



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:13 AM UTC

PDB ID : 6MU4 / pdb_00006mu4
Title : Bst DNA polymerase I FANA/DNA binary complex
Authors : Jackson, L.N.; Chim, N.; Chaput, J.C.
Deposited on : 2018-10-22
Resolution : 1.62 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
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

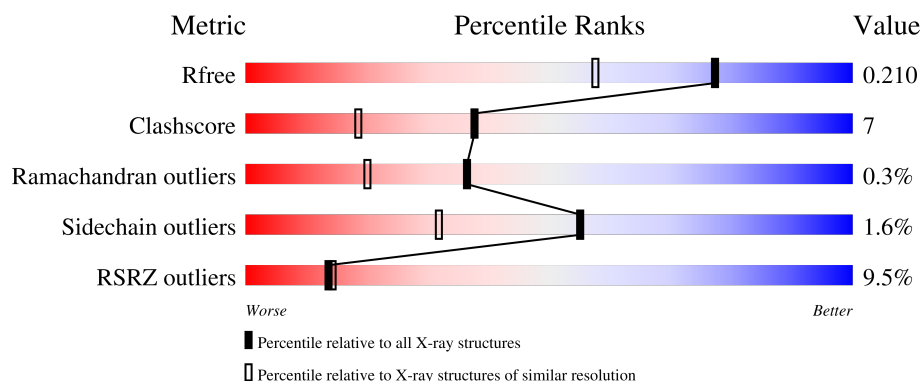
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.62 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	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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	P	11	18% 55% 45%
2	A	577	9% 87% 12%
3	T	13	38% 62%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5756 atoms, of which 42 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 DNA chain called DNA (5'-D(P*GP*CP*GP*AP*TP*CP*AP*CP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	11	Total	C	N	O	P	0	0	0
			225	107	40	67	11			

- Molecule 2 is a protein called DNA polymerase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	577	Total	C	N	O	S	0	0	0
			4632	2944	807	865	16			

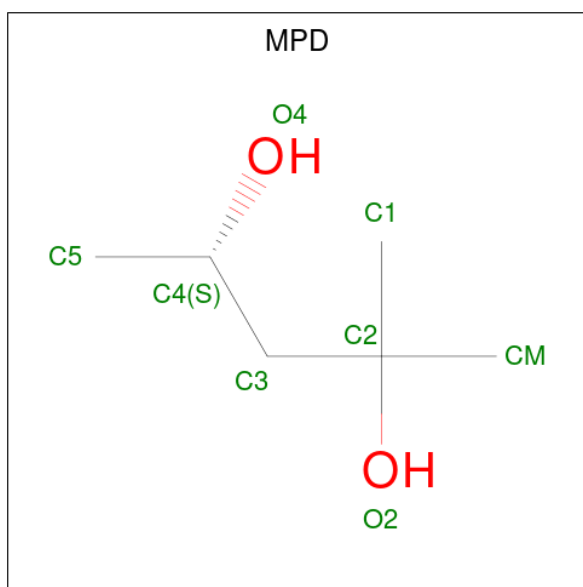
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	550	THR	SER	conflict	UNP E1C9K5

- Molecule 3 is a DNA chain called FANA (5'-D(P*(UF2)P*(A5L)P*(CFL)P*(GFL)P*(UF2)P*(GFL)P*(A5L)P*(UF2)P*(CFL)P*(GFL)P*(CFL))-3').

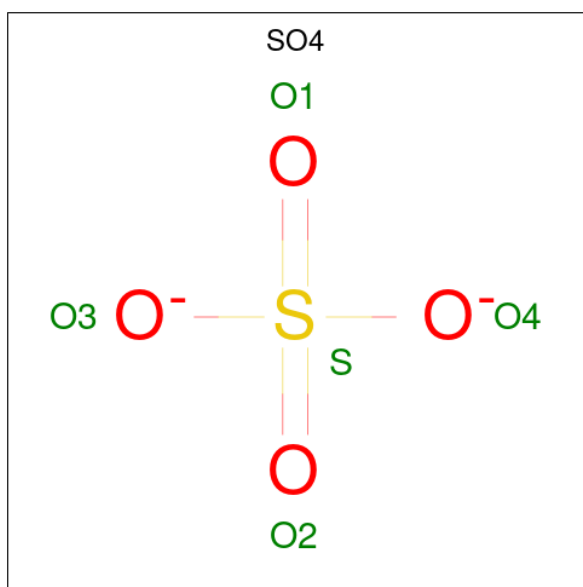
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	13	Total	C	F	N	O	P	0	0
			278	124	13	50	78	13		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			22	6	14	2		
4	A	1	Total	C	H	O	0	0
			22	6	14	2		
4	A	1	Total	C	H	O	0	0
			22	6	14	2		

- 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		

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

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

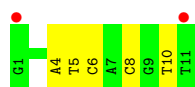
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	P	7	Total	O	0	0
			7	7		
7	A	513	Total	O	0	0
			513	513		
7	T	24	Total	O	0	0
			24	24		

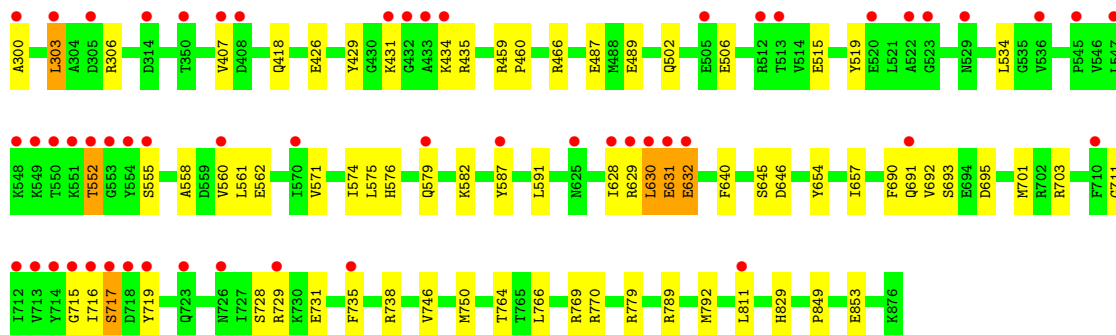
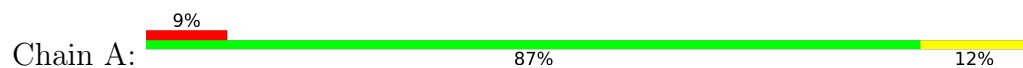
3 Residue-property plots [i](#)

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: DNA (5'-D(P*GP*CP*GP*AP*TP*CP*AP*CP*GP*T)-3')



- Molecule 2: DNA polymerase I



- Molecule 3: FANA (5'-D(P*(UF2)P*(A5L)P*(CFL)P*(GFL)P*(UF2)P*(GFL)P*(A5L)P*(UF2)P*(CFL)P*(GFL)P*(CFL))-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.83Å 93.90Å 105.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.09 – 1.62 46.09 – 1.62	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.09-1.62) 94.6 (46.09-1.62)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 1.62Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.187 , 0.210 0.192 , 0.210	Depositor DCC
R_{free} test set	2004 reflections (1.80%)	wwPDB-VP
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.480	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5756	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.10% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CFL, SO4, UF2, MPD, A5L, GFL

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	P	0.68	0/251	0.59	0/385
2	A	0.46	2/4715 (0.0%)	0.54	2/6373 (0.0%)
All	All	0.48	2/4966 (0.0%)	0.55	2/6758 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	489	GLU	C-O	-6.08	1.17	1.24
2	A	717	SER	C-O	-5.37	1.16	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	303	LEU	N-CA-C	-5.38	98.53	107.99
2	A	717	SER	CB-CA-C	-5.09	100.35	111.71

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	P	225	0	125	7	0
2	A	4632	0	4684	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	T	278	0	127	7	0
4	A	24	42	42	8	0
5	A	10	0	0	0	0
6	A	1	0	0	0	0
7	A	513	0	0	7	0
7	P	7	0	0	0	0
7	T	24	0	0	1	0
All	All	5714	42	4978	70	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 7.

All (70) 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:P:6:DC:OP1	2:A:552:THR:OG1	1.53	1.25
3:T:7:CFL:H2'	3:T:8:GFL:H5'2	1.36	1.03
2:A:459:ARG:HH21	2:A:466:ARG:HH22	1.14	0.95
2:A:431:LYS:H	2:A:434:LYS:HE3	1.32	0.91
2:A:692:VAL:HG21	2:A:701:MET:HE1	1.53	0.90
2:A:789:ARG:HD2	4:A:903:MPD:H52	1.54	0.88
2:A:426:GLU:HG3	2:A:431:LYS:HE2	1.59	0.82
1:P:4:DA:H2''	1:P:5:DT:H5''	1.66	0.75
2:A:719:TYR:CE2	2:A:729:ARG:HD3	2.24	0.73
2:A:431:LYS:N	2:A:434:LYS:HE3	2.06	0.71
2:A:534:LEU:HD11	2:A:574:ILE:HD13	1.75	0.69
2:A:426:GLU:CG	2:A:431:LYS:HE2	2.24	0.67
2:A:630:LEU:O	2:A:631:GLU:C	2.41	0.63
2:A:426:GLU:HG3	2:A:431:LYS:HG2	1.81	0.62
2:A:628:ILE:HD11	2:A:829:HIS:CE1	2.36	0.61
1:P:4:DA:C2'	1:P:5:DT:H5''	2.31	0.61
1:P:8:DC:H4'	2:A:582:LYS:HD2	1.81	0.60
3:T:4:GFL:N3	3:T:4:GFL:H3'	2.17	0.60
2:A:738:ARG:CZ	7:A:1008:HOH:O	2.49	0.59
2:A:630:LEU:O	2:A:632:GLU:N	2.36	0.58
2:A:558:ALA:O	2:A:562:GLU:HG3	2.04	0.57
2:A:692:VAL:HG21	2:A:701:MET:CE	2.32	0.57
2:A:716:ILE:O	4:A:903:MPD:H31	2.05	0.56
3:T:14:GFL:H2'	3:T:15:CFL:O4'	2.06	0.55
2:A:502:GLN:O	2:A:506:GLU:HG3	2.05	0.55
2:A:555:SER:OG	2:A:560:VAL:HG21	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:300:ALA:N	4:A:902:MPD:HO4	2.06	0.53
1:P:4:DA:H2''	1:P:5:DT:C5'	2.35	0.53
2:A:629:ARG:N	2:A:629:ARG:CD	2.72	0.52
2:A:591:LEU:HD21	2:A:640:PHE:CZ	2.44	0.51
3:T:16:A5L:OP1	7:T:101:HOH:O	2.20	0.49
2:A:628:ILE:N	2:A:628:ILE:HD12	2.29	0.48
2:A:487:GLU:HG3	7:A:1221:HOH:O	2.13	0.47
2:A:628:ILE:HD11	2:A:829:HIS:NE2	2.29	0.47
2:A:728:SER:OG	2:A:731:GLU:HG3	2.14	0.47
2:A:561:LEU:HB2	2:A:575:LEU:HD21	1.95	0.47
2:A:716:ILE:O	4:A:903:MPD:C3	2.63	0.47
2:A:426:GLU:CD	2:A:431:LYS:HE2	2.41	0.46
1:P:10:DT:H5''	2:A:628:ILE:HD13	1.97	0.46
2:A:789:ARG:HD2	4:A:903:MPD:C5	2.38	0.45
2:A:418:GLN:HA	7:A:1055:HOH:O	2.17	0.45
2:A:849:PRO:O	2:A:853:GLU:HG3	2.17	0.45
2:A:426:GLU:CG	2:A:431:LYS:HG2	2.46	0.45
2:A:789:ARG:HA	2:A:792:MET:HE3	1.99	0.44
2:A:587:TYR:O	2:A:591:LEU:HB2	2.16	0.44
2:A:561:LEU:O	2:A:571:VAL:HG11	2.18	0.44
4:A:901:MPD:H52	3:T:5:UF2:C6	2.48	0.44
2:A:459:ARG:HB3	2:A:460:PRO:HD3	1.98	0.44
2:A:429:TYR:O	2:A:435:ARG:HA	2.18	0.43
2:A:654:TYR:HB3	2:A:657:ILE:HB	2.00	0.43
3:T:14:GFL:H4'	3:T:15:CFL:O1P	2.19	0.43
2:A:426:GLU:OE2	2:A:431:LYS:HE2	2.19	0.43
2:A:576:HIS:O	2:A:579:GLN:HG2	2.19	0.43
2:A:738:ARG:NH2	7:A:1008:HOH:O	2.52	0.43
2:A:693:SER:OG	2:A:695:ASP:OD1	2.33	0.42
2:A:645:SER:O	2:A:646:ASP:HB2	2.18	0.42
2:A:764:THR:HA	2:A:769:ARG:O	2.19	0.42
2:A:770:ARG:HG3	7:A:1201:HOH:O	2.19	0.42
2:A:690:PHE:CB	2:A:701:MET:HE3	2.49	0.42
2:A:691:GLN:HG2	2:A:738:ARG:NH1	2.35	0.41
1:P:6:DC:P	2:A:552:THR:OG1	2.71	0.41
4:A:902:MPD:O4	4:A:902:MPD:O2	2.35	0.41
2:A:711:GLY:HA2	2:A:716:ILE:HG12	2.02	0.41
2:A:703:ARG:HD3	7:A:1473:HOH:O	2.20	0.41
3:T:6:A5L:H2'	3:T:7:CFL:H6	2.02	0.41
2:A:779:ARG:NH1	7:A:1031:HOH:O	2.54	0.41
2:A:715:GLY:HA2	4:A:903:MPD:H53	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:515:GLU:HG3	2:A:519:TYR:CZ	2.56	0.40
2:A:746:VAL:O	2:A:750:MET:HG2	2.22	0.40
2:A:766:LEU:HA	2:A:766:LEU:HD23	1.89	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
2	A	575/577 (100%)	562 (98%)	11 (2%)	2 (0%)	36 20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	631	GLU
2	A	407	VAL

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
2	A	493/494 (100%)	485 (98%)	8 (2%)	55 32

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	303	LEU
2	A	306	ARG
2	A	552	THR
2	A	630	LEU
2	A	632	GLU
2	A	717	SER
2	A	735	PHE
2	A	811	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	468	ASN
2	A	470	GLN
2	A	579	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

13 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	A5L	T	6	3,1	21,24,25	5.96	9 (42%)	30,35,38	2.92	15 (50%)
3	CFL	T	13	3,1	18,21,22	4.47	13 (72%)	25,30,33	1.09	2 (8%)
3	GFL	T	4	3	22,25,26	5.94	15 (68%)	32,37,40	2.18	11 (34%)
3	GFL	T	10	3,1	22,25,26	5.72	16 (72%)	32,37,40	2.34	11 (34%)
3	CFL	T	15	3,1	18,21,22	4.46	13 (72%)	25,30,33	1.12	1 (4%)
3	A5L	T	11	3,1	21,24,25	5.88	8 (38%)	30,35,38	2.96	13 (43%)
3	UF2	T	5	3,1	18,21,22	7.32	15 (83%)	25,30,33	1.86	6 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	UF2	T	9	3,1	18,21,22	7.11	15 (83%)	25,30,33	2.14	9 (36%)
3	A5L	T	16	3	21,24,25	6.08	8 (38%)	30,35,38	3.16	17 (56%)
3	CFL	T	7	3,1	18,21,22	4.48	14 (77%)	25,30,33	1.18	1 (4%)
3	UF2	T	12	3,1	18,21,22	7.10	15 (83%)	25,30,33	2.21	9 (36%)
3	GFL	T	8	3,1	22,25,26	5.85	15 (68%)	32,37,40	2.34	12 (37%)
3	GFL	T	14	3,1	22,25,26	5.94	15 (68%)	32,37,40	2.67	16 (50%)

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	A5L	T	6	3,1	-	2/7/25/26	0/3/3/3
3	CFL	T	13	3,1	-	0/7/25/26	0/2/2/2
3	GFL	T	4	3	-	2/7/25/26	0/3/3/3
3	GFL	T	10	3,1	-	0/7/25/26	0/3/3/3
3	CFL	T	15	3,1	-	2/7/25/26	0/2/2/2
3	A5L	T	11	3,1	-	0/7/25/26	0/3/3/3
3	UF2	T	5	3,1	-	1/7/25/26	0/2/2/2
3	UF2	T	9	3,1	-	0/7/25/26	0/2/2/2
3	A5L	T	16	3	-	2/7/25/26	0/3/3/3
3	CFL	T	7	3,1	-	0/7/25/26	0/2/2/2
3	UF2	T	12	3,1	-	0/7/25/26	0/2/2/2
3	GFL	T	8	3,1	-	2/7/25/26	0/3/3/3
3	GFL	T	14	3,1	-	0/7/25/26	0/3/3/3

All (171) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	14	GFL	C2'-C3'	-20.06	1.26	1.52
3	T	4	GFL	C2'-C3'	-20.04	1.26	1.52
3	T	8	GFL	C2'-C3'	-19.86	1.26	1.52
3	T	10	GFL	C2'-C3'	-19.42	1.27	1.52
3	T	16	A5L	C2'-C1'	-19.22	1.30	1.53
3	T	5	UF2	C2'-C3'	-18.68	1.28	1.52
3	T	6	A5L	C2'-C1'	-18.18	1.31	1.53
3	T	11	A5L	C2'-C1'	-17.85	1.31	1.53
3	T	12	UF2	C2'-C3'	-17.50	1.29	1.52
3	T	9	UF2	C2'-C3'	-17.34	1.29	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	5	UF2	F2'-C2'	-16.04	1.08	1.40
3	T	9	UF2	F2'-C2'	-15.50	1.09	1.40
3	T	12	UF2	F2'-C2'	-15.40	1.10	1.40
3	T	11	A5L	C2'-C3'	12.94	1.69	1.52
3	T	6	A5L	C2'-C3'	12.63	1.69	1.52
3	T	16	A5L	C2'-C3'	12.55	1.69	1.52
3	T	4	GFL	C2'-C1'	11.69	1.67	1.53
3	T	14	GFL	C2'-C1'	11.10	1.66	1.53
3	T	8	GFL	C2'-C1'	10.80	1.66	1.53
3	T	6	A5L	C3'-C4'	-10.61	1.26	1.53
3	T	12	UF2	C2'-C1'	10.52	1.65	1.53
3	T	9	UF2	C2'-C1'	10.50	1.65	1.53
3	T	11	A5L	C3'-C4'	-10.44	1.26	1.53
3	T	16	A5L	C3'-C4'	-10.35	1.26	1.53
3	T	10	GFL	C2'-C1'	10.08	1.65	1.53
3	T	5	UF2	C2'-C1'	9.80	1.64	1.53
3	T	13	CFL	C3'-C4'	-8.78	1.30	1.53
3	T	15	CFL	C3'-C4'	-8.54	1.31	1.53
3	T	7	CFL	C3'-C4'	-8.44	1.31	1.53
3	T	16	A5L	O4'-C4'	7.93	1.62	1.45
3	T	6	A5L	O4'-C4'	7.81	1.62	1.45
3	T	15	CFL	O4'-C4'	7.76	1.62	1.45
3	T	9	UF2	C2-N1	7.67	1.50	1.38
3	T	7	CFL	O4'-C4'	7.59	1.61	1.45
3	T	12	UF2	C2-N1	7.43	1.50	1.38
3	T	11	A5L	O4'-C4'	7.39	1.61	1.45
3	T	14	GFL	C4-N3	7.37	1.51	1.34
3	T	13	CFL	O4'-C4'	7.32	1.61	1.45
3	T	5	UF2	C2-N3	7.26	1.50	1.38
3	T	5	UF2	C2-N1	7.21	1.49	1.38
3	T	10	GFL	C4-N3	7.18	1.50	1.34
3	T	4	GFL	C4-N3	7.14	1.50	1.34
3	T	8	GFL	C4-N3	7.14	1.50	1.34
3	T	9	UF2	C2-N3	7.07	1.50	1.38
3	T	12	UF2	C2-N3	6.98	1.50	1.38
3	T	8	GFL	C2-N2	6.57	1.49	1.34
3	T	14	GFL	C2-N2	6.53	1.49	1.34
3	T	4	GFL	C2-N2	6.52	1.49	1.34
3	T	7	CFL	C2-N3	6.47	1.49	1.36
3	T	10	GFL	C2-N2	6.45	1.49	1.34
3	T	13	CFL	C2-N3	6.35	1.48	1.36
3	T	7	CFL	C6-C5	6.28	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	13	CFL	C6-C5	6.24	1.49	1.35
3	T	15	CFL	C6-C5	6.24	1.49	1.35
3	T	15	CFL	C2-N3	6.23	1.48	1.36
3	T	5	UF2	C6-C5	5.79	1.48	1.35
3	T	9	UF2	C6-C5	5.70	1.48	1.35
3	T	14	GFL	C2-N3	5.67	1.46	1.33
3	T	12	UF2	C6-C5	5.62	1.48	1.35
3	T	7	CFL	C4-N3	5.56	1.45	1.34
3	T	5	UF2	O4'-C1'	-5.50	1.29	1.42
3	T	8	GFL	C5'-C4'	-5.49	1.35	1.51
3	T	13	CFL	C4-N3	5.48	1.45	1.34
3	T	8	GFL	C2-N3	5.44	1.46	1.33
3	T	10	GFL	C2-N3	5.42	1.46	1.33
3	T	15	CFL	C4-N3	5.36	1.45	1.34
3	T	6	A5L	O4'-C1'	5.30	1.54	1.42
3	T	9	UF2	O4'-C1'	-5.29	1.29	1.42
3	T	4	GFL	C2-N3	5.28	1.46	1.33
3	T	14	GFL	C5'-C4'	-5.23	1.35	1.51
3	T	12	UF2	O4'-C1'	-5.22	1.29	1.42
3	T	4	GFL	C5'-C4'	-5.12	1.36	1.51
3	T	16	A5L	O4'-C1'	5.04	1.53	1.42
3	T	10	GFL	C5'-C4'	-5.02	1.36	1.51
3	T	11	A5L	O4'-C1'	4.96	1.53	1.42
3	T	15	CFL	O4'-C1'	-4.96	1.30	1.42
3	T	7	CFL	O4'-C1'	-4.87	1.30	1.42
3	T	13	CFL	O4'-C1'	-4.86	1.30	1.42
3	T	7	CFL	C4-N4	4.84	1.45	1.33
3	T	15	CFL	C4-N4	4.83	1.45	1.33
3	T	13	CFL	C4-N4	4.79	1.45	1.33
3	T	5	UF2	C4-N3	4.54	1.46	1.38
3	T	10	GFL	O4'-C1'	-4.51	1.31	1.42
3	T	8	GFL	O4'-C1'	-4.51	1.31	1.42
3	T	16	A5L	C6-N6	4.44	1.45	1.34
3	T	6	A5L	C6-N6	4.41	1.45	1.34
3	T	11	A5L	C6-N6	4.40	1.45	1.34
3	T	9	UF2	C4-N3	4.40	1.46	1.38
3	T	4	GFL	O4'-C1'	-4.29	1.32	1.42
3	T	13	CFL	C2-N1	4.27	1.49	1.40
3	T	14	GFL	O4'-C1'	-4.26	1.32	1.42
3	T	12	UF2	C4-N3	4.23	1.45	1.38
3	T	7	CFL	C2-N1	4.22	1.48	1.40
3	T	15	CFL	C2-N1	4.17	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	5	UF2	O4'-C4'	3.99	1.53	1.45
3	T	9	UF2	O4'-C4'	3.98	1.53	1.45
3	T	12	UF2	O4'-C4'	3.94	1.53	1.45
3	T	13	CFL	F-C2'	-3.81	1.32	1.40
3	T	5	UF2	C5'-C4'	-3.78	1.40	1.51
3	T	12	UF2	C5'-C4'	-3.72	1.40	1.51
3	T	15	CFL	F-C2'	-3.67	1.33	1.40
3	T	9	UF2	C5'-C4'	-3.67	1.40	1.51
3	T	7	CFL	F-C2'	-3.58	1.33	1.40
3	T	4	GFL	O6-C6	-3.49	1.16	1.23
3	T	10	GFL	O6-C6	-3.48	1.17	1.23
3	T	14	GFL	O6-C6	-3.47	1.17	1.23
3	T	4	GFL	C6-N1	3.45	1.45	1.38
3	T	8	GFL	O6-C6	-3.43	1.17	1.23
3	T	7	CFL	C6-N1	3.40	1.46	1.38
3	T	15	CFL	C6-N1	3.31	1.46	1.38
3	T	8	GFL	C6-N1	3.30	1.45	1.38
3	T	10	GFL	C6-N1	3.30	1.45	1.38
3	T	13	CFL	C6-N1	3.24	1.45	1.38
3	T	14	GFL	O3'-C3'	3.23	1.50	1.43
3	T	14	GFL	C6-N1	3.22	1.44	1.38
3	T	14	GFL	O4'-C4'	3.05	1.51	1.45
3	T	5	UF2	O3'-C3'	3.01	1.50	1.43
3	T	9	UF2	O3'-C3'	3.00	1.50	1.43
3	T	12	UF2	O3'-C3'	2.99	1.50	1.43
3	T	16	A5L	C5-C4	-2.97	1.33	1.39
3	T	5	UF2	C6-N1	2.96	1.45	1.38
3	T	4	GFL	O4'-C4'	2.96	1.51	1.45
3	T	12	UF2	O4-C4	-2.94	1.18	1.24
3	T	10	GFL	O4'-C4'	2.91	1.51	1.45
3	T	6	A5L	C5-C4	-2.89	1.33	1.39
3	T	7	CFL	O3'-C3'	2.88	1.50	1.43
3	T	11	A5L	C5-C4	-2.86	1.34	1.39
3	T	9	UF2	C6-N1	2.85	1.44	1.38
3	T	15	CFL	O3'-C3'	2.85	1.50	1.43
3	T	12	UF2	C6-N1	2.83	1.44	1.38
3	T	5	UF2	O4-C4	-2.79	1.19	1.24
3	T	7	CFL	C5-C4	2.78	1.49	1.42
3	T	13	CFL	C5-C4	2.78	1.49	1.42
3	T	14	GFL	C5-N7	-2.76	1.33	1.39
3	T	10	GFL	C3'-C4'	2.74	1.59	1.53
3	T	13	CFL	O3'-C3'	2.74	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	8	GFL	O4'-C4'	2.71	1.51	1.45
3	T	4	GFL	C2-N1	2.69	1.44	1.37
3	T	9	UF2	O4-C4	-2.66	1.19	1.24
3	T	15	CFL	C5-C4	2.63	1.49	1.42
3	T	8	GFL	C2-N1	2.63	1.44	1.37
3	T	14	GFL	C3'-C4'	2.63	1.59	1.53
3	T	6	A5L	C5-N7	-2.60	1.34	1.39
3	T	8	GFL	C5-N7	-2.59	1.33	1.39
3	T	10	GFL	C5-N7	-2.59	1.33	1.39
3	T	10	GFL	C2-N1	2.58	1.43	1.37
3	T	4	GFL	C3'-C4'	2.55	1.59	1.53
3	T	14	GFL	C2-N1	2.53	1.43	1.37
3	T	15	CFL	O2-C2	-2.53	1.19	1.23
3	T	9	UF2	C5-C4	2.51	1.49	1.43
3	T	4	GFL	C5-N7	-2.49	1.34	1.39
3	T	5	UF2	C5-C4	2.45	1.49	1.43
3	T	12	UF2	O2-C2	-2.43	1.18	1.23
3	T	4	GFL	O3'-C3'	2.43	1.49	1.43
3	T	7	CFL	O2-C2	-2.40	1.19	1.23
3	T	13	CFL	O2-C2	-2.39	1.19	1.23
3	T	9	UF2	O2-C2	-2.38	1.18	1.23
3	T	11	A5L	C5-N7	-2.38	1.34	1.39
3	T	12	UF2	C5-C4	2.33	1.48	1.43
3	T	16	A5L	C5-N7	-2.31	1.34	1.39
3	T	10	GFL	C5-C6	2.28	1.52	1.44
3	T	8	GFL	O3'-C3'	2.16	1.48	1.43
3	T	8	GFL	C5-C6	2.16	1.52	1.44
3	T	7	CFL	C2'-C3'	2.16	1.55	1.52
3	T	10	GFL	O3'-C3'	2.15	1.48	1.43
3	T	5	UF2	O2-C2	-2.15	1.19	1.23
3	T	14	GFL	C5-C6	2.11	1.52	1.44
3	T	4	GFL	C5-C6	2.10	1.52	1.44
3	T	8	GFL	C3'-C4'	2.09	1.58	1.53
3	T	6	A5L	C8-N9	-2.01	1.34	1.37
3	T	10	GFL	C1'-N9	-2.00	1.41	1.47

All (123) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	16	A5L	N6-C6-N1	-7.97	100.63	118.38
3	T	6	A5L	N6-C6-N1	-7.59	101.46	118.38
3	T	11	A5L	N6-C6-N1	-7.44	101.81	118.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	16	A5L	C5-C6-N6	6.41	139.16	123.29
3	T	6	A5L	C5-C6-N6	6.17	138.57	123.29
3	T	11	A5L	C5-C6-N6	5.90	137.90	123.29
3	T	12	UF2	C4-N3-C2	-5.86	119.34	126.61
3	T	16	A5L	N3-C2-N1	-5.81	119.79	128.58
3	T	11	A5L	N3-C2-N1	-5.80	119.81	128.58
3	T	14	GFL	C5-C4-N3	-5.74	119.26	128.39
3	T	6	A5L	N3-C2-N1	-5.64	120.05	128.58
3	T	9	UF2	C4-N3-C2	-5.45	119.85	126.61
3	T	5	UF2	C4-N3-C2	-5.26	120.08	126.61
3	T	4	GFL	C5-C4-N3	-5.19	120.14	128.39
3	T	14	GFL	C3'-C2'-C1'	5.18	109.11	103.10
3	T	8	GFL	C5-C4-N3	-5.02	120.40	128.39
3	T	10	GFL	C5-C4-N3	-4.98	120.47	128.39
3	T	11	A5L	C5-C4-N3	-4.95	119.89	126.72
3	T	6	A5L	C5-C4-N3	-4.93	119.93	126.72
3	T	4	GFL	C2-N3-C4	4.68	120.37	112.30
3	T	14	GFL	C2-N3-C4	4.68	120.35	112.30
3	T	16	A5L	N9-C8-N7	-4.54	107.49	113.94
3	T	16	A5L	C5-C4-N3	-4.53	120.48	126.72
3	T	10	GFL	C2-N3-C4	4.49	120.03	112.30
3	T	8	GFL	C2-N3-C4	4.43	119.93	112.30
3	T	11	A5L	N9-C8-N7	-4.39	107.70	113.94
3	T	8	GFL	C3'-C2'-C1'	4.37	108.17	103.10
3	T	8	GFL	C1'-N9-C4	-4.34	113.66	126.49
3	T	10	GFL	C1'-N9-C4	-4.33	113.70	126.49
3	T	16	A5L	O4'-C1'-C2'	-4.12	101.49	105.84
3	T	10	GFL	C2'-C3'-C4'	4.12	107.86	102.43
3	T	14	GFL	C2'-C3'-C4'	4.11	107.84	102.43
3	T	6	A5L	N9-C8-N7	-4.10	108.12	113.94
3	T	6	A5L	C2'-C3'-C4'	3.96	107.65	102.43
3	T	12	UF2	N3-C2-N1	3.88	119.94	114.89
3	T	12	UF2	C5-C4-N3	3.84	120.18	114.80
3	T	14	GFL	C5'-C4'-C3'	-3.83	101.41	115.21
3	T	16	A5L	C4'-O4'-C1'	-3.82	101.04	109.47
3	T	14	GFL	N9-C4-N3	3.80	133.55	125.95
3	T	10	GFL	C1'-N9-C8	3.79	137.49	126.73
3	T	8	GFL	C1'-N9-C8	3.68	137.19	126.73
3	T	9	UF2	N3-C2-N1	3.66	119.66	114.89
3	T	11	A5L	C2'-C3'-C4'	3.60	107.18	102.43
3	T	4	GFL	C1'-N9-C4	-3.59	115.88	126.49
3	T	14	GFL	C1'-N9-C4	-3.55	116.01	126.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	9	UF2	C5-C4-N3	3.52	119.73	114.80
3	T	5	UF2	N3-C2-N1	3.48	119.42	114.89
3	T	5	UF2	C5-C4-N3	3.46	119.65	114.80
3	T	8	GFL	N9-C8-N7	-3.45	107.00	113.40
3	T	12	UF2	C3'-C2'-C1'	3.42	107.07	103.10
3	T	11	A5L	C2-N3-C4	3.41	120.17	111.83
3	T	7	CFL	C2'-C3'-C4'	3.41	106.92	102.43
3	T	16	A5L	C2-N3-C4	3.39	120.11	111.83
3	T	9	UF2	C4'-O4'-C1'	-3.38	102.00	109.47
3	T	6	A5L	C2-N3-C4	3.36	120.03	111.83
3	T	11	A5L	C3'-C2'-C1'	3.31	106.94	103.10
3	T	11	A5L	N3-C4-N9	3.30	132.79	127.17
3	T	10	GFL	N9-C8-N7	-3.30	107.28	113.40
3	T	4	GFL	N9-C4-N3	3.24	132.43	125.95
3	T	16	A5L	C2'-C3'-C4'	3.22	106.67	102.43
3	T	8	GFL	N9-C4-N3	3.22	132.38	125.95
3	T	11	A5L	C4'-O4'-C1'	-3.16	102.50	109.47
3	T	4	GFL	C1'-N9-C8	3.15	135.69	126.73
3	T	14	GFL	C1'-N9-C8	3.15	135.69	126.73
3	T	10	GFL	C3'-C2'-C1'	3.12	106.72	103.10
3	T	16	A5L	C5-N7-C8	3.06	108.26	103.45
3	T	14	GFL	C2-N1-C6	-3.05	119.59	125.11
3	T	5	UF2	O4-C4-C5	-3.02	119.96	125.16
3	T	10	GFL	C2-N1-C6	-3.01	119.66	125.11
3	T	14	GFL	N9-C8-N7	-2.99	107.85	113.40
3	T	4	GFL	C2-N1-C6	-2.98	119.71	125.11
3	T	14	GFL	O3'-C3'-C4'	2.96	119.59	111.08
3	T	6	A5L	N3-C4-N9	2.96	132.20	127.17
3	T	16	A5L	C3'-C2'-C1'	-2.94	99.68	103.10
3	T	9	UF2	C2'-C3'-C4'	2.93	106.30	102.43
3	T	11	A5L	C5-N7-C8	2.93	108.06	103.45
3	T	12	UF2	C2'-C3'-C4'	2.92	106.28	102.43
3	T	4	GFL	N9-C8-N7	-2.91	108.00	113.40
3	T	10	GFL	N9-C4-N3	2.88	131.71	125.95
3	T	12	UF2	O4-C4-C5	-2.87	120.21	125.16
3	T	15	CFL	C2'-C3'-C4'	2.86	106.19	102.43
3	T	8	GFL	C2-N1-C6	-2.84	119.95	125.11
3	T	6	A5L	C5-N7-C8	2.82	107.88	103.45
3	T	10	GFL	C5-C6-N1	2.80	120.39	113.25
3	T	9	UF2	C3'-C2'-C1'	2.78	106.33	103.10
3	T	14	GFL	C5-C6-N1	2.75	120.25	113.25
3	T	4	GFL	C5-C6-N1	2.74	120.23	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	14	GFL	C2'-C1'-N9	-2.72	110.09	114.27
3	T	13	CFL	C4'-O4'-C1'	-2.68	103.55	109.47
3	T	6	A5L	F-C2'-C1'	2.68	114.25	108.88
3	T	6	A5L	C3'-C2'-C1'	2.67	106.20	103.10
3	T	11	A5L	C4-N9-C8	2.65	108.53	105.74
3	T	8	GFL	C5-C6-N1	2.62	119.92	113.25
3	T	4	GFL	O6-C6-C5	-2.60	119.68	126.53
3	T	16	A5L	C4-C5-N7	-2.59	107.62	110.58
3	T	4	GFL	C3'-C2'-C1'	2.56	106.07	103.10
3	T	5	UF2	C2'-C3'-C4'	2.52	105.76	102.43
3	T	16	A5L	C4-N9-C8	2.52	108.38	105.74
3	T	9	UF2	O4-C4-C5	-2.50	120.84	125.16
3	T	14	GFL	O6-C6-C5	-2.50	119.94	126.53
3	T	16	A5L	O4'-C1'-N9	2.48	112.86	108.09
3	T	8	GFL	C5'-C4'-C3'	-2.47	106.31	115.21
3	T	13	CFL	C2'-C3'-C4'	2.46	105.67	102.43
3	T	11	A5L	F-C2'-C1'	2.45	113.79	108.88
3	T	8	GFL	C8-N7-C5	2.45	108.62	104.26
3	T	16	A5L	N3-C4-N9	2.41	131.27	127.17
3	T	12	UF2	C4'-O4'-C1'	-2.38	104.22	109.47
3	T	8	GFL	O6-C6-C5	-2.35	120.33	126.53
3	T	5	UF2	O2-C2-N1	-2.33	119.76	122.80
3	T	9	UF2	C1'-N1-C2	2.31	121.75	117.59
3	T	14	GFL	C8-N7-C5	2.30	108.36	104.26
3	T	10	GFL	C8-N7-C5	2.24	108.26	104.26
3	T	16	A5L	C5-C4-N9	2.24	108.25	105.81
3	T	9	UF2	F2'-C2'-C3'	2.23	113.56	109.14
3	T	12	UF2	F2'-C2'-C3'	2.22	113.54	109.14
3	T	16	A5L	C2'-C1'-N9	2.21	117.87	113.92
3	T	14	GFL	O4'-C1'-C2'	2.13	108.10	105.84
3	T	6	A5L	C4-N9-C8	2.12	107.97	105.74
3	T	6	A5L	C4-C5-N7	-2.12	108.16	110.58
3	T	6	A5L	C5'-C4'-C3'	-2.09	107.67	115.21
3	T	6	A5L	C6-C5-C4	2.09	120.03	117.18
3	T	4	GFL	F-C2'-C1'	2.07	113.02	108.88
3	T	12	UF2	C1'-N1-C2	2.05	121.27	117.59

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	T	6	A5L	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
3	T	8	GFL	O4'-C4'-C5'-O5'
3	T	8	GFL	C3'-C4'-C5'-O5'
3	T	15	CFL	C3'-C4'-C5'-O5'
3	T	6	A5L	O4'-C4'-C5'-O5'
3	T	4	GFL	C3'-C4'-C5'-O5'
3	T	4	GFL	O4'-C4'-C5'-O5'
3	T	15	CFL	O4'-C4'-C5'-O5'
3	T	16	A5L	O4'-C4'-C5'-O5'
3	T	16	A5L	C3'-C4'-C5'-O5'
3	T	5	UF2	O4'-C4'-C5'-O5'

There are no ring outliers.

8 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	T	6	A5L	1	0
3	T	4	GFL	1	0
3	T	15	CFL	2	0
3	T	5	UF2	1	0
3	T	16	A5L	1	0
3	T	7	CFL	2	0
3	T	8	GFL	1	0
3	T	14	GFL	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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
4	MPD	A	903	-	7,7,7	0.43	0	9,10,10	0.78	0
5	SO4	A	905	-	4,4,4	0.23	0	6,6,6	0.10	0
5	SO4	A	904	-	4,4,4	0.25	0	6,6,6	0.14	0
4	MPD	A	901	-	7,7,7	0.40	0	9,10,10	0.55	0
4	MPD	A	902	-	7,7,7	0.32	0	9,10,10	0.40	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
4	MPD	A	901	-	-	1/5/5/5	-
4	MPD	A	903	-	-	2/5/5/5	-
4	MPD	A	902	-	-	1/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	903	MPD	C1-C2-C3-C4
4	A	902	MPD	C2-C3-C4-O4
4	A	901	MPD	C1-C2-C3-C4
4	A	903	MPD	CM-C2-C3-C4

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	903	MPD	5	0
4	A	901	MPD	1	0
4	A	902	MPD	2	0

5.7 Other polymers [i](#)

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	P	11/11 (100%)	1.53	2 (18%) 3 3	59, 73, 113, 149	0
2	A	577/577 (100%)	0.46	54 (9%) 14 14	18, 31, 60, 100	0
3	T	0/13	-	-	-	-
All	All	588/601 (97%)	0.48	56 (9%) 14 14	18, 31, 64, 149	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	632	GLU	5.8
2	A	631	GLU	5.1
2	A	300	ALA	5.1
2	A	630	LEU	4.8
2	A	628	ILE	4.1
2	A	433	ALA	3.8
2	A	713	VAL	3.7
2	A	550	THR	3.6
2	A	715	GLY	3.6
2	A	716	ILE	3.5
2	A	719	TYR	3.5
2	A	629	ARG	3.3
2	A	714	TYR	3.2
2	A	551	LYS	3.2
2	A	408	ASP	3.2
2	A	587	TYR	3.1
2	A	712	ILE	3.1
1	P	11	DT	3.0
2	A	547	LEU	3.0
2	A	555	SER	2.9
2	A	726	ASN	2.9
2	A	735	PHE	2.8
2	A	723	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
2	A	431	LYS	2.7
2	A	314	ASP	2.7
2	A	553	GLY	2.7
2	A	407	VAL	2.6
2	A	579	GLN	2.6
2	A	717	SER	2.6
1	P	1	DG	2.6
2	A	520	GLU	2.6
2	A	513	THR	2.5
2	A	552	THR	2.5
2	A	523	GLY	2.4
2	A	625	ASN	2.4
2	A	691	GLN	2.4
2	A	529	ASN	2.4
2	A	303	LEU	2.4
2	A	729	ARG	2.4
2	A	560	VAL	2.4
2	A	549	LYS	2.3
2	A	505	GLU	2.3
2	A	554	TYR	2.3
2	A	811	LEU	2.3
2	A	434	LYS	2.3
2	A	718	ASP	2.2
2	A	570	ILE	2.2
2	A	305	ASP	2.2
2	A	512	ARG	2.2
2	A	710	PHE	2.2
2	A	522	ALA	2.1
2	A	545	PRO	2.1
2	A	432	GLY	2.1
2	A	548	LYS	2.1
2	A	536	VAL	2.1
2	A	350	THR	2.0

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, 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	A5L	T	16	22/23	0.45	0.17	92,101,123,126	0
3	CFL	T	15	20/21	0.50	0.16	99,108,124,125	0
3	GFL	T	4	23/24	0.61	0.17	77,86,120,121	0
3	UF2	T	5	20/21	0.67	0.18	93,103,117,117	0
3	GFL	T	14	23/24	0.69	0.15	77,98,106,119	0
3	A5L	T	6	22/23	0.74	0.15	83,94,120,123	0
3	CFL	T	7	20/21	0.80	0.16	56,75,94,98	0
3	GFL	T	8	23/24	0.86	0.14	38,56,61,67	0
3	CFL	T	13	20/21	0.87	0.14	47,64,73,81	0
3	GFL	T	10	23/24	0.87	0.16	43,53,58,59	0
3	UF2	T	12	20/21	0.88	0.14	40,53,60,68	0
3	A5L	T	11	22/23	0.91	0.12	33,43,50,51	0
3	UF2	T	9	20/21	0.92	0.12	32,44,55,58	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
4	MPD	A	901	8/8	0.61	0.20	33,55,65,66	0
4	MPD	A	903	8/8	0.65	0.21	46,61,66,79	0
5	SO4	A	905	5/5	0.72	0.18	85,91,93,93	0
4	MPD	A	902	8/8	0.88	0.12	37,53,60,67	0
5	SO4	A	904	5/5	0.93	0.08	58,66,72,73	0
6	MG	A	906	1/1	0.95	0.13	52,52,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.