Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 09:45 PM EDT

PDB ID	:	2AXI
Title	:	HDM2 in complex with a beta-hairpin
Authors	:	Mittl, P.R.E.; Fasan, R.; Robinson, J.; Gruetter, M.G.
Deposited on	:	2005-09-05
Resolution	:	1.40 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 (i)) were used in the production of this report:

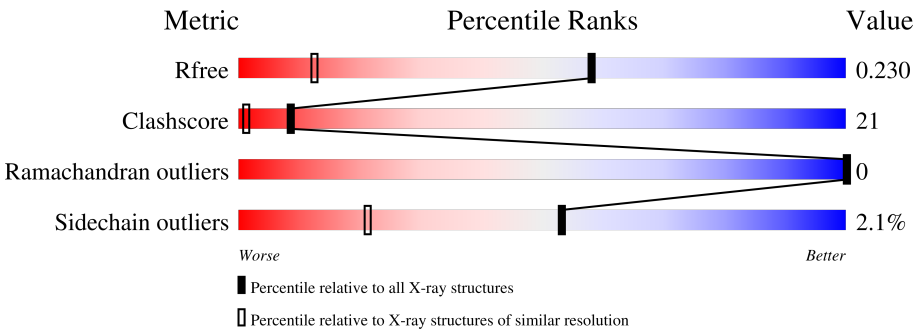
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 1.40 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	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)

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	115	56% 22% • 20%
2	B	10	90% 10%

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
3	SO4	A	302	-	X	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 1029 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 Ubiquitin-protein ligase E3 Mdm2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	92	811	534	131	142	4	0	9	0

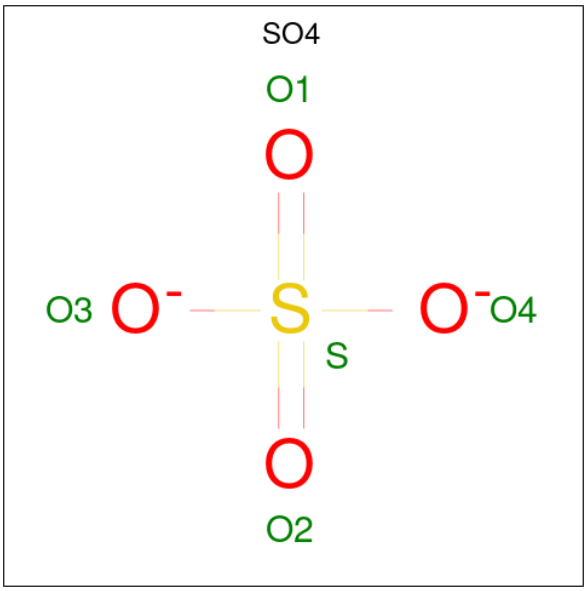
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	126	HIS	-	expression tag	UNP Q9UMT8
A	127	HIS	-	expression tag	UNP Q9UMT8
A	128	HIS	-	expression tag	UNP Q9UMT8
A	129	HIS	-	expression tag	UNP Q9UMT8
A	130	HIS	-	expression tag	UNP Q9UMT8
A	131	HIS	-	expression tag	UNP Q9UMT8

- Molecule 2 is a protein called cyclic 8-mer peptide.

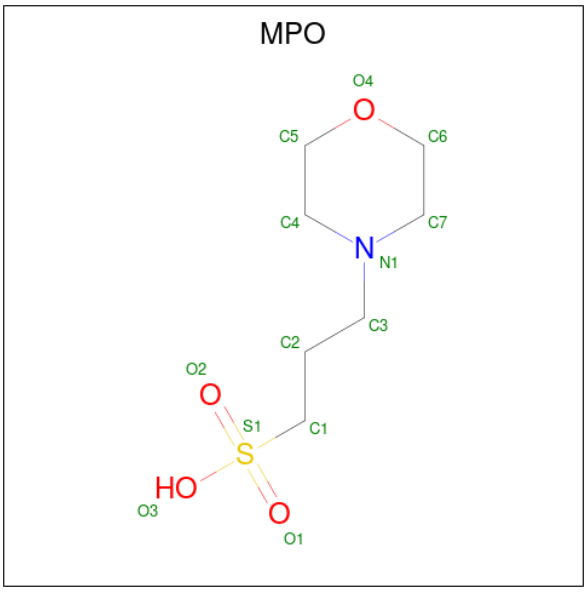
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	Cl	N	O			
2	B	10	99	70	1	12	16	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0

- Molecule 4 is 3[N-MORPHOLINO]PROPANE SULFONIC ACID (three-letter code: MPO) (formula: $C_7H_{15}NO_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O S 13 7 1 4 1	0	0

- Molecule 5 is water.

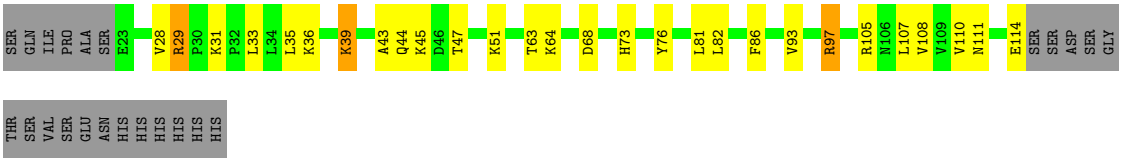
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	85	85	85	0	0
			Total	O		
5	B	11	11	11	0	0

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: Ubiquitin-protein ligase E3 Mdm2

Chain A:



- Molecule 2: cyclic 8-mer peptide

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	45.18Å 77.75Å 61.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.40 19.53 – 1.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.40) 99.7 (19.53-1.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.00 (at 1.40Å)	Xtriage
Refinement program	SHELX, SHELXL	Depositor
R, R_{free}	0.149 , 0.234 0.201 , 0.230	Depositor DCC
R_{free} test set	2230 reflections (10.34%)	wwPDB-VP
Wilson B-factor (Å^2)	18.3	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 63.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.020 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.033 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	1029	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.41% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 6CW, MPO, DPR, SO4

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	0.54	0/863	1.35	8/1163 (0.7%)
2	B	0.50	0/80	1.31	0/106
All	All	0.53	0/943	1.34	8/1269 (0.6%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	97	ARG	NE-CZ-NH2	9.54	125.07	120.30
1	A	97	ARG	NE-CZ-NH1	-7.54	116.53	120.30
1	A	51	LYS	CD-CE-NZ	6.53	126.71	111.70
1	A	29[A]	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	29[B]	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	97	ARG	CD-NE-CZ	-6.37	114.68	123.60
1	A	105	ARG	CD-NE-CZ	-6.30	114.77	123.60
1	A	105	ARG	NE-CZ-NH1	-6.14	117.23	120.30

There are no chirality outliers.

There are no planarity outliers.

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	811	0	843	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	99	0	77	0	0
3	A	10	0	0	6	0
4	A	13	0	14	0	0
5	A	85	0	0	4	0
5	B	11	0	0	0	0
All	All	1029	0	934	39	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 21.

All (39) 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:302:SO4:O2	3:A:302:SO4:S	1.98	1.21
3:A:302:SO4:S	3:A:302:SO4:O4	1.98	1.21
3:A:302:SO4:S	3:A:302:SO4:O1	1.98	1.21
3:A:302:SO4:S	3:A:302:SO4:O3	1.99	1.20
1:A:39[B]:LYS:HE2	1:A:44:GLN:HA	1.52	0.90
1:A:68:ASP:HB2	1:A:76[A]:TYR:HE1	1.40	0.87
1:A:39[B]:LYS:HD2	1:A:43:ALA:O	1.82	0.79
1:A:39[A]:LYS:HD3	1:A:44:GLN:HA	1.68	0.76
1:A:29[B]:ARG:HH22	1:A:110:VAL:HG22	1.51	0.75
1:A:39[A]:LYS:HD2	5:A:345:HOH:O	1.93	0.69
1:A:29[B]:ARG:NH2	1:A:110:VAL:HG22	2.09	0.65
1:A:73:HIS:HB2	1:A:93:VAL:HG22	1.83	0.60
1:A:35[B]:LEU:HG	1:A:39[B]:LYS:HE3	1.86	0.57
1:A:111:ASN:HB2	3:A:302:SO4:O3	2.05	0.56
1:A:82:LEU:HD11	1:A:86[B]:PHE:HE2	1.71	0.54
1:A:39[A]:LYS:HD3	1:A:44:GLN:HG2	1.89	0.54
1:A:28:VAL:HB	1:A:107:LEU:HD13	1.91	0.52
1:A:29[A]:ARG:HB2	1:A:108:VAL:HG22	1.91	0.52
1:A:35[A]:LEU:HD22	1:A:39[A]:LYS:NZ	2.25	0.51
1:A:39[A]:LYS:CD	1:A:44:GLN:HG2	2.41	0.51
1:A:82:LEU:HD11	1:A:86[B]:PHE:CE2	2.46	0.50
1:A:45:LYS:HE3	1:A:47:THR:O	2.11	0.50
1:A:33:LEU:HD11	1:A:81[B]:LEU:HG	1.94	0.49
1:A:64:LYS:HD2	5:A:319:HOH:O	2.13	0.48
1:A:97:ARG:HH11	1:A:97:ARG:HD2	1.43	0.48
1:A:33:LEU:HD11	1:A:81[B]:LEU:CG	2.45	0.46
1:A:29[B]:ARG:NH2	3:A:302:SO4:O4	2.48	0.46
1:A:39[A]:LYS:CD	1:A:44:GLN:HA	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:LYS:NZ	5:A:367:HOH:O	2.49	0.45
1:A:39[B]:LYS:HE2	1:A:44:GLN:CA	2.37	0.44
1:A:36:LYS:HA	1:A:36:LYS:HD3	1.74	0.44
1:A:35[A]:LEU:HD22	1:A:39[A]:LYS:HZ2	1.84	0.43
1:A:35[B]:LEU:HG	1:A:39[B]:LYS:CE	2.47	0.43
1:A:28:VAL:CG1	1:A:107:LEU:HD13	2.49	0.42
1:A:63[A]:THR:HG22	5:A:350:HOH:O	2.20	0.42
1:A:39[A]:LYS:HE2	1:A:39[A]:LYS:HB2	1.50	0.41

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	
1	A	99/115 (86%)	98 (99%)	1 (1%)	0	100	100
2	B	7/10 (70%)	5 (71%)	2 (29%)	0	100	100
All	All	106/125 (85%)	103 (97%)	3 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	96/108 (89%)	93 (97%)	3 (3%)	40	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	8/8 (100%)	8 (100%)	0	100	100
All	All	104/116 (90%)	101 (97%)	3 (3%)	53	11

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39[A]	LYS
1	A	39[B]	LYS
1	A	114	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	96	HIS
1	A	111	ASN

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	$\#\|Z\| > 2$
2	6CW	B	23	2	14,16,17	1.38	3 (21%)	15,22,24	2.13	5 (33%)

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	6CW	B	23	2	-	0/4/6/8	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	23	6CW	CB-CA	-2.83	1.47	1.53
2	B	23	6CW	CH2-CLL	-2.47	1.69	1.74
2	B	23	6CW	CD1-NE1	-2.27	1.32	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	23	6CW	CH2-CZ2-CE2	-5.59	114.78	119.50
2	B	23	6CW	CG-CB-CA	2.80	118.86	114.53
2	B	23	6CW	CB-CA-C	-2.78	106.26	111.47
2	B	23	6CW	CE3-CZ3-CH2	2.56	122.18	119.21
2	B	23	6CW	CB-CG-CD2	2.34	129.88	126.25

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)

3 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	$\#\|Z\| > 2$
3	SO4	A	301	-	4,4,4	0.25	0	6,6,6	0.35	0
4	MPO	A	201	-	13,13,13	1.77	1 (7%)	17,17,17	1.77	4 (23%)
3	SO4	A	302	-	4,4,4	8.09	4 (100%)	6,6,6	0.10	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
4	MPO	A	201	-	-	2/7/15/15	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	SO4	O2-S	9.64	1.98	1.46
3	A	302	SO4	O1-S	9.61	1.98	1.46
3	A	302	SO4	O3-S	6.24	1.99	1.47
3	A	302	SO4	O4-S	6.12	1.98	1.47
4	A	201	MPO	C1-S1	4.90	1.84	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	201	MPO	C2-C1-S1	-4.54	106.29	113.25
4	A	201	MPO	C5-C4-N1	-3.45	104.87	110.10
4	A	201	MPO	O3-S1-C1	2.27	109.43	105.77
4	A	201	MPO	O4-C6-C7	-2.12	107.14	111.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	201	MPO	C2-C3-N1-C4
4	A	201	MPO	C1-C2-C3-N1

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	SO4	6	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)

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

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

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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