Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:42 PM GMT

PDB ID	:	3UO7
Title	:	Crystal structure of Human Thymine DNA Glycosylase Bound to Substrate 5-carboxylcytosine
Authors	:	Zhang, L.; He, C.
Deposited on	:	2011-11-16
Resolution	:	3.00 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

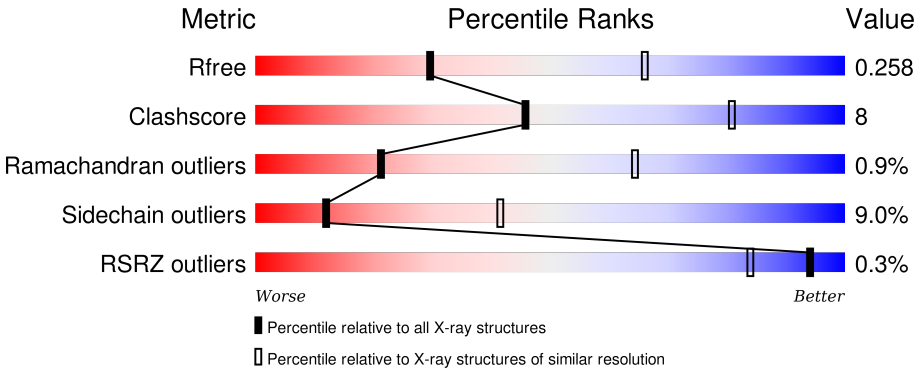
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 <=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	C	23	35% 61% .
2	D	23	4% 35% 57% 9%
3	A	201	66% 20% . 10%
3	B	201	71% 14% . 14%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3761 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*AP*GP*CP*TP*CP*TP*GP*TP*AP*CP*AP *TP*GP*AP*GP*CP*AP*GP*TP*GP*GP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	23	Total	C	N	O	P	0	0	0
			471	224	90	135	22			

- Molecule 2 is a DNA chain called 5'-D(*CP*CP*AP*CP*TP*GP*CP*TP*CP*AP*(1CC) P*GP*TP*AP*CP*AP*GP*AP*GP*CP*TP*GP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	23	Total	C	N	O	P	0	0	0
			467	223	84	138	22			

- Molecule 3 is a protein called G/T mismatch-specific thymine DNA glycosylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	181	Total	C	N	O	S	0	0	0
			1444	932	247	256	9			
3	B	173	Total	C	N	O	S	0	0	0
			1379	892	232	247	8			

There are 8 discrepancies between the modelled and reference sequences:

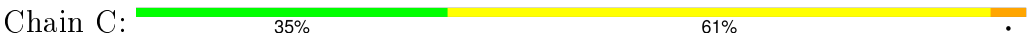
Chain	Residue	Modelled	Actual	Comment	Reference
A	108	SER	-	EXPRESSION TAG	UNP Q13569
A	109	ASN	-	EXPRESSION TAG	UNP Q13569
A	110	ALA	-	EXPRESSION TAG	UNP Q13569
A	140	ALA	ASN	ENGINEERED MUTATION	UNP Q13569
B	108	SER	-	EXPRESSION TAG	UNP Q13569
B	109	ASN	-	EXPRESSION TAG	UNP Q13569
B	110	ALA	-	EXPRESSION TAG	UNP Q13569
B	140	ALA	ASN	ENGINEERED MUTATION	UNP Q13569

3 Residue-property plots (i)

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.

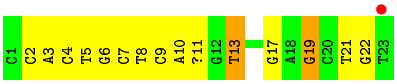
• Molecule 1: 5'-D(*CP*AP*GP*CP*TP*CP*TP*GP*TP*AP*CP*AP*TP*GP*AP*GP*CP*AP*GP*TP*GP*GP*A)-3'

Chain C:



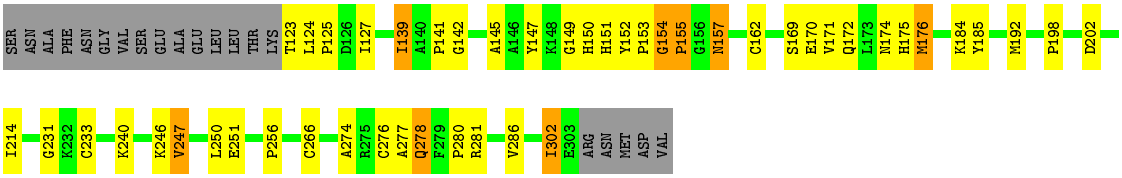
• Molecule 2: 5'-D(*CP*CP*AP*CP*TP*GP*CP*TP*CP*AP*(1CC)P*GP*TP*AP*CP*AP*GP*AP*GP*CP*TP*GP*T)-3'

Chain D:



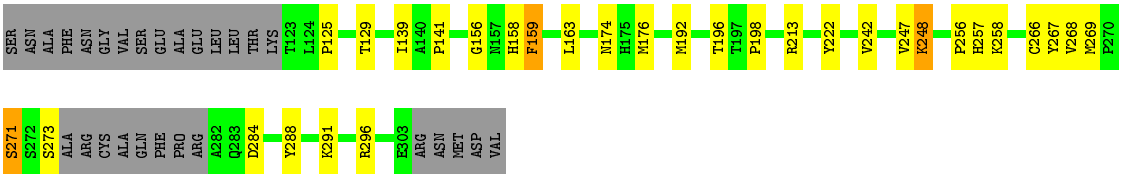
• Molecule 3: G/T mismatch-specific thymine DNA glycosylase

Chain A:



• Molecule 3: G/T mismatch-specific thymine DNA glycosylase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	164.35Å 164.35Å 57.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.61 – 3.00 36.61 – 3.00	Depositor EDS
% Data completeness (in resolution range)	81.2 (36.61-3.00) 80.9 (36.61-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.66 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.227 , 0.280 0.238 , 0.258	Depositor DCC
R_{free} test set	735 reflections (5.31%)	DCC
Wilson B-factor (Å^2)	72.0	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 28.1	EDS
Estimated twinning fraction	0.047 for h,-h-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Outliers	0 of 14639 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3761	wwPDB-VP
Average B, all atoms (Å^2)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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, 0.375 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: 1CC

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	C	0.76	0/529	1.45	8/815 (1.0%)
2	D	0.82	1/497 (0.2%)	1.41	8/762 (1.0%)
3	A	1.46	8/1481 (0.5%)	1.22	7/1997 (0.4%)
3	B	1.42	6/1413 (0.4%)	1.18	7/1904 (0.4%)
All	All	1.30	15/3920 (0.4%)	1.27	30/5478 (0.5%)

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	A	0	4
3	B	0	4
All	All	0	8

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	266	CYS	CB-SG	-9.13	1.66	1.82
3	B	266	CYS	CB-SG	-7.59	1.69	1.82
3	A	162	CYS	CB-SG	-7.18	1.70	1.82
3	A	231	GLY	CA-C	-5.85	1.42	1.51
3	A	233	CYS	CB-SG	-5.69	1.72	1.81
3	A	141	PRO	N-CD	-5.68	1.39	1.47
3	B	269	MET	CG-SD	-5.62	1.66	1.81
3	A	185	TYR	CB-CG	-5.61	1.43	1.51
3	A	256	PRO	N-CD	-5.35	1.40	1.47
3	B	141	PRO	N-CD	-5.23	1.40	1.47
3	B	125	PRO	N-CD	-5.22	1.40	1.47
3	B	198	PRO	N-CD	-5.18	1.40	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	256	PRO	N-CD	-5.13	1.40	1.47
2	D	9	DC	C3'-O3'	-5.10	1.37	1.44
3	A	276	CYS	CB-SG	-5.06	1.73	1.81

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	19	DG	O4'-C1'-N9	10.99	115.70	108.00
3	A	154	GLY	O-C-N	-10.71	100.75	121.10
3	B	222	TYR	CB-CG-CD2	-8.47	115.92	121.00
3	B	271	SER	CB-CA-C	-8.04	94.83	110.10
1	C	1	DC	O4'-C1'-N1	7.41	113.19	108.00
1	C	17	DC	O4'-C1'-N1	7.33	113.13	108.00
3	A	154	GLY	CA-C-N	7.25	137.41	117.10
3	A	247	VAL	N-CA-C	7.10	130.17	111.00
1	C	13	DT	N3-C4-O4	7.03	124.12	119.90
1	C	21	DG	O4'-C1'-N9	6.92	112.84	108.00
3	A	139	ILE	N-CA-C	6.68	129.04	111.00
3	B	222	TYR	CB-CG-CD1	6.63	124.98	121.00
2	D	7	DC	O4'-C1'-N1	6.43	112.50	108.00
2	D	13	DT	O4'-C1'-N1	6.38	112.47	108.00
3	A	139	ILE	CB-CA-C	-6.14	99.32	111.60
2	D	19	DG	O4'-C4'-C3'	-6.06	102.08	104.50
1	C	2	DA	O4'-C1'-N9	5.96	112.17	108.00
2	D	6	DG	C1'-O4'-C4'	-5.82	104.28	110.10
2	D	6	DG	O4'-C1'-N9	5.78	112.05	108.00
3	A	176	MET	CG-SD-CE	-5.69	91.09	100.20
3	A	247	VAL	CB-CA-C	-5.62	100.72	111.40
3	B	288	TYR	CB-CG-CD2	-5.43	117.74	121.00
3	B	176	MET	CA-CB-CG	-5.37	104.18	113.30
1	C	10	DA	O4'-C1'-N9	5.28	111.69	108.00
2	D	5	DT	N3-C4-O4	5.23	123.04	119.90
1	C	13	DT	C5-C4-O4	-5.20	121.26	124.90
3	B	268	VAL	CA-CB-CG2	-5.16	103.16	110.90
2	D	21	DT	N3-C4-O4	5.12	122.97	119.90
3	B	158	HIS	C-N-CA	5.10	134.46	121.70
2	D	4	DC	O4'-C1'-N1	5.03	111.52	108.00

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	147	TYR	Sidechain
3	A	154	GLY	Peptide
3	A	155	PRO	Peptide
3	A	281	ARG	Sidechain
3	B	156	GLY	Peptide
3	B	159	PHE	Mainchain
3	B	267	TYR	Sidechain
3	B	296	ARG	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	C	471	0	257	15	0
2	D	467	0	260	21	0
3	A	1444	0	1455	37	1
3	B	1379	0	1389	4	1
All	All	3761	0	3361	52	1

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 8.

All (52) 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)
3:A:246:LYS:O	3:A:247:VAL:HG12	1.52	1.07
3:A:247:VAL:O	3:A:247:VAL:HG22	1.62	0.97
2:D:11:1CC:H10	2:D:11:1CC:H3	1.57	0.87
2:D:13:DT:H1'	3:A:278:GLN:NE2	1.89	0.87
3:A:246:LYS:O	3:A:247:VAL:CG1	2.24	0.85
3:A:153:PRO:HB3	3:A:175:HIS:CG	2.13	0.84
2:D:13:DT:C1'	3:A:278:GLN:NE2	2.45	0.80
3:A:155:PRO:HA	3:A:157:ASN:H	1.47	0.79
2:D:11:1CC:OP1	3:A:157:ASN:ND2	2.17	0.77
1:C:6:DC:H42	2:D:17:DG:H1	1.40	0.68
2:D:10:DA:N3	3:A:274:ALA:HB3	2.08	0.68
3:A:246:LYS:C	3:A:247:VAL:HG12	2.16	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:13:DT:O2	3:A:278:GLN:NE2	2.22	0.63
3:A:152:TYR:N	3:A:153:PRO:HD3	2.13	0.61
1:C:12:DA:C4	3:A:277:ALA:CB	2.83	0.61
1:C:5:DT:OP2	3:A:246:LYS:NZ	2.33	0.61
2:D:13:DT:H1'	3:A:278:GLN:HE22	1.65	0.59
3:B:139:ILE:HD12	3:B:139:ILE:H	1.68	0.58
3:B:271:SER:C	3:B:273:SER:H	2.06	0.58
2:D:11:1CC:H4	3:A:142:GLY:HA3	1.86	0.57
3:A:149:GLY:O	3:A:150:HIS:CD2	2.58	0.56
3:A:124:LEU:HD12	3:A:125:PRO:HD2	1.86	0.56
1:C:22:DG:N2	2:D:2:DC:O2	2.40	0.55
3:A:155:PRO:HA	3:A:157:ASN:N	2.20	0.54
2:D:10:DA:C2	3:A:274:ALA:HB1	2.43	0.53
1:C:4:DC:H42	2:D:19:DG:H1	1.56	0.53
2:D:10:DA:N3	3:A:274:ALA:CB	2.76	0.49
1:C:12:DA:C4	3:A:277:ALA:HB2	2.47	0.49
3:A:247:VAL:O	3:A:247:VAL:HG13	2.12	0.49
1:C:1:DC:N4	2:D:22:DG:O6	2.46	0.49
2:D:13:DT:O4'	3:A:278:GLN:NE2	2.46	0.48
1:C:12:DA:N3	3:A:277:ALA:HA	2.29	0.48
3:A:152:TYR:N	3:A:153:PRO:CD	2.78	0.47
2:D:8:DT:H6	2:D:8:DT:H5"	1.79	0.47
3:A:153:PRO:HB3	3:A:175:HIS:CB	2.45	0.46
2:D:2:DC:H2"	2:D:3:DA:C8	2.49	0.46
3:A:174:ASN:H	3:A:174:ASN:ND2	2.13	0.46
1:C:3:DG:H2'	1:C:4:DC:H6	1.81	0.46
1:C:12:DA:C4	3:A:277:ALA:HB1	2.50	0.45
2:D:10:DA:C2	3:A:274:ALA:CB	3.00	0.45
2:D:11:1CC:C21	3:A:145:ALA:HB2	2.48	0.43
1:C:12:DA:C5	3:A:277:ALA:HB2	2.54	0.43
1:C:20:DT:H5'	1:C:20:DT:C6	2.53	0.43
3:A:127:ILE:HG22	3:A:127:ILE:O	2.19	0.42
3:A:153:PRO:HB3	3:A:175:HIS:CD2	2.53	0.42
1:C:14:DG:C2	2:D:10:DA:C2	3.08	0.42
3:A:151:HIS:HB3	3:A:152:TYR:HD2	1.84	0.42
3:B:248:LYS:NZ	3:B:248:LYS:CB	2.83	0.42
1:C:12:DA:H2	3:A:274:ALA:O	2.04	0.41
3:A:247:VAL:HG21	3:A:250:LEU:HD13	2.04	0.40
1:C:1:DC:H42	2:D:22:DG:H1	1.68	0.40
3:B:163:LEU:HD12	3:B:163:LEU:HA	1.94	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:302:ILE:CD1	3:B:257:HIS:NE2[6_554]	2.01	0.19

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
3	A	179/201 (89%)	170 (95%)	7 (4%)	2 (1%)	17 58
3	B	169/201 (84%)	156 (92%)	12 (7%)	1 (1%)	30 72
All	All	348/402 (87%)	326 (94%)	19 (6%)	3 (1%)	21 64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	240	LYS
3	B	159	PHE
3	A	139	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
3	A	158/175 (90%)	141 (89%)	17 (11%)	8 30
3	B	152/175 (87%)	141 (93%)	11 (7%)	18 53
All	All	310/350 (89%)	282 (91%)	28 (9%)	12 41

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	123	THR
3	A	157	ASN
3	A	169	SER
3	A	170	GLU
3	A	171	VAL
3	A	172	GLN
3	A	176	MET
3	A	184	LYS
3	A	192	MET
3	A	198	PRO
3	A	202	ASP
3	A	214	ILE
3	A	251	GLU
3	A	278	GLN
3	A	280	PRO
3	A	286	VAL
3	A	302	ILE
3	B	129	THR
3	B	174	ASN
3	B	192	MET
3	B	196	THR
3	B	213	ARG
3	B	242	VAL
3	B	247	VAL
3	B	248	LYS
3	B	258	LYS
3	B	284	ASP
3	B	291	LYS

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

Mol	Chain	Res	Type
3	A	150	HIS
3	A	151	HIS
3	A	157	ASN
3	A	174	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	1CC	D	11	2	12,23,24	0.90	1 (8%)	14,33,36	0.65	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	1CC	D	11	2	-	0/3/25/26	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	11	1CC	C5-C4	-2.60	1.39	1.43

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	11	1CC	4	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	C	23/23 (100%)	-0.16	0 100 100	87, 109, 147, 152	0
2	D	22/23 (95%)	0.09	1 (4%) 37 15	72, 119, 145, 153	0
3	A	181/201 (90%)	-0.43	0 100 100	45, 67, 84, 116	0
3	B	173/201 (86%)	-0.48	0 100 100	47, 67, 90, 106	0
All	All	399/448 (89%)	-0.41	1 (0%) 94 84	45, 69, 120, 153	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	23	DT	3.1

6.2 Non-standard residues in protein, DNA, RNA chains

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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, 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	LLDF	B-factors(Å^2)	Q<0.9
2	1CC	D	11	22/23	0.97	0.17	-	57,64,68,69	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.