



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:47 AM GMT

PDB ID : 3Q0A
Title : X-ray crystal structure of the transcription initiation complex of the N4 mini-vRNAP with P2 promoter: Mismatch complex
Authors : Murakami, K.S.
Deposited on : 2010-12-15
Resolution : 2.69 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

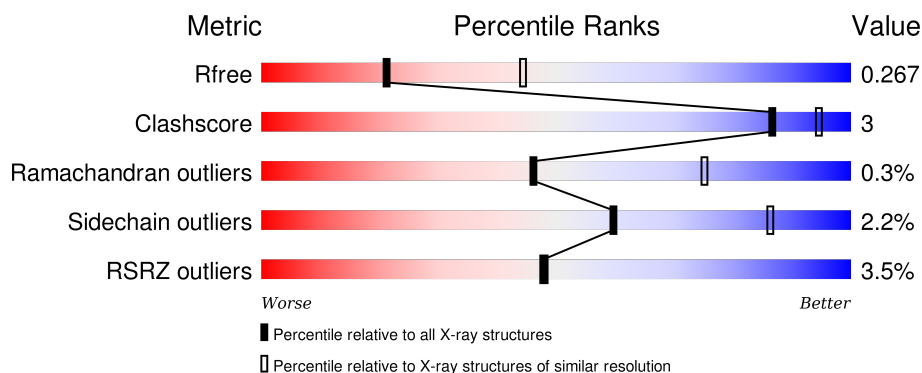
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	A	1118	<div> <div>3%</div> <div>91%</div> <div>6% ..</div> </div>
1	B	1118	<div> <div>3%</div> <div>89%</div> <div>8% ..</div> </div>
2	C	36	<div> <div>6%</div> <div>53%</div> <div>44%</div> </div>
2	D	36	<div> <div>3%</div> <div>53%</div> <div>44%</div> </div>

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
3	PO4	B	1107	-	-	-	X
4	GTP	C	26	-	-	-	X
4	GTP	D	26	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18029 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 Virion RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1095	Total	C	N	O	S	0	0	0
			8454	5306	1435	1672	41			
1	B	1094	Total	C	N	O	S	0	0	0
			8443	5299	1432	1671	41			

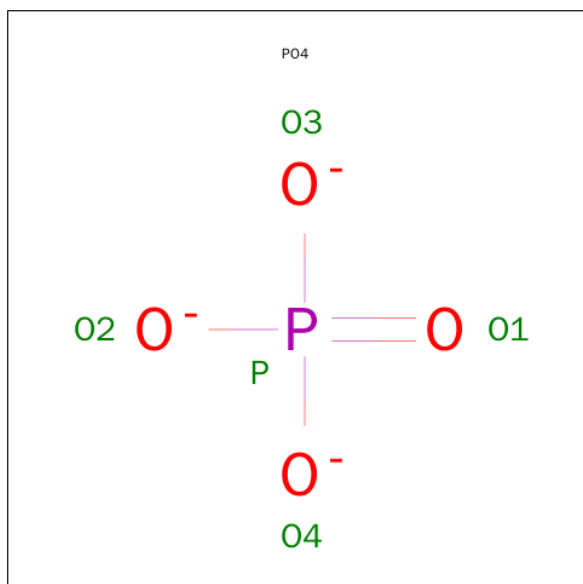
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	EXPRESSION TAG	UNP Q859P9
A	-10	GLY	-	EXPRESSION TAG	UNP Q859P9
A	-9	GLY	-	EXPRESSION TAG	UNP Q859P9
A	-8	SER	-	EXPRESSION TAG	UNP Q859P9
A	-7	HIS	-	EXPRESSION TAG	UNP Q859P9
A	-6	HIS	-	EXPRESSION TAG	UNP Q859P9
A	-5	HIS	-	EXPRESSION TAG	UNP Q859P9
A	-4	HIS	-	EXPRESSION TAG	UNP Q859P9
A	-3	HIS	-	EXPRESSION TAG	UNP Q859P9
A	-2	HIS	-	EXPRESSION TAG	UNP Q859P9
A	-1	ARG	-	EXPRESSION TAG	UNP Q859P9
A	0	SER	-	EXPRESSION TAG	UNP Q859P9
B	-11	MET	-	EXPRESSION TAG	UNP Q859P9
B	-10	GLY	-	EXPRESSION TAG	UNP Q859P9
B	-9	GLY	-	EXPRESSION TAG	UNP Q859P9
B	-8	SER	-	EXPRESSION TAG	UNP Q859P9
B	-7	HIS	-	EXPRESSION TAG	UNP Q859P9
B	-6	HIS	-	EXPRESSION TAG	UNP Q859P9
B	-5	HIS	-	EXPRESSION TAG	UNP Q859P9
B	-4	HIS	-	EXPRESSION TAG	UNP Q859P9
B	-3	HIS	-	EXPRESSION TAG	UNP Q859P9
B	-2	HIS	-	EXPRESSION TAG	UNP Q859P9
B	-1	ARG	-	EXPRESSION TAG	UNP Q859P9
B	0	SER	-	EXPRESSION TAG	UNP Q859P9

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*GP*CP*CP*TP*CP*CP*CP*AP*GP*GP*CP*A*GP*TP*CP*AP*AP*AP*AP*GP*AP*AP*GP*CP*GP*GP*AP*GP*CP*TP*TP*CP*TP*TP*C)-3').

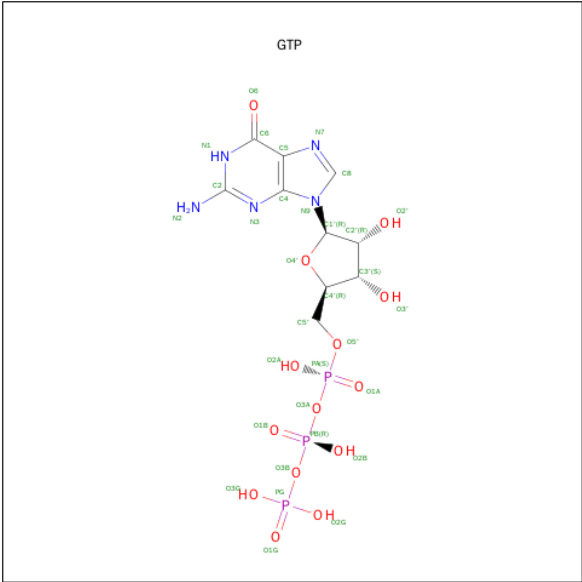
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	20	Total	C	N	O	P	0	0	0
			412	196	83	114	19			
2	D	20	Total	C	N	O	P	0	0	0
			412	196	83	114	19			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

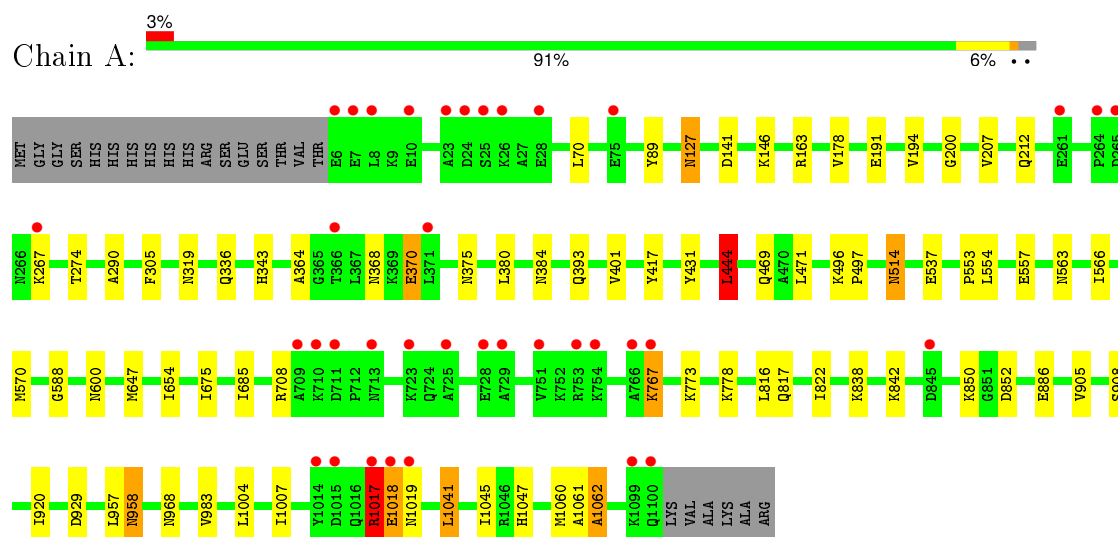
- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



3 Residue-property plots [i](#)

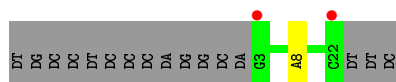
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Virion RNA polymerase



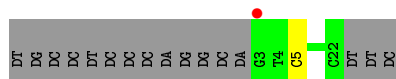
- Molecule 2: DNA (5'-D(*TP*GP*CP*CP*TP*CP*CP*CP*AP*GP*GP*CP*A*GP*TP*CP*AP*AP*AP*AP*GP*AP*AP*GP*CP*GP*GP*AP*GP*CP*TP*TP*CP*TP*TP*C)-3')

Chain C: 



- Molecule 2: DNA (5'-D(*TP*GP*CP*CP*TP*CP*CP*CP*AP*GP*GP*CP*A*GP*TP*CP*AP*AP*AP*AP*GP*AP*AP*GP*CP*GP*GP*AP*GP*CP*TP*TP*CP*TP*TP*C)-3')

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.35Å 111.38Å 275.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.69 49.39 – 2.69	Depositor EDS
% Data completeness (in resolution range)	96.8 (50.00-2.69) 96.8 (49.39-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	13.19 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.217 , 0.276 0.212 , 0.267	Depositor DCC
R_{free} test set	3440 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	31.7	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 67966 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	18029	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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, PO4

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	0.32	0/8583	0.47	1/11609 (0.0%)
1	B	0.32	0/8572	0.47	0/11596
2	C	0.62	0/464	1.15	0/715
2	D	0.63	0/464	1.13	0/715
All	All	0.34	0/18083	0.53	1/24635 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	444	LEU	CA-CB-CG	5.13	127.11	115.30

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	8454	0	8479	44	0
1	B	8443	0	8465	50	0
2	C	412	0	225	1	0
2	D	412	0	225	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	32	0	12	0	0
4	D	32	0	12	1	0
5	A	130	0	0	0	0
5	B	93	0	0	0	0
5	C	9	0	0	0	0
5	D	2	0	0	0	0
All	All	18029	0	17418	95	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 3.

All (95) 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:A:336:GLN:HE21	1:A:417:TYR:H	1.10	0.99
1:A:469:GLN:HE22	1:A:557:GLU:H	1.19	0.88
1:B:769:LYS:HG3	1:B:770:ILE:H	1.40	0.86
1:B:469:GLN:HE22	1:B:557:GLU:H	1.25	0.85
1:B:364:ALA:H	1:B:384:ASN:HD21	1.39	0.70
1:B:364:ALA:H	1:B:384:ASN:ND2	1.90	0.69
1:B:769:LYS:HG3	1:B:770:ILE:N	2.07	0.68
1:B:336:GLN:HE21	1:B:417:TYR:H	1.40	0.67
1:B:700:ARG:HE	1:B:723:LYS:HE3	1.59	0.67
1:B:191:GLU:HG3	1:B:375:ASN:HB3	1.78	0.65
1:B:816:LEU:HD23	1:B:980:ILE:HD13	1.79	0.64
1:A:444:LEU:HG	1:A:553:PRO:HB2	1.81	0.63
1:A:127:ASN:H	1:A:127:ASN:HD22	1.47	0.61
1:A:968:ASN:HD21	1:A:1060:MET:H	1.49	0.61
1:A:514:ASN:H	1:A:514:ASN:HD22	1.49	0.59
1:A:1041:LEU:O	1:A:1045:ILE:HG12	2.06	0.56
1:B:514:ASN:HD22	1:B:514:ASN:H	1.54	0.56
1:B:351:GLU:HG3	1:B:395:PHE:CE2	2.41	0.55
1:A:563:ASN:HD21	1:A:929:ASP:HB3	1.71	0.55
1:A:336:GLN:HE21	1:A:417:TYR:N	1.93	0.55
1:B:563:ASN:HD21	1:B:929:ASP:HB3	1.72	0.55
1:A:958:ASN:HD22	1:A:958:ASN:H	1.55	0.55
1:A:496:LYS:HB3	1:A:497:PRO:HD3	1.89	0.54
1:A:336:GLN:NE2	1:A:417:TYR:H	1.94	0.54
1:A:207:VAL:HG11	1:A:905:VAL:HG21	1.89	0.54
1:B:351:GLU:HG3	1:B:395:PHE:HE2	1.73	0.53
1:A:554:LEU:HD23	1:A:957:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:675:ILE:HD11	1:A:685:ILE:HG12	1.91	0.52
1:B:444:LEU:HG	1:B:553:PRO:HB2	1.91	0.52
1:B:449:THR:H	1:B:958:ASN:HD21	1.55	0.52
1:B:619:LEU:HD22	1:B:797:LEU:HD13	1.91	0.51
1:A:570:MET:O	1:A:1047:HIS:HE1	1.94	0.50
1:A:178:VAL:HG21	1:A:194:VAL:HA	1.94	0.50
1:A:816:LEU:CD1	1:A:983:VAL:HG21	2.42	0.49
1:B:37:SER:HB3	1:B:231:THR:HG22	1.94	0.49
1:B:715:SER:O	1:B:716:ALA:HB3	2.11	0.49
1:A:191:GLU:HB3	1:A:375:ASN:HD22	1.79	0.48
1:A:767:LYS:HA	1:A:767:LYS:HE3	1.94	0.48
1:A:554:LEU:O	1:A:957:LEU:HG	2.13	0.48
1:B:1061:ALA:O	1:B:1062:ALA:HB2	2.14	0.48
1:A:127:ASN:N	1:A:127:ASN:HD22	2.10	0.48
1:B:968:ASN:HD21	1:B:1060:MET:H	1.62	0.47
1:B:566:ILE:HG13	1:B:588:GLY:HA3	1.94	0.47
1:B:55:LEU:HD12	1:B:153:GLN:HG2	1.94	0.47
1:B:882:ILE:HD13	1:B:919:GLY:HA2	1.97	0.46
1:B:135:LEU:O	1:B:138:VAL:HG22	2.16	0.46
1:B:178:VAL:HG21	1:B:194:VAL:HA	1.97	0.46
1:A:838:LYS:O	1:A:842:LYS:HG2	2.15	0.46
1:B:127:ASN:H	1:B:127:ASN:HD22	1.62	0.46
1:A:200:GLY:HA2	1:A:274:THR:HG22	1.97	0.46
1:A:822:ILE:HG12	1:A:1007:ILE:HG23	1.97	0.46
1:A:968:ASN:ND2	1:A:1060:MET:H	2.11	0.46
1:B:655:ASN:HB2	1:B:663:GLU:HB3	1.98	0.45
1:B:319:ASN:HD22	1:B:319:ASN:HA	1.57	0.45
1:A:305:PHE:HE1	1:A:401:VAL:HG22	1.82	0.45
1:A:647:MET:HB3	1:A:654:ILE:HG13	1.99	0.45
1:A:1018:GLU:HG3	1:A:1019:ASN:H	1.82	0.45
1:A:1061:ALA:O	1:A:1062:ALA:CB	2.64	0.44
1:B:671:ASN:HB3	1:B:672:PRO:HD3	2.00	0.44
1:A:1061:ALA:O	1:A:1062:ALA:HB2	2.17	0.44
1:B:842:LYS:HB3	1:B:848:TRP:CD2	2.52	0.44
1:B:848:TRP:CH2	1:B:850:LYS:HA	2.53	0.44
1:B:384:ASN:HD22	1:B:384:ASN:HA	1.61	0.44
1:A:370:GLU:HA	1:A:773:LYS:HE2	2.00	0.44
1:A:817:GLN:HB2	1:A:920:ILE:HD11	2.00	0.44
1:A:393:GLN:HG2	1:A:431:TYR:HB2	2.00	0.44
1:A:141:ASP:HB2	1:A:146:LYS:HE3	1.99	0.43
1:B:802:THR:HG23	1:B:810:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:821:GLN:HE22	1:B:914:GLN:HE21	1.65	0.43
1:B:620:MET:HG3	1:B:664:LEU:HD12	2.00	0.43
1:B:783:LYS:O	1:B:787:GLU:HG2	2.18	0.43
1:B:1016:GLN:O	1:B:1020:ALA:HB2	2.19	0.42
1:B:141:ASP:HB2	1:B:146:LYS:HG2	2.02	0.42
1:A:343:HIS:HE1	1:A:537:GLU:OE2	2.03	0.42
1:A:364:ALA:H	1:A:384:ASN:HD21	1.66	0.42
1:B:598:THR:HG22	1:B:1066:PRO:HD3	2.02	0.42
1:A:89:TYR:CZ	1:A:290:ALA:HB3	2.55	0.42
1:B:563:ASN:HA	1:B:1059:GLN:HE22	1.85	0.41
1:A:566:ILE:HG13	1:A:588:GLY:HA3	2.02	0.41
1:B:920:ILE:HB	1:B:921:PRO:CD	2.50	0.41
1:A:886:GLU:HG3	1:A:908:SER:HB3	2.02	0.41
1:A:1017:ARG:O	1:A:1019:ASN:N	2.54	0.41
1:A:886:GLU:O	2:C:8:DA:H4'	2.20	0.41
1:B:668:ILE:H	1:B:668:ILE:HG13	1.73	0.41
2:D:5:DC:N3	4:D:26:GTP:N1	2.60	0.41
1:B:634:MET:N	1:B:635:PRO:HD2	2.36	0.41
1:B:61:ALA:HA	1:B:67:ARG:HB3	2.02	0.41
1:B:394:LEU:O	1:B:398:ILE:HG12	2.20	0.41
1:A:600:ASN:H	1:A:600:ASN:ND2	2.18	0.41
1:B:16:TYR:O	1:B:35:LYS:HE3	2.21	0.41
1:B:870:ALA:HB2	1:B:989:LYS:HD3	2.04	0.40
1:B:715:SER:O	1:B:716:ALA:CB	2.69	0.40
1:A:364:ALA:HB2	1:A:380:LEU:HD22	2.03	0.40
1:B:597:LYS:HE2	1:B:602:HIS:HB2	2.02	0.40
1:B:644:LEU:HD22	1:B:662:LEU:HD21	2.04	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	1093/1118 (98%)	1068 (98%)	22 (2%)	3 (0%)	46 75
1	B	1092/1118 (98%)	1064 (97%)	24 (2%)	4 (0%)	39 69
All	All	2185/2236 (98%)	2132 (98%)	46 (2%)	7 (0%)	46 75

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1018	GLU
1	A	1062	ALA
1	B	1062	ALA
1	A	1017	ARG
1	B	716	ALA
1	B	769	LYS
1	B	770	ILE

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	916/935 (98%)	896 (98%)	20 (2%)	60 86
1	B	915/935 (98%)	895 (98%)	20 (2%)	60 86
All	All	1831/1870 (98%)	1791 (98%)	40 (2%)	60 86

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	LEU
1	A	127	ASN
1	A	163	ARG
1	A	212	GLN
1	A	267	LYS
1	A	319	ASN
1	A	368	ASN
1	A	370	GLU
1	A	444	LEU

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Mol	Chain	Res	Type
1	A	471	LEU
1	A	514	ASN
1	A	708	ARG
1	A	767	LYS
1	A	778	LYS
1	A	850	LYS
1	A	852	ASP
1	A	958	ASN
1	A	1004	LEU
1	A	1017	ARG
1	A	1041	LEU
1	B	52	GLU
1	B	82	ASN
1	B	124	THR
1	B	127	ASN
1	B	163	ARG
1	B	210	LEU
1	B	319	ASN
1	B	368	ASN
1	B	406	GLU
1	B	444	LEU
1	B	447	LYS
1	B	471	LEU
1	B	514	ASN
1	B	520	ASN
1	B	656	LEU
1	B	670	LYS
1	B	817	GLN
1	B	838	LYS
1	B	929	ASP
1	B	1050	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	82	ASN
1	A	127	ASN
1	A	150	GLN
1	A	212	GLN
1	A	225	ASN
1	A	316	GLN

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Mol	Chain	Res	Type
1	A	319	ASN
1	A	324	ASN
1	A	336	GLN
1	A	343	HIS
1	A	348	GLN
1	A	368	ASN
1	A	373	ASN
1	A	375	ASN
1	A	384	ASN
1	A	414	HIS
1	A	469	GLN
1	A	506	ASN
1	A	514	ASN
1	A	563	ASN
1	A	600	ASN
1	A	602	HIS
1	A	613	GLN
1	A	639	GLN
1	A	724	GLN
1	A	781	GLN
1	A	815	GLN
1	A	817	GLN
1	A	823	GLN
1	A	954	ASN
1	A	958	ASN
1	A	968	ASN
1	A	1035	ASN
1	A	1047	HIS
1	A	1059	GLN
1	B	82	ASN
1	B	127	ASN
1	B	140	GLN
1	B	150	GLN
1	B	186	GLN
1	B	255	ASN
1	B	314	ASN
1	B	316	GLN
1	B	319	ASN
1	B	324	ASN
1	B	336	GLN
1	B	343	HIS
1	B	348	GLN

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Mol	Chain	Res	Type
1	B	368	ASN
1	B	375	ASN
1	B	384	ASN
1	B	414	HIS
1	B	454	ASN
1	B	469	GLN
1	B	514	ASN
1	B	520	ASN
1	B	602	HIS
1	B	629	ASN
1	B	639	GLN
1	B	786	GLN
1	B	803	GLN
1	B	815	GLN
1	B	817	GLN
1	B	833	GLN
1	B	878	GLN
1	B	892	ASN
1	B	893	GLN
1	B	914	GLN
1	B	954	ASN
1	B	958	ASN
1	B	968	ASN
1	B	1035	ASN
1	B	1047	HIS
1	B	1059	GLN

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

4 ligands are modelled in this entry.

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	$\# Z > 2$
3	PO4	A	1107	-	4,4,4	0.47	0	6,6,6	0.27	0
3	PO4	B	1107	-	4,4,4	0.45	0	6,6,6	0.27	0
4	GTP	C	26	-	25,34,34	0.97	2 (8%)	34,54,54	1.68	7 (20%)
4	GTP	D	26	-	25,34,34	0.94	1 (4%)	34,54,54	1.70	7 (20%)

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
3	PO4	A	1107	-	-	0/0/0/0	0/0/0/0
3	PO4	B	1107	-	-	0/0/0/0	0/0/0/0
4	GTP	C	26	-	-	0/18/38/38	0/3/3/3
4	GTP	D	26	-	-	0/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	26	GTP	C2-N1	2.02	1.39	1.35
4	D	26	GTP	C6-N1	2.98	1.38	1.33
4	C	26	GTP	C6-N1	3.19	1.39	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	26	GTP	N3-C2-N1	-4.97	119.88	127.44
4	D	26	GTP	N3-C2-N1	-4.84	120.06	127.44
4	D	26	GTP	PA-O3A-PB	-3.58	122.67	132.73
4	C	26	GTP	PA-O3A-PB	-3.41	123.16	132.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	26	GTP	PB-O3B-PG	-3.19	121.97	132.67
4	C	26	GTP	C5-C6-N1	-3.12	119.32	123.59
4	C	26	GTP	PB-O3B-PG	-3.08	122.34	132.67
4	D	26	GTP	C2'-C1'-N9	-2.94	109.80	114.29
4	D	26	GTP	C5-C6-N1	-2.92	119.59	123.59
4	C	26	GTP	C2'-C1'-N9	-2.26	110.83	114.29
4	D	26	GTP	N2-C2-N1	2.01	120.53	117.20
4	C	26	GTP	C4'-O4'-C1'	2.13	112.06	109.72
4	D	26	GTP	C6-N1-C2	2.87	119.92	115.94
4	C	26	GTP	C6-N1-C2	3.02	120.13	115.94

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
4	D	26	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, 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	1095/1118 (97%)	0.07	37 (3%) 49 49	12, 26, 49, 60	0
1	B	1094/1118 (97%)	0.09	37 (3%) 49 49	11, 26, 46, 64	0
2	C	20/36 (55%)	0.06	2 (10%) 9 7	24, 34, 52, 54	0
2	D	20/36 (55%)	-0.08	1 (5%) 32 31	17, 30, 47, 56	0
All	All	2229/2308 (96%)	0.07	77 (3%) 48 48	11, 26, 48, 64	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1018	GLU	5.7
1	A	10	GLU	4.9
1	A	7	GLU	4.7
1	A	28	GLU	4.4
1	A	1015	ASP	3.8
1	B	726	ALA	3.8
1	B	725	ALA	3.7
1	B	6	GLU	3.6
1	A	8	LEU	3.6
1	B	1018	GLU	3.5
1	B	7	GLU	3.5
1	B	264	PRO	3.4
1	A	725	ALA	3.4
1	A	1100	GLN	3.4
1	A	1014	TYR	3.3
1	B	1015	ASP	3.3
1	B	10	GLU	3.3
1	A	713	ASN	3.3
1	B	1096	GLU	3.3
1	A	754	LYS	3.2
1	A	265	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	1019	ASN	3.2
1	B	265	ASP	3.1
1	B	8	LEU	3.1
1	B	1014	TYR	3.1
1	B	769	LYS	3.0
1	B	1098	ARG	3.0
1	A	261	GLU	2.9
1	B	714	ILE	2.9
1	B	366	THR	2.9
2	D	3	DG	2.9
1	B	281	PHE	2.8
1	A	845	ASP	2.8
1	A	26	LYS	2.8
1	B	727	SER	2.8
1	A	766	ALA	2.8
1	B	713	ASN	2.8
1	B	730	HIS	2.7
1	B	723	LYS	2.7
1	A	24	ASP	2.7
1	A	729	ALA	2.7
1	A	753	ARG	2.6
1	A	264	PRO	2.6
1	B	710	LYS	2.5
1	A	267	LYS	2.5
1	B	767	LYS	2.5
1	B	42	GLU	2.5
1	A	767	LYS	2.5
1	B	43	GLU	2.4
1	A	1017	ARG	2.4
1	B	755	GLY	2.3
1	A	728	GLU	2.3
1	A	366	THR	2.3
1	B	26	LYS	2.3
1	A	711	ASP	2.3
1	B	712	PRO	2.3
1	B	763	GLY	2.3
2	C	22	DC	2.3
1	A	6	GLU	2.3
1	A	751	VAL	2.2
1	A	25	SER	2.2
1	A	723	LYS	2.2
1	B	754	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	709	ALA	2.2
1	B	722	GLY	2.2
1	B	764	THR	2.2
1	A	710	LYS	2.2
1	A	371	LEU	2.2
2	C	3	DG	2.2
1	B	768	GLY	2.1
1	A	75	GLU	2.1
1	B	704	VAL	2.1
1	B	724	GLN	2.1
1	A	1099	LYS	2.1
1	A	23	ALA	2.1
1	B	720	MET	2.0
1	B	708	ARG	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(\AA^2)	Q<0.9
4	GTP	D	26	32/32	0.80	0.28	12.27	54,58,68,68	0
3	PO4	B	1107	5/5	0.91	0.23	7.66	57,57,57,57	0
4	GTP	C	26	32/32	0.79	0.25	2.39	43,47,58,58	0
3	PO4	A	1107	5/5	0.96	0.20	1.41	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.