



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 11:34 PM UTC

PDB ID : 2OZW / pdb_00002ozw
Title : Solution structure of human phosphohistidine phosphatase 1 with phosphate ligand
Authors : Gong, W.; Cui, G.; Jin, C.; Xia, B.
Deposited on : 2007-02-27

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

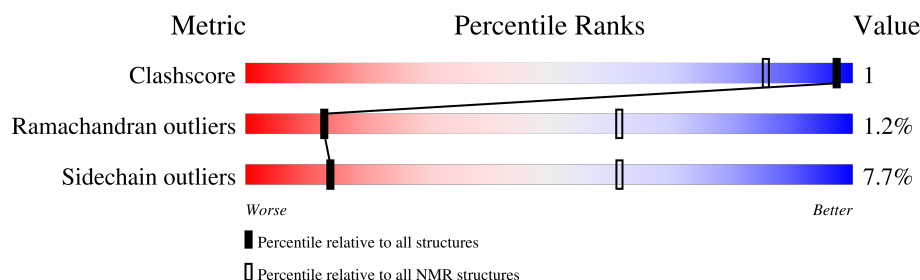
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	125	 65% 6% • 29%

2 Ensemble composition and analysis

This entry contains 21 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:4-A:14, A:20-A:31, A:39-A:79, A:89-A:110, A:118-A:120 (89)	0.33	1

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 5, 7, 9, 11, 13, 15, 16, 17, 18, 19, 21
2	2, 20
3	6, 12
4	3, 10
Single-model clusters	4; 8; 14

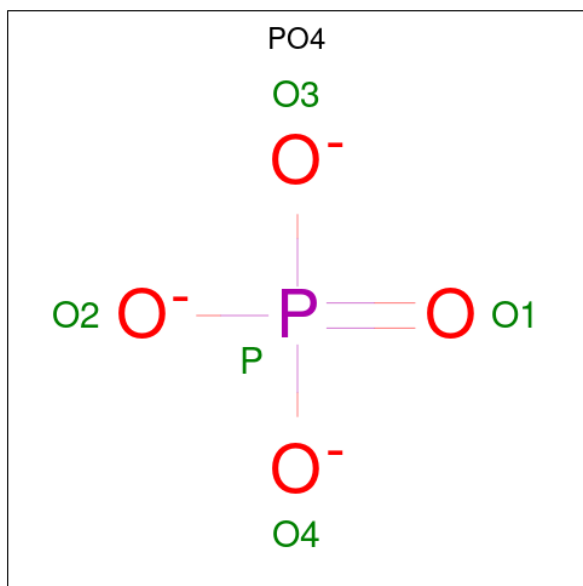
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1908 atoms, of which 931 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 14 kDa phosphohistidine phosphatase.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	125	1903	613	931	165	188	6	0

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



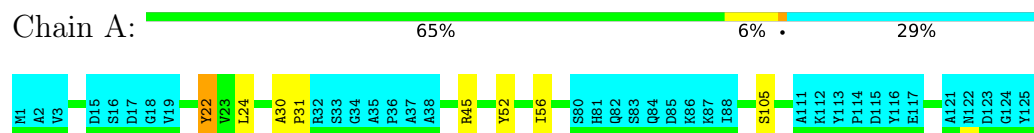
Mol	Chain	Residues	Atoms		
			Total	O	P
2	A	1	5	4	1

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: 14 kDa phosphohistidine phosphatase

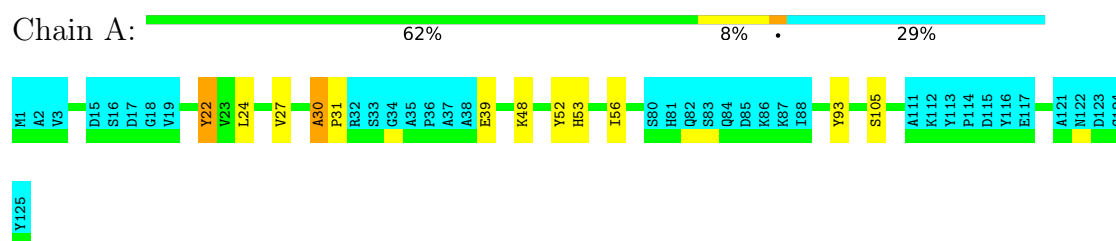


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

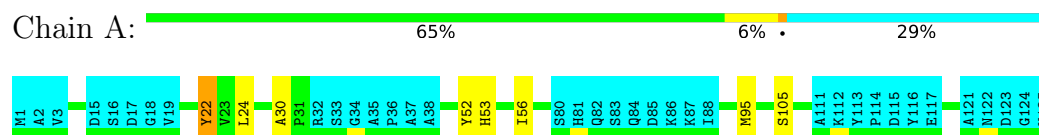
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: 14 kDa phosphohistidine phosphatase



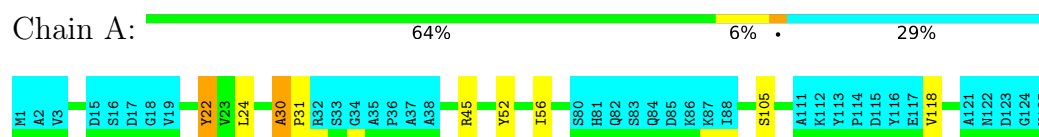
4.2.2 Score per residue for model 2

- Molecule 1: 14 kDa phosphohistidine phosphatase



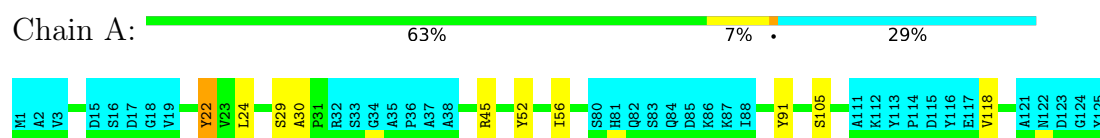
4.2.3 Score per residue for model 3

- Molecule 1: 14 kDa phosphohistidine phosphatase



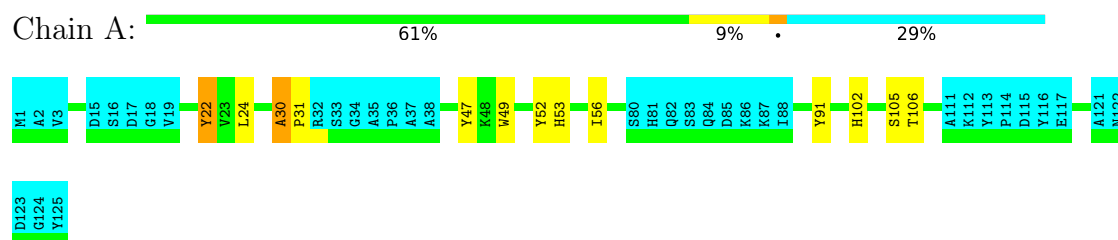
4.2.4 Score per residue for model 4

- Molecule 1: 14 kDa phosphohistidine phosphatase



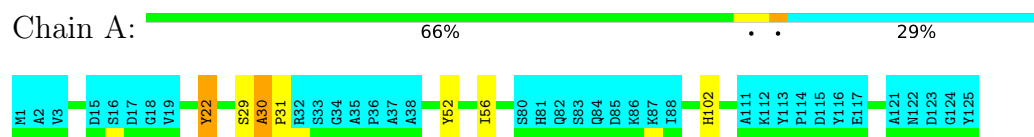
4.2.5 Score per residue for model 5

- Molecule 1: 14 kDa phosphohistidine phosphatase



4.2.6 Score per residue for model 6

- Molecule 1: 14 kDa phosphohistidine phosphatase



4.2.7 Score per residue for model 7

- Molecule 1: 14 kDa phosphohistidine phosphatase





4.2.8 Score per residue for model 8

- Molecule 1: 14 kDa phosphohistidine phosphatase



4.2.9 Score per residue for model 9

- Molecule 1: 14 kDa phosphohistidine phosphatase



4.2.10 Score per residue for model 10

- Molecule 1: 14 kDa phosphohistidine phosphatase



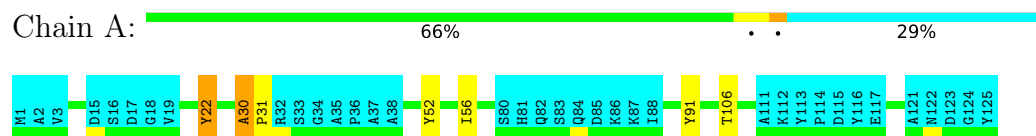
4.2.11 Score per residue for model 11

- Molecule 1: 14 kDa phosphohistidine phosphatase



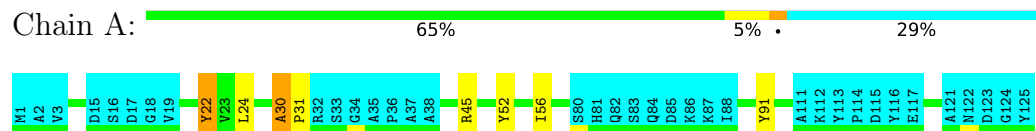
4.2.12 Score per residue for model 12

- Molecule 1: 14 kDa phosphohistidine phosphatase



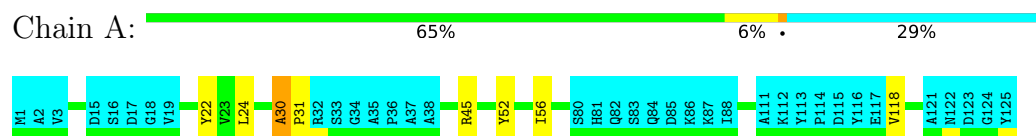
4.2.13 Score per residue for model 13

- Molecule 1: 14 kDa phosphohistidine phosphatase



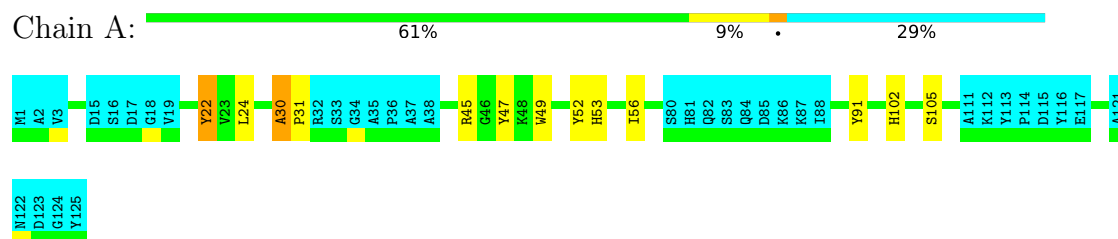
4.2.14 Score per residue for model 14

- Molecule 1: 14 kDa phosphohistidine phosphatase



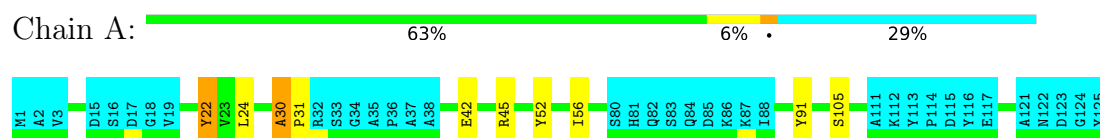
4.2.15 Score per residue for model 15

- Molecule 1: 14 kDa phosphohistidine phosphatase



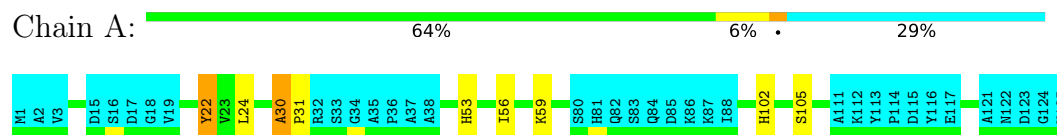
4.2.16 Score per residue for model 16

- Molecule 1: 14 kDa phosphohistidine phosphatase



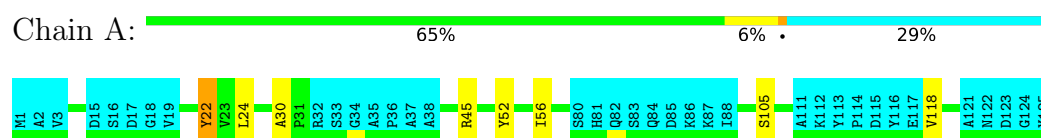
4.2.17 Score per residue for model 17

- Molecule 1: 14 kDa phosphohistidine phosphatase



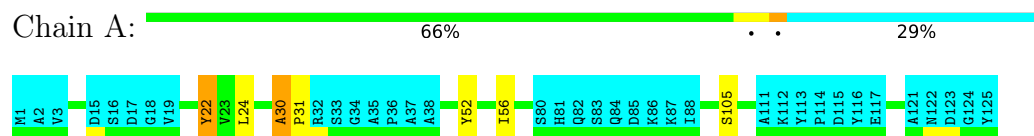
4.2.18 Score per residue for model 18

- Molecule 1: 14 kDa phosphohistidine phosphatase



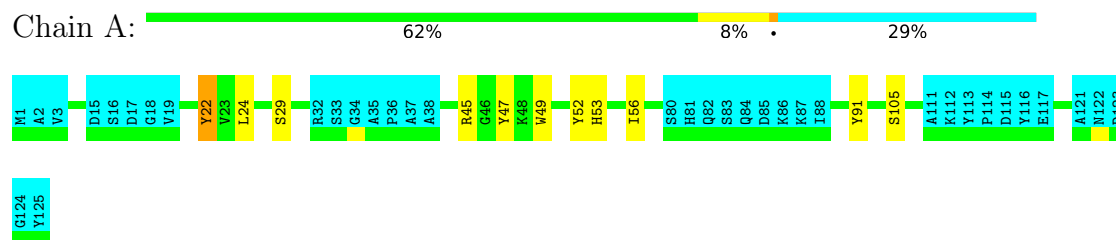
4.2.19 Score per residue for model 19

- Molecule 1: 14 kDa phosphohistidine phosphatase



4.2.20 Score per residue for model 20

- Molecule 1: 14 kDa phosphohistidine phosphatase



4.2.21 Score per residue for model 21

- Molecule 1: 14 kDa phosphohistidine phosphatase



M1	A2	V3	D15	S16	D17	G18	V19	Y22	V23	L24	A30	P31	R32	S33	G34	A35	P36	A37	A38	Y52	T56	S80	H81	Q82	S83	Q84	D85	K86	K87	I88	Y91	S105	A111	K112	Y113	P114	D115	Y116	E117	A121	N122	D123	G124	Y125
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5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics simulated annealing*.

Of the 100 calculated structures, 21 were deposited, based on the following criterion: *structures with favorable non-bond energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DYANA	structure solution	cyana2.0
Amber	refinement	7.0

No chemical shift data was provided.

6 Model quality

6.1 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 (average) 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	0.68±0.01	0±0/722 (0.0± 0.0%)	1.29±0.08	1±1/978 (0.1± 0.1%)
All	All	0.68	0/15162 (0.0%)	1.29	14/20538 (0.1%)

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	Planarity
1	A	0.0±0.0	1.6±0.7
All	All	0	34

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	39	GLU	CG-CD-OE2	19.24	162.65	118.40	1	1
1	A	39	GLU	OE1-CD-OE2	-18.91	77.52	122.90	1	1
1	A	39	GLU	CG-CD-OE1	-14.46	85.14	118.40	1	1
1	A	102	HIS	CB-CG-CD2	-5.34	124.25	131.20	11	3
1	A	53	HIS	CB-CG-CD2	-5.32	124.29	131.20	5	8

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	22	TYR	Sidechain	19

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	45	ARG	Sidechain	11
1	A	91	TYR	Sidechain	3
1	A	93	TYR	Sidechain	1

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	703	684	684	1±1
All	All	14868	14364	14364	19

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 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:ALA:N	1:A:31:PRO:CD	0.43	2.81	10	14
1:A:47:TYR:CD2	1:A:49:TRP:CZ2	0.42	3.08	20	1
1:A:47:TYR:CD1	1:A:49:TRP:CZ2	0.41	3.08	5	4

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	89/125 (71%)	86±1 (96±2%)	2±1 (3±1%)	1±1 (1±1%)	13	61
All	All	1869/2625 (71%)	1798 (96%)	48 (3%)	23 (1%)	13	61

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	30	ALA	17
1	A	29	SER	3
1	A	102	HIS	3

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	73/100 (73%)	67±1 (92±1%)	6±1 (8±1%)	14	61
All	All	1533/2100 (73%)	1415 (92%)	118 (8%)	14	61

All 15 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	22	TYR	21
1	A	56	ILE	21
1	A	52	TYR	20
1	A	24	LEU	19
1	A	105	SER	17
1	A	91	TYR	6
1	A	118	VAL	5
1	A	106	THR	2
1	A	27	VAL	1
1	A	48	LYS	1
1	A	95	MET	1
1	A	14	ILE	1
1	A	42	GLU	1
1	A	45	ARG	1
1	A	59	LYS	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	PO4	A	126	-	4,4,4	2.07±0.04	3±0 (75±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	PO4	A	126	-	6,6,6	0.69±0.05	0±0 (0±0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	126	PO4	P-O4	2.46	1.47	1.54	9	21
2	A	126	PO4	P-O3	2.42	1.47	1.54	13	21
2	A	126	PO4	P-O2	2.22	1.48	1.54	13	21

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided