



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 08:05 PM UTC

PDB ID : 3ST6 / pdb\_00003st6  
Title : Structure of a M. tuberculosis Synthase, MbtI, in Complex with an Isochorismate Analogue Inhibitor  
Authors : Chi, G.; Bulloch, E.M.M.; Manos-Turvey, A.; Payne, R.J.; Lott, J.S.; TB Structural Genomics Consortium (TBSGC)  
Deposited on : 2011-07-08  
Resolution : 1.75 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](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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

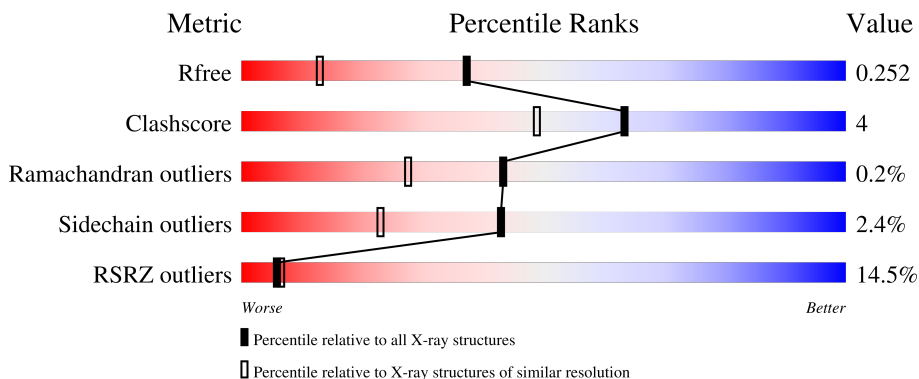
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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))
$R_{free}$	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	450	 3% 90% 6%
1	B	450	 2% 89% 8%
1	C	450	 14% 85% 9% 1% 1%
1	D	450	 36% 72% 16% 1% 1%

## 2 Entry composition [i](#)

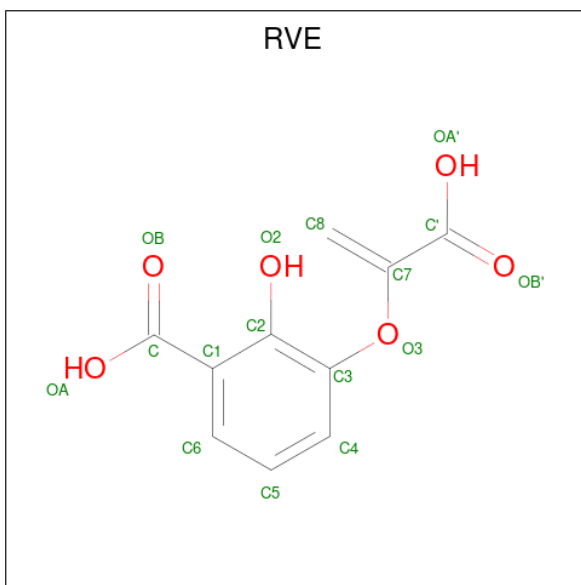
There are 3 unique types of molecules in this entry. The entry contains 13876 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Isochorismate synthase/ischorismate-pyruvate lyase mbtI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	436	Total 3332	C 2088	N 606	O 628	S 10	0	5	0
1	B	435	Total 3301	C 2070	N 594	O 627	S 10	0	1	0
1	C	424	Total 3197	C 2006	N 574	O 607	S 10	0	2	0
1	D	411	Total 3012	C 1900	N 523	O 580	S 9	0	0	0

- Molecule 2 is 3-[(1-carboxyethenyl)oxy]-2-hydroxybenzoic acid (CCD ID: RVE) (formula: C<sub>10</sub>H<sub>8</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 16	C 10	O 6	0	0
2	B	1	Total 16	C 10	O 6	0	0

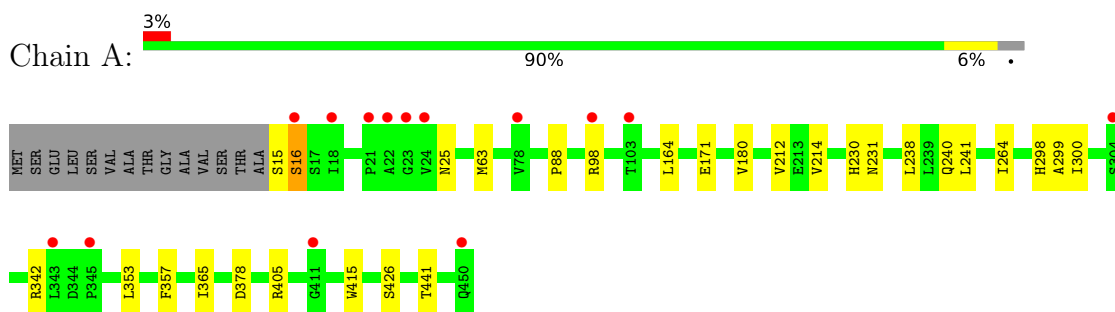
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	364	Total 364	O 364	0	0
3	B	299	Total 299	O 299	0	0
3	C	227	Total 227	O 227	0	0
3	D	112	Total 112	O 112	0	0

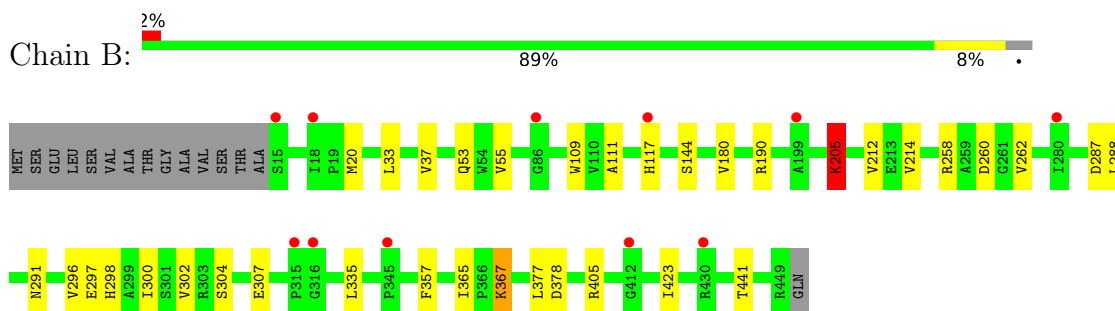
### 3 Residue-property plots

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.

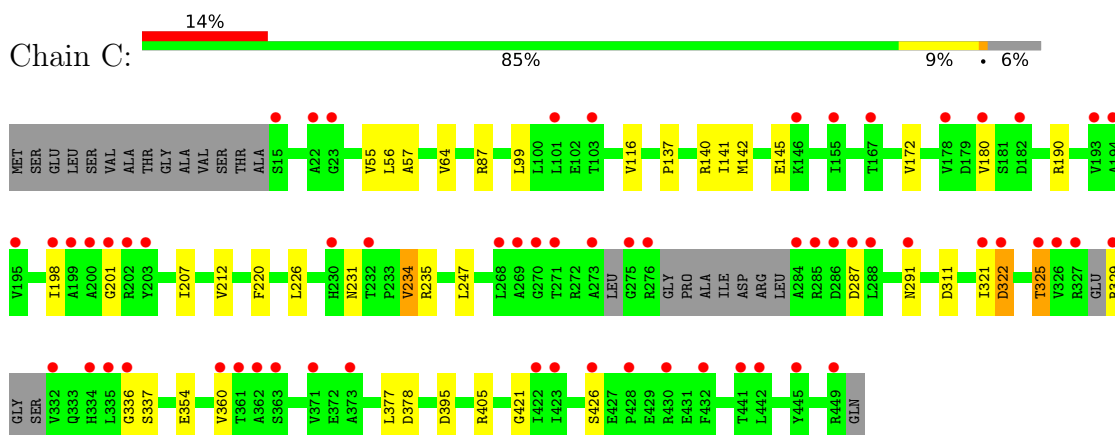
- Molecule 1: Isochorismate synthase/isochorismate-pyruvate lyase mbtI



- Molecule 1: Isochorismate synthase/isochorismate-pyruvate lyase mbtI



- Molecule 1: Isochorismate synthase/isochorismate-pyruvate lyase mbtI



- Molecule 1: Isochorismate synthase/isochorismate-pyruvate lyase mbtI



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.10Å 115.85Å 94.90Å 90.00° 91.25° 90.00°	Depositor
Resolution (Å)	29.36 – 1.75 29.36 – 1.75	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.36-1.75) 97.7 (29.36-1.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 1.75Å)	Xtrriage
Refinement program	BUSTER 2.8.0	Depositor
R, $R_{free}$	0.217 , 0.243 0.225 , 0.252	Depositor DCC
$R_{free}$ test set	9407 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtrriage
Anisotropy	0.479	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 43.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.019 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13876	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: RVE

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	0.94	5/3397 (0.1%)	1.17	5/4616 (0.1%)
1	B	0.94	3/3362 (0.1%)	1.18	6/4569 (0.1%)
1	C	0.97	4/3256 (0.1%)	1.20	6/4424 (0.1%)
1	D	0.97	2/3065 (0.1%)	1.33	6/4179 (0.1%)
All	All	0.95	14/13080 (0.1%)	1.22	23/17788 (0.1%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	238	LEU	C-O	-8.01	1.14	1.23
1	A	298	HIS	C-O	-6.53	1.16	1.24
1	B	53	GLN	C-O	-6.24	1.16	1.24
1	C	321	ILE	C-O	-5.71	1.17	1.24
1	B	205	LYS	C-O	-5.62	1.16	1.23

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	101	LEU	N-CA-C	-9.97	100.10	110.97
1	B	296	VAL	N-CA-CB	6.96	118.69	110.55
1	A	426	SER	N-CA-C	6.04	118.99	110.23
1	D	176	ARG	N-CA-C	5.97	119.20	109.59
1	C	116	VAL	CA-C-N	5.73	127.95	120.28

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	3332	0	3328	8	0
1	B	3301	0	3288	14	0
1	C	3197	0	3157	17	0
1	D	3012	0	2874	64	0
2	A	16	0	5	0	0
2	B	16	0	5	0	0
3	A	364	0	0	1	0
3	B	299	0	0	1	0
3	C	227	0	0	0	0
3	D	112	0	0	3	0
All	All	13876	0	12657	103	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 4.

The worst 5 of 103 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:D:288:LEU:HD11	1:D:335:LEU:HB2	1.13	1.13
1:D:413:ARG:HH11	1:D:415:TRP:HB3	1.20	1.04
1:D:288:LEU:CD1	1:D:335:LEU:HB2	1.89	1.03
1:D:413:ARG:NH1	1:D:415:TRP:HB3	1.86	0.89
1:D:413:ARG:NH1	1:D:415:TRP:CB	2.41	0.82

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	439/450 (98%)	431 (98%)	7 (2%)	1 (0%)	43	27
1	B	434/450 (96%)	430 (99%)	4 (1%)	0	100	100
1	C	417/450 (93%)	411 (99%)	6 (1%)	0	100	100
1	D	401/450 (89%)	383 (96%)	15 (4%)	3 (1%)	18	7
All	All	1691/1800 (94%)	1655 (98%)	32 (2%)	4 (0%)	43	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	SER
1	D	171	GLU
1	D	333	GLN
1	D	233	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	343/358 (96%)	337 (98%)	6 (2%)	53	36
1	B	340/358 (95%)	334 (98%)	6 (2%)	51	33
1	C	327/358 (91%)	321 (98%)	6 (2%)	51	33
1	D	294/358 (82%)	281 (96%)	13 (4%)	25	7
All	All	1304/1432 (91%)	1273 (98%)	31 (2%)	43	23

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	311	ASP
1	D	349	ARG
1	C	405	ARG
1	D	413	ARG
1	D	232	THR

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	25	ASN
1	A	83	GLN
1	C	61	GLN
1	C	83	GLN
1	C	291	ASN

### 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 oligosaccharides 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	RVE	A	451	-	16,16,16	3.22	8 (50%)	19,22,22	1.90	5 (26%)
2	RVE	B	451	-	16,16,16	2.79	9 (56%)	19,22,22	1.43	5 (26%)

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	RVE	A	451	-	-	2/12/12/12	0/1/1/1
2	RVE	B	451	-	-	2/12/12/12	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	451	RVE	C7-C'	9.24	1.58	1.49
2	B	451	RVE	C7-C'	6.42	1.55	1.49
2	B	451	RVE	O3-C7	-4.34	1.33	1.41
2	A	451	RVE	O3-C7	-4.16	1.33	1.41
2	A	451	RVE	O3-C3	-3.63	1.33	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	451	RVE	OB'-C'-C7	-5.04	114.19	121.79
2	A	451	RVE	OA'-C'-C7	4.22	121.11	113.91
2	B	451	RVE	OA'-C'-C7	2.80	118.68	113.91
2	A	451	RVE	O3-C3-C2	2.64	122.83	117.50
2	B	451	RVE	O3-C3-C2	2.38	122.30	117.50

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	451	RVE	OB'-C'-C7-C8
2	A	451	RVE	C4-C3-O3-C7
2	B	451	RVE	C4-C3-O3-C7
2	B	451	RVE	C2-C3-O3-C7

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	436/450 (96%)	0.24	14 (3%) 50 57	10, 24, 43, 62	5 (1%)
1	B	435/450 (96%)	0.31	11 (2%) 58 64	12, 25, 44, 59	1 (0%)
1	C	424/450 (94%)	0.90	61 (14%) 6 7	10, 30, 50, 84	2 (0%)
1	D	411/450 (91%)	1.86	161 (39%) 1 1	19, 44, 72, 100	1 (0%)
All	All	1706/1800 (94%)	0.81	247 (14%) 6 6	10, 29, 59, 100	9 (0%)

The worst 5 of 247 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	332	VAL	10.2
1	D	326	VAL	7.3
1	C	335	LEU	6.7
1	C	326	VAL	6.6
1	C	288	LEU	6.2

### 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 oligosaccharides 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( $\text{\AA}^2$ )	Q<0.9
2	RVE	A	451	16/16	0.96	0.06	15,23,29,31	0
2	RVE	B	451	16/16	0.96	0.06	19,26,32,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.