Full wwPDB X-ray Structure Validation Report ⓘ

Feb 5, 2024 – 11:49 AM EST

PDB ID	:	1SKS
Title	:	Binary 3' complex of T7 DNA polymerase with a DNA primer/template containing a cis-syn thymine dimer on the template
Authors	:	Li, Y.; Dutta, S.; Doublie, S.; Bdour, H.M.; Taylor, J.S.; Ellenberger, T.
Deposited on	:	2004-03-05
Resolution	:	2.30 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:

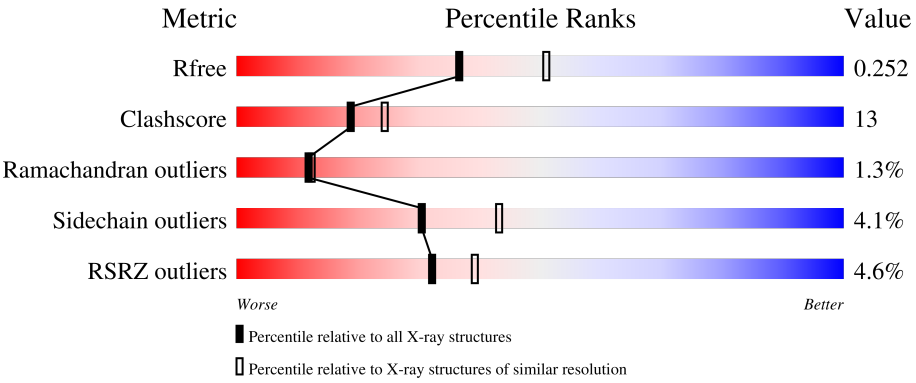
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	P	21	10% 19% 29% 5% 48%
2	T	25	8% 32% 8% 8% 52%
3	A	698	4% 71% 24%
4	B	108	6% 74% 20%

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
2	TTD	T	5	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6769 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 DNA chain called 5'-D(*CP*GP*AP*AP*AP*AP*CP*GP*AP*C*GP*GP*CP*CP*AP*GP*TP*GP*CP*CP*(2DT))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	11	Total	C	N	O	P	0	0	0
			199	96	31	62	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	12	Total	C	N	O	P	0	0	0
			266	126	48	79	13			

- Molecule 3 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	681	Total	C	N	O	S	0	0	0
			5308	3382	921	981	24			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LYS	deletion	UNP P00581
A	?	-	ARG	deletion	UNP P00581
A	?	-	PHE	deletion	UNP P00581
A	?	-	GLY	deletion	UNP P00581
A	?	-	SER	deletion	UNP P00581
A	?	-	HIS	deletion	UNP P00581

- Molecule 4 is a protein called Thioredoxin 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	105	Total	C	N	O	S	0	0	0
			798	515	128	152	3			

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

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

- Molecule 6 is water.

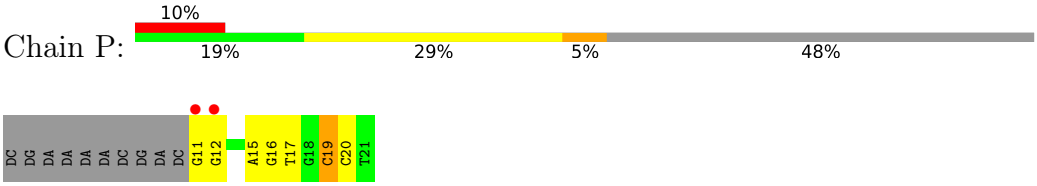
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	P	7	Total O 7 7	0	0
6	T	6	Total O 6 6	0	0
6	A	172	Total O 172 172	0	0
6	B	12	Total O 12 12	0	0

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.

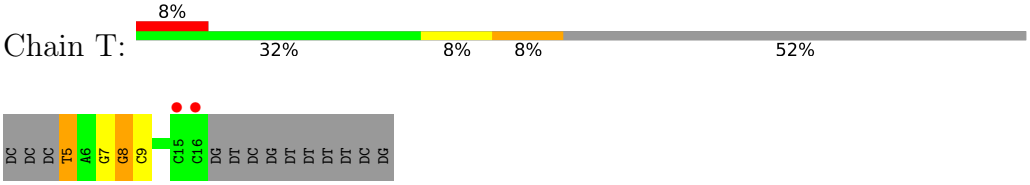
• Molecule 1: 5'-D(*CP*GP*AP*AP*AP*AP*CP*GP*AP*C*GP*GP*CP*CP*AP*GP*TP*GP*CP*CP*(2DT))-3'

Chain P:



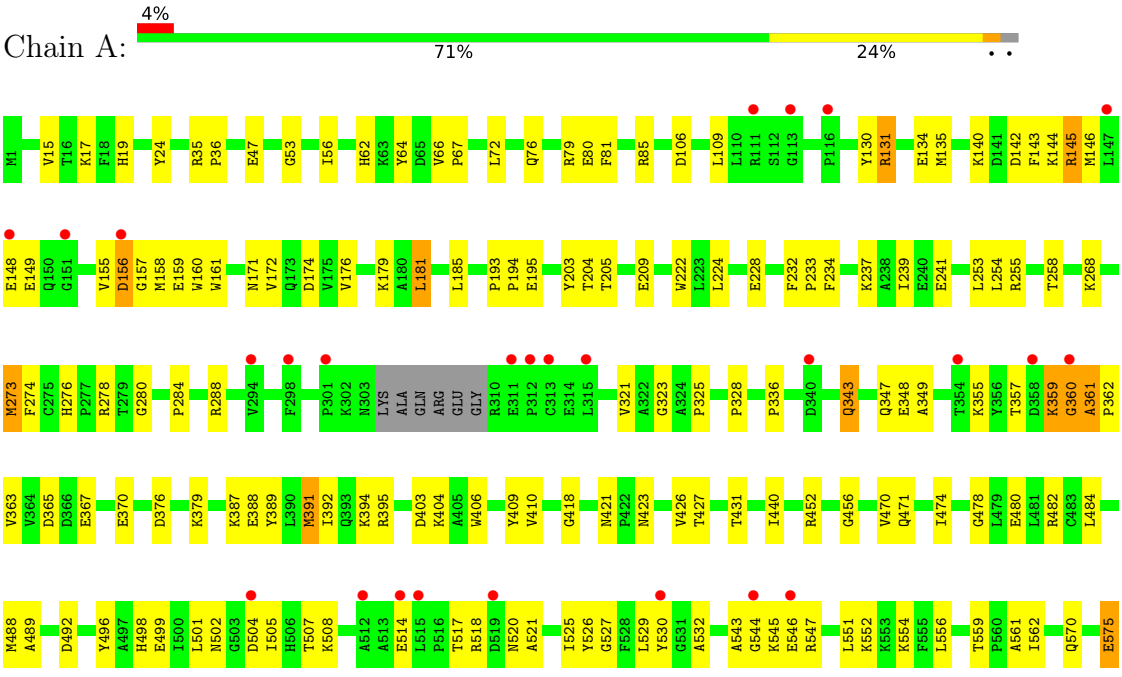
• Molecule 2: 5'-D(*CP*CP*CP*(TTD)P*AP*GP*GP*CP*AP*CP*TP*GP*GP*CP*CP*GP*TP*CP*GP*TP*TP*TP*TP*CP*G)-3'

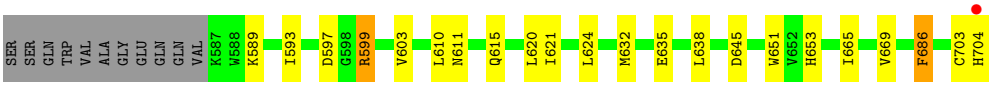
Chain T:



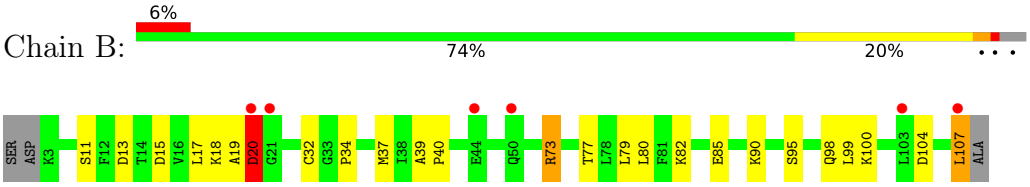
• Molecule 3: DNA polymerase

Chain A:





• Molecule 4: Thioredoxin 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	104.77Å 214.92Å 52.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 47.81 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.9 (50.00-2.30) 96.7 (47.81-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	3.91 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.235 , 0.266 0.225 , 0.252	Depositor DCC
R_{free} test set	2546 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	35.7	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 41.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	6769	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 3.79% 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

5.1 Standard geometry

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

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	0.36	0/200	0.82	0/305
2	T	0.51	0/253	0.90	0/388
3	A	0.37	0/5440	0.57	0/7382
4	B	0.32	0/813	0.55	0/1104
All	All	0.37	0/6706	0.59	0/9179

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	P	0	1
2	T	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	P	19	DC	Sidechain
2	T	8	DG	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	P	199	0	115	10	0
2	T	266	0	147	5	0
3	A	5308	0	5090	139	0
4	B	798	0	805	19	0
5	A	1	0	0	0	0
6	A	172	0	0	2	0
6	B	12	0	0	0	0
6	P	7	0	0	0	0
6	T	6	0	0	1	0
All	All	6769	0	6157	167	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 13.

All (167) 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:15:DA:H2"	1:P:16:DG:H5'	1.58	0.83
2:T:5:TTD:H2'	2:T:5:TTD:H5R2	1.58	0.83
3:A:144:LYS:O	3:A:148:GLU:HG2	1.79	0.81
3:A:328:PRO:HB3	4:B:73:ARG:HH12	1.46	0.81
3:A:35:ARG:HB3	3:A:36:PRO:HD2	1.69	0.73
1:P:16:DG:H1'	1:P:17:DT:H5"	1.73	0.71
3:A:496:TYR:CZ	3:A:505:ILE:HD11	2.26	0.70
3:A:552:LYS:O	3:A:556:LEU:HG	1.93	0.69
3:A:328:PRO:HB3	4:B:73:ARG:NH1	2.07	0.68
3:A:284:PRO:HA	3:A:288:ARG:HH22	1.59	0.68
4:B:100:LYS:NZ	4:B:100:LYS:HB3	2.10	0.67
3:A:145:ARG:HB3	3:A:145:ARG:NH1	2.11	0.66
3:A:504:ASP:OD2	3:A:507:THR:HG23	1.94	0.66
3:A:343:GLN:HG3	3:A:362:PRO:CG	2.26	0.66
3:A:140:LYS:O	3:A:144:LYS:HG3	1.97	0.65
3:A:343:GLN:HG3	3:A:362:PRO:HG2	1.77	0.64
3:A:480:GLU:CB	3:A:529:LEU:HD13	2.29	0.62
3:A:575:GLU:HB3	3:A:589:LYS:HE2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:645:ASP:HB3	3:A:665:ILE:HD13	1.81	0.61
4:B:39:ALA:HB3	4:B:40:PRO:HD3	1.82	0.61
3:A:228:GLU:HG2	3:A:418:GLY:O	2.00	0.61
3:A:452:ARG:HH21	3:A:704:HIS:HD2	1.49	0.61
3:A:158:MET:HA	3:A:161:TRP:CD2	2.35	0.60
3:A:632:MET:O	3:A:635:GLU:HG2	2.01	0.60
4:B:34:PRO:O	4:B:37:MET:HB2	2.02	0.60
3:A:237:LYS:O	3:A:241:GLU:HG3	2.01	0.60
3:A:517:THR:O	3:A:520:ASN:HB2	2.02	0.60
3:A:480:GLU:HB3	3:A:529:LEU:HD13	1.84	0.59
3:A:106:ASP:OD2	3:A:109:LEU:HD12	2.03	0.58
3:A:391:MET:O	3:A:391:MET:HE2	2.04	0.58
3:A:421:ASN:HB3	3:A:431:THR:OG1	2.05	0.57
3:A:85:ARG:HD3	6:A:5160:HOH:O	2.04	0.57
3:A:530:TYR:HA	3:A:611:ASN:ND2	2.19	0.57
3:A:131:ARG:O	3:A:135:MET:HG2	2.04	0.57
3:A:527:GLY:HA2	3:A:530:TYR:CE1	2.40	0.57
3:A:19:HIS:O	3:A:36:PRO:HD3	2.05	0.57
3:A:336:PRO:HB2	3:A:389:TYR:CD1	2.39	0.56
3:A:593:ILE:HG12	3:A:603:VAL:HG21	1.87	0.56
1:P:16:DG:H2"	1:P:17:DT:H5'	1.87	0.56
3:A:276:HIS:CD2	3:A:278:ARG:H	2.23	0.56
3:A:499:GLU:HG2	3:A:508:LYS:HD2	1.87	0.56
3:A:234:PHE:CZ	3:A:239:ILE:HG13	2.41	0.56
3:A:514:GLU:CG	3:A:554:LYS:HE3	2.36	0.56
3:A:427:THR:HG21	3:A:615:GLN:OE1	2.07	0.55
3:A:355:LYS:HG3	3:A:363:VAL:HB	1.89	0.54
3:A:145:ARG:O	3:A:149:GLU:HG3	2.06	0.54
3:A:172:VAL:O	3:A:176:VAL:HG13	2.07	0.54
3:A:254:LEU:O	3:A:258:THR:HG23	2.07	0.54
3:A:145:ARG:CB	3:A:145:ARG:HH11	2.21	0.54
3:A:66:VAL:HB	3:A:67:PRO:HD3	1.90	0.53
3:A:347:GLN:C	3:A:349:ALA:H	2.12	0.53
3:A:599:ARG:HD3	3:A:620:LEU:HD11	1.90	0.53
3:A:47:GLU:HG3	3:A:81:PHE:HE1	1.74	0.53
3:A:365:ASP:OD1	3:A:367:GLU:HB2	2.10	0.52
4:B:13:ASP:OD1	4:B:18:LYS:HE3	2.09	0.52
3:A:145:ARG:NH1	3:A:145:ARG:CB	2.72	0.52
3:A:181:LEU:HD22	3:A:185:LEU:HD11	1.90	0.52
3:A:135:MET:HG3	3:A:174:ASP:OD1	2.10	0.52
3:A:158:MET:HA	3:A:161:TRP:CE2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:15:DA:H4'	3:A:359:LYS:HZ3	1.75	0.52
3:A:489:ALA:HA	3:A:492:ASP:OD1	2.10	0.51
3:A:559:THR:HG22	3:A:562:ILE:HG13	1.93	0.51
3:A:155:VAL:O	3:A:156:ASP:C	2.50	0.51
3:A:24:TYR:CZ	3:A:179:LYS:HE3	2.46	0.51
3:A:321:VAL:HG23	4:B:90:LYS:HD2	1.94	0.50
3:A:391:MET:HE1	3:A:392:ILE:HA	1.93	0.50
3:A:273:MET:HG3	3:A:274:PHE:N	2.26	0.50
3:A:478:GLY:O	3:A:482:ARG:HG3	2.10	0.50
3:A:456:GLY:HA2	3:A:471:GLN:OE1	2.12	0.50
3:A:376:ASP:OD2	3:A:379:LYS:HD3	2.11	0.50
3:A:480:GLU:HB2	3:A:529:LEU:HD13	1.94	0.50
3:A:130:TYR:CZ	3:A:134:GLU:HG3	2.48	0.49
1:P:15:DA:H2"	1:P:16:DG:C5'	2.36	0.49
3:A:530:TYR:HA	3:A:611:ASN:HD21	1.76	0.49
1:P:16:DG:H2"	1:P:17:DT:C5'	2.43	0.49
3:A:205:THR:HG23	3:A:209:GLU:HG3	1.95	0.49
3:A:360:GLY:O	3:A:361:ALA:HB2	2.12	0.49
3:A:514:GLU:HA	3:A:514:GLU:OE1	2.13	0.49
3:A:525:ILE:HG23	3:A:526:TYR:N	2.26	0.49
3:A:130:TYR:CE2	3:A:134:GLU:HG3	2.48	0.48
3:A:155:VAL:HG12	3:A:156:ASP:N	2.28	0.48
3:A:131:ARG:HA	3:A:131:ARG:NH1	2.28	0.48
3:A:343:GLN:O	3:A:347:GLN:HG3	2.13	0.48
3:A:547:ARG:O	3:A:551:LEU:HG	2.13	0.48
4:B:73:ARG:HD2	4:B:73:ARG:O	2.14	0.48
3:A:142:ASP:O	3:A:145:ARG:HG2	2.14	0.48
4:B:95:SER:OG	4:B:98:GLN:HG3	2.12	0.48
4:B:32:CYS:SG	4:B:34:PRO:HD2	2.54	0.48
3:A:253:LEU:HD11	3:A:388:GLU:HG2	1.95	0.48
3:A:559:THR:CG2	3:A:562:ILE:HG13	2.44	0.48
3:A:64:TYR:O	3:A:67:PRO:HD2	2.14	0.47
1:P:15:DA:H4'	3:A:359:LYS:NZ	2.29	0.47
3:A:391:MET:HE3	3:A:395:ARG:HG3	1.97	0.47
3:A:544:GLY:C	3:A:546:GLU:H	2.17	0.47
3:A:130:TYR:O	3:A:134:GLU:HG2	2.15	0.47
3:A:157:GLY:HA2	3:A:159:GLU:OE1	2.14	0.47
3:A:505:ILE:HD12	3:A:508:LYS:HD3	1.96	0.47
3:A:514:GLU:HG2	3:A:554:LYS:HG2	1.96	0.47
3:A:514:GLU:HG3	3:A:554:LYS:HE3	1.96	0.47
4:B:82:LYS:O	4:B:85:GLU:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:5:TTD:H2'	2:T:5:TTD:O4R	2.15	0.46
3:A:488:MET:HE3	3:A:561:ALA:HB3	1.97	0.46
1:P:19:DC:H5'	3:A:394:LYS:HE2	1.97	0.46
3:A:143:PHE:O	3:A:146:MET:HB2	2.15	0.46
3:A:276:HIS:HD2	3:A:278:ARG:H	1.64	0.46
3:A:357:THR:OG1	3:A:361:ALA:HB3	2.16	0.46
1:P:11:DG:H2"	1:P:12:DG:O4'	2.15	0.46
3:A:203:TYR:CE1	3:A:204:THR:HG23	2.51	0.46
3:A:159:GLU:HG2	3:A:160:TRP:CD1	2.51	0.45
3:A:597:ASP:OD2	3:A:599:ARG:HD2	2.17	0.45
2:T:7:DG:H1'	6:T:5124:HOH:O	2.16	0.45
3:A:452:ARG:HH21	3:A:704:HIS:CD2	2.32	0.45
4:B:100:LYS:HB3	4:B:100:LYS:HZ3	1.81	0.45
3:A:484:LEU:O	3:A:488:MET:HG2	2.16	0.45
3:A:703:CYS:O	3:A:704:HIS:HB2	2.15	0.45
3:A:35:ARG:HH11	3:A:35:ARG:HG3	1.82	0.45
3:A:638:LEU:HD12	3:A:638:LEU:N	2.31	0.45
3:A:376:ASP:HB3	3:A:379:LYS:HB2	1.98	0.45
4:B:13:ASP:HA	4:B:17:LEU:HD12	1.97	0.45
3:A:268:LYS:O	3:A:328:PRO:HB2	2.17	0.45
3:A:440:ILE:O	3:A:452:ARG:NH1	2.50	0.45
3:A:474:ILE:HD11	3:A:669:VAL:HG12	1.99	0.45
3:A:406:TRP:CZ2	3:A:440:ILE:HD12	2.52	0.45
1:P:19:DC:H2"	1:P:20:DC:C6	2.52	0.44
3:A:24:TYR:CE2	3:A:179:LYS:HE3	2.52	0.44
3:A:17:LYS:HA	3:A:76:GLN:OE1	2.17	0.44
3:A:343:GLN:HG3	3:A:362:PRO:HG3	1.97	0.44
3:A:514:GLU:HG2	3:A:554:LYS:HE3	2.00	0.43
3:A:525:ILE:CG2	3:A:526:TYR:N	2.81	0.43
4:B:19:ALA:O	4:B:20:ASP:C	2.56	0.43
4:B:107:LEU:HD12	4:B:107:LEU:HA	1.81	0.43
3:A:518:ARG:O	3:A:521:ALA:HB3	2.19	0.43
3:A:404:LYS:HA	3:A:409:TYR:HE2	1.84	0.42
3:A:255:ARG:HG2	3:A:255:ARG:HH11	1.84	0.42
3:A:597:ASP:OD1	3:A:599:ARG:HD2	2.20	0.42
3:A:53:GLY:HA2	6:A:5022:HOH:O	2.18	0.42
3:A:193:PRO:HA	3:A:194:PRO:HD3	1.86	0.42
3:A:496:TYR:CE1	3:A:505:ILE:HD11	2.55	0.42
3:A:15:VAL:HG22	3:A:72:LEU:HD21	2.01	0.42
3:A:355:LYS:H	3:A:355:LYS:HG2	1.69	0.42
3:A:530:TYR:CZ	3:A:532:ALA:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:544:GLY:O	3:A:546:GLU:N	2.53	0.42
3:A:56:ILE:HD12	3:A:56:ILE:N	2.34	0.41
3:A:145:ARG:HH11	3:A:145:ARG:HB2	1.85	0.41
3:A:423:ASN:OD1	3:A:599:ARG:NH2	2.52	0.41
3:A:79:ARG:HG2	3:A:80:GLU:N	2.35	0.41
2:T:8:DG:H2"	2:T:9:DC:O5'	2.20	0.41
3:A:85:ARG:HG3	3:A:222:TRP:CG	2.55	0.41
3:A:145:ARG:HB3	3:A:145:ARG:CZ	2.50	0.41
4:B:11:SER:O	4:B:15:ASP:HB2	2.21	0.41
3:A:559:THR:HG21	3:A:562:ILE:CD1	2.51	0.41
3:A:323:GLY:O	3:A:325:PRO:HD3	2.20	0.41
4:B:37:MET:HB3	4:B:37:MET:HE2	1.96	0.41
3:A:205:THR:CG2	3:A:209:GLU:HG3	2.51	0.41
3:A:498:HIS:O	3:A:502:ASN:HB2	2.21	0.41
3:A:559:THR:HG22	3:A:559:THR:O	2.20	0.41
3:A:406:TRP:O	3:A:410:VAL:HG13	2.20	0.41
3:A:517:THR:OG1	3:A:520:ASN:OD1	2.39	0.41
4:B:77:THR:HG22	4:B:79:LEU:CD1	2.50	0.41
3:A:370:GLU:OE1	3:A:387:LYS:NZ	2.54	0.41
3:A:336:PRO:HB2	3:A:389:TYR:CE1	2.56	0.40
4:B:100:LYS:HB3	4:B:100:LYS:HZ2	1.83	0.40
3:A:233:PRO:HB2	3:A:456:GLY:O	2.21	0.40
3:A:470:VAL:HG12	3:A:471:GLN:N	2.35	0.40
3:A:621:ILE:HD11	3:A:686:PHE:CZ	2.56	0.40
2:T:5:TTD:H72	2:T:5:TTD:H5A1	1.91	0.40
3:A:224:LEU:HD11	3:A:651:TRP:CZ3	2.57	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	
3	A	675/698 (97%)	639 (95%)	27 (4%)	9 (1%)	12	12
4	B	103/108 (95%)	97 (94%)	5 (5%)	1 (1%)	15	17
All	All	778/806 (96%)	736 (95%)	32 (4%)	10 (1%)	12	12

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	156	ASP
3	A	543	ALA
3	A	359	LYS
3	A	360	GLY
4	B	20	ASP
3	A	348	GLU
3	A	545	LYS
3	A	653	HIS
3	A	361	ALA
3	A	280	GLY

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	
3	A	533/579 (92%)	514 (96%)	19 (4%)	35	49
4	B	84/87 (97%)	78 (93%)	6 (7%)	14	19
All	All	617/666 (93%)	592 (96%)	25 (4%)	30	43

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	62	HIS
3	A	131	ARG
3	A	145	ARG
3	A	171	ASN
3	A	181	LEU
3	A	195	GLU

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Mol	Chain	Res	Type
3	A	232	PHE
3	A	273	MET
3	A	343	GLN
3	A	391	MET
3	A	403	ASP
3	A	426	VAL
3	A	501	LEU
3	A	570	GLN
3	A	575	GLU
3	A	599	ARG
3	A	610	LEU
3	A	624	LEU
3	A	686	PHE
4	B	20	ASP
4	B	73	ARG
4	B	80	LEU
4	B	99	LEU
4	B	104	ASP
4	B	107	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	276	HIS
3	A	611	ASN
3	A	667	GLN
4	B	50	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	$\#\|Z\| > 2$
1	2DT	P	21	2,1	17,20,21	0.39	0	22,28,31	0.46	0
2	TTD	T	5	2	42,45,46	3.96	10 (23%)	62,74,77	3.42	31 (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
1	2DT	P	21	2,1	-	2/7/18/19	0/2/2/2
2	TTD	T	5	2	-	8/22/109/110	0/5/6/6

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	5	TTD	C5T-C6T	-20.08	1.32	1.55
2	T	5	TTD	C5-C6	-10.46	1.43	1.55
2	T	5	TTD	C1'-N1	6.01	1.53	1.45
2	T	5	TTD	C1R-N1T	4.82	1.51	1.45
2	T	5	TTD	C5A-C5	4.24	1.62	1.53
2	T	5	TTD	C2-N1	3.33	1.43	1.36
2	T	5	TTD	C5M-C5T	3.16	1.59	1.53
2	T	5	TTD	O4R-C1R	-2.80	1.36	1.42
2	T	5	TTD	C2-N3	-2.59	1.33	1.38
2	T	5	TTD	C2'-C3R	2.22	1.57	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	T	5	TTD	O4T-C4T-C5T	9.19	130.21	122.88
2	T	5	TTD	C5T-C5-C4	7.93	139.37	113.21
2	T	5	TTD	O4'-C1'-N1	-7.69	99.54	108.65
2	T	5	TTD	O5R-PB-O5P	-7.28	80.64	109.07
2	T	5	TTD	C2'-C1'-N1	6.92	124.93	115.59
2	T	5	TTD	C5-C5T-C6T	6.51	96.48	88.38
2	T	5	TTD	O4R-C1R-N1T	6.51	116.36	108.65
2	T	5	TTD	C5A-C5-C4	-5.90	98.05	108.22
2	T	5	TTD	C5T-C5-C6	-5.62	81.38	88.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	T	5	TTD	O4P-PB-O5R	-5.07	84.21	107.75
2	T	5	TTD	C5-C5T-C4T	-4.54	98.24	113.21
2	T	5	TTD	O4T-C4T-N3T	-4.46	113.39	120.50
2	T	5	TTD	O3R-PB-O5P	4.42	126.06	109.47
2	T	5	TTD	C5T-C6T-N1T	4.28	121.60	115.61
2	T	5	TTD	C4'-O4R-C1R	-3.79	100.29	109.45
2	T	5	TTD	C5T-C6T-C6	-3.66	83.28	89.28
2	T	5	TTD	O4'-C1'-C2'	-3.55	99.55	106.25
2	T	5	TTD	O4P-PB-O5P	3.33	128.71	112.24
2	T	5	TTD	O4-C4-C5	3.18	125.42	122.88
2	T	5	TTD	C4R-O4'-C1'	-2.78	102.74	109.45
2	T	5	TTD	C2R-C1R-N1T	-2.66	111.99	115.59
2	T	5	TTD	O4'-C4R-C3R	2.60	110.26	105.30
2	T	5	TTD	O3R-C3R-C2'	2.60	120.22	110.56
2	T	5	TTD	C5-C6-N1	2.59	119.24	115.61
2	T	5	TTD	C3'-C2R-C1R	-2.51	96.24	102.54
2	T	5	TTD	C5'-C4R-C3R	-2.48	108.87	114.53
2	T	5	TTD	C2'-C3R-C4R	-2.47	98.14	102.98
2	T	5	TTD	O3R-C3R-C4R	-2.40	101.65	108.66
2	T	5	TTD	C5M-C5T-C6T	2.30	121.23	114.16
2	T	5	TTD	C5A-C5-C5T	-2.18	110.10	116.39
2	T	5	TTD	C5A-C5-C6	-2.04	107.90	114.16

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	P	21	2DT	O4'-C4'-C5'-O5'
2	T	5	TTD	C3'-C4'-C5R-O5R
2	T	5	TTD	O4R-C4'-C5R-O5R
2	T	5	TTD	C2'-C1'-N1-C6
2	T	5	TTD	C2'-C1'-N1-C2
2	T	5	TTD	O4'-C4R-C5'-O5'
1	P	21	2DT	C3'-C4'-C5'-O5'
2	T	5	TTD	O4'-C1'-N1-C2
2	T	5	TTD	O4'-C1'-N1-C6
2	T	5	TTD	C3R-O3R-PB-O5R

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	T	5	TTD	3	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95^{th} 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	10/21 (47%)	0.56	2 (20%)	1	1	37, 49, 76, 79	0
2	T	11/25 (44%)	0.39	2 (18%)	1	1	33, 47, 69, 72	0
3	A	681/698 (97%)	0.29	27 (3%)	38	45	16, 36, 60, 69	0
4	B	105/108 (97%)	0.31	6 (5%)	23	30	33, 47, 59, 62	0
All	All	807/852 (94%)	0.30	37 (4%)	32	39	16, 38, 60, 79	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	360	GLY	5.2
3	A	313	CYS	5.1
3	A	514	GLU	4.9
3	A	294	VAL	4.5
4	B	20	ASP	4.3
3	A	358	ASP	3.6
1	P	12	DG	3.5
4	B	21	GLY	3.5
3	A	151	GLY	3.5
3	A	298	PHE	3.4
3	A	111	ARG	3.3
3	A	312	PRO	3.1
3	A	515	LEU	3.1
3	A	704	HIS	3.1
3	A	544	GLY	2.9
2	T	15	DC	2.9
3	A	354	THR	2.9
3	A	301	PRO	2.8
4	B	107	LEU	2.7
3	A	148	GLU	2.7
2	T	16	DC	2.7

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Mol	Chain	Res	Type	RSRZ
3	A	519	ASP	2.6
3	A	546	GLU	2.5
3	A	512	ALA	2.4
3	A	340	ASP	2.2
4	B	50	GLN	2.2
3	A	311	GLU	2.2
1	P	11	DG	2.2
4	B	103	LEU	2.2
3	A	156	ASP	2.1
3	A	530	TYR	2.1
4	B	44	GLU	2.1
3	A	315	LEU	2.1
3	A	113	GLY	2.1
3	A	116	PRO	2.1
3	A	504	ASP	2.0
3	A	147	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	TTD	T	5	40/41	0.64	0.48	72,79,86,87	0
1	2DT	P	21	19/20	0.95	0.14	39,41,43,44	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, 95^{th} 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	MG	A	4003	1/1	0.91	0.27	68,68,68,68	0

6.5 Other polymers (i)

There are no such residues in this entry.