



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 29, 2024 – 02:31 pm BST

PDB ID : 4ABN  
Title : Crystal structure of full length mouse Strap (TTC5)  
Authors : Pike, A.C.W.; Bullock, A.N.; Kleinekofort, W.; Zimmermann, T.; Burgess-Brown, N.; Sharpe, T.D.; Thangaratnarajah, C.; Keates, T.; Ugochukwu, E.; Bunkoczi, G.; Uppenberg, J.; von Delft, F.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Bountra, C.; La Thangue, N.B.; Knapp, S.  
Deposited on : 2011-12-09  
Resolution : 2.05 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](mailto: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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36.2  
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) : 2.36.2

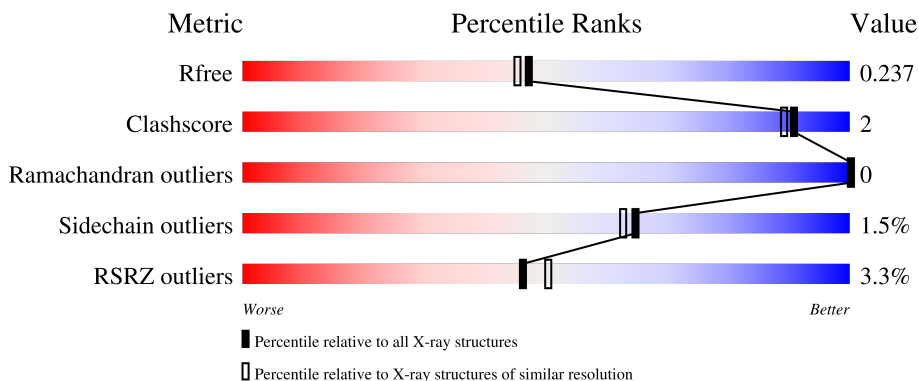
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


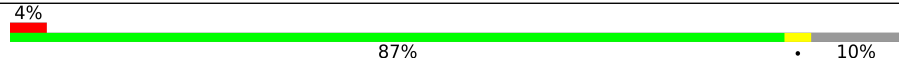
The reported resolution of this entry is 2.05 Å.

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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	474	 2% 84% 5% 11%
1	B	474	 4% 87% 10%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 6910 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 TETRATRICOPEPTIDE REPEAT PROTEIN 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	422	Total 3256	C 2058	N 558	O 625	S 15	0	4	0
1	B	426	Total 3262	C 2057	N 551	O 639	S 15	0	4	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	expression tag	UNP Q99LG4
A	-32	GLY	-	expression tag	UNP Q99LG4
A	-31	SER	-	expression tag	UNP Q99LG4
A	-30	SER	-	expression tag	UNP Q99LG4
A	-29	HIS	-	expression tag	UNP Q99LG4
A	-28	HIS	-	expression tag	UNP Q99LG4
A	-27	HIS	-	expression tag	UNP Q99LG4
A	-26	HIS	-	expression tag	UNP Q99LG4
A	-25	HIS	-	expression tag	UNP Q99LG4
A	-24	HIS	-	expression tag	UNP Q99LG4
A	-23	SER	-	expression tag	UNP Q99LG4
A	-22	SER	-	expression tag	UNP Q99LG4
A	-21	GLY	-	expression tag	UNP Q99LG4
A	-20	LEU	-	expression tag	UNP Q99LG4
A	-19	VAL	-	expression tag	UNP Q99LG4
A	-18	PRO	-	expression tag	UNP Q99LG4
A	-17	ARG	-	expression tag	UNP Q99LG4
A	-16	GLY	-	expression tag	UNP Q99LG4
A	-15	SER	-	expression tag	UNP Q99LG4
A	-14	HIS	-	expression tag	UNP Q99LG4
A	-13	MET	-	expression tag	UNP Q99LG4
A	-12	ALA	-	expression tag	UNP Q99LG4
A	-11	SER	-	expression tag	UNP Q99LG4
A	-10	MET	-	expression tag	UNP Q99LG4
A	-9	THR	-	expression tag	UNP Q99LG4

*Continued on next page...*

*Continued from previous page...*

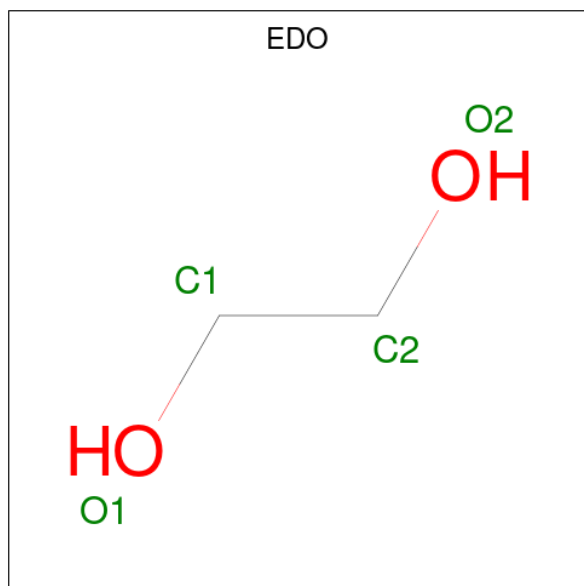
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	GLY	-	expression tag	UNP Q99LG4
A	-7	GLY	-	expression tag	UNP Q99LG4
A	-6	GLN	-	expression tag	UNP Q99LG4
A	-5	GLN	-	expression tag	UNP Q99LG4
A	-4	MET	-	expression tag	UNP Q99LG4
A	-3	GLY	-	expression tag	UNP Q99LG4
A	-2	ARG	-	expression tag	UNP Q99LG4
A	-1	GLY	-	expression tag	UNP Q99LG4
A	0	SER	-	expression tag	UNP Q99LG4
A	120	THR	ALA	SEE REMARK 999	UNP Q99LG4
A	256	ALA	VAL	SEE REMARK 999	UNP Q99LG4
B	-33	MET	-	expression tag	UNP Q99LG4
B	-32	GLY	-	expression tag	UNP Q99LG4
B	-31	SER	-	expression tag	UNP Q99LG4
B	-30	SER	-	expression tag	UNP Q99LG4
B	-29	HIS	-	expression tag	UNP Q99LG4
B	-28	HIS	-	expression tag	UNP Q99LG4
B	-27	HIS	-	expression tag	UNP Q99LG4
B	-26	HIS	-	expression tag	UNP Q99LG4
B	-25	HIS	-	expression tag	UNP Q99LG4
B	-24	HIS	-	expression tag	UNP Q99LG4
B	-23	SER	-	expression tag	UNP Q99LG4
B	-22	SER	-	expression tag	UNP Q99LG4
B	-21	GLY	-	expression tag	UNP Q99LG4
B	-20	LEU	-	expression tag	UNP Q99LG4
B	-19	VAL	-	expression tag	UNP Q99LG4
B	-18	PRO	-	expression tag	UNP Q99LG4
B	-17	ARG	-	expression tag	UNP Q99LG4
B	-16	GLY	-	expression tag	UNP Q99LG4
B	-15	SER	-	expression tag	UNP Q99LG4
B	-14	HIS	-	expression tag	UNP Q99LG4
B	-13	MET	-	expression tag	UNP Q99LG4
B	-12	ALA	-	expression tag	UNP Q99LG4
B	-11	SER	-	expression tag	UNP Q99LG4
B	-10	MET	-	expression tag	UNP Q99LG4
B	-9	THR	-	expression tag	UNP Q99LG4
B	-8	GLY	-	expression tag	UNP Q99LG4
B	-7	GLY	-	expression tag	UNP Q99LG4
B	-6	GLN	-	expression tag	UNP Q99LG4
B	-5	GLN	-	expression tag	UNP Q99LG4
B	-4	MET	-	expression tag	UNP Q99LG4
B	-3	GLY	-	expression tag	UNP Q99LG4

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	ARG	-	expression tag	UNP Q99LG4
B	-1	GLY	-	expression tag	UNP Q99LG4
B	0	SER	-	expression tag	UNP Q99LG4
B	120	THR	ALA	SEE REMARK 999	UNP Q99LG4
B	256	ALA	VAL	SEE REMARK 999	UNP Q99LG4

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
3	A	219	Total	O	0	1
			220	220		
3	B	164	Total	O	0	0
			164	164		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.92Å 91.57Å 138.61Å 90.00° 93.06° 90.00°	Depositor
Resolution (Å)	55.00 – 2.05 46.14 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (55.00-2.05) 99.8 (46.14-2.05)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 2.05Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.193 , 0.236 0.194 , 0.237	Depositor DCC
$R_{free}$ test set	3146 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.6	Xtrriage
Anisotropy	0.200	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 45.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6910	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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: EDO

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	0.77	0/3337	0.75	7/4522 (0.2%)
1	B	0.69	0/3344	0.66	0/4536
All	All	0.73	0/6681	0.71	7/9058 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ARG	NE-CZ-NH1	9.57	125.09	120.30
1	A	145[A]	VAL	CG1-CB-CG2	5.97	120.45	110.90
1	A	145[B]	VAL	CG1-CB-CG2	5.97	120.45	110.90
1	A	180	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	38	ASP	CB-CG-OD1	5.24	123.02	118.30
1	A	309[A]	TYR	CA-CB-CG	5.05	122.99	113.40
1	A	309[B]	TYR	CA-CB-CG	5.05	122.99	113.40

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	3256	0	3195	13	0
1	B	3262	0	3138	9	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	8	0	12	0	0
3	A	220	0	0	2	0
3	B	164	0	0	4	0
All	All	6910	0	6345	22	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 2.

All (22) 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:144[A]:MET:HG2	3:A:2131:HOH:O	1.95	0.67
1:B:322:LYS:O	1:B:337:VAL:HG12	2.08	0.52
1:A:235:LYS:NZ	1:A:349:GLU:OE2	2.42	0.52
1:A:101:GLU:H	1:A:101:GLU:CD	2.14	0.51
1:A:228:LEU:O	1:A:232:THR:HG23	2.10	0.51
1:A:329:PRO:O	3:A:2196:HOH:O	2.19	0.51
1:B:228:LEU:O	1:B:232:THR:HG23	2.11	0.51
1:A:226:LEU:C	1:A:226:LEU:HD23	2.32	0.50
1:A:68:ALA:CB	1:A:99:GLU:HG3	2.43	0.47
1:B:144[A]:MET:HG2	3:B:2103:HOH:O	2.15	0.46
1:A:126:PHE:CE2	1:A:141:ASN:HB3	2.52	0.45
1:A:385:ALA:HB3	1:A:417:VAL:HB	1.99	0.44
1:B:162:MET:HE2	3:B:2030:HOH:O	2.17	0.43
1:A:372:VAL:HG12	1:A:413:PRO:HD3	2.00	0.42
1:A:126:PHE:CZ	1:A:141:ASN:HB3	2.54	0.42
1:B:126:PHE:CE2	1:B:141:ASN:HB3	2.55	0.42
1:B:419:ASN:N	3:B:2147:HOH:O	2.53	0.41
1:B:273:ARG:NE	3:B:2143:HOH:O	2.48	0.41
1:B:292:MET:HB3	1:B:340:LYS:HG2	2.02	0.41
1:B:126:PHE:CZ	1:B:141:ASN:HB3	2.56	0.41
1:A:27:ARG:HD3	1:A:80:VAL:HG22	2.03	0.40

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	419/474 (88%)	415 (99%)	4 (1%)	0	100	100
1	B	426/474 (90%)	424 (100%)	2 (0%)	0	100	100
All	All	845/948 (89%)	839 (99%)	6 (1%)	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	351/405 (87%)	346 (99%)	5 (1%)	67	65
1	B	345/405 (85%)	340 (99%)	5 (1%)	67	65
All	All	696/810 (86%)	686 (99%)	10 (1%)	65	65

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	101	GLU
1	A	159	ARG
1	A	228	LEU
1	A	412	THR
1	B	69	GLN
1	B	228	LEU
1	B	340	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	412	THR
1	B	426	SER

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](#)

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	EDO	A	1433	-	3,3,3	0.68	0	2,2,2	0.30	0
2	EDO	A	1434	-	3,3,3	0.62	0	2,2,2	0.15	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
2	EDO	A	1433	-	-	0/1/1/1	-
2	EDO	A	1434	-	-	0/1/1/1	-

There are no bond length outliers.

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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	422/474 (89%)	0.03	8 (1%) 66 71	19, 39, 77, 110	0
1	B	426/474 (89%)	0.19	20 (4%) 31 33	23, 47, 89, 143	0
All	All	848/948 (89%)	0.11	28 (3%) 46 50	19, 44, 84, 143	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	422	PRO	4.7
1	A	312	ALA	4.5
1	B	324	LEU	4.2
1	B	425	SER	3.9
1	A	4	ASP	3.9
1	B	427	SER	3.6
1	B	309	TYR	3.4
1	B	321	LEU	3.1
1	B	413	PRO	3.1
1	B	327	LEU	3.0
1	B	2	MET	2.9
1	A	289	LEU	2.9
1	A	309[A]	TYR	2.8
1	B	305	GLY	2.6
1	A	297	ARG	2.6
1	A	431	ALA	2.5
1	B	418	VAL	2.5
1	B	336	VAL	2.5
1	B	292	MET	2.3
1	A	298	PRO	2.3
1	B	361	ASP	2.2
1	A	152	ASP	2.2
1	B	296	LEU	2.2
1	B	414	LEU	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	303	PRO	2.1
1	B	301	LEU	2.1
1	B	310	GLN	2.1
1	B	300	HIS	2.1

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	EDO	A	1434	4/4	0.82	0.13	56,56,58,61	0
2	EDO	A	1433	4/4	0.91	0.10	43,44,48,48	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.