



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 07:06 AM EDT

PDB ID : 2HWU  
Title : Crystal structure of the uridine phosphorylase from *Salmonella typhimurium* in complex with uridine and phosphate ion at 2.91Å resolution  
Authors : Timofeev, V.I.; Gabdulkhakov, A.G.; Dontsova, M.V.; Mikhailov, A.M.  
Deposited on : 2006-08-02  
Resolution : 2.91 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

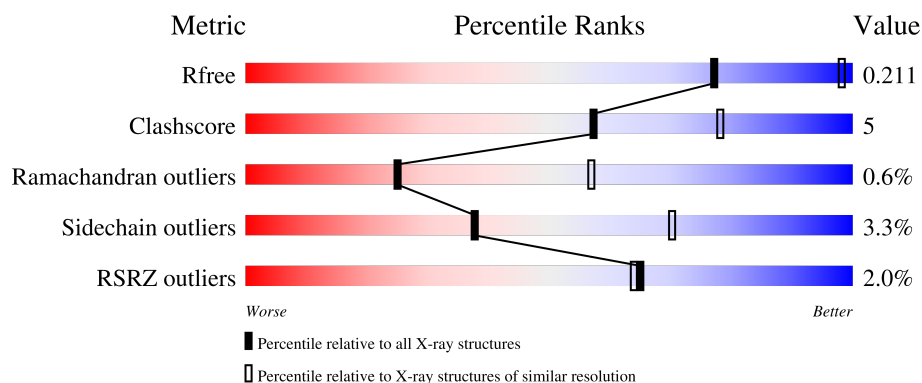
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.91 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))
$R_{free}$	130704	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	253	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>13%</div> <div>.</div> </div> </div>
1	B	253	<div> <div></div> <div> <div>82%</div> <div>13%</div> <div>.</div> <div>.</div> </div> </div>
1	C	253	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>13%</div> <div>.</div> </div> </div>
1	D	253	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>.</div> <div>.</div> </div> </div>
1	E	253	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>.</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	253	<div><div></div><div>81%</div><div>13%<div></div><div></div></div></div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11194 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 Uridine phosphorylase.

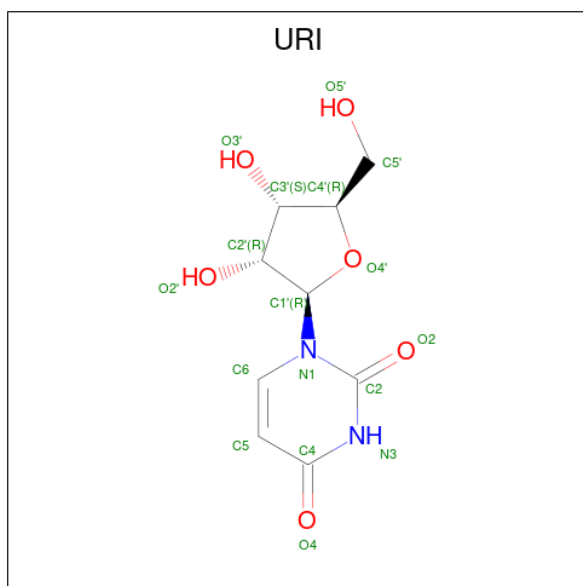
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	0	0
			1900	1188	334	365	13			
1	B	242	Total	C	N	O	S	0	1	0
			1816	1138	320	347	11			
1	C	243	Total	C	N	O	S	0	1	0
			1825	1143	322	348	12			
1	D	244	Total	C	N	O	S	0	0	0
			1833	1147	323	351	12			
1	E	242	Total	C	N	O	S	0	0	0
			1815	1136	321	347	11			
1	F	242	Total	C	N	O	S	0	1	0
			1816	1139	320	346	11			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is URIDINE (three-letter code: URI) (formula:  $C_9H_{12}N_2O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	2	6		
3	B	1	Total	C	N	O	0	0
			17	9	2	6		
3	C	1	Total	C	N	O	0	0
			17	9	2	6		
3	D	1	Total	C	N	O	0	0
			17	9	2	6		
3	E	1	Total	C	N	O	0	0
			17	9	2	6		
3	F	1	Total	C	N	O	0	0
			17	9	2	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total	O	0	0
			14	14		
4	B	18	Total	O	0	0
			18	18		
4	C	13	Total	O	0	0
			13	13		

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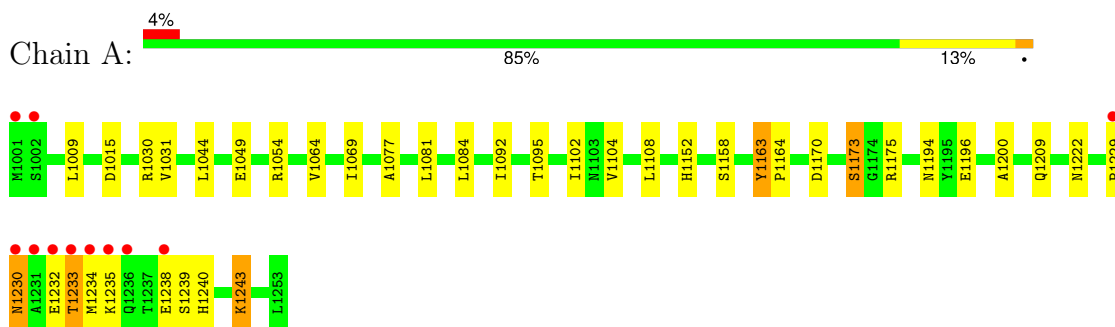
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	11	Total	O	0	0
			11	11		
4	E	14	Total	O	0	0
			14	14		
4	F	12	Total	O	0	0
			12	12		

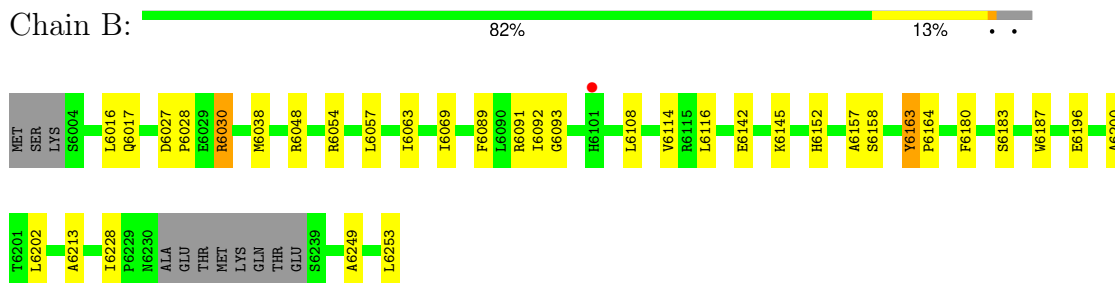
### 3 Residue-property plots [i](#)

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.

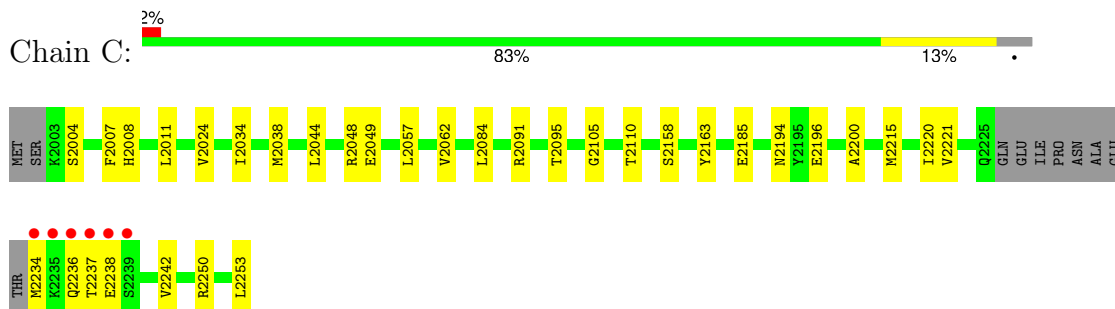
- Molecule 1: Uridine phosphorylase

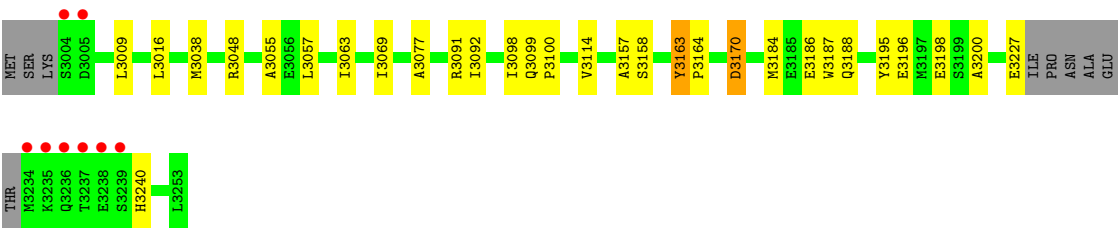


- Molecule 1: Uridine phosphorylase

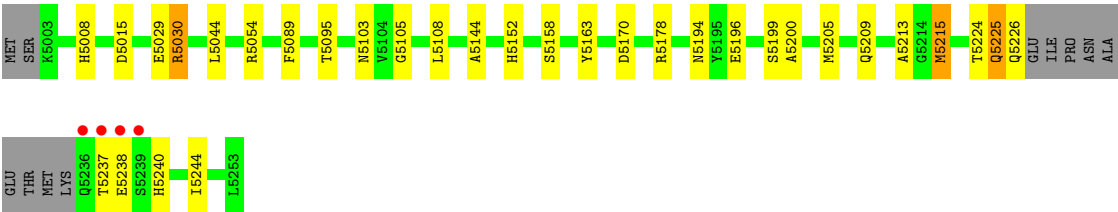
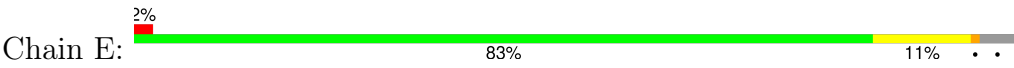


- Molecule 1: Uridine phosphorylase

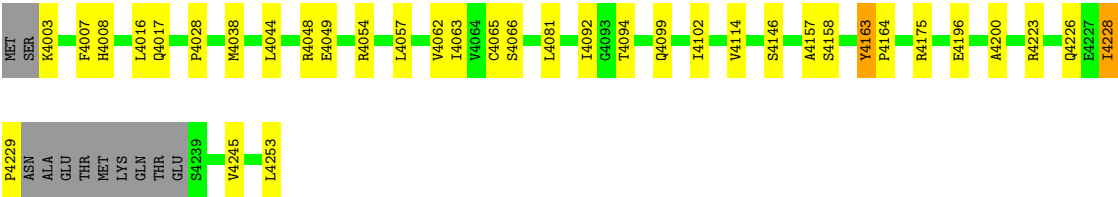
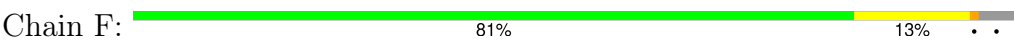




● Molecule 1: Uridine phosphorylase



● Molecule 1: Uridine phosphorylase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.88Å 123.99Å 134.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.91 – 2.91 19.97 – 2.91	Depositor EDS
% Data completeness (in resolution range)	97.7 (90.91-2.91) 98.1 (19.97-2.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.98 (at 2.93Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, $R_{free}$	0.208 , 0.256 0.204 , 0.211	Depositor DCC
$R_{free}$ test set	1625 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.1	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 12.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	11194	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	5.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: URI, PO4

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	0.31	0/1930	0.50	0/2613
1	B	0.30	0/1849	0.48	0/2505
1	C	0.31	0/1858	0.49	0/2513
1	D	0.31	0/1861	0.50	0/2518
1	E	0.31	0/1842	0.50	0/2492
1	F	0.31	0/1850	0.49	0/2505
All	All	0.31	0/11190	0.49	0/15146

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	1900	0	1914	21	0
1	B	1816	0	1826	18	0
1	C	1825	0	1844	16	0
1	D	1833	0	1844	17	0
1	E	1815	0	1828	14	0
1	F	1816	0	1833	23	0
2	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	17	0	12	1	0
3	B	17	0	12	1	0
3	C	17	0	12	1	0
3	D	17	0	12	1	0
3	E	17	0	12	1	0
3	F	17	0	12	2	0
4	A	14	0	0	0	0
4	B	18	0	0	0	0
4	C	13	0	0	0	0
4	D	11	0	0	0	0
4	E	14	0	0	0	0
4	F	12	0	0	0	0
All	All	11194	0	11161	108	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 5.

The worst 5 of 108 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:F:4228:ILE:HB	1:F:4229:PRO:HD3	1.35	1.07
1:A:1232:GLU:HB2	1:A:1235:LYS:HB2	1.59	0.84
1:F:4228:ILE:HB	1:F:4229:PRO:CD	2.18	0.73
3:A:201:URI:H2'	3:A:201:URI:O2	1.88	0.72
3:F:206:URI:H2'	3:F:206:URI:O2	1.90	0.69

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	Percentiles	
1	A	251/253 (99%)	242 (96%)	8 (3%)	1 (0%)	34	65
1	B	239/253 (94%)	232 (97%)	6 (2%)	1 (0%)	34	65
1	C	240/253 (95%)	233 (97%)	5 (2%)	2 (1%)	19	49
1	D	240/253 (95%)	230 (96%)	9 (4%)	1 (0%)	34	65
1	E	238/253 (94%)	229 (96%)	7 (3%)	2 (1%)	19	49
1	F	239/253 (94%)	227 (95%)	10 (4%)	2 (1%)	19	49
All	All	1447/1518 (95%)	1393 (96%)	45 (3%)	9 (1%)	25	57

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	5225	GLN
1	F	4228	ILE
1	A	1163	TYR
1	B	6163	TYR
1	E	5163	TYR

### 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	202/202 (100%)	193 (96%)	9 (4%)	27	59
1	B	193/202 (96%)	187 (97%)	6 (3%)	40	72
1	C	194/202 (96%)	188 (97%)	6 (3%)	40	72
1	D	194/202 (96%)	190 (98%)	4 (2%)	53	80
1	E	192/202 (95%)	184 (96%)	8 (4%)	30	62
1	F	193/202 (96%)	188 (97%)	5 (3%)	46	76
All	All	1168/1212 (96%)	1130 (97%)	38 (3%)	38	70

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	5170	ASP

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Mol	Chain	Res	Type
1	F	4146	SER
1	E	5196	GLU
1	E	5240	HIS
1	F	4245	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	5226	GLN
1	F	4047	HIS
1	F	4226	GLN
1	D	3226	GLN
1	D	3240	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](#)

7 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
3	URI	D	204	-	18,18,18	1.20	1 (5%)	26,26,26	1.97	8 (30%)
3	URI	F	206	-	18,18,18	1.20	1 (5%)	26,26,26	1.99	8 (30%)
2	PO4	A	1	-	4,4,4	0.94	0	6,6,6	0.48	0
3	URI	C	203	-	18,18,18	1.21	1 (5%)	26,26,26	1.95	7 (26%)
3	URI	A	201	-	18,18,18	1.20	1 (5%)	26,26,26	1.96	8 (30%)
3	URI	B	202	-	18,18,18	1.24	2 (11%)	26,26,26	1.99	8 (30%)
3	URI	E	205	-	18,18,18	1.22	2 (11%)	26,26,26	1.98	8 (30%)

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
3	URI	D	204	-	-	6/6/22/22	0/2/2/2
3	URI	F	206	-	-	2/6/22/22	0/2/2/2
3	URI	C	203	-	-	4/6/22/22	0/2/2/2
3	URI	A	201	-	-	4/6/22/22	0/2/2/2
3	URI	B	202	-	-	4/6/22/22	0/2/2/2
3	URI	E	205	-	-	4/6/22/22	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	205	URI	C2-N1	3.02	1.43	1.38
3	B	202	URI	C2-N1	3.01	1.43	1.38
3	C	203	URI	C2-N1	2.91	1.43	1.38
3	D	204	URI	C2-N1	2.91	1.43	1.38
3	F	206	URI	C2-N1	2.88	1.43	1.38

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	205	URI	C4-N3-C2	-4.58	120.92	126.61
3	C	203	URI	C4-N3-C2	-4.58	120.93	126.61
3	B	202	URI	C1'-N1-C2	4.34	125.39	117.59
3	D	204	URI	C4-N3-C2	-4.33	121.24	126.61
3	B	202	URI	C4-N3-C2	-4.32	121.25	126.61

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	202	URI	C3'-C4'-C5'-O5'
3	D	204	URI	C3'-C4'-C5'-O5'
3	A	201	URI	C2'-C1'-N1-C2
3	B	202	URI	C2'-C1'-N1-C2
3	E	205	URI	C2'-C1'-N1-C2

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	204	URI	1	0
3	F	206	URI	2	0
3	C	203	URI	1	0
3	A	201	URI	1	0
3	B	202	URI	1	0
3	E	205	URI	1	0

## 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<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	253/253 (100%)	-0.30	11 (4%) 35 32	2, 3, 32, 49	0
1	B	242/253 (95%)	-0.45	1 (0%) 92 92	2, 3, 11, 15	0
1	C	243/253 (96%)	-0.25	6 (2%) 57 56	2, 5, 15, 54	0
1	D	244/253 (96%)	-0.24	8 (3%) 46 42	2, 4, 19, 58	0
1	E	242/253 (95%)	-0.38	4 (1%) 70 70	2, 3, 12, 39	0
1	F	242/253 (95%)	-0.51	0 100 100	2, 3, 9, 12	0
All	All	1466/1518 (96%)	-0.36	30 (2%) 65 64	2, 3, 14, 58	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	3234	MET	6.0
1	E	5236	GLN	5.5
1	A	1234	MET	4.8
1	A	1231	ALA	4.6
1	C	2236	GLN	4.3

### 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<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	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	A	1	5/5	0.92	0.26	50,51,51,51	0
3	URI	B	202	17/17	0.95	0.14	7,8,8,8	0
3	URI	C	203	17/17	0.95	0.13	10,10,10,10	0
3	URI	E	205	17/17	0.95	0.15	12,12,12,12	0
3	URI	F	206	17/17	0.95	0.14	7,7,7,8	0
3	URI	A	201	17/17	0.96	0.11	8,9,9,9	0
3	URI	D	204	17/17	0.96	0.12	12,12,12,12	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.