



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:26 PM GMT

PDB ID : 4RXQ
Title : The structure of GTP-dUTP-bound SAMHD1
Authors : Zhu, C.F.; Wei, W.; Peng, X.; Dong, Y.H.; Gong, Y.; Yu, X.F.
Deposited on : 2014-12-11
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at 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

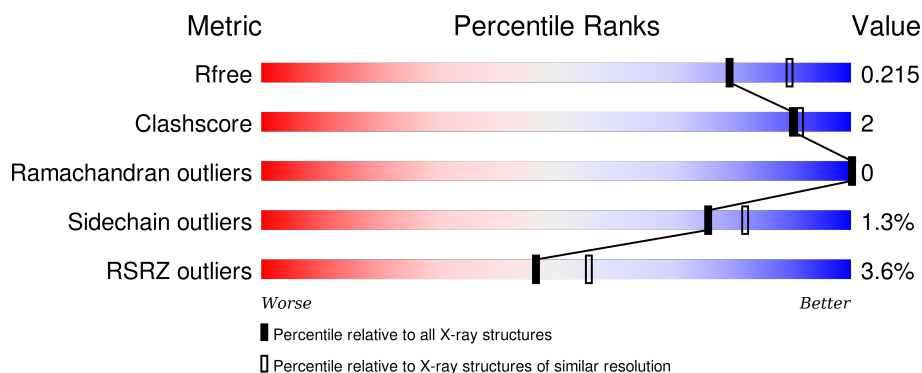
1 Overall quality at a glance

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 ≥ 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	539	<div> <div>4%</div> <div>84%</div> <div>11%</div> </div>
1	B	539	<div> <div>3%</div> <div>86%</div> <div>5%</div> <div>9%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8668 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
			3936	2522	683	712	19			
1	B	493	Total	C	N	O	S	0	0	0
			4036	2586	700	731	19			

There are 44 discrepancies between the modelled and reference sequences:

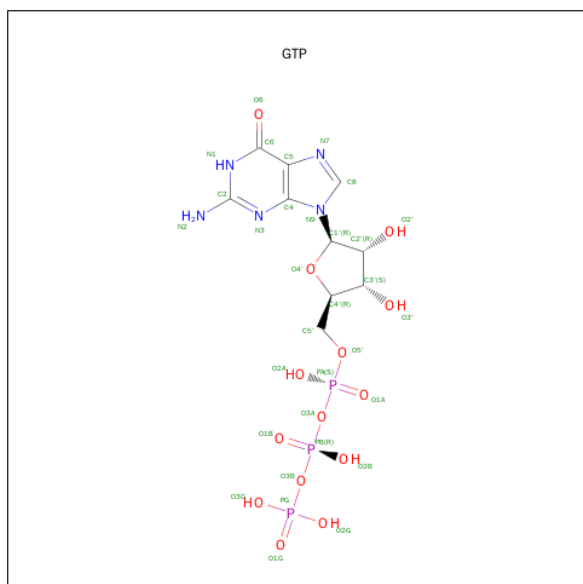
Chain	Residue	Modelled	Actual	Comment	Reference
A	88	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
A	89	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	90	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	91	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	92	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	93	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	94	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	95	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	96	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	97	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
A	98	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	99	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	100	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	101	GLU	-	EXPRESSION TAG	UNP Q9Y3Z3
A	102	ASN	-	EXPRESSION TAG	UNP Q9Y3Z3
A	103	LEU	-	EXPRESSION TAG	UNP Q9Y3Z3
A	104	TYR	-	EXPRESSION TAG	UNP Q9Y3Z3
A	105	PHE	-	EXPRESSION TAG	UNP Q9Y3Z3
A	106	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
A	107	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
A	108	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
A	266	TYR	CYS	CONFLICT	UNP Q9Y3Z3
B	88	MET	-	EXPRESSION TAG	UNP Q9Y3Z3
B	89	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	90	SER	-	EXPRESSION TAG	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	91	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	92	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	93	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	94	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	95	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	96	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	97	HIS	-	EXPRESSION TAG	UNP Q9Y3Z3
B	98	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	99	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	100	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	101	GLU	-	EXPRESSION TAG	UNP Q9Y3Z3
B	102	ASN	-	EXPRESSION TAG	UNP Q9Y3Z3
B	103	LEU	-	EXPRESSION TAG	UNP Q9Y3Z3
B	104	TYR	-	EXPRESSION TAG	UNP Q9Y3Z3
B	105	PHE	-	EXPRESSION TAG	UNP Q9Y3Z3
B	106	GLN	-	EXPRESSION TAG	UNP Q9Y3Z3
B	107	GLY	-	EXPRESSION TAG	UNP Q9Y3Z3
B	108	SER	-	EXPRESSION TAG	UNP Q9Y3Z3
B	266	TYR	CYS	CONFLICT	UNP Q9Y3Z3

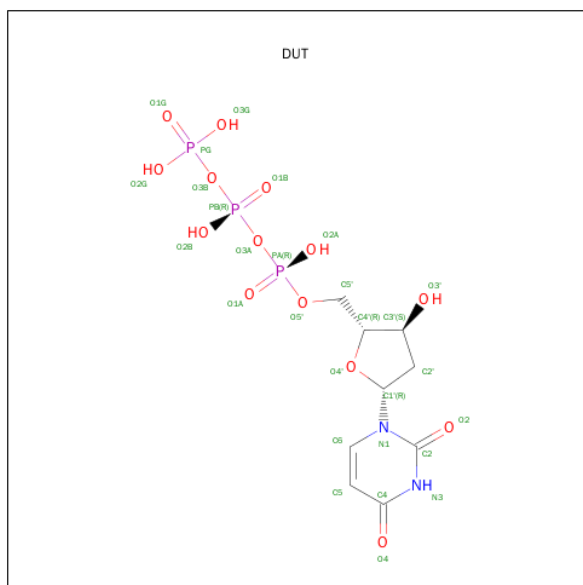
- Molecule 2 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 3 is DEOXYURIDINE-5'-TRIPHOSPHATE (three-letter code: DUT) (formula: $C_9H_{15}N_2O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	9	2	14	3		
3	A	1	Total	C	N	O	P	0	0
			28	9	2	14	3		
3	B	1	Total	C	N	O	P	0	0
			28	9	2	14	3		
3	B	1	Total	C	N	O	P	0	0
			28	9	2	14	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

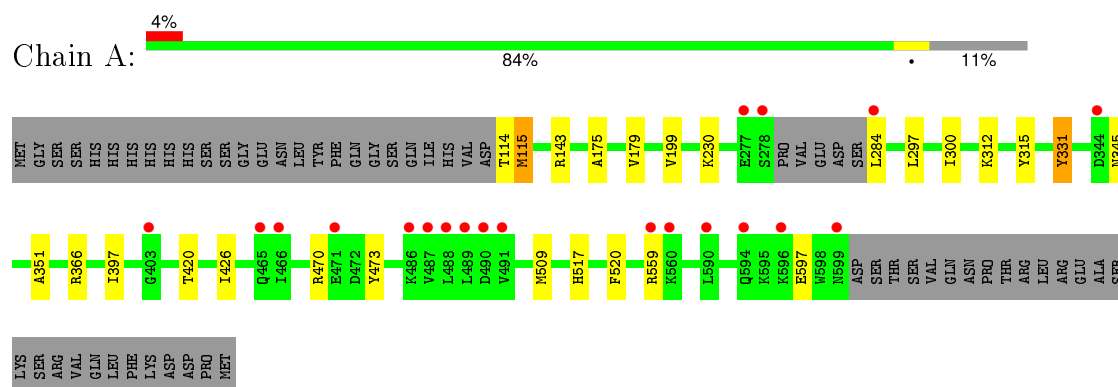
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	265	Total 265	O 265	0	0
5	B	253	Total 253	O 253	0	0

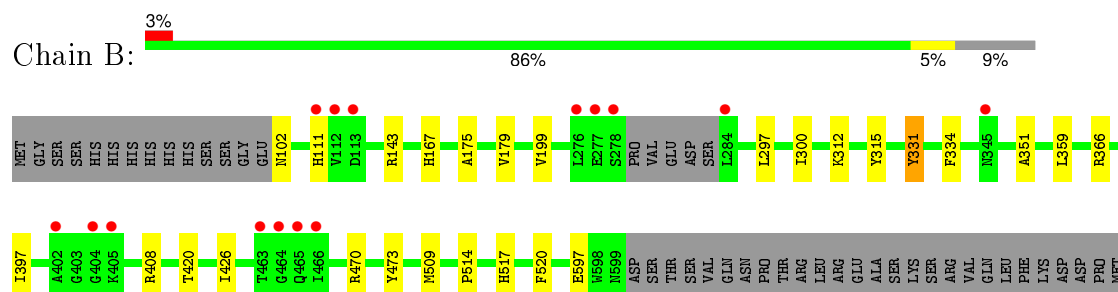
3 Residue-property plots [i](#)

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: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	150.80Å 108.92Å 92.22Å 90.00° 122.73° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 41.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.10) 99.8 (41.12-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.21 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.197 , 0.229 0.186 , 0.215	Depositor DCC
R_{free} test set	3637 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 72931 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8668	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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	0/4030	0.62	0/5441
1	B	0.48	0/4133	0.63	0/5581
All	All	0.47	0/8163	0.63	0/11022

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3936	0	3918	15	0
1	B	4036	0	4008	21	0
2	A	64	0	24	1	0
3	A	56	0	22	2	0
3	B	56	0	22	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	265	0	0	0	0
5	B	253	0	0	3	0
All	All	8668	0	7994	37	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 2.

All (37) 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:408:ARG:HH11	1:B:408:ARG:HG2	1.44	0.80
1:A:179:VAL:HG22	1:A:300:ILE:HD13	1.74	0.70
1:B:179:VAL:HG22	1:B:300:ILE:HD13	1.73	0.69
1:A:175:ALA:HB1	1:A:199:VAL:HG12	1.77	0.66
1:B:175:ALA:HB1	1:B:199:VAL:HG12	1.79	0.65
1:B:408:ARG:NH1	1:B:408:ARG:HG2	2.15	0.62
1:B:179:VAL:CG2	1:B:300:ILE:HD13	2.30	0.62
1:A:179:VAL:CG2	1:A:300:ILE:HD13	2.30	0.60
1:B:312:LYS:NZ	3:B:702:DUT:O1G	2.35	0.59
1:A:312:LYS:HG3	3:A:802:DUT:O3G	2.06	0.55
1:A:312:LYS:HE3	1:A:366:ARG:HD2	1.94	0.49
1:B:312:LYS:HE3	1:B:366:ARG:HD2	1.94	0.49
1:B:111:HIS:HB3	5:B:1000:HOH:O	2.15	0.46
1:A:470:ARG:HA	1:A:473:TYR:CE1	2.51	0.46
1:B:167:HIS:NE2	5:B:801:HOH:O	2.36	0.45
1:B:470:ARG:HA	1:B:473:TYR:CE1	2.52	0.44
1:B:351:ALA:O	1:B:520:PHE:HA	2.18	0.44
1:B:102:ASN:N	5:B:908:HOH:O	2.50	0.44
1:A:312:LYS:NZ	3:A:802:DUT:O3G	2.47	0.44
1:A:351:ALA:O	1:A:520:PHE:HA	2.17	0.44
1:A:114:THR:HG22	1:A:115:MET:O	2.18	0.43
1:A:143:ARG:HD2	1:A:420:THR:HA	1.99	0.43
1:B:509:MET:HE1	1:B:514:PRO:HA	1.99	0.43
1:A:297:LEU:HA	1:A:300:ILE:HD12	1.99	0.43
1:A:397:ILE:HG21	1:A:426:ILE:HD11	2.00	0.43
1:A:509:MET:HE1	1:A:517:HIS:CD2	2.53	0.42
1:B:509:MET:HB2	1:B:509:MET:HE2	1.83	0.42
2:A:804:GTP:H5''	3:B:703:DUT:O1B	2.19	0.42
1:B:397:ILE:HG21	1:B:426:ILE:HD11	2.01	0.42
1:A:179:VAL:HG22	1:A:300:ILE:CD1	2.47	0.42
1:B:297:LEU:HA	1:B:300:ILE:HD12	2.03	0.41
1:B:143:ARG:HD2	1:B:420:THR:HA	2.01	0.41
1:B:331:TYR:CD1	1:B:331:TYR:C	2.93	0.41
1:A:331:TYR:C	1:A:331:TYR:CD1	2.93	0.41
1:B:334:PHE:CE1	1:B:359:LEU:HD21	2.55	0.41
1:B:334:PHE:HE1	1:B:359:LEU:HD21	1.86	0.40
1:B:509:MET:HE1	1:B:517:HIS:CD2	2.56	0.40

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	477/539 (88%)	470 (98%)	7 (2%)	0	100	100
1	B	489/539 (91%)	481 (98%)	8 (2%)	0	100	100
All	All	966/1078 (90%)	951 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	427/481 (89%)	419 (98%)	8 (2%)	65	70
1	B	438/481 (91%)	435 (99%)	3 (1%)	88	92
All	All	865/962 (90%)	854 (99%)	11 (1%)	76	82

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	MET
1	A	230	LYS
1	A	284	LEU
1	A	315	TYR
1	A	331	TYR
1	A	345	ASN
1	A	559	ARG
1	A	597	GLU

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Mol	Chain	Res	Type
1	B	315	TYR
1	B	331	TYR
1	B	597	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	517	HIS
1	B	215	HIS
1	B	517	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	GTP	A	801	4	25,34,34	1.18	2 (8%)	34,54,54	1.78	7 (20%)
3	DUT	A	802	-	20,29,29	0.70	0	32,45,45	1.72	4 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DUT	A	803	4	20,29,29	0.76	1 (5%)	32,45,45	1.91	4 (12%)
2	GTP	A	804	4	25,34,34	1.13	3 (12%)	34,54,54	1.81	7 (20%)
3	DUT	B	702	-	20,29,29	0.75	1 (5%)	32,45,45	1.56	2 (6%)
3	DUT	B	703	4	20,29,29	0.84	1 (5%)	32,45,45	1.71	5 (15%)

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	GTP	A	801	4	-	0/18/38/38	0/3/3/3
3	DUT	A	802	-	-	0/18/34/34	0/2/2/2
3	DUT	A	803	4	-	0/18/34/34	0/2/2/2
2	GTP	A	804	4	-	0/18/38/38	0/3/3/3
3	DUT	B	702	-	-	0/18/34/34	0/2/2/2
3	DUT	B	703	4	-	0/18/34/34	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	703	DUT	PG-O3G	-2.19	1.46	1.54
3	B	702	DUT	C6-N1	-2.10	1.32	1.35
2	A	804	GTP	PG-O3G	-2.06	1.47	1.54
3	A	803	DUT	PG-O3G	-2.01	1.47	1.54
2	A	801	GTP	C5-C4	2.74	1.46	1.40
2	A	804	GTP	C6-C5	2.85	1.47	1.41
2	A	804	GTP	C5-C4	3.07	1.47	1.40
2	A	801	GTP	C6-C5	3.42	1.48	1.41

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	GTP	C5-C6-N1	-4.57	117.34	123.59
3	A	802	DUT	PB-O3A-PA	-4.38	120.42	132.73
3	A	803	DUT	O4'-C1'-N1	-4.34	100.21	107.72
3	B	702	DUT	PB-O3A-PA	-4.30	120.65	132.73
2	A	804	GTP	C5-C6-N1	-4.25	117.78	123.59
2	A	804	GTP	C6-C5-C4	-3.54	116.67	120.90
2	A	801	GTP	C6-C5-C4	-3.33	116.91	120.90
3	A	802	DUT	PB-O3B-PG	-2.87	123.03	132.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	804	GTP	N3-C2-N1	-2.83	123.14	127.44
2	A	801	GTP	O5'-PA-O1A	-2.51	99.87	109.62
2	A	804	GTP	PA-O3A-PB	-2.49	125.73	132.73
2	A	801	GTP	N3-C2-N1	-2.45	123.71	127.44
2	A	801	GTP	PA-O3A-PB	-2.40	125.98	132.73
3	B	703	DUT	O4'-C1'-N1	-2.40	103.56	107.72
2	A	804	GTP	O5'-PA-O1A	-2.17	101.20	109.62
3	B	703	DUT	PB-O3B-PG	-2.17	125.40	132.67
3	A	802	DUT	O2B-PB-O1B	2.04	123.61	112.53
3	B	703	DUT	O3G-PG-O2G	2.46	116.74	107.38
3	A	803	DUT	C2'-C1'-N1	2.74	120.82	114.16
3	B	703	DUT	C2'-C1'-N1	3.07	121.63	114.16
2	A	801	GTP	O3G-PG-O2G	3.60	121.07	107.38
3	A	803	DUT	O3G-PG-O2G	3.82	121.91	107.38
2	A	804	GTP	O3G-PG-O2G	3.88	122.15	107.38
2	A	801	GTP	C6-N1-C2	4.91	122.75	115.94
2	A	804	GTP	C6-N1-C2	5.07	122.98	115.94
3	B	702	DUT	C4-N3-C2	6.20	120.28	114.14
3	A	802	DUT	C4-N3-C2	6.38	120.46	114.14
3	B	703	DUT	C4-N3-C2	6.67	120.75	114.14
3	A	803	DUT	C4-N3-C2	7.22	121.29	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	DUT	2	0
2	A	804	GTP	1	0
3	B	702	DUT	1	0
3	B	703	DUT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	481/539 (89%)	0.01	20 (4%)	40 49	24, 38, 66, 96	0
1	B	493/539 (91%)	-0.09	15 (3%)	54 62	22, 38, 63, 104	0
All	All	974/1078 (90%)	-0.04	35 (3%)	46 55	22, 38, 64, 104	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	278	SER	7.8
1	A	488	LEU	7.6
1	B	278	SER	7.4
1	A	490	ASP	5.7
1	B	465	GLN	4.7
1	A	465	GLN	4.6
1	A	487	VAL	4.3
1	B	277	GLU	4.0
1	B	111	HIS	3.9
1	A	559	ARG	3.7
1	A	489	LEU	3.5
1	A	596	LYS	3.5
1	B	113	ASP	3.5
1	B	284	LEU	3.4
1	A	599	ASN	3.3
1	A	590	LEU	3.3
1	A	486	LYS	3.2
1	B	464	GLY	3.1
1	A	277	GLU	3.1
1	A	491	VAL	3.1
1	A	560	LYS	3.0
1	B	466	ILE	2.9
1	A	284	LEU	2.8
1	B	405	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	402	ALA	2.6
1	A	344	ASP	2.5
1	A	403	GLY	2.4
1	B	463	THR	2.3
1	B	345	ASN	2.3
1	B	112	VAL	2.2
1	A	466	ILE	2.2
1	A	471	GLU	2.2
1	B	404	GLY	2.1
1	A	594	GLN	2.1
1	B	276	LEU	2.0

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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	DUT	A	802	28/28	0.85	0.15	1.65	26,39,92,95	0
3	DUT	B	702	28/28	0.90	0.13	0.68	25,36,74,77	0
3	DUT	A	803	28/28	0.99	0.08	-1.19	22,27,31,32	0
2	GTP	A	804	32/32	0.99	0.07	-1.22	23,26,31,32	0
3	DUT	B	703	28/28	0.98	0.09	-1.24	21,25,29,30	0
2	GTP	A	801	32/32	0.98	0.07	-1.81	27,29,34,35	0
4	MG	A	805	1/1	0.99	0.06	-	26,26,26,26	0
4	MG	B	701	1/1	0.99	0.09	-	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.