

wwPDB X-ray Structure Validation Summary Report (i)

Feb 18, 2024 – 09:33 PM EST

PDB ID : 4GQ6

Title: Human menin in complex with MLL peptide

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Deposited on : 2012-08-22

Resolution : 1.55 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 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)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove) oteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

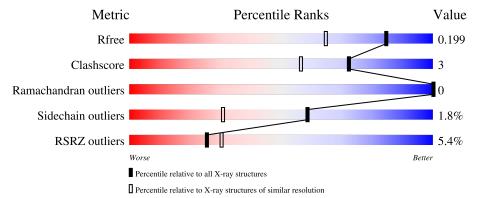
Validation Pipeline (wwPDB-VP) : 2.36

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 1.55 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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% 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	489	86%	9% • •
2	В	12	25% 67%	33%



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4321 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 Menin.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	٨	467	Total	С	N	О	S	0	0	0
1	A	407	3709	2376	633	684	16	U	0	

There are 115 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP O00255
A	-3	GLY	-	expression tag	UNP O00255
A	-2	SER	-	expression tag	UNP O00255
A	-1	SER	-	expression tag	UNP O00255
A	0	SER	-	expression tag	UNP O00255
A	?	-	ILE	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	THR	deletion	UNP O00255
A	?	-	ASN	deletion	UNP O00255
A	?	-	VAL	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	LEU	deletion	UNP O00255
A	?	-	THR	deletion	UNP O00255
A	?	-	PHE	deletion	UNP O00255
A	?	-	GLN	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	SER	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	ASP	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	_	GLU	deletion	UNP O00255

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Chain	Residue	Modelled Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	GLN	deletion	UNP O00255
A	?	-	SER	deletion	UNP O00255
A	?	-	GLN	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	THR	deletion	UNP O00255
A	?	-	GLN	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	TRP	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?		GLY	deletion	UNP O00255
A	?		PRO	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	SER	deletion	UNP O00255
A	?	_	LYS	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255
A	?	-	GLU	deletion	UNP O00255

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	LYS	deletion	UNP O00255
A	?	-	LYS	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	LEU	deletion	UNP O00255
A	?	-	ASP	deletion	UNP O00255
A	?	-	LYS	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	LEU	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	THR	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	GLN	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	VAL	deletion	UNP O00255
A	?	-	SER	deletion	UNP O00255
A	?	-	GLY	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	ARG	deletion	UNP O00255
A	?	-	LYS	deletion	UNP O00255
A	?	-	PRO	deletion	UNP O00255
A	?	-	PRO	deletion	UNP 000255
A	?	-	GLY	deletion	UNP O00255
A	?	-	THR	deletion	UNP O00255
A	?	-	VAL	deletion	UNP 000255
A	?	-	ALA	deletion	UNP 000255
A	?	_	GLY	deletion	UNP 000255
A	?	-	THR	deletion	UNP 000255
A	?	-	ALA	deletion	UNP 000255
A	?	-	ARG	deletion	UNP 000255
A	?	-	GLY	deletion	UNP 000255
A	?	-	PRO	deletion	UNP 000255
A	?	-	GLU	deletion	UNP 000255
A	?	-	GLY	deletion	UNP 000255
A	?	-	GLY	deletion	UNP 000255
A	?	-	SER	deletion	UNP O00255

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	THR	deletion	UNP O00255
A	?	-	ALA	deletion	UNP O00255
A	?	-	GLN	deletion	UNP O00255
A	541	ALA	THR	engineered mutation	UNP O00255

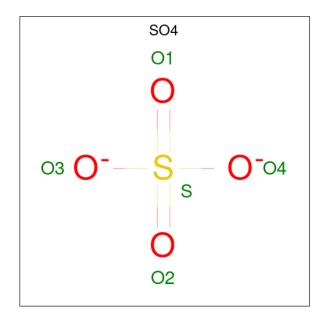
• Molecule 2 is a protein called Histone-lysine N-methyltransferase MLL.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	12	Total 99	C 63	N 22	O 14	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	4	SER	-	expression tag	UNP Q03164
В	5	ALA	-	expression tag	UNP Q03164

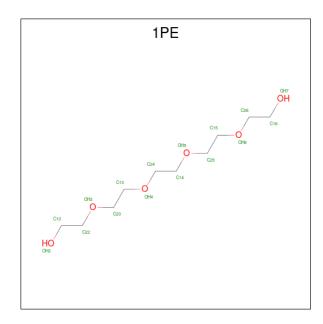
• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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
3	A	1	Total O S 5 4 1	0	0



 \bullet Molecule 4 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $\mathrm{C_{10}H_{22}O_6}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 11 7 4	0	0
4	A	1	Total C O 8 5 3	0	0

• Molecule 5 is water.

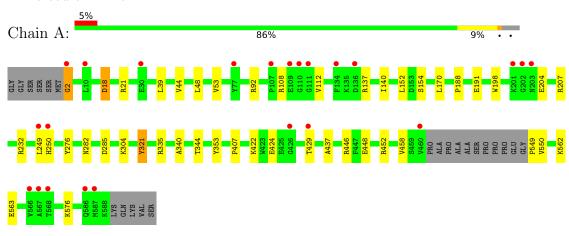
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	469	Total O 469 469	0	0
5	В	10	Total O 10 10	0	0



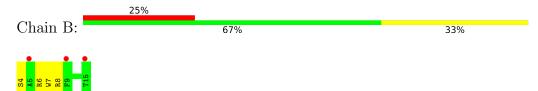
3 Residue-property plots (i)

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 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: Menin



• Molecule 2: Histone-lysine N-methyltransferase MLL





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	48.60Å 80.06Å 124.55Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 - 1.55	Depositor
rtesolution (A)	34.56 - 1.55	EDS
% Data completeness	98.6 (50.00-1.55)	Depositor
(in resolution range)	98.2 (34.56-1.55)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	1.51 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
P. P.	0.160 , 0.189	Depositor
R, R_{free}	0.172 , 0.199	DCC
R_{free} test set	3568 reflections (5.05%)	wwPDB-VP
Wilson B-factor (\mathring{A}^2)	16.5	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 49.7	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4321	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.29% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: SO4, 1PE

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 Chai	Chain		nd lengths	Bo	ond angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	1.04	6/3814 (0.2%)	1.03	12/5173~(0.2%)
2	В	1.15	1/103 (1.0%)	1.08	0/139
All	All	1.04	7/3917 (0.2%)	1.03	$12/5312 \ (0.2\%)$

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
1	A	53	VAL	C-N	7.95	1.47	1.33
1	A	424	GLU	CD-OE1	5.43	1.31	1.25
1	A	2	GLY	N-CA	5.35	1.54	1.46
2	В	7	TRP	CD2-CE2	5.34	1.47	1.41
1	A	448	GLU	CG-CD	5.27	1.59	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^{o})$
1	A	232	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	A	207	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	A	18	ASP	CB-CG-OD2	-5.59	113.27	118.30
1	A	446	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	335	ARG	NE-CZ-NH1	5.53	123.07	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	3709	0	3688	26	0
2	В	99	0	96	1	0
3	A	15	0	0	1	0
4	A	19	0	22	0	0
5	A	469	0	0	4	0
5	В	10	0	0	0	0
All	All	4321	0	3806	26	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 3.

The worst 5 of 26 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:137[B]:ARG:HH11	1:A:137[B]:ARG:HG3	0.85	0.98
1:A:137[B]:ARG:HH11	1:A:137[B]:ARG:CG	1.77	0.97
1:A:137[B]:ARG:HG3	1:A:137[B]:ARG:NH1	1.63	0.96
1:A:321:TYR:HB2	1:A:344:THR:HG22	1.72	0.69
1:A:137[B]:ARG:CG	1:A:137[B]:ARG:NH1	2.44	0.67

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	Perce	ntiles
1	A	471/489 (96%)	462 (98%)	9 (2%)	0	100	100
2	В	10/12 (83%)	10 (100%)	0	0	100	100
All	All	481/501 (96%)	472 (98%)	9 (2%)	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	Analysed Rotameric Outliers		Percentiles		
1	A	395/410 (96%)	390 (99%)	5 (1%)	69 44		
2	В	9/9 (100%)	7 (78%)	2 (22%)	1 0		
All	All	404/419 (96%)	397 (98%)	7 (2%)	59 32		

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	l Chain Res		Type
1	A	276	TYR
1	A	282	ASN
2	В	8	ARG
2	В	6	ARG
1	A	250	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

5 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	ol Type Chain Res Link			Вс	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	603	-	4,4,4	0.24	0	6,6,6	0.51	0
4	1PE	A	604	-	10,10,15	0.58	0	9,9,14	0.62	0
4	1PE	A	605	-	7,7,15	0.21	0	6,6,14	1.51	1 (16%)
3	SO4	A	602	-	4,4,4	0.40	0	6,6,6	0.92	0
3	SO4	A	601	-	4,4,4	0.54	0	6,6,6	0.41	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	1PE	A	604	_	-	0/8/8/13	-
4	1PE	A	605	-	-	2/5/5/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
4	A	605	1PE	OH3-C23-C13	-2.74	98.04	110.39

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	605	1PE	C13-C23-OH3-C22
4	A	605	1PE	OH4-C13-C23-OH3

There are no ring outliers.



1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	SO4	1	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)

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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	467/489 (95%)	0.03	23 (4%) 29 34	12, 20, 40, 68	0
2	В	12/12 (100%)	1.34	3 (25%) 0 0	18, 32, 51, 52	0
All	All	479/501 (95%)	0.06	26 (5%) 25 30	12, 20, 42, 68	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	GLY	7.1
1	A	250	HIS	5.2
1	A	587	MET	4.2
1	A	586	GLN	3.8
1	A	111	GLY	3.7

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
3	SO4	A	603	5/5	0.90	0.18	32,37,37,37	5
4	1PE	A	605	8/16	0.90	0.09	40,43,46,49	0
3	SO4	A	602	5/5	0.92	0.15	26,30,33,35	5
4	1PE	A	604	11/16	0.93	0.10	32,34,40,40	0
3	SO4	A	601	5/5	0.96	0.12	55,59,60,66	0

6.5 Other polymers (i)

There are no such residues in this entry.

