



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2023 – 04:54 PM EDT

PDB ID : 7U1B
Title : Crystal structure of EstG in complex with tantalum cluster
Authors : Chen, Z.; Gabelli, S.B.
Deposited on : 2022-02-20
Resolution : 2.62 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 ⓘ 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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

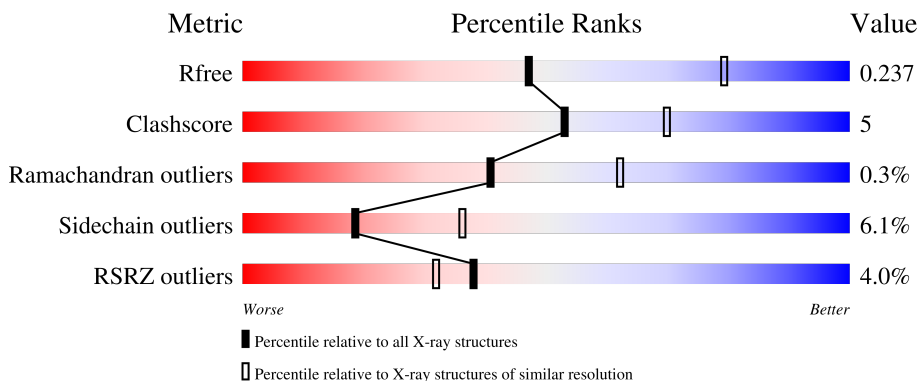
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 $\leq 5\%$. 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	469	

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 3084 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.

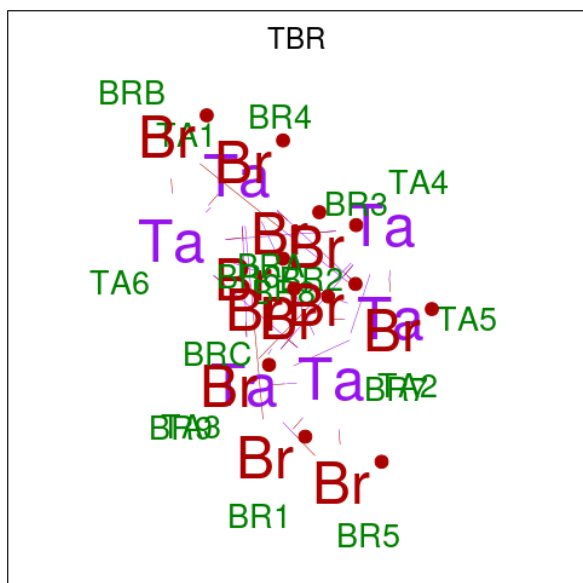
- Molecule 1 is a protein called Beta-lactamase domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	403	3032	1923	529	562	18	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

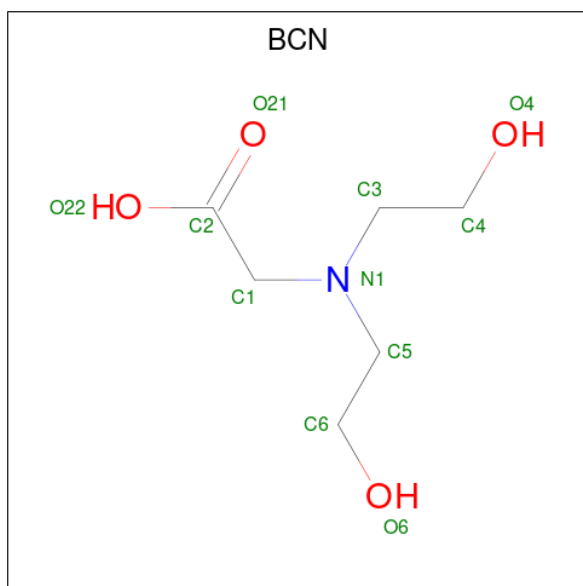
Chain	Residue	Modelled	Actual	Comment	Reference
A	463	LYS	-	expression tag	UNP Q9A800
A	464	LEU	-	expression tag	UNP Q9A800
A	465	ALA	-	expression tag	UNP Q9A800
A	466	ALA	-	expression tag	UNP Q9A800
A	467	ALA	-	expression tag	UNP Q9A800
A	468	LEU	-	expression tag	UNP Q9A800
A	469	GLU	-	expression tag	UNP Q9A800

- Molecule 2 is HEXATANTALUM DODECABROMIDE (three-letter code: TBR) (formula: $\text{Br}_{12}\text{Ta}_6$).



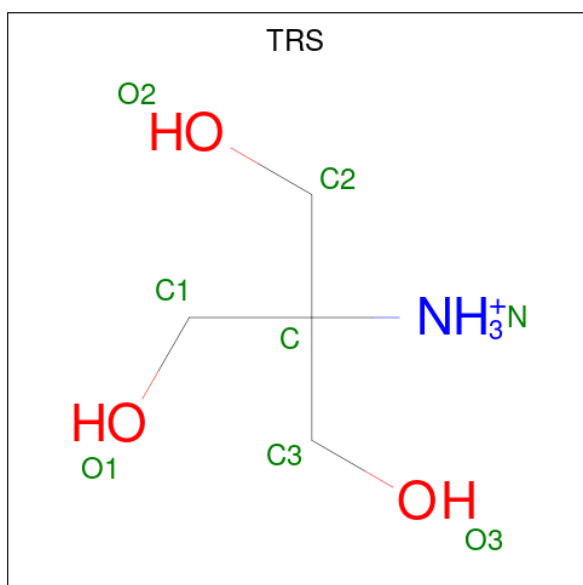
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Br	Ta		
2	A	1	18	12	6	0	0

- Molecule 3 is BICINE (three-letter code: BCN) (formula: $C_6H_{13}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	11	6	1	4	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	8	4	1	3	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

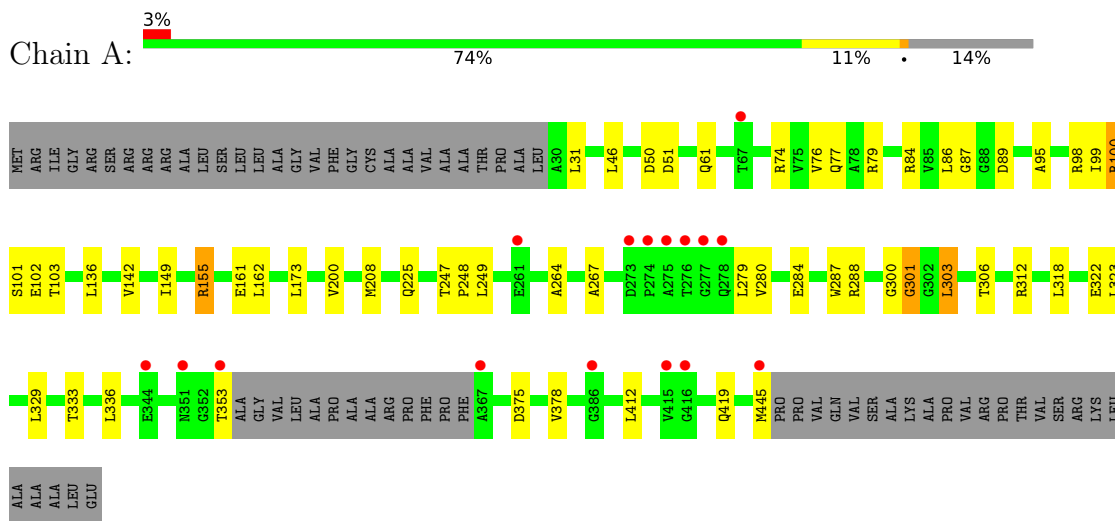
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	10	10	10	0	0

3 Residue-property plots

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: Beta-lactamase domain-containing protein



4 Data and refinement statistics i

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	111.77Å 111.77Å 57.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.96 – 2.62 27.94 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.5 (27.96-2.62) 99.6 (27.94-2.62)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 2.64Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.190 , 0.234 0.203 , 0.237	Depositor DCC
R_{free} test set	1150 reflections (5.38%)	wwPDB-VP
Wilson B-factor (Å ²)	50.0	Xtrriage
Anisotropy	0.053	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3084	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: BCN, TBR, SO4, TRS

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	0/3103	0.90	0/4216

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	87	GLY	Peptide

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	3032	0	3016	33	0
2	A	18	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	11	0	12	0	0
4	A	8	0	12	0	0
5	A	5	0	0	0	0
6	A	10	0	0	0	0
All	All	3084	0	3040	33	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 5.

All (33) 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:51:ASP:OD1	2:A:601:TBR:BR2	2.38	0.97
1:A:103:THR:HG23	1:A:303:LEU:HD22	1.61	0.81
1:A:136:LEU:HB3	1:A:208:MET:CE	2.11	0.80
1:A:136:LEU:HB3	1:A:208:MET:HE2	1.75	0.68
1:A:136:LEU:HB3	1:A:208:MET:HE1	1.76	0.67
1:A:98:ARG:H	1:A:419:GLN:HE22	1.41	0.66
1:A:51:ASP:OD1	2:A:601:TBR:BR1	2.77	0.57
1:A:412:LEU:HD12	1:A:412:LEU:C	2.25	0.57
1:A:98:ARG:H	1:A:419:GLN:NE2	2.03	0.56
1:A:101:SER:HA	1:A:300:GLY:O	2.09	0.52
1:A:173:LEU:HD21	1:A:287:TRP:CZ2	2.47	0.50
1:A:225:GLN:NE2	1:A:375:ASP:OD2	2.37	0.50
1:A:98:ARG:HB2	1:A:419:GLN:HE22	1.79	0.47
1:A:61:GLN:NE2	1:A:61:GLN:HA	2.30	0.46
1:A:50:ASP:OD1	1:A:79:ARG:HG3	2.15	0.46
1:A:84:ARG:NE	1:A:264:ALA:O	2.50	0.45
1:A:318:LEU:HD23	1:A:318:LEU:HA	1.88	0.45
1:A:100:ARG:NH1	1:A:288:ARG:HD3	2.32	0.44
1:A:155:ARG:NH2	1:A:161:GLU:OE1	2.50	0.44
1:A:247:THR:HB	1:A:248:PRO:HD3	1.98	0.44
1:A:99:ILE:HB	1:A:102:GLU:HB3	2.00	0.44
1:A:98:ARG:NH1	1:A:267:ALA:O	2.51	0.43
1:A:46:LEU:HD23	1:A:46:LEU:HA	1.87	0.43
1:A:249:LEU:O	1:A:312:ARG:NH1	2.45	0.43
1:A:95:ALA:O	1:A:306:THR:HG22	2.18	0.43
1:A:50:ASP:OD1	1:A:79:ARG:NH1	2.52	0.42
1:A:329:LEU:HD22	1:A:333:THR:HG21	2.01	0.42
1:A:61:GLN:NE2	1:A:61:GLN:CA	2.83	0.42
1:A:173:LEU:HD21	1:A:287:TRP:HZ2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ARG:NH2	1:A:284:GLU:OE2	2.46	0.41
1:A:100:ARG:O	1:A:301:GLY:HA2	2.21	0.40
1:A:51:ASP:HA	2:A:601:TBR:BR1	2.77	0.40
1:A:322:GLU:HG3	1:A:323:LEU:N	2.37	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	399/469 (85%)	389 (98%)	9 (2%)	1 (0%)	41 62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	301	GLY

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	312/358 (87%)	293 (94%)	19 (6%)	18 36

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	74	ARG
1	A	76	VAL
1	A	77	GLN
1	A	86	LEU
1	A	89	ASP
1	A	100	ARG
1	A	142	VAL
1	A	149	ILE
1	A	155	ARG
1	A	162	LEU
1	A	200	VAL
1	A	279	LEU
1	A	280	VAL
1	A	303	LEU
1	A	336	LEU
1	A	353	THR
1	A	378	VAL
1	A	445	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	165	HIS
1	A	242	GLN
1	A	419	GLN
1	A	431	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

4 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
5	SO4	A	605	-	4,4,4	0.60	0	6,6,6	0.05	0
4	TRS	A	603	-	7,7,7	0.10	0	9,9,9	0.24	0
3	BCN	A	602	-	10,10,10	0.75	0	11,11,11	0.71	0
2	TBR	A	601	-	0,36,36	-	-	-		

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	TRS	A	603	-	-	0/9/9/9	-
3	BCN	A	602	-	-	1/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	BCN	N1-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	TBR	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	403/469 (85%)	-0.04	16 (3%) 38 32	27, 46, 85, 142	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	ASP	5.7
1	A	445	MET	4.5
1	A	274	PRO	4.2
1	A	276	THR	4.1
1	A	275	ALA	3.9
1	A	278	GLN	3.3
1	A	277	GLY	3.2
1	A	386	GLY	2.9
1	A	353	THR	2.7
1	A	367	ALA	2.6
1	A	67	THR	2.6
1	A	344	GLU	2.4
1	A	351	ASN	2.3
1	A	415	VAL	2.3
1	A	416	GLY	2.2
1	A	261	GLU	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, 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
3	BCN	A	602	11/11	0.74	0.32	100,125,135,140	0
2	TBR	A	601	18/18	0.87	0.65	308,326,418,420	0
4	TRS	A	603	8/8	0.94	0.23	33,35,36,36	0
5	SO4	A	605	5/5	0.99	0.12	39,43,45,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.