



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:18 AM GMT

PDB ID : 3HT3
Title : Crystal structure of fragment DNA polymerase I from *Bacillus stearothermophilus* V713P mutant bound to G:dCTP
Authors : Wu, E.Y.; Beese, L.S.
Deposited on : 2009-06-11
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

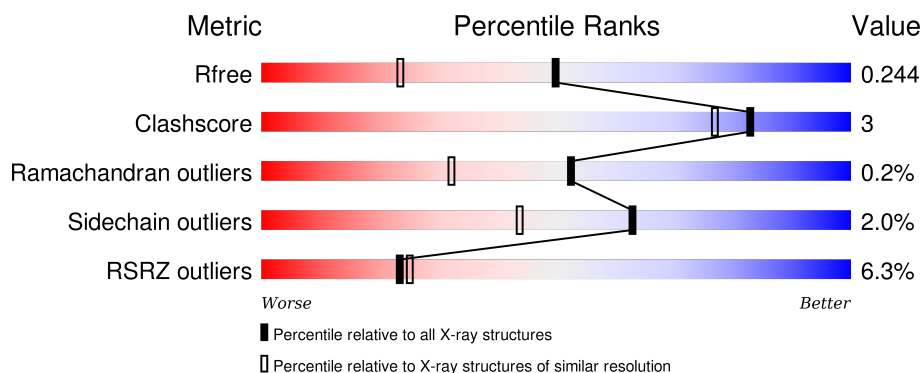
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	579	<div> <div>9%</div> <div> <div></div> <div>92%</div> <div>7%</div> </div> </div>
1	D	579	<div> <div>4%</div> <div> <div></div> <div>92%</div> <div>7%</div> </div> </div>
2	B	9	<div> <div>44%</div> <div>56%</div> </div>
2	E	9	<div> <div>56%</div> <div>44%</div> </div>
3	C	12	<div> <div>8%</div> <div> <div></div> <div>67%</div> <div>25%</div> <div>8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	12	

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
4	DCP	A	203	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 11370 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 DNA polymerase I, large fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	579	Total	C	N	O	S	0	5	0
			4678	2975	811	875	17			
1	D	579	Total	C	N	O	S	0	6	0
			4678	2978	810	872	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	598	ALA	ASP	ENGINEERED	PDB 3HT3
A	713	PRO	VAL	ENGINEERED	PDB 3HT3
D	598	ALA	ASP	ENGINEERED	PDB 3HT3
D	713	PRO	VAL	ENGINEERED	PDB 3HT3

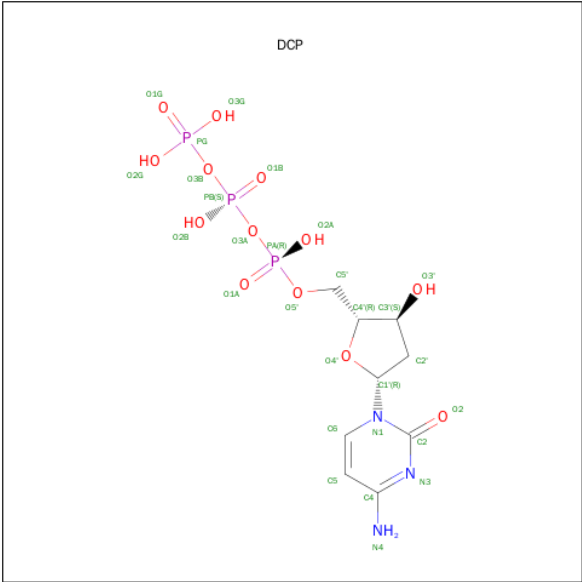
- Molecule 2 is a DNA chain called 5'-D(*CP*GP*AP*TP*CP*AP*CP*GP*(DOC))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	P	0	0	0
			178	86	34	50	8			
2	E	9	Total	C	N	O	P	0	0	0
			178	86	34	50	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	12	Total	C	N	O	P	0	0	0
			246	117	48	70	11			
3	F	12	Total	C	N	O	P	0	0	0
			246	117	48	70	11			

- Molecule 4 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C₉H₁₆N₃O₁₃P₃).

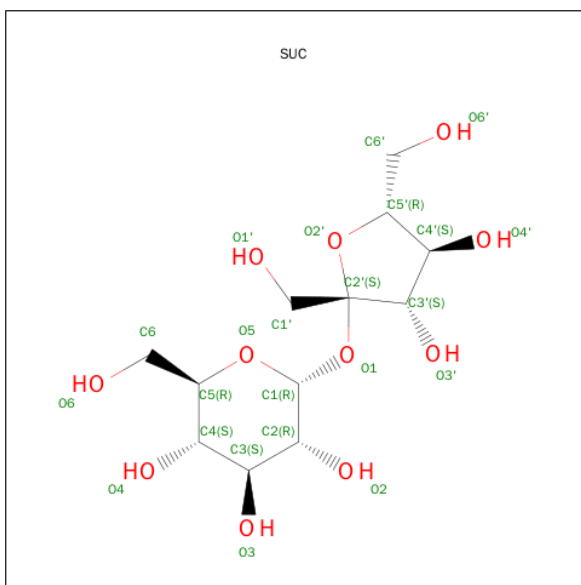


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
4	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
4	D	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

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

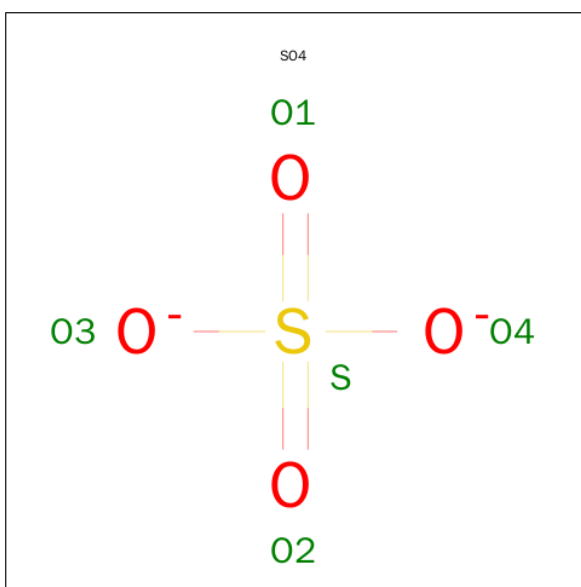
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SUGAR (SUCROSE) (three-letter code: SUC) (formula: C₁₂H₂₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			23	12	11		
6	D	1	Total	C	O	0	0
			23	12	11		
6	D	1	Total	C	O	0	0
			23	12	11		

- Molecule 7 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

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

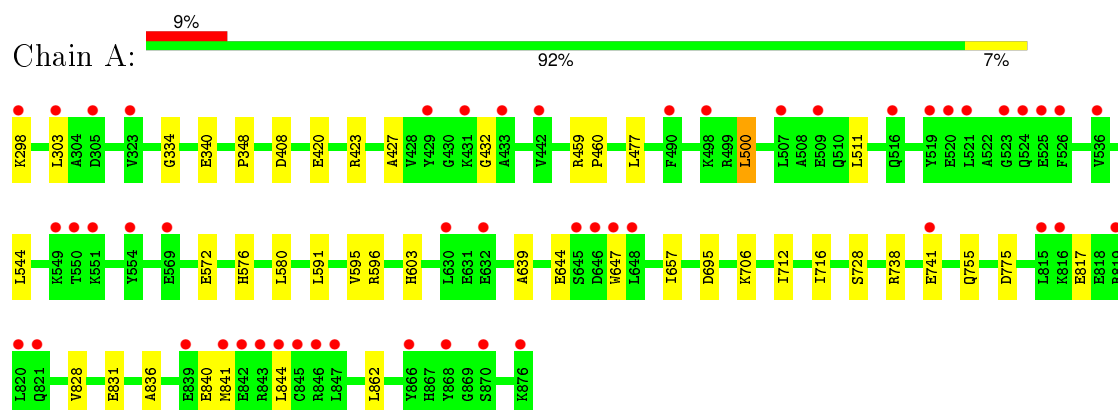
- Molecule 8 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	365	Total	O		0	0
			365	365			
8	D	521	Total	O		0	0
			521	521			
8	B	21	Total	O		0	0
			21	21			
8	C	32	Total	O		0	0
			32	32			
8	E	16	Total	O		0	0
			16	16			
8	F	41	Total	O		0	0
			41	41			

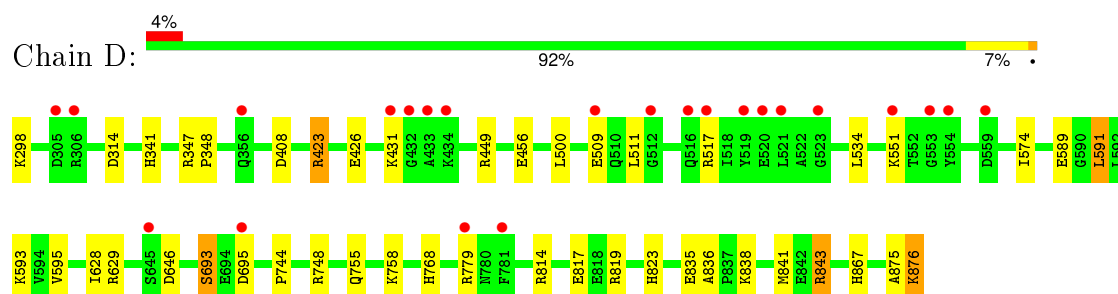
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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, large fragment



- Molecule 1: DNA polymerase I, large fragment



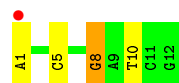
- Molecule 2: 5'-D(*CP*GP*AP*TP*CP*AP*CP*GP*(DOC))-3'



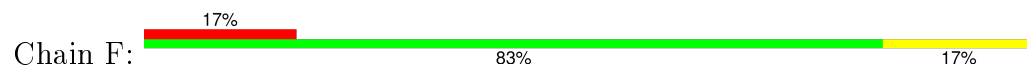
- Molecule 2: 5'-D(*CP*GP*AP*TP*CP*AP*CP*GP*(DOC))-3'



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.28Å 108.79Å 152.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.98 – 1.70 46.99 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.98-1.70) 99.8 (46.99-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.210 , 0.247 0.208 , 0.244	Depositor DCC
R_{free} test set	7528 reflections (4.64%)	DCC
Wilson B-factor (Å ²)	17.9	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 169685 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11370	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: DOC, MG, SUC, SO4, 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	0.45	0/4775	0.57	0/6452
1	D	0.52	0/4781	0.65	2/6459 (0.0%)
2	B	0.80	0/179	1.51	5/274 (1.8%)
2	E	0.82	0/179	1.61	2/274 (0.7%)
3	C	0.89	0/276	1.55	4/425 (0.9%)
3	F	0.88	0/276	1.46	3/425 (0.7%)
All	All	0.53	0/10466	0.75	16/14309 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	25	DC	O4'-C4'-C3'	-10.07	99.96	106.00
1	D	843	ARG	NE-CZ-NH2	-10.01	115.30	120.30
2	B	26	DA	O4'-C1'-N9	8.76	114.13	108.00
1	D	843	ARG	NE-CZ-NH1	8.34	124.47	120.30
3	C	1	DA	O4'-C4'-C3'	-8.11	101.14	106.00
3	F	2	DC	O4'-C1'-N1	7.43	113.20	108.00
3	C	8	DG	O4'-C1'-N9	6.88	112.82	108.00
2	B	27	DC	C4'-C3'-C2'	-6.76	97.01	103.10
2	B	25	DC	O4'-C1'-N1	6.30	112.41	108.00
3	C	10	DT	C1'-O4'-C4'	-6.13	103.97	110.10
3	F	7	DT	N3-C4-O4	5.80	123.38	119.90
2	B	27	DC	O4'-C4'-C3'	-5.76	102.19	104.50
2	B	27	DC	P-O3'-C3'	5.54	126.34	119.70
3	C	5	DC	C2-N3-C4	5.29	122.55	119.90
2	E	25	DC	C4'-C3'-C2'	-5.06	98.55	103.10
3	F	7	DT	C6-C5-C7	-5.02	119.89	122.90

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	4678	0	4736	26	0
1	D	4678	0	4751	36	0
2	B	178	0	102	1	0
2	E	178	0	102	2	0
3	C	246	0	136	1	0
3	F	246	0	136	0	0
4	A	56	0	24	1	0
4	D	28	0	12	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
6	A	23	0	22	1	0
6	D	46	0	44	2	0
7	D	15	0	0	0	0
8	A	365	0	0	7	0
8	B	21	0	0	0	0
8	C	32	0	0	1	0
8	D	521	0	0	9	0
8	E	16	0	0	0	0
8	F	41	0	0	0	0
All	All	11370	0	10065	64	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 3.

All (64) 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:D:758:LYS:HE2	8:D:972:HOH:O	1.56	1.04
1:D:423:ARG:HG2	1:D:423:ARG:HH11	1.31	0.96
1:D:876:LYS:HE3	8:D:14:HOH:O	1.74	0.86
1:D:843:ARG:HD2	8:D:180:HOH:O	1.75	0.86
1:D:456:GLU:HG2	8:D:295:HOH:O	1.74	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:819:ARG:HH11	1:D:819:ARG:HG3	1.40	0.85
1:D:408:ASP:HB2	6:D:877:SUC:H1'1	1.65	0.78
1:D:693:SER:HB2	1:D:695:ASP:OD1	1.92	0.70
1:A:657:ILE:HD13	1:A:862:LEU:HD22	1.78	0.66
1:D:867:HIS:CG	1:D:876:LYS:HA	2.32	0.65
1:D:875:ALA:O	1:D:876:LYS:HG2	1.96	0.65
1:A:423:ARG:HH11	1:A:427:ALA:HB1	1.64	0.63
1:D:534:LEU:HD11	1:D:574:ILE:HD13	1.80	0.63
1:A:596:ARG:HD3	1:A:603:HIS:CD2	2.34	0.62
1:D:298:LYS:HB3	1:D:449:ARG:NH2	2.15	0.62
1:D:875:ALA:C	1:D:876:LYS:HG2	2.22	0.60
1:A:695:ASP:HB3	8:A:996:HOH:O	2.02	0.59
1:D:819:ARG:NH1	1:D:819:ARG:HG3	2.13	0.58
1:A:459:ARG:HG3	8:A:1107:HOH:O	2.04	0.57
1:A:596:ARG:HD3	1:A:603:HIS:HD2	1.70	0.57
1:A:840:GLU:HB3	8:A:1052:HOH:O	2.04	0.57
1:D:426:GLU:OE2	1:D:431:LYS:HD3	2.05	0.56
1:D:744:PRO:HB2	1:D:748[B]:ARG:HH12	1.73	0.54
1:D:629:ARG:HH22	2:E:29:DOC:H5	1.73	0.54
1:D:423:ARG:HG2	1:D:423:ARG:NH1	2.08	0.53
1:D:456:GLU:CG	8:D:295:HOH:O	2.44	0.53
1:D:836:ALA:HB3	1:D:841:MET:CE	2.40	0.52
1:A:591:LEU:O	1:A:595:VAL:HG23	2.10	0.52
1:D:591:LEU:O	1:D:595:VAL:HG23	2.11	0.51
1:A:596:ARG:NH2	8:A:121:HOH:O	2.43	0.51
1:A:408:ASP:HB2	6:A:877:SUC:H1'1	1.92	0.51
1:D:744:PRO:HB2	1:D:748[B]:ARG:NH1	2.26	0.50
1:D:408:ASP:HB2	6:D:877:SUC:C1'	2.39	0.50
1:D:779:ARG:HD3	8:D:1115:HOH:O	2.12	0.48
1:A:706:LYS:HE3	4:A:201:DCP:O3B	2.14	0.48
1:D:646:ASP:HB3	1:D:838:LYS:HE3	1.96	0.48
1:A:738:ARG:HA	1:A:741:GLU:HG2	1.96	0.48
1:A:459:ARG:NH2	1:D:314:ASP:O	2.47	0.48
1:D:589:GLU:O	1:D:593:LYS:HG3	2.13	0.47
2:B:21:DC:H2''	2:B:22:DG:C8	2.49	0.47
2:E:21:DC:H2'	2:E:22:DG:C8	2.50	0.46
1:D:814:ARG:HA	1:D:817:GLU:HG2	1.98	0.46
1:A:459:ARG:HB3	1:A:460:PRO:HD3	1.98	0.45
1:A:334:GLY:HA2	1:A:348:PRO:HD3	2.00	0.44
1:A:828:VAL:HB	1:A:831:GLU:CG	2.48	0.44
1:D:341:HIS:HE1	8:D:930:HOH:O	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:768:HIS:HD2	8:D:1152:HOH:O	2.01	0.43
1:D:423:ARG:CG	1:D:423:ARG:NH1	2.79	0.43
1:A:755[A]:GLN:HG2	8:A:1053:HOH:O	2.17	0.43
1:D:823:HIS:HE1	1:D:835:GLU:OE2	2.02	0.43
1:D:867:HIS:CB	1:D:876:LYS:HA	2.48	0.43
1:D:755:GLN:HG2	8:D:126:HOH:O	2.19	0.42
1:A:738:ARG:HA	1:A:741:GLU:CG	2.50	0.42
1:A:500:LEU:HD13	1:A:639:ALA:CB	2.50	0.42
1:A:817:GLU:HG2	8:A:1143:HOH:O	2.19	0.42
1:A:576:HIS:CE1	1:A:580:LEU:HD11	2.55	0.42
1:A:775:ASP:HB2	8:A:67:HOH:O	2.20	0.41
1:A:712:ILE:HA	1:A:716:ILE:HG22	2.02	0.41
1:D:534:LEU:HD11	1:D:574:ILE:CD1	2.50	0.40
1:A:836:ALA:HB3	1:A:841:MET:CE	2.50	0.40
1:A:644:GLU:HB2	1:A:647:TRP:CD1	2.57	0.40
1:D:347:ARG:HA	1:D:348:PRO:HD3	1.98	0.40
3:C:8:DG:H4'	8:C:587:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	582/579 (100%)	569 (98%)	12 (2%)	1 (0%)	52	32
1	D	583/579 (101%)	572 (98%)	10 (2%)	1 (0%)	52	32
All	All	1165/1158 (101%)	1141 (98%)	22 (2%)	2 (0%)	52	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	432	GLY

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Mol	Chain	Res	Type
1	D	628	ILE

5.3.2 Protein sidechains ⓘ

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	500/495 (101%)	488 (98%)	12 (2%)	57	36
1	D	501/495 (101%)	492 (98%)	9 (2%)	66	49
All	All	1001/990 (101%)	980 (98%)	21 (2%)	63	42

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

Mol	Chain	Res	Type
1	A	298	LYS
1	A	303	LEU
1	A	340	GLU
1	A	420[A]	GLU
1	A	420[B]	GLU
1	A	477	LEU
1	A	500	LEU
1	A	511	LEU
1	A	544	LEU
1	A	572	GLU
1	A	728	SER
1	A	844	LEU
1	D	423	ARG
1	D	500	LEU
1	D	509	GLU
1	D	511	LEU
1	D	517	ARG
1	D	551	LYS
1	D	591	LEU
1	D	693	SER
1	D	876	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	579	GLN
1	A	867	HIS
1	D	341	HIS
1	D	405	GLN
1	D	502	GLN
1	D	755	GLN
1	D	768	HIS
1	D	823	HIS

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	$\# Z > 2$
2	DOC	B	29	3,2	11,19,20	0.49	0	14,26,29	1.59	1 (7%)
2	DOC	E	29	3,2	11,19,20	0.50	0	14,26,29	1.30	1 (7%)

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	DOC	B	29	3,2	-	0/3/18/19	0/2/2/2
2	DOC	E	29	3,2	-	0/3/18/19	0/2/2/2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	29	DOC	C2-N3-C4	3.21	120.14	115.61
2	B	29	DOC	C2-N3-C4	3.97	121.22	115.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	29	DOC	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	DCP	A	201	5	21,29,29	0.56	0	33,45,45	1.31	4 (12%)
4	DCP	A	203	-	21,29,29	0.55	0	33,45,45	1.44	5 (15%)
6	SUC	A	877	-	24,24,24	0.36	0	36,36,36	0.68	1 (2%)
7	SO4	D	1	-	4,4,4	0.42	0	6,6,6	0.31	0
7	SO4	D	2	-	4,4,4	0.22	0	6,6,6	0.08	0
4	DCP	D	202	5	21,29,29	0.41	0	33,45,45	1.41	5 (15%)
7	SO4	D	3	-	4,4,4	0.08	0	6,6,6	0.15	0
6	SUC	D	877	-	24,24,24	0.33	0	36,36,36	0.60	0
6	SUC	D	878	-	24,24,24	0.43	0	36,36,36	0.58	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	DCP	A	201	5	-	0/18/34/34	0/2/2/2
4	DCP	A	203	-	-	0/18/34/34	0/2/2/2
6	SUC	A	877	-	-	0/12/51/51	0/2/2/2
7	SO4	D	1	-	-	0/0/0/0	0/0/0/0
7	SO4	D	2	-	-	0/0/0/0	0/0/0/0
4	DCP	D	202	5	-	0/18/34/34	0/2/2/2
7	SO4	D	3	-	-	0/0/0/0	0/0/0/0
6	SUC	D	877	-	-	0/12/51/51	0/2/2/2
6	SUC	D	878	-	-	0/12/51/51	0/2/2/2

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	203	DCP	PB-O3B-PG	-3.75	120.09	132.67
4	D	202	DCP	C2'-C1'-N1	-3.40	105.89	114.16
4	A	201	DCP	PB-O3B-PG	-2.64	123.83	132.67
4	A	203	DCP	PB-O3A-PA	-2.53	125.61	132.73
4	D	202	DCP	PB-O3B-PG	-2.46	124.40	132.67
4	A	201	DCP	N4-C4-N3	2.03	120.21	116.50
4	D	202	DCP	O4'-C1'-N1	2.05	111.26	107.72
4	A	201	DCP	O3G-PG-O2G	2.06	115.23	107.38
4	A	203	DCP	O4'-C1'-N1	2.08	111.31	107.72
4	D	202	DCP	O3G-PG-O2G	2.20	115.75	107.38
6	A	877	SUC	C1-O5-C5	2.21	118.03	113.75
4	A	203	DCP	N4-C4-N3	2.24	120.59	116.50
4	D	202	DCP	C2-N3-C4	3.30	120.27	115.61
4	A	201	DCP	C2-N3-C4	3.61	120.71	115.61
4	A	203	DCP	C2-N3-C4	3.63	120.74	115.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	201	DCP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	877	SUC	1	0
6	D	877	SUC	2	0

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	579/579 (100%)	0.68	50 (8%) 13 14	10, 26, 42, 50	0
1	D	579/579 (100%)	0.35	23 (3%) 42 46	6, 16, 38, 45	0
2	B	8/9 (88%)	-0.03	0 100 100	14, 25, 45, 49	0
2	E	8/9 (88%)	0.17	0 100 100	11, 28, 50, 57	0
3	C	12/12 (100%)	0.35	1 (8%) 14 16	11, 26, 43, 61	0
3	F	12/12 (100%)	0.59	2 (16%) 2 2	8, 20, 47, 67	0
All	All	1198/1200 (99%)	0.51	76 (6%) 23 25	6, 21, 41, 67	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	1	DA	5.2
1	A	551	LYS	5.1
1	A	550	THR	5.0
1	A	819	ARG	4.9
1	A	820	LEU	4.9
1	D	433	ALA	4.7
1	A	844	LEU	4.6
1	A	846	ARG	4.4
1	A	298	LYS	4.1
1	A	519	TYR	3.9
3	C	1	DA	3.8
1	A	523	GLY	3.8
1	A	647	TRP	3.8
1	A	847	LEU	3.4
1	A	442	VAL	3.3
1	D	521	LEU	3.3
1	D	509	GLU	3.3
1	D	512	GLY	3.3
1	D	434	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	821	GLN	3.2
1	A	305	ASP	3.2
1	A	516	GLN	3.2
1	A	509	GLU	3.1
1	A	842	GLU	3.1
1	A	526	PHE	3.1
1	D	551	LYS	3.1
1	A	646	ASP	3.1
1	A	630	LEU	3.0
1	D	432	GLY	3.0
1	A	645	SER	3.0
1	A	569	GLU	2.8
1	A	429	TYR	2.8
1	A	741	GLU	2.8
1	D	520	GLU	2.7
1	A	525	GLU	2.6
1	A	868	TYR	2.6
1	D	356	GLN	2.6
1	D	519	TYR	2.6
1	A	632	GLU	2.6
1	D	781	PHE	2.6
1	A	433	ALA	2.6
1	A	816	LYS	2.5
1	A	303	LEU	2.5
1	D	523	GLY	2.5
1	A	520	GLU	2.5
1	A	524	GLN	2.5
1	A	815	LEU	2.5
1	D	517	ARG	2.5
1	A	554	TYR	2.5
1	D	554	TYR	2.5
1	D	305	ASP	2.4
1	D	553	GLY	2.4
1	A	843	ARG	2.4
1	A	876	LYS	2.4
1	A	845	CYS	2.4
1	A	507	LEU	2.4
1	A	521	LEU	2.4
3	F	2	DC	2.4
1	A	431	LYS	2.3
1	D	695	ASP	2.3
1	A	870	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	648	LEU	2.3
1	A	549	LYS	2.3
1	D	779	ARG	2.3
1	A	841	MET	2.2
1	A	536	VAL	2.2
1	A	498	LYS	2.2
1	A	839	GLU	2.2
1	D	431	LYS	2.2
1	A	323	VAL	2.2
1	A	866	TYR	2.2
1	D	645	SER	2.1
1	D	516	GLN	2.1
1	A	490	PHE	2.1
1	D	306	ARG	2.1
1	D	559	ASP	2.1

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q < 0.9
2	DOC	E	29	18/19	0.98	0.09	-	8,10,16,18	0
2	DOC	B	29	18/19	0.97	0.07	-	13,14,18,20	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	DCP	A	203	28/28	0.77	0.32	12.49	23,38,51,51	8
7	SO4	D	3	5/5	0.89	0.20	1.60	38,39,40,40	0
4	DCP	A	201	28/28	0.91	0.13	1.10	25,28,38,39	0
6	SUC	A	877	23/23	0.86	0.12	0.12	23,30,31,32	0
6	SUC	D	877	23/23	0.91	0.10	-0.67	11,15,17,20	0
4	DCP	D	202	28/28	0.96	0.09	-0.86	16,18,21,24	0
6	SUC	D	878	23/23	0.92	0.10	-0.93	15,16,18,20	0
5	MG	D	200	1/1	0.96	0.06	-	17,17,17,17	0
7	SO4	D	2	5/5	0.95	0.24	-	64,64,64,64	0
5	MG	A	200	1/1	0.70	0.28	-	39,39,39,39	0
7	SO4	D	1	5/5	0.97	0.13	-	26,28,31,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.