



# wwPDB X-ray Structure Validation Summary Report (i)

Feb 28, 2014 – 09:47 AM GMT

PDB ID : 2J4L  
Title : CRYSTAL STRUCTURE OF URIDYLATE KINASE FROM SULFOLOBUS  
SOLFATARICUS IN COMPLEX WITH UTP TO 2.8 ANGSTROM RESO-  
LUTION  
Authors : Jensen, K.S.; Johansson, E.; Jensen, K.F.  
Deposited on : 2006-09-01  
Resolution : 2.80 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

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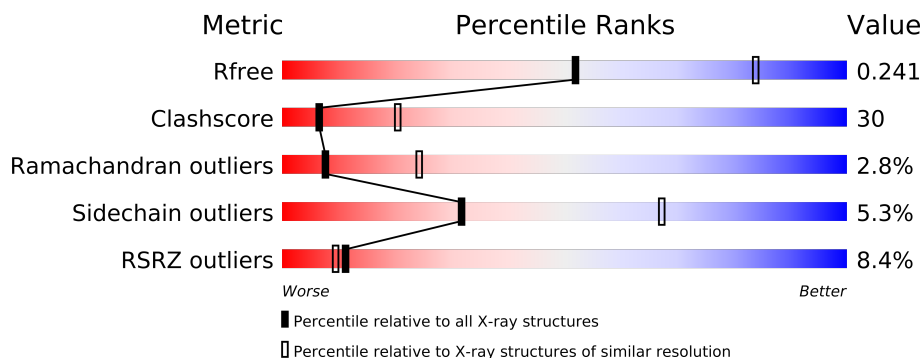
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.80 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))
$R_{free}$	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	226	
1	B	226	
1	C	226	
1	D	226	
1	E	226	
1	F	226	
1	G	226	
1	H	226	
1	I	226	
1	J	226	
1	K	226	
1	L	226	

## 2 Entry composition

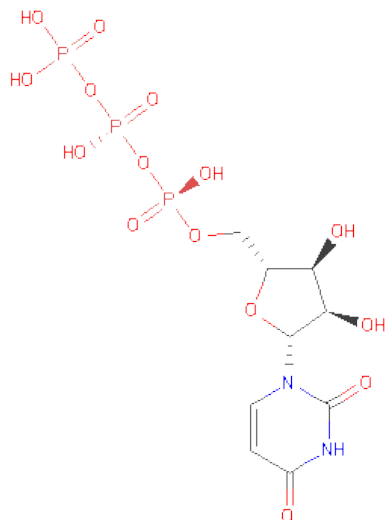
There are 3 unique types of molecules in this entry. The entry contains 19613 atoms, of which 0 are hydrogen and 0 are deuterium.

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 URIDYLATE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1674	1074	286	310	4			
1	B	213	Total	C	N	O	S	0	0	0
			1665	1069	285	307	4			
1	C	198	Total	C	N	O	S	0	0	0
			1539	991	260	284	4			
1	D	213	Total	C	N	O	S	0	0	0
			1665	1069	285	307	4			
1	E	217	Total	C	N	O	S	0	0	0
			1688	1082	287	315	4			
1	F	219	Total	C	N	O	S	0	0	0
			1714	1100	291	319	4			
1	G	212	Total	C	N	O	S	0	0	0
			1662	1070	283	305	4			
1	H	171	Total	C	N	O	S	0	0	0
			1317	850	222	241	4			
1	I	194	Total	C	N	O	S	0	0	0
			1507	970	256	277	4			
1	J	214	Total	C	N	O	S	0	0	0
			1673	1075	286	308	4			
1	K	190	Total	C	N	O	S	0	0	0
			1481	950	254	273	4			
1	L	214	Total	C	N	O	S	0	0	0
			1673	1075	286	308	4			

- Molecule 2 is URIDINE 5'-TRIPHOSPHATE (three-letter code: UTP) (formula: C<sub>9</sub>H<sub>15</sub>N<sub>2</sub>O<sub>15</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	B	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	C	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	D	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	E	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	F	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	G	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	H	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	I	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	J	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	K	1	Total	C	N	O	P	0	0
			29	9	2	15	3		
2	L	1	Total	C	N	O	P	0	0
			29	9	2	15	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

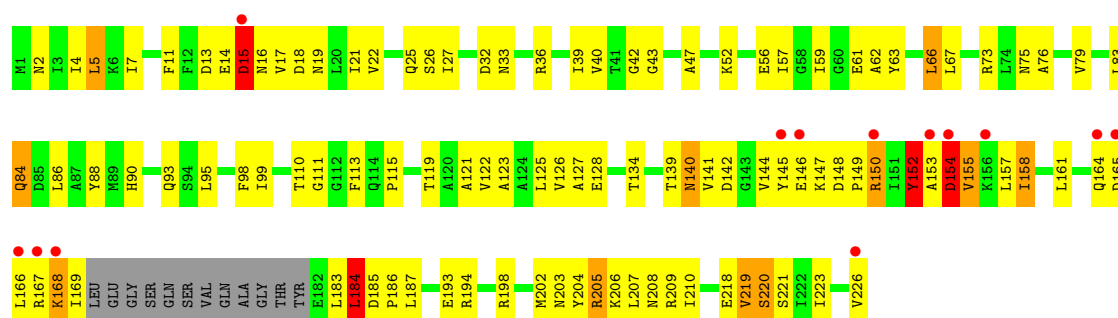
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	1	Total 1	Mg 1	0	0
3	D	1	Total 1	Mg 1	0	0
3	E	1	Total 1	Mg 1	0	0
3	B	1	Total 1	Mg 1	0	0
3	I	1	Total 1	Mg 1	0	0
3	C	1	Total 1	Mg 1	0	0
3	L	1	Total 1	Mg 1	0	0

### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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.

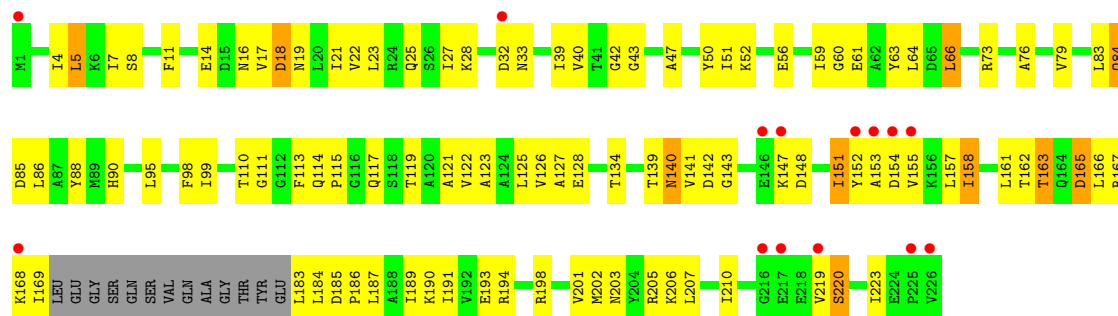
#### • Molecule 1: URIDYLATE KINASE

Chain A: 



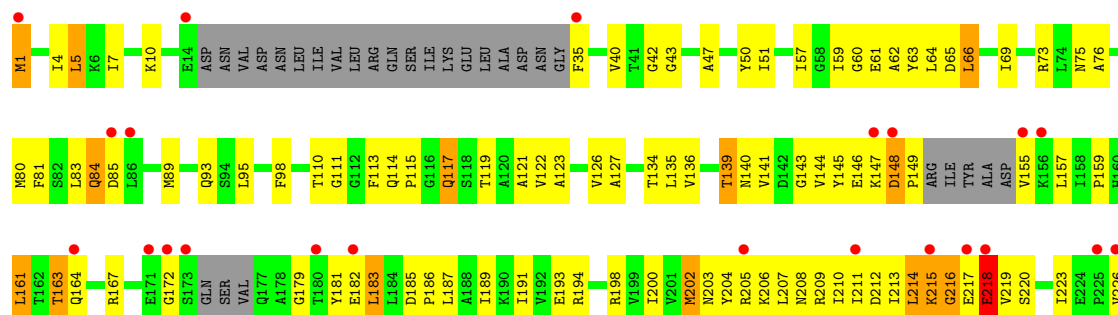
#### • Molecule 1: URIDYLATE KINASE

Chain B: 

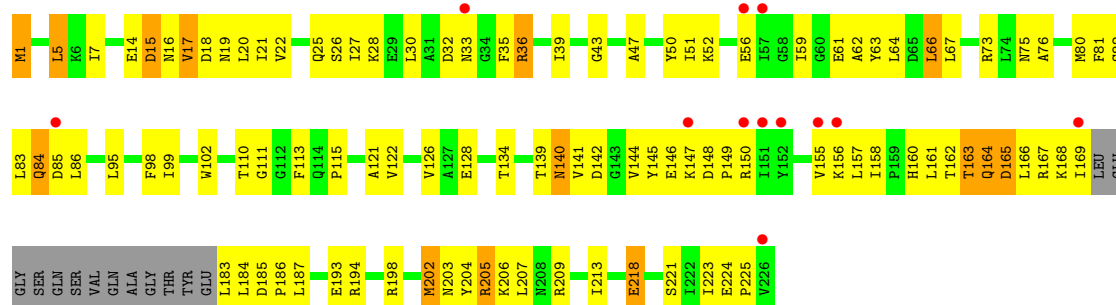


#### • Molecule 1: URIDYLATE KINASE

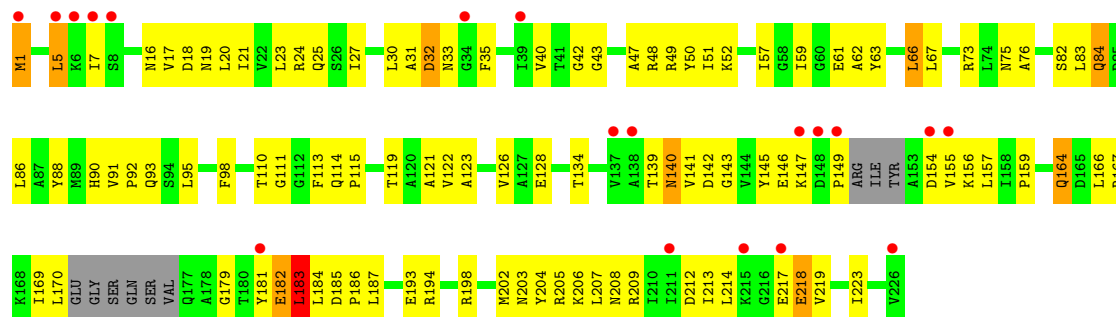
Chain C: 



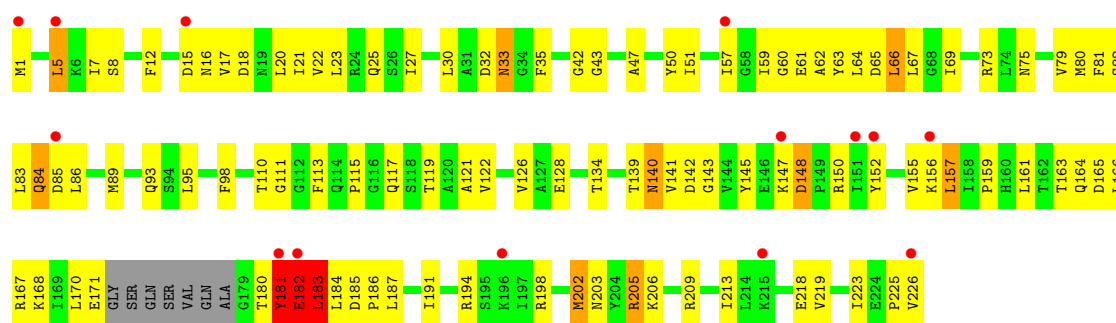
- Molecule 1: URIDYLATE KINASE

Chain D: 

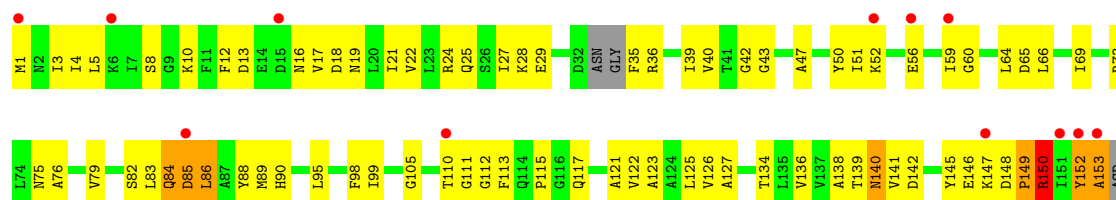
- Molecule 1: URIDYLATE KINASE

Chain E: 

- Molecule 1: URIDYLATE KINASE

Chain F: 

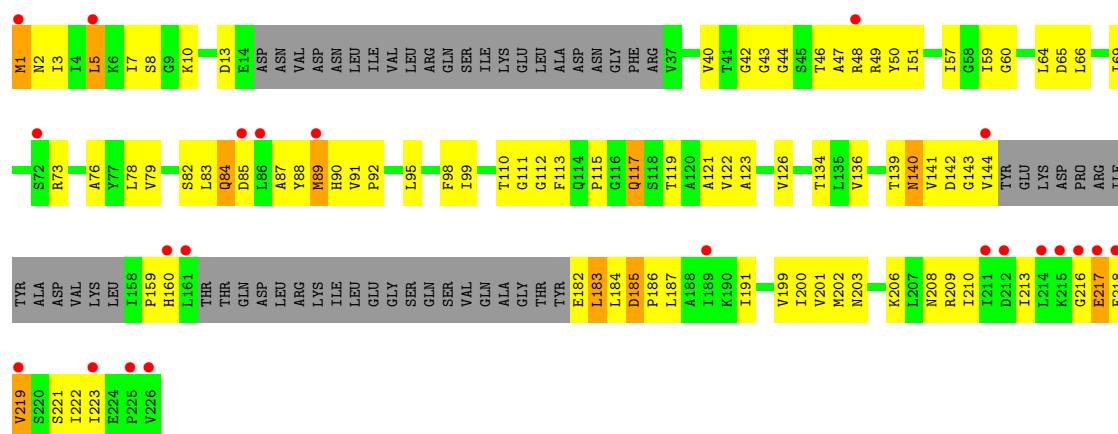
- Molecule 1: URIDYLATE KINASE

Chain G: 



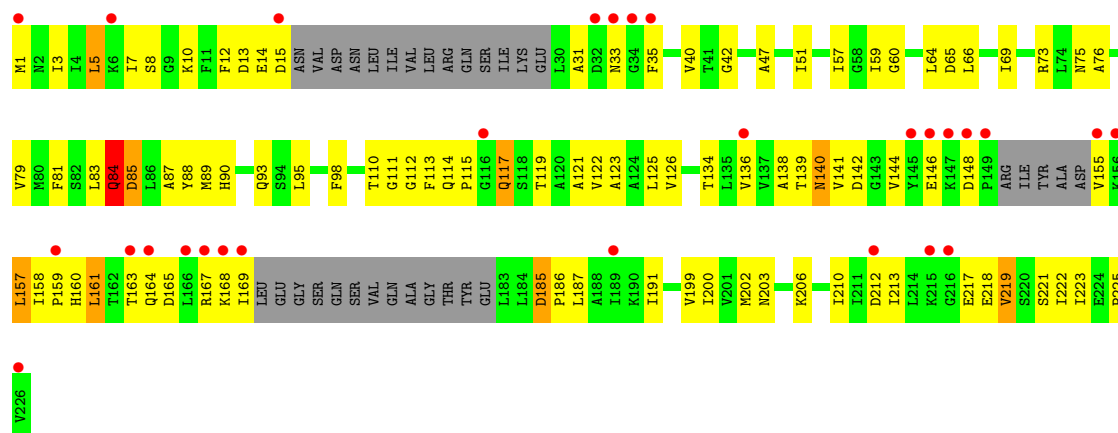
• Molecule 1: URIDYLATE KINASE

Chain H:



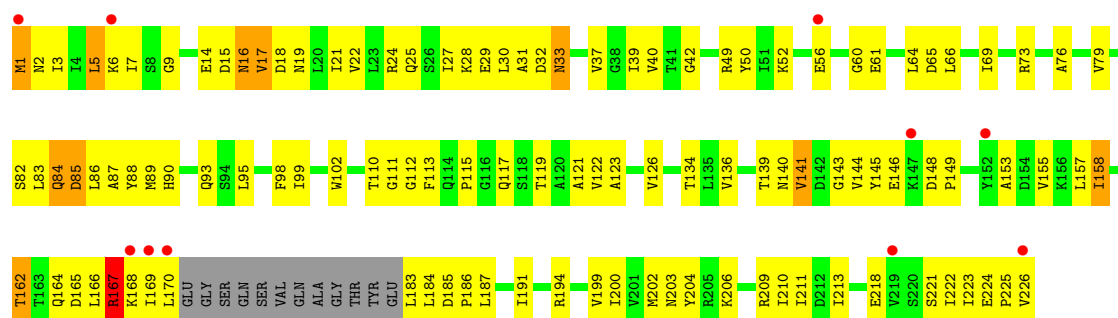
• Molecule 1: URIDYLATE KINASE

Chain I:



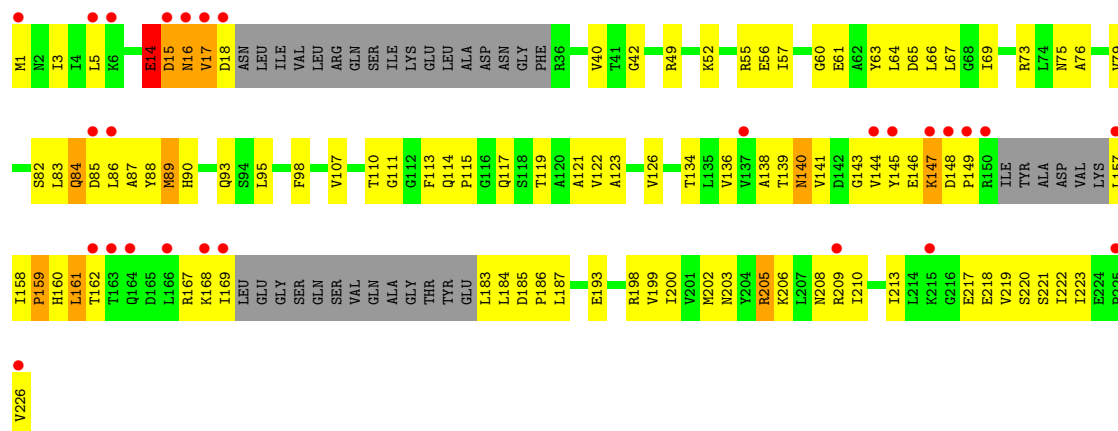
• Molecule 1: URIDYLATE KINASE

Chain J:

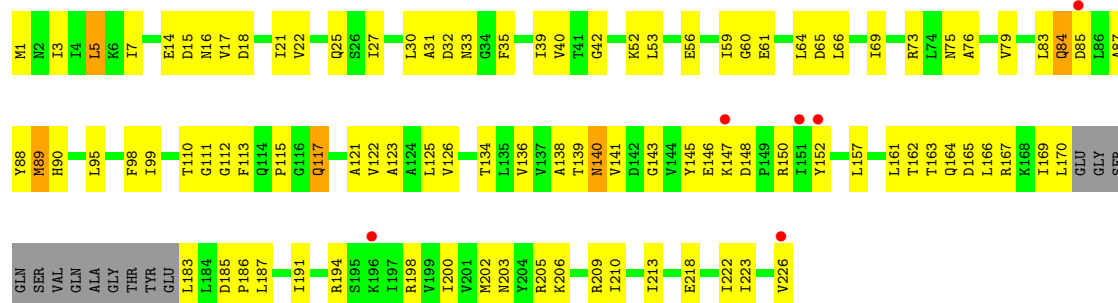


• Molecule 1: URIDYLATE KINASE



Chain K: 

● Molecule 1: URIDYLATE KINASE

Chain L: 

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	224.75Å 79.03Å 223.47Å 90.00° 96.56° 90.00°	Depositor
Resolution (Å)	29.63 – 2.80 29.63 – 2.78	Depositor EDS
% Data completeness (in resolution range)	94.6 (29.63-2.80) 93.3 (29.63-2.78)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 2.76Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.246 , 0.278 0.247 , 0.241	Depositor DCC
$R_{free}$ test set	4602 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.1	Xtriage
Anisotropy	0.498	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 92099 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	19613	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.49	0/1698	0.74	1/2296 (0.0%)
1	B	0.45	0/1689	0.69	0/2284
1	C	0.52	0/1561	0.83	6/2107 (0.3%)
1	D	0.43	0/1689	0.73	1/2284 (0.0%)
1	E	0.43	0/1711	0.70	2/2313 (0.1%)
1	F	0.50	0/1739	0.81	4/2352 (0.2%)
1	G	0.48	2/1684 (0.1%)	1.01	10/2274 (0.4%)
1	H	0.36	0/1335	0.65	1/1803 (0.1%)
1	I	0.36	0/1528	0.65	0/2063
1	J	0.39	0/1697	0.68	0/2295
1	K	0.42	0/1501	0.75	5/2027 (0.2%)
1	L	0.43	0/1697	0.68	0/2295
All	All	0.44	2/19529 (0.0%)	0.75	30/26393 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	153	ALA	C-O	-8.10	1.07	1.23
1	G	152	TYR	C-N	-5.19	1.22	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	150	ARG	O-C-N	-18.52	93.06	122.70
1	F	183	LEU	N-CA-C	-13.30	75.09	111.00
1	G	152	TYR	C-N-CA	-12.80	89.70	121.70
1	C	217	GLU	N-CA-C	-12.36	77.62	111.00
1	G	153	ALA	CA-C-O	-12.19	94.50	120.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	150	ARG	Mainchain
1	G	152	TYR	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1674	0	1742	112	0
1	B	1665	0	1736	99	0
1	C	1539	0	1599	102	0
1	D	1665	0	1736	101	0
1	E	1688	0	1751	117	0
1	F	1714	0	1778	122	0
1	G	1662	0	1738	107	0
1	H	1317	0	1374	95	0
1	I	1507	0	1569	94	0
1	J	1673	0	1747	121	0
1	K	1481	0	1541	99	0
1	L	1673	0	1747	120	0
2	A	29	0	11	0	0
2	B	29	0	11	1	0
2	C	29	0	11	2	0
2	D	29	0	11	0	0
2	E	29	0	11	2	0
2	F	29	0	11	5	0
2	G	29	0	11	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	29	0	11	2	0
2	I	29	0	11	2	0
2	J	29	0	11	3	0
2	K	29	0	11	0	0
2	L	29	0	11	1	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	L	1	0	0	0	0
All	All	19613	0	20190	1177	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 30.

The worst 5 of 1177 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:212:ASP:O	1:C:216:GLY:N	1.83	1.12
1:B:14:GLU:HB3	1:B:16:ASN:HD22	1.05	1.10
1:D:156:LYS:HG3	1:D:157:LEU:H	1.16	1.05
1:D:145:TYR:HD1	1:D:156:LYS:O	1.43	1.02
1:I:212:ASP:HB3	1:I:217:GLU:HB2	1.42	1.00

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	210/226 (93%)	190 (90%)	11 (5%)	9 (4%)	4 13
1	B	209/226 (92%)	198 (95%)	7 (3%)	4 (2%)	12 37
1	C	190/226 (84%)	166 (87%)	20 (10%)	4 (2%)	11 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	209/226 (92%)	191 (91%)	12 (6%)	6 (3%)	7	23
1	E	211/226 (93%)	187 (89%)	21 (10%)	3 (1%)	16	49
1	F	215/226 (95%)	192 (89%)	17 (8%)	6 (3%)	8	24
1	G	204/226 (90%)	182 (89%)	18 (9%)	4 (2%)	11	35
1	H	163/226 (72%)	147 (90%)	10 (6%)	6 (4%)	5	16
1	I	186/226 (82%)	169 (91%)	11 (6%)	6 (3%)	6	20
1	J	210/226 (93%)	187 (89%)	17 (8%)	6 (3%)	7	23
1	K	182/226 (80%)	159 (87%)	13 (7%)	10 (6%)	3	8
1	L	210/226 (93%)	194 (92%)	13 (6%)	3 (1%)	16	49
All	All	2399/2712 (88%)	2162 (90%)	170 (7%)	67 (3%)	8	24

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	84	GLN
1	G	218	GLU
1	H	183	LEU
1	I	84	GLN
1	J	84	GLN

### 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	183/192 (95%)	169 (92%)	14 (8%)	18	45
1	B	182/192 (95%)	171 (94%)	11 (6%)	27	61
1	C	167/192 (87%)	158 (95%)	9 (5%)	31	66
1	D	182/192 (95%)	172 (94%)	10 (6%)	30	65
1	E	184/192 (96%)	175 (95%)	9 (5%)	35	71
1	F	187/192 (97%)	176 (94%)	11 (6%)	28	62
1	G	182/192 (95%)	170 (93%)	12 (7%)	24	56
1	H	143/192 (74%)	138 (96%)	5 (4%)	48	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	164/192 (85%)	156 (95%)	8 (5%)	35	71
1	J	183/192 (95%)	171 (93%)	12 (7%)	24	56
1	K	162/192 (84%)	158 (98%)	4 (2%)	60	90
1	L	183/192 (95%)	177 (97%)	6 (3%)	50	85
All	All	2102/2304 (91%)	1991 (95%)	111 (5%)	32	67

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	164	GLN
1	F	202	MET
1	K	66	LEU
1	E	183	LEU
1	F	33	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	140	ASN
1	G	117	GLN
1	K	140	ASN
1	F	33	ASN
1	F	117	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 7 are monoatomic - leaving 12 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
2	UTP	A	1227	-	30,30,30	1.28	4 (13%)	43,47,47	1.19	5 (11%)
2	UTP	B	1227	3	30,30,30	1.20	2 (6%)	43,47,47	1.19	4 (9%)
2	UTP	C	1227	3	30,30,30	1.27	6 (20%)	43,47,47	1.08	3 (6%)
2	UTP	D	1227	3	30,30,30	1.26	2 (6%)	43,47,47	1.17	4 (9%)
2	UTP	E	1227	3	30,30,30	1.23	4 (13%)	43,47,47	1.02	2 (4%)
2	UTP	F	1227	-	30,30,30	1.29	3 (10%)	43,47,47	1.14	4 (9%)
2	UTP	G	1227	-	30,30,30	1.44	5 (16%)	43,47,47	1.05	3 (6%)
2	UTP	H	1227	-	30,30,30	1.53	4 (13%)	43,47,47	1.06	3 (6%)
2	UTP	I	1227	-	30,30,30	1.20	2 (6%)	43,47,47	1.12	3 (6%)
2	UTP	J	1227	3	30,30,30	1.64	5 (16%)	43,47,47	1.26	3 (6%)
2	UTP	K	1227	-	30,30,30	1.30	3 (10%)	43,47,47	1.13	2 (4%)
2	UTP	L	1227	3	30,30,30	1.16	3 (10%)	43,47,47	1.15	3 (6%)

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	UTP	A	1227	-	-	0/20/38/38	0/2/2/2
2	UTP	B	1227	3	-	0/20/38/38	0/2/2/2
2	UTP	C	1227	3	-	0/20/38/38	0/2/2/2
2	UTP	D	1227	3	-	0/20/38/38	0/2/2/2
2	UTP	E	1227	3	-	0/20/38/38	0/2/2/2
2	UTP	F	1227	-	-	0/20/38/38	0/2/2/2
2	UTP	G	1227	-	-	0/20/38/38	0/2/2/2
2	UTP	H	1227	-	-	0/20/38/38	0/2/2/2
2	UTP	I	1227	-	-	0/20/38/38	0/2/2/2
2	UTP	J	1227	3	-	0/20/38/38	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UTP	K	1227	-	-	0/20/38/38	0/2/2/2
2	UTP	L	1227	3	-	0/20/38/38	0/2/2/2

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	1227	UTP	C2-N1	5.78	1.44	1.38
2	H	1227	UTP	C2-N1	5.26	1.44	1.38
2	G	1227	UTP	C2-N1	4.63	1.43	1.38
2	K	1227	UTP	C2-N1	3.73	1.42	1.38
2	I	1227	UTP	C2-N1	3.57	1.42	1.38

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	1227	UTP	C3'-C2'-C1'	4.12	107.36	100.91
2	L	1227	UTP	C3'-C2'-C1'	3.86	106.94	100.91
2	C	1227	UTP	C3'-C2'-C1'	3.72	106.73	100.91
2	A	1227	UTP	C3'-C2'-C1'	3.56	106.48	100.91
2	I	1227	UTP	C3'-C2'-C1'	3.48	106.35	100.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	214/226 (94%)	0.22	13 (6%) 21 20	39, 59, 107, 116	0
1	B	213/226 (94%)	0.15	14 (6%) 18 16	42, 62, 92, 101	0
1	C	198/226 (87%)	0.43	22 (11%) 6 5	40, 65, 110, 121	0
1	D	213/226 (94%)	0.14	12 (5%) 24 23	44, 67, 96, 109	0
1	E	217/226 (96%)	0.33	19 (8%) 10 8	37, 65, 105, 114	0
1	F	219/226 (96%)	0.21	14 (6%) 19 17	41, 64, 92, 115	0
1	G	212/226 (93%)	0.45	21 (9%) 8 6	61, 83, 104, 120	0
1	H	171/226 (75%)	0.64	22 (12%) 4 3	64, 88, 131, 140	0
1	I	194/226 (85%)	0.54	28 (14%) 3 3	57, 85, 133, 153	0
1	J	214/226 (94%)	0.15	10 (4%) 30 30	53, 73, 101, 124	0
1	K	190/226 (84%)	0.58	27 (14%) 3 3	51, 86, 134, 145	0
1	L	214/226 (94%)	0.11	6 (2%) 50 52	47, 67, 89, 103	0
All	All	2469/2712 (91%)	0.32	208 (8%) 11 9	37, 72, 116, 153	0

The worst 5 of 208 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	226	VAL	13.5
1	B	226	VAL	6.8
1	I	147	LYS	6.6
1	I	33	ASN	6.6
1	H	216	GLY	6.4

### 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 ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	UTP	K	1227	29/29	0.23	0.57	83,92,131,132	0
2	UTP	B	1227	29/29	0.19	0.47	56,69,111,112	0
3	MG	C	1228	1/1	0.24	0.30	66,66,66,66	0
2	UTP	D	1227	29/29	0.17	0.01	56,69,114,115	0
2	UTP	L	1227	29/29	0.18	-0.02	71,77,110,111	0
2	UTP	J	1227	29/29	0.19	-0.02	63,72,109,110	0
2	UTP	H	1227	29/29	0.21	-0.05	78,92,128,129	0
2	UTP	E	1227	29/29	0.21	-0.20	53,62,97,98	0
3	MG	E	1228	1/1	0.21	-0.35	73,73,73,73	0
2	UTP	F	1227	29/29	0.17	-0.46	64,67,105,105	0
2	UTP	A	1227	29/29	0.15	-0.46	64,73,109,110	0
2	UTP	C	1227	29/29	0.18	-0.46	45,58,101,102	0
2	UTP	G	1227	29/29	0.16	-0.56	71,85,119,119	0
2	UTP	I	1227	29/29	0.16	-0.60	62,78,122,122	0
3	MG	J	1228	1/1	0.09	-	64,64,64,64	0
3	MG	D	1228	1/1	0.20	-	56,56,56,56	0
3	MG	B	1228	1/1	0.14	-	55,55,55,55	0
3	MG	I	1228	1/1	0.39	-	78,78,78,78	0
3	MG	L	1228	1/1	0.16	-	55,55,55,55	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.