU:HD11	2.53	0.44
1:A:416:THR:HB	1:A:438[B]:VAL:HG11	1.98	0.44
1:A:476[B]:SER:HB3	5:A:807:HOH:O	2.18	0.43
1:A:262[B]:LEU:HD21	5:A:906:HOH:O	2.17	0.43
1:A:324:LYS:CE	5:A:650:HOH:O	2.67	0.42
1:A:395:GLU:HG2	5:A:750:HOH:O	2.19	0.42
1:A:416:THR:CB	1:A:438[B]:VAL:HG11	2.50	0.42

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:503[B]:GOL:HO2	5:A:613:HOH:O[3_556]	1.47	0.13
4:A:503[A]:GOL:O3	5:A:613:HOH:O[3_556]	2.10	0.10
4:A:503[B]:GOL:O2	5:A:613:HOH:O[3_556]	2.12	0.08

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	owed Outliers		Percentiles	
1	А	333/257~(130%)	329~(99%)	4 (1%)	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	281/208~(135%)	277~(99%)	4 (1%)	67 30	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	223	MET
1	А	296[A]	LYS
1	А	296[B]	LYS
1	А	459	ARG

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)

1 non-standard protein/DNA/RNA residue is 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).

Mol	Type	Chain	Res	Link	B	ond leng	gths	Bond angles		
IVIOI	туре	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
1	CSS	А	304	1	$4,\!6,\!7$	0.90	0	$1,\!6,\!8$	0.20	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
1	CSS	А	304	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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)

4 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).

Mol	Turne	Chain	Dec	Tinle	Bo	Bond lengths			Bond angles		
	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
4	GOL	А	503[B]	-	$5,\!5,\!5$	0.67	0	$5,\!5,\!5$	1.10	0	
4	GOL	А	503[A]	-	$5,\!5,\!5$	0.74	0	$5,\!5,\!5$	1.00	0	
3	PRO	А	502	-	$5,\!8,\!8$	0.73	0	6,10,10	1.02	0	
2	BMP	А	501	-	18,23,23	1.05	2 (11%)	21,35,35	1.54	2 (9%)	

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
4	GOL	А	503[B]	-	-	2/4/4/4	-
4	GOL	А	503[A]	-	-	1/4/4/4	-
3	PRO	А	502	-	-	0/0/11/11	0/1/1/1
2	BMP	А	501	-	-	1/6/26/26	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	А	501	BMP	O1-C6	-2.46	1.25	1.32
2	А	501	BMP	C4-N3	2.38	1.37	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	501	BMP	C5-C4-N3	-5.64	117.50	124.08
2	А	501	BMP	C6-C5-C4	2.70	120.02	115.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	503[B]	GOL	O1-C1-C2-C3
4	А	503[B]	GOL	O1-C1-C2-O2
4	А	503[A]	GOL	O1-C1-C2-C3
2	А	501	BMP	O4'-C4'-C5'-O5'

There are no ring outliers.

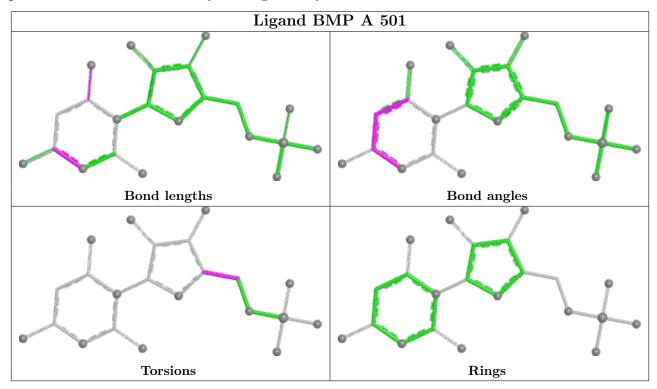
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	503[B]	GOL	0	2
4	А	503[A]	GOL	0	1

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	256/257~(99%)	2.12	125 (48%) 0 1	7, 9, 17, 39	1 (0%)

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	223	MET	12.8
1	А	478[A]	LEU	7.0
1	А	408[A]	MET	4.9
1	А	454[A]	ILE	4.4
1	А	287[A]	LEU	4.2
1	А	224[A]	GLU	4.2
1	А	388	ARG	4.1
1	А	286[A]	ILE	4.1
1	А	310[A]	PHE	3.9
1	А	245[A]	ARG	3.8
1	А	359[A]	LEU	3.8
1	А	413[A]	LEU	3.7
1	А	448	ILE	3.6
1	А	386	ALA	3.5
1	А	255	CYS	3.5
1	А	284[A]	VAL	3.4
1	А	401[A]	ILE	3.4
1	А	447	ILE	3.4
1	А	477[A]	ARG	3.3
1	А	438[A]	VAL	3.3
1	А	315	PHE	3.2
1	А	345	VAL	3.2
1	А	340	VAL	3.1
1	А	446	ILE	3.1
1	А	339	LEU	3.1
1	А	367	LEU	3.1
1	А	365 Continu	CYS	3.1



Mol	Chain	Res	Type	RSRZ
1	А	318[A]	ILE	3.1
1	А	333	ILE	3.1
1	А	361[A]	LEU	3.1
1	А	412[A]	PHE	3.0
1	А	427[A]	ASN	3.0
1	А	415	LEU	3.0
1	А	344	VAL	3.0
1	А	449	VAL	3.0
1	А	309[A]	ILE	2.9
1	А	360[A]	PRO	2.9
1	А	278	CYS	2.9
1	А	336[A]	TRP	2.9
1	А	337	ALA	2.9
1	А	419	VAL	2.9
1	А	308[A]	LEU	2.9
1	А	352[A]	LYS	2.9
1	А	368	ILE	2.9
1	А	453	ILE	2.9
1	А	234[A]	PRO	2.9
1	А	254	LEU	2.8
1	А	330[A]	ILE	2.8
1	А	316[A]	ALA	2.8
1	А	354	LEU	2.8
1	А	476[A]	SER	2.8
1	А	400	PHE	2.8
1	А	326	TYR	2.7
1	А	479[A]	GLY	2.7
1	А	355[A]	GLN	2.7
1	А	277	ILE	2.7
1	А	322	VAL	2.7
1	A	267	LEU	2.7
1	А	321	THR	2.6
1	A	356[A]	GLU	2.6
1	А	280	LEU	2.6
1	A	294[A]	VAL	2.6
1	А	243	LEU	2.6
1	A	256	LEU	2.6
1	A	395	GLU	2.6
1	A	441[A]	LYS	2.6
1	A	282	THR	2.5
1	А	244	LEU	2.5
1	А	307	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	А	351	VAL	2.5
1	А	272	ALA	2.5
1	А	288[A]	ASN	2.5
1	А	398	VAL	2.5
1	А	366	LEU	2.5
1	А	396	PHE	2.5
1	А	342	ALA	2.4
1	А	239[A]	VAL	2.4
1	А	399	GLY	2.4
1	А	293[A]	ASP	2.4
1	А	262[A]	LEU	2.4
1	А	258	ALA	2.4
1	А	440	GLY	2.4
1	А	474	TYR	2.4
1	А	235[A]	ARG	2.4
1	А	416	THR	2.3
1	А	296[A]	LYS	2.3
1	А	469	ALA	2.3
1	А	382	TYR	2.3
1	А	466[A]	TYR	2.3
1	А	424	GLY	2.3
1	А	229	ALA	2.3
1	А	334	ALA	2.3
1	А	246[A]	LEU	2.3
1	А	432	TYR	2.3
1	А	404[A]	SER	2.2
1	А	378	ALA	2.2
1	А	471	TRP	2.2
1	А	417	PRO	2.2
1	А	463	ALA	2.2
1	А	350	VAL	2.2
1	А	273	LEU	2.2
1	А	425	GLY	2.2
1	А	302	ALA	2.2
1	А	252	THR	2.2
1	А	317[A]	ASP	2.2
1	А	387	VAL	2.2
1	А	405[A]	ARG	2.2
1	А	301	LEU	2.2
1	А	423	ALA	2.2
1	А	462[A]	ALA	2.2
1	А	227	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	А	279	MET	2.1
1	А	269	LEU	2.1
1	А	450	GLY	2.1
1	А	270	ALA	2.1
1	А	374[A]	THR	2.1
1	А	297[A]	GLU	2.1
1	А	362	HIS	2.1
1	А	238[A]	PRO	2.1
1	А	331[A]	PHE	2.1
1	А	364	GLY	2.0
1	А	384	ARG	2.0
1	А	470	ALA	2.0
1	А	275	PRO	2.0
1	А	397	VAL	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	CSS	А	304	7/8	0.95	0.15	$10,\!13,\!27,\!32$	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.

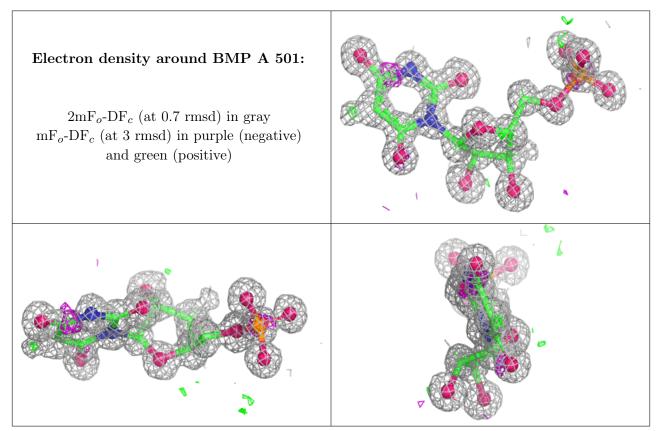
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
3	PRO	А	502	8/8	0.51	0.25	21,22,27,29	0
4	GOL	А	503[A]	6/6	0.62	0.31	16,21,23,26	14
4	GOL	А	503[B]	6/6	0.62	0.31	11,16,20,22	14



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	BMP	A	501	22/22	0.97	0.17	6,6,8,8	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.

