



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:24 AM UTC

PDB ID : 3PNS / pdb_00003pns
Title : Crystal Structure of Uridine Phosphorylase Complexed with Uracil from *Vibrio cholerae* O1 biovar El Tor
Authors : Maltseva, N.; Kim, Y.; Hasseman, J.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2010-11-19
Resolution : 2.00 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

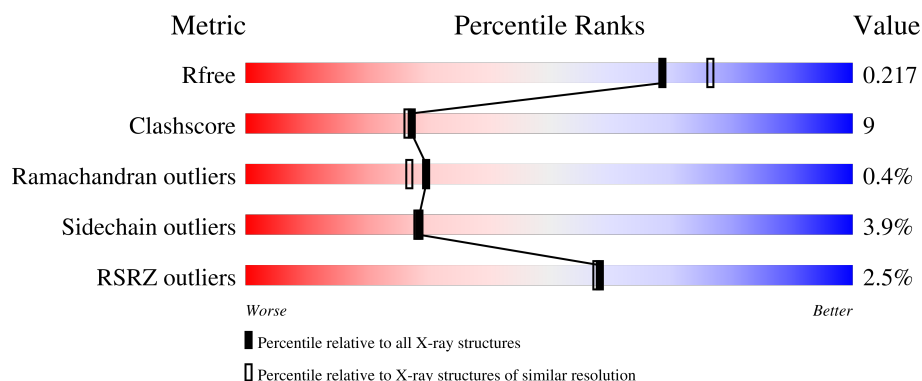
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	261	 2% 77% 16% • •
1	B	261	 2% 77% 15% • 7%
1	C	261	 4% 70% 22% • 5%
1	D	261	 2% 78% 14% • 6%
1	E	261	 5% 75% 17% • 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	261	
1	G	261	
1	H	261	
1	I	261	
1	J	261	
1	K	261	
1	L	261	

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
2	GOL	C	275	-	-	X	-
3	URA	B	271	-	X	-	-
3	URA	C	276	-	X	-	-
3	URA	D	270	-	X	-	-
3	URA	E	271	-	X	-	-
3	URA	F	274	-	X	-	-
3	URA	G	273	-	X	-	-
3	URA	H	270	-	X	-	-
3	URA	I	259	-	X	-	-
3	URA	J	271	-	X	-	-
3	URA	K	272	-	X	-	-
3	URA	L	271	-	X	-	-
6	FMT	E	273	-	-	X	-
6	FMT	H	272	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 25215 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	250	Total	C	N	O	S	Se	0	9	0
			1951	1216	346	375	4	10			
1	B	244	Total	C	N	O	S	Se	0	10	0
			1902	1183	334	371	3	11			
1	C	248	Total	C	N	O	S	Se	0	8	0
			1925	1199	341	372	3	10			
1	D	245	Total	C	N	O	S	Se	0	8	0
			1896	1183	337	363	3	10			
1	E	245	Total	C	N	O	S	Se	0	4	0
			1864	1165	327	359	3	10			
1	F	250	Total	C	N	O	S	Se	1	7	0
			1923	1202	337	370	4	10			
1	G	250	Total	C	N	O	S	Se	0	6	0
			1916	1197	334	371	3	11			
1	H	249	Total	C	N	O	S	Se	1	15	0
			1985	1235	353	383	4	10			
1	I	250	Total	C	N	O	S	Se	0	9	0
			1937	1211	334	378	4	10			
1	J	241	Total	C	N	O	S	Se	1	4	0
			1826	1142	316	354	4	10			
1	K	251	Total	C	N	O	S	Se	0	9	0
			1941	1211	335	381	4	10			
1	L	245	Total	C	N	O	S	Se	0	6	0
			1879	1173	329	364	3	10			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q9KT71
A	-1	ASN	-	expression tag	UNP Q9KT71
A	0	ALA	-	expression tag	UNP Q9KT71
B	-2	SER	-	expression tag	UNP Q9KT71
B	-1	ASN	-	expression tag	UNP Q9KT71

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	ALA	-	expression tag	UNP Q9KT71
C	-2	SER	-	expression tag	UNP Q9KT71
C	-1	ASN	-	expression tag	UNP Q9KT71
C	0	ALA	-	expression tag	UNP Q9KT71
D	-2	SER	-	expression tag	UNP Q9KT71
D	-1	ASN	-	expression tag	UNP Q9KT71
D	0	ALA	-	expression tag	UNP Q9KT71
E	-2	SER	-	expression tag	UNP Q9KT71
E	-1	ASN	-	expression tag	UNP Q9KT71
E	0	ALA	-	expression tag	UNP Q9KT71
F	-2	SER	-	expression tag	UNP Q9KT71
F	-1	ASN	-	expression tag	UNP Q9KT71
F	0	ALA	-	expression tag	UNP Q9KT71
G	-2	SER	-	expression tag	UNP Q9KT71
G	-1	ASN	-	expression tag	UNP Q9KT71
G	0	ALA	-	expression tag	UNP Q9KT71
H	-2	SER	-	expression tag	UNP Q9KT71
H	-1	ASN	-	expression tag	UNP Q9KT71
H	0	ALA	-	expression tag	UNP Q9KT71
I	-2	SER	-	expression tag	UNP Q9KT71
I	-1	ASN	-	expression tag	UNP Q9KT71
I	0	ALA	-	expression tag	UNP Q9KT71
J	-2	SER	-	expression tag	UNP Q9KT71
J	-1	ASN	-	expression tag	UNP Q9KT71
J	0	ALA	-	expression tag	UNP Q9KT71
K	-2	SER	-	expression tag	UNP Q9KT71
K	-1	ASN	-	expression tag	UNP Q9KT71
K	0	ALA	-	expression tag	UNP Q9KT71
L	-2	SER	-	expression tag	UNP Q9KT71
L	-1	ASN	-	expression tag	UNP Q9KT71
L	0	ALA	-	expression tag	UNP Q9KT71

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



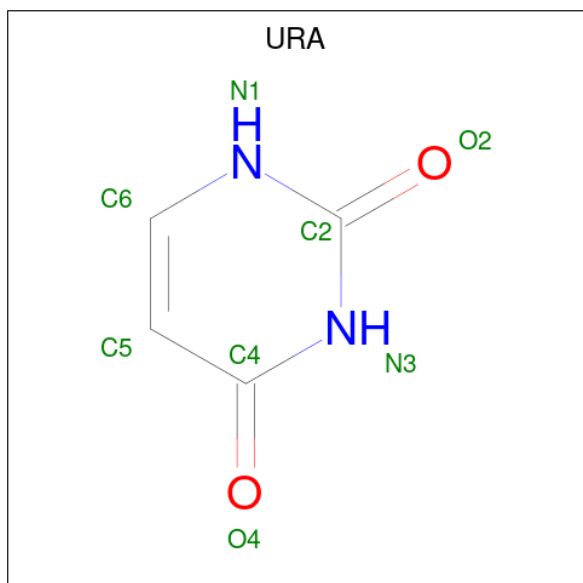
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	G	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	I	1	Total	C	O	0	0
			6	3	3		
2	I	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		
2	K	1	Total	C	O	0	0
			6	3	3		
2	K	1	Total	C	O	0	0
			6	3	3		
2	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is URACIL (CCD ID: URA) (formula: C₄H₄N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			8	4	2	2		

Continued on next page...

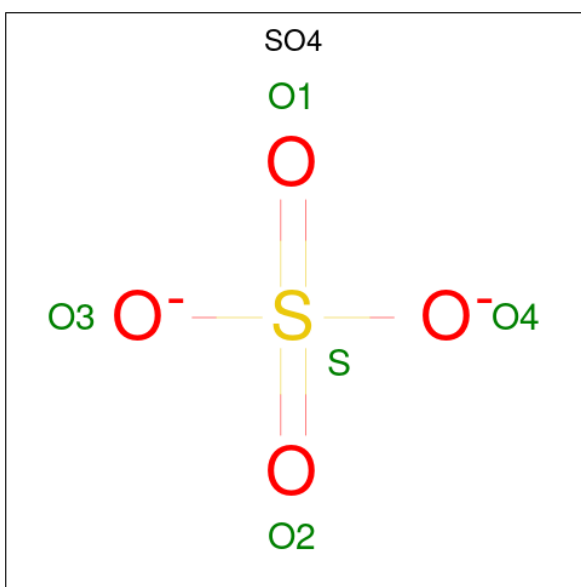
Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			8	4	2	2		
3	D	1	Total	C	N	O	0	0
			8	4	2	2		
3	E	1	Total	C	N	O	0	0
			8	4	2	2		
3	F	1	Total	C	N	O	0	0
			8	4	2	2		
3	G	1	Total	C	N	O	0	0
			8	4	2	2		
3	H	1	Total	C	N	O	0	0
			8	4	2	2		
3	I	1	Total	C	N	O	0	0
			8	4	2	2		
3	J	1	Total	C	N	O	0	0
			8	4	2	2		
3	K	1	Total	C	N	O	0	0
			8	4	2	2		
3	L	1	Total	C	N	O	0	0
			8	4	2	2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

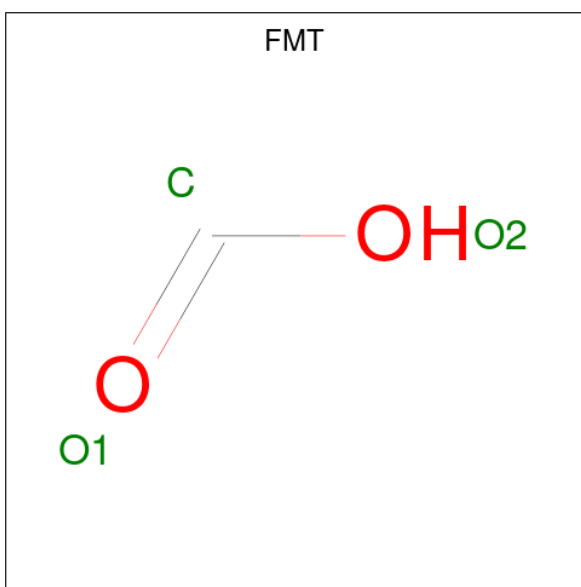
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Cl	0	0
			1	1		
4	E	1	Total	Cl	0	0
			1	1		
4	I	2	Total	Cl	0	0
			2	2		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



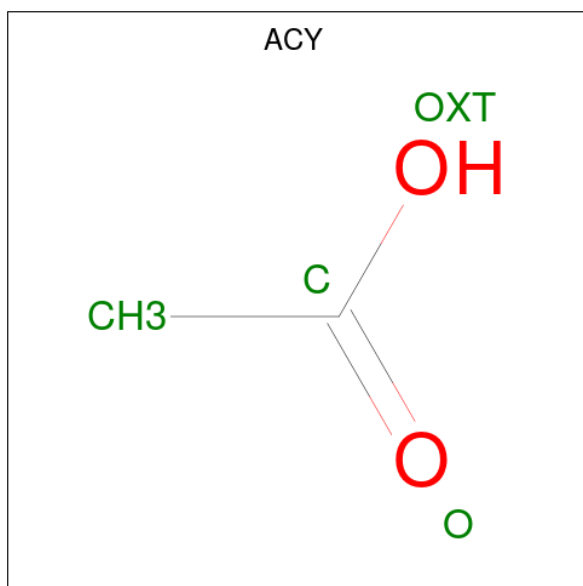
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			3	1	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	H	1	Total	C	O	0	0
			3	1	2		

- Molecule 7 is ACETIC ACID (CCD ID: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	161	Total	O	0	0
			161	161		
8	B	190	Total	O	0	0
			190	190		
8	C	132	Total	O	0	0
			132	132		
8	D	197	Total	O	0	0
			197	197		
8	E	151	Total	O	0	0
			151	151		
8	F	161	Total	O	0	0
			161	161		
8	G	165	Total	O	0	0
			165	165		

Continued on next page...

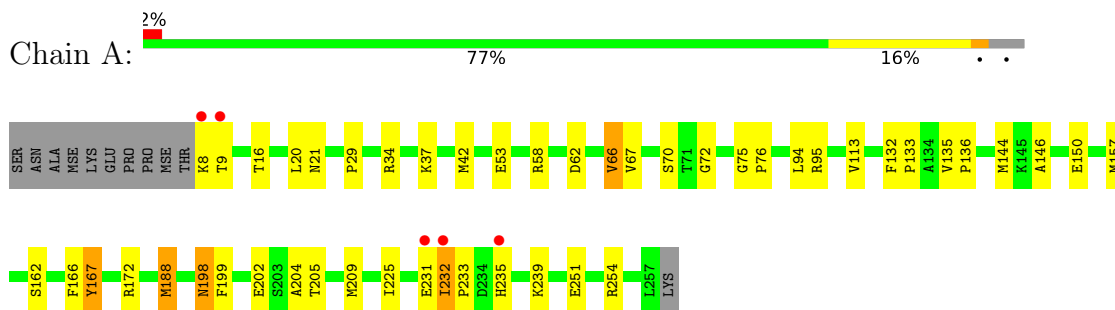
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	173	Total 173	O 173	0	0
8	I	181	Total 181	O 181	0	0
8	J	156	Total 156	O 156	0	0
8	K	171	Total 171	O 171	0	0
8	L	171	Total 171	O 171	0	0

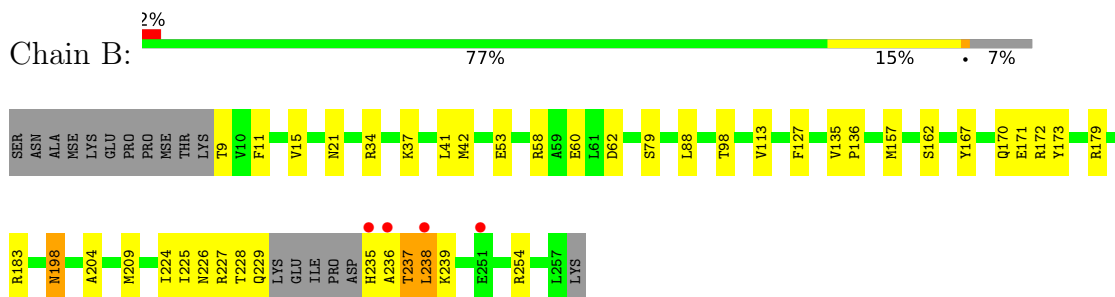
3 Residue-property plots [i](#)

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.

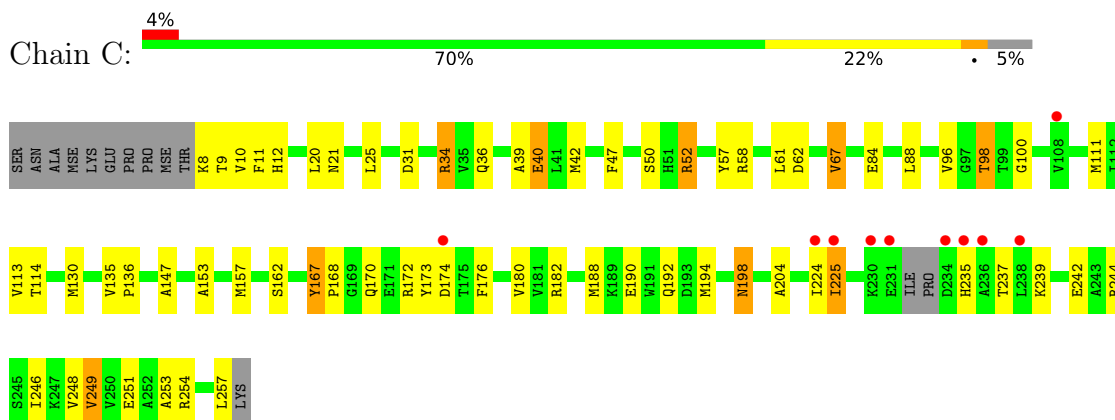
- Molecule 1: Uridine phosphorylase



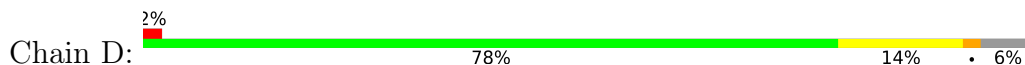
- Molecule 1: Uridine phosphorylase

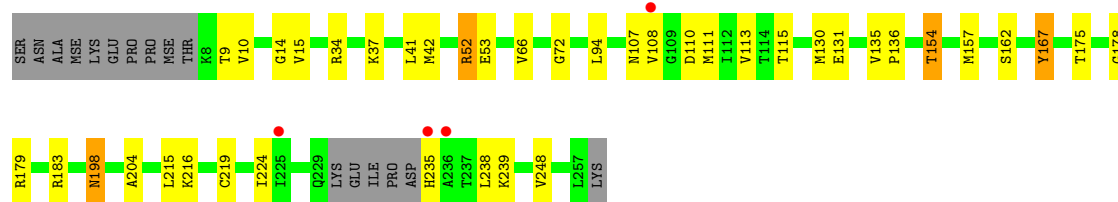


- Molecule 1: Uridine phosphorylase

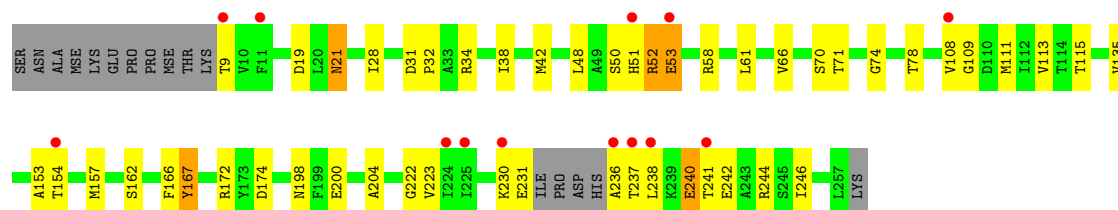
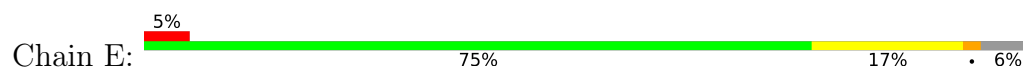


- Molecule 1: Uridine phosphorylase

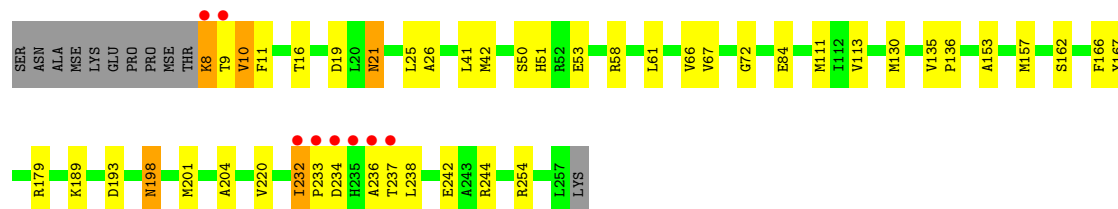
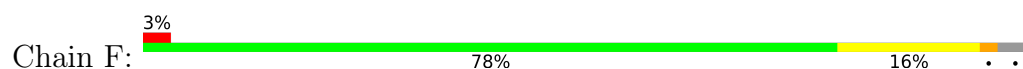




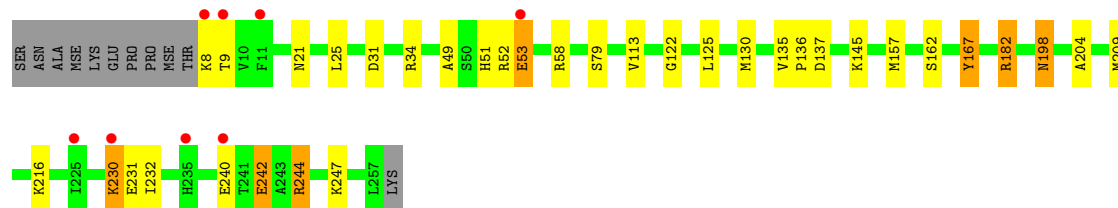
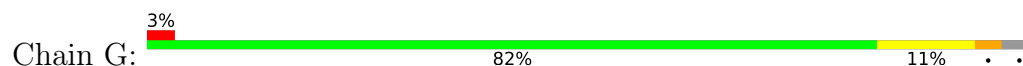
• Molecule 1: Uridine phosphorylase



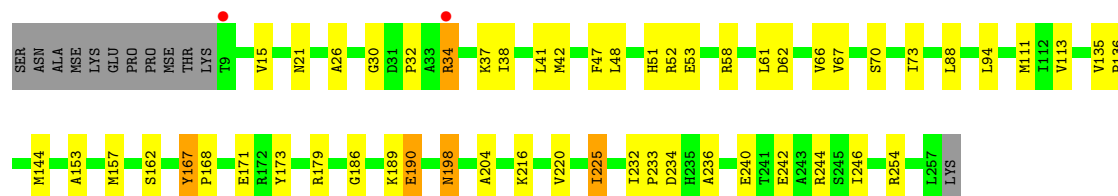
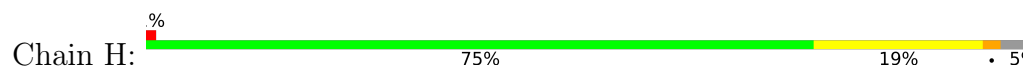
• Molecule 1: Uridine phosphorylase



• Molecule 1: Uridine phosphorylase

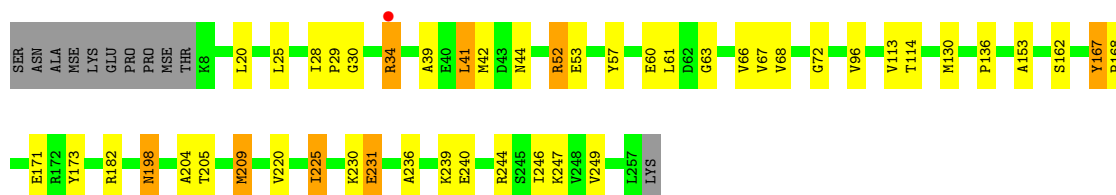


• Molecule 1: Uridine phosphorylase



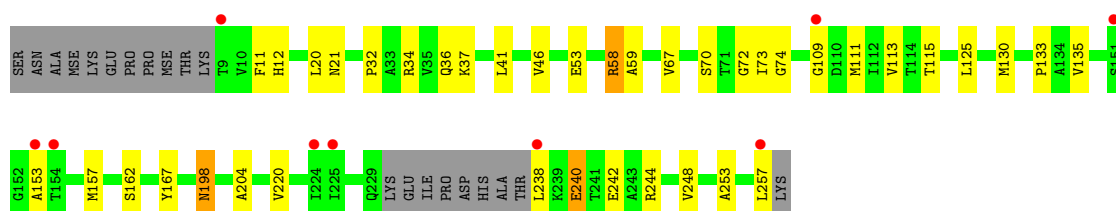
- Molecule 1: Uridine phosphorylase

Chain I:  78% 15% . .



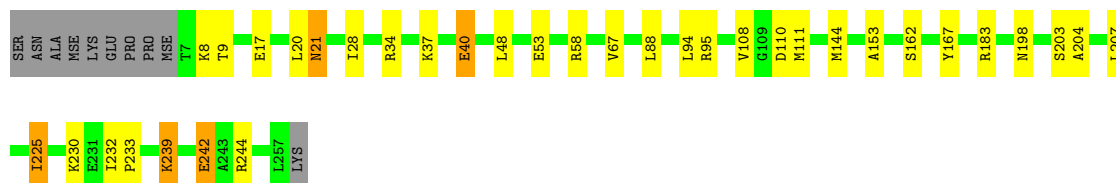
- Molecule 1: Uridine phosphorylase

Chain J:  3% 77% 14% 8%



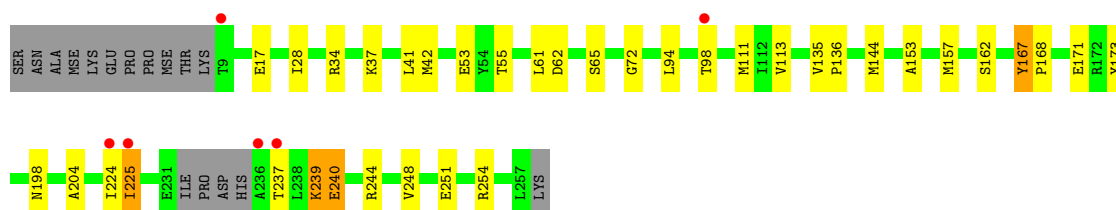
- Molecule 1: Uridine phosphorylase

Chain K:  83% 11% . .



- Molecule 1: Uridine phosphorylase

Chain L:  2% 80% 13% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.28Å 174.46Å 180.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.64 – 2.00 49.64 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.0 (49.64-2.00) 92.1 (49.64-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.174 , 0.226 0.168 , 0.217	Depositor DCC
R_{free} test set	10079 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	22.8	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	25215	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.31 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.7970e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, URA, ACY, CL, FMT, GOL

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	0.65	0/1972	0.90	0/2654
1	B	0.65	0/1921	0.87	1/2585 (0.0%)
1	C	0.62	0/1944	0.89	4/2614 (0.2%)
1	D	0.63	0/1915	0.88	2/2578 (0.1%)
1	E	0.60	0/1882	0.87	2/2534 (0.1%)
1	F	0.62	0/1945	0.86	2/2621 (0.1%)
1	G	0.65	0/1937	0.86	3/2610 (0.1%)
1	H	0.62	0/2007	0.84	1/2703 (0.0%)
1	I	0.63	0/1958	0.85	2/2640 (0.1%)
1	J	0.63	0/1844	0.87	1/2484 (0.0%)
1	K	0.64	0/1962	0.85	0/2645
1	L	0.68	0/1897	0.87	0/2553
All	All	0.64	0/23184	0.87	18/31221 (0.1%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	170	GLN	N-CA-C	-6.96	103.36	112.41
1	I	41	LEU	N-CA-C	-6.32	105.57	113.28
1	D	167	TYR	CA-C-N	-6.04	112.79	119.19
1	D	167	TYR	C-N-CA	-6.04	112.79	119.19
1	F	11	PHE	N-CA-C	5.77	117.57	111.28

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	1951	0	1944	42	0
1	B	1902	0	1877	39	0
1	C	1925	0	1915	51	0
1	D	1896	0	1894	38	0
1	E	1864	0	1866	44	0
1	F	1923	0	1916	33	0
1	G	1916	0	1910	28	0
1	H	1985	0	1970	42	0
1	I	1937	0	1925	46	0
1	J	1826	0	1818	31	0
1	K	1941	0	1924	21	0
1	L	1879	0	1874	22	0
2	A	12	0	16	0	0
2	B	12	0	16	1	0
2	C	18	0	24	7	0
2	D	12	0	16	2	0
2	E	12	0	16	1	0
2	F	12	0	16	5	0
2	G	18	0	24	0	0
2	H	6	0	8	1	0
2	I	12	0	16	0	0
2	J	12	0	16	1	0
2	K	12	0	16	3	0
2	L	6	0	8	0	0
3	B	8	0	3	2	0
3	C	8	0	3	0	0
3	D	8	0	3	0	0
3	E	8	0	3	1	0
3	F	8	0	3	2	0
3	G	8	0	3	0	0
3	H	8	0	3	0	0
3	I	8	0	3	3	0
3	J	8	0	3	0	0
3	K	8	0	3	2	0
3	L	8	0	3	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	2	0	0	0	0
5	C	5	0	0	1	0
5	G	5	0	0	1	0
5	I	5	0	0	0	0
6	E	3	0	1	2	0
6	H	3	0	1	3	0
7	F	4	0	3	0	0
8	A	161	0	0	5	0
8	B	190	0	0	1	0
8	C	132	0	0	6	0
8	D	197	0	0	9	0
8	E	151	0	0	7	0
8	F	161	0	0	4	0
8	G	165	0	0	4	0
8	H	173	0	0	3	0
8	I	181	0	0	2	0
8	J	156	0	0	6	0
8	K	171	0	0	3	0
8	L	171	0	0	3	0
All	All	25215	0	23063	423	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 9.

The worst 5 of 423 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:34[B]:ARG:HG2	1:A:34[B]:ARG:HH11	1.08	1.16
1:E:52[A]:ARG:HG3	1:E:52[A]:ARG:HH11	1.05	1.14
1:G:244:ARG:HG2	1:G:244:ARG:HH11	1.14	1.11
1:D:9:THR:HG21	1:D:14:GLY:HA2	1.33	1.05
1:D:111:MSE:HE2	1:D:248:VAL:HG21	1.37	1.05

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	257/261 (98%)	253 (98%)	3 (1%)	1 (0%)	30	27
1	B	250/261 (96%)	245 (98%)	4 (2%)	1 (0%)	30	27
1	C	252/261 (97%)	247 (98%)	4 (2%)	1 (0%)	30	27
1	D	249/261 (95%)	244 (98%)	4 (2%)	1 (0%)	30	27
1	E	245/261 (94%)	240 (98%)	4 (2%)	1 (0%)	30	27
1	F	255/261 (98%)	247 (97%)	7 (3%)	1 (0%)	30	27
1	G	254/261 (97%)	249 (98%)	3 (1%)	2 (1%)	16	11
1	H	262/261 (100%)	256 (98%)	5 (2%)	1 (0%)	30	27
1	I	257/261 (98%)	251 (98%)	5 (2%)	1 (0%)	30	27
1	J	241/261 (92%)	236 (98%)	4 (2%)	1 (0%)	30	27
1	K	258/261 (99%)	253 (98%)	4 (2%)	1 (0%)	30	27
1	L	247/261 (95%)	240 (97%)	6 (2%)	1 (0%)	30	27
All	All	3027/3132 (97%)	2961 (98%)	53 (2%)	13 (0%)	30	27

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	167	TYR
1	J	167	TYR
1	L	167	TYR
1	A	167	TYR
1	B	167	TYR

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	A	209/198 (106%)	202 (97%)	7 (3%)	33	34
1	B	204/198 (103%)	197 (97%)	7 (3%)	32	33
1	C	206/198 (104%)	193 (94%)	13 (6%)	16	13
1	D	203/198 (102%)	198 (98%)	5 (2%)	42	45
1	E	199/198 (100%)	187 (94%)	12 (6%)	17	14
1	F	207/198 (104%)	199 (96%)	8 (4%)	28	28
1	G	206/198 (104%)	194 (94%)	12 (6%)	18	15
1	H	214/198 (108%)	205 (96%)	9 (4%)	26	25
1	I	209/198 (106%)	201 (96%)	8 (4%)	29	29
1	J	196/198 (99%)	191 (97%)	5 (3%)	40	44
1	K	210/198 (106%)	201 (96%)	9 (4%)	26	25
1	L	201/198 (102%)	193 (96%)	8 (4%)	28	27
All	All	2464/2376 (104%)	2361 (96%)	103 (4%)	28	25

5 of 103 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	230	LYS
1	H	234	ASP
1	L	225	ILE
1	G	232	ILE
1	H	34[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	198	ASN
1	I	198	ASN
1	E	198	ASN
1	H	198	ASN
1	D	198	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 45 ligands modelled in this entry, 4 are monoatomic - leaving 41 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	C	259	-	4,4,4	0.29	0	6,6,6	0.06	0
2	GOL	G	271	-	5,5,5	0.33	0	5,5,5	0.59	0
2	GOL	E	259	-	5,5,5	0.51	0	5,5,5	0.84	0
2	GOL	J	273	-	5,5,5	0.34	0	5,5,5	0.41	0
3	URA	H	270	-	8,8,8	1.74	3 (37%)	10,10,10	2.80	5 (50%)
2	GOL	G	274	-	5,5,5	0.44	0	5,5,5	0.84	0
7	ACY	F	275	-	3,3,3	0.82	0	3,3,3	1.04	0
2	GOL	C	271	-	5,5,5	0.46	0	5,5,5	0.42	0
5	SO4	G	270	-	4,4,4	0.49	0	6,6,6	0.46	0
3	URA	K	272	-	8,8,8	1.73	3 (37%)	10,10,10	2.79	6 (60%)
2	GOL	J	270	-	5,5,5	0.42	0	5,5,5	0.19	0
3	URA	G	273	-	8,8,8	1.54	2 (25%)	10,10,10	3.18	6 (60%)
2	GOL	D	271	-	5,5,5	0.49	0	5,5,5	0.91	0
2	GOL	H	271	-	5,5,5	0.37	0	5,5,5	0.71	0
2	GOL	G	272	-	5,5,5	0.31	0	5,5,5	0.42	0
2	GOL	C	261	-	5,5,5	0.31	0	5,5,5	0.29	0
2	GOL	A	270	-	5,5,5	0.46	0	5,5,5	0.35	0
2	GOL	L	270	-	5,5,5	0.40	0	5,5,5	0.46	0
3	URA	C	276	-	8,8,8	1.67	3 (37%)	10,10,10	2.97	6 (60%)
2	GOL	K	271	-	5,5,5	0.47	0	5,5,5	0.60	0
2	GOL	I	270	-	5,5,5	0.37	0	5,5,5	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	D	260	-	5,5,5	0.34	0	5,5,5	0.42	0
6	FMT	H	272	-	2,2,2	0.78	0	1,1,1	0.31	0
2	GOL	F	270	-	5,5,5	0.41	0	5,5,5	0.64	0
2	GOL	C	275	-	5,5,5	0.34	0	5,5,5	0.41	0
2	GOL	K	270	-	5,5,5	0.42	0	5,5,5	0.31	0
2	GOL	B	270	-	5,5,5	0.46	0	5,5,5	0.24	0
3	URA	E	271	-	8,8,8	1.79	3 (37%)	10,10,10	3.05	6 (60%)
3	URA	L	271	-	8,8,8	1.51	2 (25%)	10,10,10	2.83	6 (60%)
2	GOL	E	272	-	5,5,5	0.43	0	5,5,5	0.71	0
2	GOL	B	261	-	5,5,5	0.34	0	5,5,5	0.38	0
5	SO4	I	271	-	4,4,4	0.42	0	6,6,6	0.19	0
3	URA	F	274	-	8,8,8	1.51	2 (25%)	10,10,10	3.09	6 (60%)
2	GOL	I	272	-	5,5,5	0.29	0	5,5,5	0.18	0
3	URA	J	271	-	8,8,8	1.70	3 (37%)	10,10,10	2.78	5 (50%)
3	URA	B	271	-	8,8,8	2.73	5 (62%)	10,10,10	2.92	6 (60%)
3	URA	D	270	-	8,8,8	1.62	2 (25%)	10,10,10	3.00	6 (60%)
6	FMT	E	273	-	2,2,2	0.74	0	1,1,1	0.27	0
2	GOL	A	260	-	5,5,5	0.36	0	5,5,5	0.40	0
2	GOL	F	273	-	5,5,5	0.39	0	5,5,5	0.29	0
3	URA	I	259	-	8,8,8	1.72	2 (25%)	10,10,10	2.78	6 (60%)

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	GOL	G	271	-	-	1/4/4/4	-
2	GOL	E	259	-	-	0/4/4/4	-
2	GOL	J	273	-	-	2/4/4/4	-
3	URA	H	270	-	-	-	0/1/1/1
2	GOL	G	274	-	-	0/4/4/4	-
2	GOL	C	271	-	-	0/4/4/4	-
3	URA	K	272	-	-	-	0/1/1/1
2	GOL	J	270	-	-	4/4/4/4	-
3	URA	G	273	-	-	-	0/1/1/1
2	GOL	D	271	-	-	3/4/4/4	-
2	GOL	H	271	-	-	2/4/4/4	-
2	GOL	G	272	-	-	0/4/4/4	-
2	GOL	C	261	-	-	2/4/4/4	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	270	-	-	0/4/4/4	-
2	GOL	L	270	-	-	2/4/4/4	-
3	URA	C	276	-	-	-	0/1/1/1
2	GOL	K	271	-	-	2/4/4/4	-
2	GOL	I	270	-	-	0/4/4/4	-
2	GOL	D	260	-	-	4/4/4/4	-
2	GOL	F	270	-	-	0/4/4/4	-
2	GOL	C	275	-	-	2/4/4/4	-
2	GOL	K	270	-	-	2/4/4/4	-
2	GOL	B	270	-	-	2/4/4/4	-
3	URA	E	271	-	-	-	0/1/1/1
3	URA	L	271	-	-	-	0/1/1/1
2	GOL	E	272	-	-	4/4/4/4	-
2	GOL	B	261	-	-	4/4/4/4	-
3	URA	F	274	-	-	-	0/1/1/1
2	GOL	I	272	-	-	2/4/4/4	-
3	URA	J	271	-	-	-	0/1/1/1
3	URA	B	271	-	-	-	0/1/1/1
3	URA	D	270	-	-	-	0/1/1/1
2	GOL	A	260	-	-	4/4/4/4	-
2	GOL	F	273	-	-	3/4/4/4	-
3	URA	I	259	-	-	-	0/1/1/1

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	271	URA	C4-N3	-4.74	1.30	1.38
3	B	271	URA	C2-N3	-3.45	1.31	1.37
3	B	271	URA	C6-N1	-3.18	1.31	1.36
3	I	259	URA	C4-N3	-2.87	1.33	1.38
3	E	271	URA	C4-N3	-2.78	1.33	1.38

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	274	URA	N1-C2-N3	5.80	121.29	115.17
3	E	271	URA	N1-C2-N3	5.49	120.95	115.17
3	G	273	URA	N1-C2-N3	5.46	120.93	115.17
3	G	273	URA	C4-N3-C2	-5.25	120.46	125.55
3	H	270	URA	N1-C2-N3	5.11	120.56	115.17

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	261	GOL	O1-C1-C2-C3
2	B	270	GOL	O1-C1-C2-C3
2	C	261	GOL	O1-C1-C2-C3
2	C	275	GOL	O1-C1-C2-C3
2	D	260	GOL	O1-C1-C2-C3

There are no ring outliers.

21 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	259	SO4	1	0
2	J	273	GOL	1	0
5	G	270	SO4	1	0
3	K	272	URA	2	0
2	D	271	GOL	1	0
2	H	271	GOL	1	0
2	C	261	GOL	1	0
2	K	271	GOL	1	0
2	D	260	GOL	1	0
6	H	272	FMT	3	0
2	F	270	GOL	2	0
2	C	275	GOL	6	0
2	K	270	GOL	2	0
2	B	270	GOL	1	0
3	E	271	URA	1	0
2	E	272	GOL	1	0
3	F	274	URA	2	0
3	B	271	URA	2	0
6	E	273	FMT	2	0
2	F	273	GOL	3	0
3	I	259	URA	3	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 ⓘ

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, 95th 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	A	240/261 (91%)	-0.42	5 (2%) 63 63	8, 20, 38, 87	14 (5%)
1	B	234/261 (89%)	-0.46	4 (1%) 69 68	8, 20, 39, 88	10 (4%)
1	C	238/261 (91%)	-0.08	10 (4%) 40 39	9, 26, 56, 102	12 (5%)
1	D	235/261 (90%)	-0.38	4 (1%) 69 68	7, 20, 43, 89	9 (3%)
1	E	235/261 (90%)	-0.10	13 (5%) 30 29	8, 25, 55, 101	9 (3%)
1	F	240/261 (91%)	-0.28	8 (3%) 49 48	7, 22, 60, 110	10 (4%)
1	G	240/261 (91%)	-0.28	8 (3%) 49 48	7, 22, 47, 83	10 (4%)
1	H	239/261 (91%)	-0.36	2 (0%) 82 82	7, 20, 45, 82	16 (6%)
1	I	240/261 (91%)	-0.43	1 (0%) 88 88	8, 21, 45, 71	11 (4%)
1	J	231/261 (88%)	-0.15	9 (3%) 43 42	9, 25, 50, 72	7 (3%)
1	K	241/261 (92%)	-0.48	0 100 100	6, 19, 42, 71	13 (5%)
1	L	235/261 (90%)	-0.35	6 (2%) 57 56	7, 20, 42, 75	10 (4%)
All	All	2848/3132 (90%)	-0.31	70 (2%) 58 58	6, 21, 49, 110	131 (4%)

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	236	ALA	5.8
1	B	236	ALA	4.4
1	D	235	HIS	4.2
1	F	8	LYS	4.2
1	B	235	HIS	4.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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, 95th 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($\text{\AA}^2$)	Q<0.9
3	URA	B	271	8/8	0.74	0.17	31,52,55,59	0
7	ACY	F	275	4/4	0.76	0.15	31,34,37,38	0
2	GOL	G	271	6/6	0.83	0.15	39,45,47,53	0
6	FMT	H	272	3/3	0.85	0.14	59,59,59,60	0
2	GOL	I	272	6/6	0.85	0.14	28,30,35,35	0
2	GOL	F	270	6/6	0.86	0.15	38,46,49,54	0
3	URA	D	270	8/8	0.86	0.12	28,45,49,52	0
3	URA	C	276	8/8	0.87	0.15	15,22,30,31	8
2	GOL	L	270	6/6	0.88	0.11	40,42,42,44	0
2	GOL	C	261	6/6	0.88	0.13	40,42,44,50	0
2	GOL	C	275	6/6	0.89	0.11	39,48,54,54	0
4	CL	C	274	1/1	0.89	0.13	59,59,59,59	0
2	GOL	K	270	6/6	0.90	0.10	28,30,35,35	0
2	GOL	J	270	6/6	0.90	0.09	33,35,37,38	0
4	CL	I	273	1/1	0.91	0.17	72,72,72,72	0
6	FMT	E	273	3/3	0.91	0.10	45,45,46,48	0
3	URA	J	271	8/8	0.91	0.09	28,33,39,39	0
2	GOL	F	273	6/6	0.91	0.10	32,39,41,42	0
2	GOL	J	273	6/6	0.92	0.11	45,46,48,49	0
4	CL	I	274	1/1	0.92	0.10	54,54,54,54	0
2	GOL	G	272	6/6	0.92	0.08	34,39,42,44	0
2	GOL	A	270	6/6	0.92	0.09	30,31,32,37	0
2	GOL	A	260	6/6	0.92	0.09	35,38,44,48	0
2	GOL	E	272	6/6	0.93	0.10	33,40,41,46	0
2	GOL	E	259	6/6	0.93	0.06	18,20,23,25	0
2	GOL	D	260	6/6	0.93	0.08	34,36,41,44	0
3	URA	L	271	8/8	0.94	0.09	19,33,34,36	0
2	GOL	B	261	6/6	0.94	0.09	36,42,45,51	0
2	GOL	C	271	6/6	0.94	0.07	26,29,30,32	0
2	GOL	D	271	6/6	0.94	0.06	16,25,27,28	0
5	SO4	C	259	5/5	0.94	0.13	37,46,49,53	0
2	GOL	K	271	6/6	0.94	0.09	22,27,30,30	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	URA	E	271	8/8	0.94	0.07	35,40,45,46	0
2	GOL	H	271	6/6	0.94	0.09	31,36,43,44	0
2	GOL	I	270	6/6	0.95	0.07	20,24,29,29	0
2	GOL	G	274	6/6	0.95	0.05	15,16,19,20	0
3	URA	F	274	8/8	0.96	0.08	18,26,31,34	0
5	SO4	I	271	5/5	0.96	0.09	29,30,34,41	0
3	URA	G	273	8/8	0.96	0.07	19,26,29,32	0
3	URA	H	270	8/8	0.96	0.05	16,20,23,24	0
2	GOL	B	270	6/6	0.96	0.06	20,21,23,23	0
3	URA	I	259	8/8	0.97	0.04	15,17,18,22	0
5	SO4	G	270	5/5	0.97	0.07	19,19,24,32	0
3	URA	K	272	8/8	0.98	0.05	11,15,21,23	0
4	CL	E	270	1/1	0.99	0.14	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.