



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 07:51 PM GMT

PDB ID : 4IRC
Title : Polymerase-DNA complex
Authors : Nair, D.T.; Sharma, A.
Deposited on : 2013-01-14
Resolution : 2.67 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

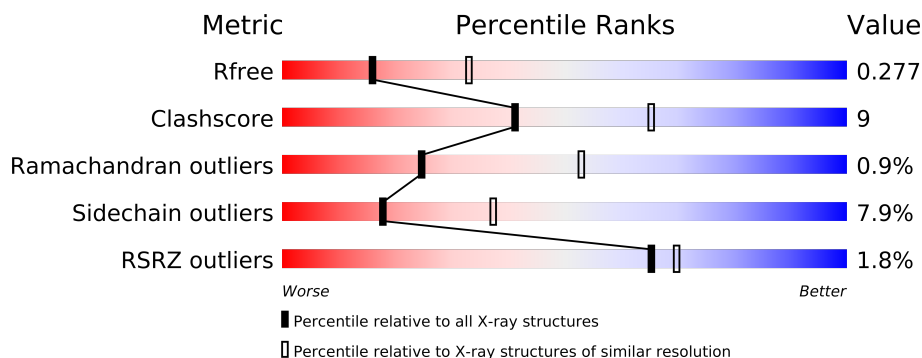
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **FAILED**
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.67 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}	66092	2010 (2.70-2.66)
Clashscore	79885	2450 (2.70-2.66)
Ramachandran outliers	78287	2410 (2.70-2.66)
Sidechain outliers	78261	2410 (2.70-2.66)
RSRZ outliers	66119	2013 (2.70-2.66)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	B	18	
1	G	18	
2	H	14	
3	C	17	
4	A	342	
4	F	342	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6887 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called DNA (5'-D(*TP*CP*TP*GP*GP*GP*GP*TP*CP*CP*TP*AP*GP*GP*AP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	18	Total	C	N	O	P	0	0	0
			365	174	66	108	17			
1	B	18	Total	C	N	O	P	0	0	0
			365	174	66	108	17			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	14	Total	C	N	O	P	0	0	0
			284	135	54	82	13			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	17	Total	C	N	O	P	0	0	0
			344	164	64	100	16			

- Molecule 4 is a protein called DNA polymerase IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	342	Total	C	N	O	S	0	0	0
			2688	1695	494	485	14			
4	A	342	Total	C	N	O	S	0	0	0
			2688	1695	494	485	14			

There are 8 discrepancies between the modelled and reference sequences:

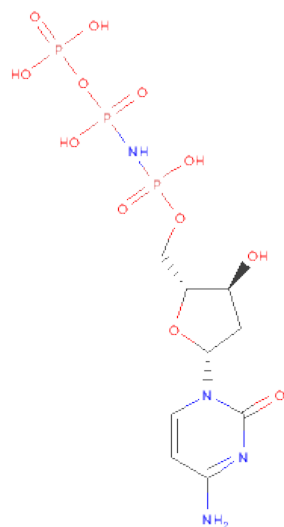
Chain	Residue	Modelled	Actual	Comment	Reference
F	0	GLY	-	EXPRESSION TAG	UNP Q47155

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1	SER	-	EXPRESSION TAG	UNP Q47155
F	64	ALA	LYS	CONFLICT	UNP Q47155
F	205	ALA	LYS	CONFLICT	UNP Q47155
A	0	GLY	-	EXPRESSION TAG	UNP Q47155
A	1	SER	-	EXPRESSION TAG	UNP Q47155
A	64	ALA	LYS	CONFLICT	UNP Q47155
A	205	ALA	LYS	CONFLICT	UNP Q47155

- Molecule 5 is 2'-DEOXY-5'-O-[(R)-HYDROXY{[(R)-HYDROXY(PHOSPHONOOXY)PHOSPHORYL]AMINO}PHOSPHORYL]CYTIDINE (three-letter code: 0KX) (formula: C₉H₁₇N₄O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	F	1	Total	C	N	O	P	0	0
			28	9	4	12	3		
5	A	1	Total	C	N	O	P	0	0
			28	9	4	12	3		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Mg	0	0
			2	2		
6	F	2	Total	Mg	0	0
			2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	G	10	Total 10	O 10	0	0
7	H	6	Total 6	O 6	0	0
7	B	2	Total 2	O 2	0	0
7	C	2	Total 2	O 2	0	0
7	F	54	Total 54	O 54	0	0
7	A	19	Total 19	O 19	0	0

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 ($RSRZ > 2$). 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.

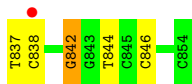
- Molecule 1: DNA (5'-D(*TP*CP*TP*GP*GP*GP*GP*TP*CP*CP*TP*AP*GP*GP*AP*CP*CP*C)-3')

Chain G: 



- Molecule 1: DNA (5'-D(*TP*CP*TP*GP*GP*GP*GP*TP*CP*CP*TP*AP*GP*GP*AP*CP*CP*C)-3')

Chain B: 



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

Chain H: 



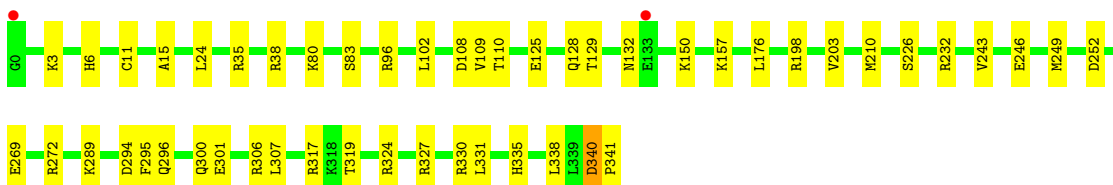
- Molecule 3: DNA (5'-D(*CP*TP*AP*GP*GP*GP*TP*CP*CP*TP*AP*GP*GP*AP*CP*CP*C)-3')

Chain C: 



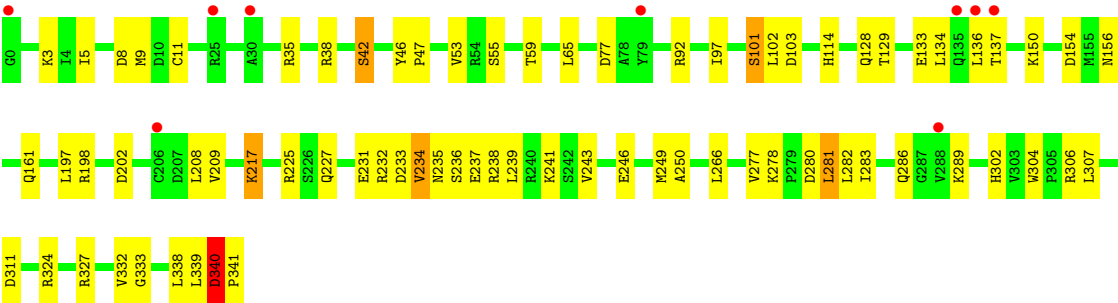
- Molecule 4: DNA polymerase IV

Chain F: 



● Molecule 4: DNA polymerase IV

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.14Å 56.95Å 110.81Å 90.00° 93.53° 90.00°	Depositor
Resolution (Å)	45.30 – 2.67 45.26 – 2.67	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.30-2.67) 99.7 (45.26-2.67)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.225 , 0.275 0.224 , 0.277	Depositor DCC
R_{free} test set	1529 reflections (5.22%)	DCC
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 36.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6887	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 0KX, 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	B	0.51	0/408	0.88	1/628 (0.2%)
1	G	0.55	0/408	0.80	0/628
2	H	0.45	0/318	0.78	0/489
3	C	0.47	0/385	0.81	0/592
4	A	0.60	0/2739	0.78	1/3699 (0.0%)
4	F	0.66	0/2739	0.81	0/3699
All	All	0.60	0/6997	0.80	2/9735 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	324	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	B	842	DG	O5'-P-OP2	-5.38	100.85	105.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	340	ASP	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	365	0	0	8	0
1	G	365	0	0	1	0
2	H	284	0	0	1	0
3	C	344	0	0	2	0
4	A	2688	0	84	33	0
4	F	2688	0	84	29	0
5	A	28	0	0	1	0
5	F	28	0	0	1	0
6	A	2	0	0	0	0
6	F	2	0	0	0	0
7	A	19	0	0	2	0
7	B	2	0	0	0	0
7	C	2	0	0	1	0
7	F	54	0	0	7	0
7	G	10	0	0	0	0
7	H	6	0	0	0	0
All	All	6887	0	168	63	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (63) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:846:DC:OP2	4:A:217:LYS:NZ	1.80	1.14
1:B:846:DC:P	4:A:217:LYS:NZ	2.43	0.90
1:G:837:DT:O3'	4:F:35:ARG:NH2	2.09	0.84
4:F:129:THR:N	7:F:503:HOH:O	2.18	0.77
4:A:92:ARG:NH2	4:A:133:GLU:OE2	2.20	0.75
4:F:11:CYS:N	5:F:401:OKX:O3G	2.20	0.74
4:A:235:ASN:HD22	4:A:238:ARG:HD3	1.53	0.73
1:B:837:DT:O3'	4:A:35:ARG:NH2	2.22	0.72
4:A:235:ASN:ND2	4:A:238:ARG:HD3	2.06	0.71
4:F:246:GLU:OE1	4:F:289:LYS:NZ	2.23	0.71
4:F:296:GLN:OE1	4:F:327:ARG:NH1	2.26	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:F:132:ASN:N	7:F:503:HOH:O	2.31	0.62
4:F:6:HIS:CG	7:F:541:HOH:O	2.52	0.61
4:A:304:TRP:CD1	4:A:306:ARG:O	2.54	0.61
4:A:327:ARG:NH1	7:A:505:HOH:O	2.32	0.61
4:F:249:MET:SD	4:F:249:MET:N	2.74	0.60
4:A:234:VAL:HG12	4:A:235:ASN:H	1.66	0.60
4:A:250:ALA:O	7:A:510:HOH:O	2.17	0.59
4:A:225:ARG:NH2	4:A:232:ARG:HE	2.01	0.58
3:C:857:DC:O5'	7:C:902:HOH:O	2.17	0.58
4:F:108:ASP:OD1	4:F:110:THR:OG1	2.21	0.58
4:F:38:ARG:NH1	4:F:252:ASP:OD1	2.36	0.58
1:B:844:DT:OP1	4:A:241:LYS:N	2.37	0.58
4:F:3:LYS:N	4:F:110:THR:CG2	2.68	0.57
3:C:873:DC:OP1	4:A:150:LYS:NZ	2.39	0.55
4:F:6:HIS:CD2	7:F:541:HOH:O	2.60	0.54
4:F:269:GLU:OE1	4:F:272:ARG:NH2	2.41	0.53
4:F:128:GLN:O	4:F:129:THR:OG1	2.27	0.53
4:F:203:VAL:CG1	4:F:226:SER:OG	2.57	0.53
4:F:306:ARG:O	4:F:307:LEU:C	2.47	0.52
4:F:300:GLN:OE1	4:F:319:THR:OG1	2.28	0.52
4:A:278:LYS:NZ	4:A:282:LEU:O	2.43	0.52
4:A:97:ILE:O	4:A:236:SER:HB3	2.08	0.52
4:A:128:GLN:O	4:A:129:THR:OG1	2.28	0.51
4:A:156:ASN:ND2	4:A:161:GLN:O	2.44	0.50
4:F:83:SER:OG	4:F:102:LEU:O	2.31	0.49
4:F:294:ASP:O	4:F:296:GLN:N	2.47	0.48
4:A:42:SER:O	4:A:55:SER:OG	2.32	0.48
1:B:846:DC:O5'	4:A:217:LYS:NZ	2.47	0.47
4:F:125:GLU:O	4:F:128:GLN:O	2.32	0.47
4:A:101:SER:OG	4:A:102:LEU:N	2.48	0.47
4:A:77:ASP:OD1	4:A:77:ASP:N	2.49	0.46
4:F:6:HIS:CE1	7:F:541:HOH:O	2.69	0.46
4:F:301:GLU:OE1	4:F:335:HIS:ND1	2.49	0.45
4:F:198:ARG:NH2	7:F:531:HOH:O	2.49	0.45
4:F:340:ASP:N	4:F:341:PRO:CD	2.80	0.45
4:F:96:ARG:NE	7:F:505:HOH:O	2.50	0.45
1:B:838:DC:P	4:A:35:ARG:NH2	2.90	0.44
4:A:302:HIS:NE2	4:A:311:ASP:OD2	2.50	0.44
1:B:842:DG:OP2	4:A:246:GLU:N	2.52	0.43
4:A:38:ARG:NH2	4:A:249:MET:O	2.52	0.42
4:F:324:ARG:O	4:F:327:ARG:N	2.52	0.42
4:A:340:ASP:CB	4:A:341:PRO:CD	2.98	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:F:11:CYS:O	4:F:11:CYS:SG	2.78	0.42
4:A:286:GLN:NE2	4:A:311:ASP:OD2	2.52	0.42
4:F:11:CYS:O	4:F:15:ALA:N	2.53	0.42
4:A:8:ASP:OD1	4:A:9:MET:O	2.37	0.42
4:A:11:CYS:N	5:A:401:OKX:O3G	2.53	0.41
4:A:289:LYS:N	4:A:333:GLY:O	2.54	0.41
4:A:46:TYR:N	4:A:47:PRO:CD	2.84	0.41
2:H:873:DC:OP1	4:F:150:LYS:NZ	2.54	0.41
4:A:280:ASP:O	4:A:282:LEU:N	2.54	0.40
1:B:838:DC:OP1	4:A:35:ARG:NH2	2.55	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	
4	A	340/342 (99%)	315 (93%)	21 (6%)	4 (1%)	19	43
4	F	340/342 (99%)	316 (93%)	22 (6%)	2 (1%)	33	64
All	All	680/684 (99%)	631 (93%)	43 (6%)	6 (1%)	25	53

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	295	PHE
4	A	340	ASP
4	A	59	THR
4	A	281	LEU
4	F	340	ASP
4	A	234	VAL

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
4	A	286/286 (100%)	253 (88%)	33 (12%)	8 18
4	F	286/286 (100%)	274 (96%)	12 (4%)	40 72
All	All	572/572 (100%)	527 (92%)	45 (8%)	18 37

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	24	LEU
4	F	80	LYS
4	F	109	VAL
4	F	157	LYS
4	F	176	LEU
4	F	210	MET
4	F	232	ARG
4	F	243	VAL
4	F	317	ARG
4	F	330	ARG
4	F	331	LEU
4	F	338	LEU
4	A	3	LYS
4	A	5	ILE
4	A	42	SER
4	A	53	VAL
4	A	65	LEU
4	A	101	SER
4	A	103	ASP
4	A	114	HIS
4	A	134	LEU
4	A	136	LEU
4	A	137	THR
4	A	154	ASP
4	A	197	LEU
4	A	198	ARG
4	A	202	ASP
4	A	208	LEU
4	A	209	VAL

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Mol	Chain	Res	Type
4	A	217	LYS
4	A	227	GLN
4	A	231	GLU
4	A	233	ASP
4	A	237	GLU
4	A	239	LEU
4	A	243	VAL
4	A	266	LEU
4	A	277	VAL
4	A	281	LEU
4	A	283	ILE
4	A	307	LEU
4	A	332	VAL
4	A	338	LEU
4	A	339	LEU
4	A	340	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 6 ligands modelled in this entry, 4 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	$\# Z > 2$
5	0KX	A	401	6	29,29,29	1.92	6 (20%)	41,45,45	2.15	10 (24%)
5	0KX	F	401	6	29,29,29	2.07	6 (20%)	41,45,45	2.12	11 (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
5	0KX	A	401	6	-	0/16/34/34	0/2/2/2
5	0KX	F	401	6	-	0/16/34/34	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	401	0KX	PA-O1A	5.69	1.53	1.46
5	F	401	0KX	PB-N3A	-4.87	1.60	1.64
5	A	401	0KX	PA-O5'	4.66	1.61	1.57
5	A	401	0KX	PB-N3A	-4.28	1.60	1.64
5	F	401	0KX	PA-O5'	4.23	1.61	1.57
5	F	401	0KX	PB-O2B	4.22	1.51	1.46
5	A	401	0KX	PA-O1A	3.78	1.50	1.46
5	A	401	0KX	C2-N1	3.67	1.42	1.38
5	A	401	0KX	PA-N3A	-3.37	1.61	1.64
5	A	401	0KX	PB-O2B	3.11	1.50	1.46
5	F	401	0KX	C2-N1	3.04	1.41	1.38
5	F	401	0KX	PA-N3A	-3.02	1.61	1.64

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	401	0KX	C6-C5-C4	8.62	121.05	117.47
5	F	401	0KX	C6-C5-C4	7.19	120.45	117.47
5	F	401	0KX	O2A-PA-O1A	4.74	120.84	109.89
5	A	401	0KX	O1B-PB-O2B	4.02	119.16	109.89
5	F	401	0KX	O1A-PA-N3A	-3.98	105.81	111.83
5	F	401	0KX	PG-O3B-PB	-3.91	118.44	131.81
5	A	401	0KX	O3B-PB-N3A	-3.59	96.64	106.59
5	A	401	0KX	C2-N3-C4	3.50	120.64	115.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	401	0KX	PB-N3A-PA	-3.32	124.88	130.03
5	A	401	0KX	O2A-PA-O1A	3.21	117.29	109.89
5	F	401	0KX	O2B-PB-N3A	-3.15	107.07	111.83
5	A	401	0KX	N4-C4-N3	2.92	122.19	116.59
5	F	401	0KX	O3B-PB-N3A	-2.74	98.99	106.59
5	F	401	0KX	O5'-PA-N3A	-2.71	99.12	106.80
5	A	401	0KX	O5'-PA-N3A	-2.60	99.43	106.80
5	F	401	0KX	O1B-PB-O2B	2.52	115.71	109.89
5	A	401	0KX	C2'-C1'-N1	-2.50	107.60	114.08
5	A	401	0KX	O1G-PG-O3G	2.43	117.08	107.61
5	A	401	0KX	C5-C4-N3	-2.09	118.85	121.68
5	F	401	0KX	C2-N3-C4	2.07	118.57	115.57
5	F	401	0KX	C5-C6-N1	-2.06	118.88	121.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	B	18/18 (100%)	-0.08	1 (5%) 24 25	55, 78, 126, 154	0
1	G	18/18 (100%)	-0.33	1 (5%) 24 25	42, 65, 137, 158	0
2	H	14/14 (100%)	-0.17	0 100 100	42, 59, 145, 147	0
3	C	17/17 (100%)	0.05	1 (5%) 22 23	58, 78, 110, 184	0
4	A	342/342 (100%)	0.15	9 (2%) 53 57	32, 72, 106, 147	0
4	F	342/342 (100%)	-0.12	2 (0%) 86 90	34, 59, 85, 107	0
All	All	751/751 (100%)	0.00	14 (1%) 65 68	32, 64, 105, 184	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	0	GLY	9.4
4	A	136	LEU	6.2
3	C	857	DC	6.0
4	A	135	GLN	2.9
1	B	838	DC	2.6
4	F	0	GLY	2.5
4	A	137	THR	2.4
4	A	79	TYR	2.3
4	A	25	ARG	2.3
4	A	288	VAL	2.3
4	F	133	GLU	2.2
4	A	30	ALA	2.2
4	A	206	CYS	2.0
1	G	837	DT	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	MG	F	402	1/1	0.22	1.41	47,47,47,47	0
6	MG	A	403	1/1	0.15	0.17	120,120,120,120	0
6	MG	F	403	1/1	0.16	0.11	78,78,78,78	0
5	0KX	F	401	28/28	0.17	0.11	39,45,49,53	0
6	MG	A	402	1/1	0.16	-0.22	50,50,50,50	0
5	0KX	A	401	28/28	0.16	-0.40	58,67,80,84	0

6.5 Other polymers

There are no such residues in this entry.