



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 03:13 pm BST

PDB ID : 6RFY
Title : Crystal structure of Eis2 form Mycobacterium abscessus
Authors : Blaise, M.; Kremer, L.; Olieric, V.; Alsarraf, H.; Ung, K.L.
Deposited on : 2019-04-16
Resolution : 2.20 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 ⓘ symbol.

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)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

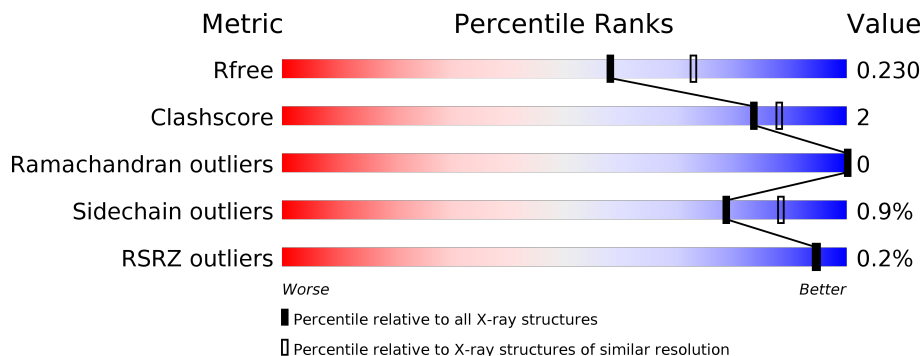
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 on 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	411	 91% 8%
1	B	411	 93% 6%
1	C	411	 94% 5%
1	D	411	 93% 6%
1	E	411	 91% 8%
1	F	411	 90% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19964 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.

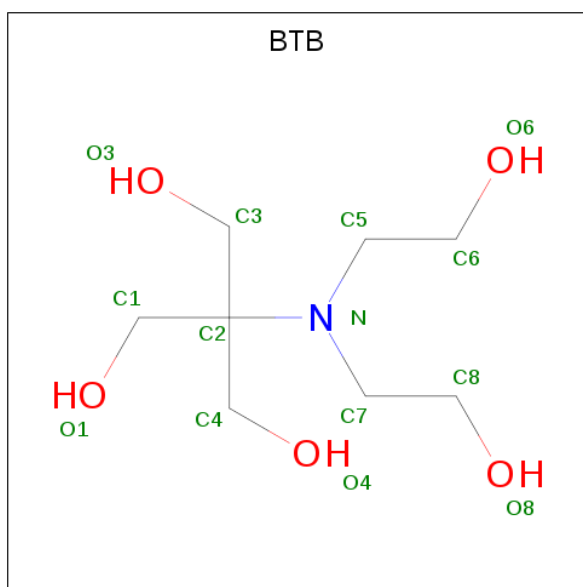
- Molecule 1 is a protein called Eis2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	3146	1982	551	603	10	0	0	0
1	B	405	3147	1984	551	602	10	0	0	0
1	C	406	3151	1986	552	603	10	0	0	0
1	D	407	3156	1989	553	604	10	0	0	0
1	E	404	3140	1979	550	601	10	0	0	0
1	F	404	3138	1979	550	599	10	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

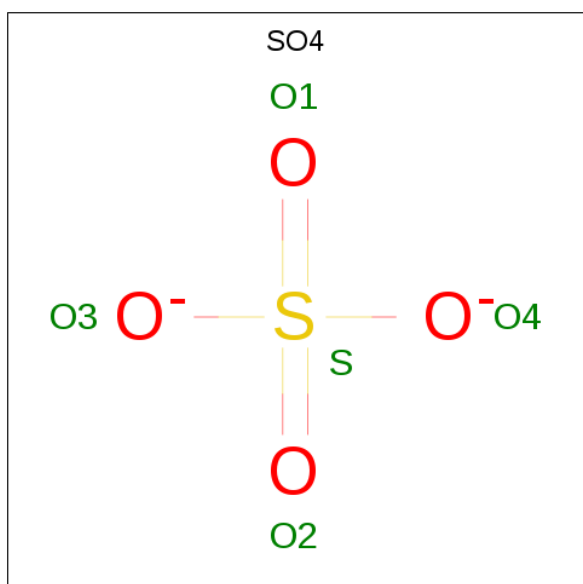
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A0A3A1BNP8
B	1	GLY	-	expression tag	UNP A0A3A1BNP8
C	1	GLY	-	expression tag	UNP A0A3A1BNP8
D	1	GLY	-	expression tag	UNP A0A3A1BNP8
E	1	GLY	-	expression tag	UNP A0A3A1BNP8
F	1	GLY	-	expression tag	UNP A0A3A1BNP8

- Molecule 2 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total 14	8	1	5	0	0
2	B	1	Total 14	8	1	5	0	0
2	D	1	Total 14	8	1	5	0	0
2	E	1	Total 14	8	1	5	0	0
2	F	1	Total 14	8	1	5	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

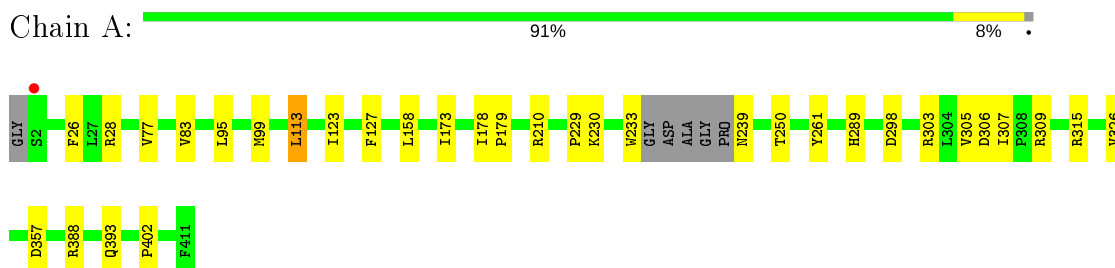
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	193	Total O 193 193	0	0
4	B	194	Total O 194 194	0	0
4	C	174	Total O 174 174	0	0
4	D	167	Total O 167 167	0	0
4	E	157	Total O 157 157	0	0
4	F	101	Total O 101 101	0	0

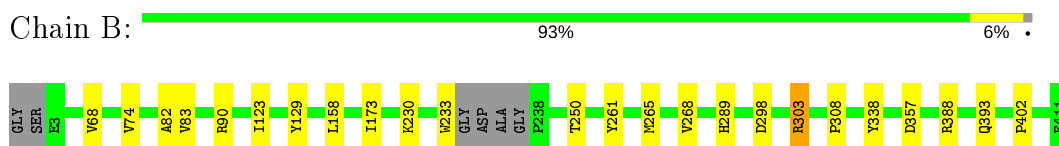
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

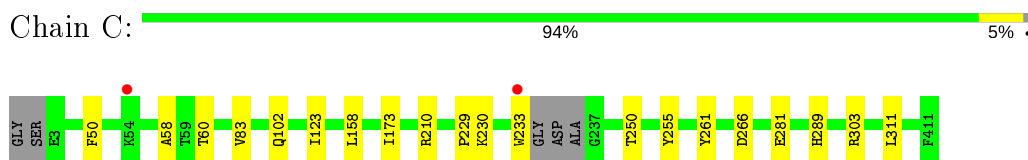
- Molecule 1: Eis2



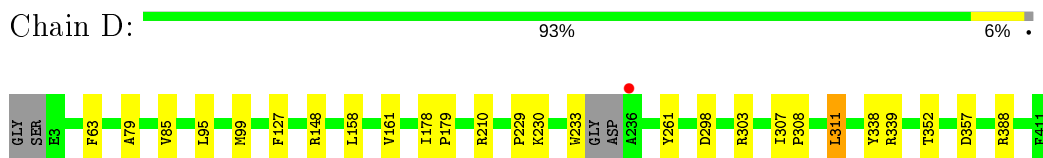
- Molecule 1: Eis2



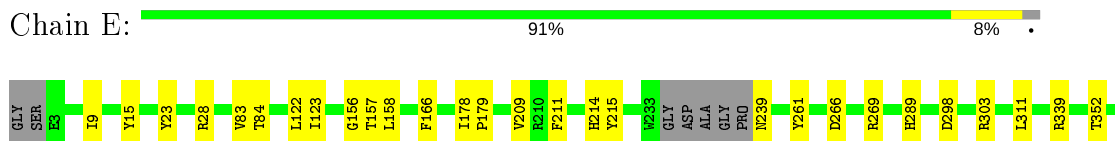
- Molecule 1: Eis2



- Molecule 1: Eis2



- Molecule 1: Eis2





- Molecule 1: Eis2

Chain F: 90% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	112.69Å 79.86Å 152.83Å 90.00° 90.24° 90.00°	Depositor
Resolution (Å)	49.52 – 2.20 49.52 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.52-2.20) 99.9 (49.52-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.20Å)	Xtrriage
Refinement program	PHENIX (1.15rc3_3435: ???)	Depositor
R, R_{free}	0.199 , 0.230 0.200 , 0.230	Depositor DCC
R_{free} test set	2006 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	42.3	Xtrriage
Anisotropy	0.312	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 29.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19964	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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: SO4, BTB

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	0.25	0/3213	0.45	0/4368
1	B	0.25	0/3215	0.45	0/4371
1	C	0.25	0/3219	0.45	0/4377
1	D	0.25	0/3224	0.45	0/4384
1	E	0.25	0/3207	0.45	0/4360
1	F	0.25	0/3206	0.45	0/4359
All	All	0.25	0/19284	0.45	0/26219

There are no bond length outliers.

There are no bond angle outliers.

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	3146	0	3082	19	0
1	B	3147	0	3085	15	0
1	C	3151	0	3087	9	0
1	D	3156	0	3092	13	0
1	E	3140	0	3077	16	0
1	F	3138	0	3079	18	0
2	A	14	0	19	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	14	0	19	2	0
2	D	14	0	19	3	0
2	E	14	0	19	3	0
2	F	14	0	19	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	193	0	0	2	0
4	B	194	0	0	0	0
4	C	174	0	0	0	0
4	D	167	0	0	1	0
4	E	157	0	0	0	0
4	F	101	0	0	0	0
All	All	19964	0	18597	91	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.

The worst 5 of 91 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:F:112:SER:HB3	1:F:309:ARG:HH11	1.54	0.73
1:B:90:ARG:NH2	1:E:266:ASP:OD1	2.26	0.64
1:A:239:ASN:N	4:A:602:HOH:O	2.33	0.61
1:A:402:PRO:HG2	1:B:393:GLN:HG2	1.82	0.60
1:A:393:GLN:HG2	1:B:402:PRO:HG2	1.86	0.58

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	401/411 (98%)	396 (99%)	5 (1%)	0	100	100
1	B	401/411 (98%)	395 (98%)	6 (2%)	0	100	100
1	C	402/411 (98%)	396 (98%)	6 (2%)	0	100	100
1	D	403/411 (98%)	398 (99%)	5 (1%)	0	100	100
1	E	400/411 (97%)	395 (99%)	5 (1%)	0	100	100
1	F	400/411 (97%)	393 (98%)	7 (2%)	0	100	100
All	All	2407/2466 (98%)	2373 (99%)	34 (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	330/332 (99%)	326 (99%)	4 (1%)	71	83
1	B	330/332 (99%)	329 (100%)	1 (0%)	92	97
1	C	330/332 (99%)	327 (99%)	3 (1%)	78	88
1	D	330/332 (99%)	327 (99%)	3 (1%)	78	88
1	E	329/332 (99%)	326 (99%)	3 (1%)	78	88
1	F	329/332 (99%)	325 (99%)	4 (1%)	71	83
All	All	1978/1992 (99%)	1960 (99%)	18 (1%)	78	88

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	161	VAL
1	D	303	ARG
1	F	161	VAL
1	C	303	ARG
1	C	311	LEU

Some 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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

11 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
3	SO4	B	502	-	4,4,4	0.14	0	6,6,6	0.07	0
3	SO4	F	502	-	4,4,4	0.13	0	6,6,6	0.09	0
3	SO4	A	502	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	C	501	-	4,4,4	0.14	0	6,6,6	0.14	0
3	SO4	E	502	-	4,4,4	0.14	0	6,6,6	0.11	0
2	BTB	B	501	-	13,13,13	0.52	0	7,16,16	0.68	0
2	BTB	A	501	-	13,13,13	0.51	0	7,16,16	0.44	0
2	BTB	F	501	-	13,13,13	0.50	0	7,16,16	0.50	0
2	BTB	E	501	-	13,13,13	0.43	0	7,16,16	0.43	0
2	BTB	D	501	-	13,13,13	0.46	0	7,16,16	0.43	0
3	SO4	D	502	-	4,4,4	0.14	0	6,6,6	0.10	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	BTB	F	501	-	-	4/21/21/21	-
2	BTB	E	501	-	-	5/21/21/21	-
2	BTB	D	501	-	-	6/21/21/21	-
2	BTB	B	501	-	-	13/21/21/21	-
2	BTB	A	501	-	-	1/21/21/21	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	BTB	O1-C1-C2-C3
2	B	501	BTB	O1-C1-C2-C4
2	B	501	BTB	O1-C1-C2-N
2	B	501	BTB	C3-C2-C4-O4
2	B	501	BTB	C1-C2-N-C5

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	BTB	2	0
2	A	501	BTB	1	0
2	F	501	BTB	2	0
2	E	501	BTB	3	0
2	D	501	BTB	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	405/411 (98%)	-0.50	1 (0%) 95 94	31, 46, 70, 119	0
1	B	405/411 (98%)	-0.44	0 100 100	31, 47, 71, 99	0
1	C	406/411 (98%)	-0.46	2 (0%) 91 90	34, 49, 68, 100	0
1	D	407/411 (99%)	-0.30	1 (0%) 95 94	34, 53, 78, 106	0
1	E	404/411 (98%)	-0.45	0 100 100	36, 52, 73, 106	0
1	F	404/411 (98%)	-0.08	1 (0%) 95 94	39, 69, 93, 106	0
All	All	2431/2466 (98%)	-0.37	5 (0%) 95 94	31, 51, 82, 119	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	SER	3.5
1	D	236	ALA	2.9
1	C	54	LYS	2.6
1	F	54	LYS	2.4
1	C	233	TRP	2.3

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 carbohydrates 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
2	BTB	E	501	14/14	0.81	0.22	81,88,95,95	0
2	BTB	D	501	14/14	0.83	0.20	82,87,88,90	0
2	BTB	B	501	14/14	0.84	0.21	75,81,84,85	0
2	BTB	F	501	14/14	0.87	0.17	81,86,88,89	0
2	BTB	A	501	14/14	0.89	0.18	79,88,91,94	0
3	SO4	D	502	5/5	0.95	0.14	59,63,69,70	0
3	SO4	C	501	5/5	0.96	0.13	52,57,61,68	0
3	SO4	F	502	5/5	0.97	0.09	72,72,75,75	0
3	SO4	A	502	5/5	0.98	0.10	58,61,62,62	0
3	SO4	B	502	5/5	0.99	0.08	55,56,58,59	0
3	SO4	E	502	5/5	0.99	0.07	60,61,64,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.