



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2017 – 03:55 PM EDT

PDB ID : 5XOJ  
Title : Crystal structure of Xpo1p-PKI-Nup42p-Gsp1p-GTP complex  
Authors : Koyama, M.; Shirai, N.; Matsuura, Y.  
Deposited on : unknown  
Resolution : 2.20 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](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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20030345

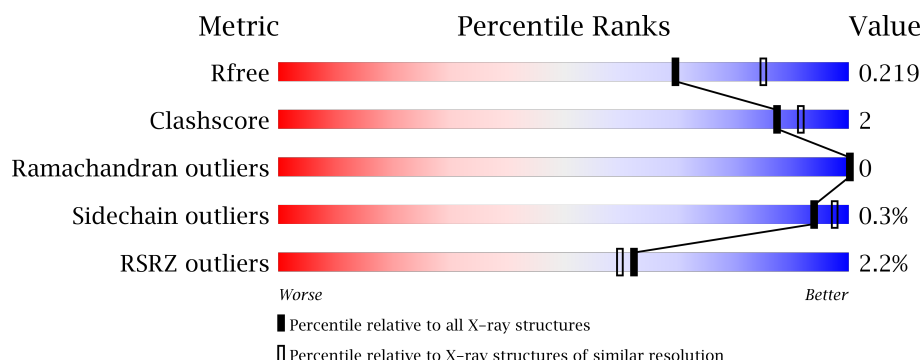
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	182	<div> <div>2%</div> <div>87%</div> <div>6%</div> <div>7%</div> </div>
2	C	1047	<div> <div>2%</div> <div>90%</div> <div>5%</div> <div>5%</div> </div>
3	D	76	<div> <div>3%</div> <div>18%</div> <div>7%</div> <div>75%</div> </div>
4	E	35	<div> <div>9%</div> <div>20%</div> <div>80%</div> </div>
4	F	35	<div> <div>20%</div> <div>6%</div> <div>74%</div> </div>

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Mol	Chain	Length	Quality of chain
4	G	35	<div><div><div></div><div></div><div></div></div><div>3%20%77%</div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10250 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 GTP-binding nuclear protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	0	0
			1373	896	234	239	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	LEU	GLN	engineered mutation	UNP E7KFU1

- Molecule 2 is a protein called Exportin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	999	Total	C	N	O	S	0	0	0
			8052	5180	1322	1512	38			

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	VAL	deletion	UNP P30822
C	?	-	GLN	deletion	UNP P30822
C	?	-	ARG	deletion	UNP P30822
C	?	-	LEU	deletion	UNP P30822
C	?	-	PRO	deletion	UNP P30822
C	?	-	ALA	deletion	UNP P30822
C	?	-	THR	deletion	UNP P30822
C	?	-	GLU	deletion	UNP P30822
C	?	-	MET	deletion	UNP P30822
C	?	-	SER	deletion	UNP P30822
C	?	-	PRO	deletion	UNP P30822
C	?	-	LEU	deletion	UNP P30822
C	?	-	ILE	deletion	UNP P30822
C	?	-	GLN	deletion	UNP P30822
C	?	-	LEU	deletion	UNP P30822

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	SER	deletion	UNP P30822
C	?	-	VAL	deletion	UNP P30822
C	?	-	GLY	deletion	UNP P30822
C	?	-	SER	deletion	UNP P30822
C	?	-	GLN	deletion	UNP P30822
C	?	-	ALA	deletion	UNP P30822
C	?	-	ILE	deletion	UNP P30822
C	?	-	SER	deletion	UNP P30822
C	?	-	THR	deletion	UNP P30822
C	?	-	GLY	deletion	UNP P30822
C	?	-	SER	deletion	UNP P30822
C	?	-	GLY	deletion	UNP P30822
C	?	-	ALA	deletion	UNP P30822
C	?	-	LEU	deletion	UNP P30822
C	?	-	ASN	deletion	UNP P30822
C	?	-	PRO	deletion	UNP P30822
C	?	-	GLU	deletion	UNP P30822
C	?	-	TYR	deletion	UNP P30822
C	?	-	MET	deletion	UNP P30822
C	?	-	LYS	deletion	UNP P30822
C	?	-	ARG	deletion	UNP P30822
C	?	-	PHE	deletion	UNP P30822

- Molecule 3 is a protein called cAMP-dependent protein kinase inhibitor alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	19	Total	C	N	O	0	0	0
			141	88	24	29			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	35	LEU	SER	engineered mutation	UNP P61925

- Molecule 4 is a protein called Nup42p.

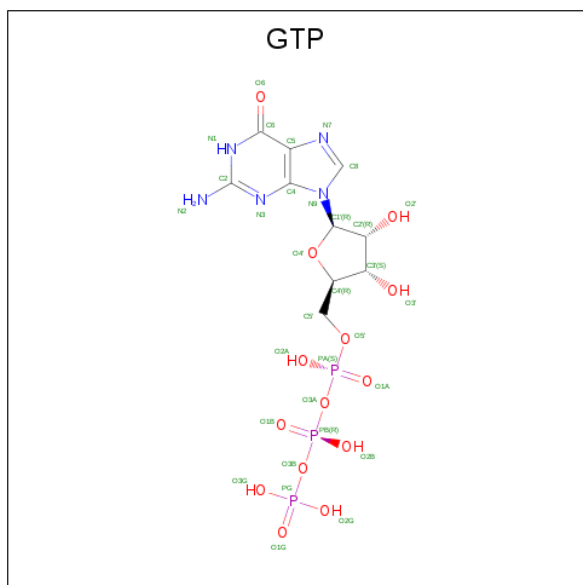
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	7	Total	C	N	O	0	0	0
			48	34	7	7			
4	F	9	Total	C	N	O	0	0	0
			57	39	9	9			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	8	Total	C	N	O	0	0	0
			52	33	8	11			

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



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

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	110	Total	O	0	0
			110	110		
7	C	376	Total	O	0	0
			376	376		
7	D	6	Total	O	0	0
			6	6		

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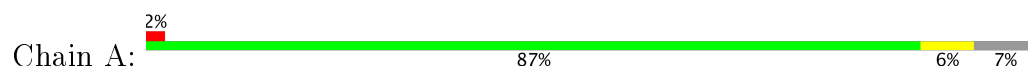
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	F	1	Total	O	0	0
			1	1		
7	G	1	Total	O	0	0
			1	1		

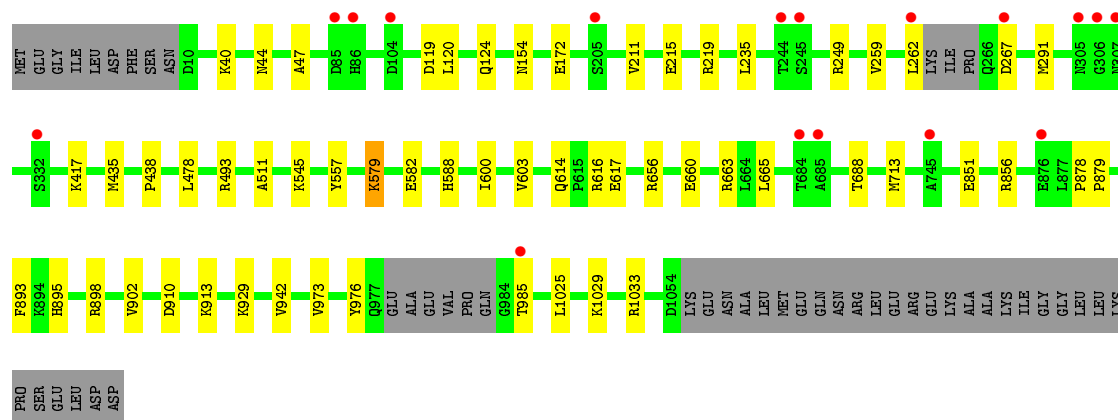
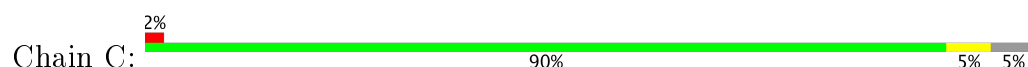
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

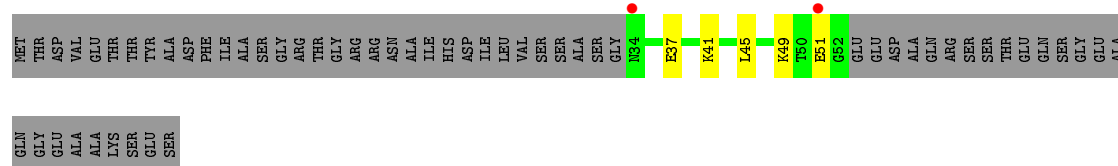
- Molecule 1: GTP-binding nuclear protein



- Molecule 2: Exportin-1



- Molecule 3: cAMP-dependent protein kinase inhibitor alpha



- Molecule 4: Nup42p



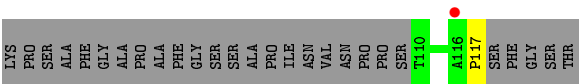




● Molecule 4: Nup42p



● Molecule 4: Nup42p



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.64Å 107.56Å 149.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.58 – 2.20 31.58 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.6 (31.58-2.20) 97.6 (31.58-2.20)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.09 (at 2.20Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.191 , 0.220 0.191 , 0.219	Depositor DCC
$R_{free}$ test set	4148 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.9	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10250	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	A	0.23	0/1408	0.42	0/1905
2	C	0.22	0/8205	0.39	0/11122
3	D	0.23	0/140	0.43	0/187
4	E	0.26	0/50	0.43	0/67
4	F	0.26	0/59	0.34	0/79
4	G	0.25	0/53	0.41	0/72
All	All	0.22	0/9915	0.39	0/13432

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 [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	1373	0	1376	7	0
2	C	8052	0	8114	35	0
3	D	141	0	148	4	0
4	E	48	0	42	0	0
4	F	57	0	47	1	0
4	G	52	0	47	1	0
5	A	32	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
7	A	110	0	0	1	0
7	C	376	0	0	3	0
7	D	6	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
All	All	10250	0	9786	46	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 (46) 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)
2:C:851:GLU:O	2:C:856:ARG:NH2	2.18	0.75
2:C:493:ARG:NH2	7:C:1107:HOH:O	2.27	0.66
2:C:856:ARG:HD3	2:C:895:HIS:NE2	2.14	0.62
3:D:37:GLU:HG2	3:D:41:LYS:HE2	1.81	0.62
1:A:97:ARG:NH2	7:A:301:HOH:O	2.33	0.62
2:C:172:GLU:HG2	2:C:1033:ARG:HD3	1.81	0.61
2:C:40:LYS:NZ	7:C:1115:HOH:O	2.35	0.59
2:C:579:LYS:HD3	3:D:45:LEU:HB3	1.86	0.58
2:C:976:TYR:OH	2:C:985:THR:O	2.19	0.57
2:C:929:LYS:HE3	2:C:973:VAL:HG11	1.86	0.56
2:C:435:MET:HG3	2:C:511:ALA:HB2	1.89	0.54
2:C:688:THR:HA	4:G:117:PRO:HG3	1.90	0.54
2:C:898:ARG:O	2:C:902:VAL:HG23	2.09	0.53
2:C:267:ASP:OD1	2:C:267:ASP:N	2.42	0.50
1:A:119:ILE:HB	1:A:146:LEU:HD22	1.94	0.49
2:C:417:LYS:HD2	2:C:478:LEU:HD22	1.94	0.49
2:C:893:PHE:HB3	2:C:942:VAL:HG11	1.96	0.48
2:C:545:LYS:HE2	2:C:588:HIS:HB2	1.95	0.47
1:A:31:ARG:HG2	1:A:159:PHE:CZ	2.49	0.47
2:C:249:ARG:NH1	7:C:1111:HOH:O	2.31	0.47
2:C:600:ILE:HA	2:C:603:VAL:HG22	1.97	0.46
3:D:49:LYS:HA	3:D:49:LYS:HD2	1.64	0.46
2:C:119:ASP:OD2	2:C:154:ASN:ND2	2.42	0.46
2:C:259:VAL:HA	2:C:262:LEU:HG	1.98	0.45
2:C:44:ASN:HB3	2:C:47:ALA:HB2	1.99	0.45
1:A:125:LYS:HG2	5:A:201:GTP:C6	2.52	0.45
4:F:94:ALA:HA	4:F:95:PRO:HD3	1.86	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:235:LEU:HD21	2:C:259:VAL:HG11	1.98	0.45
2:C:438:PRO:HG3	2:C:557:TYR:OH	2.16	0.45
2:C:910:ASP:HA	2:C:913:LYS:HE3	1.99	0.44
3:D:49:LYS:HG3	3:D:51:GLU:OE1	2.18	0.44
2:C:120:LEU:O	2:C:124:GLN:HG2	2.18	0.44
2:C:616:ARG:HG3	2:C:616:ARG:HH11	1.84	0.43
1:A:31:ARG:NH1	1:A:153:ALA:O	2.51	0.43
1:A:141:HIS:HB2	1:A:146:LEU:HB2	2.00	0.43
2:C:1025:LEU:HD11	2:C:1029:LYS:HE3	2.01	0.43
2:C:215:GLU:O	2:C:219:ARG:NH2	2.51	0.43
2:C:235:LEU:HA	2:C:235:LEU:HD23	1.92	0.42
1:A:17:LEU:HD13	1:A:89:ILE:HB	2.02	0.41
2:C:660:GLU:OE1	2:C:663:ARG:NH1	2.53	0.41
2:C:878:PRO:HA	2:C:879:PRO:HD3	1.87	0.41
2:C:665:LEU:HD13	2:C:713:MET:SD	2.60	0.41
2:C:614:GLN:HB2	2:C:617:GLU:HG3	2.02	0.41
2:C:211:VAL:O	2:C:215:GLU:HG2	2.21	0.40
2:C:579:LYS:NZ	2:C:582:GLU:OE2	2.43	0.40
2:C:656:ARG:HD3	2:C:656:ARG:HA	1.74	0.40

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	168/182 (92%)	164 (98%)	4 (2%)	0	100	100
2	C	993/1047 (95%)	978 (98%)	15 (2%)	0	100	100
3	D	17/76 (22%)	16 (94%)	1 (6%)	0	100	100
4	E	5/35 (14%)	5 (100%)	0	0	100	100
4	F	7/35 (20%)	7 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	G	6/35 (17%)	3 (50%)	3 (50%)	0	100	100
All	All	1196/1410 (85%)	1173 (98%)	23 (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	146/156 (94%)	145 (99%)	1 (1%)	87	93
2	C	907/955 (95%)	905 (100%)	2 (0%)	94	98
3	D	15/59 (25%)	15 (100%)	0	100	100
4	E	3/25 (12%)	3 (100%)	0	100	100
4	F	3/25 (12%)	3 (100%)	0	100	100
4	G	5/25 (20%)	5 (100%)	0	100	100
All	All	1079/1245 (87%)	1076 (100%)	3 (0%)	94	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
2	C	291	MET
2	C	579	LYS

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

Mol	Chain	Res	Type
2	C	623	GLN
2	C	867	ASN
2	C	930	ASN

### 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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	GTP	A	201	6	27,34,34	0.96	1 (3%)	27,54,54	1.68	4 (14%)

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	GTP	A	201	6	-	0/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	201	GTP	C6-N1	3.09	1.38	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
5	A	201	GTP	N3-C2-N1	-4.99	120.17	127.46
5	A	201	GTP	C5-C6-N1	-2.77	119.53	123.48
5	A	201	GTP	C6-N1-C2	2.70	119.95	116.06
5	A	201	GTP	C2-N3-C4	4.29	120.17	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	201	GTP	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, 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	170/182 (93%)	-0.26	4 (2%) 59 57	15, 28, 56, 76	0
2	C	999/1047 (95%)	-0.21	17 (1%) 70 68	17, 40, 64, 87	0
3	D	19/76 (25%)	0.42	2 (10%) 7 6	35, 53, 95, 105	0
4	E	7/35 (20%)	1.60	3 (42%) 0 0	60, 67, 71, 72	0
4	F	9/35 (25%)	0.39	0 100 100	49, 53, 60, 63	0
4	G	8/35 (22%)	0.66	1 (12%) 4 4	43, 59, 66, 66	0
All	All	1212/1410 (85%)	-0.18	27 (2%) 62 60	15, 39, 65, 105	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	305	ASN	6.5
2	C	244	THR	5.5
2	C	267	ASP	4.5
4	E	91	ALA	4.2
3	D	51	GLU	3.8
3	D	34	ASN	3.4
2	C	262	LEU	3.2
2	C	306	GLY	3.1
1	A	55	TYR	3.0
2	C	985	THR	2.9
2	C	245	SER	2.9
1	A	10	VAL	2.8
4	E	94	ALA	2.7
2	C	205	SER	2.6
4	G	116	ALA	2.6
2	C	745	ALA	2.6
2	C	307	ASN	2.5
2	C	685	ALA	2.5
2	C	684	THR	2.4

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Mol	Chain	Res	Type	RSRZ
2	C	104	ASP	2.3
2	C	86	HIS	2.3
2	C	332	SER	2.3
2	C	85	ASP	2.2
2	C	876	GLU	2.2
4	E	92	PHE	2.1
1	A	175	GLN	2.1
1	A	11	PRO	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, 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
6	MG	A	202	1/1	0.97	0.12	0.00	26,26,26,26	0
5	GTP	A	201	32/32	0.99	0.11	-0.38	21,25,30,44	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.