



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:00 PM GMT

PDB ID : 1I9Z  
Title : CRYSTAL STRUCTURE OF INOSITOL POLYPHOSPHATE 5-PHOSPHATASE DOMAIN (IPP5C) OF SPSYNAPTOJANIN IN COMPLEX WITH INOSITOL (1,4)-BISPHOSPHATE AND CALCIUM ION  
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Deposited on : 2001-03-21  
Resolution : 1.80 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  
<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

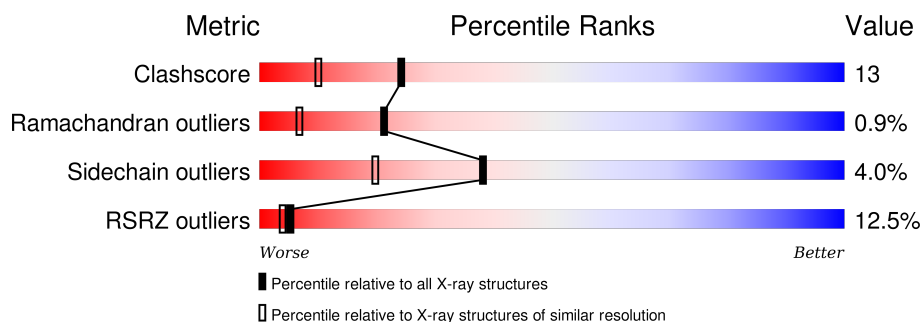
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	347	

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	A	301	-	-	-	X
3	2IP	A	302	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3011 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.

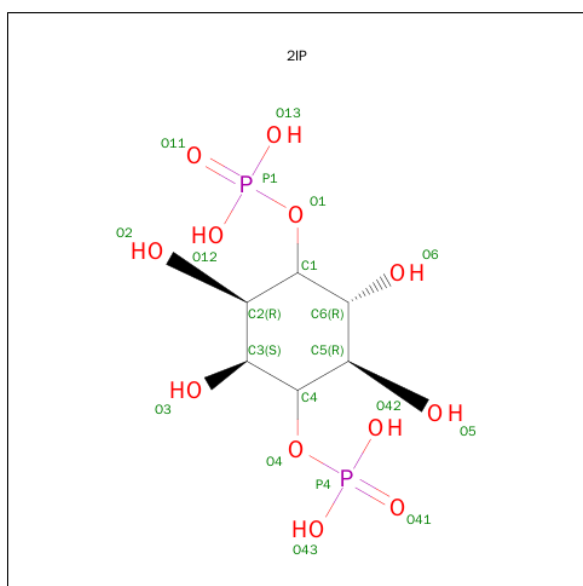
- Molecule 1 is a protein called PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	1	0
			2766	1771	473	513	9			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is D-MYO-INOSITOL-1,4-BISPHOSPHATE (three-letter code: 2IP) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>12</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			20	6	12	2		

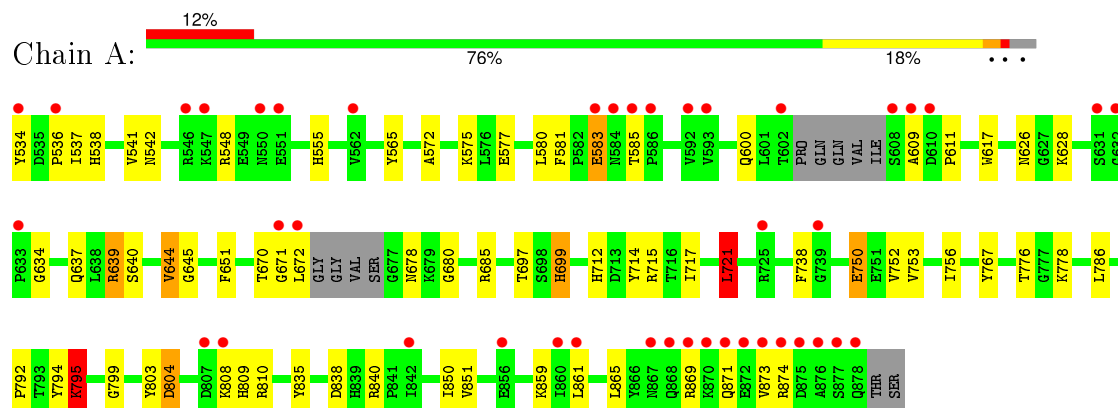
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	224	Total 224	O 224	0	0

### 3 Residue-property plots [i](#)

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: PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	149.00Å 67.70Å 51.99Å 90.00° 106.15° 90.00°	Depositor
Resolution (Å)	32.00 – 1.80 27.82 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (32.00-1.80) 93.3 (27.82-1.80)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.76 (at 1.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.191 , 0.218 0.200 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	19.0	Xtriage
Anisotropy	0.891	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 52.0	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	0 of 44082 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3011	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.34% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 2IP

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	1.04	4/2835 (0.1%)	1.17	12/3834 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	752	VAL	CB-CG2	5.98	1.65	1.52
1	A	795	LYS	CB-CG	-5.75	1.37	1.52
1	A	767	TYR	CD1-CE1	5.57	1.47	1.39
1	A	803	TYR	CG-CD2	5.03	1.45	1.39

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	639	ARG	NE-CZ-NH1	25.91	133.26	120.30
1	A	639	ARG	NE-CZ-NH2	-23.05	108.77	120.30
1	A	794	TYR	C-N-CA	17.05	164.33	121.70
1	A	794	TYR	O-C-N	11.74	141.49	122.70
1	A	794	TYR	CA-C-N	-10.06	95.06	117.20
1	A	639	ARG	CD-NE-CZ	8.72	135.81	123.60
1	A	721	LEU	CA-CB-CG	7.47	132.48	115.30
1	A	639	ARG	CB-CG-CD	7.33	130.65	111.60
1	A	838	ASP	CB-CG-OD2	-6.26	112.66	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	838	ASP	CB-CG-OD1	6.17	123.86	118.30
1	A	840	ARG	NE-CZ-NH1	5.83	123.21	120.30
1	A	840	ARG	NE-CZ-NH2	-5.29	117.66	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	714	TYR	Sidechain

## 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	2766	0	2686	71	1
2	A	1	0	0	0	0
3	A	20	0	9	2	0
4	A	224	0	0	11	1
All	All	3011	0	2695	71	1

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 13.

All (71) 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:756:ILE:CD1	1:A:756:ILE:CG1	1.78	1.59
1:A:600:GLN:HG3	4:A:221:HOH:O	1.31	1.23
1:A:753:VAL:O	1:A:756:ILE:HG13	1.46	1.15
1:A:808:LYS:C	1:A:809[B]:HIS:N	2.06	1.07
1:A:776:THR:OG1	1:A:778:LYS:HG3	1.70	0.90
1:A:795:LYS:HG3	1:A:804:ASP:HB2	1.60	0.83
1:A:809[A]:HIS:C	1:A:810:ARG:N	2.32	0.81
1:A:639:ARG:HD3	4:A:35:HOH:O	1.81	0.79
1:A:753:VAL:O	1:A:756:ILE:CG1	2.29	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:583:GLU:HB2	1:A:585:THR:HG23	1.67	0.76
1:A:678:ASN:HB2	4:A:54:HOH:O	1.87	0.75
1:A:712:HIS:HA	1:A:715:ARG:NH1	2.02	0.74
1:A:639:ARG:CD	4:A:35:HOH:O	2.36	0.71
1:A:611:PRO:HD2	4:A:111:HOH:O	1.91	0.71
1:A:537:ILE:HG23	1:A:869:ARG:CG	2.21	0.70
1:A:808:LYS:HE2	1:A:808:LYS:HA	1.74	0.69
1:A:795:LYS:CG	1:A:804:ASP:HB2	2.23	0.68
1:A:671:GLY:HA2	4:A:125:HOH:O	1.93	0.68
1:A:672:LEU:HB2	1:A:712:HIS:ND1	2.09	0.68
1:A:577:GLU:H	1:A:577:GLU:CD	1.98	0.67
1:A:555:HIS:CD2	1:A:851:VAL:HG22	2.30	0.66
1:A:750:GLU:HG2	4:A:195:HOH:O	1.95	0.65
1:A:810:ARG:NH2	3:A:302:2IP:H3	2.12	0.65
1:A:672:LEU:HB2	1:A:712:HIS:CE1	2.32	0.64
1:A:639:ARG:HG2	1:A:640:SER:N	2.13	0.63
1:A:537:ILE:HG23	1:A:869:ARG:HG2	1.82	0.62
1:A:548:ARG:NH2	1:A:861:LEU:HD22	2.14	0.62
1:A:537:ILE:HG23	1:A:869:ARG:HG3	1.82	0.61
1:A:717:ILE:HG23	1:A:721:LEU:HD22	1.82	0.61
1:A:548:ARG:HH22	1:A:861:LEU:HD22	1.63	0.60
1:A:717:ILE:CG2	1:A:721:LEU:HD22	2.31	0.60
1:A:537:ILE:O	1:A:541:VAL:HG23	2.02	0.59
1:A:583:GLU:OE1	1:A:585:THR:OG1	2.21	0.58
1:A:672:LEU:HD13	1:A:672:LEU:C	2.25	0.56
1:A:861:LEU:O	1:A:865:LEU:HD23	2.05	0.56
1:A:538:HIS:CE1	1:A:542:ASN:HD21	2.23	0.56
1:A:575:LYS:HA	1:A:577:GLU:OE2	2.06	0.55
1:A:699:HIS:HD2	4:A:14:HOH:O	1.89	0.55
1:A:639:ARG:HG2	1:A:640:SER:H	1.71	0.54
1:A:575:LYS:HE2	1:A:575:LYS:HA	1.88	0.54
1:A:795:LYS:HB3	4:A:10:HOH:O	2.07	0.53
1:A:672:LEU:HB2	1:A:712:HIS:HD1	1.76	0.51
1:A:809[A]:HIS:O	1:A:810:ARG:N	2.41	0.51
1:A:644:VAL:HG12	1:A:645:GLY:N	2.27	0.50
1:A:548:ARG:HH21	1:A:865:LEU:HD21	1.77	0.50
1:A:869:ARG:O	1:A:869:ARG:HD3	2.12	0.49
1:A:808:LYS:O	1:A:809[A]:HIS:C	2.50	0.49
1:A:778:LYS:HB3	4:A:150:HOH:O	2.12	0.49
1:A:809[A]:HIS:CA	1:A:810:ARG:N	2.75	0.49
1:A:626:ASN:OD1	1:A:634:GLY:HA3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:534:TYR:CE1	1:A:536:PRO:HG3	2.48	0.48
1:A:750:GLU:CD	1:A:750:GLU:H	2.18	0.47
1:A:871:GLN:NE2	1:A:874:ARG:NH1	2.62	0.47
1:A:869:ARG:O	1:A:873:VAL:HG23	2.16	0.46
1:A:808:LYS:C	1:A:809[B]:HIS:CA	2.75	0.45
1:A:697:THR:HA	1:A:738:PHE:O	2.17	0.45
1:A:581:PHE:CZ	1:A:628:LYS:HG3	2.52	0.45
1:A:712:HIS:HA	1:A:715:ARG:HH12	1.76	0.45
1:A:795:LYS:HG3	1:A:795:LYS:O	2.17	0.44
1:A:639:ARG:HD2	4:A:35:HOH:O	2.10	0.44
1:A:670:THR:HG23	1:A:680:GLY:HA2	1.99	0.44
1:A:799:GLY:HA2	1:A:835:TYR:HB3	2.00	0.44
1:A:753:VAL:C	1:A:756:ILE:HG13	2.30	0.43
1:A:572:ALA:HA	1:A:617:TRP:CZ2	2.53	0.43
1:A:871:GLN:NE2	1:A:874:ARG:HH11	2.17	0.41
1:A:795:LYS:HG2	1:A:810:ARG:HB2	2.01	0.41
1:A:534:TYR:HE1	1:A:536:PRO:HG3	1.86	0.41
1:A:637:GLN:HB2	1:A:651:PHE:CE2	2.56	0.41
1:A:810:ARG:NE	3:A:302:2IP:H5	2.36	0.40
1:A:583:GLU:OE1	1:A:585:THR:N	2.51	0.40
1:A:672:LEU:HD22	1:A:672:LEU:HA	1.65	0.40

All (1) 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:715:ARG:NH1	4:A:216:HOH:O[4_546]	1.80	0.40

## 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	329/347 (95%)	319 (97%)	7 (2%)	3 (1%)	21 7

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	609	ALA
1	A	804	ASP
1	A	644	VAL

### 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	301/309 (97%)	289 (96%)	12 (4%)	38 20

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	565	TYR
1	A	580	LEU
1	A	583	GLU
1	A	685	ARG
1	A	699	HIS
1	A	721	LEU
1	A	750	GLU
1	A	786	LEU
1	A	792	PRO
1	A	795	LYS
1	A	850	ILE
1	A	859	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	542	ASN

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Mol	Chain	Res	Type
1	A	555	HIS
1	A	568	ASN
1	A	578	ASN
1	A	600	GLN
1	A	699	HIS
1	A	849	ASN
1	A	871	GLN
1	A	878	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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$
3	2IP	A	302	-	20,20,20	1.38	4 (20%)	28,32,32	2.59	5 (17%)

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	2IP	A	302	-	-	0/10/34/34	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	2IP	P1-O1	-3.04	1.50	1.60
3	A	302	2IP	P4-O42	-2.25	1.46	1.54
3	A	302	2IP	P4-O41	2.02	1.57	1.51
3	A	302	2IP	C6-C1	2.04	1.58	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	2IP	O6-C6-C5	-3.75	101.89	110.34
3	A	302	2IP	C5-C4-C3	-2.79	107.21	110.89
3	A	302	2IP	O1-C1-C6	3.87	116.84	108.38
3	A	302	2IP	P1-O1-C1	4.93	133.38	121.56
3	A	302	2IP	O1-C1-C2	9.77	129.75	108.38

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
3	A	302	2IP	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 ⓘ

### 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<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	336/347 (96%)	0.38	42 (12%) 5 4	13, 22, 65, 75	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	602	THR	7.2
1	A	608	SER	5.8
1	A	583	GLU	5.4
1	A	633	PRO	5.2
1	A	871	GLN	5.2
1	A	609	ALA	4.7
1	A	860	ILE	4.7
1	A	874	ARG	4.7
1	A	631	SER	4.3
1	A	877	SER	3.9
1	A	632	GLY	3.8
1	A	584	ASN	3.7
1	A	856	GLU	3.7
1	A	876	ALA	3.3
1	A	873	VAL	3.3
1	A	878	GLN	3.2
1	A	585	THR	3.2
1	A	867	ASN	3.2
1	A	861	LEU	3.1
1	A	725	ARG	3.1
1	A	875	ASP	3.1
1	A	671	GLY	3.0
1	A	550	ASN	2.9
1	A	808	LYS	2.9
1	A	592	VAL	2.8
1	A	610	ASP	2.7
1	A	842	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	534	TYR	2.5
1	A	807	ASP	2.5
1	A	551	GLU	2.4
1	A	870	LYS	2.4
1	A	536	PRO	2.3
1	A	672	LEU	2.2
1	A	868	GLN	2.2
1	A	547	LYS	2.2
1	A	869	ARG	2.2
1	A	739	GLY	2.2
1	A	546	ARG	2.1
1	A	872	GLU	2.1
1	A	586	PRO	2.1
1	A	562	VAL	2.1
1	A	593	VAL	2.1

## 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(Å <sup>2</sup> )	Q<0.9
3	2IP	A	302	20/20	0.64	0.43	14.32	50,55,60,61	20
2	CA	A	301	1/1	0.20	0.30	6.62	31,31,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.