wwPDB X-ray Structure Validation Summary Report (i)

Jun 24, 2024 – 09:59 PM EDT

PDB ID	:	5WRU
Title	:	Crystal structure of type I inorganic pyrophosphatase from P falciparum
Authors	:	Jamwal, A.; Yogavel, M.; Sharma, A.
Deposited on	:	2016-12-03
Resolution	:	3.19 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 (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:

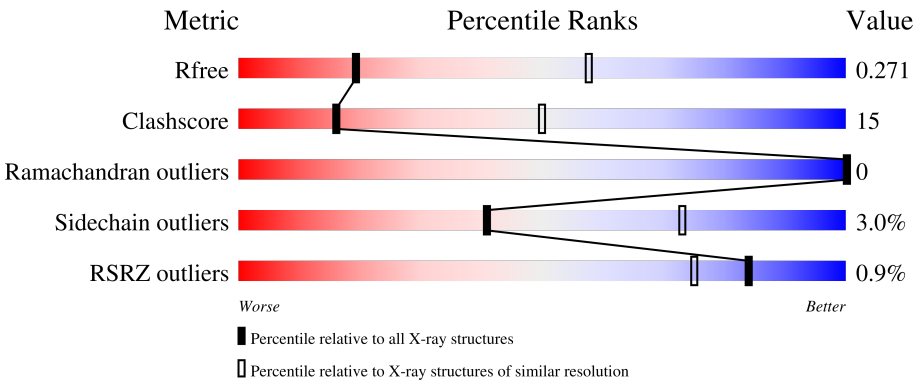
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.19 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	380	.% 62% 18% • 18%
1	B	380	59% 20% • 19%
1	C	380	.% 53% 25% • 19%
1	D	380	2% 51% 28% • 19%
1	E	380	57% 23% • 18%

2 Entry composition (i)

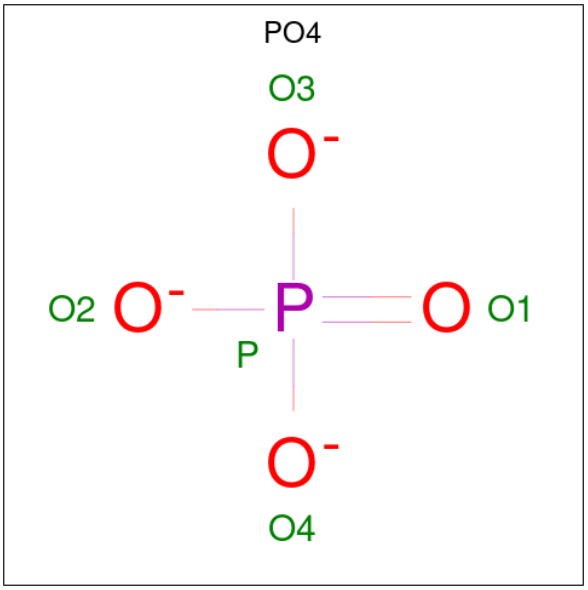
There are 2 unique types of molecules in this entry. The entry contains 13039 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Probable inorganic pyrophosphatase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	310	2626	1703	423	495	1	4	0	0	0
1	B	308	2614	1697	419	493	1	4	0	0	0
1	C	308	2589	1675	416	493	1	4	0	0	0
1	D	306	2575	1672	411	487	1	4	0	0	0
1	E	311	2625	1702	422	496	1	4	0	0	0

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



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

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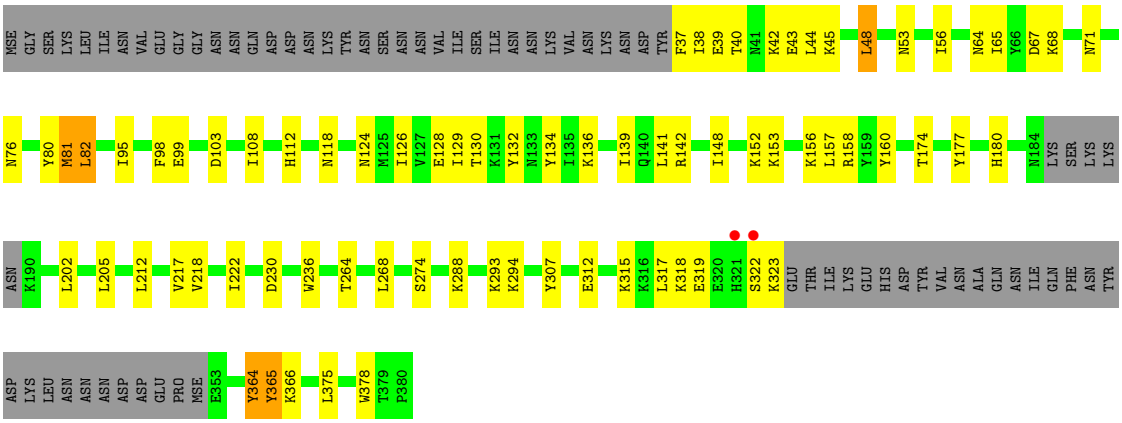
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	C	1	5	4	1	0	0

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.

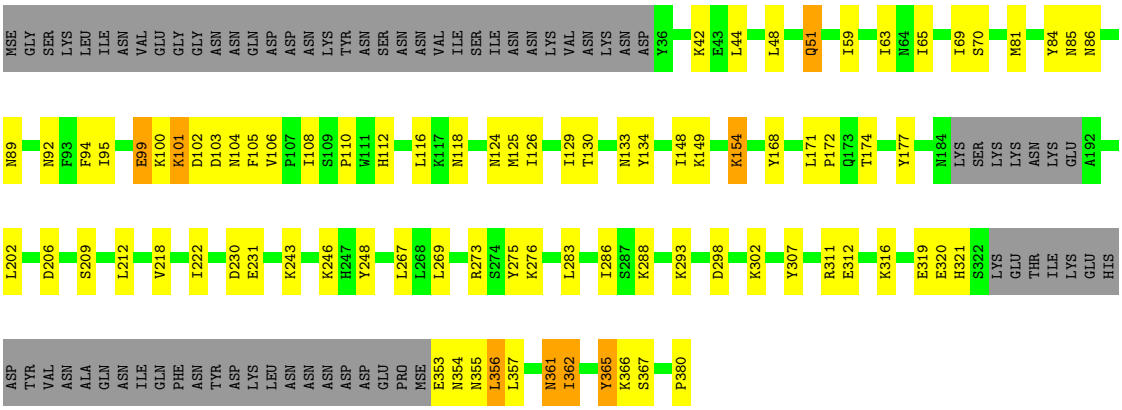
• Molecule 1: Probable inorganic pyrophosphatase

Chain A:



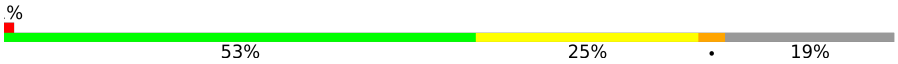
• Molecule 1: Probable inorganic pyrophosphatase

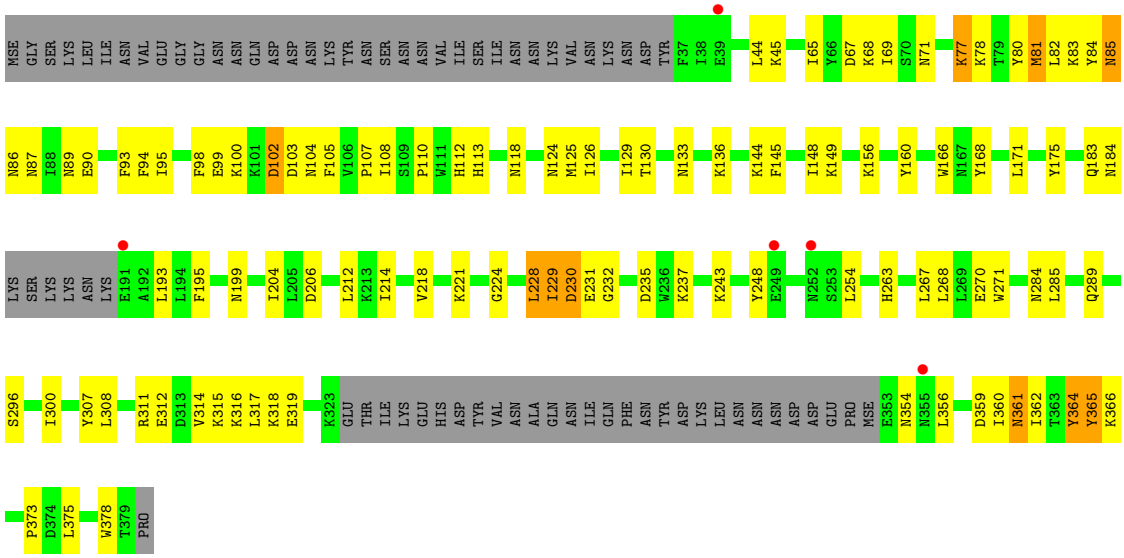
Chain B:



• Molecule 1: Probable inorganic pyrophosphatase

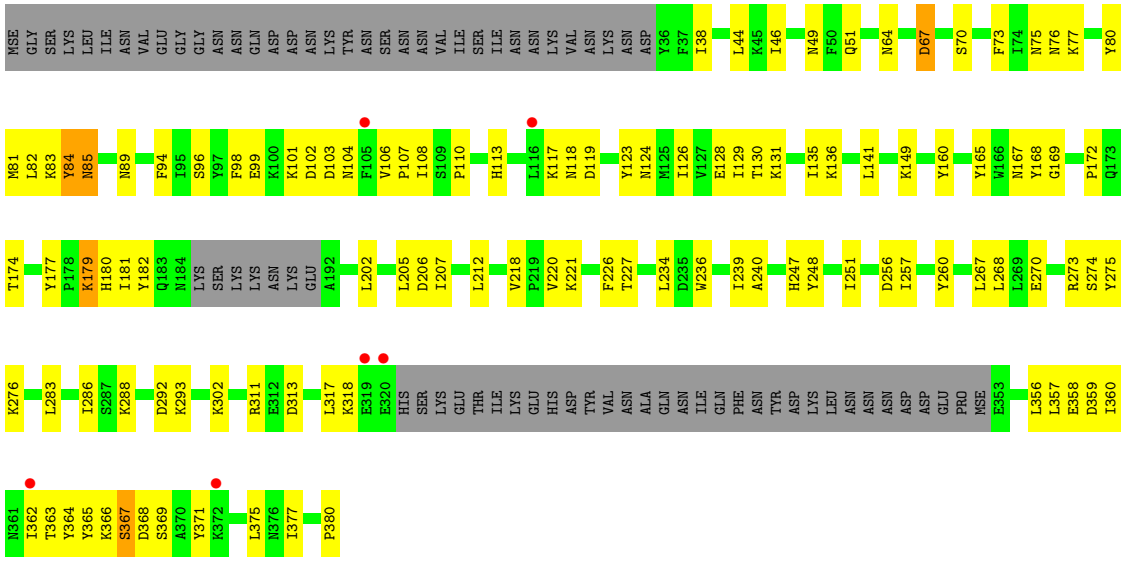
Chain C:





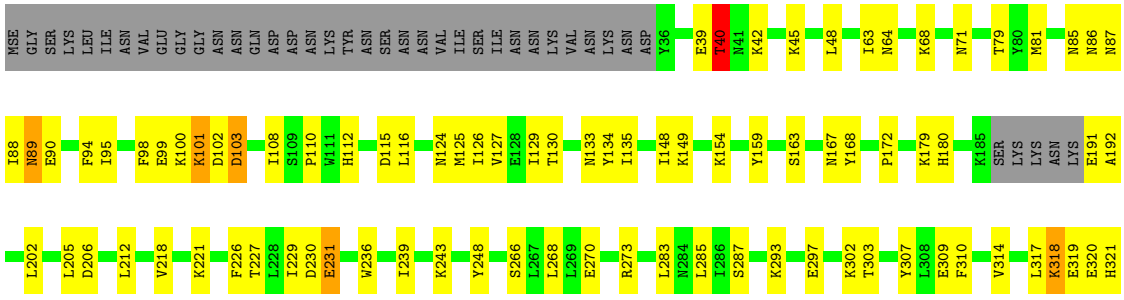
- Molecule 1: Probable inorganic pyrophosphatase

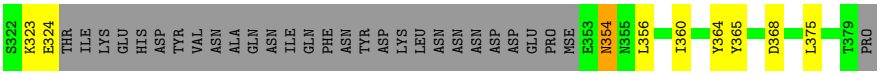
Chain D:



- Molecule 1: Probable inorganic pyrophosphatase

Chain E:




S322
K323
E324
THR
ILE
LYS
GLU
HIS
ASP
TYR
VAL
ASN
ALA
GLN
ASN
ILE
GLN
PHE
ASN
TYR
ASP
LYS
LEU
ASN
ASN
ASN
ASP
ASP
GLU
PRO
MSE
E353
N354
N355
L356
I360
Y364
Y365
D368
L375
T379
PRO

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	253.34Å 85.22Å 108.44Å 90.00° 114.95° 90.00°	Depositor
Resolution (Å)	44.91 – 3.19 49.16 – 3.19	Depositor EDS
% Data completeness (in resolution range)	94.6 (44.91-3.19) 94.1 (49.16-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.71 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.234 , 0.277 0.234 , 0.271	Depositor DCC
R_{free} test set	1997 reflections (5.78%)	wwPDB-VP
Wilson B-factor (Å^2)	54.7	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 15.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	13039	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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 (i)

5.1 Standard geometry (i)

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	0.77	6/2684 (0.2%)	0.57	0/3615
1	B	0.62	2/2673 (0.1%)	0.57	3/3604 (0.1%)
1	C	0.58	1/2645 (0.0%)	0.59	0/3568
1	D	0.48	1/2632 (0.0%)	0.58	0/3551
1	E	0.64	1/2681 (0.0%)	0.58	3/3612 (0.1%)
All	All	0.63	11/13315 (0.1%)	0.58	6/17950 (0.0%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	364	TYR	CE1-CZ	-7.49	1.28	1.38
1	A	80	TYR	CE1-CZ	-7.39	1.28	1.38
1	A	134	TYR	CE1-CZ	-6.88	1.29	1.38
1	B	84	TYR	CE1-CZ	-6.58	1.29	1.38
1	A	132	TYR	CE1-CZ	-6.26	1.30	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	101	LYS	N-CA-C	-7.74	90.11	111.00
1	B	365	TYR	N-CA-C	7.63	131.60	111.00
1	B	365	TYR	CB-CA-C	-6.96	96.49	110.40
1	E	231	GLU	N-CA-C	-6.88	92.41	111.00
1	E	40	THR	N-CA-C	-5.24	96.85	111.00

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	2626	0	2591	55	0
1	B	2614	0	2571	64	0
1	C	2589	0	2522	115	0
1	D	2575	0	2518	92	0
1	E	2625	0	2585	67	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
All	All	13039	0	12787	375	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 15.

The worst 5 of 375 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:C:85:ASN:ND2	1:C:94:PHE:CE2	1.73	1.55
1:C:184:ASN:CB	1:C:360:ILE:HD11	1.42	1.50
1:D:83:LYS:CB	1:D:96:SER:OG	1.67	1.40
1:C:356:LEU:CA	1:C:359:ASP:OD1	1.72	1.35
1:A:82:LEU:HD11	1:A:95:ILE:CG2	1.64	1.24

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	304/380 (80%)	292 (96%)	12 (4%)	0	100	100
1	B	302/380 (80%)	293 (97%)	9 (3%)	0	100	100
1	C	302/380 (80%)	289 (96%)	13 (4%)	0	100	100
1	D	300/380 (79%)	289 (96%)	11 (4%)	0	100	100
1	E	305/380 (80%)	293 (96%)	12 (4%)	0	100	100
All	All	1513/1900 (80%)	1456 (96%)	57 (4%)	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	294/355 (83%)	286 (97%)	8 (3%)	44	75
1	B	293/355 (82%)	284 (97%)	9 (3%)	40	72
1	C	287/355 (81%)	275 (96%)	12 (4%)	30	65
1	D	285/355 (80%)	277 (97%)	8 (3%)	43	74
1	E	292/355 (82%)	285 (98%)	7 (2%)	49	77
All	All	1451/1775 (82%)	1407 (97%)	44 (3%)	41	73

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	365	TYR
1	D	367	SER
1	D	67	ASP
1	D	179	LYS
1	E	40	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	133	ASN
1	E	89	ASN
1	C	289	GLN
1	C	76	ASN
1	D	53	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	C	401	-	4,4,4	1.03	0	6,6,6	0.44	0
2	PO4	B	401	1	4,4,4	1.05	0	6,6,6	0.51	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.

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 (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	306/380 (80%)	-0.15	2 (0%) 87 81	29, 38, 54, 70	0
1	B	304/380 (80%)	-0.11	0 100 100	30, 44, 62, 92	0
1	C	304/380 (80%)	0.19	5 (1%) 72 59	46, 66, 82, 90	0
1	D	302/380 (79%)	0.31	6 (1%) 65 51	53, 74, 87, 94	0
1	E	307/380 (80%)	-0.18	0 100 100	27, 34, 52, 75	0
All	All	1523/1900 (80%)	0.01	13 (0%) 84 75	27, 49, 82, 94	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	355	ASN	3.3
1	D	319	GLU	2.8
1	D	320	GLU	2.8
1	A	322	SER	2.6
1	A	321	HIS	2.6

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, 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	PO4	B	401	5/5	0.76	0.28	47,48,52,55	0
2	PO4	C	401	5/5	0.85	0.32	70,72,75,77	0

6.5 Other polymers (i)

There are no such residues in this entry.