wwPDB X-ray Structure Validation Summary Report (i)

Oct 19, 2026 – 08:08 PM EDT

PDB ID	:	9YVW / pdb_00009yvw
Title	:	HIV-1 RT F227C with DNA and islatravir-triphosphate
Authors	:	Snyder, A.A.; Kirby, K.A.; Sarafianos, S.G.
Deposited on	:	2025-10-23
Resolution	:	1.80 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

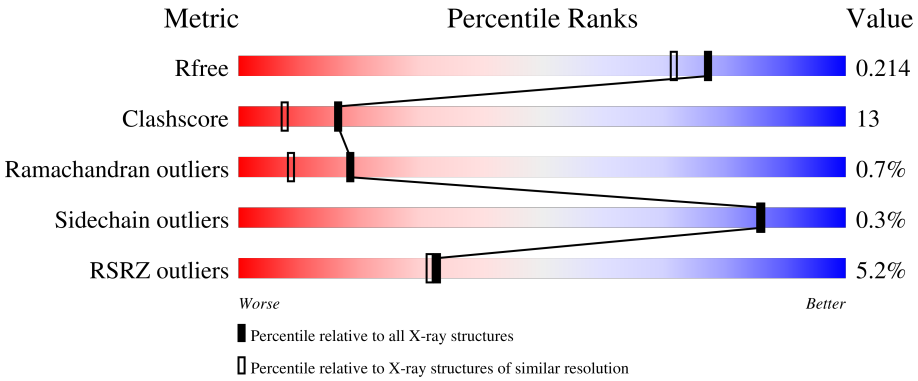
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	2% 83% 17%
2	B	452	9% 64% 24% • 11%
3	P	21	57% 38% 5%
4	T	27	59% 33% 7%

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
6	EDO	A	605	-	-	X	-

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 9864 atoms, of which 12 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 P66.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	558	Total	C	N	O	S	0	3	0
			4559	2942	764	844	9			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	THR	ALA	conflict	UNP A7YKL0
A	64	LYS	ARG	conflict	UNP A7YKL0
A	227	CYS	PHE	engineered mutation	UNP A7YKL0
A	258	CYS	GLN	conflict	UNP A7YKL0
A	280	SER	CYS	conflict	UNP A7YKL0

- Molecule 2 is a protein called P51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	401	Total	C	N	O	S	0	1	0
			3322	2159	553	604	6			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	MET	-	expression tag	UNP A7YKL0
B	-10	GLY	-	expression tag	UNP A7YKL0
B	-9	SER	-	expression tag	UNP A7YKL0
B	-8	SER	-	expression tag	UNP A7YKL0
B	-7	HIS	-	expression tag	UNP A7YKL0
B	-6	HIS	-	expression tag	UNP A7YKL0
B	-5	HIS	-	expression tag	UNP A7YKL0
B	-4	HIS	-	expression tag	UNP A7YKL0
B	-3	HIS	-	expression tag	UNP A7YKL0
B	-2	HIS	-	expression tag	UNP A7YKL0
B	-1	SER	-	expression tag	UNP A7YKL0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	expression tag	UNP A7YKL0
B	39	THR	ALA	conflict	UNP A7YKL0
B	64	LYS	ARG	conflict	UNP A7YKL0
B	280	SER	CYS	conflict	UNP A7YKL0

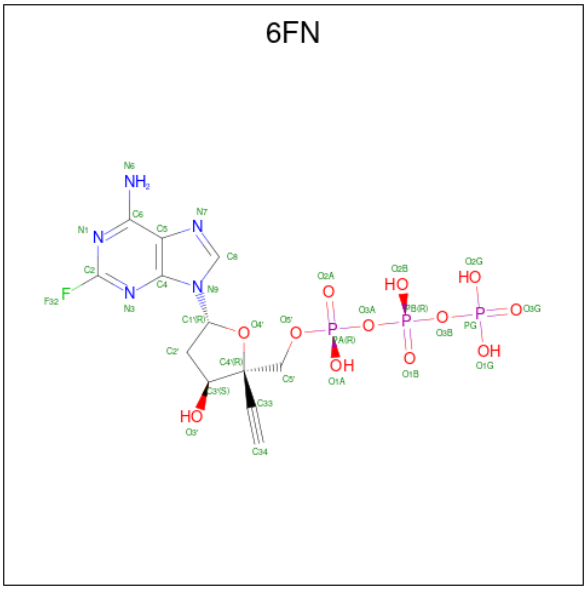
- Molecule 3 is a DNA chain called Primer.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
3	P	21	431	205	77	127	21	1	1	0	0

- Molecule 4 is a DNA chain called Template.

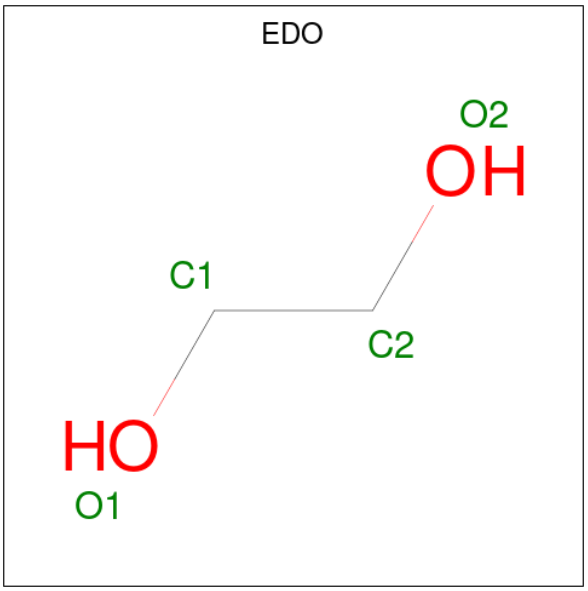
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	T	25	518	243	102	148	25	0	0	0

- Molecule 5 is 2'-deoxy-4'-ethynyl-2-fluoroadenosine 5'-(tetrahydrogen triphosphate) (CCD ID: 6FN) (formula: $C_{12}H_{15}FN_5O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C H O 10 2 6 2	0	0
6	P	1	Total C H O 10 2 6 2	0	0

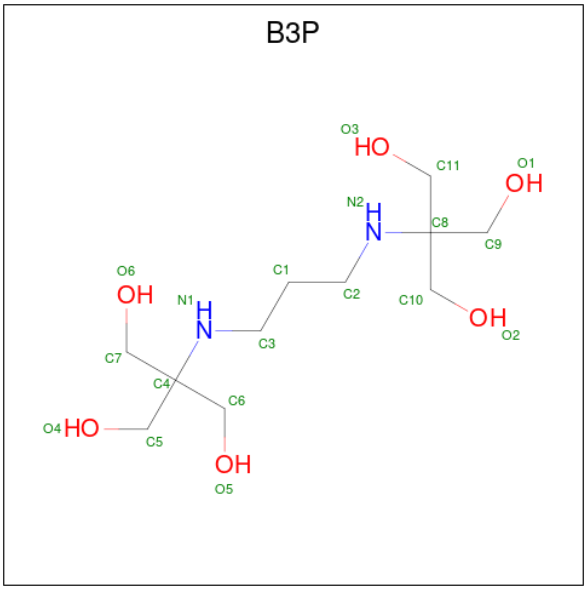
- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total Mg 2 2	0	0
7	P	1	Total Mg 1 1	0	0
7	T	1	Total Mg 1 1	0	0

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0

- Molecule 9 is 2-[3-(2-HYDROXY-1,1-DIHYDROXYMETHYL-ETHYLAMINO)-PROPYLAMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: B3P) (formula: $C_{11}H_{26}N_2O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	T	1	Total C N O 19 11 2 6	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	523	Total O 523 523	0	0
10	B	275	Total O 275 275	0	0
10	P	62	Total O 62 62	0	0
10	T	69	Total O 69 69	0	0

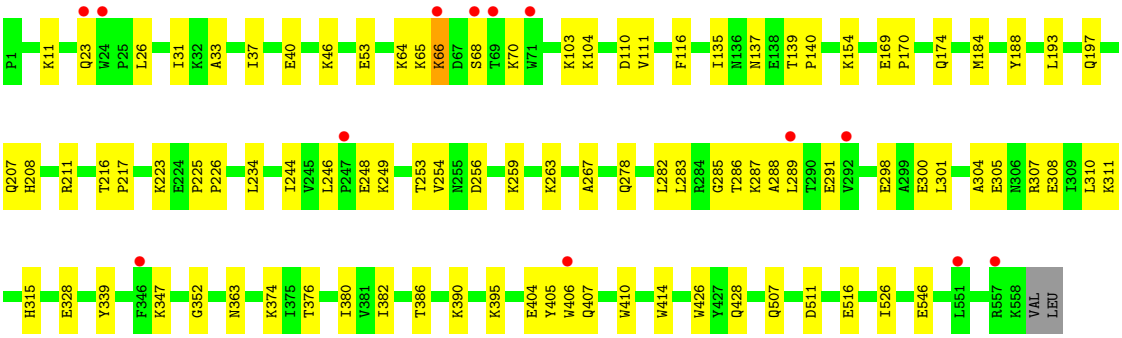
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: P66

Chain A:

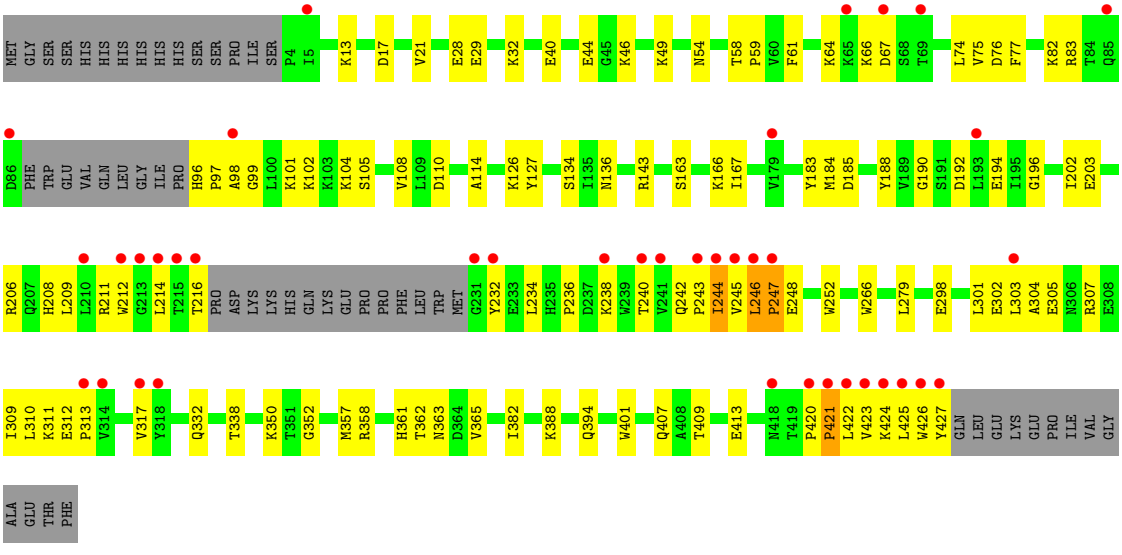




- Molecule 2: P51

Chain B:

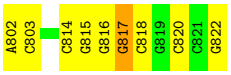




- Molecule 3: Primer

Chain P:

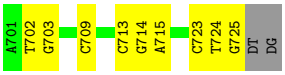




• Molecule 4: Template

Chain T:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	83.99Å 100.68Å 92.49Å 90.00° 113.95° 90.00°	Depositor
Resolution (Å)	43.30 – 1.80 43.30 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.9 (43.30-1.80) 99.1 (43.30-1.80)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.65 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.186 , 0.214 0.185 , 0.214	Depositor DCC
R_{free} test set	6310 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å^2)	38.9	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 49.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	9864	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6FN, MRG, EDO, MG, B3P, CL

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	0/4681	0.46	0/6357
2	B	0.25	0/3415	0.41	0/4638
3	P	0.93	0/451	0.97	1/690 (0.1%)
4	T	0.96	1/582 (0.2%)	0.87	0/897
All	All	0.42	1/9129 (0.0%)	0.52	1/12582 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	T	709	DC	C3'-O3'	-5.82	1.36	1.44

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	820	DC	O4'-C4'-C3'	-5.25	102.85	106.00

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	A	4559	0	4617	99	0
2	B	3322	0	3352	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	P	431	0	239	11	0
4	T	518	0	279	8	0
5	A	33	0	0	0	0
6	A	20	0	30	7	0
6	B	12	6	18	1	0
6	P	4	6	6	0	0
7	A	2	0	0	0	0
7	P	1	0	0	0	0
7	T	1	0	0	0	0
8	A	1	0	0	0	0
9	T	19	0	26	0	0
10	A	523	0	0	28	1
10	B	275	0	0	19	1
10	P	62	0	0	0	0
10	T	69	0	0	2	0
All	All	9852	12	8567	228	1

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 13.

The worst 5 of 228 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:207:GLN:NE2	10:A:701:HOH:O	1.89	1.02
2:B:312:GLU:HG3	2:B:313:PRO:CD	1.93	0.97
2:B:167:ILE:HD13	2:B:214:LEU:HD11	1.44	0.96
2:B:266:TRP:HZ3	2:B:425:LEU:HD22	1.28	0.95
2:B:244:ILE:HD13	2:B:310:LEU:HD13	1.48	0.95

All (1) 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)
10:A:1183:HOH:O	10:B:626:HOH:O[2_545]	2.01	0.19

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	559/560 (100%)	545 (98%)	13 (2%)	1 (0%)	43 31
2	B	396/452 (88%)	378 (96%)	12 (3%)	6 (2%)	8 2
All	All	955/1012 (94%)	923 (97%)	25 (3%)	7 (1%)	18 8

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	LYS
2	B	247	PRO
2	B	243	PRO
2	B	248	GLU
2	B	421	PRO

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	501/500 (100%)	500 (100%)	1 (0%)	87 87
2	B	365/411 (89%)	363 (100%)	2 (0%)	81 80
All	All	866/911 (95%)	863 (100%)	3 (0%)	86 86

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

Mol	Chain	Res	Type
1	A	188	TYR

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Mol	Chain	Res	Type
2	B	134	SER
2	B	244	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	207	GLN
2	B	315	HIS
2	B	418	ASN
1	A	373	GLN
1	A	507	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	25,28,29	1.89	5 (20%)	32,39,42	1.86	8 (25%)

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	-	2/12/26/27	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	817	MRG	O6-C6	5.52	1.34	1.23
3	P	817	MRG	C2-N3	4.40	1.40	1.32
3	P	817	MRG	C2-N2	2.87	1.40	1.34
3	P	817	MRG	C8-N9	2.20	1.42	1.37
3	P	817	MRG	C6-N1	-2.16	1.34	1.38

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	817	MRG	C2-N1-C6	-5.94	117.37	124.55
3	P	817	MRG	C5-C6-N1	4.11	123.72	113.25
3	P	817	MRG	C6-C5-C4	-2.75	114.69	118.83
3	P	817	MRG	O6-C6-C5	-2.73	119.32	126.53
3	P	817	MRG	C5-C4-N3	-2.54	124.34	128.39

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	P	817	MRG	C22-C21-N2-C2
3	P	817	MRG	C21-C22-C23-S24

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	817	MRG	7	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 5 are monoatomic - leaving 11 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	$\#\|Z\| > 2$
9	B3P	T	802	-	18,18,18	0.51	0	23,23,23	1.30	2 (8%)
6	EDO	P	901	-	3,3,3	0.45	0	2,2,2	0.73	0
6	EDO	A	602	-	3,3,3	0.41	0	2,2,2	0.45	0
6	EDO	B	502	-	3,3,3	0.45	0	2,2,2	0.33	0
6	EDO	A	609	-	3,3,3	0.55	0	2,2,2	0.26	0
5	6FN	A	601	7	31,35,35	3.24	16 (51%)	38,56,56	3.60	17 (44%)
6	EDO	B	503	-	3,3,3	0.41	0	2,2,2	0.43	0
6	EDO	A	604	-	3,3,3	0.50	0	2,2,2	0.31	0
6	EDO	A	605	-	3,3,3	0.46	0	2,2,2	0.38	0
6	EDO	B	501	-	3,3,3	0.58	0	2,2,2	0.26	0
6	EDO	A	603	-	3,3,3	0.47	0	2,2,2	0.37	0

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
9	B3P	T	802	-	-	0/28/28/28	-
6	EDO	P	901	-	-	0/1/1/1	-
6	EDO	A	602	-	-	1/1/1/1	-
6	EDO	B	502	-	-	0/1/1/1	-
6	EDO	A	609	-	-	0/1/1/1	-
5	6FN	A	601	7	-	4/23/50/50	0/3/3/3
6	EDO	B	503	-	-	0/1/1/1	-
6	EDO	A	604	-	-	1/1/1/1	-
6	EDO	A	605	-	-	0/1/1/1	-
6	EDO	B	501	-	-	1/1/1/1	-
6	EDO	A	603	-	-	0/1/1/1	-

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	6FN	C8-N9	-8.12	1.23	1.37
5	A	601	6FN	PB-O3A	6.74	1.66	1.59
5	A	601	6FN	C4-N9	-6.70	1.23	1.37
5	A	601	6FN	O4'-C1'	5.70	1.51	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	6FN	C6-N6	4.57	1.45	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	601	6FN	C4-N9-C8	13.07	119.46	105.74
5	A	601	6FN	C5-C4-N3	-8.04	118.71	127.18
5	A	601	6FN	N3-C4-N9	7.40	136.38	126.99
5	A	601	6FN	N1-C2-N3	-5.88	122.10	130.60
5	A	601	6FN	C4-C5-N7	-5.55	104.23	110.58

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	6FN	PB-O3B-PG-O1G
6	A	604	EDO	O1-C1-C2-O2
5	A	601	6FN	PA-O3A-PB-O2B
6	A	602	EDO	O1-C1-C2-O2
6	B	501	EDO	O1-C1-C2-O2

There are no ring outliers.

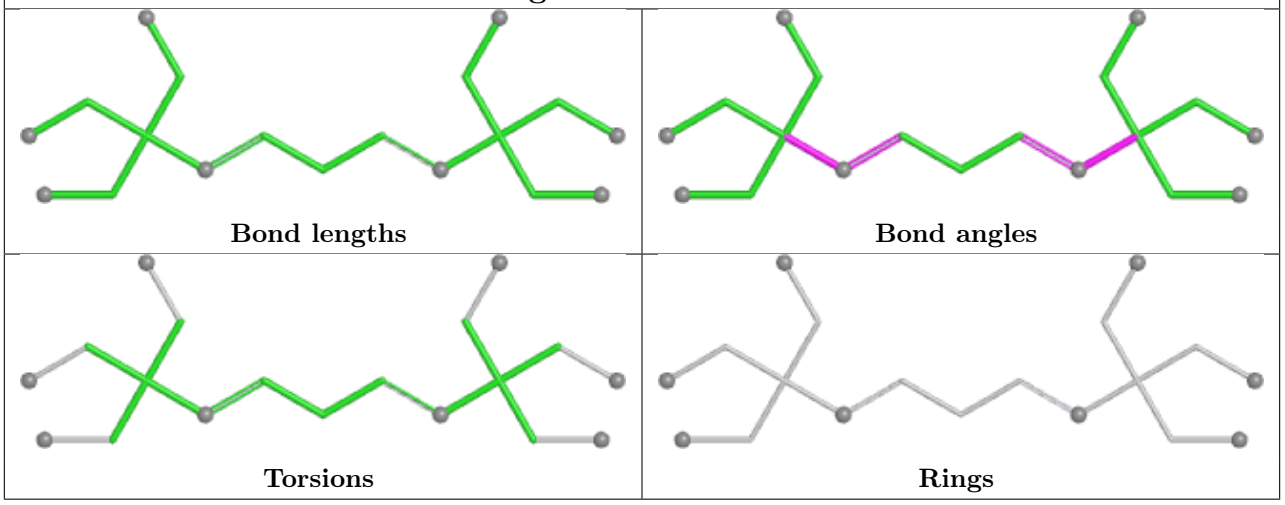
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	609	EDO	1	0
6	B	503	EDO	1	0
6	A	604	EDO	1	0
6	A	605	EDO	5	0
6	A	603	EDO	1	0

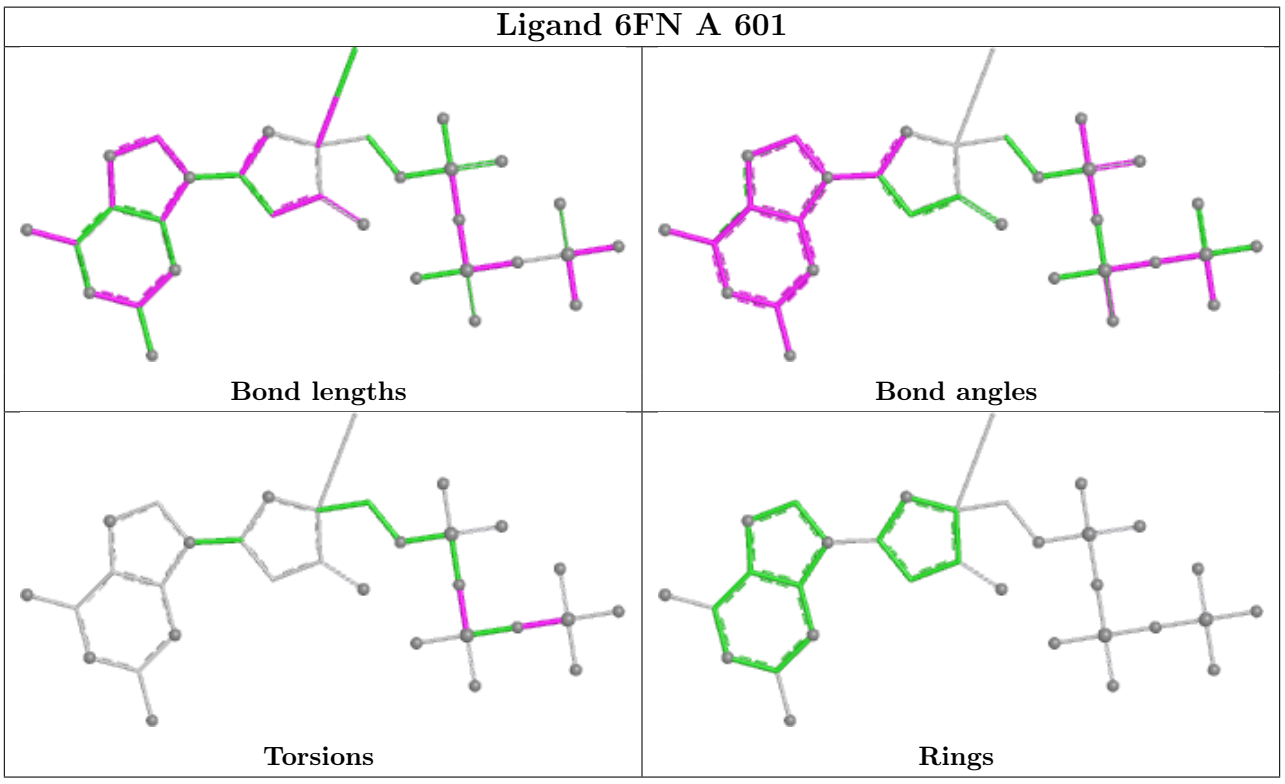
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.

Ligand B3P T 802



Ligand 6FN A 601



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^{th} 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%)	0.37	13 (2%) 61 61	27, 48, 85, 125	4 (0%)
2	B	401/452 (88%)	0.80	39 (9%) 13 11	32, 57, 111, 164	4 (0%)
3	P	20/21 (95%)	-0.09	0 100 100	39, 55, 95, 101	1 (5%)
4	T	25/27 (92%)	-0.01	0 100 100	33, 62, 95, 109	0
All	All	1004/1060 (94%)	0.52	52 (5%) 33 31	27, 52, 99, 164	9 (0%)

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	422	LEU	6.2
2	B	212[A]	TRP	6.0
2	B	427	TYR	5.2
2	B	232	TYR	4.8
2	B	244	ILE	4.5

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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
3	MRG	P	817	26/27	0.94	0.10	42,57,72,78	0

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands (i)

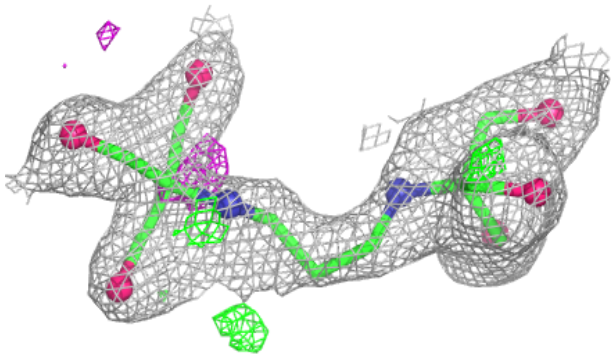
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

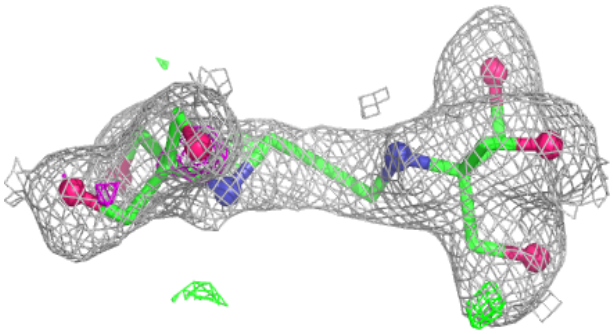
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	EDO	B	503	4/4	0.67	0.12	86,93,96,103	0
6	EDO	A	602	4/4	0.79	0.14	75,76,77,87	0
6	EDO	P	901	4/4	0.79	0.16	78,87,100,107	0
6	EDO	B	502	4/4	0.84	0.18	57,63,66,67	0
9	B3P	T	802	19/19	0.85	0.14	57,70,77,81	0
6	EDO	A	609	4/4	0.86	0.15	50,56,63,63	0
7	MG	P	902	1/1	0.87	0.11	79,79,79,79	0
6	EDO	A	604	4/4	0.87	0.16	68,72,73,78	0
6	EDO	B	501	4/4	0.89	0.15	48,54,56,64	0
6	EDO	A	605	4/4	0.89	0.12	59,59,74,79	0
6	EDO	A	603	4/4	0.91	0.12	51,56,61,62	0
5	6FN	A	601	33/33	0.97	0.07	36,43,48,49	3
7	MG	A	606	1/1	0.98	0.07	48,48,48,48	0
7	MG	T	801	1/1	0.98	0.05	59,59,59,59	0
7	MG	A	607	1/1	0.98	0.09	31,31,31,31	0
8	CL	A	608	1/1	0.99	0.05	45,45,45,45	0

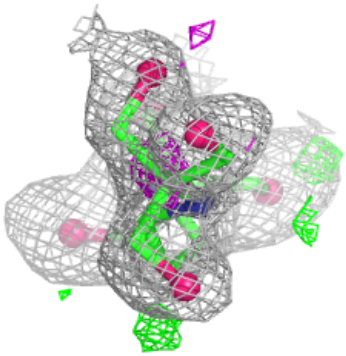
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around B3P T 802:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

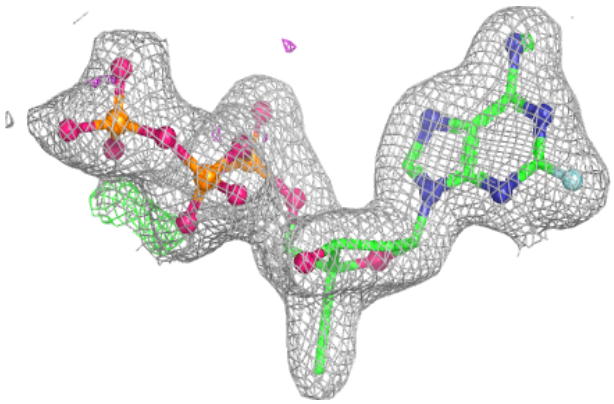


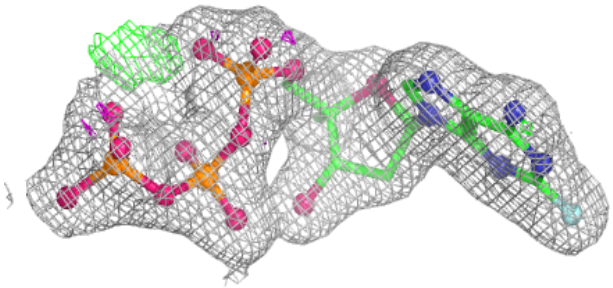


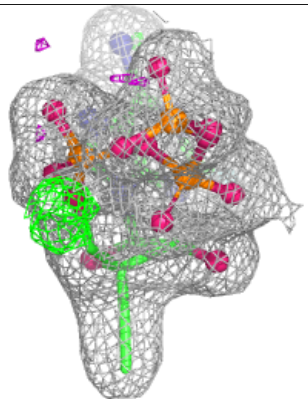


Electron density around 6FN A 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.