Full wwPDB X-ray Structure Validation Report (i)

Feb 4, 2024 – 03:10 AM EST

PDB ID	:	1OMK
Title	:	The Crystal Structure of d(CACG(5IU)G)
Authors	:	Schuerman, G.; Van Hecke, K.; Van Meervelt, L.
Deposited on	:	2003-02-25
Resolution	:	1.30 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 (i) 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 (1)) were used in the production of this report:

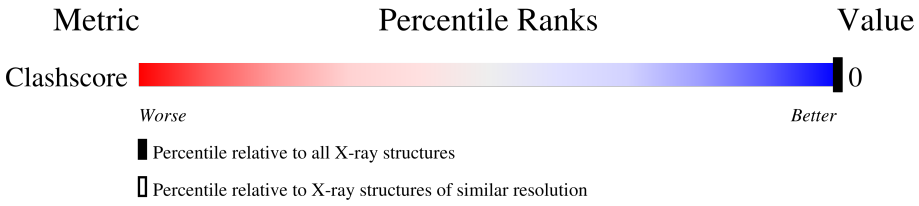
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 1.30 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))
Clashscore	141614	1101 (1.30-1.30)

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%

Mol	Chain	Length	Quality of chain
1	A	6	100%
1	B	6	100%

2 Entry composition (i)

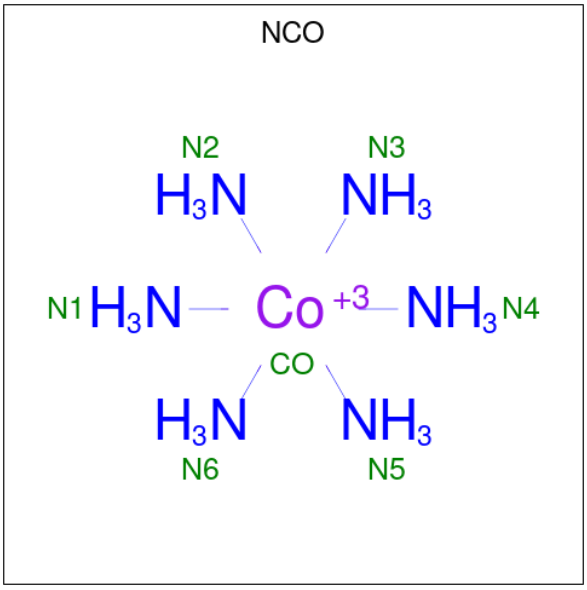
There are 3 unique types of molecules in this entry. The entry contains 297 atoms, of which 0 are hydrogens and 0 are deuteriums.

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*CP*GP*(5IU)P*G)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	6	Total	C	I	N	O	P	0	0	0
			120	57	1	23	34	5			
1	B	6	Total	C	I	N	O	P	0	0	0
			120	57	1	23	34	5			

- Molecule 2 is COBALT HEXAMMINE(III) (three-letter code: NCO) (formula: $CoH_{18}N_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	Co	N		0	0
			7	1	6			
2	A	1	Total	Co	N		0	0
			7	1	6			

- Molecule 3 is water.

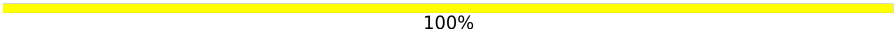
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	23	Total O 23 23	0	0
3	B	20	Total O 20 20	0	0

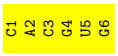
3 Residue-property plots (i)

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. 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. 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*CP*GP*(5IU)P*G)-3'

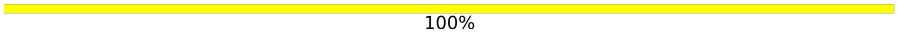
Chain A:

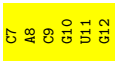




- Molecule 1: 5'-D(*CP*AP*CP*GP*(5IU)P*G)-3'

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	18.16Å 30.03Å 41.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.30 17.21 – 1.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (20.00-1.30) 97.6 (17.21-1.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.61 (at 1.30Å)	Xtriage
Refinement program	SHELXL	Depositor
R, R_{free}	(Not available) , (Not available) 0.161 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	11.3	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 84.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	297	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.91 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.5068e-03.*

[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 (i)

5.1 Standard geometry (i)

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

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	1.55	0/111	2.60	11/167 (6.6%)
1	B	1.81	1/111 (0.9%)	3.06	15/167 (9.0%)
All	All	1.69	1/222 (0.5%)	2.84	26/334 (7.8%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	10	DG	P-O5'	7.30	1.67	1.59

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	8	DA	O4'-C4'-C3'	-9.43	100.34	106.00
1	B	12	DG	C6-N1-C2	-9.39	119.47	125.10
1	B	8	DA	O4'-C1'-N9	-9.00	101.70	108.00
1	A	6	DG	O4'-C1'-N9	-8.13	102.31	108.00
1	B	12	DG	C5-C6-N1	7.30	115.15	111.50
1	A	2	DA	O4'-C1'-N9	-7.24	102.93	108.00
1	B	10	DG	O4'-C1'-N9	-7.21	102.95	108.00
1	B	7	DC	C5-C6-N1	7.13	124.57	121.00
1	B	8	DA	N1-C6-N6	7.06	122.83	118.60
1	B	12	DG	O4'-C1'-N9	-6.92	103.16	108.00
1	B	9	DC	P-O5'-C5'	6.86	131.87	120.90
1	B	10	DG	C2-N3-C4	6.78	115.29	111.90
1	A	3	DC	N1-C2-O2	-6.76	114.84	118.90
1	B	7	DC	O4'-C1'-C2'	-6.75	100.50	105.90
1	B	12	DG	N3-C4-C5	-6.71	125.24	128.60
1	A	3	DC	N3-C2-O2	6.54	126.47	121.90
1	B	10	DG	N3-C2-N2	6.29	124.31	119.90
1	A	4	DG	N7-C8-N9	6.11	116.16	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	4	DG	C2-N3-C4	6.05	114.92	111.90
1	B	12	DG	C5-C6-O6	-5.90	125.06	128.60
1	A	1	DC	C2-N3-C4	5.87	122.84	119.90
1	A	1	DC	N3-C2-O2	5.82	125.97	121.90
1	A	2	DA	N1-C2-N3	-5.65	126.47	129.30
1	A	4	DG	O4'-C1'-N9	-5.34	104.26	108.00
1	A	4	DG	C8-N9-C4	-5.19	104.32	106.40
1	B	12	DG	C2-N3-C4	5.00	114.40	111.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	120	0	66	0	0
1	B	120	0	66	0	0
2	A	14	0	0	0	0
3	A	23	0	0	0	0
3	B	20	0	0	0	0
All	All	297	0	132	0	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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

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	5IU	B	11	1	18,21,22	1.81	4 (22%)	26,30,33	2.18	5 (19%)
1	5IU	A	5	1	18,21,22	1.55	7 (38%)	26,30,33	1.27	5 (19%)

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	5IU	B	11	1	-	0/7/21/22	0/2/2/2
1	5IU	A	5	1	-	0/7/21/22	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	11	5IU	O4-C4	5.39	1.33	1.23
1	A	5	5IU	O4-C4	3.64	1.30	1.23
1	B	11	5IU	C4-N3	-2.40	1.34	1.38
1	A	5	5IU	C2-N3	-2.35	1.33	1.38
1	B	11	5IU	C1'-N1	-2.26	1.42	1.48
1	A	5	5IU	C1'-N1	-2.21	1.42	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	11	5IU	C4-C5	-2.14	1.40	1.45
1	A	5	5IU	C4-N3	-2.11	1.34	1.38
1	A	5	5IU	O3'-C3'	2.10	1.47	1.43
1	A	5	5IU	C2-N1	2.02	1.41	1.38
1	A	5	5IU	C4-C5	-2.00	1.41	1.45

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	11	5IU	C4-N3-C2	-6.51	118.92	127.35
1	B	11	5IU	N3-C2-N1	4.41	120.74	114.89
1	B	11	5IU	C5-C4-N3	4.26	120.96	113.86
1	B	11	5IU	O2-C2-N1	-4.03	117.43	122.79
1	A	5	5IU	C4-N3-C2	-2.99	123.48	127.35
1	A	5	5IU	C5-C4-N3	2.97	118.82	113.86
1	B	11	5IU	O4-C4-C5	-2.62	121.02	125.69
1	A	5	5IU	O2-C2-N1	-2.31	119.72	122.79
1	A	5	5IU	O4-C4-N3	-2.12	116.06	120.12
1	A	5	5IU	O4'-C1'-C2'	-2.05	102.38	106.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	NCO	A	31	-	6,6,6	1.28	0	-		
2	NCO	A	30	-	6,6,6	1.19	1 (16%)	-		

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	30	NCO	CO-N4	2.25	2.04	1.96

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.