



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:17 PM GMT

PDB ID : 4OE1  
Title : Crystal structure of the pentatricopeptide repeat protein PPR10 (C256S/C430S/C449S) in complex with an 18-nt PSAJ rna element  
Authors : Li, Q.; Yan, C.; Wu, J.; Yin, P.; Yan, N.  
Deposited on : 2014-01-11  
Resolution : 2.80 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

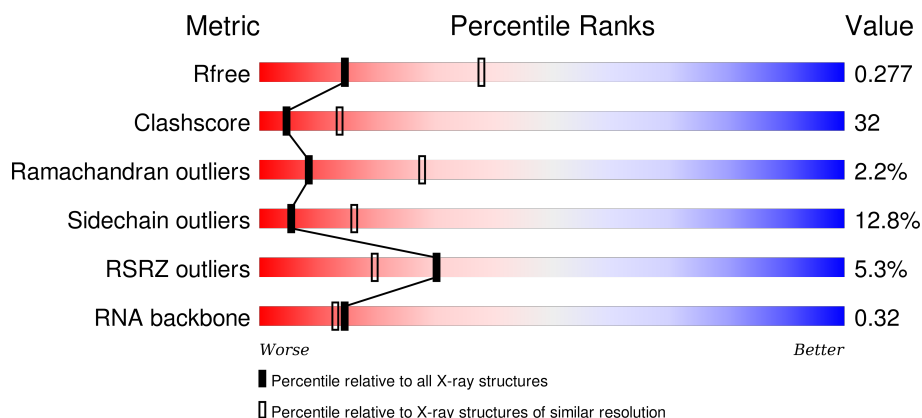
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)
RNA backbone	2183	1091 (3.20-2.40)

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	718	<div> <div>5%</div> <div>49%</div> <div>38%</div> <div>7%</div> <div>• •</div> </div>
1	B	718	<div> <div>5%</div> <div>56%</div> <div>33%</div> <div>6%</div> <div>5%</div> </div>
2	C	18	<div> <div>44%</div> <div>11%</div> <div>22%</div> <div>22%</div> </div>
2	D	18	<div> <div>6%</div> <div>11%</div> <div>39%</div> <div>50%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11033 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 Chloroplast pentatricopeptide repeat protein 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	687	Total	C	N	O	S	16	0	0
			5202	3284	890	985	43			
1	B	683	Total	C	N	O	S	14	0	0
			5179	3273	891	973	42			

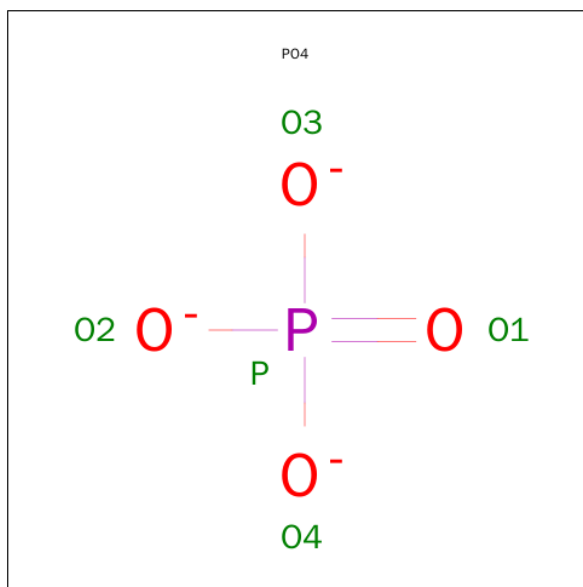
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	256	SER	CYS	ENGINEERED MUTATION	UNP B8Y6I0
A	430	SER	CYS	ENGINEERED MUTATION	UNP B8Y6I0
A	449	SER	CYS	ENGINEERED MUTATION	UNP B8Y6I0
B	256	SER	CYS	ENGINEERED MUTATION	UNP B8Y6I0
B	430	SER	CYS	ENGINEERED MUTATION	UNP B8Y6I0
B	449	SER	CYS	ENGINEERED MUTATION	UNP B8Y6I0

- Molecule 2 is a RNA chain called psaJ RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	18	Total	C	N	O	P	3	0	0
			368	167	53	131	17			
2	C	14	Total	C	N	O	P	4	0	0
			279	126	41	99	13			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).

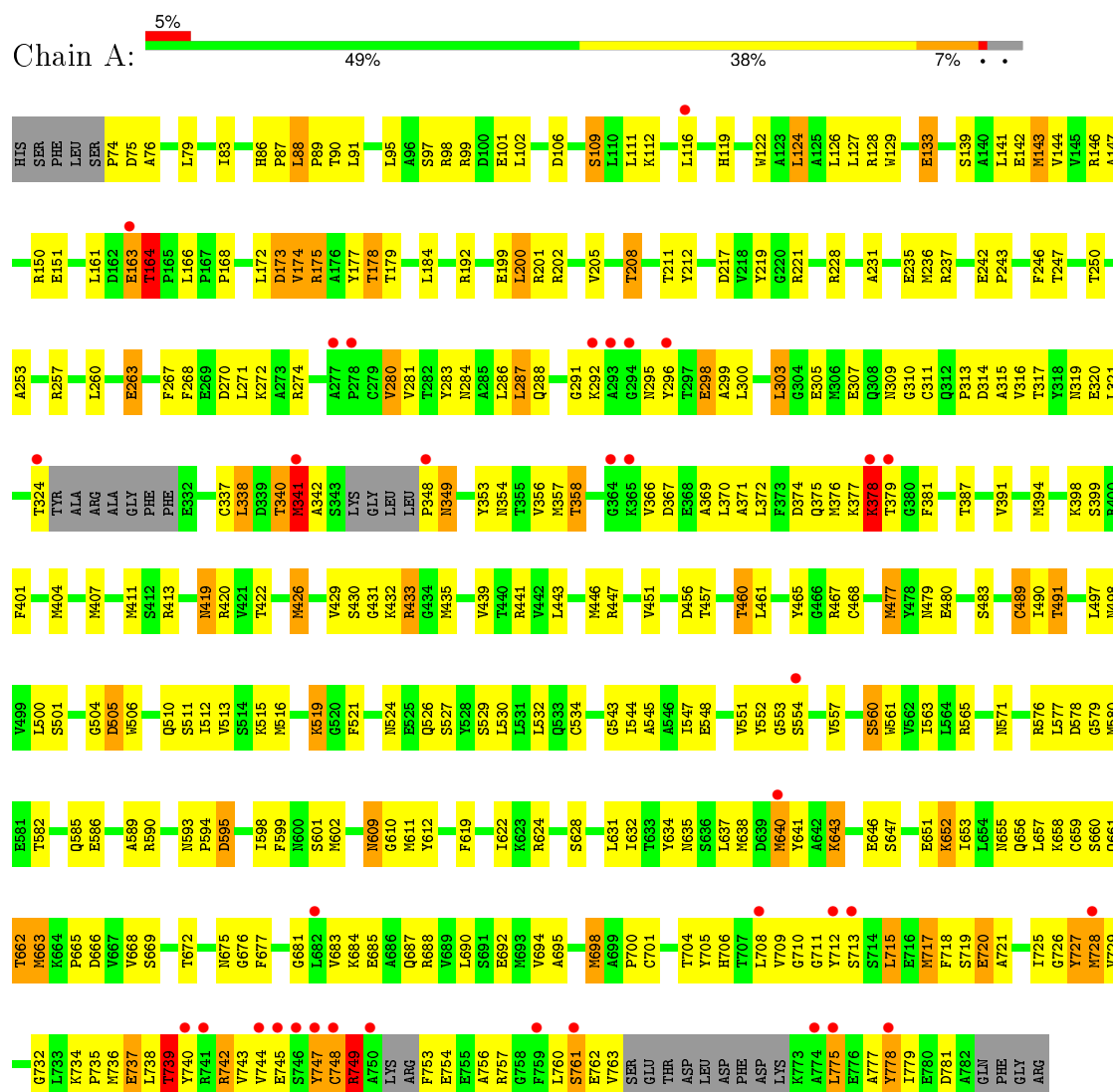


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	P	5	0
			5	4	1		

### 3 Residue-property plots

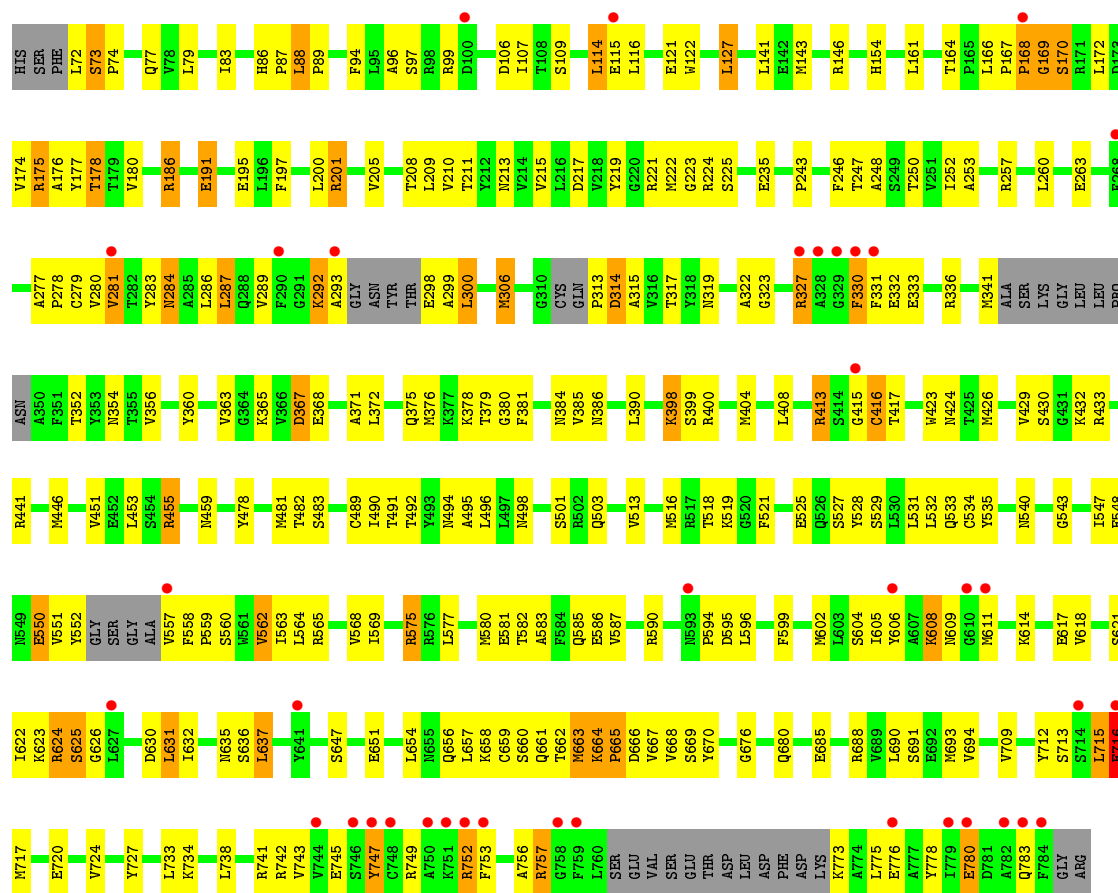
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ( $\text{RSRZ} > 2$ ). 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: Chloroplast pentatricopeptide repeat protein 10



- Molecule 1: Chloroplast pentatricopeptide repeat protein 10

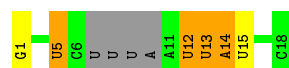




• Molecule 2: psaJ RNA



• Molecule 2: psaJ RNA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.32Å 83.32Å 225.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.26 – 2.80 34.26 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.2 (34.26-2.80) 98.2 (34.26-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.263 , 0.278 0.265 , 0.277	Depositor DCC
$R_{free}$ test set	1845 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	67.0	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 55.6	EDS
Estimated twinning fraction	0.054 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 37060 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	11033	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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: 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	0.72	1/5294 (0.0%)	0.53	0/7177
1	B	0.78	1/5269 (0.0%)	0.58	1/7136 (0.0%)
2	C	0.27	0/308	0.72	0/474
2	D	0.33	0/408	0.66	0/631
All	All	0.73	2/11279 (0.0%)	0.56	1/15418 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	548	GLU	C-N	-7.04	1.17	1.34
1	A	468	CYS	CB-SG	-5.76	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	313	PRO	N-CA-CB	6.03	110.54	103.30

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	5202	0	5106	380	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5179	0	5067	272	1
2	C	279	0	146	10	0
2	D	368	0	189	60	0
3	B	5	0	0	0	0
All	All	11033	0	10508	688	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 32.

The worst 5 of 688 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:706:HIS:CE1	1:A:738:LEU:HD22	1.19	1.62
1:A:296:TYR:CE1	1:A:300:LEU:HD11	1.38	1.59
1:A:489:CYS:SG	1:A:491:THR:HG22	1.50	1.51
1:A:79:LEU:HD13	1:A:98:ARG:NH2	1.32	1.43
1:A:515:LYS:NZ	1:A:519:LYS:HE3	1.21	1.43

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)
1:A:168:PRO:O	1:A:447:ARG:NH1[1_565]	1.96	0.24
1:A:413:ARG:NE	1:B:518:THR:O[3_744]	2.16	0.04

## 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	677/718 (94%)	599 (88%)	65 (10%)	13 (2%)	10	32
1	B	671/718 (94%)	605 (90%)	50 (8%)	16 (2%)	7	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1348/1436 (94%)	1204 (89%)	115 (8%)	29 (2%)	8	28

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	168	PRO
1	B	315	ALA
1	B	665	PRO
1	A	511	SER
1	A	698	MET

### 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	539/587 (92%)	456 (85%)	83 (15%)	3	10
1	B	530/587 (90%)	476 (90%)	54 (10%)	9	26
All	All	1069/1174 (91%)	932 (87%)	137 (13%)	5	16

5 of 137 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	643	LYS
1	A	747	TYR
1	B	625	SER
1	A	659	CYS
1	A	720	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	731	HIS
1	B	153	GLN
1	B	655	ASN

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Mol	Chain	Res	Type
1	A	706	HIS
1	B	656	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	12/18 (66%)	5 (41%)	2 (16%)
2	D	17/18 (94%)	9 (52%)	3 (17%)
All	All	29/36 (80%)	14 (48%)	5 (17%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	D	6	C
2	D	7	U
2	D	9	U
2	D	10	A
2	D	11	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	D	5	U
2	D	9	U
2	D	14	A
2	C	12	U
2	C	13	U

## 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](#)

1 ligand is 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	$\# Z  > 2$
3	PO4	B	801	-	4,4,4	0.48	0	6,6,6	0.27	0

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
3	PO4	B	801	-	-	0/0/0/0	0/0/0/0

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, 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	687/718 (95%)	0.20	35 (5%) 32 21	32, 75, 135, 243	104 (15%)
1	B	683/718 (95%)	0.27	38 (5%) 28 18	40, 74, 128, 237	86 (12%)
2	C	14/18 (77%)	-0.03	0 100 100	56, 82, 108, 120	4 (28%)
2	D	18/18 (100%)	0.45	1 (5%) 28 18	73, 89, 135, 158	7 (38%)
All	All	1402/1472 (95%)	0.24	74 (5%) 30 20	32, 75, 133, 243	201 (14%)

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	784	PHE	12.2
1	B	329	GLY	7.8
1	B	780	GLU	6.1
1	B	748	CYS	6.1
1	B	750	ALA	5.8

### 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( $\text{\AA}^2$ )	Q<0.9
3	PO4	B	801	5/5	-	-	-	78,79,79,79	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.