



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:20 PM GMT

PDB ID : 4RJI  
Title : Acetolactate synthase from Bacillus subtilis bound to ThDP - crystal form I  
Authors : Sommer, B.; von Moeller, H.; Haack, M.; Qoura, F.; Langner, C.; Bourenkov, G.; Garbe, D.; Brueck, T.; Loll, B.  
Deposited on : 2014-10-09  
Resolution : 3.20 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](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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

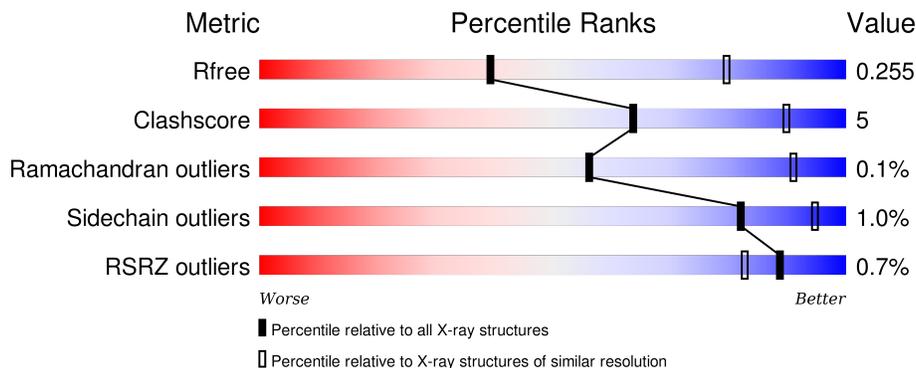
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	587	
1	B	587	
1	C	587	
1	D	587	

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
4	PG4	B	603	-	-	-	X

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 16994 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 Acetolactate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	539	Total 4119	C 2610	N 710	O 788	S 11	0	0	0
1	B	552	Total 4227	C 2681	N 726	O 808	S 12	0	0	0
1	C	555	Total 4252	C 2697	N 731	O 812	S 12	0	0	0
1	D	555	Total 4252	C 2697	N 731	O 812	S 12	0	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	572	LEU	-	EXPRESSION TAG	UNP V5MX36
A	573	SER	-	EXPRESSION TAG	UNP V5MX36
A	574	GLY	-	EXPRESSION TAG	UNP V5MX36
A	575	ARG	-	EXPRESSION TAG	UNP V5MX36
A	576	PRO	-	EXPRESSION TAG	UNP V5MX36
A	577	VAL	-	EXPRESSION TAG	UNP V5MX36
A	578	LEU	-	EXPRESSION TAG	UNP V5MX36
A	579	GLY	-	EXPRESSION TAG	UNP V5MX36
A	580	SER	-	EXPRESSION TAG	UNP V5MX36
A	581	SER	-	EXPRESSION TAG	UNP V5MX36
A	582	HIS	-	EXPRESSION TAG	UNP V5MX36
A	583	HIS	-	EXPRESSION TAG	UNP V5MX36
A	584	HIS	-	EXPRESSION TAG	UNP V5MX36
A	585	HIS	-	EXPRESSION TAG	UNP V5MX36
A	586	HIS	-	EXPRESSION TAG	UNP V5MX36
A	587	HIS	-	EXPRESSION TAG	UNP V5MX36
B	572	LEU	-	EXPRESSION TAG	UNP V5MX36
B	573	SER	-	EXPRESSION TAG	UNP V5MX36
B	574	GLY	-	EXPRESSION TAG	UNP V5MX36
B	575	ARG	-	EXPRESSION TAG	UNP V5MX36
B	576	PRO	-	EXPRESSION TAG	UNP V5MX36

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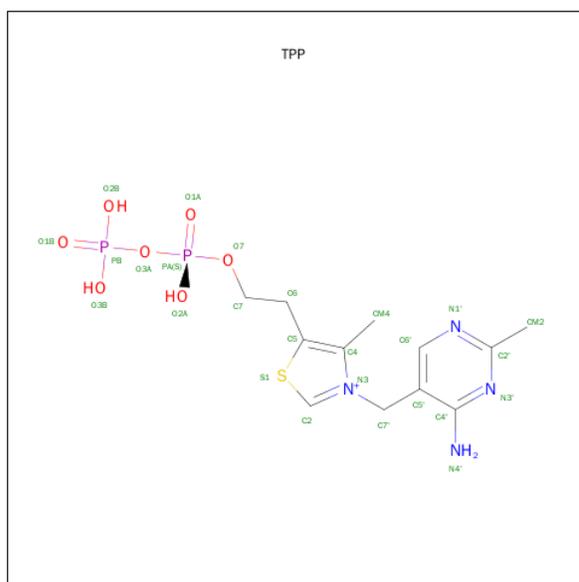
Chain	Residue	Modelled	Actual	Comment	Reference
B	577	VAL	-	EXPRESSION TAG	UNP V5MX36
B	578	LEU	-	EXPRESSION TAG	UNP V5MX36
B	579	GLY	-	EXPRESSION TAG	UNP V5MX36
B	580	SER	-	EXPRESSION TAG	UNP V5MX36
B	581	SER	-	EXPRESSION TAG	UNP V5MX36
B	582	HIS	-	EXPRESSION TAG	UNP V5MX36
B	583	HIS	-	EXPRESSION TAG	UNP V5MX36
B	584	HIS	-	EXPRESSION TAG	UNP V5MX36
B	585	HIS	-	EXPRESSION TAG	UNP V5MX36
B	586	HIS	-	EXPRESSION TAG	UNP V5MX36
B	587	HIS	-	EXPRESSION TAG	UNP V5MX36
C	572	LEU	-	EXPRESSION TAG	UNP V5MX36
C	573	SER	-	EXPRESSION TAG	UNP V5MX36
C	574	GLY	-	EXPRESSION TAG	UNP V5MX36
C	575	ARG	-	EXPRESSION TAG	UNP V5MX36
C	576	PRO	-	EXPRESSION TAG	UNP V5MX36
C	577	VAL	-	EXPRESSION TAG	UNP V5MX36
C	578	LEU	-	EXPRESSION TAG	UNP V5MX36
C	579	GLY	-	EXPRESSION TAG	UNP V5MX36
C	580	SER	-	EXPRESSION TAG	UNP V5MX36
C	581	SER	-	EXPRESSION TAG	UNP V5MX36
C	582	HIS	-	EXPRESSION TAG	UNP V5MX36
C	583	HIS	-	EXPRESSION TAG	UNP V5MX36
C	584	HIS	-	EXPRESSION TAG	UNP V5MX36
C	585	HIS	-	EXPRESSION TAG	UNP V5MX36
C	586	HIS	-	EXPRESSION TAG	UNP V5MX36
C	587	HIS	-	EXPRESSION TAG	UNP V5MX36
D	572	LEU	-	EXPRESSION TAG	UNP V5MX36
D	573	SER	-	EXPRESSION TAG	UNP V5MX36
D	574	GLY	-	EXPRESSION TAG	UNP V5MX36
D	575	ARG	-	EXPRESSION TAG	UNP V5MX36
D	576	PRO	-	EXPRESSION TAG	UNP V5MX36
D	577	VAL	-	EXPRESSION TAG	UNP V5MX36
D	578	LEU	-	EXPRESSION TAG	UNP V5MX36
D	579	GLY	-	EXPRESSION TAG	UNP V5MX36
D	580	SER	-	EXPRESSION TAG	UNP V5MX36
D	581	SER	-	EXPRESSION TAG	UNP V5MX36
D	582	HIS	-	EXPRESSION TAG	UNP V5MX36
D	583	HIS	-	EXPRESSION TAG	UNP V5MX36
D	584	HIS	-	EXPRESSION TAG	UNP V5MX36
D	585	HIS	-	EXPRESSION TAG	UNP V5MX36
D	586	HIS	-	EXPRESSION TAG	UNP V5MX36

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Chain	Residue	Modelled	Actual	Comment	Reference
D	587	HIS	-	EXPRESSION TAG	UNP V5MX36

- Molecule 2 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C<sub>12</sub>H<sub>19</sub>N<sub>4</sub>O<sub>7</sub>P<sub>2</sub>S).

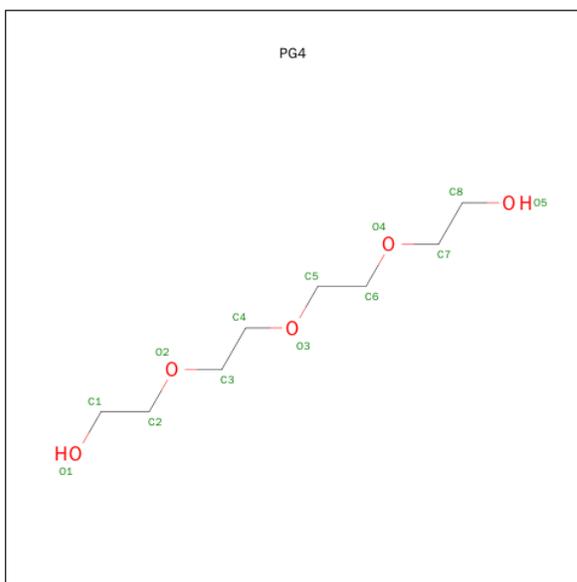


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
2	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
2	B	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
2	C	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
2	D	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total 1 Mg	0	0
3	A	1	Total 1 Mg	0	0
3	D	1	Total 1 Mg	0	0
3	C	1	Total 1 Mg	0	0

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).

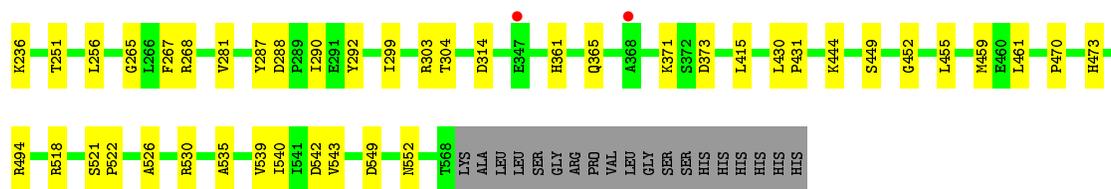


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	C O	0	0
			13	8 5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	O	0	0
			3	3		
5	B	6	Total	O	0	0
			6	6		
5	C	7	Total	O	0	0
			7	7		
5	D	7	Total	O	0	0
			7	7		





- Molecule 1: Acetolactate synthase

Chain D: 83% 11% 5%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	140.65Å 140.65Å 238.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.66 – 3.20 29.66 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.66-3.20) 99.7 (29.66-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 3.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.187 , 0.253 0.195 , 0.255	Depositor DCC
$R_{free}$ test set	2007 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.5	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 51.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 40142 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	16994	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.18% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PG4, MG, TPP

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	0.28	0/4195	0.47	0/5704
1	B	0.29	0/4308	0.47	0/5859
1	C	0.30	0/4333	0.49	0/5891
1	D	0.31	0/4333	0.49	0/5891
All	All	0.29	0/17169	0.48	0/23345

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	4119	0	4131	55	0
1	B	4227	0	4232	56	0
1	C	4252	0	4265	42	0
1	D	4252	0	4265	43	0
2	A	26	0	16	0	0
2	B	26	0	16	0	0
2	C	26	0	16	0	0
2	D	26	0	16	2	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	13	0	18	0	0
5	A	3	0	0	0	0
5	B	6	0	0	0	0
5	C	7	0	0	0	0
5	D	7	0	0	0	0
All	All	16994	0	16975	175	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.

The worst 5 of 175 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:228:ILE:HG12	1:D:251:THR:HG22	1.66	0.77
1:C:228:ILE:HG12	1:C:251:THR:HG22	1.66	0.77
1:B:299:ILE:O	1:B:303:ARG:NH2	2.17	0.77
1:C:218:VAL:HG11	1:C:251:THR:HG21	1.67	0.74
1:D:218:VAL:HG11	1:D:251:THR:HG21	1.70	0.71

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	535/587 (91%)	521 (97%)	12 (2%)	2 (0%)	39 80
1	B	550/587 (94%)	540 (98%)	10 (2%)	0	100 100
1	C	553/587 (94%)	542 (98%)	11 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	553/587 (94%)	540 (98%)	13 (2%)	0	100	100
All	All	2191/2348 (93%)	2143 (98%)	46 (2%)	2 (0%)	56	91

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	300	ASN
1	A	299	ILE

### 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	440/482 (91%)	435 (99%)	5 (1%)	80	94
1	B	451/482 (94%)	447 (99%)	4 (1%)	84	95
1	C	454/482 (94%)	452 (100%)	2 (0%)	93	98
1	D	454/482 (94%)	447 (98%)	7 (2%)	72	91
All	All	1799/1928 (93%)	1781 (99%)	18 (1%)	82	95

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

Mol	Chain	Res	Type
1	B	543	VAL
1	C	221	LYS
1	D	341	VAL
1	B	221	LYS
1	B	459	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	TPP	A	1000	3	20,27,27	2.10	4 (20%)	31,40,40	1.98	12 (38%)
2	TPP	B	601	3	20,27,27	2.07	5 (25%)	31,40,40	1.94	10 (32%)
4	PG4	B	603	-	12,12,12	0.63	0	11,11,11	0.74	0
2	TPP	C	1000	3	20,27,27	2.18	4 (20%)	31,40,40	1.85	9 (29%)
2	TPP	D	1000	3	20,27,27	2.08	3 (15%)	31,40,40	1.91	13 (41%)

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	TPP	A	1000	3	-	0/16/17/17	0/2/2/2
2	TPP	B	601	3	-	0/16/17/17	0/2/2/2
4	PG4	B	603	-	-	0/10/10/10	0/0/0/0
2	TPP	C	1000	3	-	0/16/17/17	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPP	D	1000	3	-	0/16/17/17	0/2/2/2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1000	TPP	C4-N3	-6.53	1.34	1.39
2	D	1000	TPP	C4-N3	-5.96	1.34	1.39
2	A	1000	TPP	C4-N3	-5.92	1.34	1.39
2	B	601	TPP	C4-N3	-5.62	1.34	1.39
2	B	601	TPP	C7'-C5'	2.00	1.55	1.51

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1000	TPP	PA-O3A-PB	-3.86	119.74	132.67
2	B	601	TPP	CM4-C4-C5	-3.80	120.35	128.90
2	A	1000	TPP	CM4-C4-C5	-3.60	120.81	128.90
2	C	1000	TPP	N1'-C2'-N3'	-3.53	119.08	125.60
2	A	1000	TPP	N1'-C2'-N3'	-3.38	119.35	125.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1000	TPP	2	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	539/587 (91%)	-0.08	8 (1%) 76 63	31, 80, 131, 184	0
1	B	552/587 (94%)	-0.33	3 (0%) 91 87	31, 63, 104, 153	0
1	C	555/587 (94%)	-0.48	3 (0%) 91 87	28, 56, 94, 147	0
1	D	555/587 (94%)	-0.51	1 (0%) 95 94	32, 53, 86, 127	0
All	All	2201/2348 (93%)	-0.35	15 (0%) 89 83	28, 61, 112, 184	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	450	GLY	4.1
1	A	347	GLU	3.8
1	A	493	ASN	3.8
1	B	493	ASN	3.1
1	A	258	ASP	2.9

### 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( $\text{\AA}^2$ )	Q<0.9
4	PG4	B	603	13/13	0.72	0.46	8.71	66,84,97,99	0
3	MG	D	1001	1/1	0.97	0.18	0.70	34,34,34,34	0
2	TPP	A	1000	26/26	0.94	0.24	0.12	73,108,112,116	0
2	TPP	D	1000	26/26	0.96	0.17	0.09	41,47,53,56	0
2	TPP	B	601	26/26	0.94	0.20	-0.28	60,79,86,94	0
2	TPP	C	1000	26/26	0.96	0.16	-0.30	53,70,78,81	0
3	MG	A	1001	1/1	0.95	0.20	-0.53	96,96,96,96	0
3	MG	B	602	1/1	0.95	0.15	-1.35	63,63,63,63	0
3	MG	C	1001	1/1	0.94	0.04	-4.55	43,43,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.