



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:20 PM UTC

PDB ID : 4A21 / pdb\_00004a21  
Title : Structure of Mycobacterium tuberculosis fructose 1,6-bisphosphate aldolase bound to sulfate  
Authors : Coincon, M.; De la Paz Santangelo, M.; Gest, P.M.; Guerin, M.E.; Pham, H.; Ryan, G.; Puckett, S.E.; Spencer, J.S.; Gonzalez-Juarrero, M.; Daher, R.; Lenaerts, A.J.; Schnappinger, D.; Therisod, M.; Ehrt, S.; Jackson, M.; Sygusch, J.  
Deposited on : 2011-09-21  
Resolution : 2.35 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

<https://www.wwpdb.org/validation/2017/FAQs#types>.

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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)

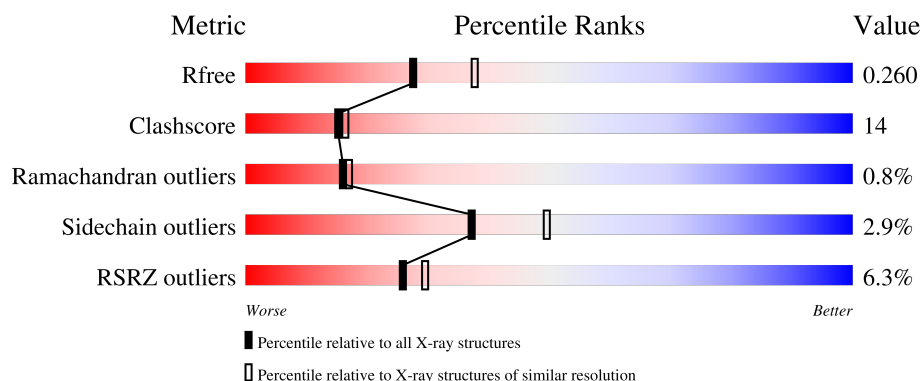
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	344	 6% 74% 17% 9%
1	B	344	 4% 64% 25% 9%
1	C	344	 8% 65% 23% 9%
1	D	344	 5% 70% 18% 9%

Validation Pipeline (wwPDB-VP) : 2.49

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
2	SO4	D	1345	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 19522 atoms, of which 9296 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 FRUCTOSE-BISPHOSPHATE ALDOLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	314	Total	C	H	N	O	S	0	0	0
			4671	1488	2325	395	453	10			
1	B	314	Total	C	H	N	O	S	0	0	0
			4671	1488	2325	395	453	10			
1	C	314	Total	C	H	N	O	S	0	0	0
			4669	1488	2323	395	453	10			
1	D	314	Total	C	H	N	O	S	0	0	0
			4669	1488	2323	395	453	10			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Na	0	0
			2	2		

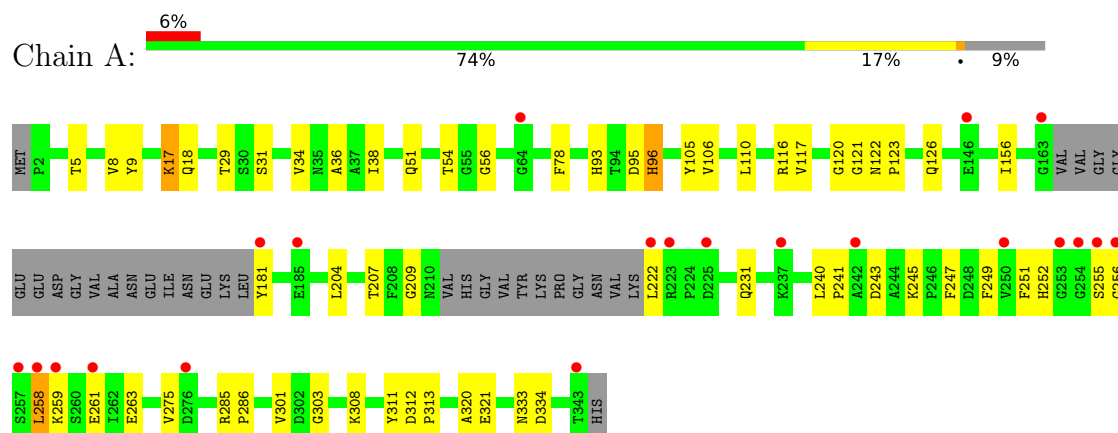
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	215	Total	O	0	0
			215	215		
4	B	205	Total	O	0	0
			205	205		
4	C	185	Total	O	0	0
			185	185		
4	D	195	Total	O	0	0
			195	195		

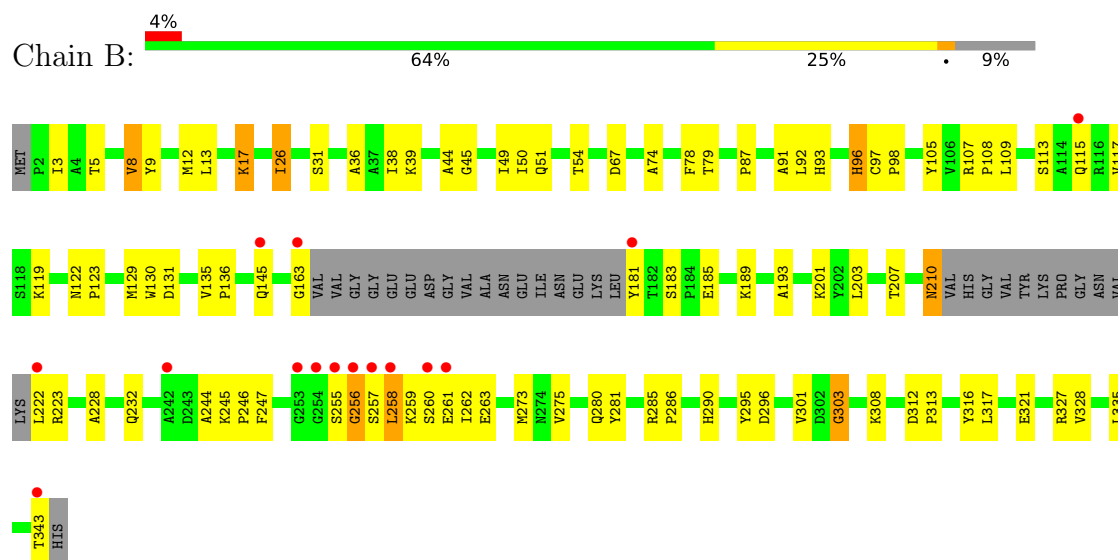
### 3 Residue-property plots

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.

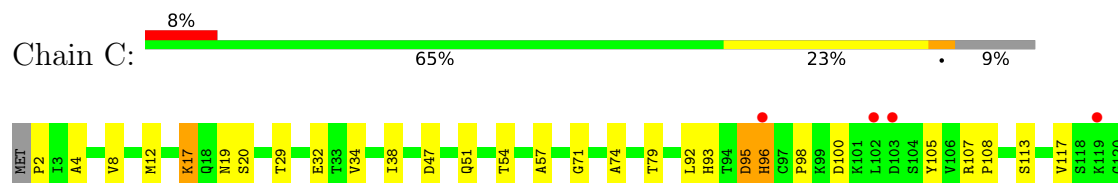
#### • Molecule 1: FRUCTOSE-BISPHOSPHATE ALDOLASE

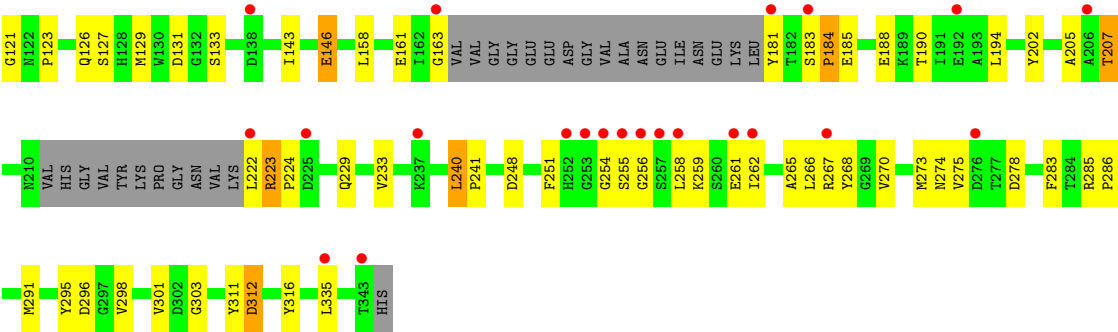


#### • Molecule 1: FRUCTOSE-BISPHOSPHATE ALDOLASE

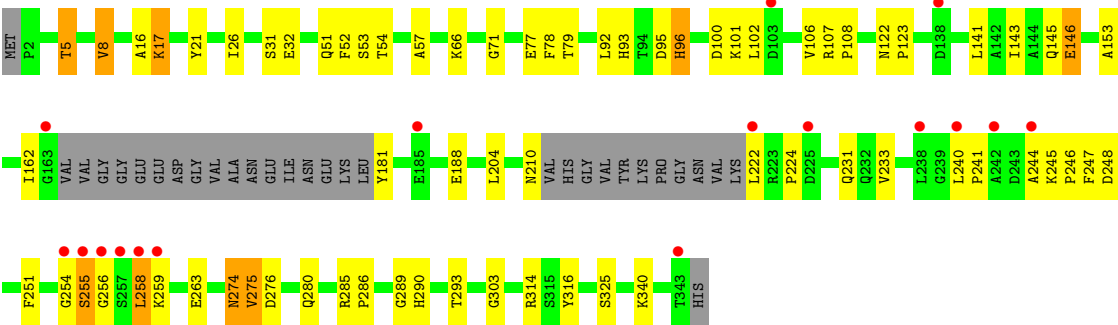


#### • Molecule 1: FRUCTOSE-BISPHOSPHATE ALDOLASE





● Molecule 1: FRUCTOSE-BISPHOSPHATE ALDOLASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	336.94Å 43.23Å 103.02Å 90.00° 99.57° 90.00°	Depositor
Resolution (Å)	42.87 – 2.35 42.87 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.2 (42.87-2.35) 99.1 (42.87-2.35)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 2.34Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.211 , 0.261 0.220 , 0.260	Depositor DCC
$R_{free}$ test set	4634 reflections (7.49%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.4	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 49.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	19522	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, SO4

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	0.50	0/2391	0.83	1/3236 (0.0%)
1	B	0.49	0/2391	0.81	0/3236
1	C	0.45	0/2391	0.78	0/3236
1	D	0.48	0/2391	0.80	2/3236 (0.1%)
All	All	0.48	0/9564	0.81	3/12944 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	VAL	N-CA-C	5.74	115.93	110.42
1	D	5	THR	CA-C-N	-5.08	113.69	119.28
1	D	5	THR	C-N-CA	-5.08	113.69	119.28

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	2346	2325	2323	54	0
1	B	2346	2325	2323	72	0
1	C	2346	2323	2323	71	0
1	D	2346	2323	2323	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	10	0	0	2	0
2	B	10	0	0	0	0
2	C	10	0	0	0	0
2	D	10	0	0	2	0
3	A	2	0	0	0	0
4	A	215	0	0	20	1
4	B	205	0	0	22	1
4	C	185	0	0	22	1
4	D	195	0	0	14	0
All	All	10226	9296	9292	254	2

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 14.

The worst 5 of 254 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:258:LEU:HB3	4:A:2170:HOH:O	1.58	1.02
1:B:257:SER:HA	4:B:2161:HOH:O	1.61	0.99
1:A:181:TYR:CZ	4:A:2138:HOH:O	2.22	0.92
1:C:267:ARG:HA	4:C:2033:HOH:O	1.68	0.92
1:C:163:GLY:HA3	1:C:207:THR:OG1	1.84	0.78

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2126:HOH:O	4:A:2211:HOH:O[1_545]	2.17	0.03
4:B:2180:HOH:O	4:C:2159:HOH:O[1_565]	2.17	0.03

## 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	308/344 (90%)	297 (96%)	10 (3%)	1 (0%)	36	43
1	B	308/344 (90%)	293 (95%)	12 (4%)	3 (1%)	12	12
1	C	308/344 (90%)	290 (94%)	14 (4%)	4 (1%)	9	8
1	D	308/344 (90%)	296 (96%)	10 (3%)	2 (1%)	21	24
All	All	1232/1376 (90%)	1176 (96%)	46 (4%)	10 (1%)	16	17

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	255	SER
1	A	96	HIS
1	C	96	HIS
1	D	96	HIS
1	B	303	GLY

### 5.3.2 Protein sidechains ⓘ

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	242/266 (91%)	237 (98%)	5 (2%)	47	61
1	B	242/266 (91%)	234 (97%)	8 (3%)	33	44
1	C	242/266 (91%)	233 (96%)	9 (4%)	30	40
1	D	242/266 (91%)	236 (98%)	6 (2%)	42	55
All	All	968/1064 (91%)	940 (97%)	28 (3%)	37	49

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	95	ASP
1	D	275	VAL
1	C	207	THR
1	D	146	GLU
1	C	146	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	19	ASN
1	C	122	ASN
1	D	330	GLN
1	D	280	GLN
1	D	294	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](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

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	SO4	B	1345	-	4,4,4	0.33	0	6,6,6	0.14	0
2	SO4	C	1344	-	4,4,4	0.25	0	6,6,6	0.11	0
2	SO4	D	1345	-	4,4,4	0.28	0	6,6,6	0.32	0
2	SO4	B	1344	-	4,4,4	0.23	0	6,6,6	0.25	0
2	SO4	A	1345	-	4,4,4	0.25	0	6,6,6	0.21	0
2	SO4	C	1345	-	4,4,4	0.26	0	6,6,6	0.24	0
2	SO4	A	1344	-	4,4,4	0.20	0	6,6,6	0.13	0
2	SO4	D	1344	-	4,4,4	0.26	0	6,6,6	0.28	0

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.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1345	SO4	2	0
2	A	1345	SO4	1	0
2	A	1344	SO4	1	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, 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	314/344 (91%)	0.55	21 (6%) 24 27	15, 29, 57, 89	0
1	B	314/344 (91%)	0.48	15 (4%) 35 41	16, 28, 54, 99	0
1	C	314/344 (91%)	0.75	26 (8%) 17 19	17, 37, 68, 107	0
1	D	314/344 (91%)	0.44	17 (5%) 31 37	16, 29, 55, 83	0
All	All	1256/1376 (91%)	0.56	79 (6%) 26 29	15, 31, 60, 107	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	254	GLY	8.3
1	C	163	GLY	6.5
1	D	163	GLY	5.1
1	A	163	GLY	4.8
1	C	255	SER	4.8

### 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	SO4	B	1345	5/5	0.70	0.17	50,54,67,83	0
2	SO4	D	1345	5/5	0.70	0.16	57,59,68,88	0
3	NA	A	1347	1/1	0.76	0.21	43,43,43,43	0
2	SO4	C	1344	5/5	0.78	0.20	51,67,74,83	0
2	SO4	D	1344	5/5	0.78	0.13	38,43,63,87	0
2	SO4	C	1345	5/5	0.80	0.12	50,50,68,80	0
3	NA	A	1346	1/1	0.85	0.16	47,47,47,47	0
2	SO4	B	1344	5/5	0.87	0.14	41,44,65,75	0
2	SO4	A	1345	5/5	0.87	0.18	38,46,52,60	0
2	SO4	A	1344	5/5	0.92	0.10	52,55,64,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.