



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:36 PM GMT

PDB ID : 4TO4  
Title : Structure basis of cellular dNTP regulation, SAMHD1-GTP-dGTP-dCTP complex  
Authors : Ji, X.; Tang, C.; Zhao, Q.; Wang, W.; Xiong, Y.  
Deposited on : 2014-06-05  
Resolution : 2.10 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.

---

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

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

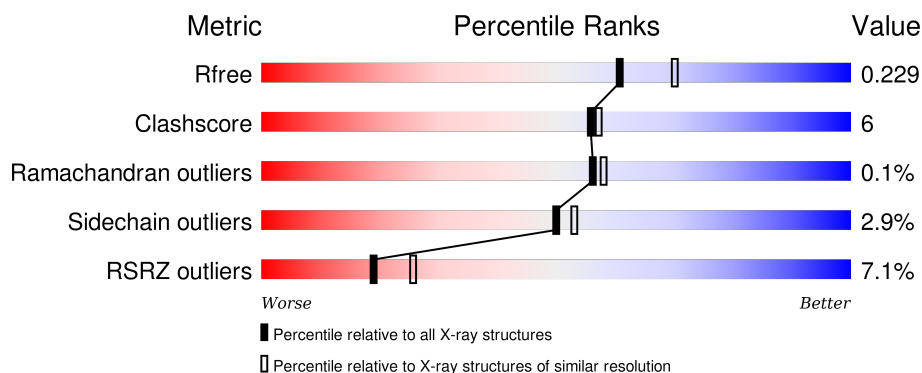
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	514	<div> <div>8%</div> <div>83% 10% • 6%</div> </div>
1	B	514	<div> <div>8%</div> <div>80% 12% • 6%</div> </div>
1	C	514	<div> <div>2%</div> <div>80% 12% • 6%</div> </div>
1	D	514	<div> <div>8%</div> <div>81% 12% • 6%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16513 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.

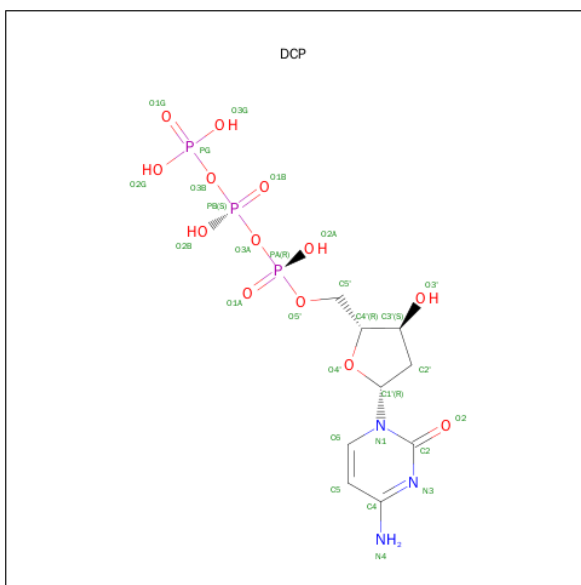
- Molecule 1 is a protein called Deoxynucleoside triphosphate triphosphohydrolase SAMHD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	S	0	0	0
			3933	2517	685	711	20			
1	B	481	Total	C	N	O	S	0	0	0
			3933	2517	685	711	20			
1	C	481	Total	C	N	O	S	0	2	0
			3945	2523	687	715	20			
1	D	484	Total	C	N	O	S	0	1	0
			3963	2536	691	716	20			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
A	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
B	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
B	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
C	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
C	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
D	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
D	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3

- Molecule 2 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C<sub>9</sub>H<sub>16</sub>N<sub>3</sub>O<sub>13</sub>P<sub>3</sub>).

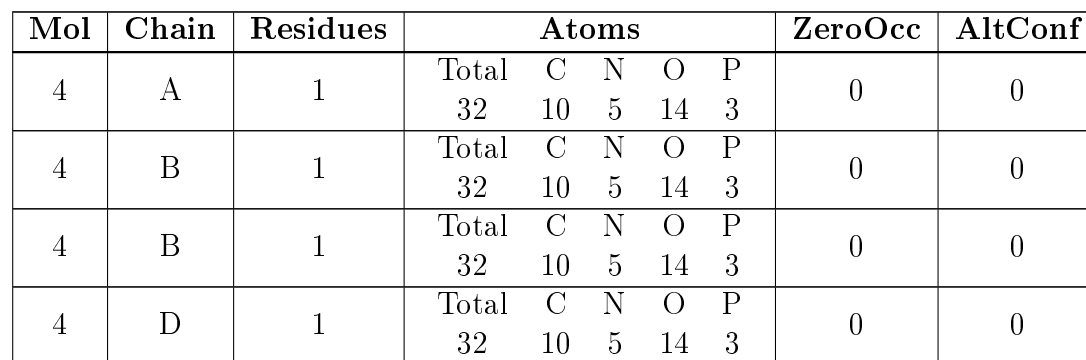


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	B	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	C	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	D	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mg	0	0
			2	2		
3	A	2	Total	Mg	0	0
			2	2		
3	D	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).



- [illegible]

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
5	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
5	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
5	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

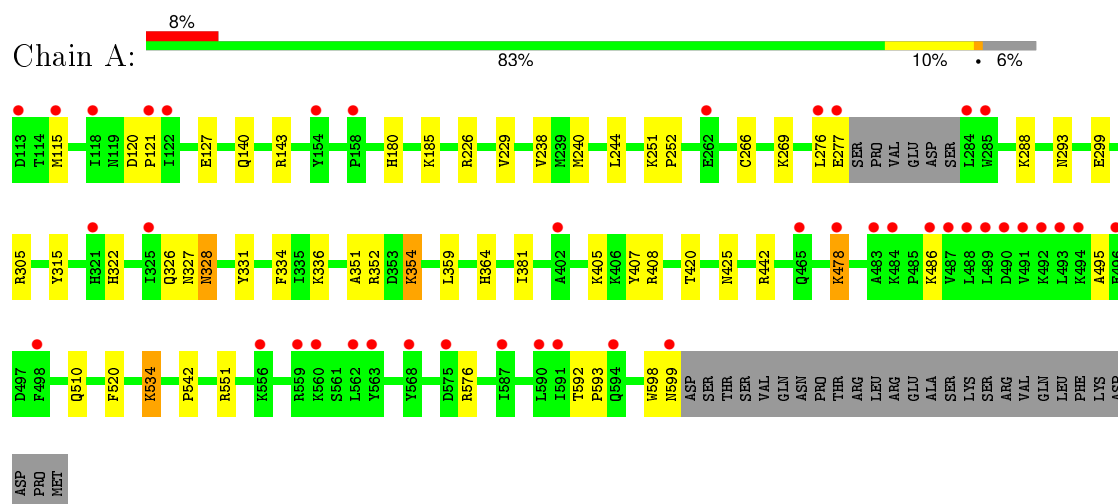
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	93	Total	O	0	0
			93	93		
6	B	86	Total	O	0	0
			86	86		
6	C	117	Total	O	0	0
			117	117		
6	D	71	Total	O	0	0
			71	71		

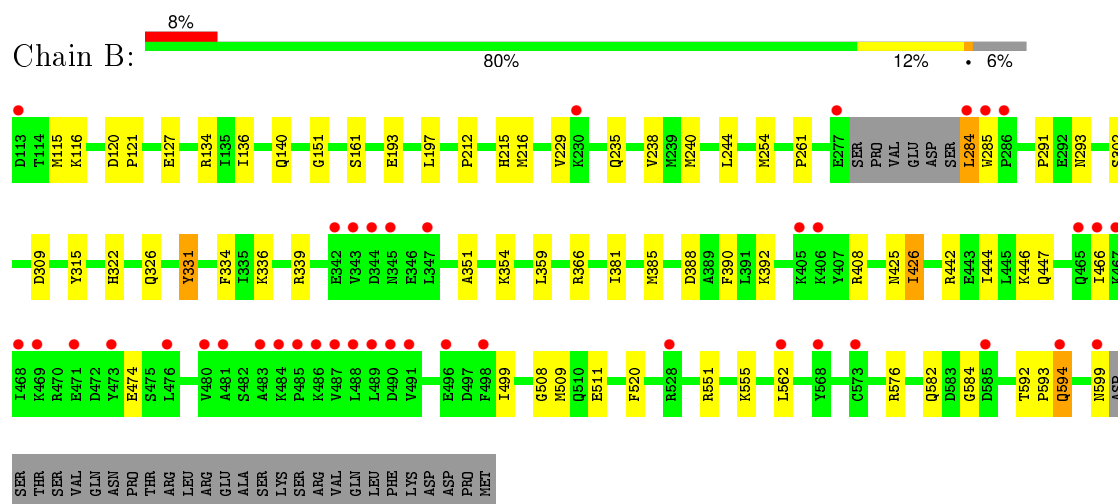
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

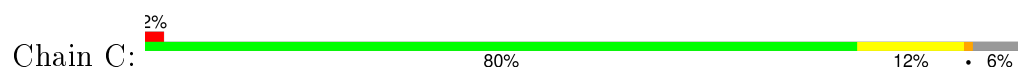
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

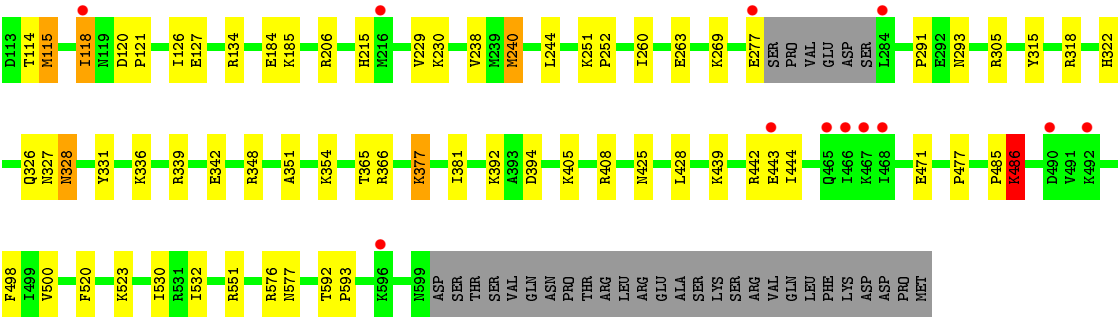


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

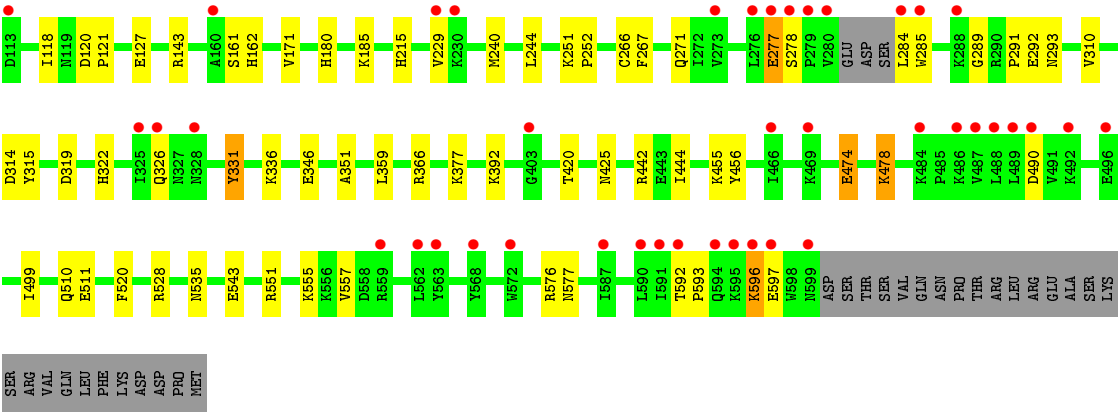
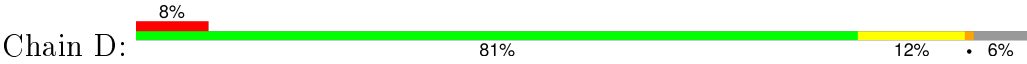


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1





● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.71Å 145.84Å 98.65Å 90.00° 114.75° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 47.06 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.1 (50.00-2.10) 99.1 (47.06-2.10)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.197 , 0.225 0.202 , 0.229	Depositor DCC
$R_{free}$ test set	6476 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.8	Xtriage
Anisotropy	0.579	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.3	EDS
Estimated twinning fraction	0.024 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 128443 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	16513	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

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

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	0.72	0/4025	0.81	6/5433 (0.1%)
1	B	0.70	1/4025 (0.0%)	0.80	7/5433 (0.1%)
1	C	0.77	2/4037 (0.0%)	0.83	7/5449 (0.1%)
1	D	0.69	1/4057 (0.0%)	0.77	6/5478 (0.1%)
All	All	0.72	4/16144 (0.0%)	0.80	26/21793 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	161	SER	CB-OG	5.83	1.49	1.42
1	D	161	SER	CB-OG	5.77	1.49	1.42
1	C	342	GLU	CD-OE2	5.39	1.31	1.25
1	C	318	ARG	CZ-NH1	5.09	1.39	1.33

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	442	ARG	NE-CZ-NH1	7.03	123.81	120.30
1	B	366	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	C	318	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	C	551	ARG	NE-CZ-NH1	-6.18	117.21	120.30
1	B	442	ARG	NE-CZ-NH1	6.01	123.30	120.30

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	3933	0	3921	43	0
1	B	3933	0	3921	53	0
1	C	3945	0	3929	60	0
1	D	3963	0	3948	49	0
2	A	28	0	12	0	0
2	B	28	0	12	2	0
2	C	28	0	12	2	0
2	D	28	0	12	2	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	32	0	12	1	0
4	B	64	0	24	1	0
4	D	32	0	12	0	0
5	A	31	0	12	1	0
5	B	31	0	12	2	0
5	C	31	0	12	0	0
5	D	31	0	12	0	0
6	A	93	0	0	12	0
6	B	86	0	0	22	0
6	C	117	0	0	31	0
6	D	71	0	0	25	0
All	All	16513	0	15863	199	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 6.

The worst 5 of 199 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:B:216:MET:HE2	6:B:853:HOH:O	1.44	1.16
1:D:331:TYR:HE2	6:D:831:HOH:O	1.38	1.05
1:C:240:MET:SD	6:C:838:HOH:O	2.16	1.01
4:A:703:GTP:O3'	6:A:893:HOH:O	1.77	1.01

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:266:CYS:HB3	6:D:860:HOH:O	1.60	1.01

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	477/514 (93%)	467 (98%)	10 (2%)	0	100	100
1	B	477/514 (93%)	468 (98%)	9 (2%)	0	100	100
1	C	479/514 (93%)	469 (98%)	9 (2%)	1 (0%)	52	53
1	D	481/514 (94%)	471 (98%)	10 (2%)	0	100	100
All	All	1914/2056 (93%)	1875 (98%)	38 (2%)	1 (0%)	56	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	486	LYS

### 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	427/459 (93%)	417 (98%)	10 (2%)	58	62

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	427/459 (93%)	414 (97%)	13 (3%)	48	51
1	C	429/459 (94%)	416 (97%)	13 (3%)	48	51
1	D	431/459 (94%)	417 (97%)	14 (3%)	46	48
All	All	1714/1836 (93%)	1664 (97%)	50 (3%)	50	53

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	594	GLN
1	C	229	VAL
1	D	490	ASP
1	C	115	MET
1	C	134	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	235	GLN
1	C	326	GLN
1	D	328	ASN
1	B	527	ASN
1	D	233	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 20 ligands modelled in this entry, 8 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	DCP	A	701	3	21,29,29	1.03	1 (4%)	33,45,45	1.59	7 (21%)
4	GTP	A	703	3	25,34,34	1.31	3 (12%)	34,54,54	1.94	8 (23%)
5	DGT	A	704	3	25,33,33	1.25	3 (12%)	35,52,52	1.88	9 (25%)
2	DCP	B	701	3	21,29,29	0.75	0	33,45,45	1.55	6 (18%)
4	GTP	B	703	3	25,34,34	1.38	3 (12%)	34,54,54	1.77	7 (20%)
4	GTP	B	705	3	25,34,34	1.35	4 (16%)	34,54,54	1.86	9 (26%)
5	DGT	B	706	3	25,33,33	1.41	2 (8%)	35,52,52	2.11	11 (31%)
5	DGT	C	701	3	25,33,33	1.37	3 (12%)	35,52,52	1.90	9 (25%)
2	DCP	C	703	3	21,29,29	1.00	0	33,45,45	1.82	6 (18%)
5	DGT	D	702	3	25,33,33	1.16	2 (8%)	35,52,52	1.83	11 (31%)
2	DCP	D	703	-	21,29,29	1.00	0	33,45,45	1.54	7 (21%)
4	GTP	D	705	3	25,34,34	1.79	5 (20%)	34,54,54	2.05	11 (32%)

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	DCP	A	701	3	-	0/18/34/34	0/2/2/2
4	GTP	A	703	3	-	0/18/38/38	0/3/3/3
5	DGT	A	704	3	-	0/18/34/34	0/3/3/3
2	DCP	B	701	3	-	0/18/34/34	0/2/2/2
4	GTP	B	703	3	-	0/18/38/38	0/3/3/3
4	GTP	B	705	3	-	0/18/38/38	0/3/3/3
5	DGT	B	706	3	-	0/18/34/34	0/3/3/3
5	DGT	C	701	3	-	0/18/34/34	0/3/3/3
2	DCP	C	703	3	-	0/18/34/34	0/2/2/2
5	DGT	D	702	3	-	0/18/34/34	0/3/3/3

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DCP	D	703	-	-	0/18/34/34	0/2/2/2
4	GTP	D	705	3	-	0/18/38/38	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	705	GTP	PA-O1A	-3.33	1.39	1.51
4	B	705	GTP	PA-O2A	-3.15	1.41	1.54
5	C	701	DGT	PG-O2G	-2.93	1.44	1.54
4	D	705	GTP	PG-O2G	-2.78	1.44	1.54
4	B	703	GTP	PG-O2G	-2.26	1.46	1.54

The worst 5 of 101 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	706	DGT	C6-C5-C4	-5.23	114.65	120.90
4	D	705	GTP	C5-C6-N1	-4.95	116.83	123.59
4	A	703	GTP	C5-C6-N1	-4.77	117.07	123.59
5	A	704	DGT	C5-C6-N1	-4.69	117.17	123.59
4	B	703	GTP	PA-O3A-PB	-4.62	119.75	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	703	GTP	1	0
5	A	704	DGT	1	0
2	B	701	DCP	2	0
4	B	705	GTP	1	0
5	B	706	DGT	2	0
2	C	703	DCP	2	0
2	D	703	DCP	2	0

## 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 [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	481/514 (93%)	0.37	42 (8%) 13 17	25, 48, 81, 111	0
1	B	481/514 (93%)	0.43	41 (8%) 13 18	26, 52, 87, 123	0
1	C	481/514 (93%)	0.10	12 (2%) 61 67	22, 41, 71, 99	1 (0%)
1	D	484/514 (94%)	0.51	41 (8%) 13 18	27, 53, 84, 161	0
All	All	1927/2056 (93%)	0.35	136 (7%) 19 26	22, 48, 82, 161	1 (0%)

The worst 5 of 136 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	280	VAL	16.1
1	D	279	PRO	12.8
1	A	488	LEU	8.7
1	D	488	LEU	7.4
1	A	490	ASP	6.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	DGT	A	704	31/31	0.97	0.14	-0.13	25,29,37,37	0
5	DGT	C	701	31/31	0.98	0.12	-0.43	29,32,42,44	0
2	DCP	A	701	28/28	0.92	0.12	-0.48	31,40,72,78	0
2	DCP	B	701	28/28	0.91	0.11	-0.68	37,43,71,73	0
2	DCP	D	703	28/28	0.92	0.11	-0.84	35,42,76,80	0
4	GTP	B	705	32/32	0.98	0.11	-0.93	27,31,36,37	0
5	DGT	D	702	31/31	0.98	0.11	-0.98	29,33,41,42	0
4	GTP	A	703	32/32	0.98	0.11	-1.01	31,36,40,45	0
5	DGT	B	706	31/31	0.97	0.11	-1.01	29,34,42,45	0
2	DCP	C	703	28/28	0.95	0.10	-1.02	26,30,59,62	0
4	GTP	D	705	32/32	0.97	0.10	-1.18	33,38,43,47	0
4	GTP	B	703	32/32	0.98	0.10	-1.20	30,36,40,45	0
3	MG	D	704	1/1	0.82	0.09	-	111,111,111,111	0
3	MG	D	701	1/1	0.94	0.04	-	37,37,37,37	0
3	MG	C	704	1/1	0.96	0.03	-	60,60,60,60	0
3	MG	B	702	1/1	0.87	0.14	-	123,123,123,123	0
3	MG	A	702	1/1	0.88	0.06	-	73,73,73,73	0
3	MG	B	704	1/1	0.97	0.03	-	30,30,30,30	0
3	MG	C	702	1/1	0.82	0.08	-	37,37,37,37	0
3	MG	A	705	1/1	0.99	0.05	-	41,41,41,41	0

## 6.5 Other polymers

There are no such residues in this entry.