Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 12:00 PM EDT

PDB ID	:	1URB
Title	:	ALKALINE PHOSPHATASE (N51MG)
Authors	:	Tibbitts, T.T.; Murphy, J.E.; Kantrowitz, E.R.
Deposited on	:	1996-02-03
Resolution	:	2.14 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

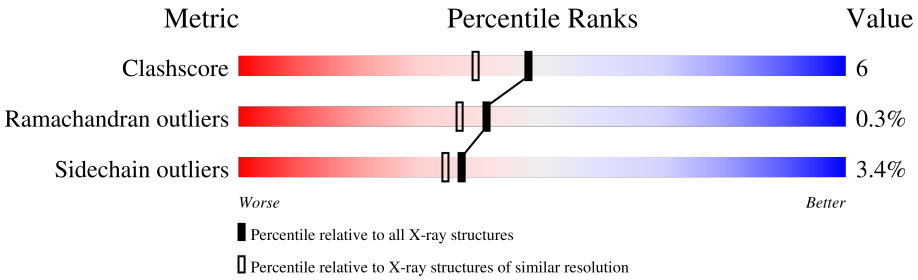
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.14 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	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)

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 >=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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	446	85% 14%
1	B	446	85% 14%

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
4	PO4	A	457	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7025 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 ALKALINE PHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3281	2028	579	662	12			
1	B	446	Total	C	N	O	S	0	0	0
			3281	2028	579	662	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ASN	ASP	engineered mutation	UNP P00634
B	51	ASN	ASP	engineered mutation	UNP P00634

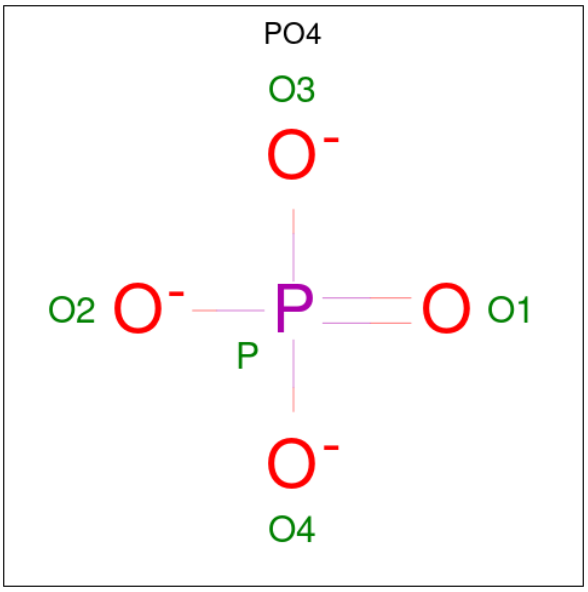
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	248	Total O 248 248	0	0
5	B	191	Total O 191 191	0	0

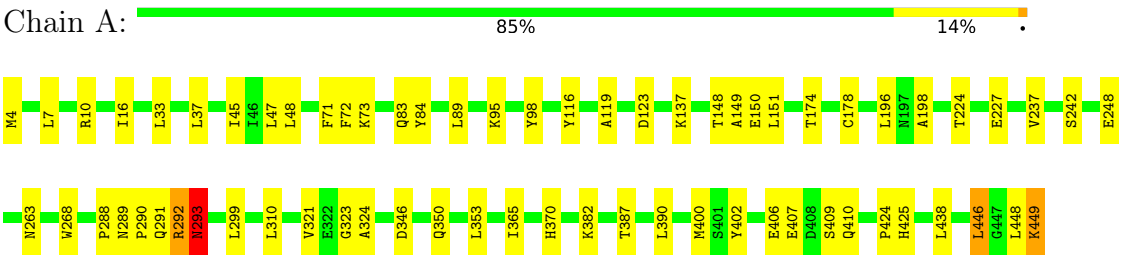
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

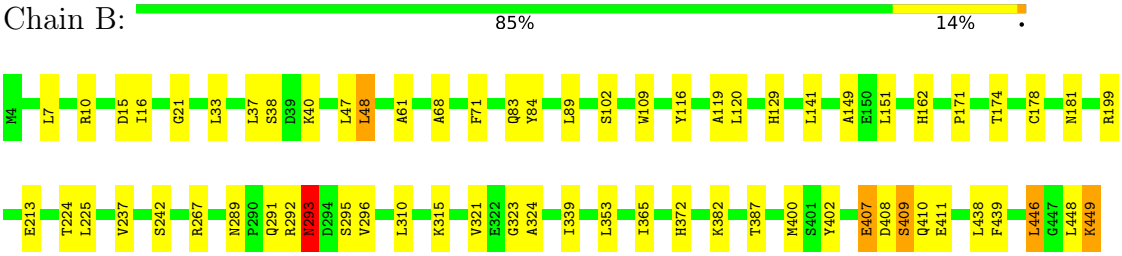
• Molecule 1: ALKALINE PHOSPHATASE

Chain A:



• Molecule 1: ALKALINE PHOSPHATASE

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	195.72Å 168.48Å 76.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.14	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.14)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.193 , 0.241	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7025	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 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	0.68	5/3335 (0.1%)	0.84	10/4526 (0.2%)
1	B	0.68	2/3335 (0.1%)	0.80	4/4526 (0.1%)
All	All	0.68	7/6670 (0.1%)	0.82	14/9052 (0.2%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	291	GLN	CG-CD	9.45	1.72	1.51
1	B	291	GLN	CB-CG	-8.99	1.28	1.52
1	A	406	GLU	C-N	-7.84	1.16	1.34
1	A	293	ASN	C-O	7.00	1.36	1.23
1	A	407	GLU	CA-CB	-6.94	1.38	1.53
1	A	406	GLU	CA-C	-6.34	1.36	1.52
1	A	407	GLU	N-CA	-5.91	1.34	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	406	GLU	CA-C-O	9.42	139.89	120.10
1	A	293	ASN	O-C-N	7.88	135.31	122.70
1	A	291	GLN	O-C-N	6.77	133.53	122.70
1	A	406	GLU	C-N-CA	-6.53	105.37	121.70
1	A	407	GLU	CB-CA-C	6.25	122.89	110.40
1	A	406	GLU	CA-C-N	-6.05	103.88	117.20
1	A	292	ARG	NE-CZ-NH2	5.85	123.22	120.30
1	B	48	LEU	CA-CB-CG	5.69	128.38	115.30
1	B	293	ASN	N-CA-C	5.64	126.22	111.00
1	B	409	SER	CA-C-O	-5.54	108.46	120.10
1	A	293	ASN	N-CA-C	5.46	125.75	111.00
1	B	323	GLY	N-CA-C	-5.29	99.88	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	323	GLY	N-CA-C	-5.08	100.39	113.10
1	A	390	LEU	CA-CB-CG	5.03	126.86	115.30

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	3281	0	3229	43	0
1	B	3281	0	3228	45	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	10	0	0	3	0
4	B	10	0	0	0	0
5	A	248	0	0	9	1
5	B	191	0	0	5	0
All	All	7025	0	6457	80	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 6.

All (80) 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:290:PRO:HB2	5:A:701:HOH:O	1.76	0.84
1:B:10:ARG:HB2	1:B:71:PHE:CE1	2.17	0.80
1:A:73:LYS:HE2	5:A:463:HOH:O	1.81	0.79
1:B:402:TYR:HB3	1:B:410:GLN:HG3	1.63	0.79
1:B:237:VAL:HG13	1:B:242:SER:HB2	1.69	0.75
1:A:402:TYR:HB3	1:A:410:GLN:HG3	1.70	0.74
1:B:408:ASP:OD1	1:B:409:SER:N	2.24	0.71
1:A:292:ARG:O	1:A:293:ASN:HB2	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:PRO:HB3	1:A:292:ARG:CZ	2.23	0.69
1:B:48:LEU:HD13	1:B:321:VAL:HB	1.76	0.66
1:A:293:ASN:ND2	5:A:580:HOH:O	2.29	0.66
1:B:293:ASN:HB3	1:B:295:SER:H	1.60	0.65
1:A:237:VAL:HG13	1:A:242:SER:HB2	1.79	0.64
1:A:370:HIS:HB2	5:A:683:HOH:O	1.97	0.64
1:B:411:GLU:HG2	5:B:541:HOH:O	1.97	0.64
1:B:267:ARG:O	1:B:292:ARG:NH1	2.29	0.64
1:A:289:ASN:O	1:A:292:ARG:HG2	1.97	0.63
1:A:365:ILE:HD13	1:A:438:LEU:HD11	1.79	0.63
1:B:449:LYS:H	1:B:449:LYS:HD2	1.65	0.62
1:A:16:ILE:HG22	1:B:89:LEU:HD21	1.80	0.62
1:A:48:LEU:HD13	1:A:321:VAL:HB	1.82	0.61
1:A:83:GLN:HE21	1:B:83:GLN:HE21	1.50	0.60
1:A:73:LYS:HB2	1:A:350:GLN:NE2	2.17	0.59
1:B:293:ASN:HB2	1:B:296:VAL:HG23	1.83	0.59
1:A:16:ILE:CG2	1:B:89:LEU:HD21	2.34	0.57
1:A:116:TYR:CZ	1:A:119:ALA:HB2	2.39	0.57
1:A:89:LEU:HD21	1:B:16:ILE:CG2	2.36	0.55
1:A:89:LEU:HD21	1:B:16:ILE:HG22	1.87	0.55
1:B:365:ILE:HD13	1:B:438:LEU:HD11	1.88	0.55
1:A:292:ARG:NH2	4:A:457:PO4:O1	2.40	0.54
1:B:149:ALA:HB2	1:B:324:ALA:CB	2.38	0.54
1:A:288:PRO:HB3	1:A:292:ARG:NH2	2.24	0.53
1:B:10:ARG:HB2	1:B:71:PHE:CD1	2.44	0.51
1:B:129:HIS:O	1:B:162:HIS:HE1	1.93	0.51
1:A:37:LEU:HD21	1:B:33:LEU:HD23	1.93	0.50
1:B:446:LEU:HB3	1:B:448:LEU:HD13	1.93	0.50
1:B:178:CYS:HB3	1:B:181:ASN:OD1	2.12	0.49
1:A:268:TRP:HD1	1:A:292:ARG:HH21	1.60	0.48
1:B:120:LEU:O	1:B:162:HIS:HA	2.13	0.48
1:B:267:ARG:HG3	5:B:493:HOH:O	2.14	0.48
1:A:73:LYS:CE	5:A:463:HOH:O	2.51	0.48
1:A:449:LYS:H	1:A:449:LYS:HD2	1.79	0.48
1:A:149:ALA:HB2	1:A:324:ALA:CB	2.44	0.48
1:A:248:GLU:HA	5:A:688:HOH:O	2.14	0.47
1:B:213:GLU:O	1:B:224:THR:HA	2.15	0.47
1:B:16:ILE:HG12	5:B:520:HOH:O	2.15	0.46
1:B:38:SER:OG	1:B:40:LYS:HG2	2.16	0.46
1:B:407:GLU:HB3	1:B:408:ASP:H	1.55	0.46
1:A:424:PRO:O	1:A:425:HIS:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:THR:OG1	1:A:227:GLU:HG3	2.16	0.46
1:B:199:ARG:O	1:B:199:ARG:HG2	2.16	0.46
1:B:292:ARG:O	1:B:296:VAL:HB	2.15	0.46
1:A:123:ASP:HB2	5:A:596:HOH:O	2.17	0.45
1:B:289:ASN:O	1:B:292:ARG:HD3	2.17	0.44
1:A:174:THR:HG23	1:A:178:CYS:HB2	1.99	0.44
1:A:387:THR:HA	1:A:400:MET:O	2.18	0.43
1:B:411:GLU:HA	5:B:541:HOH:O	2.18	0.43
1:A:148:THR:HG23	1:A:299:LEU:HD13	2.00	0.43
1:B:174:THR:HG23	1:B:178:CYS:HB2	2.00	0.43
1:A:45:ILE:HD12	1:A:446:LEU:HD22	2.00	0.42
1:A:292:ARG:NH1	4:A:457:PO4:O1	2.53	0.42
1:A:98:TYR:HE1	1:B:68:ALA:HB2	1.85	0.42
1:A:137:LYS:HE3	1:A:198:ALA:O	2.20	0.42
1:A:10:ARG:HB2	1:A:71:PHE:CE1	2.55	0.42
1:A:72:PHE:HB3	1:A:346:ASP:OD1	2.20	0.41
1:A:95:LYS:HB2	5:A:695:HOH:O	2.20	0.41
1:B:141:LEU:HD23	1:B:315:LYS:HB3	2.03	0.41
1:B:61:ALA:HA	1:B:339:ILE:HG23	2.03	0.41
1:B:109:TRP:O	1:B:439:PHE:HB2	2.20	0.41
1:B:33:LEU:HD12	1:B:33:LEU:HA	1.87	0.41
1:A:4:MET:HB3	5:A:534:HOH:O	2.21	0.41
1:A:150:GLU:HG3	1:A:263:ASN:OD1	2.21	0.41
1:B:15:ASP:O	1:B:21:GLY:HA3	2.21	0.41
1:B:116:TYR:CZ	1:B:119:ALA:HB2	2.55	0.41
1:B:446:LEU:HD12	1:B:446:LEU:HA	1.92	0.41
1:A:33:LEU:HD23	1:B:37:LEU:HD21	2.03	0.40
1:A:292:ARG:CZ	4:A:457:PO4:O1	2.69	0.40
1:B:171:PRO:HD3	1:B:225:LEU:HD11	2.03	0.40
1:B:387:THR:HA	1:B:400:MET:O	2.20	0.40
1:B:400:MET:HE2	5:B:579:HOH:O	2.21	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)
5:A:505:HOH:O	5:A:505:HOH:O[3_656]	2.13	0.07

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	444/446 (100%)	430 (97%)	13 (3%)	1 (0%)	47	45
1	B	444/446 (100%)	432 (97%)	10 (2%)	2 (0%)	29	22
All	All	888/892 (100%)	862 (97%)	23 (3%)	3 (0%)	41	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	407	GLU
1	B	293	ASN
1	A	293	ASN

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	337/337 (100%)	325 (96%)	12 (4%)	35	32
1	B	337/337 (100%)	326 (97%)	11 (3%)	38	35
All	All	674/674 (100%)	651 (97%)	23 (3%)	37	34

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	47	LEU
1	A	84	TYR

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Mol	Chain	Res	Type
1	A	151	LEU
1	A	196	LEU
1	A	310	LEU
1	A	353	LEU
1	A	382	LYS
1	A	409	SER
1	A	446	LEU
1	A	448	LEU
1	A	449	LYS
1	B	7	LEU
1	B	47	LEU
1	B	84	TYR
1	B	102	SER
1	B	151	LEU
1	B	310	LEU
1	B	353	LEU
1	B	372	HIS
1	B	382	LYS
1	B	446	LEU
1	B	449	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	350	GLN
1	A	370	HIS
1	B	329	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)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
4	PO4	B	457	-	4,4,4	1.29	1 (25%)	6,6,6	1.06	0
4	PO4	A	457	-	4,4,4	1.83	2 (50%)	6,6,6	0.78	0
4	PO4	B	453	2	4,4,4	1.23	0	6,6,6	1.08	0
4	PO4	A	453	2	4,4,4	1.26	0	6,6,6	1.12	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	457	PO4	P-O1	-2.52	1.44	1.50
4	B	457	PO4	P-O2	-2.21	1.48	1.54
4	A	457	PO4	P-O4	-2.15	1.48	1.54

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 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	457	PO4	3	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	406:GLU	C	407:GLU	N	1.16

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.