



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 09:27 PM GMT

PDB ID : 3Q0D  
Title : Crystal structure of SUVH5 SRA- hemi methylated CG DNA complex  
Authors : Eerappa, R.; Simanshu, D.K.; Patel, D.J.  
Deposited on : 2010-12-15  
Resolution : 2.37 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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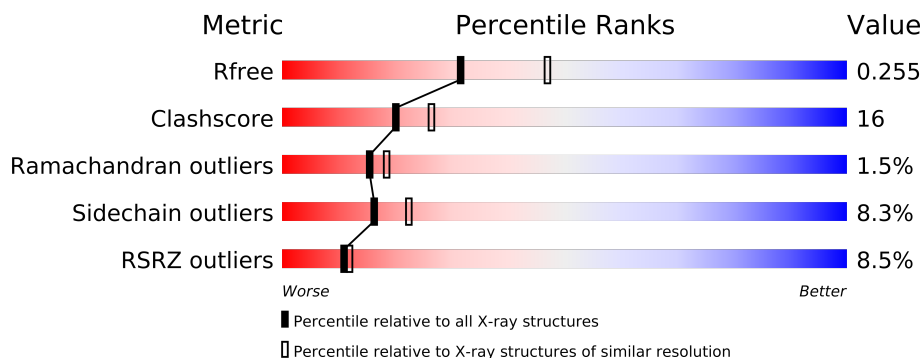
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.37 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))
$R_{free}$	66092	2963 (2.40-2.36)
Clashscore	79885	3668 (2.40-2.36)
Ramachandran outliers	78287	3600 (2.40-2.36)
Sidechain outliers	78261	3602 (2.40-2.36)
RSRZ outliers	66119	2966 (2.40-2.36)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	167	
1	X	167	
2	B	10	
3	C	10	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3035 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	140	Total	C	N	O	S	0	0	0
			1066	678	182	204	2			
1	A	145	Total	C	N	O	S	0	0	0
			1107	703	189	213	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	10	Total	C	N	O	P	0	10	0
			400	194	72	116	18			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	P	0	10	0
			410	196	80	116	18			

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	X	22	Total	O	0	0
			22	22		
5	A	18	Total	O	0	0
			18	18		

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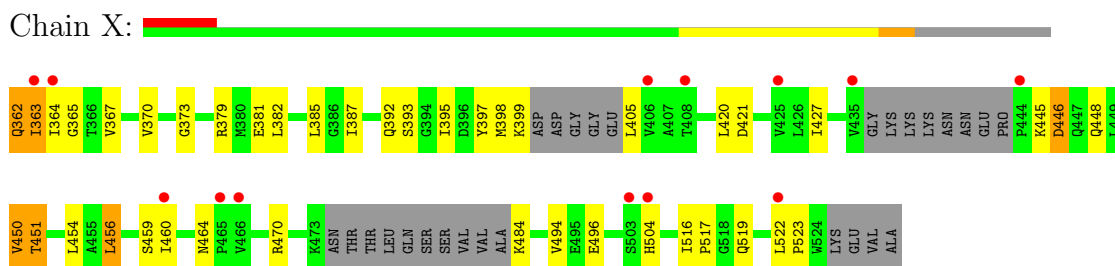
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	7	Total	O	0	0
			7	7		
5	C	4	Total	O	0	0
			4	4		

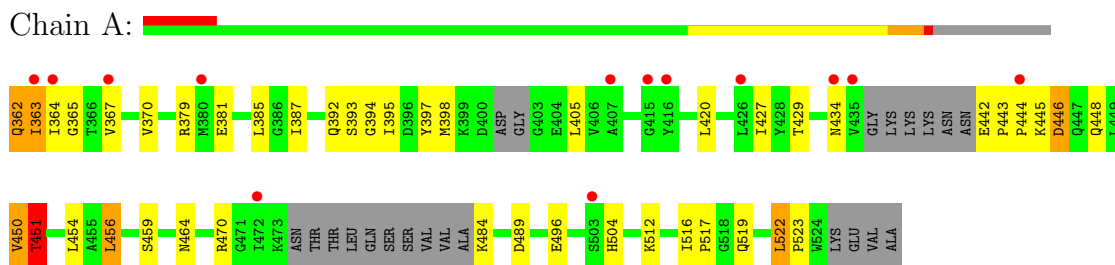
### 3 Residue-property plots

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: Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5



- Molecule 1: Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5



- Molecule 2: DNA (5'-D(\*TP\*CP\*CP\*AP\*(5CM)P\*GP\*TP\*CP\*AP\*G)-3')



- Molecule 3: DNA (5'-D(\*CP\*TP\*GP\*AP\*CP\*GP\*TP\*GP\*GP\*A)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.38Å 76.38Å 74.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.09 – 2.37 43.68 – 2.36	Depositor EDS
% Data completeness (in resolution range)	98.8 (19.09-2.37) 98.5 (43.68-2.36)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.56 (at 2.37Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.225 , 0.263 0.216 , 0.255	Depositor DCC
$R_{free}$ test set	881 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	58.8	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 87.4	EDS
Estimated twinning fraction	0.026 for -h,-l,-k 0.021 for -h,l,k 0.024 for l,-k,h 0.027 for -l,-k,-h 0.468 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 17399 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3035	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5CM, CL

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	0.49	0/1126	0.69	0/1527
1	X	0.48	0/1084	0.70	0/1471
2	B	1.46	2/400 (0.5%)	1.51	12/608 (2.0%)
3	C	0.66	0/460	1.27	6/708 (0.8%)
All	All	0.72	2/3070 (0.1%)	0.96	18/4314 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	9[A]	DA	P-O5'	-5.38	1.54	1.59
2	B	9[B]	DA	P-O5'	-5.38	1.54	1.59

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	8[A]	DC	O4'-C1'-N1	-6.48	103.46	108.00
2	B	8[B]	DC	O4'-C1'-N1	-6.48	103.46	108.00
3	C	2[A]	DT	N3-C4-O4	5.88	123.43	119.90
3	C	2[B]	DT	N3-C4-O4	5.88	123.43	119.90
2	B	10[A]	DG	C3'-C2'-C1'	-5.81	95.53	102.50
2	B	10[B]	DG	C3'-C2'-C1'	-5.81	95.53	102.50
2	B	7[A]	DT	C1'-O4'-C4'	-5.70	104.40	110.10
2	B	7[B]	DT	C1'-O4'-C4'	-5.70	104.40	110.10
3	C	5[A]	DC	O4'-C1'-N1	-5.68	104.02	108.00
3	C	5[B]	DC	O4'-C1'-N1	-5.68	104.02	108.00
2	B	1[A]	DT	N3-C4-O4	5.24	123.04	119.90
2	B	1[B]	DT	N3-C4-O4	5.24	123.04	119.90
2	B	1[A]	DT	C5-C4-O4	-5.13	121.31	124.90
2	B	1[B]	DT	C5-C4-O4	-5.13	121.31	124.90
2	B	7[A]	DT	O4'-C1'-C2'	-5.13	101.79	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	7[B]	DT	O4'-C1'-C2'	-5.13	101.79	105.90
3	C	2[A]	DT	C5-C4-O4	-5.11	121.33	124.90
3	C	2[B]	DT	C5-C4-O4	-5.11	121.33	124.90

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1107	0	1065	35	0
1	X	1066	0	1022	29	0
2	B	400	0	196	20	0
3	C	410	0	202	17	0
4	A	1	0	0	0	0
5	A	18	0	0	1	0
5	B	7	0	0	0	0
5	C	4	0	0	0	0
5	X	22	0	0	2	0
All	All	3035	0	2485	87	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

All (87) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:X:421:ASP:OD2	5:X:17:HOH:O	1.91	0.87
1:A:379:ARG:HG3	3:C:6[B]:DG:H4'	1.64	0.79
2:B:9[A]:DA:H2''	2:B:10[A]:DG:C8	2.26	0.69
3:C:7[A]:DT:H2''	3:C:8[A]:DG:C8	2.27	0.69
1:X:370:VAL:HG21	1:X:387:ILE:HD11	1.77	0.66
1:A:370:VAL:HG21	1:A:387:ILE:HD11	1.80	0.64
1:A:489:ASP:OD1	1:A:522:LEU:HD11	1.97	0.64
3:C:6[A]:DG:H2''	3:C:7[A]:DT:H5''	1.79	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:X:392:GLN:OE1	2:B:6[A]:DG:N2	2.31	0.63
1:X:362:GLN:OE1	1:X:398:MET:HB3	2.00	0.62
3:C:8[B]:DG:H2''	3:C:9[B]:DG:O5'	2.01	0.60
2:B:6[B]:DG:H5'	2:B:6[B]:DG:H8	1.67	0.60
1:A:362:GLN:OE1	1:A:398:MET:HB3	2.03	0.59
1:A:364:ILE:HG22	1:A:365:GLY:N	2.17	0.59
1:X:364:ILE:HG22	1:X:365:GLY:N	2.16	0.59
1:A:434:ASN:ND2	1:A:443:PRO:O	2.37	0.58
1:X:379:ARG:HG3	2:B:6[B]:DG:H4'	1.87	0.56
1:A:392:GLN:OE1	3:C:6[A]:DG:N2	2.39	0.56
2:B:6[B]:DG:H5'	2:B:6[B]:DG:C8	2.41	0.55
1:A:496:GLU:OE1	1:A:512:LYS:HD3	2.07	0.54
1:A:429:THR:O	2:B:5[A]:5CM:N4	2.40	0.53
2:B:6[A]:DG:C8	2:B:7[A]:DT:H72	2.43	0.53
2:B:9[B]:DA:H2''	2:B:10[B]:DG:C8	2.44	0.53
3:C:9[B]:DG:H2''	3:C:10[B]:DA:C8	2.44	0.52
1:X:395:ILE:HD13	1:X:456:LEU:CD2	2.40	0.52
1:A:379:ARG:N	3:C:7[B]:DT:OP1	2.30	0.51
1:X:364:ILE:CG2	1:X:365:GLY:N	2.74	0.51
2:B:5[B]:5CM:O5'	2:B:5[B]:5CM:H6	2.10	0.51
3:C:8[A]:DG:H2''	3:C:9[A]:DG:O5'	2.11	0.51
1:X:379:ARG:NH2	1:X:393:SER:O	2.43	0.50
2:B:1[B]:DT:O4	3:C:10[B]:DA:N6	2.45	0.50
1:A:364:ILE:CG2	1:A:365:GLY:N	2.74	0.49
1:A:395:ILE:HD13	1:A:456:LEU:CD2	2.42	0.49
1:A:363:ILE:HD13	1:A:367:VAL:HG22	1.94	0.49
1:X:363:ILE:HD13	1:X:367:VAL:HG22	1.95	0.49
2:B:10[A]:DG:O6	3:C:1[A]:DC:N4	2.37	0.48
2:B:9[A]:DA:H2''	2:B:10[A]:DG:H8	1.75	0.48
1:A:379:ARG:NH2	1:A:393:SER:O	2.45	0.47
3:C:7[A]:DT:H2''	3:C:8[A]:DG:H8	1.76	0.47
1:X:363:ILE:HG12	1:X:363:ILE:O	2.07	0.47
3:C:6[B]:DG:H2''	3:C:7[B]:DT:H5''	1.96	0.47
1:A:450:VAL:HG23	1:A:451:THR:OG1	2.15	0.47
1:A:450:VAL:O	1:A:451:THR:C	2.53	0.47
1:X:373:GLY:HA2	1:X:522:LEU:HD21	1.95	0.46
1:X:392:GLN:HG2	3:C:6[A]:DG:O4'	2.15	0.46
1:A:445:LYS:C	1:A:446:ASP:O	2.54	0.46
1:X:450:VAL:O	1:X:451:THR:C	2.54	0.46
1:A:393:SER:HA	2:B:4[A]:DA:O3'	2.17	0.45
1:A:392:GLN:HG2	2:B:6[A]:DG:O4'	2.16	0.45
1:A:394:GLY:N	2:B:5[A]:5CM:OP1	2.48	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:X:395:ILE:HD13	1:X:456:LEU:HD22	1.98	0.45
2:B:3[B]:DC:H2''	2:B:4[B]:DA:C8	2.52	0.45
1:X:420:LEU:HD23	1:X:470:ARG:HD2	2.00	0.44
1:A:420:LEU:HD23	1:A:470:ARG:HD2	1.99	0.44
1:A:363:ILE:HG12	1:A:363:ILE:O	2.11	0.44
1:X:516:ILE:HA	1:X:517:PRO:HD3	1.83	0.44
1:A:443:PRO:HA	1:A:444:PRO:HD3	1.59	0.44
2:B:7[A]:DT:O4	3:C:4[A]:DA:N6	2.51	0.43
1:A:381:GLU:O	1:A:385:LEU:HD13	2.18	0.43
1:X:381:GLU:O	1:X:385:LEU:HD13	2.18	0.43
3:C:1[A]:DC:H2''	3:C:2[A]:DT:OP2	2.18	0.43
2:B:8[B]:DC:H2''	2:B:9[B]:DA:C8	2.54	0.43
1:X:445:LYS:C	1:X:446:ASP:O	2.55	0.43
1:X:399:LYS:C	5:X:3:HOH:O	2.57	0.42
2:B:8[A]:DC:H2'	2:B:9[A]:DA:C8	2.55	0.42
1:X:420:LEU:N	1:X:420:LEU:HD12	2.35	0.42
1:A:496:GLU:HG3	1:A:512:LYS:HB3	2.00	0.42
1:A:442:GLU:N	5:A:13:HOH:O	2.53	0.42
1:X:397:TYR:CD2	1:X:405:LEU:HD22	2.55	0.41
1:A:420:LEU:N	1:A:420:LEU:HD12	2.36	0.41
1:A:459:SER:CB	1:A:464:ASN:HD21	2.32	0.41
1:A:405:LEU:HD12	1:A:454:LEU:HD23	2.01	0.41
1:X:522:LEU:HD23	1:X:522:LEU:HA	1.83	0.41
1:X:522:LEU:HD23	1:X:523:PRO:HD2	2.03	0.41
2:B:8[B]:DC:O2	3:C:3[B]:DG:N2	2.40	0.41
1:X:405:LEU:HD12	1:X:454:LEU:HD23	2.03	0.41
1:A:516:ILE:O	1:A:519:GLN:HG3	2.20	0.41
1:A:522:LEU:HA	1:A:523:PRO:HD3	1.76	0.41
1:A:395:ILE:HD13	1:A:456:LEU:HD22	2.03	0.41
1:A:445:LYS:O	1:A:446:ASP:O	2.39	0.41
1:X:516:ILE:O	1:X:519:GLN:HG3	2.20	0.41
1:A:397:TYR:CD2	1:A:405:LEU:HD22	2.56	0.41
1:X:459:SER:CB	1:X:464:ASN:HD21	2.34	0.41
1:X:382:LEU:O	1:X:387:ILE:N	2.53	0.40
1:X:460:ILE:HA	1:X:494:VAL:O	2.22	0.40
3:C:3[A]:DG:H8	3:C:3[A]:DG:OP2	2.05	0.40
1:A:516:ILE:HA	1:A:517:PRO:HD3	1.90	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	137/167 (82%)	124 (90%)	10 (7%)	3 (2%)	10	10
1	X	132/167 (79%)	119 (90%)	12 (9%)	1 (1%)	27	37
All	All	269/334 (80%)	243 (90%)	22 (8%)	4 (2%)	15	18

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	446	ASP
1	A	446	ASP
1	A	451	THR
1	A	450	VAL

### 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	117/144 (81%)	108 (92%)	9 (8%)	18	26
1	X	112/144 (78%)	102 (91%)	10 (9%)	14	19
All	All	229/288 (80%)	210 (92%)	19 (8%)	16	22

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

Mol	Chain	Res	Type
1	X	362	GLN
1	X	363	ILE
1	X	427	ILE
1	X	448	GLN
1	X	450	VAL

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Mol	Chain	Res	Type
1	X	451	THR
1	X	456	LEU
1	X	484	LYS
1	X	496	GLU
1	X	504	HIS
1	A	362	GLN
1	A	363	ILE
1	A	427	ILE
1	A	448	GLN
1	A	451	THR
1	A	456	LEU
1	A	484	LYS
1	A	504	HIS
1	A	522	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	461	ASN
1	X	464	ASN
1	A	431	GLN
1	A	434	ASN
1	A	461	ASN
1	A	464	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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	5CM	B	5[A]	2	19,21,22	7.30	9 (47%)	24,30,33	1.31	1 (4%)
2	5CM	B	5[B]	2	19,21,22	7.29	9 (47%)	24,30,33	1.47	2 (8%)

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	5CM	B	5[A]	2	-	0/5/21/22	0/2/2/2
2	5CM	B	5[B]	2	-	0/5/21/22	0/2/2/2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	5[A]	5CM	P-OP1	16.35	1.65	1.46
2	B	5[B]	5CM	P-OP1	16.12	1.65	1.46
2	B	5[A]	5CM	C2-N1	15.99	1.55	1.38
2	B	5[B]	5CM	C2-N1	15.91	1.55	1.38
2	B	5[B]	5CM	C4-N3	11.66	1.51	1.32
2	B	5[A]	5CM	C4-N3	11.45	1.51	1.32
2	B	5[B]	5CM	C5-C4	10.16	1.57	1.41
2	B	5[A]	5CM	C5-C4	10.12	1.57	1.41
2	B	5[B]	5CM	O2-C2	8.23	1.40	1.23
2	B	5[A]	5CM	C6-N1	8.14	1.54	1.34
2	B	5[B]	5CM	C6-N1	8.13	1.54	1.34
2	B	5[A]	5CM	O2-C2	8.06	1.40	1.23
2	B	5[A]	5CM	C2-N3	7.96	1.56	1.35
2	B	5[B]	5CM	C2-N3	7.95	1.56	1.35
2	B	5[A]	5CM	C6-C5	5.80	1.56	1.40
2	B	5[B]	5CM	C6-C5	5.59	1.55	1.40
2	B	5[B]	5CM	C4-N4	4.73	1.46	1.34
2	B	5[A]	5CM	C4-N4	4.45	1.45	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5[B]	5CM	C2-N3-C4	5.68	120.55	115.41
2	B	5[A]	5CM	C2-N3-C4	4.95	119.90	115.41
2	B	5[B]	5CM	C6-N1-C2	2.84	120.02	118.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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.

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	145/167 (86%)	0.75	13 (8%) 10 10	37, 58, 82, 98	0
1	X	140/167 (83%)	0.75	13 (9%) 9 10	38, 57, 81, 99	0
2	B	10/10 (100%)	0.34	0 100 100	41, 49, 67, 76	0
3	C	10/10 (100%)	0.24	0 100 100	40, 48, 61, 68	0
All	All	305/354 (86%)	0.72	26 (8%) 11 12	37, 57, 82, 99	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	444	PRO	5.5
1	A	364	ILE	5.0
1	X	504	HIS	4.1
1	A	363	ILE	3.6
1	A	434	ASN	3.4
1	X	406	VAL	3.2
1	X	503	SER	3.1
1	X	363	ILE	3.1
1	X	465	PRO	3.0
1	X	522	LEU	3.0
1	A	367	VAL	2.8
1	A	503	SER	2.6
1	X	435	VAL	2.6
1	A	380	MET	2.5
1	X	466	VAL	2.5
1	X	460	ILE	2.5
1	A	416	TYR	2.4
1	X	364	ILE	2.4
1	A	407	ALA	2.3
1	A	435	VAL	2.3
1	A	444	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	X	425	VAL	2.2
1	A	415	GLY	2.2
1	A	426	LEU	2.1
1	X	408	THR	2.0
1	A	472	ILE	2.0

## 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<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	5CM	B	5[B]	20/21	0.19	1.36	41,46,63,67	20
2	5CM	B	5[A]	20/21	0.19	0.65	41,46,63,67	20

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	CL	A	1	1/1	0.17	-0.33	74,74,74,74	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.