wwPDB X-ray Structure Validation Summary Report (i)

Aug 23, 2023 – 05:48 AM EDT

PDB ID	:	3D85
Title	:	Crystal structure of IL-23 in complex with neutralizing FAB
Authors	:	Beyer, B.M.; Ingram, R.; Ramanathan, L.; Reichert, P.; Le, H.; Madison, V.
Deposited on	:	2008-05-22
Resolution	:	1.90 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 (i)) were used in the production of this report:

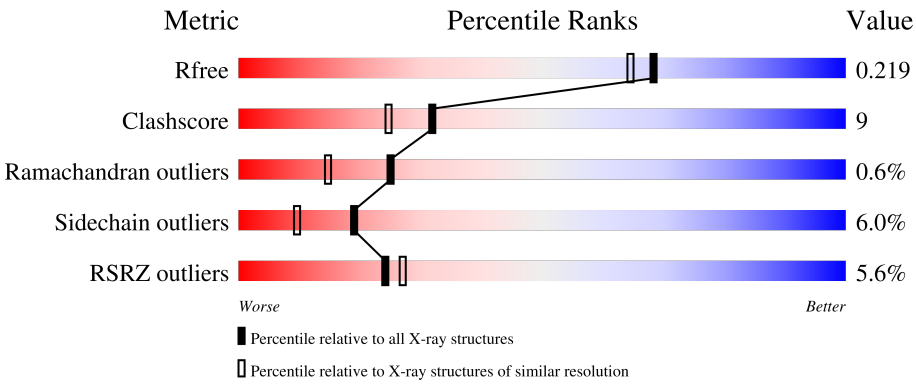
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	214	84% 14% •
2	B	223	3% 84% 11% • •
3	C	178	5% 62% 11% •• 25%
4	D	306	10% 72% 20% • • 5%

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
6	MPD	B	501	X	-	-	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7509 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 FAB of antibody 7G10, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	213	1643	1025	279	334	5	0	1	0

- Molecule 2 is a protein called FAB of antibody 7G10, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	216	1632	1034	266	325	7	0	3	0

- Molecule 3 is a protein called Interleukin-23 subunit p19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	133	1031	662	183	181	5	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	171	GLY	-	expression tag	UNP Q9NPF7
C	172	SER	-	expression tag	UNP Q9NPF7
C	173	HIS	-	expression tag	UNP Q9NPF7
C	174	HIS	-	expression tag	UNP Q9NPF7
C	175	HIS	-	expression tag	UNP Q9NPF7
C	176	HIS	-	expression tag	UNP Q9NPF7
C	177	HIS	-	expression tag	UNP Q9NPF7
C	178	HIS	-	expression tag	UNP Q9NPF7

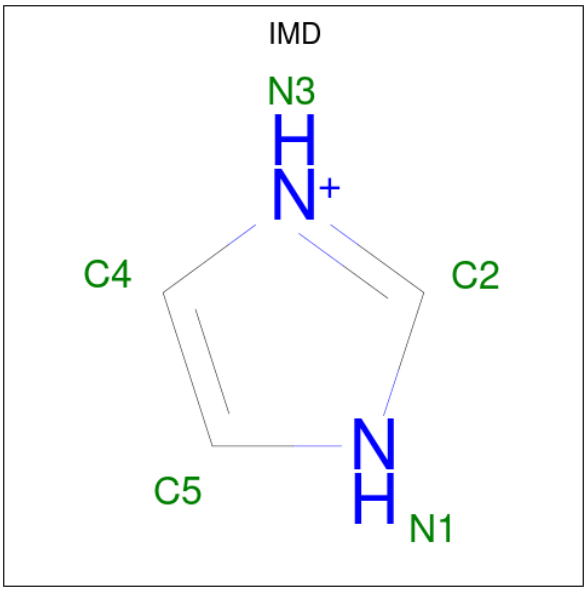
- Molecule 4 is a protein called Interleukin-12 subunit p40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	290	2276	1445	364	455	12	0	0	0

There is a discrepancy between the modelled and reference sequences:

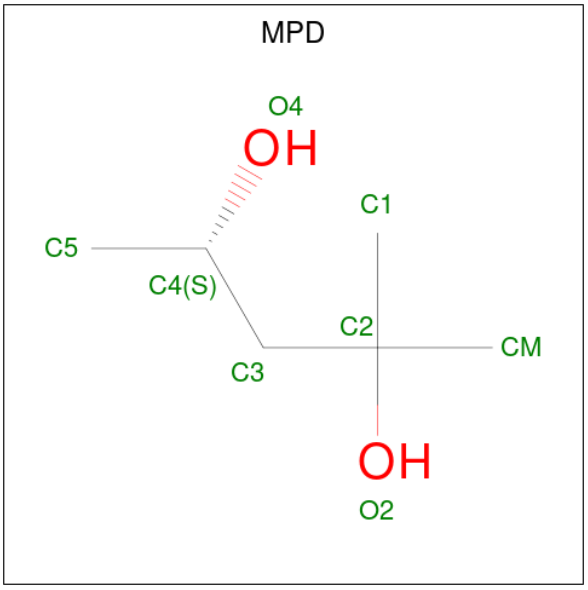
Chain	Residue	Modelled	Actual	Comment	Reference
D	200	GLN	ASN	engineered mutation	UNP P29460

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	N		
5	A	1	5	3	2	0	0

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	8	6	2	0	0
			Total	C	O		
6	B	1	8	6	2	0	0

- Molecule 7 is water.

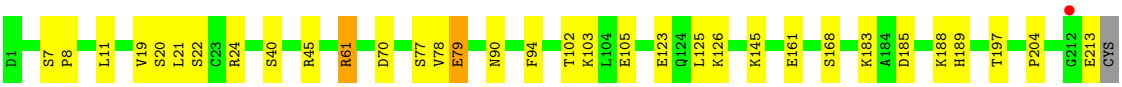
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	256	256	256	0	0
			Total	O		
7	B	281	281	281	0	0
			Total	O		
7	C	101	101	101	0	0
			Total	O		
7	D	268	268	268	0	0

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.

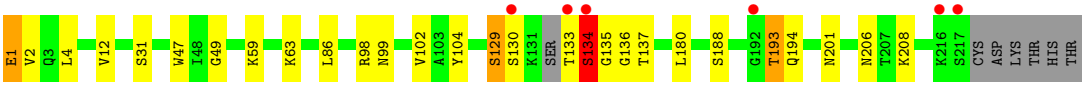
- Molecule 1: FAB of antibody 7G10, light chain

Chain A:



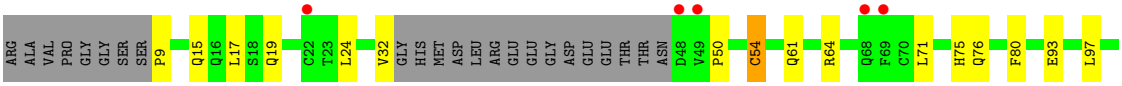
- Molecule 2: FAB of antibody 7G10, heavy chain

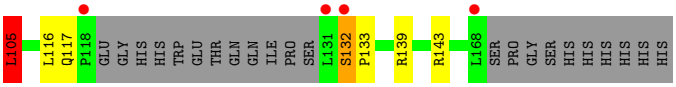
Chain B:



- Molecule 3: Interleukin-23 subunit p19

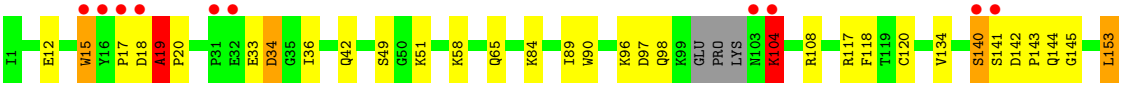
Chain C:

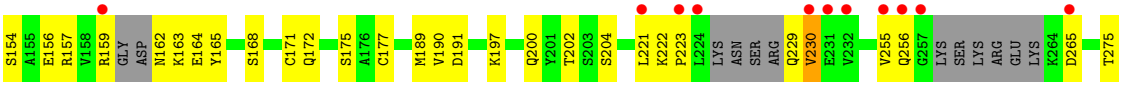


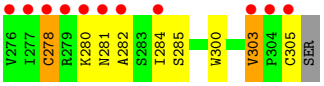


- Molecule 4: Interleukin-12 subunit p40

Chain D:






V276
I277
C278
R279
K280
N281
A282
S283
I284
S285
W300
V303
P304
C305
SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	75.39Å 62.09Å 107.26Å 90.00° 97.44° 90.00°	Depositor
Resolution (Å)	106.60 – 1.90 34.16 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.0 (106.60-1.90) 99.3 (34.16-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.67 (at 1.91Å)	Xtriage
Refinement program	BUSTER-TNT 2.1.1	Depositor
R, R_{free}	0.171 , 0.214 0.171 , 0.219	Depositor DCC
R_{free} test set	1541 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	28.2	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 63.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7509	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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: MPD, IMD

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	0.70	0/1685	0.79	0/2285
2	B	0.79	0/1683	0.84	0/2290
3	C	0.55	0/1056	0.68	1/1435 (0.1%)
4	D	0.54	0/2330	0.73	2/3169 (0.1%)
All	All	0.65	0/6754	0.76	3/9179 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	19	ALA	C-N-CD	-8.73	101.39	120.60
4	D	19	ALA	C-N-CA	5.89	146.73	122.00
3	C	105	LEU	CA-CB-CG	5.21	127.28	115.30

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	1643	0	1587	24	0
2	B	1632	0	1606	28	0
3	C	1031	0	1036	18	0
4	D	2276	0	2148	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	5	0	5	0	0
6	A	8	0	14	1	0
6	B	8	0	14	3	0
7	A	256	0	0	4	0
7	B	281	0	0	3	0
7	C	101	0	0	6	0
7	D	268	0	0	5	0
All	All	7509	0	6410	116	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 9.

The worst 5 of 116 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)
4:D:104:LYS:HE3	4:D:104:LYS:H	1.13	1.07
4:D:189:MET:HE3	4:D:200:GLN:HG3	1.38	1.05
1:A:61:ARG:HH21	1:A:61:ARG:HG3	1.32	0.95
2:B:31:SER:HA	6:B:501:MPD:H52	1.49	0.94
2:B:134:SER:HB3	2:B:135:GLY:C	1.91	0.92

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	212/214 (99%)	206 (97%)	6 (3%)	0	100 100
2	B	215/223 (96%)	208 (97%)	6 (3%)	1 (0%)	29 18
3	C	127/178 (71%)	125 (98%)	2 (2%)	0	100 100
4	D	280/306 (92%)	265 (95%)	11 (4%)	4 (1%)	11 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	834/921 (91%)	804 (96%)	25 (3%)	5 (1%)	25 15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	134	SER
4	D	19	ALA
4	D	104	LYS
4	D	18	ASP
4	D	17	PRO

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	191/191 (100%)	180 (94%)	11 (6%)	20 10
2	B	186/191 (97%)	179 (96%)	7 (4%)	33 24
3	C	113/151 (75%)	108 (96%)	5 (4%)	28 19
4	D	253/277 (91%)	232 (92%)	21 (8%)	11 4
All	All	743/810 (92%)	699 (94%)	44 (6%)	19 10

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	96	LYS
4	D	175	SER
4	D	104	LYS
4	D	144	GLN
4	D	229	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	76	GLN
4	D	98	GLN
4	D	229	GLN
4	D	200	GLN
3	C	72	GLN

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)

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	$\#\|Z\| > 2$
6	MPD	A	502	-	7,7,7	1.07	0	9,10,10	1.02	0
5	IMD	A	503	-	3,5,5	0.14	0	4,5,5	0.55	0
6	MPD	B	501	-	7,7,7	0.59	0	9,10,10	1.43	1 (11%)

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
6	MPD	B	501	-	1/1/2/2	1/5/5/5	-
5	IMD	A	503	-	-	-	0/1/1/1
6	MPD	A	502	-	-	0/5/5/5	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	501	MPD	CM-C2-C1	2.42	115.61	110.57

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	B	501	MPD	C4

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	501	MPD	C2-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	502	MPD	1	0
6	B	501	MPD	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 (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, 95th 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	213/214 (99%)	-0.22	1 (0%) 91 92	19, 30, 49, 77	0
2	B	216/223 (96%)	-0.22	6 (2%) 53 56	16, 25, 50, 91	0
3	C	133/178 (74%)	0.12	9 (6%) 17 19	22, 36, 68, 80	0
4	D	290/306 (94%)	0.16	32 (11%) 5 6	25, 40, 77, 101	0
All	All	852/921 (92%)	-0.04	48 (5%) 24 27	16, 33, 67, 101	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	17	PRO	6.2
4	D	278	CYS	6.1
3	C	131	LEU	4.8
4	D	224	LEU	4.7
2	B	134	SER	4.6

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, 95th 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
5	IMD	A	503	5/5	0.69	0.15	77,78,78,79	0
6	MPD	B	501	8/8	0.92	0.11	43,45,47,49	0
6	MPD	A	502	8/8	0.95	0.09	37,37,40,42	0

6.5 Other polymers (i)

There are no such residues in this entry.