



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:02 AM UTC

PDB ID : 6P1I / pdb_00006p1i
Title : Structure of HIV-1 Reverse Transcriptase (RT) in complex with dsDNA and dCTP
Authors : Bertoletti, N.; Anderson, K.S.
Deposited on : 2019-05-19
Resolution : 2.74 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

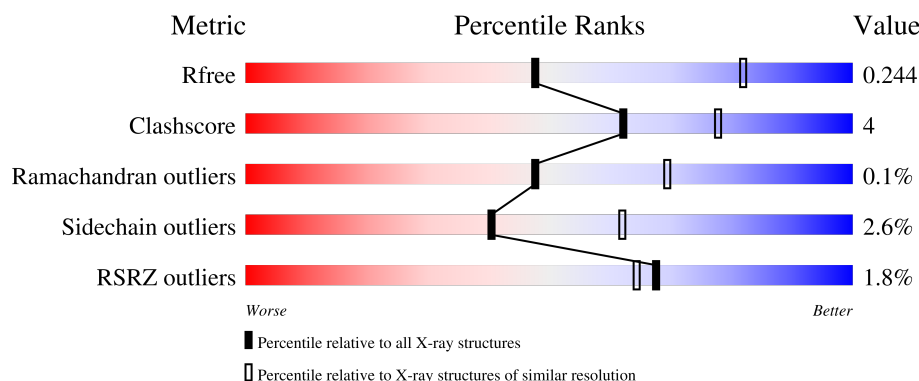
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.74 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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 $\leq 5\%$. 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	85% 12% ..
2	B	452	3% 78% 8% 13%
3	P	21	62% 19% 5% 14%
4	T	27	52% 33% 15%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8411 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	0	0
			4393	2844	733	808	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 p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	392	Total	C	N	O	S	0	0	0
			3117	2029	512	571	5			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	MET	-	expression tag	UNP P04585
B	-10	GLY	-	expression tag	UNP P04585
B	-9	SER	-	expression tag	UNP P04585
B	-8	SER	-	expression tag	UNP P04585
B	-7	HIS	-	expression tag	UNP P04585
B	-6	HIS	-	expression tag	UNP P04585
B	-5	HIS	-	expression tag	UNP P04585
B	-4	HIS	-	expression tag	UNP P04585
B	-3	HIS	-	expression tag	UNP P04585
B	-2	HIS	-	expression tag	UNP P04585
B	-1	SER	-	expression tag	UNP P04585
B	0	SER	-	expression tag	UNP P04585
B	280	SER	CYS	engineered mutation	UNP P04585

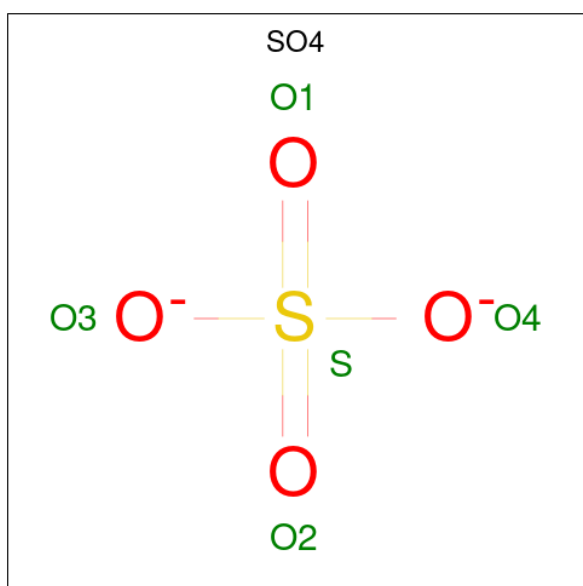
- Molecule 3 is a DNA chain called DNA Primer 20-mer.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	P	18	Total	C	N	O	P	S	0	0	0
			366	175	64	109	17	1			

- Molecule 4 is a DNA chain called DNA template 27-mer.

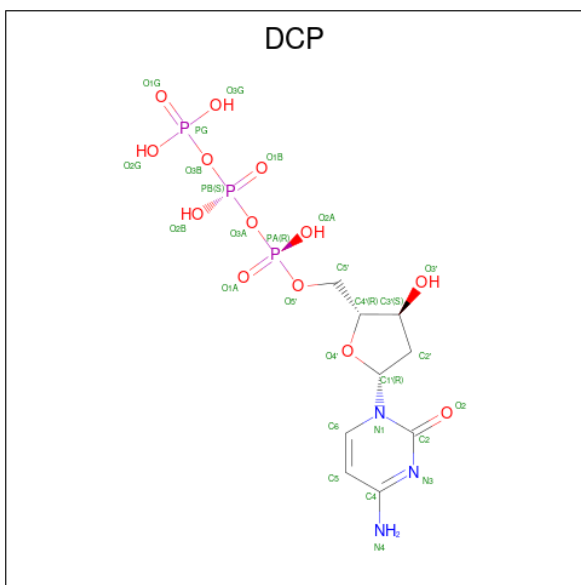
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	T	23	Total	C	N	O	P		0	0	0
			479	223	98	135	23				

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	T	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (CCD ID: DCP) (formula: C₉H₁₆N₃O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- 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

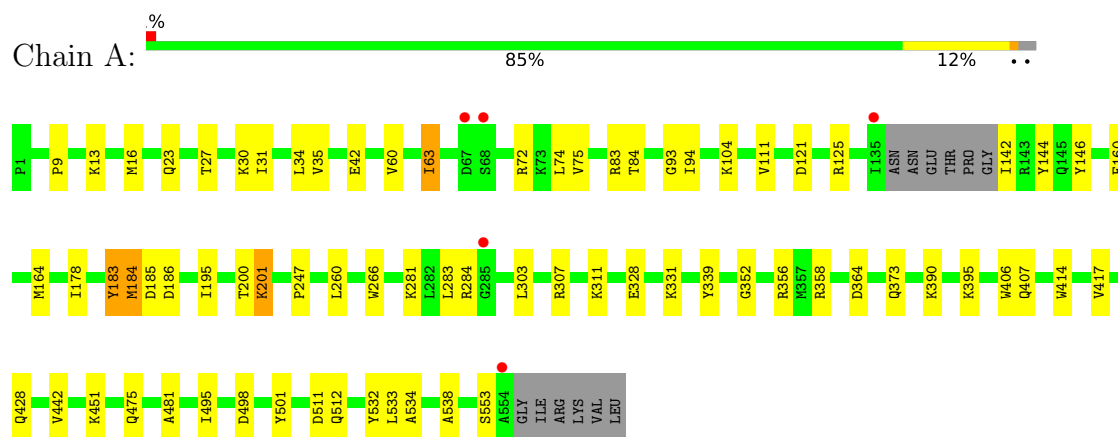
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	12	Total O 12 12	0	0
8	B	3	Total O 3 3	0	0
8	P	1	Total O 1 1	0	0

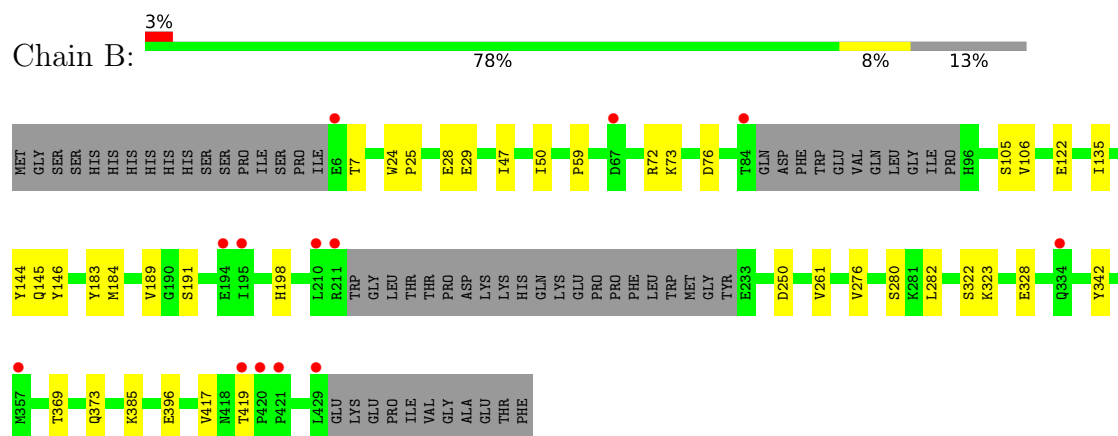
3 Residue-property plots [i](#)

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: Reverse transcriptase/ribonuclease H



- Molecule 2: p51 RT



- Molecule 3: DNA Primer 20-mer



- Molecule 4: DNA template 27-mer



DA	G703	G705	G706	G707	G708	G709	G710	G711	G712	G713	G725	DT	DG
DT	G704												

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	166.42Å 169.50Å 103.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.93 – 2.74 28.93 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.1 (28.93-2.74) 99.5 (28.93-2.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 2.72Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.183 , 0.236 0.188 , 0.244	Depositor DCC
R_{free} test set	1925 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	60.0	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8411	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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: SO4, G47, MG, DDG, DCP

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	0/4508	0.51	0/6141
2	B	0.30	0/3203	0.48	0/4373
3	P	0.36	0/355	0.50	0/543
4	T	0.33	0/539	0.49	0/831
All	All	0.31	0/8605	0.50	0/11888

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
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	TYR	Peptide

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	4393	0	4368	44	0
2	B	3117	0	3047	15	0
3	P	366	0	207	4	0
4	T	479	0	255	6	0
5	A	5	0	0	0	0
5	T	5	0	0	0	0
6	A	28	0	12	1	0
7	A	2	0	0	0	0
8	A	12	0	0	0	0
8	B	3	0	0	0	0
8	P	1	0	0	0	0
All	All	8411	0	7889	66	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 4.

All (66) 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)
4:T:703:DG:H2''	4:T:704:DG:H5''	1.64	0.79
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.19	0.76
2:B:261:VAL:HG13	2:B:276:VAL:HG11	1.72	0.71
1:A:60:VAL:HG12	1:A:75:VAL:HG22	1.80	0.63
1:A:331:LYS:NZ	1:A:364:ASP:OD2	2.33	0.61
3:P:816:DG:H2'	3:P:817:G47:C8	2.31	0.60
1:A:284:ARG:NH1	4:T:713:DC:OP1	2.36	0.58
3:P:816:DG:H2'	3:P:817:G47:H8	1.86	0.57
2:B:191:SER:HB3	2:B:198:HIS:ND1	2.21	0.56
1:A:72:ARG:HH21	6:A:602:DCP:H3'	1.72	0.55
4:T:711:DC:H2'	4:T:712:DC:C6	2.42	0.54
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.42	0.53
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.89	0.53
2:B:50:ILE:HD13	2:B:145:GLN:HB3	1.90	0.53
1:A:16:MET:HE3	1:A:83:ARG:HG2	1.91	0.53
1:A:328:GLU:HG3	1:A:390:LYS:HB2	1.92	0.52
1:A:406:TRP:HD1	1:A:407:GLN:HE21	1.56	0.52
1:A:339:TYR:CZ	1:A:352:GLY:HA3	2.45	0.51
1:A:42:GLU:HG3	1:A:144:TYR:HE1	1.75	0.51
1:A:495:ILE:HB	1:A:533:LEU:HD12	1.93	0.50
1:A:178:ILE:CD1	1:A:201:LYS:HG2	2.42	0.49
1:A:30:LYS:O	1:A:34:LEU:HG	2.13	0.49
1:A:13:LYS:HE2	1:A:84:THR:O	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:498:ASP:HB2	1:A:538:ALA:HB2	1.95	0.49
1:A:183:TYR:O	1:A:184:MET:C	2.56	0.48
1:A:31:ILE:O	1:A:35:VAL:HG13	2.14	0.48
2:B:47:ILE:HD12	2:B:144:TYR:CD1	2.48	0.48
2:B:59:PRO:HG2	2:B:76:ASP:HB3	1.96	0.47
1:A:451:LYS:NZ	3:P:808:DC:OP1	2.48	0.47
1:A:27:THR:O	1:A:31:ILE:HG12	2.15	0.47
1:A:281:LYS:O	1:A:284:ARG:HG2	2.13	0.47
1:A:23:GLN:HE22	1:A:60:VAL:HG22	1.80	0.46
1:A:406:TRP:CD1	1:A:407:GLN:HE21	2.32	0.46
1:A:356:ARG:CZ	1:A:358:ARG:HD3	2.46	0.46
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.51	0.46
2:B:183:TYR:O	2:B:184:MET:C	2.60	0.45
2:B:369:THR:HG22	2:B:373:GLN:HE21	1.81	0.45
1:A:63:ILE:HD13	1:A:74:LEU:HD11	1.97	0.45
1:A:475:GLN:H	1:A:475:GLN:CD	2.24	0.45
1:A:532:TYR:CE2	1:A:534:ALA:HB2	2.52	0.45
2:B:24:TRP:HB2	2:B:25:PRO:HD2	1.98	0.45
2:B:250:ASP:OD2	2:B:250:ASP:N	2.49	0.45
1:A:247:PRO:O	1:A:307:ARG:NH1	2.49	0.44
1:A:9:PRO:HA	1:A:121:ASP:OD2	2.17	0.44
4:T:710:DG:H2'	4:T:711:DC:C6	2.52	0.44
2:B:328:GLU:HG3	2:B:342:TYR:HE1	1.83	0.44
1:A:160:PHE:CZ	1:A:164:MET:HE2	2.53	0.44
1:A:93:GLY:C	1:A:94:ILE:HD13	2.43	0.43
1:A:442:VAL:HB	1:A:481:ALA:HB1	2.00	0.43
4:T:707:DG:H2'	4:T:708:DG:C8	2.53	0.43
1:A:23:GLN:NE2	1:A:60:VAL:HG22	2.34	0.43
4:T:706:DC:H2'	4:T:707:DG:C8	2.54	0.42
1:A:184:MET:HE2	1:A:184:MET:HB2	1.89	0.42
1:A:266:TRP:CE2	3:P:820:DC:H4'	2.55	0.42
2:B:28:GLU:HA	2:B:135:ILE:HD11	2.02	0.42
1:A:125:ARG:HG2	1:A:146:TYR:O	2.19	0.42
1:A:511:ASP:OD1	1:A:512:GLN:HG2	2.20	0.42
2:B:396:GLU:H	2:B:396:GLU:HG2	1.65	0.42
1:A:307:ARG:O	1:A:311:LYS:HG3	2.20	0.42
2:B:323:LYS:O	2:B:385:LYS:HE2	2.20	0.42
1:A:93:GLY:O	1:A:94:ILE:HD13	2.20	0.41
1:A:260:LEU:HD21	1:A:303:LEU:HD13	2.02	0.41
1:A:72:ARG:HD3	1:A:74:LEU:HD21	2.02	0.41
1:A:195:ILE:HD12	1:A:195:ILE:HA	1.90	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:TRP:CD1	1:A:407:GLN:HG2	2.55	0.41
2:B:106:VAL:HA	2:B:189:VAL:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	544/560 (97%)	526 (97%)	17 (3%)	1 (0%)	43	62
2	B	386/452 (85%)	377 (98%)	9 (2%)	0	100	100
All	All	930/1012 (92%)	903 (97%)	26 (3%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	MET

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	470/500 (94%)	459 (98%)	11 (2%)	44	65
2	B	328/411 (80%)	318 (97%)	10 (3%)	36	58
All	All	798/911 (88%)	777 (97%)	21 (3%)	40	62

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	ILE
1	A	104	LYS
1	A	142	ILE
1	A	186	ASP
1	A	200	THR
1	A	201	LYS
1	A	283	LEU
1	A	373	GLN
1	A	417	VAL
1	A	428	GLN
1	A	553	SER
2	B	7	THR
2	B	29	GLU
2	B	72	ARG
2	B	105	SER
2	B	122	GLU
2	B	280	SER
2	B	282	LEU
2	B	322	SER
2	B	417	VAL
2	B	419	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	GLN
1	A	207	GLN
1	A	278	GLN
1	A	315	HIS
1	A	407	GLN
1	A	487	GLN
1	A	500	GLN
1	A	520	GLN
1	A	547	GLN
2	B	137	ASN
2	B	147	ASN
2	B	161	GLN
2	B	182	GLN
2	B	208	HIS
2	B	235	HIS
2	B	265	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	269	GLN
2	B	373	GLN
2	B	394	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	G47	P	817	1,3,4	23,27,28	1.26	3 (13%)	31,38,41	2.29	5 (16%)
3	DDG	P	822	3,4	20,23,24	1.35	3 (15%)	27,33,36	2.48	8 (29%)

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	G47	P	817	1,3,4	-	5/11/25/26	0/3/3/3
3	DDG	P	822	3,4	-	0/7/18/19	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	822	DDG	C5-C4	3.29	1.47	1.38
3	P	817	G47	C5-C4	3.22	1.47	1.38
3	P	822	DDG	C5-N7	-2.41	1.34	1.39
3	P	817	G47	C6-N1	-2.34	1.34	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	817	G47	C5-N7	-2.16	1.34	1.39
3	P	822	DDG	C6-N1	-2.15	1.34	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	817	G47	C2-N3-C4	7.77	121.72	112.00
3	P	822	DDG	C5-C4-N3	-6.31	118.35	128.39
3	P	817	G47	C5-C4-N3	-6.21	118.50	128.39
3	P	822	DDG	C2'-C1'-N9	-5.06	102.81	112.40
3	P	822	DDG	C2-N3-C4	4.71	120.42	112.30
3	P	822	DDG	N9-C4-N3	4.66	135.27	125.95
3	P	822	DDG	O4'-C1'-N9	4.09	115.12	107.86
3	P	817	G47	N9-C4-N3	3.95	133.85	125.95
3	P	817	G47	C6-C5-N7	3.45	136.57	130.29
3	P	817	G47	C4-C5-N7	-2.81	106.22	110.67
3	P	822	DDG	C6-C5-N7	2.50	134.84	130.29
3	P	822	DDG	O6-C6-C5	-2.39	120.22	126.53
3	P	822	DDG	C4-C5-N7	-2.28	107.06	110.67

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	P	817	G47	O4'-C4'-C5'-O5'
3	P	817	G47	C3'-C4'-C5'-O5'
3	P	817	G47	N2-C6A-C7A-SG
3	P	817	G47	N3-C2-N2-C6A
3	P	817	G47	N1-C2-N2-C6A

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	817	G47	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	SO4	T	801	-	4,4,4	0.24	0	6,6,6	0.22	0
6	DCP	A	602	7	28,29,29	0.58	0	41,45,45	0.61	0
5	SO4	A	601	-	4,4,4	0.22	0	6,6,6	0.19	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
6	DCP	A	602	7	-	2/22/34/34	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	602	DCP	PG-O3B-PB-O2B
6	A	602	DCP	PB-O3A-PA-O2A

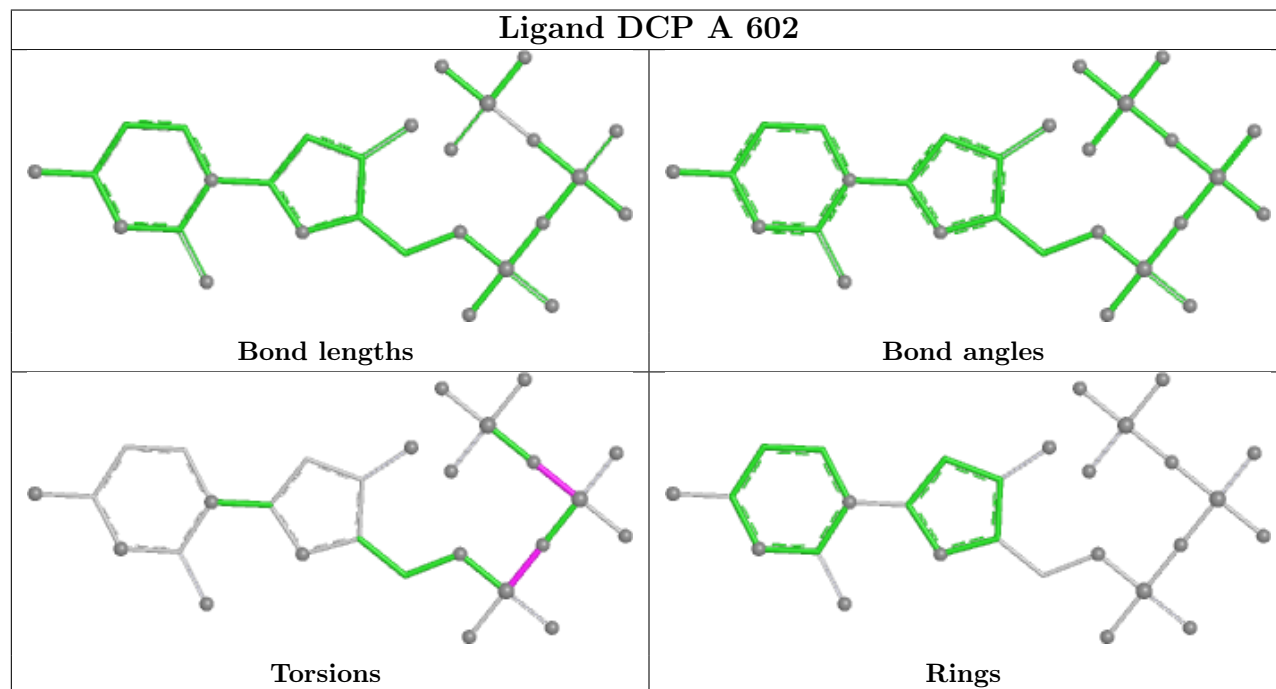
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	602	DCP	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 than 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.



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	548/560 (97%)	-0.41	5 (0%) 81 81	29, 47, 83, 119	0
2	B	392/452 (86%)	-0.18	13 (3%) 49 47	31, 56, 97, 141	0
3	P	16/21 (76%)	-0.58	0 100 100	42, 65, 79, 93	0
4	T	23/27 (85%)	-0.40	0 100 100	43, 71, 103, 110	0
All	All	979/1060 (92%)	-0.32	18 (1%) 67 64	29, 52, 92, 141	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	429	LEU	4.9
2	B	420	PRO	4.5
2	B	195	ILE	4.3
2	B	419	THR	4.1
1	A	135	ILE	4.0
2	B	211	ARG	3.0
1	A	554	ALA	3.0
2	B	67	ASP	2.9
2	B	84	THR	2.8
2	B	357	MET	2.7
1	A	67	ASP	2.6
2	B	6	GLU	2.5
2	B	421	PRO	2.5
1	A	285	GLY	2.3
2	B	210	LEU	2.2
1	A	68	SER	2.1
2	B	334	GLN	2.0
2	B	194	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 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	B-factors($\text{\AA}^2$)	Q<0.9
3	G47	P	817	25/26	0.91	0.09	47,53,67,70	0
3	DDG	P	822	21/22	0.98	0.06	30,34,37,46	0

6.3 Carbohydrates [i](#)

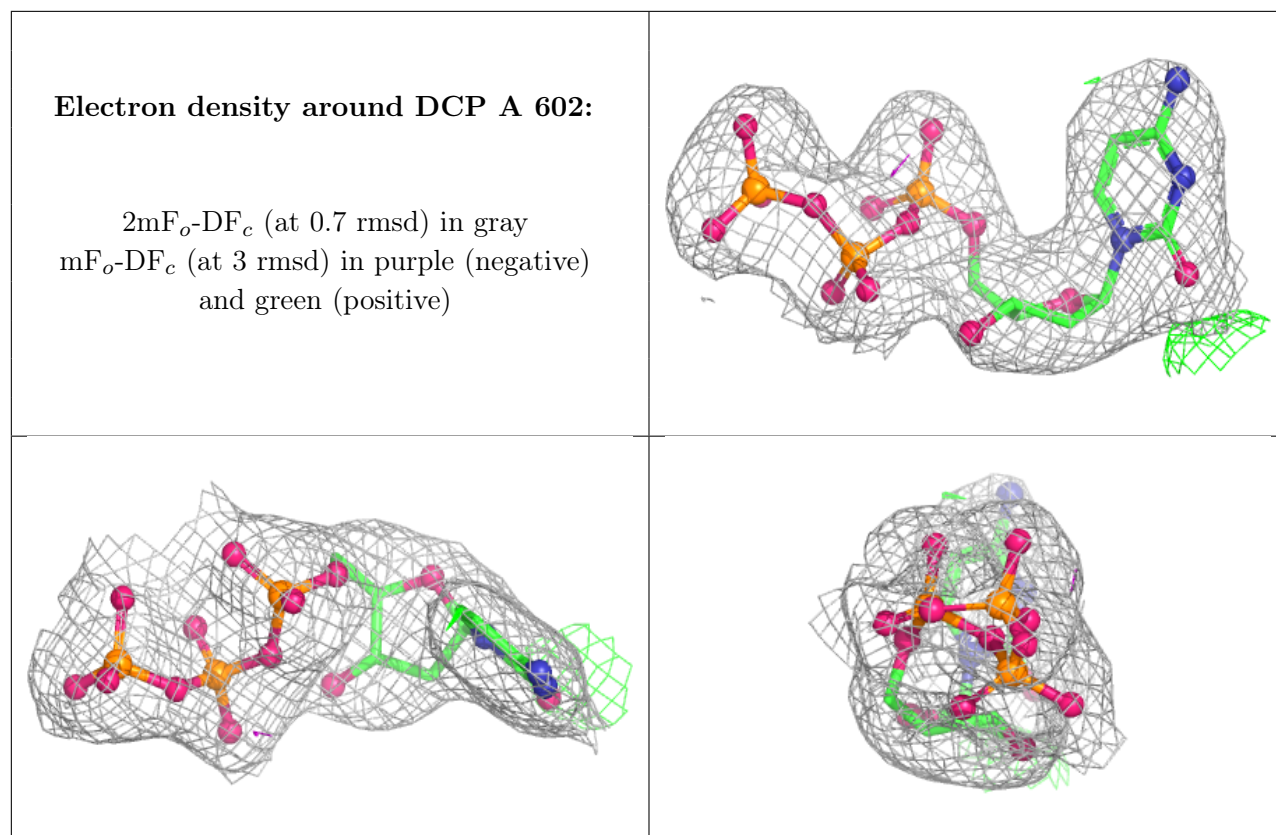
There are no oligosaccharides in this entry.

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, 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	B-factors($\text{\AA}^2$)	Q<0.9
7	MG	A	604	1/1	0.85	0.20	47,47,47,47	0
5	SO4	T	801	5/5	0.89	0.14	106,108,110,112	0
5	SO4	A	601	5/5	0.94	0.09	76,82,84,87	0
6	DCP	A	602	28/28	0.97	0.07	30,37,44,47	0
7	MG	A	603	1/1	0.99	0.05	26,26,26,26	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.