



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:22 AM GMT

PDB ID : 2A2Z  
Title : Crystal Structure of human deoxycytidine kinase in complex with deoxycytidine and uridine diphosphate  
Authors : Godsey, M.H.; Ort, S.; Sabini, E.; Konrad, M.; Lavie, A.  
Deposited on : 2005-06-23  
Resolution : 3.02 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](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

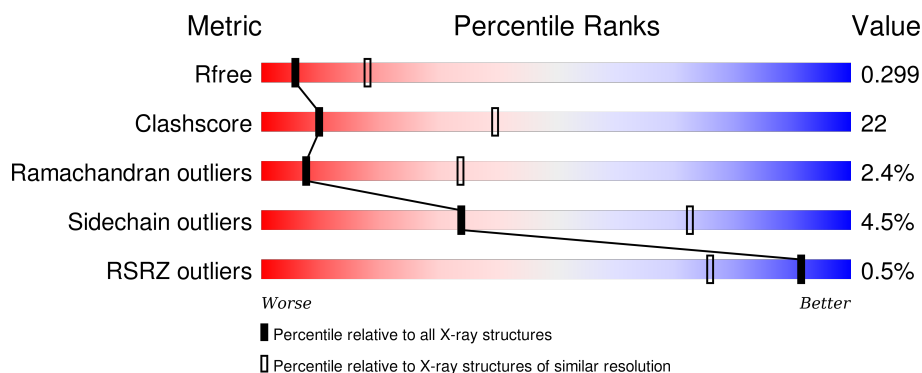
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.02 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	1773 (3.04-3.00)
Clashscore	102246	2117 (3.04-3.00)
Ramachandran outliers	100387	2050 (3.04-3.00)
Sidechain outliers	100360	2053 (3.04-3.00)
RSRZ outliers	91569	1788 (3.04-3.00)

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	248	
1	B	248	
1	C	248	
1	D	248	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7406 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 Deoxycytidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1796	1156	299	332	9			
1	B	221	Total	C	N	O	S	0	0	0
			1795	1156	295	335	9			
1	C	222	Total	C	N	O	S	0	0	0
			1800	1158	299	334	9			
1	D	220	Total	C	N	O	S	0	0	0
			1778	1148	293	328	9			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	CLONING ARTIFACT	UNP P27707
A	-1	SER	-	CLONING ARTIFACT	UNP P27707
A	0	HIS	-	CLONING ARTIFACT	UNP P27707
A	?	-	GLN	DELETION	UNP P27707
A	?	-	ASP	DELETION	UNP P27707
A	?	-	GLU	DELETION	UNP P27707
A	?	-	PHE	DELETION	UNP P27707
A	?	-	GLU	DELETION	UNP P27707
A	?	-	GLU	DELETION	UNP P27707
A	?	-	LEU	DELETION	UNP P27707
A	?	-	THR	DELETION	UNP P27707
A	?	-	MET	DELETION	UNP P27707
A	?	-	SER	DELETION	UNP P27707
A	?	-	GLN	DELETION	UNP P27707
A	?	-	LYS	DELETION	UNP P27707
A	?	-	ASN	DELETION	UNP P27707
A	?	-	GLY	DELETION	UNP P27707
A	?	-	GLY	DELETION	UNP P27707
B	-2	GLY	-	CLONING ARTIFACT	UNP P27707
B	-1	SER	-	CLONING ARTIFACT	UNP P27707
B	0	HIS	-	CLONING ARTIFACT	UNP P27707

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLN	DELETION	UNP P27707
B	?	-	ASP	DELETION	UNP P27707
B	?	-	GLU	DELETION	UNP P27707
B	?	-	PHE	DELETION	UNP P27707
B	?	-	GLU	DELETION	UNP P27707
B	?	-	GLU	DELETION	UNP P27707
B	?	-	LEU	DELETION	UNP P27707
B	?	-	THR	DELETION	UNP P27707
B	?	-	MET	DELETION	UNP P27707
B	?	-	SER	DELETION	UNP P27707
B	?	-	GLN	DELETION	UNP P27707
B	?	-	LYS	DELETION	UNP P27707
B	?	-	ASN	DELETION	UNP P27707
B	?	-	GLY	DELETION	UNP P27707
B	?	-	GLY	DELETION	UNP P27707
C	-2	GLY	-	CLONING ARTIFACT	UNP P27707
C	-1	SER	-	CLONING ARTIFACT	UNP P27707
C	0	HIS	-	CLONING ARTIFACT	UNP P27707
C	?	-	GLN	DELETION	UNP P27707
C	?	-	ASP	DELETION	UNP P27707
C	?	-	GLU	DELETION	UNP P27707
C	?	-	PHE	DELETION	UNP P27707
C	?	-	GLU	DELETION	UNP P27707
C	?	-	GLU	DELETION	UNP P27707
C	?	-	LEU	DELETION	UNP P27707
C	?	-	THR	DELETION	UNP P27707
C	?	-	MET	DELETION	UNP P27707
C	?	-	SER	DELETION	UNP P27707
C	?	-	GLN	DELETION	UNP P27707
C	?	-	LYS	DELETION	UNP P27707
C	?	-	ASN	DELETION	UNP P27707
C	?	-	GLY	DELETION	UNP P27707
C	?	-	GLY	DELETION	UNP P27707
D	-2	GLY	-	CLONING ARTIFACT	UNP P27707
D	-1	SER	-	CLONING ARTIFACT	UNP P27707
D	0	HIS	-	CLONING ARTIFACT	UNP P27707
D	?	-	GLN	DELETION	UNP P27707
D	?	-	ASP	DELETION	UNP P27707
D	?	-	GLU	DELETION	UNP P27707
D	?	-	PHE	DELETION	UNP P27707
D	?	-	GLU	DELETION	UNP P27707
D	?	-	GLU	DELETION	UNP P27707

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	LEU	DELETION	UNP P27707
D	?	-	THR	DELETION	UNP P27707
D	?	-	MET	DELETION	UNP P27707
D	?	-	SER	DELETION	UNP P27707
D	?	-	GLN	DELETION	UNP P27707
D	?	-	LYS	DELETION	UNP P27707
D	?	-	ASN	DELETION	UNP P27707
D	?	-	GLY	DELETION	UNP P27707
D	?	-	GLY	DELETION	UNP P27707

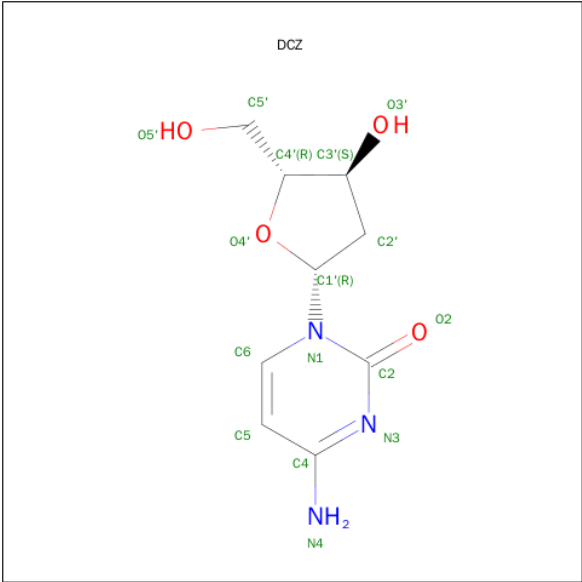
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

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

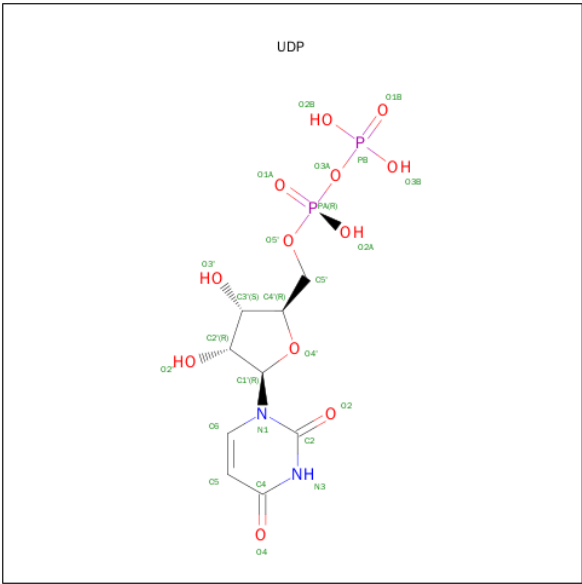
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is 2'-DEOXYCYTIDINE (three-letter code: DCZ) (formula: C<sub>9</sub>H<sub>13</sub>N<sub>3</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			16	9	3	4		
4	B	1	Total	C	N	O	0	0
			16	9	3	4		
4	C	1	Total	C	N	O	0	0
			16	9	3	4		
4	D	1	Total	C	N	O	0	0
			16	9	3	4		

- Molecule 5 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C<sub>9</sub>H<sub>14</sub>N<sub>2</sub>O<sub>12</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
5	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
5	C	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
5	D	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

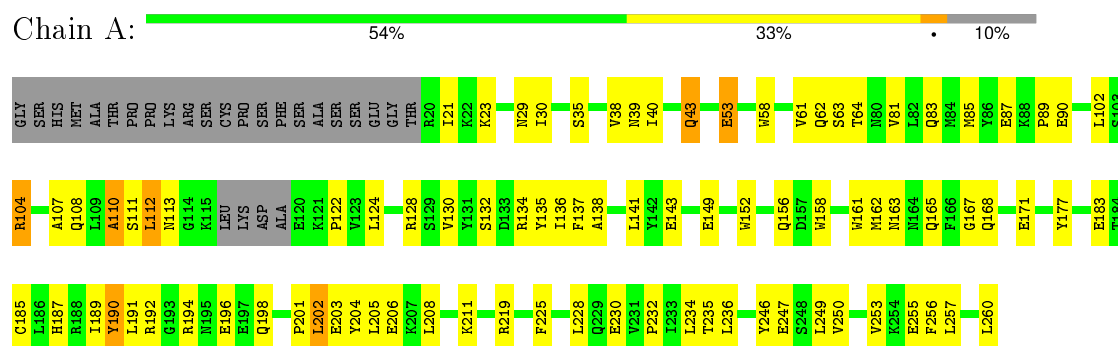
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	23	Total	O	0	0
			23	23		
6	B	15	Total	O	0	0
			15	15		
6	C	22	Total	O	0	0
			22	22		
6	D	7	Total	O	0	0
			7	7		

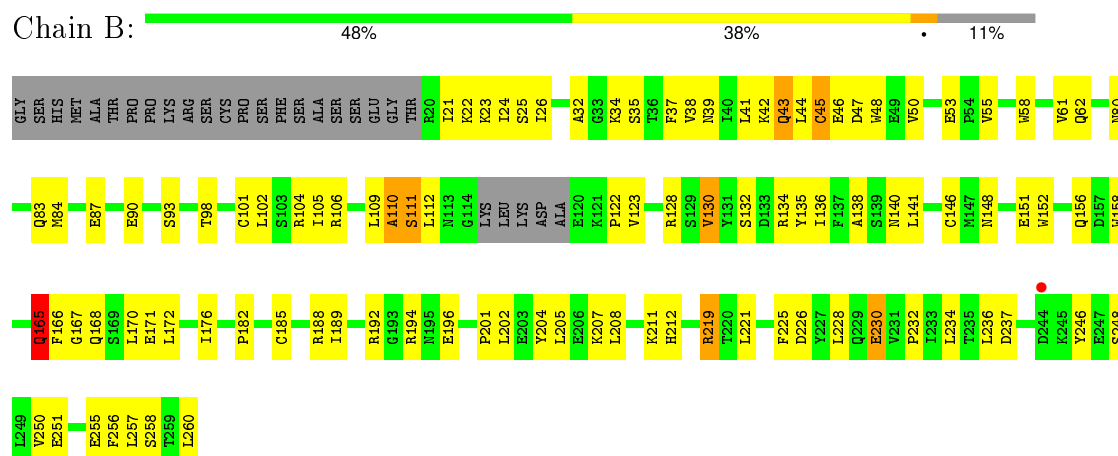
### 3 Residue-property plots

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.

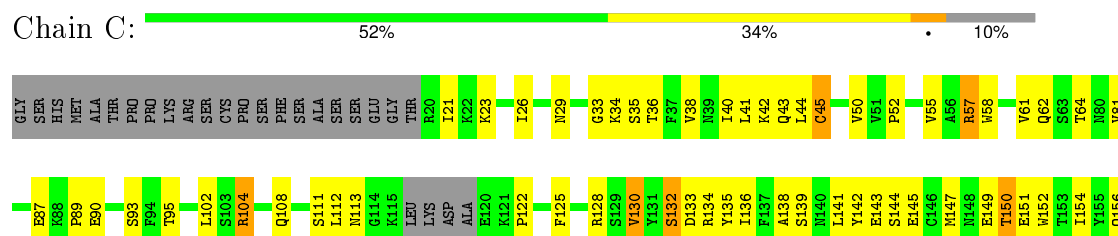
#### • Molecule 1: Deoxycytidine kinase



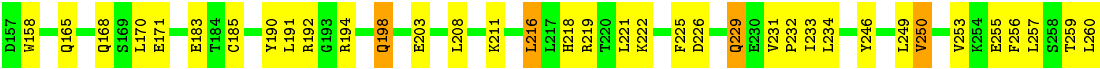
#### • Molecule 1: Deoxycytidine kinase



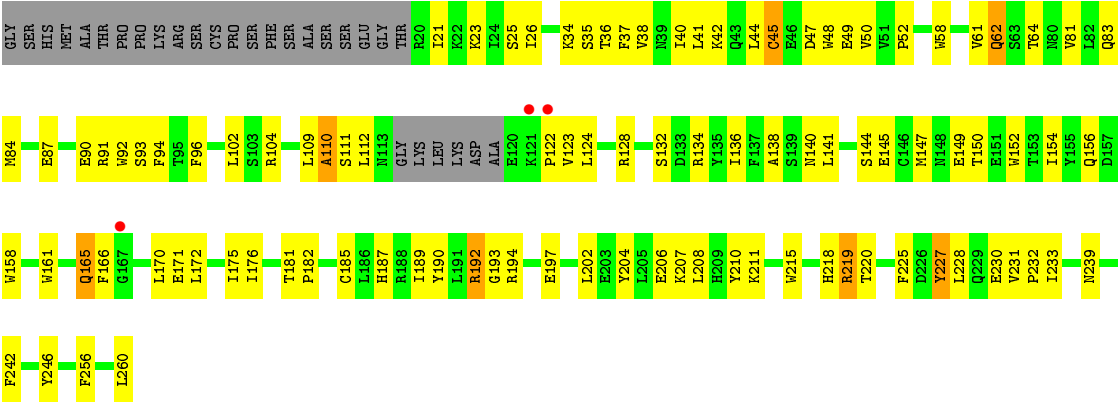
#### • Molecule 1: Deoxycytidine kinase







● Molecule 1: Deoxycytidine kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.18Å 110.85Å 155.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.66 – 3.02 29.66 – 3.02	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.66-3.02) 99.4 (29.66-3.02)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.246 , 0.300 0.248 , 0.299	Depositor DCC
$R_{free}$ test set	2244 reflections (10.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.5	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 60.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	3 of 22297 reflections (0.013%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7406	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	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 53.89 % 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 3.9513e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.47	0/1841	0.64	0/2505
1	B	0.46	1/1840 (0.1%)	0.62	0/2502
1	C	0.46	0/1845	0.63	0/2510
1	D	0.44	0/1823	0.61	0/2481
All	All	0.46	1/7349 (0.0%)	0.62	0/9998

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	146	CYS	CB-SG	-5.03	1.73	1.81

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1796	0	1694	70	0
1	B	1795	0	1699	88	0
1	C	1800	0	1698	82	0
1	D	1778	0	1679	83	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	16	0	13	0	0
4	B	16	0	13	0	0
4	C	16	0	13	0	0
4	D	16	0	13	0	0
5	A	25	0	11	0	0
5	B	25	0	11	2	0
5	C	25	0	11	3	0
5	D	25	0	11	0	0
6	A	23	0	0	4	0
6	B	15	0	0	1	0
6	C	22	0	0	2	0
6	D	7	0	0	1	0
All	All	7406	0	6866	315	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 22.

The worst 5 of 315 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:C:257:LEU:HA	1:C:260:LEU:HD12	1.48	0.92
1:C:246:TYR:O	1:C:250:VAL:HG23	1.73	0.88
1:A:21:ILE:HG23	1:A:122:PRO:HB2	1.58	0.86
1:D:150:THR:O	1:D:154:ILE:HG13	1.78	0.84
1:A:234:LEU:HG	1:A:236:LEU:HD21	1.60	0.83

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	218/248 (88%)	187 (86%)	27 (12%)	4 (2%)	11	43
1	B	217/248 (88%)	183 (84%)	27 (12%)	7 (3%)	5	26
1	C	218/248 (88%)	192 (88%)	21 (10%)	5 (2%)	8	35
1	D	216/248 (87%)	192 (89%)	19 (9%)	5 (2%)	8	35
All	All	869/992 (88%)	754 (87%)	94 (11%)	21 (2%)	7	34

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	230	GLU
1	D	45	CYS
1	D	230	GLU
1	B	45	CYS
1	B	110	ALA

### 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	189/228 (83%)	180 (95%)	9 (5%)	31	70
1	B	191/228 (84%)	184 (96%)	7 (4%)	41	78
1	C	190/228 (83%)	176 (93%)	14 (7%)	17	50
1	D	187/228 (82%)	183 (98%)	4 (2%)	61	89
All	All	757/912 (83%)	723 (96%)	34 (4%)	34	73

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	226	ASP
1	C	104	ARG
1	D	192	ARG

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Mol	Chain	Res	Type
1	C	57	ARG
1	A	205	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	165	GLN
1	C	108	GLN
1	D	163	ASN
1	B	224	ASN
1	C	62	GLN

### 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](#)

Of 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 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	UDP	A	301	3	18,26,26	1.87	3 (16%)	26,40,40	2.66	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	DCZ	A	304	-	13,17,17	0.98	1 (7%)	18,24,24	1.24	2 (11%)
5	UDP	B	401	3	18,26,26	2.04	3 (16%)	26,40,40	2.75	3 (11%)
4	DCZ	B	404	-	13,17,17	1.20	2 (15%)	18,24,24	1.17	2 (11%)
5	UDP	C	501	3	18,26,26	2.07	3 (16%)	26,40,40	2.73	3 (11%)
4	DCZ	C	504	-	13,17,17	1.07	2 (15%)	18,24,24	1.10	2 (11%)
5	UDP	D	601	3	18,26,26	1.95	3 (16%)	26,40,40	2.78	4 (15%)
4	DCZ	D	604	-	13,17,17	1.31	2 (15%)	18,24,24	1.21	2 (11%)

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
5	UDP	A	301	3	-	0/12/32/32	0/2/2/2
4	DCZ	A	304	-	-	0/2/18/18	0/2/2/2
5	UDP	B	401	3	-	0/12/32/32	0/2/2/2
4	DCZ	B	404	-	-	0/2/18/18	0/2/2/2
5	UDP	C	501	3	-	0/12/32/32	0/2/2/2
4	DCZ	C	504	-	-	0/2/18/18	0/2/2/2
5	UDP	D	601	3	-	0/12/32/32	0/2/2/2
4	DCZ	D	604	-	-	0/2/18/18	0/2/2/2

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	604	DCZ	C6-C5	-2.93	1.31	1.38
4	B	404	DCZ	C5-C4	-2.89	1.34	1.40
4	D	604	DCZ	C5-C4	-2.83	1.34	1.40
4	C	504	DCZ	C5-C4	-2.67	1.34	1.40
4	A	304	DCZ	C5-C4	-2.39	1.35	1.40

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	601	UDP	PA-O3A-PB	-2.99	122.64	132.67
5	D	601	UDP	C5-C4-N3	-2.82	115.89	123.12
4	B	404	DCZ	C6-N1-C2	-2.68	116.94	121.28
5	A	301	UDP	C5-C4-N3	-2.65	116.33	123.12
4	A	304	DCZ	C6-N1-C2	-2.64	117.01	121.28

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	401	UDP	2	0
5	C	501	UDP	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, 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	222/248 (89%)	-0.44	0 <span>100</span> <span>100</span>	20, 41, 67, 78	0
1	B	221/248 (89%)	-0.29	1 (0%) <span>91</span> <span>76</span>	23, 44, 68, 77	0
1	C	222/248 (89%)	-0.44	0 <span>100</span> <span>100</span>	19, 40, 68, 80	0
1	D	220/248 (88%)	-0.28	3 (1%) <span>78</span> <span>51</span>	26, 48, 74, 85	0
All	All	885/992 (89%)	-0.36	4 (0%) <span>91</span> <span>76</span>	19, 43, 71, 85	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	122	PRO	2.2
1	D	121	LYS	2.2
1	B	244	ASP	2.1
1	D	167	GLY	2.0

### 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	DCZ	C	504	16/16	0.96	0.22	0.59	22,24,26,29	0
4	DCZ	B	404	16/16	0.94	0.24	0.55	40,43,46,50	0
3	MG	B	402	1/1	0.89	0.27	0.30	39,39,39,39	0
5	UDP	C	501	25/25	0.94	0.19	-0.12	37,53,60,61	0
4	DCZ	D	604	16/16	0.96	0.19	-0.16	36,40,44,46	0
5	UDP	A	301	25/25	0.93	0.18	-0.43	33,52,59,62	0
4	DCZ	A	304	16/16	0.95	0.17	-0.49	13,16,21,21	0
3	MG	D	602	1/1	0.78	0.17	-0.59	35,35,35,35	0
5	UDP	D	601	25/25	0.93	0.15	-1.02	41,55,62,63	0
2	CA	A	261	1/1	0.92	0.11	-1.36	61,61,61,61	0
5	UDP	B	401	25/25	0.95	0.13	-1.66	34,43,48,51	0
3	MG	C	502	1/1	0.89	0.17	-	38,38,38,38	0
3	MG	A	302	1/1	0.90	0.19	-	46,46,46,46	0
2	CA	C	261	1/1	0.94	0.09	-	59,59,59,59	0

## 6.5 Other polymers

There are no such residues in this entry.