



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 03:52 AM EDT

PDB ID : 7JUK  
Title : Crystal structure of PTEN with a tetra-phosphorylated tail (4p-crPTEN-13sp-T2, SDTTDSDPENEG)  
Authors : Dempsey, D.; Phan, K.; Cole, P.; Gabelli, S.B.  
Deposited on : 2020-08-19  
Resolution : 3.15 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](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

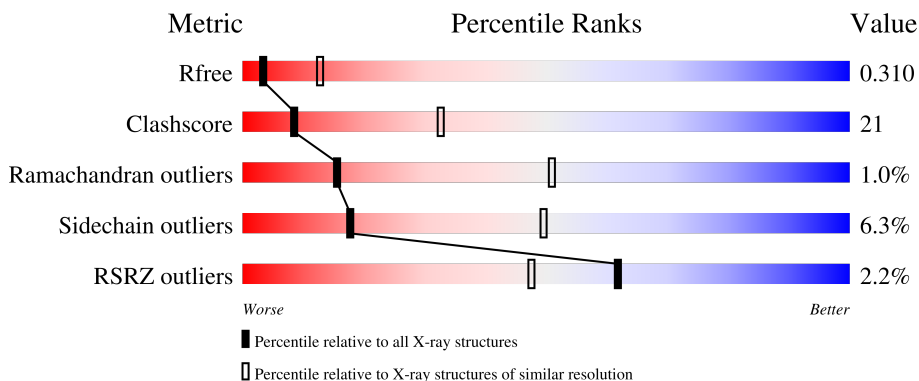
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	349	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2627 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 Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	2621	1698	448	459	16	0	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	MET	-	initiating methionine	UNP P60484
A	354	THR	-	linker	UNP P60484
A	355	GLY	-	linker	UNP P60484
A	356	GLY	-	linker	UNP P60484
A	357	GLY	-	linker	UNP P60484
A	358	SER	-	linker	UNP P60484
A	359	GLY	-	linker	UNP P60484
A	360	GLY	-	linker	UNP P60484
A	361	THR	-	linker	UNP P60484
A	362	GLY	-	linker	UNP P60484
A	363	GLY	-	linker	UNP P60484
A	364	CYS	-	linker	UNP P60484
A	378	GLY	-	cloning artifact	UNP P60484

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

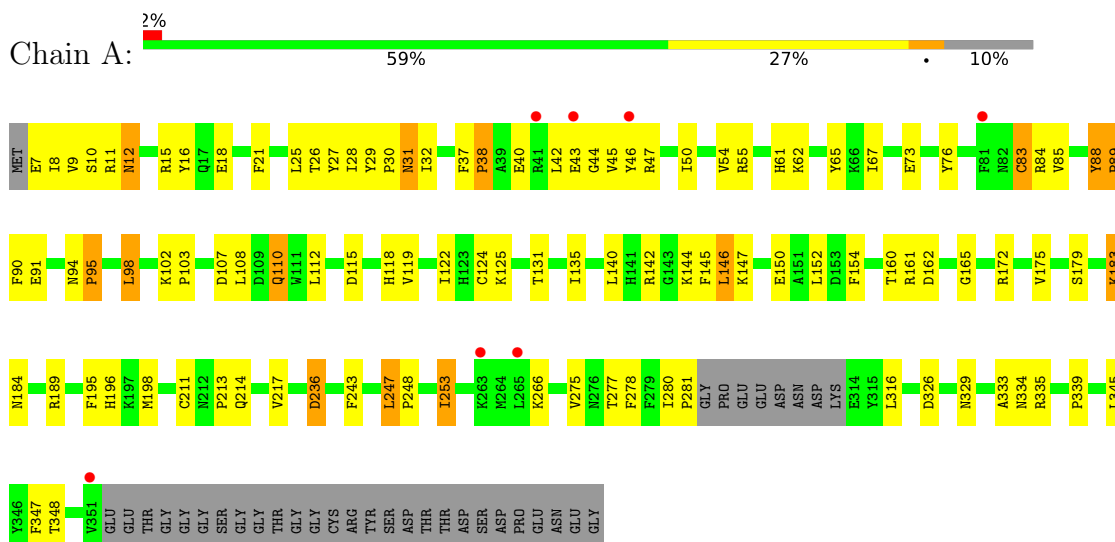
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	1	1	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: Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN



## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.44Å 113.44Å 57.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.52 – 3.15 28.50 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (28.52-3.15) 99.4 (28.50-3.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 3.17Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.184 , 0.289 0.214 , 0.310	Depositor DCC
$R_{free}$ test set	322 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	85.7	Xtrriage
Anisotropy	0.545	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 56.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.038 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2627	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	97.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.63% 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: 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	0.76	7/2695 (0.3%)	0.79	5/3635 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	38	PRO	N-CA	13.22	1.69	1.47
1	A	89	PRO	N-CA	13.07	1.69	1.47
1	A	95	PRO	N-CA	12.70	1.68	1.47
1	A	189	ARG	C-N	8.57	1.50	1.34
1	A	37	PHE	C-N	5.93	1.45	1.34
1	A	88	TYR	C-N	5.90	1.45	1.34
1	A	94	ASN	C-N	5.63	1.45	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	PRO	CA-N-CD	-8.13	100.11	111.50
1	A	38	PRO	CA-N-CD	-7.74	100.66	111.50
1	A	95	PRO	CA-N-CD	-7.42	101.11	111.50
1	A	95	PRO	N-CA-C	-5.28	98.37	112.10
1	A	90	PHE	CB-CA-C	5.22	120.85	110.40

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	2621	0	2575	108	2
2	A	5	0	0	0	1
3	A	1	0	0	0	0
All	All	2627	0	2575	108	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 21.

All (108) 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:95:PRO:N	1:A:95:PRO:CA	1.68	1.42
1:A:89:PRO:CA	1:A:89:PRO:N	1.69	1.38
1:A:38:PRO:N	1:A:38:PRO:CA	1.69	1.32
1:A:142:ARG:HH11	1:A:142:ARG:HG3	1.32	0.94
1:A:102:LYS:HB3	1:A:103:PRO:HD3	1.48	0.93
1:A:8:ILE:HG21	1:A:45:VAL:HA	1.50	0.91
1:A:9:VAL:CG1	1:A:47:ARG:HH12	1.84	0.90
1:A:9:VAL:HG13	1:A:47:ARG:HH12	1.44	0.81
1:A:25:LEU:HD12	1:A:25:LEU:O	1.85	0.77
1:A:152:LEU:HD23	1:A:172:ARG:CZ	2.15	0.76
1:A:102:LYS:HB3	1:A:103:PRO:CD	2.16	0.76
1:A:122:ILE:HG22	1:A:131:THR:HG23	1.69	0.75
1:A:142:ARG:HG3	1:A:142:ARG:NH1	2.03	0.74
1:A:183:LYS:HB3	1:A:183:LYS:NZ	2.04	0.72
1:A:333:ALA:HB3	1:A:335:ARG:HG3	1.71	0.71
1:A:95:PRO:N	1:A:95:PRO:C	2.43	0.71
1:A:42:LEU:HD12	1:A:42:LEU:O	1.90	0.70
1:A:8:ILE:CG2	1:A:45:VAL:HA	2.20	0.70
1:A:9:VAL:CG1	1:A:47:ARG:NH1	2.52	0.70
1:A:110:GLN:CA	1:A:110:GLN:HE21	2.04	0.70
1:A:110:GLN:HE21	1:A:110:GLN:HA	1.59	0.67
1:A:29:TYR:HB3	1:A:30:PRO:HD2	1.76	0.67
1:A:316:LEU:N	1:A:316:LEU:HD12	2.10	0.67
1:A:333:ALA:CB	1:A:335:ARG:HG3	2.25	0.67
1:A:18:GLU:HA	1:A:18:GLU:OE1	1.95	0.65
1:A:9:VAL:HG12	1:A:47:ARG:HH12	1.59	0.65
1:A:38:PRO:N	1:A:38:PRO:C	2.50	0.65
1:A:9:VAL:HG12	1:A:47:ARG:NH1	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:TYR:HA	1:A:119:VAL:O	1.97	0.64
1:A:108:LEU:O	1:A:108:LEU:HD23	1.97	0.64
1:A:9:VAL:HG13	1:A:47:ARG:NH1	2.11	0.63
1:A:183:LYS:HB3	1:A:183:LYS:HZ1	1.61	0.63
1:A:115:ASP:HB3	1:A:118:HIS:ND1	2.15	0.62
1:A:42:LEU:HD12	1:A:42:LEU:C	2.22	0.60
1:A:91:GLU:OE2	1:A:91:GLU:HA	2.03	0.58
1:A:122:ILE:CG2	1:A:131:THR:HG23	2.33	0.58
1:A:8:ILE:HG21	1:A:45:VAL:CA	2.28	0.58
1:A:12:ASN:HD22	1:A:12:ASN:N	2.02	0.57
1:A:140:LEU:HD13	1:A:179:SER:HB2	1.88	0.56
1:A:28:ILE:HD12	1:A:135:ILE:HD13	1.87	0.55
1:A:110:GLN:O	1:A:110:GLN:NE2	2.40	0.55
1:A:29:TYR:OH	1:A:144:LYS:HG2	2.07	0.54
1:A:25:LEU:HD12	1:A:25:LEU:C	2.27	0.54
1:A:122:ILE:HD12	1:A:122:ILE:N	2.23	0.54
1:A:98:LEU:HD13	1:A:98:LEU:O	2.09	0.53
1:A:88:TYR:N	1:A:89:PRO:CD	2.72	0.53
1:A:211:CYS:O	1:A:213:PRO:HD3	2.09	0.53
1:A:198:MET:HG2	1:A:345:LEU:CD2	2.40	0.52
1:A:28:ILE:HD12	1:A:135:ILE:HG21	1.91	0.52
1:A:115:ASP:HB3	1:A:118:HIS:CE1	2.44	0.51
1:A:316:LEU:N	1:A:316:LEU:CD1	2.73	0.51
1:A:334:ASN:ND2	1:A:339:PRO:HD3	2.25	0.51
1:A:102:LYS:CB	1:A:103:PRO:HD3	2.30	0.51
1:A:124:CYS:SG	1:A:125:LYS:N	2.85	0.50
1:A:147:LYS:O	1:A:147:LYS:HG2	2.11	0.50
1:A:28:ILE:CD1	1:A:135:ILE:HD13	2.41	0.50
1:A:83:CYS:SG	1:A:84:ARG:N	2.84	0.49
1:A:110:GLN:CA	1:A:110:GLN:NE2	2.73	0.49
1:A:115:ASP:HB3	1:A:118:HIS:CG	2.48	0.49
1:A:147:LYS:HB3	1:A:150:GLU:HG3	1.94	0.49
1:A:12:ASN:N	1:A:12:ASN:ND2	2.60	0.48
1:A:198:MET:HG2	1:A:345:LEU:HD23	1.96	0.48
1:A:7:GLU:O	1:A:10:SER:N	2.43	0.48
1:A:280:ILE:HB	1:A:281:PRO:HD3	1.96	0.47
1:A:28:ILE:CD1	1:A:135:ILE:HG21	2.44	0.47
1:A:8:ILE:HG23	1:A:11:ARG:HD3	1.95	0.47
1:A:26:THR:HG22	1:A:27:TYR:N	2.30	0.47
1:A:50:ILE:O	1:A:54:VAL:HG23	2.14	0.47
1:A:31:ASN:ND2	1:A:32:ILE:HG13	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LEU:HD23	1:A:172:ARG:NH2	2.29	0.46
1:A:142:ARG:NH1	1:A:142:ARG:CG	2.73	0.46
1:A:152:LEU:CD1	1:A:175:VAL:HG11	2.45	0.46
1:A:183:LYS:NZ	1:A:183:LYS:CB	2.74	0.46
1:A:12:ASN:HA	1:A:15:ARG:HH12	1.81	0.46
1:A:277:THR:HA	1:A:280:ILE:HD12	1.97	0.46
1:A:8:ILE:HA	1:A:11:ARG:HG3	1.98	0.45
1:A:67:ILE:HB	1:A:85:VAL:HG22	1.98	0.45
1:A:115:ASP:CB	1:A:118:HIS:CE1	2.99	0.45
1:A:147:LYS:N	1:A:150:GLU:OE2	2.48	0.45
1:A:31:ASN:C	1:A:31:ASN:HD22	2.18	0.45
1:A:42:LEU:C	1:A:42:LEU:CD1	2.85	0.45
1:A:95:PRO:HG2	1:A:95:PRO:O	2.16	0.45
1:A:146:LEU:CD2	1:A:146:LEU:C	2.85	0.45
1:A:42:LEU:HB2	1:A:46:TYR:O	2.17	0.45
1:A:278:PHE:CD1	1:A:278:PHE:O	2.70	0.45
1:A:280:ILE:N	1:A:281:PRO:CD	2.80	0.45
1:A:160:THR:HG21	1:A:165:GLY:H	1.82	0.44
1:A:217:VAL:HG13	1:A:253:ILE:HD11	1.99	0.44
1:A:316:LEU:HD13	1:A:348:THR:HA	1.99	0.44
1:A:88:TYR:N	1:A:89:PRO:HD2	2.32	0.43
1:A:108:LEU:HD23	1:A:108:LEU:C	2.39	0.43
1:A:107:ASP:OD1	1:A:107:ASP:C	2.57	0.43
1:A:196:HIS:O	1:A:243:PHE:HD2	2.02	0.43
1:A:145:PHE:HZ	1:A:154:PHE:CD2	2.36	0.42
1:A:108:LEU:HD21	1:A:112:LEU:HD11	2.01	0.42
1:A:110:GLN:NE2	1:A:110:GLN:C	2.73	0.42
1:A:183:LYS:HG3	1:A:184:ASN:ND2	2.35	0.42
1:A:146:LEU:HD22	1:A:146:LEU:N	2.35	0.41
1:A:161:ARG:HB3	1:A:161:ARG:CZ	2.51	0.41
1:A:247:LEU:HD23	1:A:248:PRO:HD2	2.01	0.41
1:A:12:ASN:HD22	1:A:12:ASN:H	1.68	0.41
1:A:29:TYR:CZ	1:A:144:LYS:HG2	2.55	0.41
1:A:31:ASN:ND2	1:A:31:ASN:H	2.18	0.41
1:A:12:ASN:HA	1:A:15:ARG:HH22	1.86	0.40
1:A:16:TYR:N	1:A:16:TYR:CD1	2.89	0.40
1:A:326:ASP:O	1:A:329:ASN:ND2	2.54	0.40
1:A:61:HIS:CD2	1:A:119:VAL:HG21	2.55	0.40
1:A:40:GLU:OE2	1:A:76:TYR:HB2	2.21	0.40

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:43:GLU:OE2	2:A:401:PO4:O4[6_444]	1.93	0.27
1:A:84:ARG:NH1	1:A:236:ASP:OD1[4_555]	2.06	0.14

### 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	309/349 (88%)	277 (90%)	29 (9%)	3 (1%)	15 51

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	LYS
1	A	44	GLY
1	A	236	ASP

#### 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	285/313 (91%)	267 (94%)	18 (6%)	18 49

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	21	PHE

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Mol	Chain	Res	Type
1	A	31	ASN
1	A	55	ARG
1	A	73	GLU
1	A	83	CYS
1	A	98	LEU
1	A	110	GLN
1	A	146	LEU
1	A	162	ASP
1	A	183	LYS
1	A	195	PHE
1	A	214	GLN
1	A	247	LEU
1	A	253	ILE
1	A	266	LYS
1	A	275	VAL
1	A	347	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	31	ASN
1	A	82	ASN
1	A	110	GLN
1	A	171	GLN
1	A	228	ASN
1	A	261	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](#)

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
2	PO4	A	401	-	4,4,4	0.70	0	6,6,6	0.43	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	PO4	0	1

## 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	313/349 (89%)	-0.07	7 (2%) 62 47	62, 90, 144, 178	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	265	LEU	6.4
1	A	263	LYS	4.1
1	A	46	TYR	2.8
1	A	43	GLU	2.7
1	A	81	PHE	2.7
1	A	41	ARG	2.2
1	A	351	VAL	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<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	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	A	401	5/5	0.86	0.67	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.