Full wwPDB X-ray Structure Validation Report (i)

Sep 5, 2023 – 11:28 AM EDT

PDB ID	:	3TS7
Title	:	CRYSTAL STRUCTURE OF FARNESYL DIPHOSPHATE SYNTHASE (TARGET EFI-501951) FROM Methylococcus capsulatus
Authors	:	Patskovsky, Y.; Toro, R.; Bhosle, R.; Hillerich, B.; Seidel, R.D.; Washington, E.; Scott Glenn, A.; Chowdhury, S.; Evans, B.; Hammonds, J.; Zencheck, W.D.; Imker, H.J.; Poulter, C.D.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)
Deposited on	:	2011-09-12
Resolution	:	1.94 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) 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 (i)) were used in the production of this report:

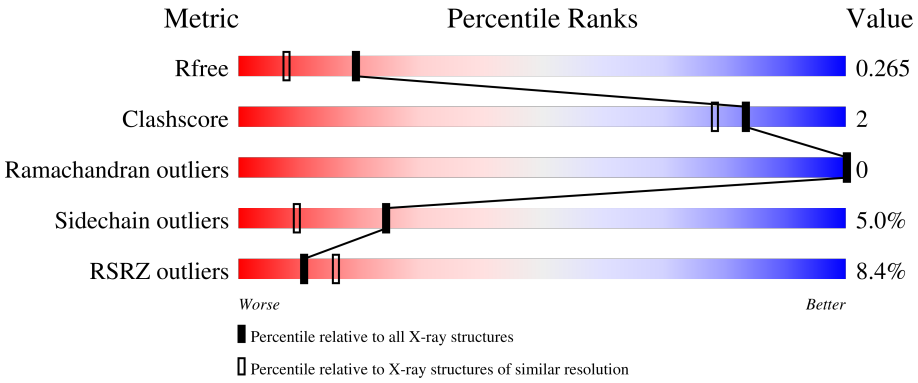
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 >=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 <=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	324	7% 79% 10% 11%
1	B	324	8% 86% 5% 8%

Validation Pipeline (wwPDB-VP) : 2.35

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4724 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 Geranyltranstransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	7	0
			2243	1406	405	419	13			
1	B	297	Total	C	N	O	S	0	3	0
			2284	1428	410	433	13			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP Q60AN0
A	0	VAL	-	expression tag	UNP Q60AN0
A	301	ALA	-	expression tag	UNP Q60AN0
A	302	GLU	-	expression tag	UNP Q60AN0
A	303	ASN	-	expression tag	UNP Q60AN0
A	304	LEU	-	expression tag	UNP Q60AN0
A	305	TYR	-	expression tag	UNP Q60AN0
A	306	PHE	-	expression tag	UNP Q60AN0
A	307	GLN	-	expression tag	UNP Q60AN0
A	308	SER	-	expression tag	UNP Q60AN0
A	309	HIS	-	expression tag	UNP Q60AN0
A	310	HIS	-	expression tag	UNP Q60AN0
A	311	HIS	-	expression tag	UNP Q60AN0
A	312	HIS	-	expression tag	UNP Q60AN0
A	313	HIS	-	expression tag	UNP Q60AN0
A	314	HIS	-	expression tag	UNP Q60AN0
A	315	TRP	-	expression tag	UNP Q60AN0
A	316	SER	-	expression tag	UNP Q60AN0
A	317	HIS	-	expression tag	UNP Q60AN0
A	318	PRO	-	expression tag	UNP Q60AN0
A	319	GLN	-	expression tag	UNP Q60AN0
A	320	PHE	-	expression tag	UNP Q60AN0
A	321	GLU	-	expression tag	UNP Q60AN0
A	322	LYS	-	expression tag	UNP Q60AN0
B	-1	MET	-	expression tag	UNP Q60AN0

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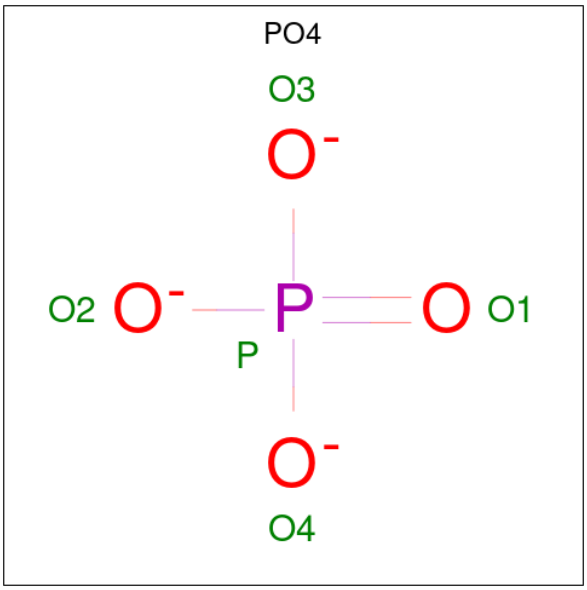
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	VAL	-	expression tag	UNP Q60AN0
B	301	ALA	-	expression tag	UNP Q60AN0
B	302	GLU	-	expression tag	UNP Q60AN0
B	303	ASN	-	expression tag	UNP Q60AN0
B	304	LEU	-	expression tag	UNP Q60AN0
B	305	TYR	-	expression tag	UNP Q60AN0
B	306	PHE	-	expression tag	UNP Q60AN0
B	307	GLN	-	expression tag	UNP Q60AN0
B	308	SER	-	expression tag	UNP Q60AN0
B	309	HIS	-	expression tag	UNP Q60AN0
B	310	HIS	-	expression tag	UNP Q60AN0
B	311	HIS	-	expression tag	UNP Q60AN0
B	312	HIS	-	expression tag	UNP Q60AN0
B	313	HIS	-	expression tag	UNP Q60AN0
B	314	HIS	-	expression tag	UNP Q60AN0
B	315	TRP	-	expression tag	UNP Q60AN0
B	316	SER	-	expression tag	UNP Q60AN0
B	317	HIS	-	expression tag	UNP Q60AN0
B	318	PRO	-	expression tag	UNP Q60AN0
B	319	GLN	-	expression tag	UNP Q60AN0
B	320	PHE	-	expression tag	UNP Q60AN0
B	321	GLU	-	expression tag	UNP Q60AN0
B	322	LYS	-	expression tag	UNP Q60AN0

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 3 is water.

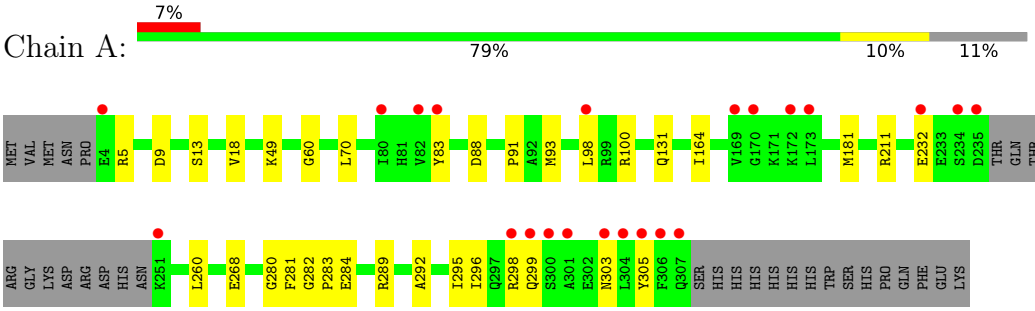
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	86	Total O 86 86	0	0
3	B	86	Total O 86 86	0	0

3 Residue-property plots (i)

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.

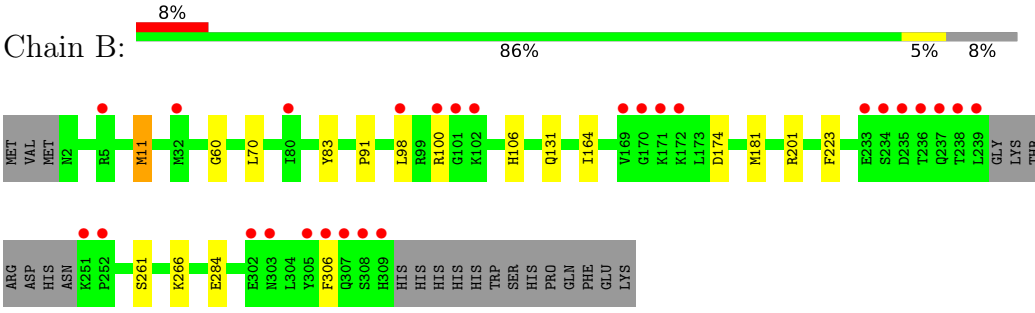
• Molecule 1: Geranyltranstransferase

Chain A:



• Molecule 1: Geranyltranstransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	114.59Å 114.59Å 113.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.94 40.26 – 1.94	Depositor EDS
% Data completeness (in resolution range)	93.8 (50.00-1.94) 93.9 (40.26-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	1.19 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.219 , 0.266 0.219 , 0.265	Depositor DCC
R_{free} test set	1631 reflections (3.09%)	wwPDB-VP
Wilson B-factor (Å^2)	39.3	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 40.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.013 for -h,-l,-k 0.005 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4724	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PO4

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	0.55	0/2290	0.66	0/3092
1	B	0.51	0/2331	0.61	0/3148
All	All	0.53	0/4621	0.64	0/6240

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

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	2243	0	2247	17	0
1	B	2284	0	2292	5	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
3	A	86	0	0	2	0
3	B	86	0	0	0	0
All	All	4724	0	4539	22	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.

All (22) 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:282[A]:GLY:C	1:A:284[A]:GLU:H	1.80	0.83
1:A:282[A]:GLY:C	1:A:284[A]:GLU:N	2.35	0.78
1:A:211:ARG:HH11	1:A:211:ARG:HG2	1.53	0.73
1:A:282[A]:GLY:O	1:A:284[A]:GLU:N	2.36	0.57
1:B:60:GLY:HA3	1:B:70:LEU:HD11	1.87	0.56
1:B:164:ILE:HG22	1:B:181:MET:HG3	1.89	0.53
1:A:211:ARG:HG2	1:A:211:ARG:NH1	2.20	0.51
1:A:232:GLU:HG2	1:A:260:LEU:HD13	1.94	0.50
1:A:281[B]:PHE:O	1:A:283[B]:PRO:HD2	2.15	0.47
1:A:295:ILE:HG22	1:A:296:ILE:HD13	1.98	0.45
1:A:164:ILE:HG22	1:A:181:MET:HG3	1.99	0.44
1:A:49:LYS:HE3	1:A:100[B]:ARG:HH12	1.82	0.43
1:B:174:ASP:N	1:B:174:ASP:OD2	2.49	0.43
1:A:282[B]:GLY:O	1:A:289:ARG:NH2	2.43	0.43
1:A:88:ASP:O	1:A:93:MET:HB2	2.19	0.42
1:A:292:ALA:O	1:A:296:ILE:HG12	2.19	0.42
1:A:280:GLY:HA2	3:A:368:HOH:O	2.19	0.42
1:B:11:MET:HE3	1:B:11:MET:HB3	1.90	0.42
1:A:60:GLY:HA3	1:A:70:LEU:HD11	2.01	0.42
1:B:91:PRO:HD3	1:B:106:HIS:CE1	2.55	0.41
1:A:211:ARG:NH1	3:A:337:HOH:O	2.53	0.41
1:A:295:ILE:HA	1:A:299:GLN:HB2	2.04	0.40

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	292/324 (90%)	286 (98%)	6 (2%)	0	100	100
1	B	296/324 (91%)	292 (99%)	4 (1%)	0	100	100
All	All	588/648 (91%)	578 (98%)	10 (2%)	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	228/258 (88%)	216 (95%)	12 (5%)	22 9
1	B	236/258 (92%)	225 (95%)	11 (5%)	26 11
All	All	464/516 (90%)	441 (95%)	23 (5%)	24 9

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ARG
1	A	9	ASP
1	A	13	SER
1	A	18	VAL
1	A	83	TYR
1	A	91	PRO
1	A	98	LEU
1	A	131	GLN
1	A	268	GLU
1	A	298	ARG
1	A	303	ASN
1	A	305	TYR
1	B	11	MET
1	B	83	TYR
1	B	98	LEU
1	B	100	ARG
1	B	131	GLN
1	B	201	ARG
1	B	223	PHE
1	B	261	SER
1	B	266	LYS
1	B	284	GLU
1	B	306	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	GLN
1	B	131	GLN
1	B	224	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	PO4	B	324	-	4,4,4	0.99	0	6,6,6	0.50	0
2	PO4	A	324	-	4,4,4	1.09	0	6,6,6	0.73	0
2	PO4	A	323	-	4,4,4	2.06	3 (75%)	6,6,6	1.17	0
2	PO4	B	325	-	4,4,4	0.79	0	6,6,6	0.59	0
2	PO4	B	323	-	4,4,4	1.01	0	6,6,6	0.49	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	323	PO4	P-O4	-2.38	1.47	1.54
2	A	323	PO4	P-O3	-2.33	1.47	1.54
2	A	323	PO4	P-O2	-2.02	1.48	1.54

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 (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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^{th} 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	289/324 (89%)	0.47	22 (7%) 13 19	27, 41, 81, 125	0
1	B	297/324 (91%)	0.41	27 (9%) 9 14	27, 42, 77, 100	0
All	All	586/648 (90%)	0.44	49 (8%) 11 16	27, 42, 79, 125	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	306	PHE	9.6
1	A	300	SER	8.6
1	A	304	LEU	8.3
1	A	301	ALA	7.8
1	B	305	TYR	7.3
1	A	235	ASP	6.9
1	A	305	TYR	5.8
1	B	101	GLY	5.8
1	A	170	GLY	5.7
1	B	236	THR	5.5
1	A	303	ASN	5.5
1	A	307	GLN	5.3
1	B	169	VAL	5.3
1	B	172	LYS	5.3
1	B	309	HIS	5.1
1	B	239	LEU	5.1
1	B	235	ASP	4.6
1	B	238	THR	4.4
1	A	172	LYS	4.2
1	A	169	VAL	4.2
1	A	234	SER	4.2
1	B	237	GLN	4.2
1	B	98	LEU	3.8
1	B	251	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	100	ARG	3.5
1	A	306	PHE	3.3
1	A	98	LEU	3.3
1	A	4	GLU	3.1
1	B	171	LYS	3.1
1	A	173	LEU	3.1
1	B	302	GLU	3.0
1	B	303	ASN	2.9
1	A	298	ARG	2.9
1	B	102[A]	LYS	2.6
1	B	5	ARG	2.6
1	A	251	LYS	2.5
1	B	170	GLY	2.5
1	A	82	VAL	2.5
1	A	232	GLU	2.5
1	B	307	GLN	2.4
1	B	234	SER	2.4
1	B	80	ILE	2.4
1	A	83	TYR	2.3
1	B	233	GLU	2.2
1	A	299	GLN	2.2
1	B	308	SER	2.2
1	B	32	MET	2.1
1	B	252	PRO	2.1
1	A	80	ILE	2.0

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 monosaccharides 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^{th} 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	PO4	B	325	5/5	0.93	0.18	50,50,69,71	0
2	PO4	B	323	5/5	0.94	0.13	62,70,77,77	0
2	PO4	B	324	5/5	0.94	0.14	77,78,88,95	0
2	PO4	A	323	5/5	0.94	0.12	55,59,74,83	0
2	PO4	A	324	5/5	0.98	0.12	42,49,50,67	0

6.5 Other polymers (i)

There are no such residues in this entry.