Full wwPDB X-ray Structure Validation Report (i)

Aug 29, 2023 – 01:51 PM EDT

PDB ID	:	3PV8
Title	:	Crystal Structure of Bacillus DNA Polymerase I Large Fragment Bound to DNA and ddTTP-dA in Closed Conformation
Authors	:	Wang, W.; Beese, L.S.
Deposited on	:	2010-12-06
Resolution	:	1.52 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 (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:

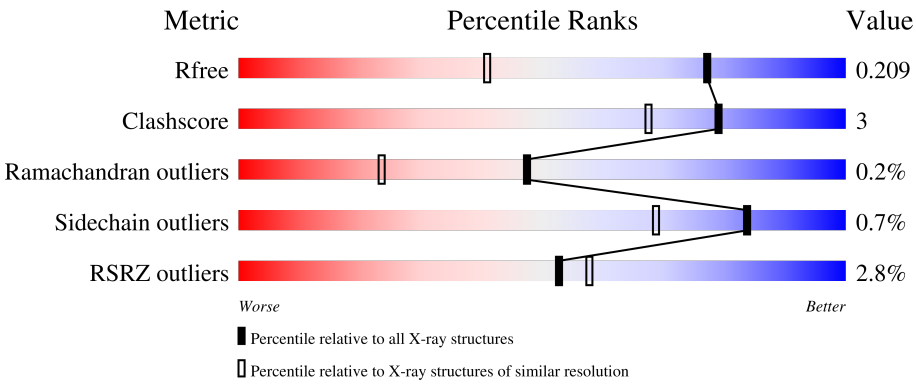
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 1.52 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}	130704	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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	592	5%, 91%, 6% •
1	D	592	92%, 6% •
2	B	9	56%, 44%
2	E	9	67%, 11%, 22%
3	C	13	54%, 38%, 8%

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Mol	Chain	Length	Quality of chain
3	F	13	54% 38% 8%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 22076 atoms, of which 9986 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 DNA polymerase I.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	579	9387	2962	4728	809	871	17	0	3	0
1	D	579	9447	2980	4760	812	878	17	0	11	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	598	ALA	ASP	engineered mutation	UNP Q5KWC1
A	710	TYR	PHE	engineered mutation	UNP Q5KWC1
A	823	HIS	ARG	SEE REMARK 999	UNP Q5KWC1
D	598	ALA	ASP	engineered mutation	UNP Q5KWC1
D	710	TYR	PHE	engineered mutation	UNP Q5KWC1
D	823	HIS	ARG	SEE REMARK 999	UNP Q5KWC1

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P			
2	B	9	277	86	102	28	53	8	0	0	0
2	E	9	277	86	102	28	53	8	0	0	0

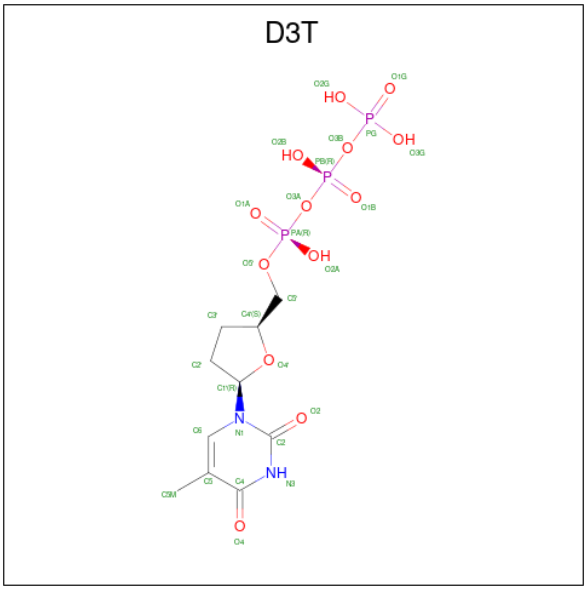
- Molecule 3 is a DNA chain called DNA (5'-D(*C*AP*TP*AP*AP*GP*AP*GP*TP*CP*AP*GP*G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P			
3	C	12	384	119	135	52	67	11	0	0	0
3	F	12	384	119	135	52	67	11	0	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

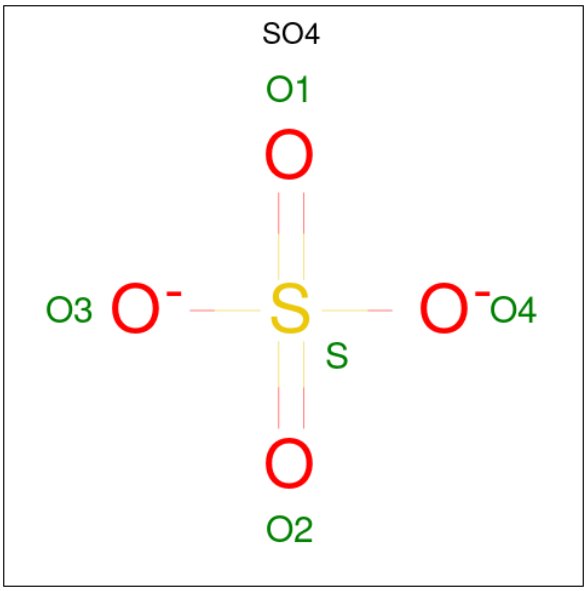
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0
4	D	1	1	1	0	0

- Molecule 5 is 2',3'-DIDEOXY-THYMIDINE-5'-TRIPHOSPHATE (three-letter code: D3T) (formula: $C_{10}H_{17}N_2O_{13}P_3$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
5	A	1	40	10	12	2	13	3	0	0
5	D	1	40	10	12	2	13	3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 7 is water.

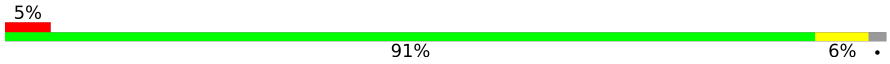
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	635	Total O 635 635	0	0
7	D	913	Total O 913 913	0	0
7	B	48	Total O 48 48	0	0
7	C	85	Total O 85 85	0	0
7	E	50	Total O 50 50	0	0
7	F	92	Total O 92 92	0	0

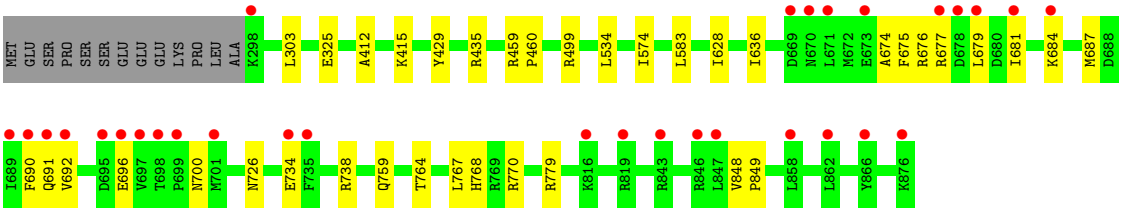
3 Residue-property plots (i)

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: DNA polymerase I

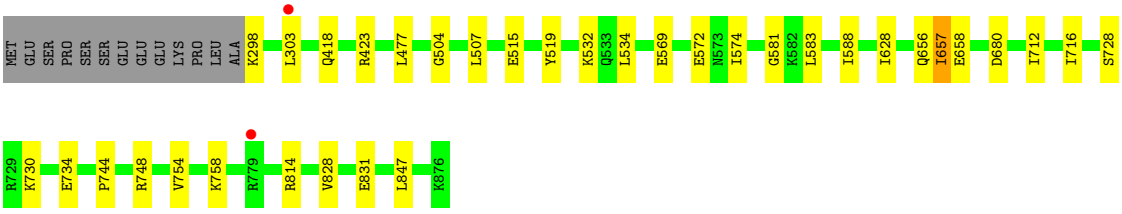
Chain A:





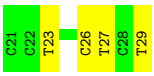
• Molecule 1: DNA polymerase I

Chain D:



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

Chain B:

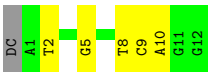


• Molecule 2: DNA (5'-D(*CP*CP*TP*GP*AP*CP*TP*CP*(2DT))-3')

Chain E:

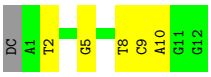
• Molecule 3: DNA (5'-D(*C*AP*TP*AP*AP*GP*AP*GP*TP*CP*AP*GP*G)-3')

Chain C:



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

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	93.89Å 109.30Å 150.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.42 – 1.52 88.42 – 1.52	Depositor EDS
% Data completeness (in resolution range)	93.9 (88.42-1.52) 93.9 (88.42-1.52)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.91 (at 1.52Å)	Xtriage
Refinement program	PHENIX 1.7.1_743, REFMAC 5.5.0109	Depositor
R, R_{free}	0.185 , 0.211 0.184 , 0.209	Depositor DCC
R_{free} test set	10323 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å^2)	15.4	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 50.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	22076	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MG, 2DT, D3T

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	0.37	0/4755	0.52	0/6427
1	D	0.48	0/4815	0.61	0/6507
2	B	0.93	0/173	1.71	4/264 (1.5%)
2	E	1.08	0/173	1.79	6/264 (2.3%)
3	C	0.96	0/281	1.64	5/433 (1.2%)
3	F	0.97	0/281	1.56	6/433 (1.4%)
All	All	0.50	0/10478	0.75	21/14328 (0.1%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	23	DT	O4'-C1'-N1	-9.41	101.42	108.00
2	E	26	DC	O4'-C1'-N1	9.12	114.39	108.00
3	C	8	DT	O4'-C1'-N1	-7.79	102.55	108.00
3	C	2	DT	O4'-C1'-N1	7.75	113.42	108.00
2	E	23	DT	O4'-C1'-N1	-7.44	102.79	108.00
3	F	8	DT	O4'-C1'-N1	-6.89	103.17	108.00
3	F	2	DT	O4'-C1'-N1	6.60	112.62	108.00
2	E	26	DC	O4'-C4'-C3'	6.30	109.78	106.00
2	E	27	DT	O5'-P-OP2	-6.28	100.05	105.70
2	E	27	DT	C4'-C3'-C2'	-6.18	97.54	103.10
3	C	2	DT	C1'-O4'-C4'	-5.56	104.54	110.10
3	C	5	DG	C8-N9-C4	-5.49	104.20	106.40
3	F	5	DG	O4'-C4'-C3'	-5.48	102.31	104.50
2	B	26	DC	O4'-C1'-N1	5.42	111.80	108.00
2	B	26	DC	O4'-C4'-C3'	5.39	109.23	106.00
3	F	2	DT	C1'-O4'-C4'	-5.34	104.76	110.10
3	F	2	DT	O4'-C1'-C2'	-5.24	101.71	105.90
2	B	27	DT	C4'-C3'-C2'	-5.24	98.39	103.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	5	DG	O4'-C4'-C3'	-5.15	102.44	104.50
3	F	2	DT	C6-C5-C7	-5.11	119.84	122.90
2	E	27	DT	OP1-P-OP2	5.08	127.22	119.60

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	4659	4728	4707	28	0
1	D	4687	4760	4715	26	0
2	B	175	102	104	0	0
2	E	175	102	104	1	0
3	C	249	135	136	1	0
3	F	249	135	136	1	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
5	A	28	12	13	0	0
5	D	28	12	13	0	0
6	A	5	0	0	0	0
6	D	10	0	0	0	0
7	A	635	0	0	7	3
7	B	48	0	0	0	0
7	C	85	0	0	0	0
7	D	913	0	0	13	4
7	E	50	0	0	1	0
7	F	92	0	0	0	0
All	All	12090	9986	9928	57	5

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 3.

All (57) 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:690:PHE:O	1:A:691:GLN:HB3	1.86	0.73
1:D:572:GLU:HG3	7:D:1786:HOH:O	1.87	0.73
1:A:734:GLU:HG2	7:A:1648:HOH:O	1.89	0.71
1:A:499:ARG:NE	7:A:971:HOH:O	2.26	0.69
1:D:583:LEU:HG	7:E:1397:HOH:O	1.94	0.68
1:A:779:ARG:NH2	7:A:1609:HOH:O	2.26	0.68
1:A:325:GLU:OE2	1:A:435:ARG:NH1	2.24	0.66
1:A:848:VAL:HB	1:A:849:PRO:HD3	1.79	0.64
3:F:9:DC:H2"	3:F:10:DA:C8	2.35	0.61
1:A:738:ARG:HD3	7:A:1392:HOH:O	1.99	0.61
1:D:504:GLY:HA2	1:D:588[B]:ILE:HD13	1.81	0.61
1:A:499:ARG:CZ	7:A:971:HOH:O	2.47	0.61
1:A:692:VAL:HB	1:A:696:GLU:HB3	1.82	0.60
3:C:9:DC:H2"	3:C:10:DA:C8	2.38	0.59
1:A:691:GLN:HG2	1:A:691:GLN:O	2.05	0.57
1:D:828:VAL:HB	1:D:831[B]:GLU:CG	2.34	0.57
1:A:675:PHE:CE2	1:A:681:ILE:HD13	2.41	0.56
1:D:504:GLY:CA	1:D:588[B]:ILE:HD13	2.37	0.55
1:D:569:GLU:CD	7:D:1752:HOH:O	2.45	0.55
1:D:748:ARG:HD3	7:D:1288:HOH:O	2.07	0.55
1:A:759:GLN:HG2	7:D:1616:HOH:O	2.08	0.54
1:D:507:LEU:HD23	1:D:588[B]:ILE:HD12	1.89	0.54
1:A:764:THR:HG22	1:A:770:ARG:HG2	1.89	0.53
1:A:459:ARG:HB3	1:A:460:PRO:HD3	1.90	0.53
1:D:734:GLU:HG3	7:D:889:HOH:O	2.09	0.52
1:D:754:VAL:HG12	1:D:758:LYS:HE2	1.91	0.51
1:D:423:ARG:NH1	7:D:1766:HOH:O	2.43	0.51
1:D:814:ARG:NH1	7:D:1357:HOH:O	2.44	0.50
1:D:754:VAL:CG1	1:D:758:LYS:HE2	2.42	0.49
1:D:657:ILE:HG23	1:D:658:GLU:N	2.27	0.49
1:A:684:LYS:HA	1:A:687:MET:HE3	1.95	0.49
1:D:418:GLN:HA	7:D:1018:HOH:O	2.13	0.49
1:D:534:LEU:HD11	1:D:574:ILE:HD13	1.94	0.49
1:D:581:GLY:HA3	7:D:1196:HOH:O	2.12	0.49
1:A:303:LEU:HD23	7:A:1416:HOH:O	2.12	0.48
1:A:412:ALA:O	1:A:415:LYS:HG2	2.13	0.48
1:A:412:ALA:O	1:A:415:LYS:HE2	2.14	0.48
1:A:325:GLU:H	1:A:325:GLU:CD	2.17	0.47
1:A:674:ALA:HA	1:A:679:LEU:HD12	1.98	0.46
1:A:681:ILE:N	1:A:681:ILE:HD12	2.31	0.46
1:D:744:PRO:O	1:D:748:ARG:HG3	2.15	0.45
1:D:831[B]:GLU:CD	7:D:1822:HOH:O	2.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:LYS:N	7:D:1389:HOH:O	2.50	0.44
1:D:847:LEU:C	1:D:847:LEU:HD23	2.38	0.44
1:D:572:GLU:CD	7:D:1787:HOH:O	2.55	0.44
1:A:677:ARG:HD2	1:A:679:LEU:HD11	1.99	0.44
1:A:687:MET:HB3	1:A:692:VAL:O	2.18	0.43
1:A:429:TYR:O	1:A:435:ARG:HA	2.19	0.43
1:D:515:GLU:HG2	1:D:519:TYR:CE2	2.54	0.43
1:D:656[A]:GLN:NE2	1:D:680:ASP:HA	2.35	0.42
1:A:676:ARG:HD3	7:A:1746:HOH:O	2.19	0.42
1:A:767:LEU:O	1:A:768:HIS:HB2	2.21	0.41
1:A:583:LEU:HD11	1:A:636:ILE:CG1	2.51	0.41
1:D:712:ILE:HA	1:D:716:ILE:HG22	2.03	0.40
1:A:534:LEU:HD11	1:A:574:ILE:HD13	2.03	0.40
1:D:532:LYS:HG3	7:D:1699:HOH:O	2.20	0.40
2:E:26:DC:H2'	2:E:27:DT:H71	2.02	0.40

All (5) 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:1802:HOH:O	7:D:1799:HOH:O[2_755]	2.03	0.17
7:D:1388:HOH:O	7:D:1419:HOH:O[4_545]	2.05	0.15
7:A:1795:HOH:O	7:A:1798:HOH:O[3_755]	2.11	0.09
7:A:1747:HOH:O	7:D:1762:HOH:O[2_745]	2.15	0.05
7:D:1120:HOH:O	7:D:1183:HOH:O[4_445]	2.18	0.02

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	580/592 (98%)	564 (97%)	15 (3%)	1 (0%)	47 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	588/592 (99%)	575 (98%)	12 (2%)	1 (0%)	47	23
All	All	1168/1184 (99%)	1139 (98%)	27 (2%)	2 (0%)	47	23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	628	ILE
1	D	628	ILE

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	498/507 (98%)	496 (100%)	2 (0%)	91	82
1	D	505/507 (100%)	500 (99%)	5 (1%)	76	56
All	All	1003/1014 (99%)	996 (99%)	7 (1%)	84	69

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	700	ASN
1	A	726	ASN
1	D	303	LEU
1	D	477	LEU
1	D	657	ILE
1	D	728	SER
1	D	730	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	704	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)

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	$\#\|Z\| > 2$
2	2DT	B	29	3,2	17,20,21	0.58	0	22,28,31	0.97	1 (4%)
2	2DT	E	29	3,2	17,20,21	0.58	0	22,28,31	0.82	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
2	2DT	B	29	3,2	-	0/7/18/19	0/2/2/2
2	2DT	E	29	3,2	-	0/7/18/19	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	29	2DT	O4-C4-C5	-2.09	122.48	124.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 2 are 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	$\#\|Z\| > 2$
6	SO4	D	1	-	4,4,4	0.14	0	6,6,6	0.43	0
5	D3T	A	201	4	25,29,29	2.09	5 (20%)	35,45,45	2.12	14 (40%)
5	D3T	D	202	4	25,29,29	1.87	4 (16%)	35,45,45	2.26	10 (28%)
6	SO4	D	3	-	4,4,4	0.16	0	6,6,6	0.09	0
6	SO4	A	2	-	4,4,4	0.16	0	6,6,6	0.08	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
5	D3T	D	202	4	-	1/22/31/31	0/2/2/2
5	D3T	A	201	4	-	4/22/31/31	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	201	D3T	O4-C4	7.78	1.38	1.23
5	D	202	D3T	O4-C4	6.24	1.35	1.23
5	D	202	D3T	C6-C5	3.42	1.40	1.34
5	D	202	D3T	C3'-C2'	-2.95	1.45	1.54
5	A	201	D3T	C6-C5	2.72	1.39	1.34
5	A	201	D3T	C3'-C2'	-2.71	1.46	1.54
5	A	201	D3T	C4-C5	-2.56	1.40	1.44
5	A	201	D3T	C4-N3	-2.05	1.35	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	202	D3T	C2-N3	-2.04	1.34	1.38

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	202	D3T	C5-C4-N3	7.07	121.35	115.31
5	A	201	D3T	N3-C2-N1	5.27	121.89	114.89
5	D	202	D3T	C4-N3-C2	-5.08	120.78	127.35
5	A	201	D3T	C4-N3-C2	-4.37	121.69	127.35
5	A	201	D3T	O4'-C1'-N1	3.97	114.96	107.86
5	D	202	D3T	N3-C2-N1	3.76	119.89	114.89
5	A	201	D3T	C5-C6-N1	-3.59	119.64	123.34
5	D	202	D3T	C2'-C1'-N1	-3.37	106.00	112.40
5	D	202	D3T	C5-C6-N1	-3.35	119.89	123.34
5	D	202	D3T	O4-C4-C5	-3.03	121.39	124.90
5	A	201	D3T	C5M-C5-C6	-3.03	118.80	122.85
5	A	201	D3T	C2'-C1'-N1	-2.89	106.92	112.40
5	D	202	D3T	O4'-C1'-N1	2.89	113.02	107.86
5	A	201	D3T	C5-C4-N3	2.87	117.76	115.31
5	D	202	D3T	O3G-PG-O3B	2.83	114.13	104.64
5	A	201	D3T	O2G-PG-O3B	2.79	113.99	104.64
5	A	201	D3T	C6-N1-C2	-2.44	118.83	121.30
5	A	201	D3T	PB-O3A-PA	-2.40	124.59	132.83
5	A	201	D3T	O2-C2-N1	-2.39	119.60	122.79
5	D	202	D3T	O3B-PG-O1G	-2.39	97.94	111.19
5	A	201	D3T	C6-C5-C4	2.30	119.96	118.03
5	A	201	D3T	C5M-C5-C4	2.20	121.19	118.77
5	A	201	D3T	C3'-C2'-C1'	2.11	105.21	102.78
5	D	202	D3T	C5M-C5-C4	2.00	120.97	118.77

There are no chirality outliers.

All (5) torsion outliers are listed below:

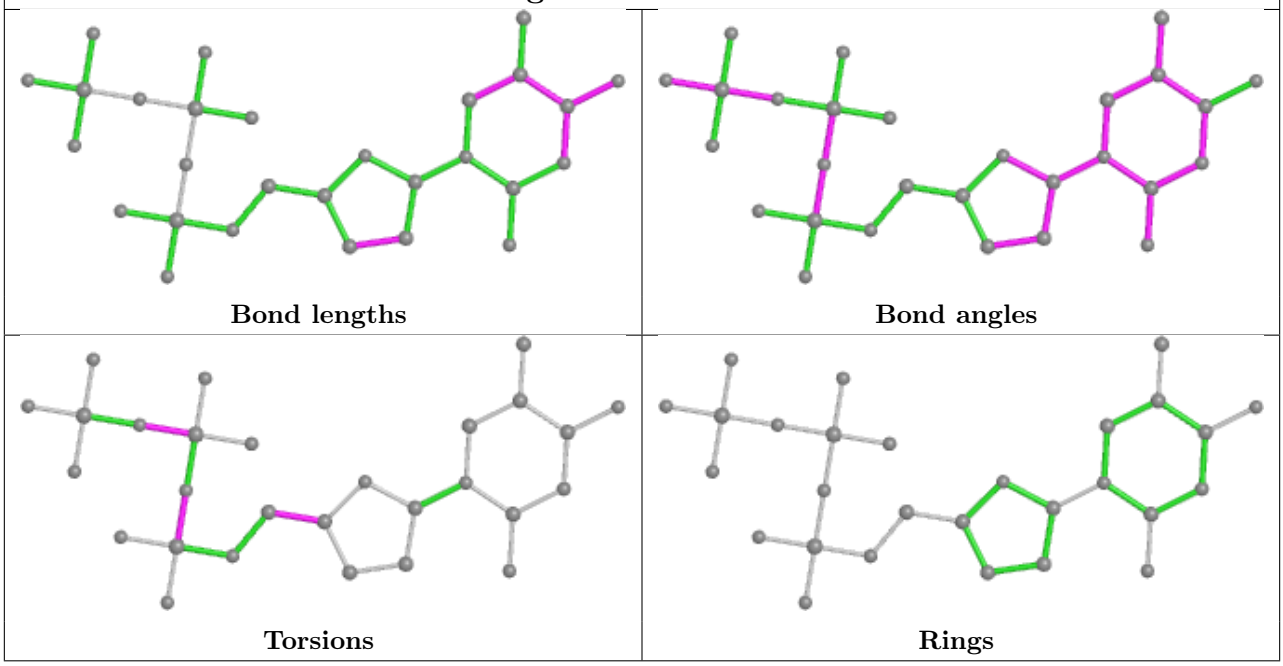
Mol	Chain	Res	Type	Atoms
5	A	201	D3T	O4'-C4'-C5'-O5'
5	A	201	D3T	PG-O3B-PB-O2B
5	D	202	D3T	PG-O3B-PB-O2B
5	A	201	D3T	PB-O3A-PA-O2A
5	A	201	D3T	PG-O3B-PB-O1B

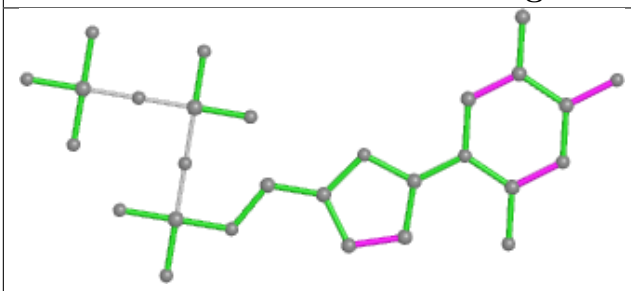
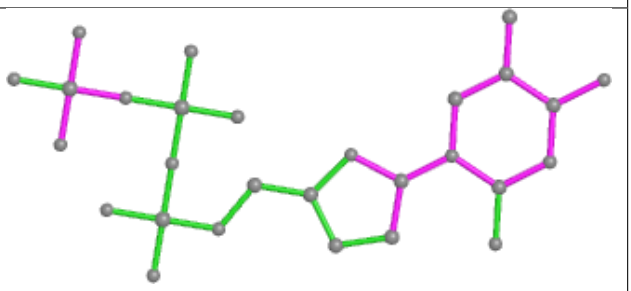
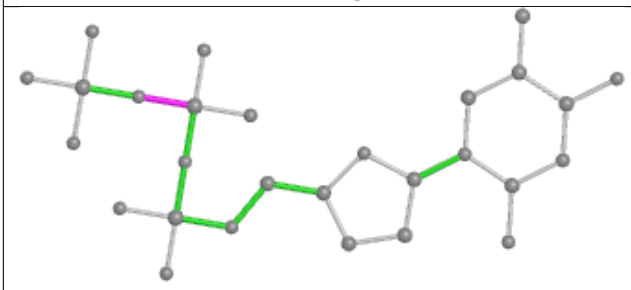
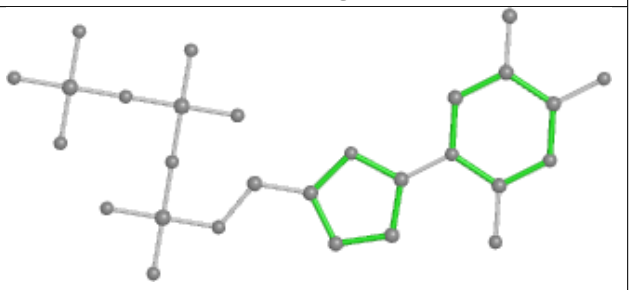
There are no ring outliers.

No monomer is involved in short contacts.

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 D3T A 201



Ligand D3T D 202	
 Bond lengths	 Bond angles
 Torsions	 Rings

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	579/592 (97%)	0.26	31 (5%) 25 28	13, 25, 44, 63	0
1	D	579/592 (97%)	-0.07	2 (0%) 94 95	6, 15, 31, 43	0
2	B	8/9 (88%)	-0.43	0 100 100	14, 16, 27, 31	0
2	E	8/9 (88%)	-0.37	0 100 100	10, 15, 25, 30	0
3	C	12/13 (92%)	-0.18	0 100 100	13, 18, 39, 52	0
3	F	12/13 (92%)	0.02	0 100 100	8, 13, 38, 52	0
All	All	1198/1228 (97%)	0.09	33 (2%) 53 58	6, 20, 39, 63	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	692	VAL	5.4
1	A	690	PHE	5.1
1	A	673	GLU	4.7
1	A	681	ILE	4.3
1	A	298	LYS	3.9
1	A	819	ARG	3.8
1	A	699	PRO	3.7
1	A	698	THR	3.5
1	A	695	ASP	3.5
1	A	866	TYR	3.5
1	A	691	GLN	3.5
1	A	677	ARG	3.4
1	A	697	VAL	3.2
1	A	679	LEU	3.0
1	A	735	PHE	3.0
1	A	846	ARG	3.0
1	A	669	ASP	2.9
1	A	876	LYS	2.9
1	A	862	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	670	ASN	2.8
1	A	689	ILE	2.8
1	A	701	MET	2.6
1	A	696	GLU	2.5
1	D	303	LEU	2.4
1	A	671	LEU	2.4
1	A	858	LEU	2.4
1	A	734	GLU	2.3
1	A	843	ARG	2.3
1	D	779	ARG	2.3
1	A	847	LEU	2.2
1	A	684	LYS	2.2
1	A	816	LYS	2.2
1	A	678	ASP	2.2

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(Å^2)	Q<0.9
2	2DT	B	29	19/20	0.97	0.07	12,15,19,22	0
2	2DT	E	29	19/20	0.99	0.09	7,9,13,14	0

6.3 Carbohydrates (i)

There are no monosaccharides 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(Å^2)	Q<0.9
5	D3T	A	201	28/28	0.93	0.10	15,19,27,27	0
6	SO4	D	3	5/5	0.94	0.15	34,42,47,47	0

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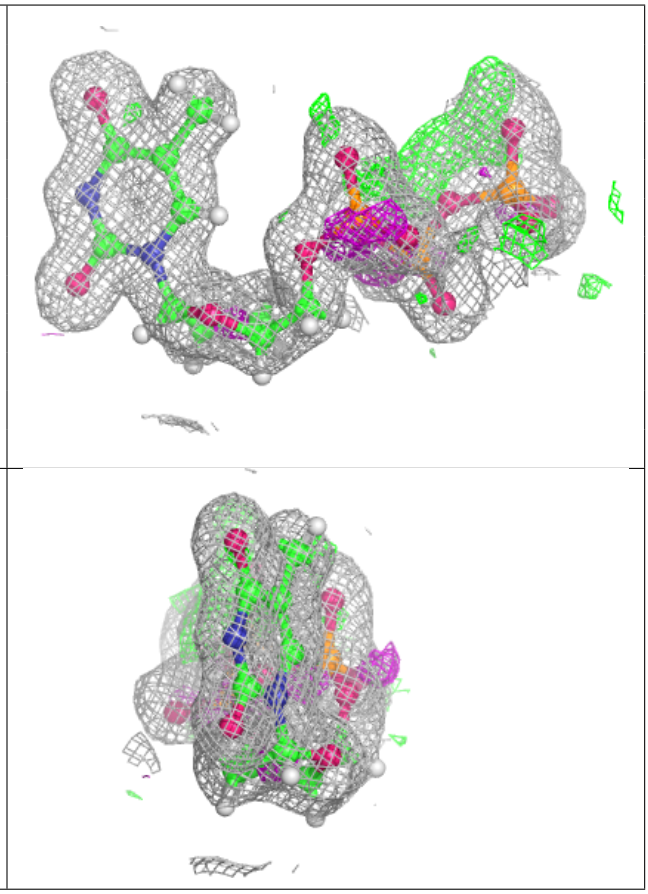
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	D3T	D	202	28/28	0.97	0.09	8,11,16,22	0
6	SO4	A	2	5/5	0.97	0.10	29,42,50,53	0
6	SO4	D	1	5/5	0.97	0.08	26,29,37,38	0
4	MG	A	1	1/1	0.97	0.06	23,23,23,23	0
4	MG	D	2	1/1	0.98	0.06	14,14,14,14	0

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.

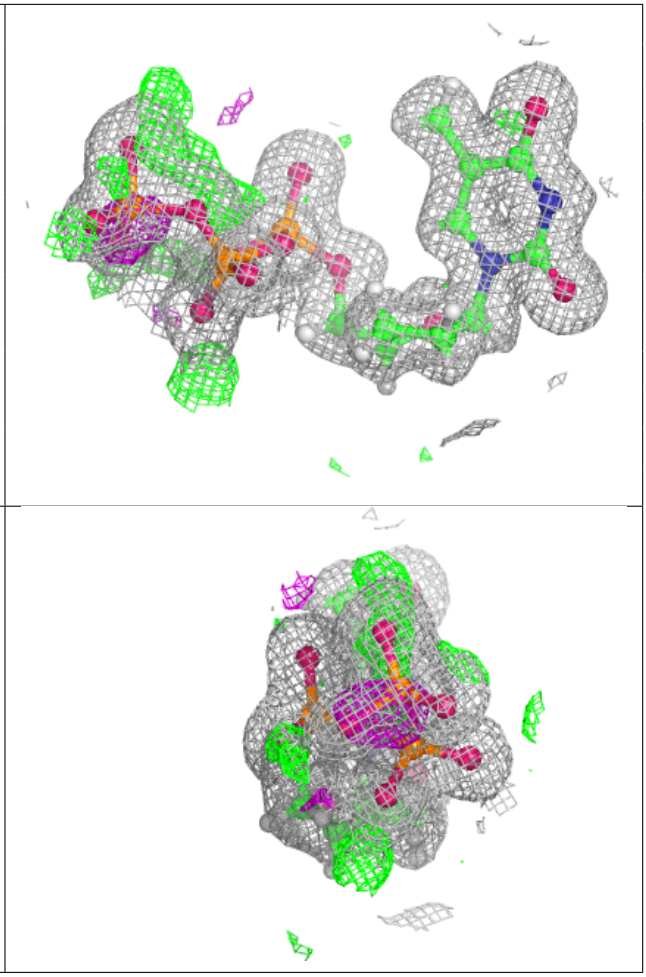
Electron density around D3T A 201:

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 D3T D 202:

$2mF_o$-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.