wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 12:17 am BST

PDB ID	:	6FPX
Title	:	Structure of S. pombe Mmi1 in complex with 11-mer RNA
Authors	:	Stowell, J.A.W.; Hill, C.H.; Yu, M.; Wagstaff, J.L.; McLaughlin, S.H.; Freund, S.M.V.; Passmore, L.A.
Deposited on	:	2018-02-12
Resolution	:	1.97 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references (1)) were used in the production of this report:

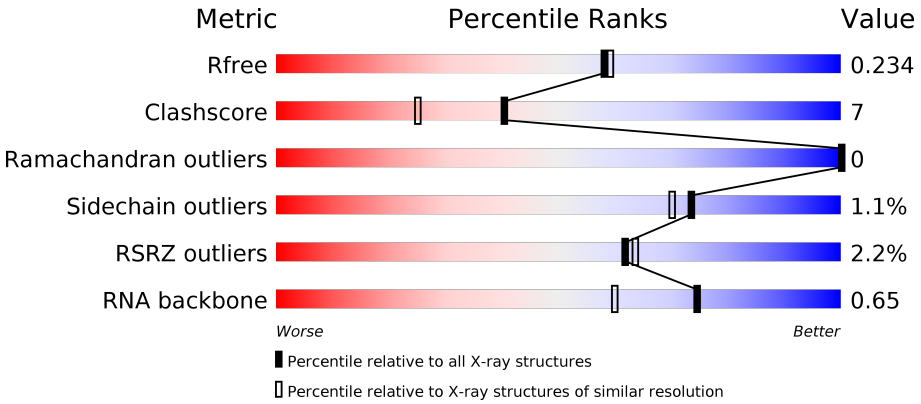
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.97 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.



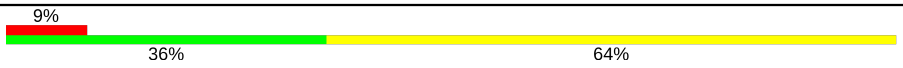
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)
RNA backbone	3102	1105 (2.50-1.46)

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 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	A	192	2% 81% 11% 8%
1	C	192	% 77% 13% • 8%
1	E	192	3% 73% 18% • 9%
2	B	11	27% 64% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	11	
2	F	11	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5013 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 YTH domain-containing protein mmi1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1400	876	251	263	10			
1	C	176	Total	C	N	O	S	0	0	0
			1401	876	253	262	10			
1	E	175	Total	C	N	O	S	0	0	0
			1392	870	252	260	10			

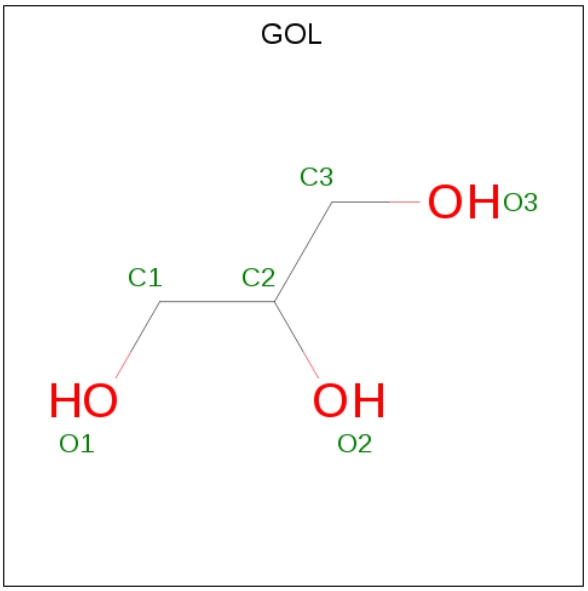
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	GLY	-	expression tag	UNP O74958
A	298	PRO	-	expression tag	UNP O74958
C	297	GLY	-	expression tag	UNP O74958
C	298	PRO	-	expression tag	UNP O74958
E	297	GLY	-	expression tag	UNP O74958
E	298	PRO	-	expression tag	UNP O74958

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*UP*AP*AP*AP*CP*CP*UP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	10	Total	C	N	O	P	0	0	0
			208	94	34	70	10			
2	D	11	Total	C	N	O	P	0	0	0
			205	93	32	70	10			
2	F	9	Total	C	N	O	P	0	0	0
			169	75	27	58	9			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

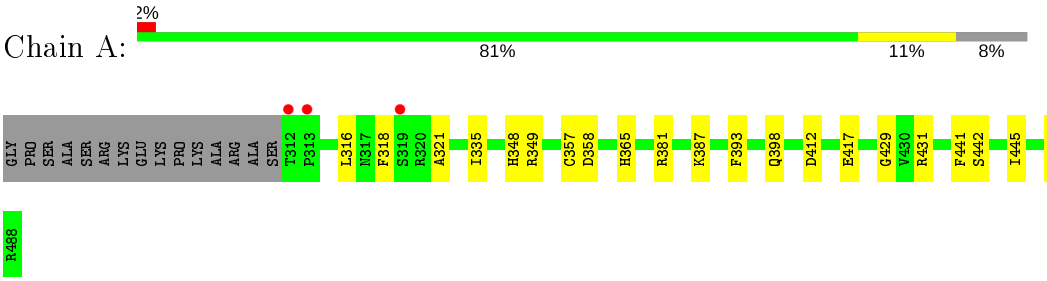
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	95	Total O 95 95	0	0
4	B	8	Total O 8 8	0	0
4	C	66	Total O 66 66	0	0
4	D	1	Total O 1 1	0	0
4	E	47	Total O 47 47	0	0
4	F	3	Total O 3 3	0	0

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 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.

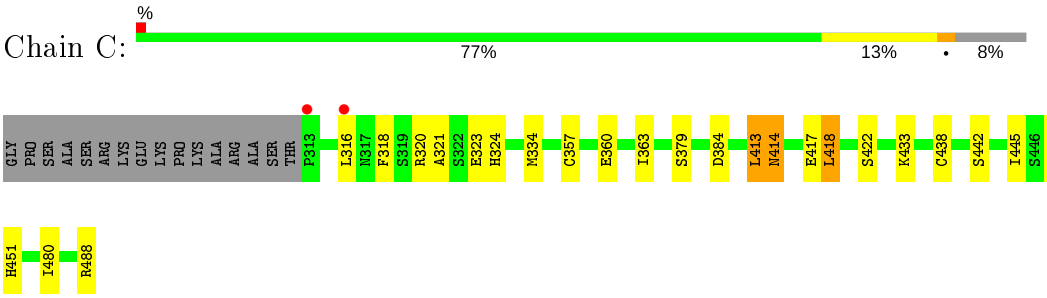
- Molecule 1: YTH domain-containing protein mmi1

Chain A:



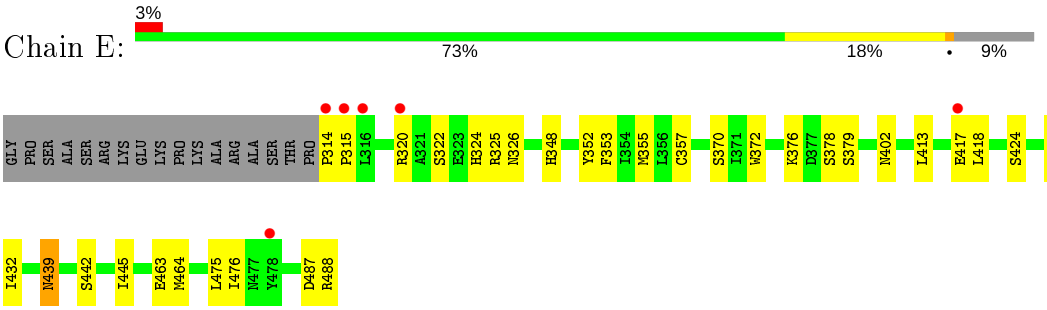
- Molecule 1: YTH domain-containing protein mmi1

Chain C:



- Molecule 1: YTH domain-containing protein mmi1

Chain E:



- Molecule 2: RNA (5'-R(P*UP*UP*UP*AP*AP*AP*CP*CP*UP*A)-3')

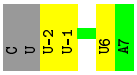
Chain B:

• Molecule 2: RNA (5'-R(P*UP*UP*UP*AP*AP*AP*CP*CP*UP*A)-3')

Chain D:

• Molecule 2: RNA (5'-R(P*UP*UP*UP*AP*AP*AP*CP*CP*UP*A)-3')

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	105.33Å 105.33Å 66.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.61 – 1.97 45.61 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.61-1.97) 99.7 (45.61-1.97)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.47 (at 1.97Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.200 , 0.234 0.200 , 0.234	Depositor DCC
R_{free} test set	1983 reflections (3.38%)	wwPDB-VP
Wilson B-factor (Å^2)	39.3	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 33.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l 0.368 for h,-h-k,-l 0.036 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	5013	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% 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: GOL

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	0.86	3/1429 (0.2%)	0.83	1/1924 (0.1%)
1	C	0.72	0/1430	0.79	1/1923 (0.1%)
1	E	0.66	0/1420	0.80	2/1908 (0.1%)
2	B	1.04	0/231	1.78	9/356 (2.5%)
2	D	0.84	0/227	1.46	5/350 (1.4%)
2	F	0.86	0/187	1.38	3/287 (1.0%)
All	All	0.78	3/4924 (0.1%)	0.96	21/6748 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	450	SER	CA-CB	6.91	1.63	1.52
1	A	441	PHE	CE2-CZ	5.20	1.47	1.37
1	A	393	PHE	CD1-CE1	5.02	1.49	1.39

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	A	N7-C8-N9	-8.35	109.63	113.80
2	B	1	A	C8-N9-C4	7.69	108.88	105.80
1	E	320	ARG	CG-CD-NE	-7.32	96.42	111.80
1	A	381	ARG	NE-CZ-NH2	-6.72	116.94	120.30
2	B	2	A	O5'-P-OP2	-6.55	99.81	105.70

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	1400	0	1368	14	0
1	C	1401	0	1378	28	0
1	E	1392	0	1366	23	0
2	B	208	0	107	0	0
2	D	205	0	104	2	0
2	F	169	0	85	0	0
3	A	6	0	8	1	0
3	C	12	0	16	6	0
4	A	95	0	0	4	2
4	B	8	0	0	0	0
4	C	66	0	0	9	0
4	D	1	0	0	0	0
4	E	47	0	0	6	0
4	F	3	0	0	0	0
All	All	5013	0	4432	66	2

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 7.

The worst 5 of 66 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:A:357:CYS:SG	4:A:693:HOH:O	2.24	0.96
1:C:418:LEU:HD21	1:C:422:SER:OG	1.66	0.95
1:C:360:GLU:O	4:C:601:HOH:O	1.83	0.95
1:E:418:LEU:HD11	1:E:428:GLY:HA2	1.55	0.88
1:C:450:SER:N	4:C:602:HOH:O	2.09	0.85

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:612:HOH:O	4:A:622:HOH:O[2_544]	1.81	0.39
4:A:607:HOH:O	4:A:686:HOH:O[2_544]	1.99	0.21

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	175/192 (91%)	171 (98%)	4 (2%)	0	100	100
1	C	174/192 (91%)	170 (98%)	4 (2%)	0	100	100
1	E	173/192 (90%)	170 (98%)	3 (2%)	0	100	100
All	All	522/576 (91%)	511 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	151/165 (92%)	151 (100%)	0	100	100
1	C	152/165 (92%)	150 (99%)	2 (1%)	69	64
1	E	150/165 (91%)	147 (98%)	3 (2%)	55	48
All	All	453/495 (92%)	448 (99%)	5 (1%)	73	70

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	413	LEU
1	C	414	ASN
1	E	348	HIS
1	E	378	SER
1	E	439	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	398	GLN
1	E	439	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	9/11 (81%)	3 (33%)	0
2	D	9/11 (81%)	1 (11%)	0
2	F	7/11 (63%)	1 (14%)	0
All	All	25/33 (75%)	5 (20%)	0

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	-1	U
2	B	6	U
2	B	7	A
2	D	-1	U
2	F	-1	U

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	GOL	C	501	-	5,5,5	0.61	0	5,5,5	0.72	0
3	GOL	A	501	-	5,5,5	0.46	0	5,5,5	0.59	0
3	GOL	C	502	-	5,5,5	0.56	0	5,5,5	1.17	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
3	GOL	C	501	-	-	2/4/4/4	-
3	GOL	A	501	-	-	2/4/4/4	-
3	GOL	C	502	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	501	GOL	C1-C2-C3-O3
3	A	501	GOL	O1-C1-C2-O2
3	A	501	GOL	O1-C1-C2-C3
3	C	502	GOL	O1-C1-C2-C3
3	C	501	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	501	GOL	3	0
3	A	501	GOL	1	0
3	C	502	GOL	3	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

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	A	177/192 (92%)	-0.15	3 (1%) 70 71	28, 42, 72, 103	0
1	C	176/192 (91%)	-0.30	2 (1%) 80 82	31, 47, 82, 118	0
1	E	175/192 (91%)	0.31	6 (3%) 45 48	51, 64, 92, 131	0
2	B	10/11 (90%)	-0.20	0 100 100	42, 53, 102, 118	0
2	D	11/11 (100%)	-0.14	1 (9%) 9 10	48, 69, 139, 143	0
2	F	9/11 (81%)	-0.29	0 100 100	66, 79, 117, 145	0
All	All	558/609 (91%)	-0.05	12 (2%) 62 63	28, 54, 89, 145	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	314	PRO	6.0
1	A	312	THR	5.2
1	C	313	PRO	3.9
1	A	313	PRO	3.7
1	E	315	PRO	3.6

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

There are no non-standard protein/DNA/RNA residues in this entry.

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. 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
3	GOL	C	501	6/6	0.78	0.37	57,69,69,70	0
3	GOL	A	501	6/6	0.78	0.23	66,68,72,72	0
3	GOL	C	502	6/6	0.88	0.30	45,56,59,65	0

6.5 Other polymers

There are no such residues in this entry.