



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 01:11 am GMT

PDB ID : 2E67  
Title : Crystal structure of the hypothetical protein TTHB029 from *Thermus thermophilus* HB8  
Authors : Imagawa, T.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2006-12-26  
Resolution : 2.90 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

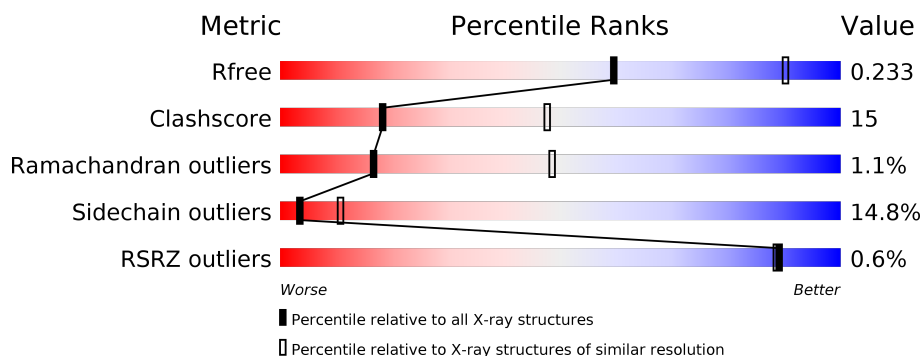
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	100719	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	264	<div> <div>71%</div> <div>23%</div> <div>5%</div> </div>
1	B	264	<div> <div>61%</div> <div>31%</div> <div>6%</div> </div>
1	C	264	<div> <div>2%</div> <div>54%</div> <div>39%</div> <div>6%</div> </div>
1	D	264	<div> <div>67%</div> <div>27%</div> <div>5%</div> </div>
1	E	264	<div> <div>%</div> <div>72%</div> <div>22%</div> <div>5%</div> </div>
1	F	264	<div> <div>%</div> <div>72%</div> <div>21%</div> <div>6%</div> </div>

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	MG	D	304	-	-	-	X
2	MG	E	305	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12678 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 Hypothetical protein TTHB029.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			2090	1352	364	372	2			
1	B	263	Total	C	N	O	S	0	0	0
			2090	1352	364	372	2			
1	C	263	Total	C	N	O	S	0	0	0
			2090	1352	364	372	2			
1	D	263	Total	C	N	O	S	0	0	0
			2090	1352	364	372	2			
1	E	263	Total	C	N	O	S	0	0	0
			2090	1352	364	372	2			
1	F	263	Total	C	N	O	S	0	0	0
			2090	1352	364	372	2			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Mg	0	0
			1	1		
2	E	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	F	1	Total	Mg	0	0
			1	1		

- Molecule 3 is water.

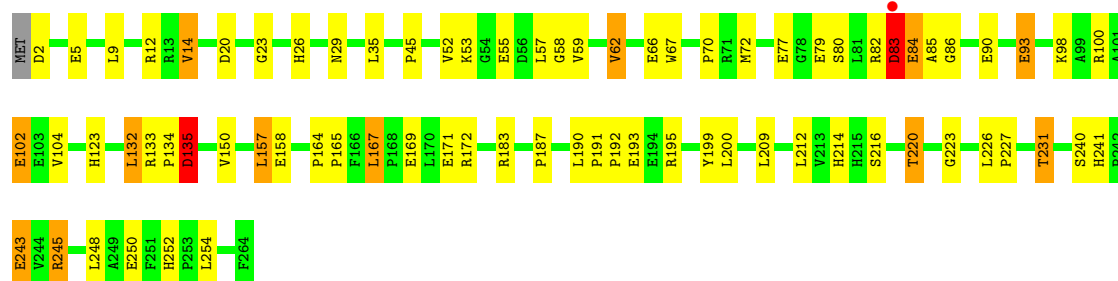
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	25	Total 25	O 25	0	0
3	B	29	Total 29	O 29	0	0
3	C	16	Total 16	O 16	0	0
3	D	26	Total 26	O 26	0	0
3	E	15	Total 15	O 15	0	0
3	F	21	Total 21	O 21	0	0

### 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.

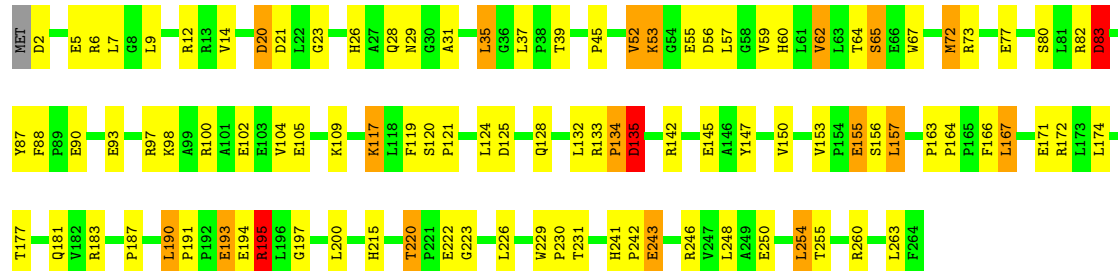
#### • Molecule 1: Hypothetical protein TTHB029

Chain A: 



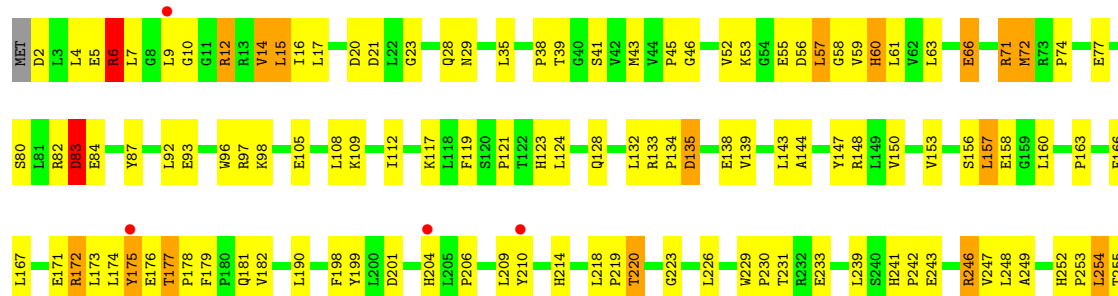
#### • Molecule 1: Hypothetical protein TTHB029

Chain B: 



#### • Molecule 1: Hypothetical protein TTHB029

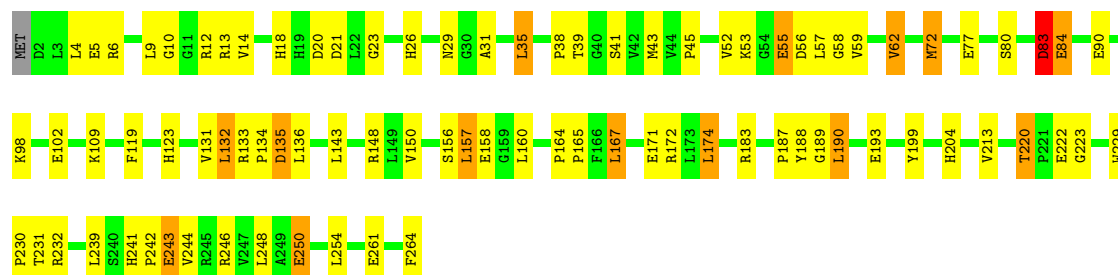
Chain C: 





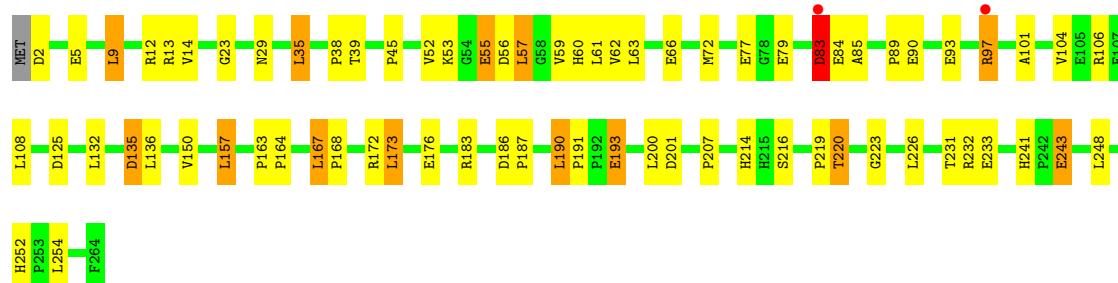
• Molecule 1: Hypothetical protein TTHB029

Chain D: 67% 27% 5%



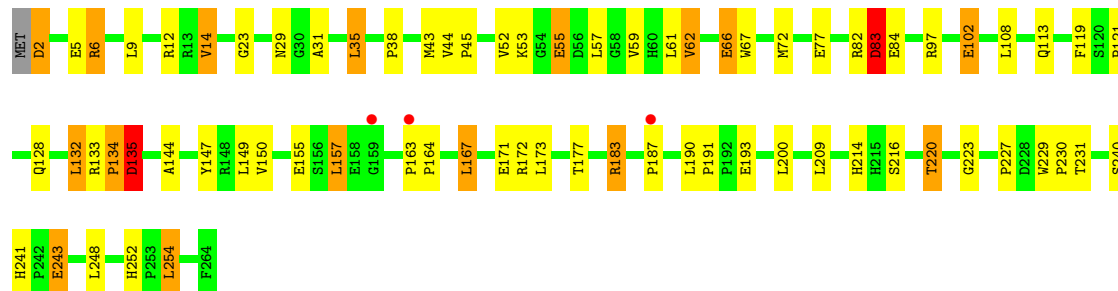
• Molecule 1: Hypothetical protein TTHB029

Chain E: 72% 22% 5%



• Molecule 1: Hypothetical protein TTHB029

Chain F: 72% 21% 6%



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	202.01Å 202.01Å 345.29Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.90 48.05 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.90) 100.0 (48.05-2.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.21 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.219 , 0.259 0.193 , 0.233	Depositor DCC
$R_{free}$ test set	3035 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.7	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 43.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12678	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% 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: MG

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	0.92	1/2156 (0.0%)	0.93	3/2948 (0.1%)
1	B	0.87	0/2156	0.92	3/2948 (0.1%)
1	C	0.88	1/2156 (0.0%)	0.93	2/2948 (0.1%)
1	D	0.87	3/2156 (0.1%)	0.89	4/2948 (0.1%)
1	E	0.78	1/2156 (0.0%)	0.88	4/2948 (0.1%)
1	F	0.77	0/2156	0.84	2/2948 (0.1%)
All	All	0.85	6/12936 (0.0%)	0.90	18/17688 (0.1%)

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	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	1
1	F	0	2
All	All	0	11

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	83	ASP	CB-CG	6.87	1.66	1.51
1	D	83	ASP	CB-CG	6.64	1.65	1.51
1	D	55	GLU	CG-CD	5.67	1.60	1.51
1	C	138	GLU	CG-CD	5.60	1.60	1.51
1	E	55	GLU	CG-CD	5.33	1.59	1.51

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	263	LEU	CA-CB-CG	7.36	132.22	115.30
1	A	245	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	A	135	ASP	N-CA-CB	-5.80	100.16	110.60
1	E	57	LEU	CB-CG-CD1	5.73	120.73	111.00
1	C	71	ARG	NE-CZ-NH2	-5.71	117.44	120.30

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	134	PRO	Peptide
1	A	83	ASP	Peptide
1	B	134	PRO	Peptide
1	B	83	ASP	Peptide
1	C	83	ASP	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	2090	0	2067	54	1
1	B	2090	0	2067	75	0
1	C	2090	0	2067	87	0
1	D	2090	0	2067	64	0
1	E	2090	0	2067	49	0
1	F	2090	0	2067	55	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	25	0	0	6	0
3	B	29	0	0	9	0
3	C	16	0	0	7	0
3	D	26	0	0	13	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	15	0	0	6	0
3	F	21	0	0	7	0
All	All	12678	0	12402	374	1

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 15.

The worst 5 of 374 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:84:GLU:HA	3:A:325:HOH:O	1.11	1.26
1:C:84:GLU:HA	3:C:318:HOH:O	1.34	1.25
3:B:330:HOH:O	1:C:178:PRO:HD3	1.32	1.23
1:F:84:GLU:HA	3:F:327:HOH:O	1.45	1.16
1:B:220:THR:HG22	1:B:223:GLY:H	1.02	1.14

All (1) 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)
1:A:250:GLU:CG	3:D:330:HOH:O[10_455]	2.11	0.09

## 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	261/264 (99%)	253 (97%)	7 (3%)	1 (0%)	38 72
1	B	261/264 (99%)	244 (94%)	13 (5%)	4 (2%)	12 39
1	C	261/264 (99%)	225 (86%)	31 (12%)	5 (2%)	9 33
1	D	261/264 (99%)	239 (92%)	18 (7%)	4 (2%)	12 39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	261/264 (99%)	239 (92%)	19 (7%)	3 (1%)	17	48
1	F	261/264 (99%)	248 (95%)	12 (5%)	1 (0%)	38	72
All	All	1566/1584 (99%)	1448 (92%)	100 (6%)	18 (1%)	17	48

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	ASP
1	B	135	ASP
1	B	195	ARG
1	C	135	ASP
1	C	201	ASP

### 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	216/217 (100%)	186 (86%)	30 (14%)	4	12
1	B	216/217 (100%)	181 (84%)	35 (16%)	3	8
1	C	216/217 (100%)	177 (82%)	39 (18%)	2	6
1	D	216/217 (100%)	186 (86%)	30 (14%)	4	12
1	E	216/217 (100%)	189 (88%)	27 (12%)	5	16
1	F	216/217 (100%)	185 (86%)	31 (14%)	4	11
All	All	1296/1302 (100%)	1104 (85%)	192 (15%)	3	11

5 of 192 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	160	LEU
1	D	20	ASP
1	F	150	VAL
1	C	172	ARG
1	C	220	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	214	HIS
1	D	29	ASN
1	F	214	HIS
1	C	241	HIS
1	D	214	HIS

### 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](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	263/264 (99%)	-0.34	1 (0%) 92 92	7, 20, 41, 57	0
1	B	263/264 (99%)	-0.27	0 100 100	7, 26, 49, 61	0
1	C	263/264 (99%)	-0.02	4 (1%) 74 72	8, 32, 62, 79	0
1	D	263/264 (99%)	-0.13	0 100 100	7, 26, 49, 60	0
1	E	263/264 (99%)	-0.15	2 (0%) 86 85	11, 35, 70, 82	0
1	F	263/264 (99%)	0.01	3 (1%) 80 79	10, 36, 62, 70	0
All	All	1578/1584 (99%)	-0.15	10 (0%) 89 88	7, 29, 59, 82	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	175	TYR	4.2
1	F	187	PRO	3.3
1	E	83	ASP	3.1
1	A	83	ASP	3.0
1	F	163	PRO	2.8

### 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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MG	D	304	1/1	0.90	0.23	5.92	13,13,13,13	0
2	MG	E	305	1/1	0.91	0.18	2.49	14,14,14,14	0
2	MG	C	303	1/1	0.88	0.23	1.98	20,20,20,20	0
2	MG	B	302	1/1	0.94	0.19	1.90	17,17,17,17	0
2	MG	A	301	1/1	0.97	0.15	0.29	10,10,10,10	0
2	MG	F	306	1/1	0.96	0.14	-0.15	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.