



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2018 – 02:59 am GMT

PDB ID : 2C2R
Title : Efficient and High Fidelity Incorporation of dCTP Opposite 7,8- Dihydro-8-o
xodeoxyguanosine by Sulfolobus solfataricus DNA Polymerase Dpo4
Authors : Irimia, A.; Loukachevitch, L.V.; Egli, M.
Deposited on : 2005-09-29
Resolution : 2.55 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

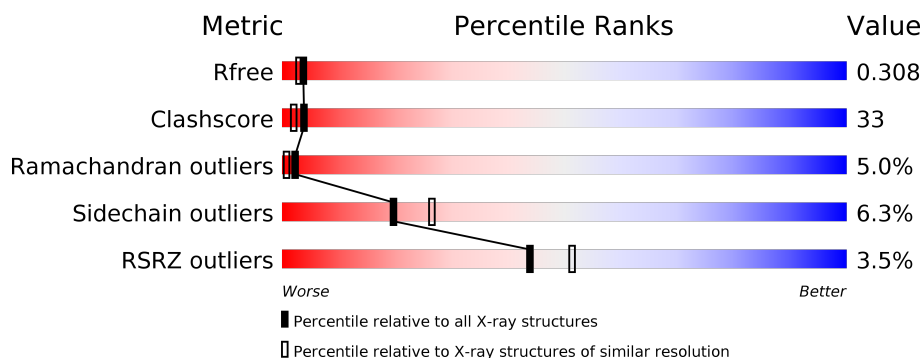
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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}	111664	1053 (2.56-2.52)
Clashscore	122126	1098 (2.56-2.52)
Ramachandran outliers	120053	1088 (2.56-2.52)
Sidechain outliers	120020	1088 (2.56-2.52)
RSRZ outliers	108989	1043 (2.56-2.52)

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	358	<div> <div>3%</div> <div> <div></div> <div>42%</div> <div>46%</div> <div>7%</div> <div>• •</div> </div> </div>
2	P	14	<div> <div>29%</div> <div>71%</div> </div>
3	T	18	<div> <div>6%</div> <div> <div></div> <div>50%</div> <div>33%</div> <div>6%</div> <div>11%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3498 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 IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	1	1
			2753	1765	474	507	7			

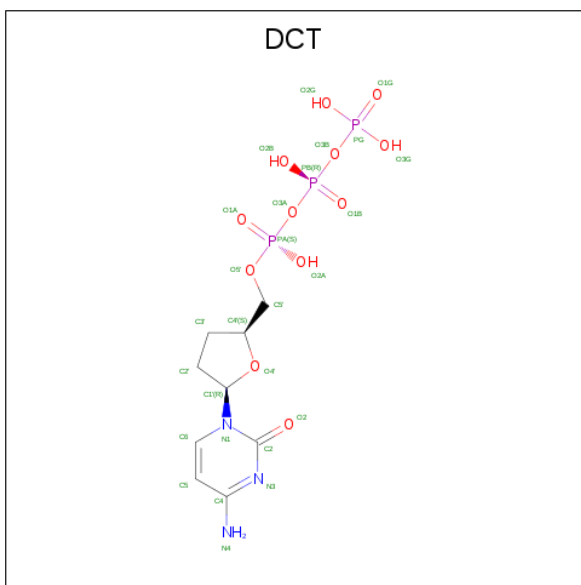
- Molecule 2 is a DNA chain called 5'-D(*GP*GP*GP*GP*GP*AP*AP*GP*GP*AP*TP*TP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	14	Total	C	N	O	P	0	0	0
			291	138	60	80	13			

- Molecule 3 is a DNA chain called 5'-D(*TP*CP*AP*C 8OGP*GP*AP*AP*TP*CP*CP *TP*TP*CP*CP*CP*CP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	16	Total	C	N	O	P	1	0	0
			317	152	55	95	15			

- Molecule 4 is 2',3'-DIDEOXYCYTIDINE 5'-TRIPHOSPHATE (three-letter code: DCT) (formula: C₉H₁₆N₃O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	9	3	12	3		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	4	Total Ca 4 4	0	0

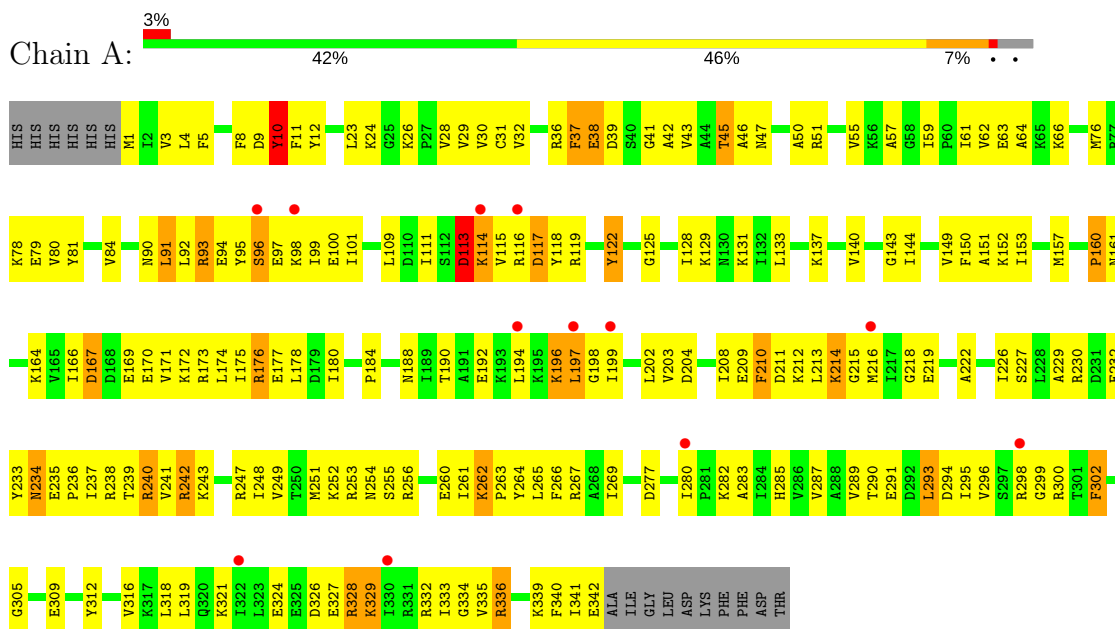
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	67	Total O 67 67	0	0
6	P	20	Total O 20 20	0	0
6	T	19	Total O 19 19	0	0

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 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.

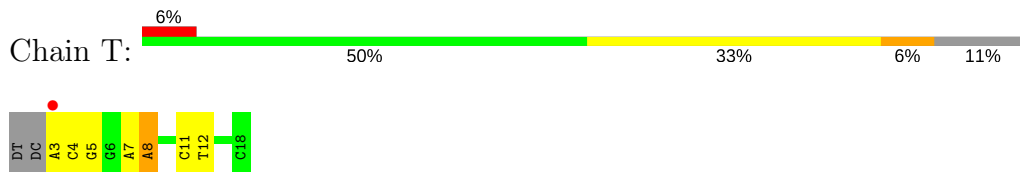
• Molecule 1: DNA POLYMERASE IV



• Molecule 2: 5'-D(*GP*GP*GP*GP*GP*AP*AP*GP*GP*AP *TP*TP*C)-3'



• Molecule 3: 5'-D(*TP*CP*AP*C 8OGP*GP*AP*AP*TP*CP*CP *TP*TP*CP*CP*CP*CP*C)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.20Å 100.15Å 52.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.99 – 2.55 42.99 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.8 (42.99-2.55) 98.9 (42.99-2.55)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.54Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.251 , 0.310 0.248 , 0.308	Depositor DCC
R_{free} test set	817 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	51.7	Xtriage
Anisotropy	0.658	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3498	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 8OG, CA, DCT, DOC

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	0.47	0/2792	0.67	0/3750
2	P	0.71	0/308	0.72	0/476
3	T	0.76	0/326	0.86	0/496
All	All	0.53	0/3426	0.69	0/4722

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	T	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	T	8	DA	Sidechain

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	2753	0	2894	196	0
2	P	291	0	158	14	0
3	T	317	0	181	14	0
4	A	27	0	12	2	0
5	A	4	0	0	0	0
6	A	67	0	0	16	0
6	P	20	0	0	1	0
6	T	19	0	0	2	0
All	All	3498	0	3245	215	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 33.

All (215) 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:76:MET:HA	6:A:2017:HOH:O	1.53	1.09
2:P:13:DC:H4'	2:P:14:DOC:H5'	1.47	0.94
1:A:91:LEU:HD21	1:A:131:LYS:HD3	1.54	0.90
1:A:91:LEU:O	1:A:94:GLU:HG2	1.71	0.89
1:A:79:GLU:H	1:A:79:GLU:CD	1.77	0.85
1:A:309[B]:GLU:OE1	6:A:2058:HOH:O	1.95	0.84
2:P:14:DOC:H2'	2:P:14:DOC:O2	1.80	0.82
1:A:248:ILE:HG13	6:A:2062:HOH:O	1.81	0.81
1:A:242:ARG:HD2	6:T:2011:HOH:O	1.81	0.81
1:A:43:VAL:HG12	1:A:57:ALA:HA	1.62	0.79
1:A:98:LYS:HE3	1:A:114:LYS:NZ	2.00	0.77
1:A:252:LYS:HE3	1:A:264:TYR:OH	1.87	0.74
1:A:197:LEU:HG	1:A:216:MET:SD	2.28	0.73
1:A:192:GLU:HG3	6:A:2035:HOH:O	1.89	0.73
1:A:98:LYS:HE3	1:A:114:LYS:HZ2	1.51	0.73
1:A:100:GLU:OE1	1:A:240:ARG:HD2	1.88	0.72
1:A:188:ASN:O	1:A:192:GLU:HG2	1.88	0.72
1:A:30:VAL:HG13	6:A:2017:HOH:O	1.87	0.72
1:A:328:ARG:H	1:A:328:ARG:HD3	1.54	0.72
1:A:167:ASP:O	1:A:171:VAL:HG23	1.91	0.71
1:A:218:GLY:HA3	3:T:12:DT:OP1	1.91	0.70
1:A:214:LYS:HG3	1:A:219:GLU:HG2	1.74	0.70
1:A:336:ARG:NH2	3:T:7:DA:H2''	2.06	0.69
1:A:31:CYS:HB3	1:A:61:ILE:HD11	1.74	0.69
1:A:133:LEU:O	1:A:137:LYS:HA	1.93	0.69
1:A:329:LYS:HD2	1:A:329:LYS:H	1.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ILE:HG12	1:A:194:LEU:HD13	1.74	0.67
1:A:4:LEU:HD12	1:A:111:ILE:HD13	1.76	0.66
1:A:291:GLU:HG2	1:A:329:LYS:NZ	2.10	0.66
1:A:91:LEU:CD2	1:A:131:LYS:HD3	2.26	0.66
1:A:122:TYR:HD2	1:A:122:TYR:C	1.98	0.65
1:A:45:THR:HG21	6:A:2065:HOH:O	1.95	0.65
1:A:336:ARG:NH2	3:T:7:DA:C2'	2.60	0.64
1:A:122:TYR:CD2	1:A:122:TYR:C	2.71	0.64
1:A:176:ARG:HG3	1:A:177:GLU:HG2	1.80	0.64
1:A:8:PHE:HA	1:A:140:VAL:HG12	1.81	0.63
1:A:23:LEU:HA	1:A:26:LYS:HD2	1.80	0.63
3:T:11:DC:H2''	3:T:12:DT:H72	1.79	0.63
1:A:32:VAL:O	1:A:32:VAL:HG23	1.99	0.63
1:A:98:LYS:NZ	1:A:98:LYS:HB2	2.14	0.63
1:A:114:LYS:H	1:A:114:LYS:HD2	1.64	0.62
1:A:96:SER:HA	1:A:114:LYS:HE2	1.82	0.62
1:A:59:ILE:HD11	1:A:64:ALA:HB2	1.81	0.62
1:A:10:TYR:CD1	1:A:47:ASN:HB3	2.35	0.62
1:A:116:ARG:O	1:A:117:ASP:CB	2.48	0.62
1:A:262:LYS:HD3	1:A:266:PHE:CE2	2.35	0.62
1:A:36:ARG:HG2	1:A:37:PHE:CD2	2.35	0.62
1:A:46:ALA:HB1	1:A:50:ALA:HB3	1.81	0.61
1:A:232:GLU:HG2	1:A:232:GLU:O	2.00	0.61
1:A:248:ILE:HA	1:A:334:GLY:HA3	1.83	0.61
1:A:80:VAL:O	1:A:84:VAL:HG23	2.02	0.60
1:A:219:GLU:O	1:A:222:ALA:HB3	2.00	0.60
1:A:262:LYS:HD3	1:A:266:PHE:HE2	1.66	0.60
1:A:174:LEU:HD22	1:A:178:LEU:HB2	1.83	0.60
1:A:149:VAL:O	1:A:153:ILE:HG13	2.02	0.59
1:A:100:GLU:HA	6:A:2021:HOH:O	2.03	0.59
1:A:114:LYS:O	1:A:115:VAL:HG23	2.02	0.59
1:A:166:ILE:HA	1:A:170:GLU:OE1	2.03	0.59
1:A:329:LYS:CD	1:A:329:LYS:H	2.14	0.59
1:A:95:TYR:O	1:A:96:SER:HB2	2.02	0.59
1:A:291:GLU:CB	1:A:329:LYS:HD3	2.32	0.58
1:A:241:VAL:O	1:A:243:LYS:HG3	2.03	0.58
1:A:199:ILE:HG23	1:A:204:ASP:HB2	1.85	0.58
1:A:36:ARG:HG2	1:A:37:PHE:HD2	1.68	0.58
1:A:116:ARG:O	1:A:117:ASP:HB3	2.04	0.58
2:P:4:DG:H1'	2:P:5:DG:H5''	1.85	0.58
1:A:97:GLU:HG3	1:A:97:GLU:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:SER:C	1:A:98:LYS:H	2.07	0.57
1:A:9:ASP:O	1:A:11:PHE:N	2.38	0.57
1:A:113:ASP:O	1:A:115:VAL:N	2.37	0.57
1:A:236:PRO:HG2	1:A:238:ARG:NH1	2.20	0.57
1:A:1:MET:H1	1:A:116:ARG:HH12	1.53	0.56
2:P:14:DOC:O2	2:P:14:DOC:C2'	2.47	0.56
1:A:289:VAL:HB	1:A:332:ARG:HB2	1.88	0.56
1:A:190:THR:O	1:A:194:LEU:HG	2.06	0.56
1:A:248:ILE:CG1	6:A:2062:HOH:O	2.48	0.56
1:A:263:PRO:O	1:A:267:ARG:HG3	2.05	0.56
1:A:93:ARG:HG2	1:A:97:GLU:OE1	2.06	0.55
1:A:133:LEU:HD12	1:A:137:LYS:HA	1.88	0.55
1:A:169:GLU:OE1	1:A:173:ARG:NH1	2.40	0.55
1:A:291:GLU:HB2	1:A:329:LYS:HD3	1.89	0.55
1:A:99:ILE:HG12	1:A:100:GLU:N	2.22	0.55
1:A:133:LEU:HD12	1:A:133:LEU:O	2.07	0.54
1:A:256:ARG:HG2	1:A:256:ARG:HH11	1.72	0.54
1:A:214:LYS:HE2	1:A:219:GLU:OE2	2.07	0.54
1:A:230:ARG:C	1:A:232:GLU:N	2.58	0.54
1:A:312:TYR:O	1:A:316:VAL:HG23	2.08	0.54
4:A:1342:DCT:H2'	6:A:2066:HOH:O	2.07	0.54
1:A:298:ARG:NH1	2:P:8:DG:H3'	2.23	0.53
1:A:153:ILE:O	1:A:157:MET:HG3	2.08	0.53
1:A:23:LEU:O	1:A:26:LYS:HB2	2.09	0.53
1:A:41:GLY:HA2	3:T:5:8OG:C5'	2.39	0.52
1:A:157:MET:HE1	1:A:164:LYS:HE2	1.91	0.52
1:A:254:ASN:O	1:A:255:SER:HB3	2.09	0.52
1:A:247:ARG:CZ	1:A:249:VAL:HG12	2.40	0.52
1:A:98:LYS:HZ2	1:A:98:LYS:HB2	1.75	0.52
1:A:237:ILE:N	1:A:237:ILE:HD12	2.25	0.52
1:A:32:VAL:HG22	1:A:42:ALA:O	2.10	0.52
1:A:336:ARG:HH22	3:T:7:DA:H2''	1.74	0.52
1:A:9:ASP:O	1:A:10:TYR:C	2.49	0.51
2:P:4:DG:H2''	2:P:5:DG:H5'	1.93	0.51
3:T:11:DC:H2''	3:T:12:DT:C7	2.40	0.51
1:A:196:LYS:O	1:A:198:GLY:N	2.44	0.51
1:A:157:MET:CE	1:A:164:LYS:HE2	2.40	0.51
1:A:95:TYR:CD2	1:A:128:ILE:HD11	2.46	0.51
1:A:230:ARG:C	1:A:232:GLU:H	2.14	0.51
1:A:321:LYS:O	1:A:324:GLU:HB2	2.11	0.51
1:A:175:ILE:CG2	1:A:229:ALA:HA	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ALA:HB2	1:A:339:LYS:HD2	1.92	0.50
1:A:99:ILE:HG13	1:A:109:LEU:HD23	1.93	0.50
1:A:150:PHE:HE2	1:A:174:LEU:HD12	1.76	0.50
1:A:92:LEU:C	1:A:94:GLU:H	2.13	0.50
1:A:280:ILE:CG2	1:A:305:GLY:HA3	2.42	0.50
1:A:29:VAL:CG1	1:A:43:VAL:HG22	2.42	0.50
1:A:203:VAL:HG13	1:A:204:ASP:N	2.27	0.50
1:A:28:VAL:HG23	1:A:47:ASN:HD21	1.76	0.50
1:A:175:ILE:HG23	1:A:229:ALA:HA	1.93	0.50
1:A:5:PHE:CD2	1:A:152:LYS:HA	2.47	0.50
1:A:212:LYS:NZ	6:A:2036:HOH:O	2.45	0.50
1:A:226:ILE:O	1:A:230:ARG:HG3	2.11	0.50
1:A:1:MET:N	1:A:116:ARG:HH12	2.10	0.49
1:A:210:PHE:CD2	1:A:210:PHE:C	2.85	0.49
1:A:282:LYS:HD3	1:A:341:ILE:HG12	1.93	0.49
1:A:140:VAL:O	1:A:140:VAL:HG23	2.13	0.49
1:A:233:TYR:CD2	1:A:234:ASN:N	2.81	0.49
1:A:293:LEU:HD21	3:T:4:DC:OP1	2.12	0.49
1:A:269:ILE:HG12	1:A:335:VAL:HG11	1.95	0.48
3:T:7:DA:H2''	3:T:8:DA:H5'	1.95	0.48
1:A:248:ILE:HD12	6:T:2006:HOH:O	2.13	0.48
1:A:62:VAL:HG23	6:A:2007:HOH:O	2.13	0.48
1:A:291:GLU:HG2	1:A:329:LYS:HZ2	1.79	0.48
1:A:41:GLY:HA2	3:T:5:8OG:H4'	1.95	0.48
1:A:280:ILE:O	1:A:340:PHE:HA	2.14	0.47
1:A:92:LEU:C	1:A:94:GLU:N	2.68	0.47
1:A:293:LEU:N	1:A:293:LEU:CD2	2.77	0.47
1:A:287:VAL:O	1:A:333:ILE:HD12	2.14	0.47
1:A:92:LEU:O	1:A:94:GLU:N	2.47	0.47
1:A:166:ILE:HG23	1:A:170:GLU:OE1	2.15	0.47
3:T:7:DA:H2''	3:T:8:DA:C5'	2.45	0.47
1:A:336:ARG:HH22	3:T:7:DA:C2'	2.27	0.46
1:A:342:GLU:N	6:A:2064:HOH:O	2.47	0.46
1:A:256:ARG:NH2	1:A:326:ASP:O	2.48	0.46
1:A:78:LYS:HA	1:A:81:TYR:CD2	2.51	0.46
1:A:118:TYR:CE2	1:A:167:ASP:HA	2.51	0.46
1:A:262:LYS:HB3	1:A:266:PHE:CE2	2.51	0.46
1:A:290:THR:HG23	1:A:294:ASP:O	2.15	0.46
1:A:197:LEU:HD22	1:A:212:LYS:HG2	1.98	0.46
1:A:79:GLU:CD	1:A:79:GLU:N	2.56	0.46
2:P:4:DG:H1'	2:P:5:DG:C5'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ARG:HD2	1:A:260:GLU:OE2	2.14	0.46
1:A:93:ARG:HH22	1:A:101:ILE:HD11	1.81	0.46
1:A:10:TYR:CE1	1:A:47:ASN:HB3	2.51	0.46
1:A:295:ILE:HG23	1:A:295:ILE:O	2.16	0.45
1:A:125:GLY:O	1:A:129:LYS:N	2.42	0.45
1:A:227:SER:OG	1:A:233:TYR:HA	2.16	0.45
1:A:298:ARG:O	1:A:318:LEU:HD13	2.17	0.45
1:A:3:VAL:CG2	1:A:237:ILE:HD11	2.46	0.45
1:A:41:GLY:HA2	3:T:5:8OG:C4'	2.47	0.45
1:A:38:GLU:O	1:A:39:ASP:HB2	2.17	0.45
1:A:32:VAL:O	1:A:41:GLY:HA3	2.16	0.45
1:A:99:ILE:HD12	1:A:109:LEU:HD21	1.99	0.45
1:A:117:ASP:OD2	1:A:119:ARG:HB3	2.17	0.44
1:A:190:THR:OG1	2:P:12:DT:OP1	2.24	0.44
1:A:265:LEU:HD22	1:A:319:LEU:HD22	1.98	0.44
1:A:150:PHE:CE2	1:A:174:LEU:HD12	2.53	0.44
1:A:8:PHE:CD1	1:A:8:PHE:N	2.84	0.44
1:A:90:ASN:HA	1:A:93:ARG:HB2	1.99	0.44
1:A:99:ILE:HG13	1:A:109:LEU:CD2	2.48	0.44
2:P:8:DG:H2''	2:P:9:DG:OP2	2.17	0.44
2:P:9:DG:H1'	2:P:10:DA:H5'	1.99	0.44
1:A:235:GLU:HG2	1:A:236:PRO:HD2	2.00	0.44
1:A:23:LEU:O	1:A:26:LYS:N	2.45	0.44
1:A:247:ARG:NH1	1:A:248:ILE:O	2.51	0.44
1:A:261:ILE:O	1:A:262:LYS:C	2.56	0.44
1:A:122:TYR:HD2	1:A:122:TYR:O	1.99	0.44
1:A:192:GLU:CG	6:A:2035:HOH:O	2.59	0.43
2:P:5:DG:H2''	2:P:6:DA:H8	1.84	0.43
1:A:143:GLY:HA3	1:A:151:ALA:O	2.19	0.43
1:A:169:GLU:CD	1:A:169:GLU:C	2.76	0.43
1:A:169:GLU:O	1:A:172:LYS:HB2	2.17	0.43
1:A:296:VAL:HG13	1:A:296:VAL:O	2.18	0.43
1:A:293:LEU:N	1:A:293:LEU:HD22	2.34	0.43
1:A:99:ILE:HG12	1:A:100:GLU:H	1.84	0.43
1:A:232:GLU:HB2	6:A:2043:HOH:O	2.18	0.42
1:A:299:GLY:HA2	1:A:318:LEU:HD13	1.99	0.42
1:A:188:ASN:ND2	6:A:2034:HOH:O	2.44	0.42
1:A:230:ARG:O	1:A:232:GLU:N	2.52	0.42
1:A:237:ILE:N	1:A:237:ILE:CD1	2.82	0.42
1:A:93:ARG:HG3	1:A:93:ARG:HH11	1.83	0.42
1:A:285:HIS:HB2	1:A:336:ARG:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:GLU:O	1:A:210:PHE:C	2.58	0.42
1:A:213:LEU:O	1:A:215:GLY:N	2.52	0.42
1:A:28:VAL:HB	1:A:47:ASN:ND2	2.34	0.42
1:A:327:GLU:O	1:A:328:ARG:O	2.38	0.42
1:A:150:PHE:O	1:A:166:ILE:HD12	2.20	0.42
1:A:208:ILE:CG2	1:A:209:GLU:N	2.82	0.42
1:A:300:ARG:HG2	1:A:302:PHE:CE1	2.55	0.41
4:A:1342:DCT:PA	6:A:2067:HOH:O	2.77	0.41
1:A:66:LYS:HB3	1:A:66:LYS:HE2	1.86	0.41
2:P:5:DG:OP2	6:P:2009:HOH:O	2.21	0.41
3:T:3:DA:N3	3:T:3:DA:H2'	2.35	0.41
1:A:51:ARG:HA	1:A:55:VAL:O	2.20	0.41
1:A:4:LEU:HG	1:A:144:ILE:HG12	2.02	0.41
1:A:251:MET:SD	1:A:261:ILE:HG12	2.60	0.41
1:A:208:ILE:HG22	1:A:209:GLU:N	2.35	0.41
2:P:3:DG:H2''	2:P:4:DG:C8	2.56	0.41
1:A:129:LYS:HG3	1:A:140:VAL:O	2.20	0.41
1:A:218:GLY:O	1:A:222:ALA:HB2	2.21	0.41
1:A:96:SER:HA	1:A:114:LYS:CE	2.51	0.41
1:A:59:ILE:HD11	1:A:64:ALA:CB	2.49	0.40
1:A:12:TYR:N	1:A:12:TYR:CD1	2.88	0.40
2:P:5:DG:H2''	2:P:6:DA:C8	2.56	0.40
1:A:93:ARG:HG3	1:A:93:ARG:NH1	2.37	0.40
1:A:160:PRO:O	1:A:161:ASN:C	2.59	0.40
1:A:256:ARG:NH1	1:A:256:ARG:HG2	2.36	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	341/358 (95%)	287 (84%)	37 (11%)	17 (5%)	2 1

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	TYR
1	A	96	SER
1	A	114	LYS
1	A	117	ASP
1	A	234	ASN
1	A	328	ARG
1	A	113	ASP
1	A	167	ASP
1	A	197	LEU
1	A	214	LYS
1	A	240	ARG
1	A	93	ARG
1	A	37	PHE
1	A	196	LYS
1	A	239	THR
1	A	277	ASP
1	A	262	LYS

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	301/315 (96%)	282 (94%)	19 (6%)	20	26

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	TYR
1	A	24	LYS
1	A	38	GLU
1	A	45	THR
1	A	63	GLU
1	A	91	LEU
1	A	113	ASP
1	A	122	TYR

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Mol	Chain	Res	Type
1	A	160	PRO
1	A	176	ARG
1	A	184	PRO
1	A	202	LEU
1	A	210	PHE
1	A	211	ASP
1	A	242	ARG
1	A	293	LEU
1	A	302	PHE
1	A	329	LYS
1	A	336	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	P	14	2,5	13,19,20	0.87	0	12,26,29	1.07	1 (8%)
3	8OG	T	5	3	17,25,26	1.35	2 (11%)	22,37,40	2.05	4 (18%)

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	P	14	2,5	-	0/3/18/19	0/2/2/2
3	8OG	T	5	3	-	0/3/21/22	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	5	8OG	C2-N1	2.86	1.40	1.35
3	T	5	8OG	C6-N1	4.19	1.40	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	5	8OG	N3-C2-N1	-5.17	119.83	127.41
3	T	5	8OG	C5-C6-N1	-3.15	118.99	123.47
2	P	14	DOC	C2'-C1'-N1	2.22	116.66	112.48
3	T	5	8OG	C6-N1-C2	2.38	119.48	116.06
3	T	5	8OG	C2-N3-C4	5.46	121.53	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	14	DOC	3	0
3	T	5	8OG	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	DCT	A	1342	5	22,28,28	1.49	3 (13%)	23,43,43	1.95	6 (26%)

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	DCT	A	1342	5	-	0/18/31/31	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1342	DCT	PG-O1G	3.05	1.60	1.50
4	A	1342	DCT	C4-N3	3.08	1.40	1.35
4	A	1342	DCT	C6-N1	3.80	1.40	1.35

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1342	DCT	O4'-C1'-C2'	-4.75	101.53	106.67
4	A	1342	DCT	C3'-C2'-C1'	-4.13	97.85	102.80
4	A	1342	DCT	PB-O3A-PA	-3.47	120.96	132.63
4	A	1342	DCT	PB-O3B-PG	-2.80	123.23	132.63
4	A	1342	DCT	N4-C4-N3	2.10	119.98	116.56
4	A	1342	DCT	O4'-C1'-N1	2.90	112.67	107.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1342	DCT	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 [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	342/358 (95%)	0.35	12 (3%) 44 51	29, 54, 74, 83	38 (11%)
2	P	13/14 (92%)	-0.32	0 100 100	30, 49, 61, 61	0
3	T	15/18 (83%)	0.14	1 (6%) 18 21	30, 53, 76, 88	1 (6%)
All	All	370/390 (94%)	0.32	13 (3%) 44 51	29, 54, 74, 88	39 (10%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	T	3	DA	6.1
1	A	197	LEU	3.2
1	A	116	ARG	3.1
1	A	96	SER	3.1
1	A	194	LEU	2.9
1	A	98	LYS	2.6
1	A	322	ILE	2.5
1	A	199	ILE	2.3
1	A	114	LYS	2.3
1	A	298	ARG	2.2
1	A	330	ILE	2.2
1	A	280	ILE	2.2
1	A	216	MET	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. 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(\AA^2)	Q<0.9
2	DOC	P	14	18/19	0.94	0.15	33,52,59,60	0
3	8OG	T	5	23/24	0.95	0.15	30,42,61,63	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. 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(\AA^2)	Q<0.9
4	DCT	A	1342	27/27	0.86	0.24	49,60,74,79	0
5	CA	A	1345	1/1	0.86	0.10	72,72,72,72	0
5	CA	A	1344	1/1	0.91	0.22	41,41,41,41	0
5	CA	A	1343	1/1	0.96	0.14	50,50,50,50	0
5	CA	A	1346	1/1	0.97	0.27	64,64,64,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.