



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 10, 2017 – 06:49 PM EDT

PDB ID : 5J2M
Title : HIV-1 reverse transcriptase in complex with DNA and EFdA-triphosphate, a translocation-defective RT inhibitor
Authors : Salie, Z.L.; Kirby, K.A.; Sarafianos, S.G.
Deposited on : unknown
Resolution : 2.43 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
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-20029824

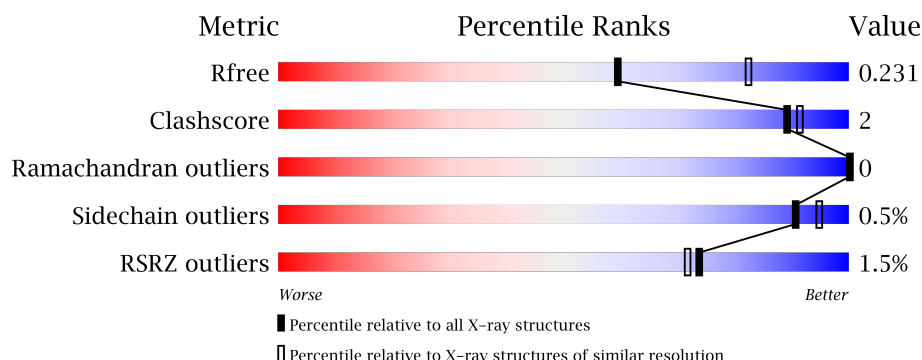
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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	1152 (2.46-2.42)
Clashscore	112137	1224 (2.46-2.42)
Ramachandran outliers	110173	1217 (2.46-2.42)
Sidechain outliers	110143	1217 (2.46-2.42)
RSRZ outliers	101464	1158 (2.46-2.42)

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	560	<div> <div style="width: 93%;"></div> <div style="width: 7%;"></div> </div>
2	B	440	<div> <div style="width: 3%;"></div> <div style="width: 86%;"></div> <div style="width: 5%;"></div> <div style="width: 10%;"></div> </div>
3	P	21	<div> <div style="width: 57%;"></div> <div style="width: 29%;"></div> <div style="width: 14%;"></div> </div>
4	T	27	<div> <div style="width: 4%;"></div> <div style="width: 74%;"></div> <div style="width: 15%;"></div> <div style="width: 11%;"></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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MG	A	602	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 9107 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 HIV-1 reverse transcriptase p51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	558	Total	C	N	O	S	7	0	0
			4542	2935	760	839	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	258	CYS	GLN	engineered mutation	UNP P04585
A	280	SER	CYS	engineered mutation	UNP P04585

- Molecule 2 is a protein called HIV-1 reverse transcriptase p51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	398	Total	C	N	O	S	16	0	0
			3281	2132	548	595	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P04585

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	18	Total	C	N	O	P	0	0	0
			370	176	64	111	18			

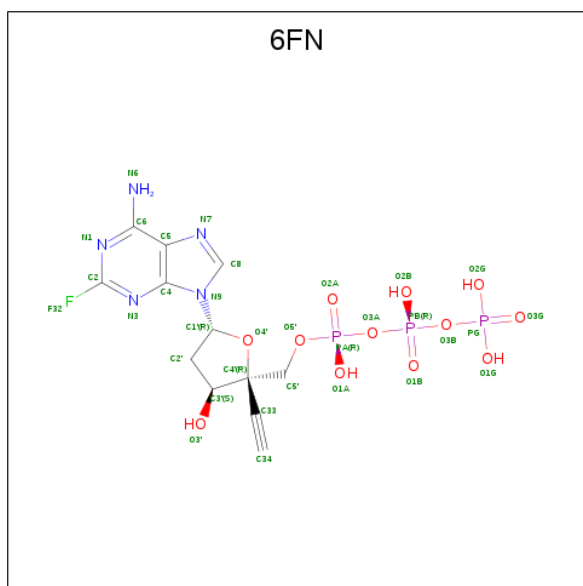
- Molecule 4 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	T	24	Total	C	N	O	P	0	0	0
			494	233	97	141	23			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Mg	0	0
			3	3		

- Molecule 6 is 2'-deoxy-4'-ethynyl-2-fluoroadenosine 5'-(tetrahydrogen triphosphate) (three-letter code: 6FN) (formula: C₁₂H₁₅FN₅O₁₂P₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	F	N	O	P	0	0
			33	12	1	5	12	3		

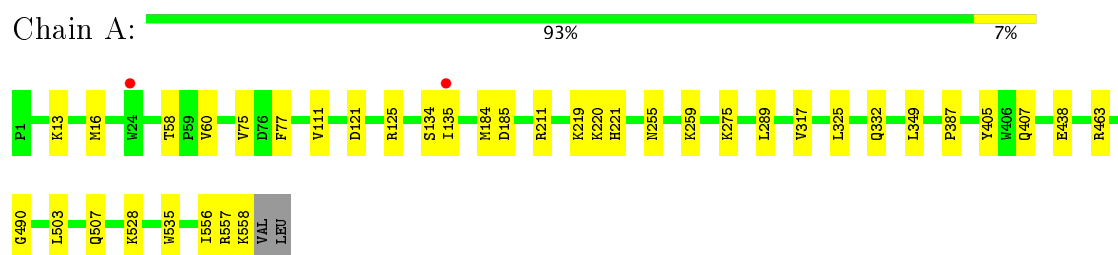
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	219	Total	O	0	0
			219	219		
7	B	131	Total	O	0	0
			131	131		
7	P	15	Total	O	0	0
			15	15		
7	T	19	Total	O	0	0
			19	19		

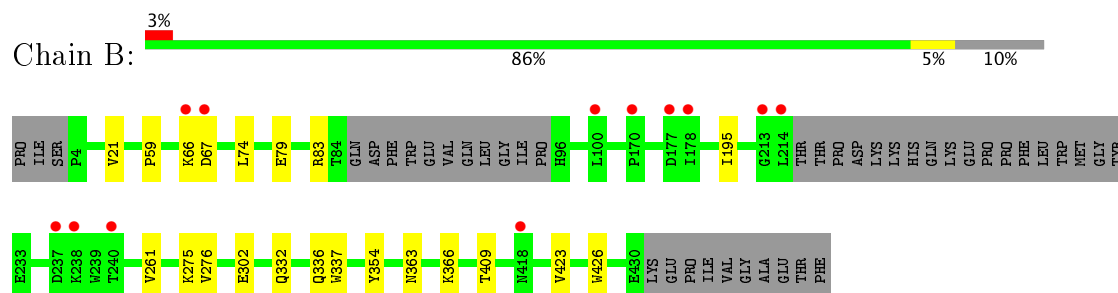
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: HIV-1 reverse transcriptase p51 subunit



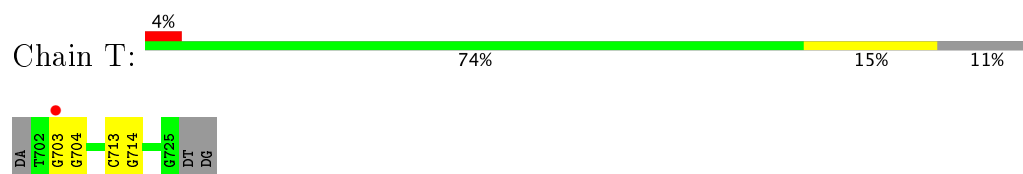
- Molecule 2: HIV-1 reverse transcriptase p51 subunit



- Molecule 3: DNA (5'-D(*AP*CP*AP*GP*TP*CP*CP*CP*TP*GP*TP*TP*CP*GP*GP*(M RG)P*CP*GP*CP*CP*G)-3')



- Molecule 4: DNA (27-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	167.47Å 169.76Å 101.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.23 – 2.43 65.23 – 2.43	Depositor EDS
% Data completeness (in resolution range)	99.5 (65.23-2.43) 99.5 (65.23-2.43)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.199 , 0.233 0.197 , 0.231	Depositor DCC
R_{free} test set	2764 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.343	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9107	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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, 0.333 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: 6FN, MG, MRG

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	0/4659	0.41	0/6328
2	B	0.24	0/3370	0.41	0/4575
3	P	0.51	0/382	0.90	0/584
4	T	0.48	0/555	0.80	0/856
All	All	0.27	0/8966	0.48	0/12343

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	4542	0	4599	22	0
2	B	3281	0	3320	10	0
3	P	370	0	206	5	0
4	T	494	0	269	2	0
5	A	3	0	0	0	0
6	A	33	0	0	0	0
7	A	219	0	0	3	2
7	B	131	0	0	0	0
7	P	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	T	19	0	0	0	0
All	All	9107	0	8394	37	2

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)
2:B:275:LYS:HE3	2:B:302:GLU:HG3	1.80	0.63
1:A:275:LYS:HD2	1:A:332:GLN:HG2	1.82	0.60
3:P:816:DG:H2'	3:P:817:MRG:C8	2.35	0.55
1:A:259:LYS:HA	3:P:819:DG:H5'	1.88	0.55
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.90	0.54
1:A:60:VAL:HG12	1:A:75:VAL:HG22	1.90	0.54
1:A:184:MET:HG3	3:P:822:DG:H1'	1.89	0.54
1:A:13:LYS:HB2	1:A:16:MET:HG3	1.90	0.54
1:A:556:ILE:HD12	1:A:557:ARG:HG3	1.91	0.52
1:A:558:LYS:NZ	7:A:718:HOH:O	2.43	0.51
1:A:332:GLN:O	7:A:701:HOH:O	2.20	0.50
4:T:713:DC:H2'	4:T:714:DG:C8	2.48	0.49
2:B:79:GLU:HG3	2:B:83:ARG:HE	1.78	0.47
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.97	0.46
1:A:255:ASN:HB2	1:A:289:LEU:HB3	1.96	0.46
4:T:703:DG:H2'	4:T:704:DG:C4	2.52	0.45
1:A:557:ARG:HB3	1:A:558:LYS:HD2	1.98	0.45
1:A:317:VAL:HG23	1:A:349:LEU:HD23	1.98	0.44
1:A:325:LEU:HB3	1:A:387:PRO:HB3	1.99	0.43
1:A:134:SER:OG	1:A:135:ILE:N	2.52	0.43
2:B:74:LEU:HD21	2:B:409:THR:HA	2.01	0.43
1:A:220:LYS:NZ	7:A:711:HOH:O	2.38	0.42
1:A:58:THR:HG21	1:A:77:PHE:CD1	2.54	0.42
2:B:332:GLN:HB2	2:B:336:GLN:HB2	2.01	0.42
2:B:423:VAL:HA	2:B:426:TRP:CD1	2.55	0.42
3:P:816:DG:H2'	3:P:817:MRG:H8	2.01	0.41
1:A:507:GLN:HB3	1:A:507:GLN:HE21	1.74	0.41
2:B:363:ASN:HB3	2:B:366:LYS:HB3	2.01	0.41
1:A:121:ASP:O	1:A:125:ARG:HG3	2.20	0.41
2:B:261:VAL:HG13	2:B:276:VAL:HG21	2.03	0.41
2:B:66:LYS:HG3	2:B:67:ASP:H	1.84	0.41
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:GLU:OE2	1:A:463:ARG:HD3	2.21	0.41
1:A:111:VAL:HB	1:A:185:ASP:HB2	2.03	0.41
2:B:337:TRP:O	2:B:354:TYR:N	2.49	0.40
3:P:810:DT:H2"	3:P:811:DG:H8	1.86	0.40
1:A:490:GLY:O	1:A:528:LYS:NZ	2.43	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:882:HOH:O	7:A:889:HOH:O[7_444]	2.15	0.05
7:A:790:HOH:O	7:A:889:HOH:O[7_444]	2.16	0.04

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	556/560 (99%)	543 (98%)	13 (2%)	0	100	100
2	B	392/440 (89%)	378 (96%)	14 (4%)	0	100	100
All	All	948/1000 (95%)	921 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	498/500 (100%)	495 (99%)	3 (1%)	89	93
2	B	360/400 (90%)	359 (100%)	1 (0%)	94	96
All	All	858/900 (95%)	854 (100%)	4 (0%)	91	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	211	ARG
1	A	219	LYS
1	A	221	HIS
2	B	195	ILE

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 molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	MRG	P	817	1,3,4	21,28,29	1.81	3 (14%)	24,39,42	1.49	4 (16%)

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	MRG	P	817	1,3,4	-	0/8/26/27	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	817	MRG	O5'-C5'	-2.65	1.41	1.44
3	P	817	MRG	C2-N2	3.99	1.40	1.34
3	P	817	MRG	O6-C6	4.37	1.35	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	817	MRG	C6-C5-C4	-5.38	115.50	120.84
3	P	817	MRG	C2'-C3'-C4'	-2.08	98.30	102.73
3	P	817	MRG	C22-C21-N2	2.09	117.03	111.46
3	P	817	MRG	C4-C5-N7	2.70	112.02	109.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	817	MRG	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are 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
6	6FN	A	604	5	24,35,35	2.29	9 (37%)	28,56,56	2.94	10 (35%)

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
6	6FN	A	604	5	-	0/23/50/50	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	604	6FN	C2'-C3'	-3.19	1.45	1.53
6	A	604	6FN	PG-O1G	-2.00	1.46	1.54
6	A	604	6FN	C2-N3	2.41	1.33	1.31
6	A	604	6FN	C5-N7	2.46	1.44	1.35
6	A	604	6FN	PG-O2G	2.54	1.65	1.54
6	A	604	6FN	C2-N1	3.21	1.34	1.31
6	A	604	6FN	PG-O3B	3.22	1.65	1.60
6	A	604	6FN	C6-N6	4.43	1.45	1.34
6	A	604	6FN	O4'-C1'	5.47	1.50	1.42

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	604	6FN	N3-C2-N1	-6.91	121.14	130.36
6	A	604	6FN	C8-N7-C5	-5.70	104.63	113.66
6	A	604	6FN	C2'-C1'-N9	-5.09	109.39	115.61
6	A	604	6FN	O1G-PG-O3G	-2.33	101.39	110.50
6	A	604	6FN	O1A-PA-O2A	-2.15	101.17	112.28
6	A	604	6FN	O2B-PB-O1B	-2.05	101.69	112.28
6	A	604	6FN	N6-C6-N1	2.77	121.10	117.00
6	A	604	6FN	F32-C2-N1	4.94	119.41	114.81
6	A	604	6FN	F32-C2-N3	4.98	119.45	114.81
6	A	604	6FN	N3-C4-N9	6.93	135.83	126.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	A	558/560 (99%)	-0.08	2 (0%) 92 93	26, 42, 75, 122	2 (0%)
2	B	398/440 (90%)	0.17	12 (3%) 51 46	27, 53, 87, 110	5 (1%)
3	P	17/21 (80%)	-0.57	0 100 100	36, 54, 70, 70	0
4	T	24/27 (88%)	-0.17	1 (4%) 37 34	35, 60, 87, 117	0
All	All	997/1048 (95%)	0.01	15 (1%) 74 72	26, 47, 84, 122	7 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	67	ASP	3.6
2	B	238	LYS	3.3
1	A	24	TRP	3.3
2	B	177	ASP	3.2
1	A	135	ILE	3.0
2	B	214	LEU	3.0
2	B	178	ILE	2.7
2	B	213	GLY	2.7
2	B	66	LYS	2.7
2	B	170	PRO	2.6
4	T	703	DG	2.6
2	B	418	ASN	2.3
2	B	237	ASP	2.2
2	B	100	LEU	2.1
2	B	240	THR	2.1

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

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	MRG	P	817	26/27	0.94	0.15	-	45,54,81,91	0

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
5	MG	A	602	1/1	0.70	0.24	5.87	57,57,57,57	0
5	MG	A	601	1/1	0.96	0.17	1.98	22,22,22,22	0
6	6FN	A	604	33/33	0.98	0.13	-0.33	27,35,42,45	0
5	MG	A	603	1/1	0.93	0.41	-	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.