



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:25 AM GMT

PDB ID : 3ICQ
Title : Karyopherin nuclear state
Authors : Cook, A.G.; Fukuhara, N.; Jinek, M.; Conti, E.
Deposited on : 2009-07-18
Resolution : 3.20 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
<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

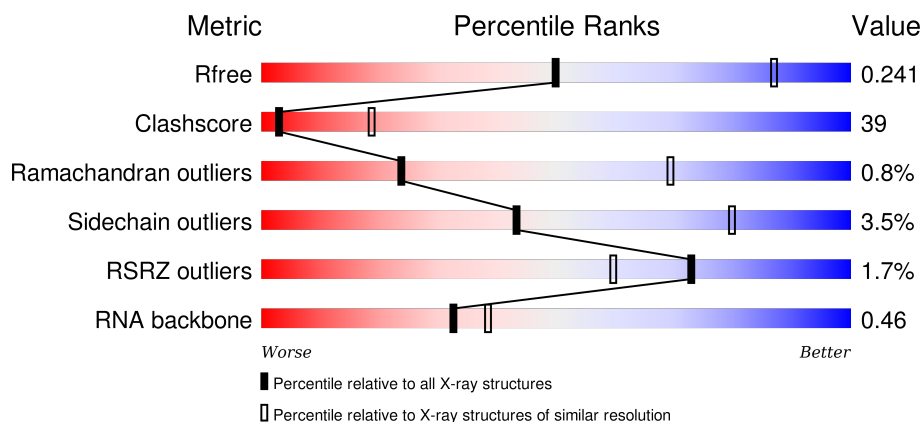
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)
RNA backbone	2183	1079 (3.70-2.70)

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	T	980	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 44%, green 50%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 50% 44% • • </div> </div>
1	U	980	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 42%, green 53%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 53% 42% • • </div> </div>
2	B	171	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 48%, green 47%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 48% 47% • • </div> </div>
2	C	171	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 49%, green 44%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 44% 49% • 5% </div> </div>

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Mol	Chain	Length	Quality of chain
3	D	67	
3	E	67	

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
4	GTP	C	250	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19125 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 Exportin-T.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	949	Total	C	N	O	S	0	0	0
			7032	4529	1133	1336	34			
1	U	943	Total	C	N	O	S	0	0	0
			6864	4431	1112	1288	33			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	-1	GLY	-	EXPRESSION TAG	UNP O94258
T	0	PRO	-	EXPRESSION TAG	UNP O94258
U	-1	GLY	-	EXPRESSION TAG	UNP O94258
U	0	PRO	-	EXPRESSION TAG	UNP O94258

- Molecule 2 is a protein called GTP-binding nuclear protein GSP1/CNR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	167	Total	C	N	O	S	0	0	0
			1290	838	219	229	4			
2	C	163	Total	C	N	O	S	0	0	0
			1236	801	208	223	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	71	LEU	GLN	ENGINEERED	UNP P32835
C	71	LEU	GLN	ENGINEERED	UNP P32835

- Molecule 3 is a RNA chain called RNA (62-MER).

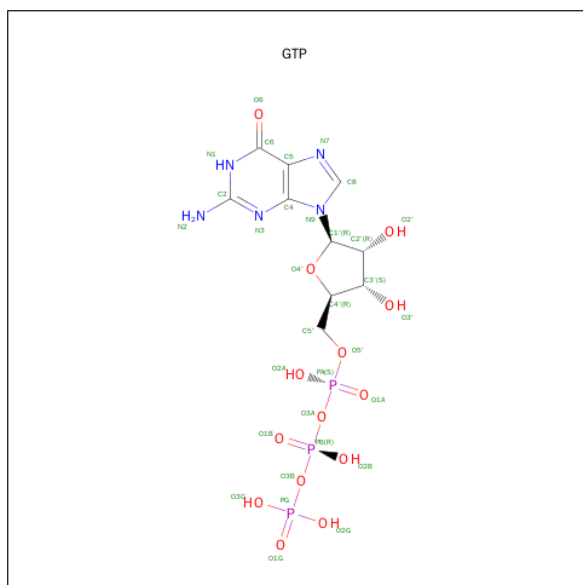
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	62	Total	C	N	O	P	0	0	0
			1318	587	236	433	62			

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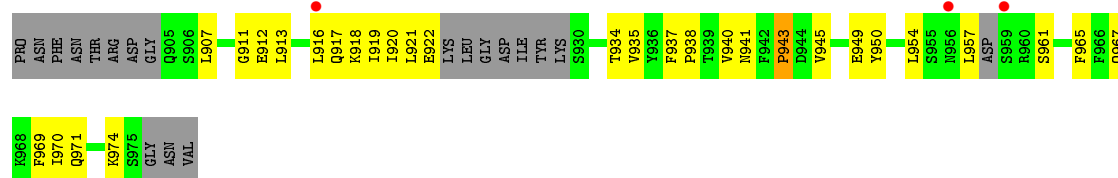
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	62	Total	C	N	O	P	0	0	0
			1315	586	234	433	62			

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

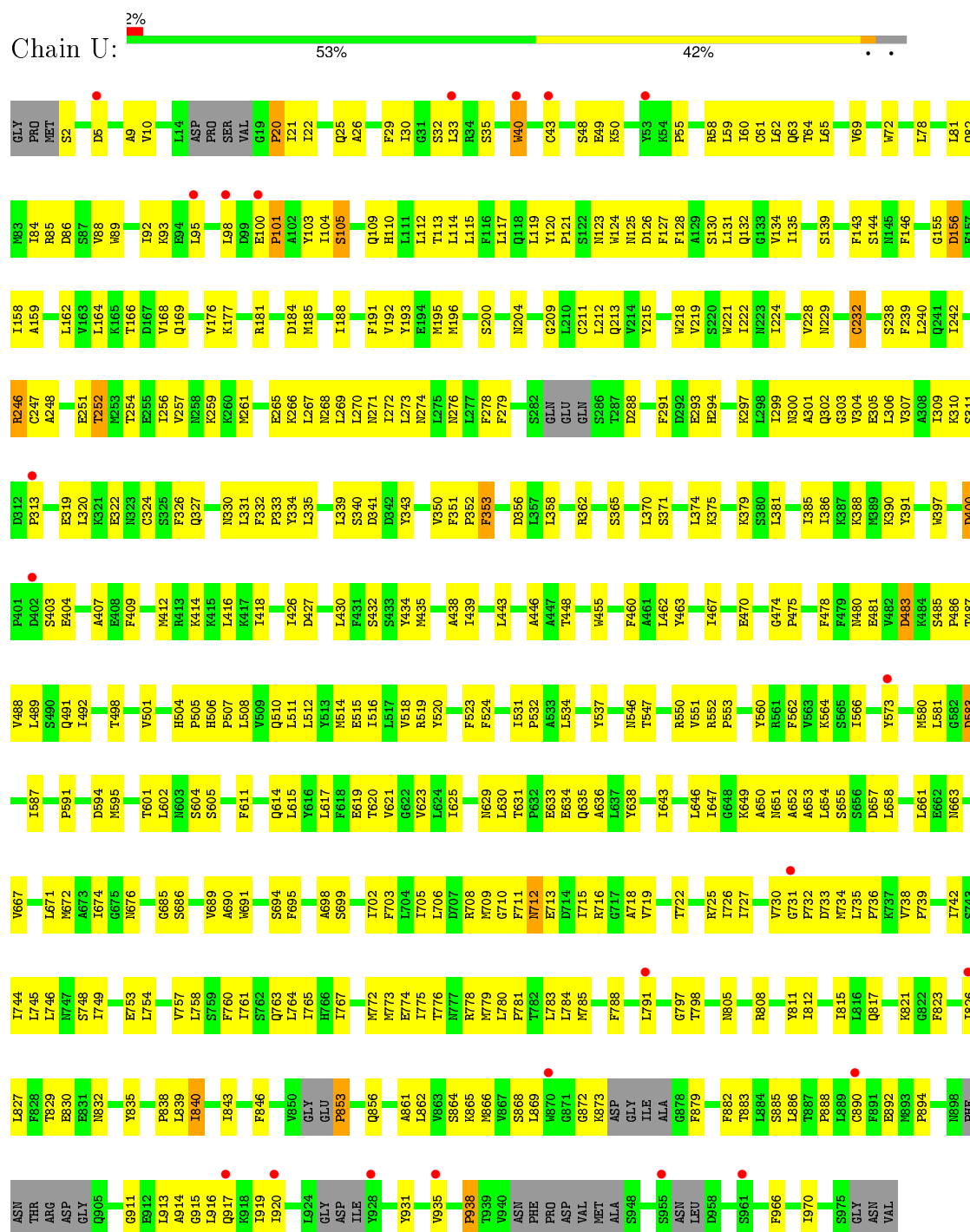


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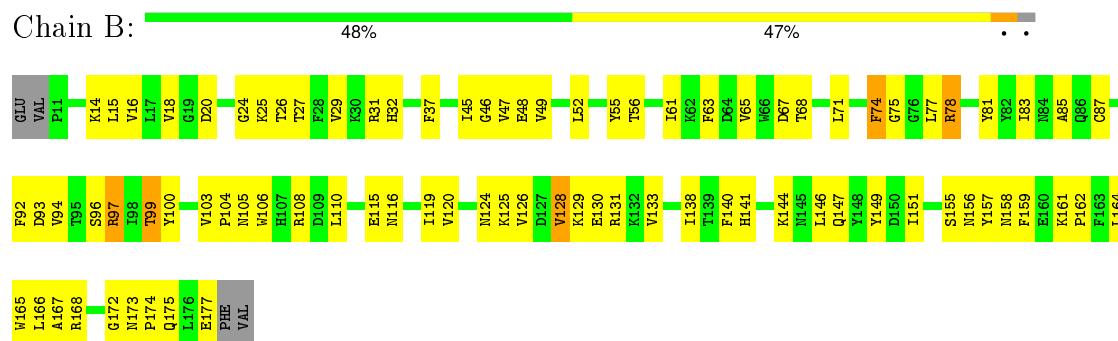
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	2	Total	O	0	0
			2	2		



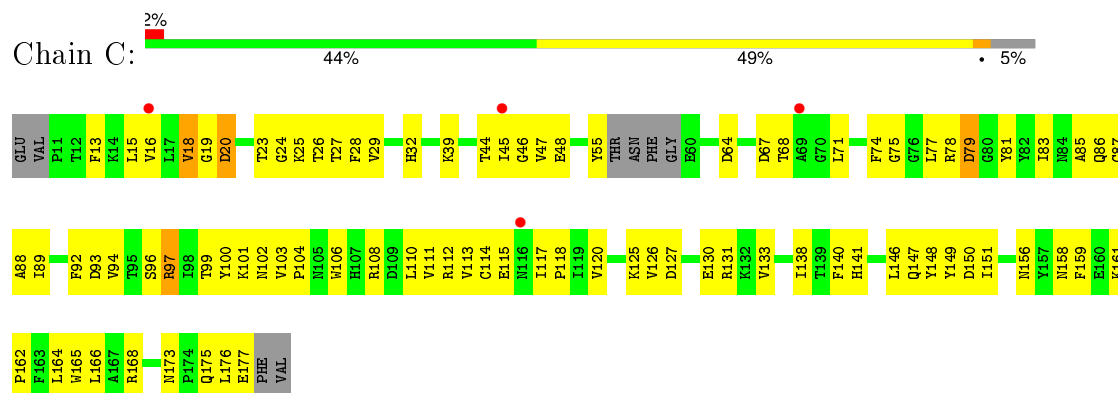
• Molecule 1: Exportin-T



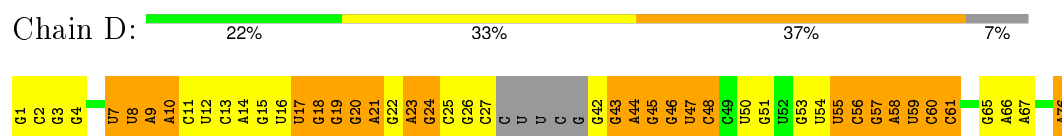
• Molecule 2: GTP-binding nuclear protein GSP1/CNR1



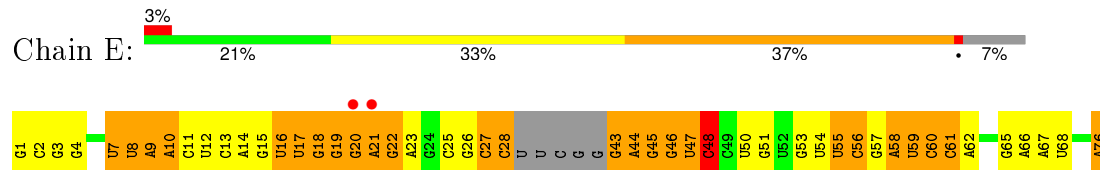
- Molecule 2: GTP-binding nuclear protein GSP1/CNR1



- Molecule 3: RNA (62-MER)



- Molecule 3: RNA (62-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	143.00Å 143.80Å 166.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.20 72.08 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.00-3.20) 100.0 (72.08-3.20)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 3.19Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.294 0.248 , 0.241	Depositor DCC
R_{free} test set	2863 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 87.3	EDS
Estimated twinning fraction	0.030 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 57388 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	19125	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, 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	T	0.49	0/7171	0.68	1/9788 (0.0%)
1	U	0.49	1/6995 (0.0%)	0.69	3/9554 (0.0%)
2	B	0.56	1/1323 (0.1%)	0.74	1/1798 (0.1%)
2	C	0.56	1/1267 (0.1%)	0.68	1/1728 (0.1%)
3	D	0.54	1/1472 (0.1%)	0.75	0/2289
3	E	0.64	3/1468 (0.2%)	0.96	7/2282 (0.3%)
All	All	0.52	7/19696 (0.0%)	0.72	13/27439 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	97	ARG	NE-CZ	12.42	1.49	1.33
2	B	97	ARG	NE-CZ	12.19	1.48	1.33
3	E	43	G	C6-O6	11.11	1.34	1.24
3	E	1	G	OP3-P	-6.88	1.52	1.61
3	D	1	G	OP3-P	-6.69	1.53	1.61

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	43	G	N3-C2-N2	-15.66	108.94	119.90
3	E	43	G	C5-C6-N1	12.02	117.51	111.50
2	B	97	ARG	CD-NE-CZ	-10.72	108.59	123.60
3	E	43	G	C6-N1-C2	-10.63	118.72	125.10
2	C	97	ARG	CD-NE-CZ	-9.17	110.76	123.60

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	T	7032	0	6550	511	0
1	U	6864	0	6299	487	0
2	B	1290	0	1230	87	0
2	C	1236	0	1145	101	0
3	D	1318	0	666	127	0
3	E	1315	0	666	101	0
4	B	32	0	12	7	0
4	C	32	0	12	9	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
6	B	2	0	0	3	0
6	C	2	0	0	3	0
All	All	19125	0	16580	1384	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 39.

The worst 5 of 1384 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:U:95:LEU:HB3	1:U:143:PHE:CZ	1.26	1.57
3:D:44:A:H2'	3:D:45:G:C8	1.46	1.47
1:U:95:LEU:CB	1:U:143:PHE:HZ	1.36	1.37
1:U:95:LEU:HD22	1:U:143:PHE:CE2	1.61	1.33
3:D:20:G:H4'	3:D:21:A:C5'	1.57	1.33

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	T	933/980 (95%)	838 (90%)	84 (9%)	11 (1%)	16	60
1	U	925/980 (94%)	833 (90%)	87 (9%)	5 (0%)	34	78
2	B	165/171 (96%)	149 (90%)	16 (10%)	0	100	100
2	C	159/171 (93%)	145 (91%)	13 (8%)	1 (1%)	30	75
All	All	2182/2302 (95%)	1965 (90%)	200 (9%)	17 (1%)	24	69

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	T	314	SER
1	T	501	VAL
1	T	830	GLU
1	U	101	PRO
1	U	938	PRO

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	T	708/880 (80%)	679 (96%)	29 (4%)	37	76
1	U	662/880 (75%)	646 (98%)	16 (2%)	57	86
2	B	129/150 (86%)	123 (95%)	6 (5%)	32	73
2	C	121/150 (81%)	115 (95%)	6 (5%)	30	71
All	All	1620/2060 (79%)	1563 (96%)	57 (4%)	43	80

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T	762	SER
2	B	74	PHE
2	C	20	ASP

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Mol	Chain	Res	Type
1	T	768	TYR
1	T	840	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	856	GLN
1	U	77	ASN
1	U	763	GLN
1	T	941	ASN
2	B	116	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	D	60/67 (89%)	24 (40%)	8 (13%)
3	E	60/67 (89%)	22 (36%)	9 (15%)
All	All	120/134 (89%)	46 (38%)	17 (14%)

5 of 46 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	D	4	G
3	D	8	U
3	D	9	A
3	D	10	A
3	D	17	U

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	D	60	C
3	E	7	U
3	E	46	G
3	D	58	A
3	E	48	C

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
4	GTP	B	250	5	25,34,34	1.29	3 (12%)	34,54,54	2.45	10 (29%)
4	GTP	C	250	5	25,34,34	1.35	3 (12%)	34,54,54	2.42	9 (26%)

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
4	GTP	B	250	5	-	0/18/38/38	0/3/3/3
4	GTP	C	250	5	-	0/18/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	250	GTP	C8-N7	-2.55	1.29	1.34
4	C	250	GTP	C6-C5	2.34	1.45	1.41
4	C	250	GTP	C6-N1	2.35	1.37	1.33
4	C	250	GTP	O4'-C1'	2.36	1.44	1.41
4	B	250	GTP	O4'-C1'	2.45	1.44	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	250	GTP	PB-O3B-PG	-7.35	108.01	132.67
4	C	250	GTP	PA-O3A-PB	-7.11	112.77	132.73
4	B	250	GTP	PA-O3A-PB	-7.02	113.00	132.73
4	C	250	GTP	PB-O3B-PG	-6.85	109.72	132.67
4	C	250	GTP	C5-C6-N1	-4.40	117.57	123.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	250	GTP	7	0
4	C	250	GTP	9	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 [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, 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	T	949/980 (96%)	0.06	11 (1%) 81 69	18, 66, 122, 194	0
1	U	943/980 (96%)	0.07	22 (2%) 64 49	22, 66, 124, 186	0
2	B	167/171 (97%)	-0.02	0 100 100	20, 60, 102, 120	0
2	C	163/171 (95%)	0.23	4 (2%) 61 47	34, 68, 111, 148	0
3	D	62/67 (92%)	0.26	0 100 100	42, 80, 161, 173	0
3	E	62/67 (92%)	0.21	2 (3%) 51 36	47, 79, 144, 176	0
All	All	2346/2436 (96%)	0.08	39 (1%) 73 60	18, 66, 124, 194	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	313	PRO	5.4
1	U	33	LEU	3.9
1	T	543	GLY	3.9
1	U	791	LEU	3.6
1	U	53	TYR	3.4

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
4	GTP	B	250	32/32	0.94	0.26	0.73	67,74,88,88	0
4	GTP	C	250	32/32	0.94	0.23	-0.16	67,74,88,88	0
5	MG	C	5	1/1	0.96	0.07	-2.41	49,49,49,49	0
5	MG	B	2	1/1	0.93	0.14	-	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.