



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:16 AM GMT

PDB ID : 3OH3  
Title : Protein structure of USP from L. major bound to URIDINE-5'-DIPHOSPHATE -Arabinose  
Authors : Dickmanns, A.; Damerow, S.; Neumann, P.; Schulz, E.-C.; Lamerz, A.; Routier, F.; Ficner, R.  
Deposited on : 2010-08-17  
Resolution : 2.03 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

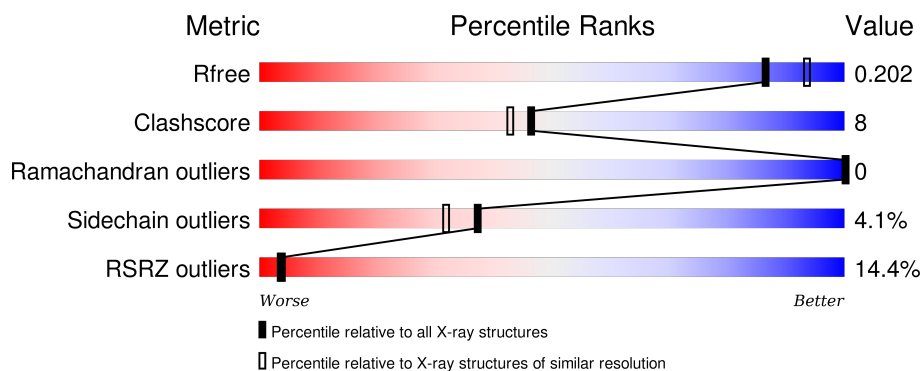
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.03 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ . 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	A	641	

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	643	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4983 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.

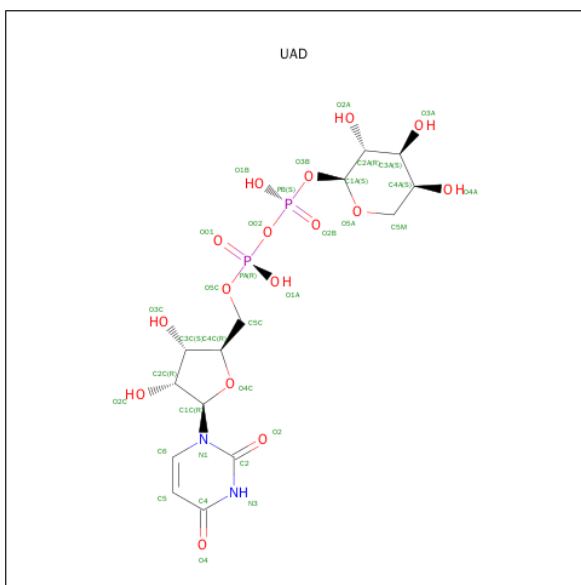
- Molecule 1 is a protein called UDP-sugar pyrophosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	585	4599	2913	798	869	19	0	6	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	630	LEU	-	EXPRESSION TAG	UNP D3G6S4
A	631	MET	-	EXPRESSION TAG	UNP D3G6S4
A	632	ARG	-	EXPRESSION TAG	UNP D3G6S4
A	633	ARG	-	EXPRESSION TAG	UNP D3G6S4
A	634	LEU	-	EXPRESSION TAG	UNP D3G6S4
A	635	GLU	-	EXPRESSION TAG	UNP D3G6S4
A	636	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	637	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	638	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	639	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	640	HIS	-	EXPRESSION TAG	UNP D3G6S4
A	641	HIS	-	EXPRESSION TAG	UNP D3G6S4

- Molecule 2 is [(2R,3S,4R,5R)-5-(2,4-DIOXO-3,4-DIHYDROPYRIMIDIN-1(2H)-YL)-3,4-DIHYDROXYTETRAHYDROFURAN-2-YL]METHYL (2S,3R,4S,5S)-3,4,5-TRIHYDROXYTETRAHYDRO-2H-PYRAN-2-YL DIHYDROGEN DIPHOSPHATE (three-letter code: UAD) (formula: C<sub>14</sub>H<sub>22</sub>N<sub>2</sub>O<sub>16</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			34	14	2	16	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $\text{C}_3\text{H}_8\text{O}_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0

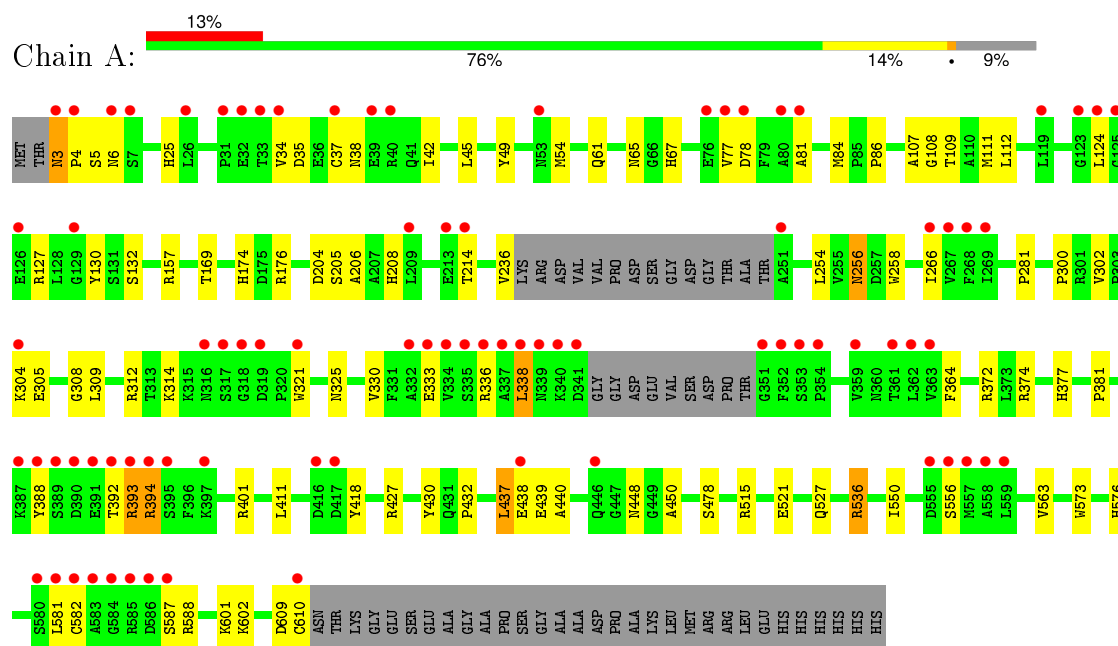
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	338	Total 338	O 338	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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: UDP-sugar pyrophosphorylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.16Å 122.51Å 61.06Å 90.00° 105.30° 90.00°	Depositor
Resolution (Å)	27.17 – 2.03 27.17 – 2.03	Depositor EDS
% Data completeness (in resolution range)	99.1 (27.17-2.03) 99.2 (27.17-2.03)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.74 (at 2.03Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, $R_{free}$	0.176 , 0.204 0.175 , 0.202	Depositor DCC
$R_{free}$ test set	2374 reflections (5.14%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.0	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 55.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 48582 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, UAD

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	A	0.27	0/4694	0.46	0/6375

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

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	A	4599	0	4558	70	0
2	A	34	0	20	0	0
3	A	12	0	16	0	0
4	A	338	0	0	5	0
All	All	4983	0	4594	70	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 8.

All (70) 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:308:GLY:HA3	1:A:325:ASN:HD21	1.42	0.83
1:A:157:ARG:HH12	1:A:556:SER:HB3	1.45	0.81
1:A:388:TYR:HE1	1:A:394:ARG:HG3	1.50	0.74
1:A:388:TYR:CE1	1:A:394:ARG:HG3	2.23	0.73
1:A:581:LEU:N	1:A:581:LEU:HD12	2.04	0.71
1:A:204:ASP:OD1	1:A:208:HIS:HD2	1.73	0.70
1:A:81:ALA:HB3	1:A:314:LYS:HB2	1.75	0.69
1:A:3:ASN:N	1:A:4:PRO:HD2	2.10	0.67
1:A:381:PRO:HG2	1:A:411:LEU:HD12	1.80	0.64
1:A:77:VAL:HG11	1:A:330:VAL:HG13	1.81	0.63
1:A:300:PRO:HG2	1:A:427:ARG:HG3	1.81	0.61
1:A:256:ASN:ND2	1:A:374:ARG:HH21	1.99	0.61
1:A:302:VAL:HG23	1:A:305:GLU:HB2	1.82	0.61
1:A:581:LEU:H	1:A:581:LEU:HD12	1.64	0.61
1:A:438:GLU:HG3	4:A:814:HOH:O	2.04	0.58
1:A:78:ASP:OD2	1:A:338:LEU:HD21	2.03	0.57
1:A:440:ALA:HB1	1:A:450:ALA:HB1	1.86	0.57
1:A:372:ARG:HD3	1:A:418:TYR:CE2	2.41	0.56
1:A:37:CYS:HB2	1:A:42:ILE:HD11	1.87	0.55
1:A:6:ASN:O	1:A:34:VAL:HG21	2.08	0.54
1:A:3:ASN:ND2	1:A:3:ASN:N	2.56	0.54
1:A:256:ASN:N	1:A:256:ASN:HD22	2.06	0.53
1:A:124:LEU:HD21	1:A:176:ARG:NH2	2.24	0.53
1:A:372:ARG:HD3	1:A:418:TYR:CZ	2.43	0.53
1:A:61:GLN:HE21	1:A:65:ASN:HD21	1.55	0.52
1:A:61:GLN:HE21	1:A:65:ASN:ND2	2.07	0.52
1:A:176:ARG:HD3	4:A:873:HOH:O	2.10	0.52
1:A:521[B]:GLU:H	1:A:521[B]:GLU:CD	2.14	0.51
1:A:169:THR:OG1	1:A:174:HIS:HD2	1.93	0.51
1:A:38:ASN:O	1:A:42:ILE:HG12	2.09	0.51
1:A:4:PRO:HB3	1:A:49:TYR:CD2	2.46	0.50
1:A:550:ILE:HD13	1:A:563:VAL:HG21	1.93	0.50
1:A:581:LEU:N	1:A:581:LEU:CD1	2.73	0.50
1:A:109:THR:HA	1:A:112:LEU:HD12	1.95	0.48
1:A:430:TYR:CZ	1:A:432:PRO:HG3	2.49	0.48
1:A:266:ILE:HG23	1:A:364:PHE:HB2	1.96	0.48
1:A:3:ASN:N	1:A:4:PRO:CD	2.77	0.47
1:A:536:ARG:HD2	1:A:556:SER:O	2.15	0.47
1:A:581:LEU:CD1	1:A:581:LEU:H	2.27	0.47
1:A:609:ASP:O	1:A:610:CYS:CB	2.63	0.47
1:A:308:GLY:HA3	1:A:325:ASN:ND2	2.20	0.47
1:A:515:ARG:HD2	4:A:935:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:TYR:HE1	1:A:394:ARG:CG	2.26	0.46
1:A:204:ASP:OD1	1:A:208:HIS:CD2	2.62	0.46
1:A:312:ARG:HG2	1:A:321:TRP:CE3	2.51	0.46
1:A:204:ASP:HB2	4:A:895:HOH:O	2.16	0.45
1:A:205:SER:HB3	1:A:394:ARG:HG2	1.99	0.45
1:A:309:LEU:HD12	1:A:309:LEU:N	2.32	0.45
1:A:107:ALA:O	1:A:111:MET:HG3	2.17	0.44
1:A:304:LYS:HB2	1:A:448:ASN:HD21	1.81	0.44
1:A:381:PRO:HG2	1:A:411:LEU:CD1	2.48	0.43
1:A:302:VAL:HG22	1:A:305:GLU:OE2	2.18	0.43
1:A:3:ASN:HD22	1:A:3:ASN:N	2.17	0.43
1:A:437:LEU:HA	1:A:437:LEU:HD12	1.90	0.43
1:A:393:ARG:O	1:A:393:ARG:HG2	2.18	0.43
1:A:84:MET:HE3	1:A:84:MET:HB2	1.90	0.43
1:A:4:PRO:HB3	1:A:49:TYR:CE2	2.54	0.42
1:A:127:ARG:HD3	1:A:439[A]:GLU:OE1	2.19	0.42
1:A:34:VAL:HG13	1:A:42:ILE:HD12	2.01	0.42
1:A:35:ASP:N	1:A:35:ASP:OD2	2.53	0.42
1:A:478:SER:H	1:A:527:GLN:NE2	2.18	0.41
1:A:573:TRP:CD1	1:A:602:LYS:HA	2.54	0.41
1:A:254:LEU:HG	1:A:258:TRP:CZ2	2.55	0.41
1:A:576:HIS:HE1	1:A:601:LYS:HD3	1.86	0.41
1:A:67:HIS:HE1	1:A:206:ALA:O	2.04	0.41
1:A:34:VAL:HG13	1:A:42:ILE:CD1	2.51	0.40
1:A:86:PRO:HD2	4:A:765:HOH:O	2.20	0.40
1:A:130:TYR:CZ	1:A:132[A]:SER:HB2	2.57	0.40
1:A:108:GLY:HA3	1:A:281:PRO:O	2.22	0.40
1:A:25:HIS:CE1	1:A:208:HIS:HB3	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	Percentiles	
1	A	585/641 (91%)	569 (97%)	16 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	A	498/536 (93%)	478 (96%)	20 (4%)	38	33

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	5	SER
1	A	45	LEU
1	A	54	MET
1	A	214	THR
1	A	236	VAL
1	A	256	ASN
1	A	333	GLU
1	A	336	ARG
1	A	338	LEU
1	A	377	HIS
1	A	392	THR
1	A	393	ARG
1	A	394	ARG
1	A	401	ARG
1	A	437	LEU
1	A	536	ARG
1	A	582	CYS
1	A	587	SER
1	A	588	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	65	ASN
1	A	67	HIS
1	A	106	ASN
1	A	144	ASN
1	A	156	GLN
1	A	174	HIS
1	A	179	GLN
1	A	190	ASN
1	A	208	HIS
1	A	252	GLN
1	A	256	ASN
1	A	325	ASN
1	A	448	ASN
1	A	480	GLN
1	A	527	GLN
1	A	576	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

3 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	UAD	A	642	-	27,36,36	1.76	7 (25%)	40,55,55	2.31	11 (27%)
3	GOL	A	643	-	5,5,5	0.31	0	5,5,5	0.24	0
3	GOL	A	644	-	5,5,5	0.33	0	5,5,5	0.17	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	UAD	A	642	-	-	0/17/54/54	0/3/3/3
3	GOL	A	643	-	-	0/4/4/4	0/0/0/0
3	GOL	A	644	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	642	UAD	PA-O01	2.04	1.58	1.51
2	A	642	UAD	C5C-C4C	2.07	1.58	1.51
2	A	642	UAD	C5M-C4A	2.08	1.57	1.52
2	A	642	UAD	PB-O2B	2.15	1.59	1.51
2	A	642	UAD	C6-N1	2.76	1.39	1.35
2	A	642	UAD	C4A-C3A	2.81	1.56	1.52
2	A	642	UAD	O4-C4	4.74	1.36	1.24

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	642	UAD	C1A-C2A-C3A	-4.55	101.01	109.97
2	A	642	UAD	O5A-C1A-O3B	-4.34	105.63	111.36
2	A	642	UAD	C6-N1-C2	-3.10	116.26	121.28
2	A	642	UAD	O2A-C2A-C3A	2.16	115.19	110.34
2	A	642	UAD	O5A-C5M-C4A	2.68	115.21	110.86
2	A	642	UAD	O02-PB-O3B	3.46	113.58	103.63
2	A	642	UAD	O3B-C1A-C2A	3.48	114.89	108.39
2	A	642	UAD	O4C-C1C-N1	4.11	116.75	108.08
2	A	642	UAD	C4-N3-C2	4.66	118.76	114.14
2	A	642	UAD	C4C-O4C-C1C	4.72	114.90	109.72
2	A	642	UAD	O02-PA-O5C	5.89	118.57	102.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	585/641 (91%)	0.57	84 (14%) 3 4	22, 43, 106, 209	4 (0%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	341	ASP	16.1
1	A	584	GLY	12.5
1	A	338	LEU	9.7
1	A	583	ALA	9.0
1	A	585	ARG	8.0
1	A	351	GLY	7.4
1	A	335	SER	7.4
1	A	352	PHE	7.2
1	A	80	ALA	7.0
1	A	340	LYS	6.9
1	A	582	CYS	6.8
1	A	3	ASN	6.4
1	A	581	LEU	5.8
1	A	339	ASN	5.8
1	A	354	PRO	5.7
1	A	304	LYS	5.7
1	A	336	ARG	5.7
1	A	337	ALA	5.6
1	A	334	VAL	5.2
1	A	353	SER	5.2
1	A	586	ASP	5.0
1	A	610	CYS	5.0
1	A	81	ALA	4.9
1	A	391	GLU	4.9
1	A	559	LEU	4.8
1	A	124	LEU	4.7
1	A	251	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	318	GLY	4.2
1	A	580	SER	4.2
1	A	393	ARG	4.0
1	A	6	ASN	4.0
1	A	388	TYR	3.9
1	A	389	SER	3.8
1	A	332	ALA	3.7
1	A	39	GLU	3.7
1	A	390	ASP	3.6
1	A	558	ALA	3.5
1	A	319	ASP	3.5
1	A	394	ARG	3.5
1	A	387	LYS	3.5
1	A	557	MET	3.4
1	A	397	LYS	3.4
1	A	392	THR	3.4
1	A	317	SER	3.4
1	A	78	ASP	3.4
1	A	269	ILE	3.3
1	A	32	GLU	3.3
1	A	40	ARG	3.2
1	A	214	THR	3.2
1	A	316	ASN	3.1
1	A	7	SER	3.1
1	A	126	GLU	3.1
1	A	213	GLU	3.1
1	A	556	SER	3.1
1	A	362	LEU	3.0
1	A	438	GLU	3.0
1	A	77	VAL	2.9
1	A	363	VAL	2.8
1	A	34	VAL	2.8
1	A	76	GLU	2.8
1	A	587	SER	2.8
1	A	361	THR	2.7
1	A	33	THR	2.5
1	A	321	TRP	2.5
1	A	395	SER	2.5
1	A	266	ILE	2.5
1	A	268	PHE	2.5
1	A	53[A]	ASN	2.4
1	A	333	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	416	ASP	2.4
1	A	446	GLN	2.4
1	A	26	LEU	2.4
1	A	555	ASP	2.3
1	A	37	CYS	2.2
1	A	209	LEU	2.2
1	A	4	PRO	2.2
1	A	31	PRO	2.2
1	A	267	VAL	2.2
1	A	359	VAL	2.2
1	A	119	LEU	2.2
1	A	125	GLY	2.1
1	A	129	GLY	2.1
1	A	123	GLY	2.0
1	A	417	ASP	2.0

## 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	A	643	6/6	0.70	0.27	9.16	71,76,77,77	0
2	UAD	A	642	34/34	0.90	0.15	0.11	34,53,82,204	0
3	GOL	A	644	6/6	0.75	0.33	-	67,73,74,76	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.